GRAS NOTICE OF

CANOLA CONCENTRATE (RAPESEED CONCENTRATE)

Appendix 2

Reports of analysis from stability studies

HAMILTON

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REPORT OF ANALYSIS No. 275903/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03#35 protein concentrate, point T=0, storage in 25 Celsius** **Tests were performed: 17.05.2021**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-05-24**	**Order of 2021-05-12**
Report dated:	**2021-05-24**	The samples were delivered by Client

Test	Method	Unit	Result
Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	43,7 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	4,3 ± 0,3
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$6{,}2x10^3$ $[3{,}9x10^3;9{,}9x10^3]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1{,}0x10^1$
Enumeration of yeast		cfu/g	$<1{,}0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Escherichia coli in 10g	PN-ISO 7251:2006		not detected in 10 g
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Senior Specialist Analyst, Microbiology Laboratory Gdynia
Katarzyna Duczek, Specialist Analyst, Microbiology Laboratory Gdynia
Sandra Gumowska, Expert Analyst, Classical Analysis Laboratory
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

The results relate to the analysed samples only. Unless otherwise specified given expanded measurement uncertainty was estimated for the coverage factor k=2 at 95% confidence level. Sampling uncertainty has not been taken into consideration. Unless otherwise specified when conformity is stated J.S. Hamilton Poland Sp. z o.o. applies the simple acceptance decision rule in accordance with ILAC-G8:09/2019. This Report cannot be reproduced partially without a prior written consent of J.S. Hamilton Poland Sp. z o.o. Responsibility of J.S. Hamilton Poland Sp. z o.o. is restricted exclusively to the results and statements presented in original copy of the Report. The service confirmed by this Report is subject to the General Terms and Conditions of Services of J.S. Hamilton Poland Sp. z o.o. published on www.hamilton.com.pl

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REPORT OF ANALYSIS No. 275904/21/SGDY

Client **NAPIFERYN BIOTECH SP. Z O.O.** DUBOIS 114/116 93-465 ŁÓDŹ	Sample description *(according to declaration of Client)* **R-03#35 protein concentrate, point T=1, storage in 25 Celsius** **Test was performed: 24.05.2021** **Samples were stored in the chamber 25°C, 60% humidity**
Sample received: **2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity): **2021-05-31**	**Order of 2021-05-12**
Report dated: **2021-05-31**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	43,9 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	7,1 ± 0,5
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$4{,}8x10^3$ [$2{,}9x10^3$;$7{,}9x10^3$]
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1{,}0x10^1$
Enumeration of yeast		cfu/g	$<1{,}0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Senior Specialyst Analyst, Microbiology Laboratory Gdynia
Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Joanna Śpiewak, Senior Specialyst Analyst, Classical Analysis Laboratory
Katarzyna Duczek, Specialist Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275994/21/SGDY

Client **NAPIFERYN BIOTECH SP. Z O.O.** DUBOIS 114/116 93-465 ŁÓDŹ	Sample description *(according to declaration of Client)* **R-03#35 protein concentrate, point T=1, storage in 40 Celsius** **Test was performed: 24.05.2021** **Samples were stored in the chamber 40°C, 75% humidity**
Sample received: **2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity): **2021-05-31**	**Order of 2021-05-12**
Report dated: **2021-05-31**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	44,7 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	5,1 ± 0,4
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$<1,0x10^1$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Senior Specialyst Analyst, Microbiology Laboratory Gdynia
Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Joanna Śpiewak, Senior Specialyst Analyst, Classical Analysis Laboratory
Katarzyna Duczek, Specialist Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275905/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03#35 protein concentrate, point T=2, storage in 25 Celsius, 60% humidity** **Test was performed on: 31.05.2021**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-06-09**	**Order of 2021-05-12**
Report dated:	**2021-06-09**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	44,5 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	5,2 ± 0,4
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$6,5x10^3$ $[4,0x10^3;1,1x10^4]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Expert Analyst, Microbiology Laboratory Gdynia
Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Joanna Śpiewak, Senior Specialyst Analyst, Classical Analysis Laboratory
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

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REPORT OF ANALYSIS No. 275995/21/SGDY

Client **NAPIFERYN BIOTECH SP. Z O.O.** DUBOIS 114/116 93-465 ŁÓDŹ	Sample description *(according to declaration of Client)* **R-03#35 protein concentrate, point T=2, storage in 40 Celsius, 75% humidity** **Test was performed on: 31.05.2021**
Sample received: **2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity): **2021-06-09**	**Order of 2021-05-12**
Report dated: **2021-06-09**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	44,5 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	4,6 ± 0,3
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$3,0x10^3$ $[1,8x10^3;5,1x10^3]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Expert Analyst, Microbiology Laboratory Gdynia
Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
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REPORT OF ANALYSIS No. 275906/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03 # 35 protein concentrate,** **Point T = 4,** **Date of analysis: 14.06.2021** **The samples were stored in a 25 ° C, 60% humidity chamber**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-06-21**	**Order of 2021-05-12**
Report dated:	**2021-06-21**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% s.m.	42,9 ± 2,1
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	6,6 ± 0,5
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$1,1x10^3$ $[6,8x10^2;1,8x10^3]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Expert Analyst, Microbiology Laboratory Gdynia
Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Katarzyna Duczek, Senior Specialist Analyst, Microbiology Laboratory Gdynia
Sandra Gumowska, Expert Analyst, Classical Analysis Laboratory
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275996/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03 # 35 protein concentrate, point T = 4** **Date of analysis: 14.06.2021** **The samples were stored in a 40°C, 75% humidity chamber**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-06-21**	**Order of 2021-05-12**
Report dated:	**2021-06-21**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% s.m.	43,4 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	6,0 ± 0,4
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$9{,}3x10^{2}$ $[5{,}7x10^{2};1{,}5x10^{3}]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1{,}0x10^{1}$
Enumeration of yeast		cfu/g	$<1{,}0x10^{1}$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Expert Analyst, Microbiology Laboratory Gdynia
Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Katarzyna Duczek, Senior Specialist Analyst, Microbiology Laboratory Gdynia
Sandra Gumowska, Expert Analyst, Classical Analysis Laboratory
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275907/21/SGDY

Client **NAPIFERYN BIOTECH SP. Z O.O.** DUBOIS 114/116 93-465 ŁÓDŹ	Sample description *(according to declaration of Client)* **R-03#35 protein concentrate, point T=8, storage in 25 Celsius, 60% humidity** **Test was performed: 12.07.2021**
Sample received: **2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity): **2021-07-26**	**Order of 2021-05-12**
Report dated: **2021-07-26**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	42,1 ± 2,1
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	6,6 ± 0,5
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$5,3x10^3$ [$3,3x10^3$;$8,4x10^3$]
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Expert Analyst, Microbiology Laboratory Gdynia
Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Katarzyna Duczek, Senior Specialist Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275997/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03#35 protein concentrate, point T=8, storage in 40 Celsius, 75% humidity** **Test was performed: 12.07.2021**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-07-19**	**Order of 2021-05-12**
Report dated:	**2021-07-19**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% s.m.	47,7 ± 2,4
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	6,8 ± 0,5
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$1,0x10^3$ $[5,3x10^2; 1,9x10^3]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Ewelina Kłosowska, Expert Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275908/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03#35 protein concentrate** **point T=12,** **Date of analysis: 09.08.2021** **The samples were stored in a 25 ° C, 60% humidity chamber**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-08-16**	**Order of 2021-05-12**
Report dated:	**2021-08-16**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% s.m.	43,4 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	7,9 ± 0,6
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$8{,}2x10^3$ $[5{,}2x10^3;1{,}3x10^4]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1{,}0x10^1$
Enumeration of yeast		cfu/g	$<1{,}0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Katarzyna Duczek, Senior Specialist Analyst, Microbiology Laboratory Gdynia
Paulina Połosak, Expert Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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AB 079

REPORT OF ANALYSIS No. 275998/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03#35 protein concentrate, point T=12** **Date of analysis: 09.08.2021** **The samples were stored in a 40°C, 75% humidity chamber**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-08-16**	**Order of 2021-05-12**
Report dated:	**2021-08-16**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% s.m.	47,9 ± 2,4
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	8,8 ± 0,6
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$7,5x10^3$ $[4,7x10^3;1,2x10^4]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Alicja Nowak, Senior Specialist Analyst, Classical Analysis Laboratory
Katarzyna Duczek, Senior Specialist Analyst, Microbiology Laboratory Gdynia
Paulina Połosak, Expert Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275909/21/SGDY

Client **NAPIFERYN BIOTECH SP. Z O.O.** DUBOIS 114/116 93-465 ŁÓDŹ		Sample description *(according to declaration of Client)* **R-03#35 protein concentrate, point T=16, storage in 25 Celsius** **Test was performed on: 06.09.2021** **Samples were stored in the chamber 25°C, 60% humidity**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-09-13**	**Order of 2021-05-12**
Report dated:	**2021-09-13**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% s.m.	41,2 ± 2,1
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	5,9 ± 0,4
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$7,9x10^2$ $[4,9x10^2;1,3x10^3]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Expert Analyst, Microbiology Laboratory Gdynia
Joanna Śpiewak, Expert Analyst, Classical Analysis Laboratory
Paulina Połosak, Expert Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275999/21/SGDY

Client **NAPIFERYN BIOTECH SP. Z O.O.** DUBOIS 114/116 93-465 ŁÓDŹ	Sample description *(according to declaration of Client)* **R-03#35 protein concentrate, point T=16, storage in 40 Celsius** **Test was performed on: 06.09.2021** **Samples were stored in the chamber 40 °C, 75% humidity**
Sample received: **2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity): **2021-09-13**	**Order of 2021-05-12**
Report dated: **2021-09-13**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% s.m.	48,2 ± 2,4
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	8,9 ± 0,6
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$7,6x10^3$ [$4,7x10^3$;$1,2x10^4$]
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	<$1,0x10^1$
Enumeration of yeast		cfu/g	<$1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		not detected in 25 g

THE END OF THE REPORT

Authorized by: Agnieszka Duda, Expert Analyst, Microbiology Laboratory Gdynia
Joanna Śpiewak, Expert Analyst, Classical Analysis Laboratory
Paulina Połosak, Expert Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275910/21/SGDY

Client **NAPIFERYN BIOTECH SP. Z O.O.** DUBOIS 114/116 93-465 ŁÓDŹ	Sample description *(according to declaration of Client)* **R-03#35 protein concentrate, point T=20, storage in 25 Celsius, 60% humidity** **Test was performed on: 04.10.2021**
Sample received: **2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity): **2021-10-11**	**Order of 2021-05-12**
Report dated: **2021-10-11**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	43,0 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	5,0 ± 0,4
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$5{,}0x10^3$ [$3{,}0x10^3$;$8{,}3x10^3$]
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1{,}0x10^1$
Enumeration of yeast		cfu/g	$<1{,}0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		Not detected in 25 g

THE END OF THE REPORT

Authorized by: Joanna Śpiewak, Expert Analyst, Classical Analysis Laboratory
Paulina Połosak, Expert Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 276000/21/SGDY

Client **NAPIFERYN BIOTECH SP. Z O.O.** DUBOIS 114/116 93-465 ŁÓDŹ	Sample description *(according to declaration of Client)* **R-03#35 protein concentrate, point T=20, storage in 40 Celsius, 75% humidity** **Test was performed on: 04.10.2021**
Sample received: **2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity): **2021-10-11**	**Order of 2021-05-12**
Report dated: **2021-10-11**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	43,5 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	9,9 ± 0,6
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$3,6x10^3$ [$2,1x10^3$;$6,0x10^3$]
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		Not detected in 25 g

THE END OF THE REPORT

Authorized by: Joanna Śpiewak, Expert Analyst, Classical Analysis Laboratory
Paulina Połosak, Expert Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 275911/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03#35 protein concentrate, point T=24, storage in 25 Celsius** **Test was performed on: 02.11.2021** **Samples were stored in 25°C, 60% humidity**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-11-10**	**Order of 2021-05-12**
Report dated:	**2021-11-10**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% d.m.	43,6 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	6,9 ± 0,5
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$4,5x10^3$ $[2,8x10^3;7,2x10^3]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		Not detected in 25 g

THE END OF THE REPORT

Authorized by: Joanna Śpiewak, Expert Analyst, Classical Analysis Laboratory
Paulina Połosak, Expert Analyst, Microbiology Laboratory Gdynia
Renata Żywicka, Senior Specialyst Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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REPORT OF ANALYSIS No. 276001/21/SGDY

Client		Sample description *(according to declaration of Client)*
NAPIFERYN BIOTECH SP. Z O.O. DUBOIS 114/116 93-465 ŁÓDŹ		**R-03#35 protein concentrate, point T=24, storage in 40 Celsius** **Date of analysis: 02.11.2021** **Samples were stored in a chamber at 40 degrees C, 75% humidity**
Sample received:	**2021-05-17**	**Sample without any visible damages**
Analysis completed (the date of performance of the laboratory activity):	**2021-11-10**	**Order of 2021-05-12**
Report dated:	**2021-11-10**	The samples were delivered by Client

Test	Method	Unit	Result
* Protein (N*6,25) on dry matter	PB-116 ed. III of 11.08.2020	% s.m.	43,5 ± 2,2
* Moisture	PB-285 ed. I of 26.09.2014 p. 1	%	10,6 ± 0,7
* Enumeration of mesophilic aerobic bacteria	PN-EN ISO 4833-1:2013-12	cfu/g	$3,5x10^3$ $[2,2x10^3;5,6x10^3]$
* Enumeration of yeast and moulds	PN-ISO 21527-2:2009		
Enumeration of moulds		cfu/g	$<1,0x10^1$
Enumeration of yeast		cfu/g	$<1,0x10^1$
* The most probable number of coliforms	PN-IS0 4831:2007	MPN/g	0
* Detection of Salmonella spp.	PN-EN ISO 6579-1:2017-04		Not detected in 25 g

THE END OF THE REPORT

Authorized by: Joanna Śpiewak, Expert Analyst, Classical Analysis Laboratory
Paulina Połosak, Expert Analyst, Microbiology Laboratory Gdynia
Renata Żywicka, Senior Specialyst Analyst, Microbiology Laboratory Gdynia
Approved by: Hanna Wachowska, Laboratory Director *(Approved with electronic signature)*

Laboratory: Gdynia 81-571, Chwaszczyńska 180

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Appendix 3

Raptein™30 Estimated Daily Intake Report

RAPTEIN™30 ESTIMATED DAILY INTAKE REPORT

A. INTENDED EFFECT

Raptein™30 is intended to be added to select general foods and beverages as described in the table below.

Table 1. Raptein™30 Intended Uses and Use Levels

Intended uses	Max. use level (g Raptein™30/100 g of food as consumed)
Bakery products (e.g. breads, rolls, pies etc.) and baking mixes	20
Breakfast cereals (e.g. oatmeal, grits, ready to eat breakfast cereal etc.)	35
Grain products, pastas (e.g., noodles, macaroni, etc.)	20
Bars (e.g. nutritional, protein etc.)	20
Protein-fibre and nutritional powders	100*
Beverages and beverage bases non-alcoholic (e.g. fruit and/or vegetable drinks, smoothies, energy drinks etc.)	7
Milk products and dairy analogs (e.g. cheeses, yoghurts, creams, frozen desserts etc.)	15
Coffee and tea (including instant coffee and tea)	7
Meat product analogs (e.g. sausages, burgers, chops etc.)	20
Fat, oils and salad dressings (e.g. mayonnaise-type dressings, margarine-like spreads etc.)	10
Egg substitutes (e.g. powdered egg analogs etc.) and egg products analogs	7
Soup and soup mixes	15
Sauces, gravies, condiments and dips	10
Nut products (e.g. nut spreads, nut butters etc.)	30
Snack foods (e.g. popcorn, chips etc.)	40
Fruit and water ices	7
Confections, candies and frostings (e.g. baking chocolates, marshmallows, non-chocolate candies etc.)	20
Sweet sauces, toppings, and syrups	10
Jams, jellies, gelatins, puddings, fillings (including mixes)	30
Processed fruits, vegetables, legumes (e.g. vegetable spreads)	30
Batter/breadings	10
Spice and seasoning mixes[a]	5
Processed meat and poultry	15

*As is basis (content for dry powder), proposed serving – 30 g (one serving a day)
[a]No NHANES data exists; calculated independently

B. ESTIMATED DAILY INTAKE

1. Assessment of Raptein™30 Use

Food consumption data was provided by the National Center for Health Statistics' (NCHS) 2017-2018 National Health and Nutrition Examination Surveys (NHANES) (CDC, 2018; USDA, 2018). The Food and Nutrition Database for Dietary Studies (FNDDS) for the corresponding biennial NHANES survey food categories was used to identify 2582 food codes for Raptein™30 that represent the proposed food categories listed for both ingredients in Table 1. The identified food codes are described in the supplemental tables. Mean and 90th percentile estimated daily intakes (EDIs) of Raptein™30 from the intended uses were calculated using those food codes and maximum use levels described in Table 1.

2. Food Consumption Survey Data

a. Survey Description

The most recent National Health and Nutrition Examination Surveys (NHANES) for the years 2017-2018 are available for public use. NHANES are conducted as a continuous, annual survey, and are released in 2-year cycles. In each cycle, approximately 10,000 people across the U.S. completed the health examination component of the survey. Any combination of consecutive years of data collection is a nationally representative sample of the U.S. population. It is well established that the length of a dietary survey affects the estimated consumption of individual users and that short-term surveys, such as the typical 1-day dietary survey, overestimate consumption over longer time periods (Kruger et al., 2014). Because two 24-hour dietary recalls administered on 2 non-consecutive days (Day 1 and Day 2) are available from the NHANES 2017-2017 survey, these data were used to generate estimates for the current intake analysis.

The NHANES provide the most appropriate data for evaluating food-use and food-consumption patterns in the United States, containing 2 years of data on individuals selected via stratified multistage probability sample of civilian non-institutionalized population of the U.S. NHANES survey data were collected from individuals and households via 24-hour dietary recalls administered on 2 non-consecutive days (Day 1 and Day 2) throughout all 4 seasons of the year. Day 1 data were collected in-person in the Mobile Examination Center (MEC), and Day 2 data were collected by telephone in the following 3 to 10 days, on different days of the week, to achieve the desired degree of statistical independence. The data were collected by first selecting Primary Sampling Units (PSUs), which were counties throughout the U.S. Small counties were combined to attain a minimum population size. These PSUs were segmented and households were chosen within each segment. One or more participants within a household were interviewed. Fifteen PSUs are visited each year. For example, in the 2009-2010 NHANES, there were 13,272 persons selected; of these 10,253 were considered respondents to the MEC examination and data

collection. 9754 of the MEC respondents provided complete dietary intakes for Day 1 and of those providing the Day 1 data, 8,405 provided complete dietary intakes for Day 2. The release data do not necessarily include all the questions asked in a section. Data items may have been removed due to confidentiality, quality, or other considerations. For this reason, it is possible that a dataset does not completely match all the questions asked in a questionnaire section. Each data file has been edited to include only those sample persons eligible for that particular section or component, so the numbers vary.

In addition to collecting information on the types and quantities of foods being consumed, the NHANES surveys collect socioeconomic, physiological, and demographic information from individual participants in the survey, such as sex, age, height and weight, and other variables useful in characterizing consumption. The inclusion of this information allows for further assessment of food intake based on consumption by specific population groups of interest within the total population.

Sample weights are incorporated with NHANES surveys to compensate for the potential under-representation of intakes from specific population groups as a result of sample variability due to survey design, differential non-response rates, or other factors, such as deficiencies in the sampling frame (CDC, 2006; USDA, 2020).

b. Statistical Methods

Consumption data from individual dietary records, detailing food items ingested by each survey participant, were collated in Octave and used to generate estimates for the intake of Raptein™30 by the U.S. population. Estimates for the daily intake of Raptein™30 represent projected 2-day averages for each individual from Day 1 and Day 2 of NHANES data; these average amounts comprised the distribution from which mean and percentile intake estimates were produced. Mean and percentile estimates were generated incorporating sample weights in order to provide representative intakes for the entire U.S. population. “All-user” intake refers to the estimated intake of Raptein™30 by those individuals consuming food products containing Raptein™30. Individuals were considered users if they consumed 1 or more food products containing Raptein™30 on either Day 1 or Day 2 of the survey.

3. Food Survey Results

The estimated “all-user” total intakes of Raptein™30 from 2582 proposed food uses, as described in Table 1, in the U.S. by population group are summarized in Table 2.

In summary, 79.66% of the total U.S. population 2+ years of age were identified as consumers from the selected food uses in the 2017-2018 survey (Table 2). The mean intakes of Raptein™30 from consumers ages 2+ from the selected food uses were estimated to be 19.29 g

Raptein™30/person/day or 0.28 g Raptein™30/kg body weight/day. The heavy consumer (90th percentile) intakes were estimated to be 40.80 g Raptein™30/person/day or 0.59 g/kg body weight/day.

Table 2. Estimated "All-user" Daily Intake (EDI) of Raptein™30 in Targeted Foods by Population Group (2017-2018 NHANES Data)

	N users	N population	% Users	Mean mass (kg)	Mean EDI (g)	90th % EDI (g)	Mean EDI (g/kg)	90th % EDI (g/kg)
ages 1-2	453	642	70.56	13.24	11.71	26.97	0.88	2.04
ages 3-5	365	529	69.00	21.08	13.46	30.00	0.64	1.42
ages 6-12	941	1258	74.80	41.89	16.37	36.6	0.39	0.87
ages 13-19	775	886	87.47	70.32	20.78	44.59	0.30	0.63
ages 20 and up	4632	5493	84.33	81.7	20.32	43.00	0.25	0.53
ages 2 and up	6713	8427	79.66	69.41	19.29	40.80	0.28	0.59

There are no food codes that can be used for stand-alone spice and seasoning mixes in NHANES. Accordingly, to calculate the estimated daily intakes of Raptein™30 from the use in spice and seasoning mix, surrogate products were used to estimate its intake level. A surrogate product called Bernard Jensen's Protein Seasoning (https://www.amazon.com/Bernard-Jensens-Protein-Seasoning-Veggies/dp/B07DVW5Z5C) was cited by the Client as a product that could include Raptein™30 as an ingredient. The recommended serving is 1 g. SCG assumes that a daily intake would not exceed one serving. Other products can be used to corroborate the estimate of intake from spice and seasoning mixes. If Raptein™30 will be used to create a flavored salt, the daily sodium intake consumed by Americans can be used to conservatively estimate the intake of Raptein™30 from flavored salts. According to the 2013-2016 What We Eat In America (WWEIA) report through NHANES, the mean sodium intake of males and females ages 1+ is 3393 mg/day (USDA, 2020). Using the very conservative estimate that half the daily sodium intake (1697 mg) is provided by Raptein™30 salt (5% maximum use level), the estimated intake of Raptein™30 from salt would be 84.85 mg/day. Alternatively, if Raptein™30 is going to be used as a flavor enhancer like monosodium glutamate, FDA estimates typical intake of MSG to be < 0.5 g/day (https://www.fda.gov/food/food-additives-petitions/questions-and-answers-monosodium-glutamate-msg). Therefore, it is expected that 1 g would be a conservative daily intake.

The intakes of Raptein™30 for all food uses, including spices and seasonings at 1 g/day, are estimated to be the EDIs (calculated above) + 1 g. The resulting mean EDI for Raptein™30 of 20.29 g/person/day or 0.29 g/kg body weight/day and the heavy consumer (90th percentile) EDI of 41.8 g/person/day or 0.60 g/kg body weight/day.

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GRAS NOTICE OF

CANOLA CONCENTRATE (RAPESEED CONCENTRATE)

Appendix 4

Allergenicity analysis of rapeseed concentrate Raptein™30 for food safety evaluation

CUSTOMER REPORT VTT-CR-00678-21

Allergenicity analysis of rapeseed protein-fiber concentrate Raptein™30 for food safety evaluation

Authors: Gopal Peddinti
Waltteri Hosia

Version: 3.9.2021

VTT

beyond the obvious

Report's title

Allergenicity analysis of rapeseed protein-fiber concentrate Raptein™30 for food safety evaluation

Customer, contact person, address	**Order reference**
NapiFeryn BioTech, Magdalena Kozłowska (m.kozlowska@napiferyn.pl), NapiFeryn BioTech Sp. z o.o., ul. Dubois 114/116, 93-465 Łódź, Poland	VTT-174239-21
Project name	**Project number/Short name**
Rapeseed product protein identification and allergenicity	131092 Rapeseed_Allergenicity

Summary

The aim of this project was to identify proteins in the rapeseed protein-fiber concentrate Raptein™30 and perform bioinformatics search of the identified proteins in AllergenOnline.org database and Celiac Database for allergenicity evaluation.

Potential risks of food allergy and celiac disease were evaluated based on full-length and sliding window 80-mer sequence identity matches (FASTA algorithm) to known allergens in FARRP allergenic protein database version 21 (AllergenOnline.org), exact peptide matches and full-length alignments with Celiac Database (CD) of AllergenOnline.org to known CD inducing glutens or gliadins. In addition, sequence homology searches with BLASTP were performed against NCBI non-redundant protein sequence database were performed to provide a functional annotation in terms of all homologous proteins, irrespective of the evidence of their allergenicity.

Three cruciferins (11S globulins), Napin-3 (1.7S seed storage proteins), Oleosin S2-2, and Squalene monooxygenase 1,2 were found in the Raptein™30 samples. The sequence searches with FARRP allergen protein database version 21 provided several hits characterizing the possible allergenic effects of the proteins found in Raptein™30. The full-length FASTA search results should we be interpreted with > 35 % as the minimum identity threshold to an allergenic protein to infer any indication of possible allergenic cross-reactivity, although typically a minimum of > 50 % sequence identity may be required for a reliable allergenic indication. Likewise, the sequence similarity found in 80-mer FASTA searches may need to be interpreted in combination with the full-length FASTA searches. The BLASTP searches against the NCBI protein database found 467 sequences homologous to the query sequences, but did not include any new allergenic proteins apart from ten that were already found during the FARRP database searches.

The Raptein™30 proteins did not match any peptides using the word search against the CD peptide dataset, which the primary tool to indicate elicitation of CD search. Likewise, the full-length FASTA search against the CD protein dataset also did not indicate high sequence similarity with the Raptein™30 proteins with the criteria of E-value < 10^{-15} and identity > 45 %. This result indicates that the Raptein™30 proteins are unlikely to elicit CD.

Espoo 27.7.2022

Written by Gopal Peddinti, Senior Scientist, and Waltteri Hosia, Senior Scientist

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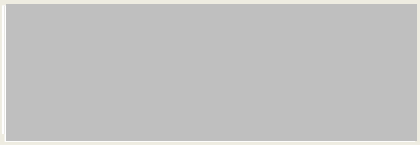
Approval

VTT TECHNICAL RESEARCH CENTRE OF FINLAND LTD

Date:	3.9.2021
Signature:	
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Contents

1. Description and objectives

The aim of the *Rapeseed Allergenicity* project was to perform protein analysis and bioinformatics searches to provide information for allergenicity report for NapiFeryn BioTech's rapeseed protein-fiber concentrate Raptein^{TM}30.

2. Methods

2.1 Protein identification

Protein characterization and identification was performed in three different levels. SDS-PAGE gel was run to evaluate the general protein content and character of the samples, intact mass LC-MS to detect the presence of napin and cruciferin proteins, and finally the peptide map LC-MS to allow accurate mass & sequence based identification of proteins present in the samples.

2.2 Sample preparation

Sample stocks of 35 mg/ml were made by weighing aliquots of dry samples to Eppendorf tubes, adding correct amount of 150 mM NaCl to give 35 mg/ml concentration and vortexing with 150 mM NaCl solution for 40 min. Subsequent samples were made from these stocks or diluted stocks.

2.3 SDS PAGE

A standard denaturing SDS-Page was run for the samples. Raptein^{TM}30 samples were run as reduced and non-reduced samples. Mini Protean 12 % SDS-PAGE gel (Bio-Rad) stained with PageBlue Coomassie stain. (Thermo Scientific) was used. 1 µl of 1:100 diluted stock sample (0.35 µg) was pipetted per lane.

2.4 Intact mass analysis

For intact mass analysis, 10 µl of the stock samples as above, was diluted to 1ml (0.35 µg/µl) and centrifuged 5 min at 14000 rpm, supernatant was loaded into LC-MS vials

Different amounts of sample were injected after initial testing and reverse phase gradient was used. Buffer A was 0.1 % formic acid and Buffer B was 100 % acetonitrile. The flow was set to 350 µl starting at 10 % B from 0 to 1 min and then ramping to 75 % B over 6 min before a 95 % B wash and equilibration phase at 10 % B. Column temperature was

65 °C A Waters acquity CSH 1.7 µm C4 50 x 2.1mm column was used. The flow from the column was passed into Waters Synapt G2 QTOF mass spectrometer. MS only acquisition was used. Source parameters were following:

Polarity	ES+
Capillary (kV)	2.9
Source Temperature (°C)	140
Sampling Cone	130 V
Source Offset	75 V
Desolvation Temperature (°C)	600
Cone Gas Flow (L/Hr)	34
Desolvation Gas Flow (L/Hr)	900

2.5 Peptide Map analysis

2.5.1 Trypsin digestion

Stock samples were used. 1.5 µl of Raptein^{TM}30 stock (slurry of solubilized and insolubilized material as homogenous mix) was taken yielding 52.5 µg of sample material. To 52 µg of protein concentrate 20 µl of 8 M µrea with 6 mM DTT was added, and the sample was incubated with shake in 50 °C for 60 min. Then, 2 µl of iodoacetamide (IAM) was added to a final IAM concentration of 18 mM. The sample was incubated with shake in dark (lid on) for 30 min in RT. 90 µl of 100 mM Tris pH 7.8 was added to dilute urea below 1.5 M, the sample was mixed and 1:25 (w/w) sequencing grade trypsin was added. Digestion was carried overnight in 37 °C with slow shaking.

2.5.2 Chromatography and Mass spectrometry

Mass spectrometry was done with Synapt G2 Q-TOF mass spectrometer, Acquity UPLC system. 2.1 x 100 mm Waters CSH C18 column was used. Column temperature 60 °C. A gradient from 2 % to 40 % acetonitrile is applied from 2 to 17 min, after which a saw tooth wash phase and equilibration phase were applied. A MSe acquisition mode (Data independent fragmentation) is used. Source parameters were the following:

Polarity	ES+
Capillary (kV)	2.85

Source Temperature (°C)	135
Sampling Cone (V)	36
Source Offset (V)	56
Desolvation Temperature (°C)	420
Cone Gas Flow (L/Hr)	17
Desolvation Gas Flow (L/Hr)	900

MSe acquisition parameters:

Mass Range (m/z)	50-1995
Collision Ramp energy (Low mass-High mass) (eV)	25.0 to 85.0
Scan Time (s)	0.3

2.6 Bioinformatics search for peptide identification

Mascot Server v. 2.8 and Mascot Distiller v. 2.8 software were used to search the peptide mapping data against the database. The parameters used were following:

Database	SwissProt 2021_03 (565,254 sequences; 203,850,821 residues)
Taxonomy	Other green plants (19,756 sequences)
Type of search	MS/MS Ion Search
Enzyme	Trypsin/P
Fixed modifications	Carbamidomethyl (C)
Variable modifications	Deamidated (NQ), Gln->pyro-Glu (N-term Q), Glu->pyro-Glu (N-term E), Oxidation (M)
Mass values	Monoisotopic
Protein mass	Unrestricted
Peptide mass tolerance	0.1 Da
Fragment mass tolerance	0.1 Da
Max missed cleavages	2

Instrument type	ESI-QUAD-TOF
Significance threshold p <	0.05
Max. number of families	AUTO
Ions score or expect cut-off	0
Min. number of sig. unique sequences	1

2.7 Sequence similarity searches

The bioinformatics searches for sequence similarity to known allergen proteins or Celiac Disease-eliciting proteins rely primarily on the use of the FASTA3 algorithm developed by Pearson at the University of Virginia (Pearson and Lipman, 1988) and BLASTP (Altschul et al. 1990).

Databases

The identified proteins were searched in the following publicly accessible databases to identify potential allergenicity.

AllergenOnline.org

The FARRP allergic protein database (Food Allergy Research and Resource Program, www.allergenonline.org) includes known and putative allergens that have been identified as IgE binding proteins from food, airway, contact and venom allergen sources. The FARRP database version 21 (February 14, 2021) contained a list of 2233 known or putative allergens from 912 allergenic taxonomic protein groups, and was used in the bioinformatics searches in this project. The database version 21 is freely accessible as a web resource (http://www.allergenonline.com/AllergenOnlineV21.pdf).

Celiac Peptide and Gluten Protein database

AllergenOnline also includes a set of 1013 peptides were identified from grains of the wheat and wheat relatives (barley, rye and oats) including native and deamidated peptides of glutens (gliadins and glutenins) that have been shown to elicit celiac disease (CD), activate Major Histocompatibility Class (MHC) II restricted T cells of subjects with CD, or stimulating toxicity in intestinal epithelia or intestinal inflammatory cells in subjects

with CD. The peptides are used in searches for exact peptide (AA) matches within any query sequence. The peptides are all based on binding to MHC DQ2.5, DQ8 or the nearly identical (DQ2.2, DQ8.5) receptors, but in addition, stimulated MHC restricted T cells from subjects with CD; or alternatively had specific toxic effects such as stimulating signal induction through the EGFR receptor of intestinal epithelial cells, stimulating IL-15 production by intestinal macrophages, inducing TNF expression from dendritic cells increasing HLA-E expression in intestinal epithelial cells, increasing intestinal permeability or signalling antigen presenting cells through TLR4 to secrete inflammatory cytokines (Jabri and Sollid, 2009).

Seventy-two representative gluten proteins containing at least one of the CD peptides are also provided at AllergenOnline.org CD database, for rapid screening using FASTA3 with criteria that allows for some AA substitutions, but conserved overall identity matches that might represent some risk from the query protein. This set of 72 proteins is to be used for screening with FASTA algorithm, in addition to the exact peptide match criterion with the 1013 peptides, with minimum percent identity of 45 and maximum E-value of 10^{-16}. The FARRP Celiac Disease database is publicly accessible from http://www.allergenonline.com/celiachome.shtml.

NCBI Protein

This is an uncurated database of general proteins maintained by the National Library of Medicine, National Institute of Health in the USA (http://www.ncbi.nlm.nih.gov/protein). It is updated every few days. Many sequences in NCBI that are designated as allergens or associated with allergy by keywords are not included in the AllergenOnline.org database because they lack any published proof of allergy. The NCBI database may be searched by keywords or by sequence comparison (BLASTP). As the FARRP database version 21 released in Feb 2021, has been curated by experts based on the published evidence for allergenicity from the latest NCBI protein database available at the time, the NCBI protein entries last updated prior to 2021 can be considered to have been reviewed by the FARRP database team and to have been included in the FARRP database if evidence for their potential allergenicity exists. Therefore, we can safely assume that the proteins whose information was last updated on NCBI protein database prior to 2021 and not included in FARRP database, even if they are homologous to the query proteins, do not provide any evidence for the potential allergenicity if the FARRP allergenicity database is

used for screening allergenicity. Such homologous proteins, however, may provide hints for assigning gene functions to the query proteins.

Search algorithms

The most important searches for risk assessment of allergenicity are amino acid sequence identity searches (FASTA or BLAST) comparing the query sequence to known allergens, looking for matches of >50% identity over the full length of the sequences. Since many sequences are labelled as allergens in the public NCBI database often without full validation of allergenicity, the use of the curated AllergenOnline.org database is the primary search database. A full-length FASTA3 search is the algorithm for optimum alignment. As a conservative assessment, Codex (2003) recommends a search for matches of >35% identity over 80 amino acid segments and the "sliding window" approach on the www.AllergenOnline.org website is a useful and convenient tool for that step. Some countries still demand a search for identity matches of 8 amino acids and the word search method with www.AllergenOnline.org is effective to meet those demands. In addition, it is sometimes useful to run BLASTP on the NCBI Protein database using a keyword limit ("allergen") to verify that the www.AllergenOlinc.org database did not omit an important allergenic homologue of the novel protein that matches with at least 50% identity over the full-length. To help evaluate BLASTP results, a second BLASTP search should be performed without keyword limits to understand the similarity of the novel protein to other proteins, many of which humans are likely to have been exposed to without sensitizing or eliciting allergic responses. Details are provided below.

Searching FARRP DB with full-length FASTA3

The primary search algorithm for allergenicity searching is a full-length FASTA3 search that gives optimum alignments using the default criteria defined by Pearson (2000). The default scoring matrix is BLOSUM 50 (Henikoff and Henikoff: 1992 and 1996). The penalty for each gap inserted into query or searched sequences to obtain optimal alignments is calculated as (-q + -r*k), where q (10) is an initial penalty for each independent gap, r (2) is a penalty for each amino acid position within the gap and k is the number of amino acid positions within the gap (Reese and Pearson. 2002). The default word size (ktup) is two (Pearson, 2000). The FASTA3 version used in these searches was 36.3.8h May, 2020 (https://github.com/wrpearson/fasta36). Very small expectation values (E values) indicate probable evolutionary homology, and structural similarity. While the default E value for FASTA3 is 10, a value that does not indicate

significant similarity, distantly related sequences will generally have E values less than 0.01, and highly similar sequences that probably represent close homology are more likely to have E values much less than 10^{-7}. If the E value calculated for an alignment between the query protein and any one allergen appear to indicate significant similarity, the percent identity over the length of the intact proteins may be evaluated for possible cross-reactivity in those sensitized to the matched allergen. As discussed by Aalberse (2000), a protein sharing greater than 70 % identity over its length, relative to an allergen is likely to be cross-reactive, or share IgE binding. Those that have less than 50 % identity are not very likely to be cross-reactive.

Searching FARRP DB with sliding window of 80 AA

The identification of relatively short regions of high identity shared by a query sequence and an allergen may indicate similarities that could also share IgE binding, or cross-reactivity. Based on the recommendation of Codex (2003), the FASTA3 algorithm was used to compare all possible contiguous amino acid segments of each query protein sequence against all sequences listed in AllergenOnline. Every possible contiguous 80-amino acid sequence of each query protein was searched, beginning with amino acids 1-80, then 2-81, 3-82 and so on until the last 80 amino acid segment of each protein was compared with the database using the same FASTA3 algorithm used for the full-length sequence comparison. The same criterion of 35 % identity is maintained as per the recommendation of Codex (2003). The rationale by Codex (2003) for recommending that alignments of >35% identity over segments as short as 80 amino acids is that proteins sometimes contain structural motifs that are comprised of sequences much shorter than the intact protein, and that these structural motifs may include a conformational IgE binding epitope. In such a situation, the overall sequence identity for the aligned proteins may be significantly less than 35%, even though a short region could contain an important cross-reactive epitope. This criterion is more conservative than empirical data would suggest is common for cross-reactive proteins (Aalbersee, 2000). It should also help to identify potentially cross-reactive proteins that are not true homologues of an allergen but have significant local identities that might provide an immunological target for IgE antibodies in those with allergies to the matched allergen. The output of the 80 amino acid FASTA3 search includes a table of each allergen that was matched, and the total number of 80-amino acid matches of greater than 35 % identity.

Searching FARRP DB with 8-mer exact match

The eight amino acid identity match often requested for GM crop protein evaluation is essentially a “word” matching program that looks for segments of 8 contiguous amino acids (8-mer) with a 100 % identity match to any 8-mer segment of any allergen in the database. It is a very conservative estimator for cross-reactivity and over-predicts potential allergic cross-reactivity (Hileman et al., 2002; Silvanovich et al, 2006; Cressman and Ladics, 2009). Therefore, this search was not performed to evaluate the Raptein™30 proteins.

Searching the FARRP Celiac Database

The primary search is for any exact amino acid sequence match between the query sequences (Table 1) and the CD peptide dataset containing 1013 peptide sequences in the FARRP database. The search is done as a word search requiring an exact peptide sequence match. The secondary search is a FASTA search against the CD full-length protein dataset containing 72 proteins. The FASTA search results should be evaluated to look for matches with E-values smaller than 10^{-15} and greater than 45 % identity.

Searching NCBI Protein using BLASTP

In addition to searching for homologous sequences in the curated FARRP database, a protein-protein BLAST search (blastp) was performed against the whole of NCBI non-redundant sequence database (nr database), to find any possible homologous sequences to the sequences found in Raptein™90 samples (Table 1). The default BLASTP parameters were used for the search (E-value < 0.05, Hitlist size 100, Word size 6, Matrix BLOSUM62).

3. Results

3.1 Sample dissolution

Sample dissolution to 150 mM NaCl was unsuccessful for Raptein™30 samples. As the main experiments would nevertheless use strong denaturing the Raptein™30 stock was decided to be used as slurry. The Raptein™30 slurry did dissolve to 8 M urea/6 mM DTT used for trypsin digestion and to SDS-PAGE sample buffer.

3.2 SDS PAGE

Cruciferin is known to exist natively as multimeric protein composed of several subunits, which separate in SDS PAGE, napin has two main chains of 9 kDa and 4 kDa. In addition, it was known here that Raptein^{TM}30 sample was expected to have some degree of hydrolysis. SDS page results (Figure 1) were in accordance with the above and the previously published SDS Page results for cruciferin and napin [1, 2]

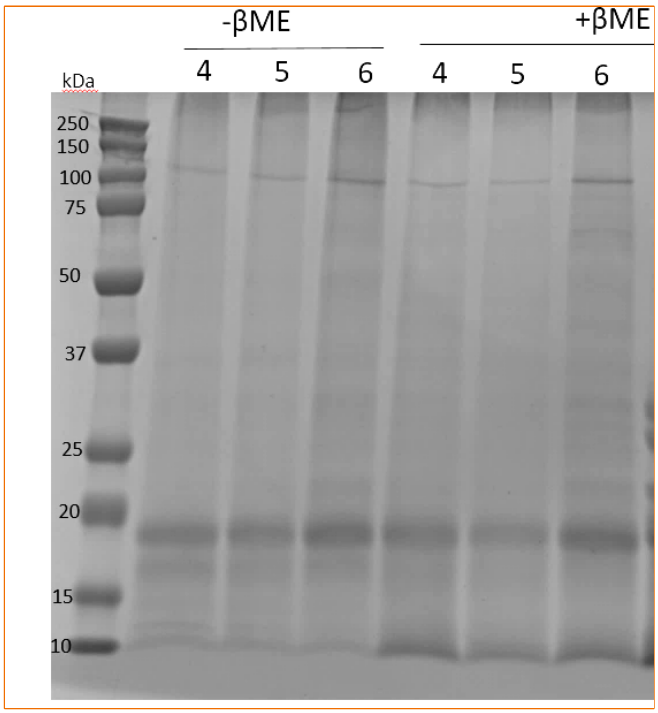


Figure 1. SDS PAGE gel of the RapteinTM30 samples. The lanes in the Coomassie stained gel were:
-βME, 4 = R09#41_RapteinTM30, 5 = R06#60_RapteinTM30, 6 = R03#35_RapteinTM30
+βME, 4 = R09#41_RapteinTM30, 5 = R06#60_RapteinTM30, 6 = R03#35_RapteinTM30

3.3 Intact mass spectrometry

Raptein^{TM}30 samples were very sparingly soluble to 150mM NaCl, and the water diluted samples gave almost no signal at all. Then dilution with 8 M urea was tested, and that resulted in a strong signal. TIC chromatogram of Raptein^{TM}30 did not show chromatographic separation (Figure 2). As was expected due to heterogeneous nature of the samples, including partial hydrolysis of Raptein^{TM}30 samples, and polymerizing propensity of cruciferin, only few proteins could be observed as separable concise mass in intact LC-MS (Figure 3).

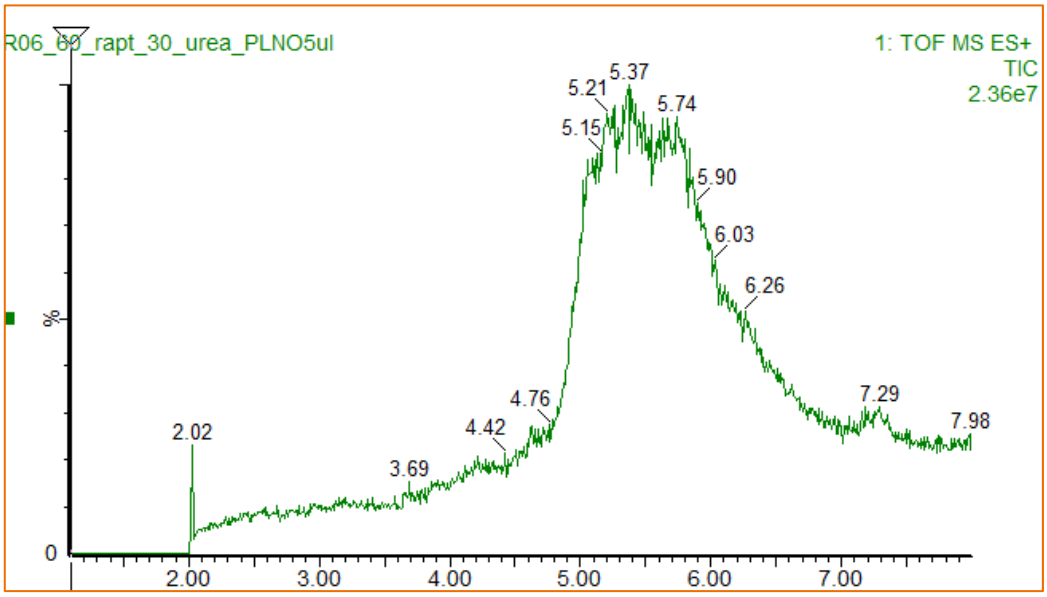


Figure 2. TIC Chromatogram of a representative Raptein^{TM}30 sample

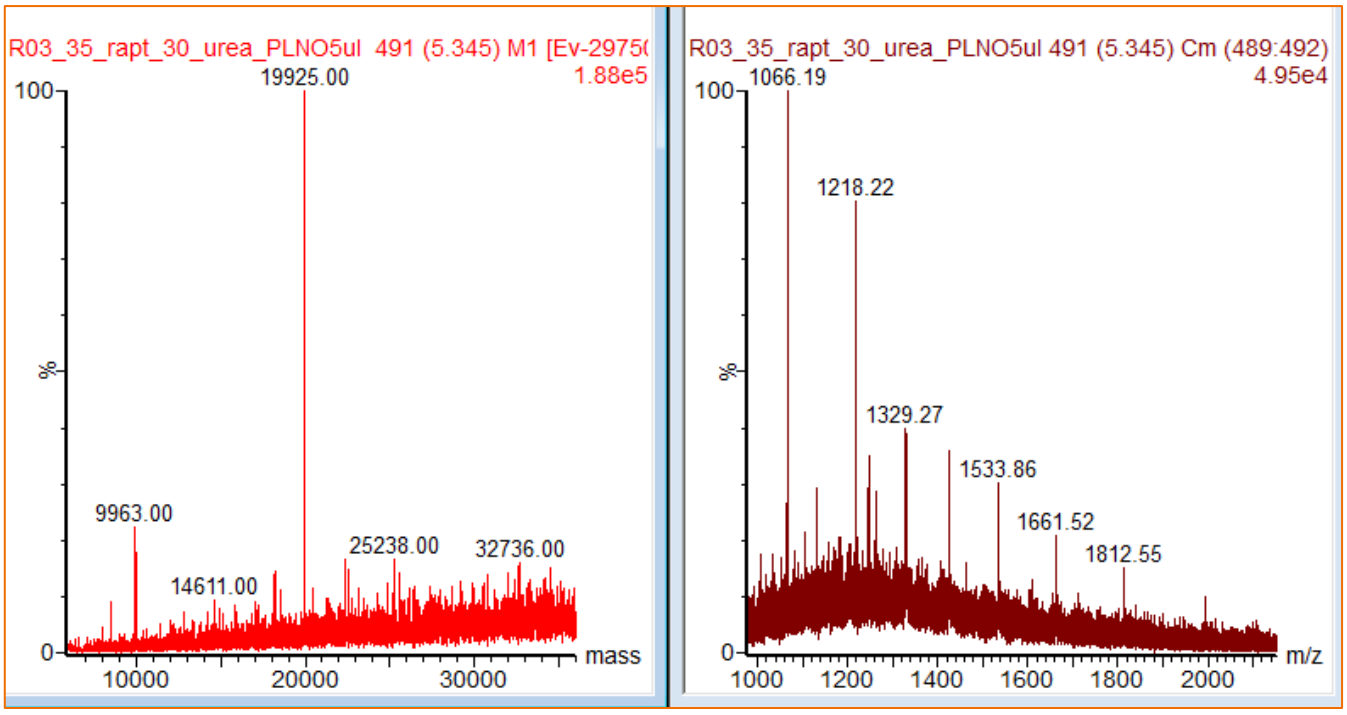


Figure 3. Deconvoluted (left) and original (right) mass spectrum of intact protein LC-MS of R03_35 Raptein^{TM}30 sample (Urea dissolved) of one relatively pure spectrum. Deconvoluted mass is 860 Da from expected mass of Brassica napus Napin-3 (2SS3_BRANA, access P80208 theoretical mass 20785 Da).

3.4 Peptide mapping

The Raptein^{TM}30 samples were not solubilized by NaCl but it was observed in intact mass and SDS-PAGE studies that the sample solubilized with strong denaturants. Therefore, the slurry was used as such, dissolved with 8 M urea/ 6 mM DTT. Despite the observed complete solubilization the peptide map TIC intensities were relatively low for Raptein^{TM}30 samples (Figure 4). Reason for this is unknown, there were no substantial undigested higher Mw residuals in the digests. Thus, the digestion had proceeded normally, which was evident also in the successful identification of cruciferin peptides. The amount of napin peptides were so low in two of the Raptein^{TM}30 samples that the presence of them had to be manually confirmed, because of the Mascot thresholds (please, see Methods). Figures 4, 5 and 6 show the TIC chromatograms, and exemplary MS and MSe channel data, respectively, for the QQQGQQGQQLQQVISR peptide of napin in Raptein^{TM}30.

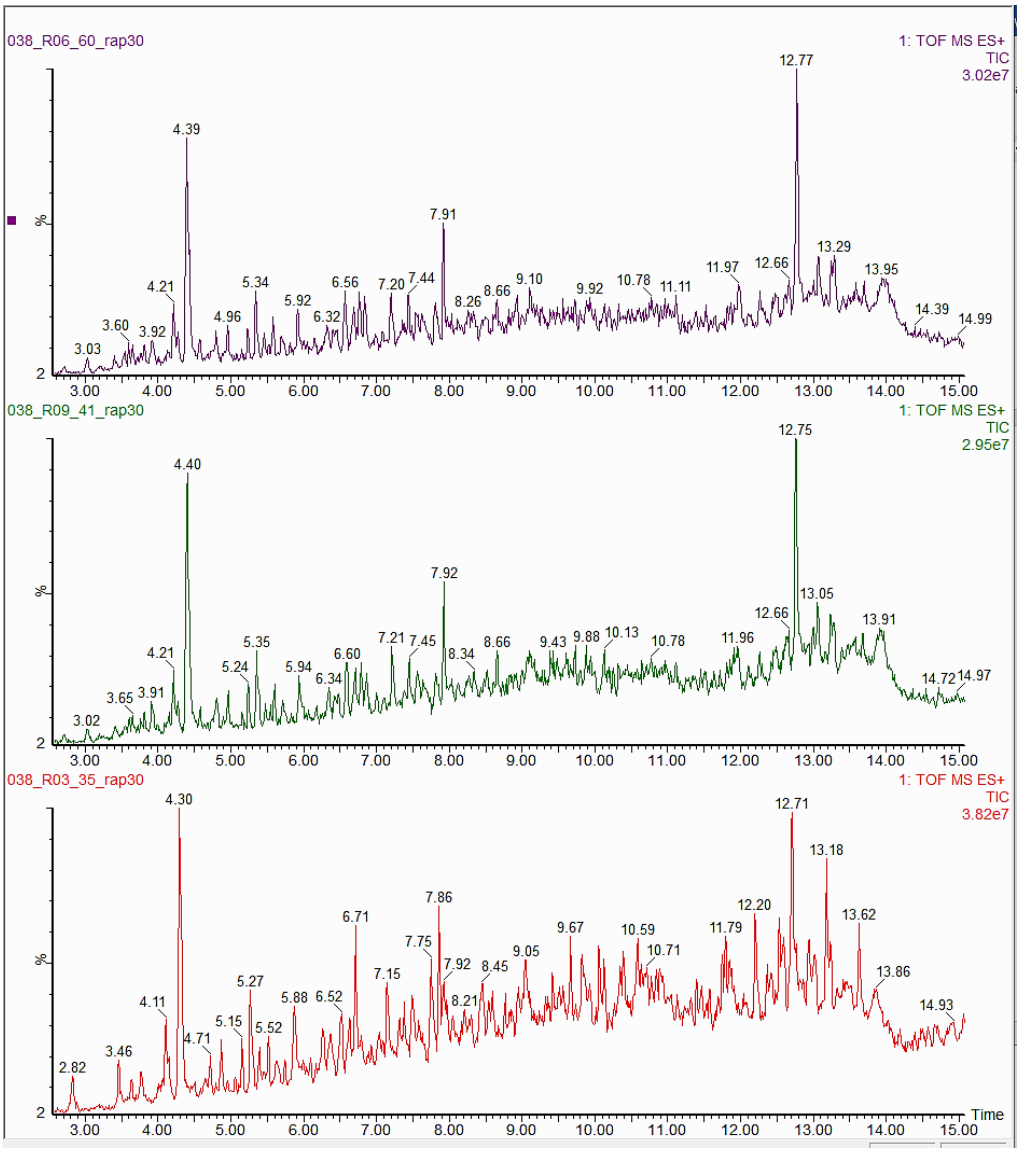
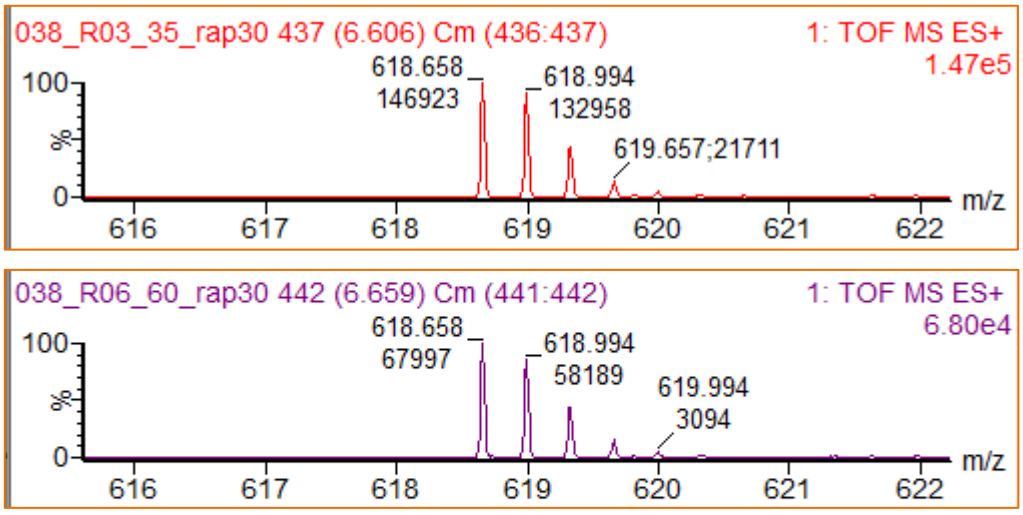


Figure 4. TIC chromatograms of Raptein^{TM}30 tryptic digests (Peptide map)



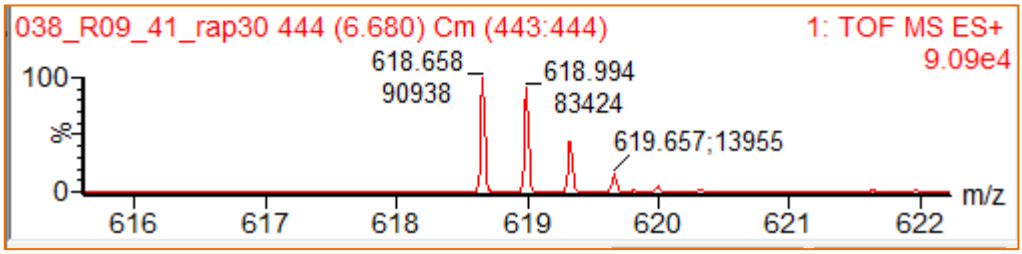


Figure 5. HR MS Spectrum of napin peptide QQQGQQGQQLQQVISR 3+ charge state of Raptein™30 samples.

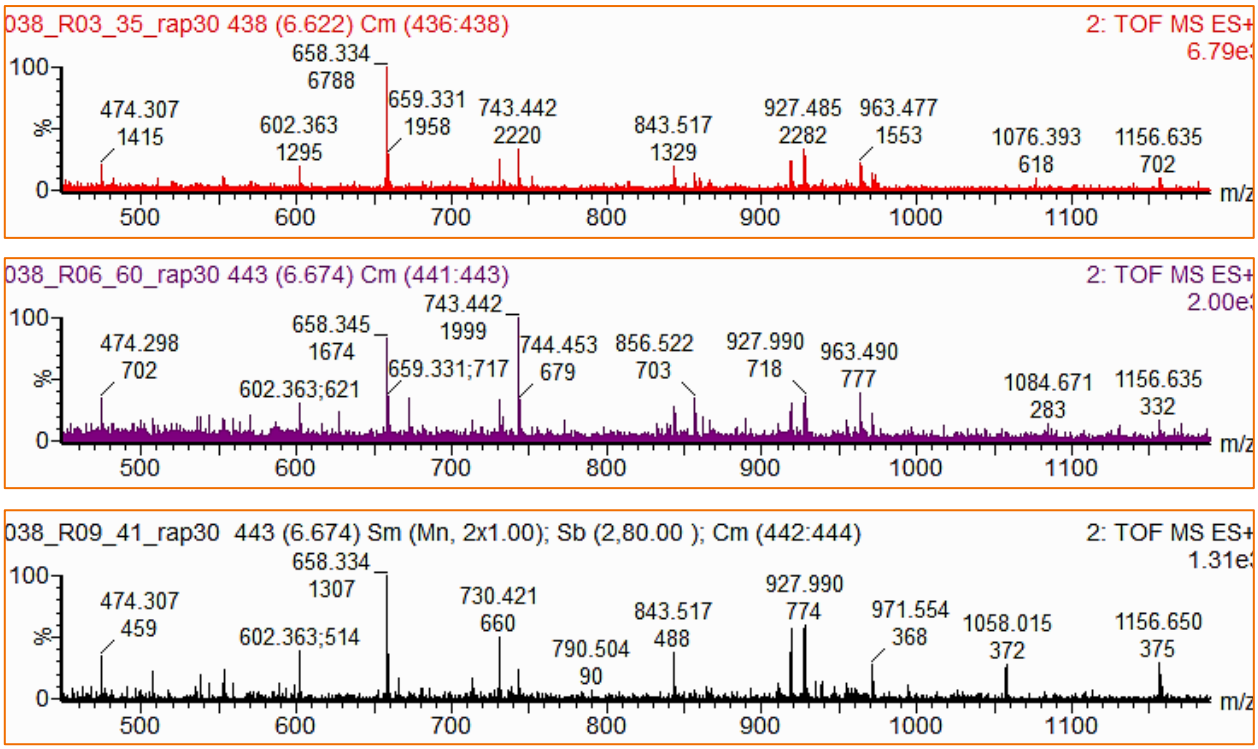


Figure 6. Mse high energy fragment spectrum evidence for Napin peptide QQQGQQGQQLQQVISR. For example y7 (1156.6), y9 (971.6), y10 (843.5), y11 (730.4), y12 (602.4), and y13 (474.3) can be seen in all Raptein™30 samples.

3.5 Mascot search

Uniprot-SwissProt is a high quality manually curated protein database (https://www.uniprot.org/) with small amount of redundancy and know to contain > 300 *Barssica napus* protein sequences. SwissProt database was searched with Mascot server parameters said in materials and methods via Mascot distiller using slightly adjusted peak picking parameters for MS and vendor (Waters) supplied peak picking parameters for MSe channels.

The search was limited to taxonomy of “other green plants” which served also as secondary functional control of searches so that we got hits also for proteins of other plants with overlapping sequences with Brassica.

Generally, the cruciferin was the most abundant protein found, it was found with Mascot in all samples directly. Napin was directly found in 1/3 samples but manually confirmed in all samples (as shown above). A representative result list for (filtered for *Brassica napus*) is shown in Table 1.

Table 1. Mascot search results for a representative sample of Raptein^{TM}30

Accession	Score	Mass (Da)	Relative abundance	Description
CRU4_BRANA	554	51630	0.82	Cruciferin CRU4 OS=Brassica napus OX=3708 GN=CRU4 PE=1 SV=1
CRU3_BRANA	302	56867	0.65	Cruciferin CRU1 OS=Brassica napus OX=3708 GN=CRU1 PE=3 SV=1
CRU1_BRANA	399	54076	0.53	Cruciferin BnC1 OS=Brassica napus OX=3708 GN=BnC1 PE=3 SV=2
OLES2_BRANA	147	19867	0.46	Oleosin S2-2 OS=Brassica napus OX=3708 GN=S2 PE=1 SV=1
2SS3_BRANA	23	14482	0.41	Napin-3 OS=Brassica napus OX=3708 PE=1 SV=1
ERG12_BRANA	20	57819	0.05	Squalene monooxygenase 1,2 OS=Brassica napus OX=3708 GN=SQP1,2 PE=2 SV=1

3.6 Sequence matches from FARRP database

Full-length FASTA matches for Cruciferin CRU4

NCBI-GI	opt	bits	E(2233)	%_id	%_sim	alen
62240390	1388	219.9	3.30E-58	0.55	0.781	471
62240392	1355	215	1.10E-56	0.533	0.768	482
110349085	1303	207.2	2.10E-54	0.456	0.743	471
82469930	1300	206.7	2.80E-54	0.425	0.755	461
156001070	1296	206.1	4.30E-54	0.454	0.743	471
30313867	1240	197.7	1.50E-51	0.43	0.728	463
1534918238	1228	195.9	4.60E-51	0.437	0.744	430
13183173	1218	194.4	1.60E-50	0.421	0.701	489
5381325	1072	172.4	5.90E-44	0.362	0.75	428
110349083	1043	168	1.30E-42	0.449	0.728	481
584592120	1013	163.6	2.70E-41	0.366	0.745	415
584592116	1012	163.4	3.00E-41	0.366	0.745	415
25991543	983	159	6.30E-40	0.459	0.735	464

112677	889	144.9	1.20E-35	0.409	0.691	447
307159112	673	112.3	8.70E-26	0.409	0.664	538
158998782	668	111.6	1.30E-25	0.433	0.701	515
158998780	667	111.5	1.50E-25	0.431	0.697	515
258588247	666	111.3	1.70E-25	0.414	0.672	515
56788031	663	110.9	2.20E-25	0.433	0.709	499
1126299828	662	110.7	2.50E-25	0.439	0.703	501
557792009	658	110.1	3.80E-25	0.441	0.719	501
18479082	654	109.5	5.80E-25	0.444	0.715	502
29839419	643	107.8	1.90E-24	0.378	0.701	482
307159114	640	107.4	2.40E-24	0.449	0.707	492
29839254	639	107.2	3.10E-24	0.355	0.655	507
113200131	636	106.8	3.80E-24	0.416	0.748	452
29839255	589	99.7	5.00E-22	0.397	0.737	448
169973	546	93.3	4.30E-20	0.381	0.671	486
18615	545	93.1	4.80E-20	0.381	0.671	486
18639	530	90.9	2.20E-19	0.386	0.675	471
218265	524	90	4.20E-19	0.375	0.682	472
18609	524	90	4.20E-19	0.375	0.682	472
224036293	510	87.8	1.90E-18	0.348	0.635	488
199732457	510	87.8	2.00E-18	0.351	0.635	504
112380623	498	86	6.70E-18	0.347	0.655	490
169969	498	86	6.80E-18	0.347	0.633	502
21314465	496	85.7	8.80E-18	0.349	0.629	518
3703107	492	85.1	1.20E-17	0.339	0.643	487
312233065	491	85	1.40E-17	0.345	0.653	490
10566449	491	85	1.40E-17	0.357	0.643	502
169971	479	83.5	1.90E-17	0.396	0.728	202
732706	484	83.9	3.30E-17	0.327	0.599	544
18641	484	83.9	3.30E-17	0.325	0.594	545
4249568	484	83.9	3.30E-17	0.328	0.598	545
806556	484	83.9	3.30E-17	0.327	0.6	545
22135348	464	81.2	8.00E-17	0.384	0.664	211
5712199	472	82.1	1.10E-16	0.333	0.623	504
523916668	299	56.5	1.80E-09	0.48	0.68	175
71084277	154	34.1	0.045	0.285	0.527	207
13183177	150	33.6	0.046	0.226	0.532	359
158251953	145	33	0.056	0.228	0.58	312
410067729	145	32.9	0.06	0.206	0.513	433
187766755	144	32.8	0.063	0.201	0.512	457
187766747	141	32.4	0.067	0.205	0.54	346
187766751	141	32.4	0.067	0.21	0.536	347
187766749	141	32.4	0.067	0.21	0.539	347
9967357	140	32.1	0.12	0.24	0.558	416
18536	140	32.1	0.14	0.24	0.558	416

288860106	136	31.4	0.32	0.294	0.512	170
9967361	128	30.3	0.43	0.232	0.582	323
21914823	127	30.2	0.46	0.235	0.566	327
21666498	126	30	0.5	0.232	0.566	327
980951548	127	30.1	0.53	0.233	0.521	305
15425631	126	30	0.61	0.236	0.581	322
736319	127	30	0.8	0.328	0.557	174
980951568	123	29.5	0.8	0.228	0.54	324
980951518	123	29.5	0.81	0.217	0.51	314
169950562	123	29.5	0.81	0.217	0.51	314

Matches with 80-mer FASTA for Cruciferin CRU4

Hit #	NCBI-gi	Species	Best %ID	# Hits > 35%	Full-align E-val	Full-align %ID	Full-align len
1	62240390	Sinapis alba	70.01 %	386of386	3.30E-58	55.00 %	471
2	62240392	Sinapis alba	65.03 %	386of386	1.10E-56	53.30 %	482
3	110349085	Pistacia vera	61.30 %	379of386	2.10E-54	45.60 %	471
4	156001070	Pistacia vera	61.30 %	375of386	4.30E-54	45.40 %	471
5	110349083	Pistacia vera	60.04 %	365of386	1.30E-42	44.90 %	481
6	25991543	Anacardium occidentale	59.30 %	377of386	6.30E-40	45.90 %	464
7	18479082	Corylus avellana	58.76 %	386of386	5.80E-25	44.40 %	502
8	557792009	Corylus avellana	58.76 %	386of386	3.80E-25	44.10 %	501
9	112677	Cucurbita maxima	58.00 %	330of386	1.20E-35	40.90 %	447
10	307159112	Prunus dulcis	57.52 %	380of386	8.70E-26	40.90 %	538
11	258588247	Prunus dulcis	57.52 %	367of386	1.70E-25	41.40 %	515
12	113200131	Fagopyrum tataricum	56.30 %	297of386	3.80E-24	41.60 %	452
13	307159114	Prunus dulcis	56.29 %	386of386	2.40E-24	44.90 %	492
14	523916668	Prunus dulcis	56.29 %	126of386	1.80E-09	48.00 %	175
15	158998780	Carya illinoinensis	55.60 %	386of386	1.50E-25	43.10 %	515

16	158998782	Carya illinoinensis	55.60 %	386of386	1.30E-25	43.30 %	515
17	1126299828	Juglans nigra	55.60 %	379of386	2.50E-25	43.90 %	501
18	29839254	Fagopyrum esculentum	55.00 %	233of386	3.10E-24	35.50 %	507
19	29839255	Fagopyrum esculentum	55.00 %	293of386	5.00E-22	39.70 %	448
20	13183173	Sesamum indicum	54.99 %	369of386	1.60E-50	42.10 %	489
21	56788031	Juglans regia	54.30 %	386of386	2.20E-25	43.30 %	499
22	29839419	Fagopyrum esculentum	53.80 %	229of386	1.90E-24	37.80 %	482
23	82469930	Actinidia chinensis	52.54 %	348of386	2.80E-54	42.50 %	461
24	10566449	Glycine max	52.50 %	262of386	1.40E-17	35.70 %	502
25	30313867	Bertholletia excelsa	52.50 %	386of386	1.50E-51	43.00 %	463
26	1534918238	Bertholletia excelsa	52.50 %	379of386	4.60E-51	43.70 %	430
27	169971	Glycine max	51.25 %	120of386	1.90E-17	39.60 %	202
28	169973	Glycine max	51.20 %	256of386	4.30E-20	38.10 %	486
29	18639	Glycine max	51.20 %	303of386	2.20E-19	38.60 %	471
30	806556	Glycine soja	51.20 %	237of386	3.30E-17	32.70 %	545
31	4249568	Glycine max	51.20 %	237of386	3.30E-17	32.80 %	545
32	732706	Glycine max	51.20 %	226of386	3.30E-17	32.70 %	544
33	18615	Glycine max	51.20 %	256of386	4.80E-20	38.10 %	486
34	18641	Glycine max	51.20 %	226of386	3.30E-17	32.50 %	545
35	169969	Glycine max	50.00 %	244of386	6.80E-18	34.70 %	502
36	213144665	Arachis hypogaea	48.78 %	232of386	8.80E-18	34.90 %	518
37	224036293	Arachis hypogaea	48.75 %	204of386	1.90E-18	34.80 %	488
38	199732457	Arachis hypogaea	48.75 %	215of386	2.00E-18	35.10 %	504

39	5381325	Sesamum indicum	48.70 %	189of386	5.90E-44	36.20 %	428
40	18609	Glycine max	48.70 %	254of386	4.20E-19	37.50 %	472
41	218265	Glycine max	48.70 %	254of386	4.20E-19	37.50 %	472
42	3122330 65	Arachis hypogaea	47.50 %	190of386	1.40E-17	34.50 %	490
43	1123806 23	Arachis hypogaea	47.50 %	192of386	6.70E-18	34.70 %	490
44	5712199	Arachis hypogaea	47.50 %	188of386	1.10E-16	33.30 %	504
45	3703107	Arachis hypogaea	46.30 %	211of386	1.20E-17	33.90 %	487
46	2213534 8	Arachis hypogaea	45.03 %	100of386	8.00E-17	38.40 %	211
47	5845921 16	Fagopyrum esculentum	43.80 %	203of386	3.00E-41	36.60 %	415
48	5845921 20	Fagopyrum esculentum	43.80 %	203of386	2.70E-41	36.60 %	415
49	736319	Triticum aestivum	39.00 %	12of386	0.8	32.80 %	174
50	21743	Triticum aestivum	37.80 %	7of386	2.5	29.50 %	173
51	170743	Triticum aestivum	37.80 %	7of386	2.4	28.60 %	185
52	5087326 25	Triticum aestivum	37.80 %	7of386	2.3	28.60 %	185
53	2086053 46	Triticum aestivum	35.40 %	1of386	29	25.80 %	93
54	2086053 48	Triticum aestivum	35.40 %	1of386	39	26.40 %	91
55	7391249 6	Triticum aestivum	35.40 %	1of386	64	34.50 %	84

Full-length FASTA matches for Cruciferin CRU1

NCBI-GI	opt	bits	E(2233)	%_id	%_sim	alen
62240390	3155	725.4	2.50E-210	0.916	0.969	510
62240392	2382	549.2	2.80E-157	0.901	0.948	523
170734	134	37.1	0.0019	0.5	0.611	54
508732627	134	37	0.0024	0.5	0.611	54
21773	134	36.9	0.0026	0.5	0.611	54
523916668	373	91.8	4.90E-20	0.497	0.692	195
62550933	116	32.8	0.049	0.493	0.638	69

886967	118	33.3	0.029	0.489	0.644	45
897811	157	43.4	1.00E-05	0.484	0.641	64
307159114	672	159.4	5.80E-40	0.47	0.713	513
258588247	829	195.2	1.00E-50	0.463	0.731	521
1706883247	109	31.3	0.11	0.463	0.611	54
25991543	1150	268.4	8.30E-73	0.462	0.723	487
307159112	835	196.6	4.20E-51	0.461	0.733	536
18479082	991	232.1	7.70E-62	0.456	0.697	528
557792009	994	232.8	4.80E-62	0.455	0.699	528
508732623	109	31.2	0.17	0.455	0.576	66
158998782	985	230.8	1.90E-61	0.447	0.686	535
56788031	1018	238.3	1.10E-63	0.445	0.685	533
158998780	991	232.1	7.50E-62	0.445	0.688	535
1126299828	980	229.6	4.30E-61	0.433	0.69	533
13183173	1008	236	5.00E-63	0.421	0.688	478
156001070	891	209.4	5.10E-55	0.419	0.702	513
110349085	887	208.5	9.50E-55	0.417	0.702	513
82469930	1097	256.3	3.60E-69	0.414	0.71	500
1534918238	947	222.2	6.50E-59	0.411	0.683	467
110349083	831	195.7	7.00E-51	0.411	0.707	518
170730	162	43.3	3.10E-05	0.405	0.582	79
170732	162	43.3	3.40E-05	0.405	0.582	79
169971	492	118.7	5.20E-28	0.398	0.754	191
30313867	954	223.7	2.40E-59	0.397	0.674	506
112677	891	209.4	5.20E-55	0.373	0.649	504
18615	769	181.5	1.30E-46	0.371	0.642	517
169973	765	180.6	2.40E-46	0.371	0.64	517
29839419	737	174.2	2.20E-44	0.368	0.747	486
929075511	126	34.8	0.054	0.364	0.606	66
929097893	122	33.9	0.1	0.364	0.621	66
18639	661	156.9	3.10E-39	0.36	0.645	516
113200131	732	173.1	4.60E-44	0.356	0.675	523
18609	520	124.8	1.50E-29	0.354	0.64	503
218265	520	124.8	1.50E-29	0.354	0.64	503
5381325	875	205.7	6.20E-54	0.35	0.68	503
288860106	309	76.6	8.40E-15	0.348	0.527	224
1079717942	130	35.8	0.027	0.348	0.545	66
22135348	290	72.7	3.30E-14	0.347	0.599	242
29839254	712	168.5	1.20E-42	0.346	0.683	540
10566449	505	121.4	1.70E-28	0.344	0.626	546
584592116	500	120.2	3.30E-28	0.343	0.667	496
29839255	690	163.5	3.40E-41	0.342	0.703	512
27806257	123	34.2	0.081	0.342	0.526	76
584592120	500	120.2	3.30E-28	0.341	0.667	496
71084277	248	62.7	1.20E-10	0.341	0.512	252

112380623	481	115.9	7.60E-27	0.335	0.634	516
169969	307	76.2	6.70E-15	0.335	0.619	546
312233065	473	114.1	2.70E-26	0.333	0.632	516
736319	258	65	2.60E-11	0.333	0.541	207
21314465	460	111.1	2.20E-25	0.332	0.595	548
224036293	482	116.1	6.40E-27	0.327	0.611	511
199732457	482	116.1	6.70E-27	0.327	0.611	511
929312453	123	34.2	0.08	0.325	0.558	77
929244458	123	34.2	0.08	0.325	0.558	77
170736	121	34.1	0.016	0.323	0.542	155
3703107	463	111.8	1.30E-25	0.321	0.607	511
21743	270	67.7	3.90E-12	0.318	0.509	267
4249568	517	124.1	2.90E-29	0.317	0.597	580
806556	515	123.6	3.90E-29	0.317	0.597	580
5712199	433	104.9	1.60E-23	0.317	0.603	511
508732625	266	66.8	7.00E-12	0.315	0.513	267
170743	266	66.8	7.20E-12	0.315	0.513	267
18641	517	124.1	2.90E-29	0.314	0.593	580
732706	508	122	1.20E-28	0.313	0.596	579
508732621	140	38.4	0.0009	0.31	0.527	203
22090	248	62.7	1.10E-10	0.306	0.536	222
21751	231	58.9	1.40E-09	0.305	0.492	266
226437844	93	28.1	0.57	0.304	0.696	56
1063270	119	33.6	0.025	0.301	0.523	193
21757	150	40.6	0.0002	0.298	0.528	178
170738	133	36.7	0.0033	0.298	0.49	208
1137166044	184	48.4	9.20E-07	0.297	0.523	195
170708	118	33.3	0.031	0.295	0.525	200
170740	144	39.2	0.00052	0.294	0.514	177
170710	142	38.8	0.00078	0.294	0.506	235
208605346	156	42	7.00E-05	0.292	0.469	209
170718	181	47.7	1.60E-06	0.291	0.474	234
21765	179	47.2	2.20E-06	0.291	0.474	234
73912496	186	48.7	1.10E-06	0.29	0.484	217
170712	164	43.8	2.20E-05	0.29	0.514	183
21673	188	49.3	5.20E-07	0.288	0.481	243
1079717864	123	34.2	0.086	0.284	0.505	95
170724	172	45.6	6.20E-06	0.283	0.483	240
170702	114	32.4	0.061	0.282	0.521	188
1304264	133	36.8	0.0025	0.281	0.517	178
170728	117	33.4	0.019	0.28	0.506	164
75317968	148	40.1	0.00037	0.279	0.524	208
170722	168	44.8	9.90E-06	0.276	0.53	185
21930	176	46.6	3.10E-06	0.275	0.573	171
170726	120	33.8	0.022	0.275	0.495	204

21755	174	46.1	4.30E-06	0.274	0.536	179
170720	168	44.7	1.10E-05	0.274	0.525	179
886963	111	31.8	0.067	0.274	0.555	146
208605348	157	42.1	8.10E-05	0.272	0.508	250
288709	123	34.5	0.014	0.271	0.479	192
1708280	123	34.5	0.014	0.271	0.479	192
21761	157	42.2	6.40E-05	0.268	0.52	179
21779	188	49	1.30E-06	0.266	0.476	418
75219081	166	44.3	1.50E-05	0.266	0.561	173
208605344	108	31	0.2	0.264	0.455	231
21783	147	39.9	0.00041	0.262	0.504	240
283476402	143	39	0.00057	0.259	0.487	228
886965	126	35.2	0.0075	0.259	0.496	228
21926	160	42.9	4.10E-05	0.241	0.557	174
187766751	172	45.5	8.30E-06	0.228	0.559	347
335331566	124	34.6	0.016	0.221	0.505	321
187766747	172	45.5	8.30E-06	0.219	0.565	347
187766749	172	45.5	8.30E-06	0.219	0.559	347
410067729	171	45.2	1.30E-05	0.219	0.556	347
108743976	104	30	0.49	0.216	0.56	334
187766755	175	46.2	6.60E-06	0.214	0.554	370

Matches with 80-mer FASTA for Cruciferin CRU1

Hit #	NCBI-gi	Species	Best %ID	# Hits > 35%	Full-align E-val	Full-align %ID	Full-align len
1	gi|62240390	Sinapis alba	98.80 %	430of430	2.50E-210	91.60 %	510
2	gi|62240392	Sinapis alba	97.50 %	430of430	2.80E-157	90.10 %	523
3	gi|158998780	Carya illinoinensis	65.00 %	355of430	7.50E-62	44.50 %	535
4	gi|158998782	Carya illinoinensis	65.00 %	358of430	1.90E-61	44.70 %	535
5	gi|56788031	Juglans regia	63.79 %	368of430	1.10E-63	44.50 %	533
6	gi|1126299828	Juglans nigra	63.79 %	373of430	4.30E-61	43.30 %	533
7	gi|523916668	Prunus dulcis	60.04 %	168of430	4.90E-20	49.70 %	195
8	gi|307159114	Prunus dulcis	60.04 %	425of430	5.80E-40	47.00 %	513
9	gi|25991543	Anacardium occidentale	60.04 %	379of430	8.30E-73	46.20 %	487
10	gi|557792009	Corylus avellana	58.79 %	391of430	4.80E-62	45.50 %	528
11	gi|18479082	Corylus avellana	58.79 %	394of430	7.70E-62	45.60 %	528
12	gi|307159112	Prunus dulcis	58.40 %	430of430	4.20E-51	46.10 %	536

13	gi|258588247	Prunus dulcis	58.40 %	423of430	1.00E-50	46.30 %	521
14	gi|82469930	Actinidia chinensis	56.30 %	327of430	3.60E-69	41.40 %	500
15	gi|736319	Triticum aestivum	56.26 %	70of430	2.60E-11	33.30 %	207
16	gi|288860106	Triticum aestivum	55.60 %	79of430	8.40E-15	34.80 %	224
17	gi|110349085	Pistacia vera	55.00 %	359of430	9.50E-55	41.70 %	513
18	gi|156001070	Pistacia vera	55.00 %	361of430	5.10E-55	41.90 %	513
19	gi|110349083	Pistacia vera	55.00 %	345of430	7.00E-51	41.10 %	518
	gi|71084277	Triticum aestivum	55.00 %	75of430	1.20E-10	34.10 %	252
21	gi|113200131	Fagopyrum tataricum	53.80 %	255of430	4.60E-44	35.60 %	523
22	gi|13183173	Sesamum indicum	53.80 %	343of430	5.00E-63	42.10 %	478
23	gi|112677	Cucurbita maxima	52.50 %	273of430	5.20E-55	37.30 %	504
24	gi|1534918238	Bertholletia excelsa	52.50 %	309of430	6.50E-59	41.10 %	467
25	gi|30313867	Bertholletia excelsa	52.50 %	309of430	2.40E-59	39.70 %	506
26	gi|29839254	Fagopyrum esculentum	51.25 %	240of430	1.20E-42	34.60 %	540
27	gi|10566449	Glycine max	51.25 %	264of430	1.70E-28	34.40 %	546
28	gi|18639	Glycine max	51.20 %	267of430	3.10E-39	36.00 %	516
29	gi|18641	Glycine max	50.60 %	239of430	2.90E-29	31.40 %	580
	gi|4249568	Glycine max	50.60 %	256of430	2.90E-29	31.70 %	580
31	gi|806556	Glycine soja	50.60 %	256of430	3.90E-29	31.70 %	580
32	gi|22090	Triticum aestivum	50.02 %	69of430	1.10E-10	30.60 %	222
33	gi|29839419	Fagopyrum esculentum	50.00 %	236of430	2.20E-44	36.80 %	486
34	gi|170743	Triticum aestivum	50.00 %	70of430	7.20E-12	31.50 %	267
35	gi|21743	Triticum aestivum	50.00 %	69of430	3.90E-12	31.80 %	267
36	gi|18615	Glycine max	50.00 %	267of430	1.30E-46	37.10 %	517
37	gi|29839255	Fagopyrum esculentum	50.00 %	213of430	3.40E-41	34.20 %	512
38	gi|508732625	Triticum aestivum	50.00 %	70of430	7.00E-12	31.50 %	267
39	gi|169969	Glycine max	50.00 %	242of430	6.70E-15	33.50 %	546
	gi|169973	Glycine max	50.00 %	267of430	2.40E-46	37.10 %	517
41	gi|732706	Glycine max	49.40 %	237of430	1.20E-28	31.30 %	579

42	gi|21751	Triticum aestivum	48.78 %	71of430	1.40E-09	30.50 %	266
43	gi|218265	Glycine max	48.70 %	244of430	1.50E-29	35.40 %	503
44	gi|18609	Glycine max	48.70 %	244of430	1.50E-29	35.40 %	503
45	gi|5381325	Sesamum indicum	48.10 %	238of430	6.20E-54	35.00 %	503
46	gi|199732457	Arachis hypogaea	47.50 %	187of430	6.70E-27	32.70 %	511
47	gi|224036293	Arachis hypogaea	47.50 %	187of430	6.40E-27	32.70 %	511
48	gi|5712199	Arachis hypogaea	47.50 %	145of430	1.60E-23	31.70 %	511
49	gi|22135348	Arachis hypogaea	47.50 %	77of430	3.30E-14	34.70 %	242
	gi|169971	Glycine max	47.50 %	116of430	5.20E-28	39.80 %	191
51	gi|21314465	Arachis hypogaea	47.50 %	219of430	2.20E-25	33.20 %	548
52	gi|21779	Triticum aestivum	47.50 %	68of430	1.30E-06	26.60 %	418
53	gi|3703107	Arachis hypogaea	46.90 %	174of430	1.30E-25	32.10 %	511
54	gi|584592120	Fagopyrum esculentum	46.30 %	218of430	3.30E-28	34.10 %	496
55	gi|584592116	Fagopyrum esculentum	46.30 %	228of430	3.30E-28	34.30 %	496
56	gi|112380623	Arachis hypogaea	46.22 %	186of430	7.60E-27	33.50 %	516
57	gi|312233065	Arachis hypogaea	46.22 %	170of430	2.70E-26	33.30 %	516
58	gi|21930	Triticum turgidum subsp. durum	43.80 %	35of430	3.10E-06	27.50 %	171
59	gi|170738	Triticum aestivum	43.79 %	20of430	0.0033	29.80 %	208
	gi|170730	Triticum aestivum	43.71 %	38of430	3.10E-05	40.50 %	79
61	gi|170732	Triticum aestivum	43.71 %	38of430	3.40E-05	40.50 %	79
62	gi|75219081	Triticum aestivum	42.52 %	37of430	1.50E-05	26.60 %	173
63	gi|62550933	Triticum aestivum	42.52 %	29of430	0.049	49.30 %	69
64	gi|2834764402	Triticum aestivum	41.29 %	36of430	0.00057	25.90 %	228
65	gi|170736	Triticum aestivum	41.28 %	35of430	0.016	32.30 %	155
66	gi|508732621	Triticum aestivum	41.28 %	33of430	0.0009	31.00 %	203
67	gi|1137166044	Triticum monococcum subsp. aegilopoides	40.01 %	39of430	9.20E-07	29.70 %	195
68	gi|897811	Triticum aestivum	40.01 %	38of430	1.00E-05	48.40 %	64
69	gi|208605346	Triticum aestivum	40.00 %	21of430	7.00E-05	29.20 %	209
	gi|208605348	Triticum aestivum	40.00 %	21of430	8.10E-05	27.20 %	250

71	gi|21757	Triticum aestivum	39.99 %	35of430	0.0002	29.80 %	178
72	gi|21761	Triticum aestivum	38.79 %	14of430	6.40E-05	26.80 %	179
73	gi|21926	Triticum turgidum subsp. durum	38.78 %	36of430	4.10E-05	24.10 %	174
74	gi|170724	Triticum aestivum	38.76 %	18of430	6.20E-06	28.30 %	240
75	gi|170708	Triticum aestivum	38.75 %	19of430	0.031	29.50 %	200
76	gi|73912496	Triticum aestivum	38.72 %	27of430	1.10E-06	29.00 %	217
77	gi|1063270	Triticum aestivum	38.72 %	1of430	0.025	30.10 %	193
78	gi|170702	Triticum aestivum	38.72 %	17of430	0.061	28.20 %	188
79	gi|508732623	Triticum aestivum	37.54 %	16of430	0.17	45.50 %	66
80	gi|21673	Triticum aestivum	37.52 %	30of430	5.20E-07	28.80 %	243
81	gi|170740	Triticum urartu	37.52 %	30of430	0.00052	29.40 %	177
82	gi|21783	Triticum aestivum	37.00 %	3of430	0.00041	26.20 %	240
83	gi|75317968	Triticum aestivum	36.27 %	2of430	0.00037	27.90 %	208
84	gi|170726	Triticum aestivum	36.24 %	10of430	0.022	27.50 %	204
85	gi|21765	Triticum aestivum	35.04 %	3of430	2.20E-06	29.10 %	234
86	gi|170718	Triticum aestivum	35.04 %	3of430	1.60E-06	29.10 %	234
87	gi|170712	Triticum aestivum	35.02 %	15of430	2.20E-05	29.00 %	183

Full-length FASTA matches for Cruciferin BnC1

NCBI-GI	opt	bits	E(2233)	%_id	%_sim	alen
62240390	1281	172.1	8.60E-44	0.589	0.824	501
62240392	601	87.6	2.50E-18	0.572	0.814	512
523916668	349	56.5	1.90E-09	0.482	0.679	193
307159114	639	92.3	9.10E-20	0.451	0.695	508
18479082	682	97.6	2.30E-21	0.447	0.684	532
25991543	698	99.7	5.00E-22	0.444	0.712	493
258588247	655	94.3	2.40E-20	0.441	0.704	521
557792009	689	98.5	1.20E-21	0.436	0.68	541
307159112	651	93.8	3.60E-20	0.436	0.697	544
1534918238	747	105.8	6.80E-24	0.434	0.702	456
291482310	114	27.3	0.87	0.432	0.636	44
158998782	664	95.4	1.10E-20	0.43	0.663	537
158998780	663	95.3	1.10E-20	0.43	0.663	537
1126299828	662	95.2	1.30E-20	0.427	0.661	531
82469930	1069	145.8	6.60E-36	0.426	0.707	498

56788031	660	94.9	1.50E-20	0.424	0.656	538
110349085	991	136.1	5.60E-33	0.418	0.706	493
156001070	984	135.2	1.00E-32	0.416	0.706	493
30313867	750	106.1	5.80E-24	0.416	0.693	495
110349083	813	113.9	2.70E-26	0.409	0.7	504
113200131	874	121.5	1.50E-28	0.405	0.695	479
75219081	125	28.5	0.81	0.405	0.635	74
169971	464	70.7	1.40E-13	0.404	0.718	188
170730	132	29.4	0.48	0.403	0.584	77
170732	132	29.4	0.51	0.403	0.584	77
112677	684	97.9	1.80E-21	0.397	0.628	506
29839419	551	81.3	1.90E-16	0.396	0.715	480
29839255	834	116.5	4.60E-27	0.395	0.701	471
13183173	984	135.2	1.10E-32	0.391	0.669	517
18639	719	102.3	8.70E-23	0.378	0.638	503
29839254	556	82	1.30E-16	0.377	0.659	528
169973	546	80.7	2.70E-16	0.376	0.636	511
18615	545	80.6	2.90E-16	0.376	0.636	511
18609	721	102.5	7.40E-23	0.362	0.64	506
218265	721	102.5	7.40E-23	0.362	0.64	506
112380623	527	78.4	1.40E-15	0.355	0.655	516
312233065	520	77.5	2.60E-15	0.353	0.653	516
584592120	761	107.5	2.20E-24	0.344	0.682	468
584592116	761	107.5	2.20E-24	0.344	0.682	468
10566449	471	71.4	1.80E-13	0.344	0.604	538
22135348	242	43.1	2.50E-05	0.341	0.629	229
21314465	491	73.9	3.40E-14	0.336	0.607	545
5381325	797	112	9.90E-26	0.334	0.684	488
199732457	499	74.9	1.70E-14	0.334	0.609	557
224036293	499	74.9	1.60E-14	0.333	0.605	531
508732625	200	37.6	0.0041	0.333	0.519	156
170743	200	37.6	0.0042	0.333	0.519	156
21743	196	37.1	0.0061	0.333	0.513	156
169969	296	49.6	6.40E-07	0.331	0.595	538
3703107	483	72.9	6.30E-14	0.33	0.601	531
288860106	204	38.1	0.0031	0.324	0.553	188
5712199	458	69.8	5.70E-13	0.323	0.606	538
4249568	491	73.9	3.60E-14	0.321	0.558	591
18641	491	73.9	3.60E-14	0.32	0.553	591
806556	494	74.2	2.70E-14	0.318	0.557	591
732706	495	74.4	2.50E-14	0.317	0.558	590
736319	207	38.5	0.0024	0.3	0.529	227
71084277	149	31.3	0.33	0.294	0.513	228
21779	142	30.4	0.49	0.286	0.492	199
22090	174	34.4	0.034	0.278	0.545	198

46560476	144	30.8	0.25	0.277	0.672	119
375332427	159	32.7	0.067	0.275	0.614	153
347447588	159	32.7	0.067	0.275	0.614	153
21751	140	30.2	0.57	0.271	0.502	203
21930	123	28.3	0.96	0.261	0.522	180
187766751	164	33.3	0.038	0.243	0.618	152
29539111	131	29.2	0.74	0.238	0.515	344
187766749	164	33.3	0.038	0.213	0.538	338
187766747	164	33.3	0.038	0.207	0.538	338
410067729	168	33.8	0.036	0.198	0.539	479
187766755	176	34.8	0.017	0.196	0.545	455

Matches with 80-mer FASTA for Cruciferin BnC1

Hit #	NCBI-gi	Species	Best %ID	# Hits > 35%	Full-align E-val	Full-align %ID	Full-align len
1	62240390	Sinapis alba	76.50 %	411of411	8.60E-44	58.90 %	501
2	62240392	Sinapis alba	74.10 %	411of411	2.50E-18	57.20 %	512
3	557792009	Corylus avellana	63.70 %	374of411	1.20E-21	43.60 %	541
4	18479082	Corylus avellana	63.70 %	383of411	2.30E-21	44.70 %	532
5	523916668	Prunus dulcis	62.51 %	161of411	1.90E-09	48.20 %	193
6	307159114	Prunus dulcis	62.51 %	410of411	9.10E-20	45.10 %	508
7	25991543	Anacardium occidentale	61.30 %	367of411	5.00E-22	44.40 %	493
8	112677	Cucurbita maxima	60.50 %	294of411	1.80E-21	39.70 %	506
9	258588247	Prunus dulcis	58.79 %	391of411	2.40E-20	44.10 %	521
10	158998780	Carya illinoinensis	58.79 %	347of411	1.10E-20	43.00 %	537
11	158998782	Carya illinoinensis	58.79 %	347of411	1.10E-20	43.00 %	537
12	1126299828	Juglans nigra	58.79 %	343of411	1.30E-20	42.70 %	531
13	307159112	Prunus dulcis	58.79 %	392of411	3.60E-20	43.60 %	544
14	56788031	Juglans regia	57.52 %	351of411	1.50E-20	42.40 %	538
15	82469930	Actinidia chinensis	56.30 %	342of411	6.60E-36	42.60 %	498
16	156001070	Pistacia vera	56.30 %	371of411	1.00E-32	41.60 %	493
17	110349085	Pistacia vera	56.30 %	379of411	5.60E-33	41.80 %	493
18	113200131	Fagopyrum tataricum	55.00 %	303of411	1.50E-28	40.50 %	479
19	110349083	Pistacia vera	55.00 %	346of411	2.70E-26	40.90 %	504

	29839255	Fagopyrum esculentum	55.00 %	271of411	4.60E-27	39.50 %	471
21	18639	Glycine max	53.80 %	277of411	8.70E-23	37.80 %	503
22	29839419	Fagopyrum esculentum	53.80 %	259of411	1.90E-16	39.60 %	480
23	1534918238	Bertholletia excelsa	53.80 %	352of411	6.80E-24	43.40 %	456
24	30313867	Bertholletia excelsa	53.80 %	364of411	5.80E-24	41.60 %	495
25	29839254	Fagopyrum esculentum	53.80 %	247of411	1.30E-16	37.70 %	528
26	18615	Glycine max	52.54 %	270of411	2.90E-16	37.60 %	511
27	169973	Glycine max	52.54 %	270of411	2.70E-16	37.60 %	511
28	4249568	Glycine max	52.50 %	244of411	3.60E-14	32.10 %	591
29	10566449	Glycine max	52.50 %	256of411	1.80E-13	34.40 %	538
	169971	Glycine max	52.50 %	122of411	1.40E-13	40.40 %	188
31	806556	Glycine soja	52.50 %	244of411	2.70E-14	31.80 %	591
32	18641	Glycine max	52.50 %	244of411	3.60E-14	32.00 %	591
33	732706	Glycine max	52.50 %	223of411	2.50E-14	31.70 %	590
34	13183173	Sesamum indicum	52.46 %	320of411	1.10E-32	39.10 %	517
35	218265	Glycine max	51.29 %	230of411	7.40E-23	36.20 %	506
36	18609	Glycine max	51.29 %	230of411	7.40E-23	36.20 %	506
37	71084277	Triticum aestivum	51.20 %	66of411	0.33	29.40 %	228
38	288860106	Triticum aestivum	50.00 %	74of411	0.0031	32.40 %	188
39	22135348	Arachis hypogaea	49.40 %	50of411	2.50E-05	34.10 %	229
	3703107	Arachis hypogaea	49.40 %	180of411	6.30E-14	33.00 %	531
41	21314465	Arachis hypogaea	49.40 %	219of411	3.40E-14	33.60 %	545
42	169969	Glycine max	48.78 %	239of411	6.40E-07	33.10 %	538
43	112380623	Arachis hypogaea	48.70 %	214of411	1.40E-15	35.50 %	516
44	312233065	Arachis hypogaea	48.70 %	208of411	2.60E-15	35.30 %	516
45	736319	Triticum aestivum	47.60 %	70of411	0.0024	30.00 %	227
46	170743	Triticum aestivum	47.50 %	72of411	0.0042	33.30 %	156
47	508732625	Triticum aestivum	47.50 %	72of411	0.0041	33.30 %	156
48	5712199	Arachis hypogaea	46.30 %	148of411	5.70E-13	32.30 %	538

49	224036293	Arachis hypogaea	46.22 %	179of411	1.60E-14	33.30 %	531
50	199732457	Arachis hypogaea	46.22 %	179of411	1.70E-14	33.40 %	557
51	5381325	Sesamum indicum	46.22 %	187of411	9.90E-26	33.40 %	488
52	21743	Triticum aestivum	44.00 %	72of411	0.0061	33.30 %	156
53	584592120	Fagopyrum esculentum	43.80 %	197of411	2.20E-24	34.40 %	468
54	584592116	Fagopyrum esculentum	43.80 %	197of411	2.20E-24	34.40 %	468
55	21779	Triticum aestivum	42.00 %	55of411	0.49	28.60 %	199
56	22090	Triticum aestivum	41.50 %	54of411	0.034	27.80 %	198
57	21751	Triticum aestivum	40.01 %	46of411	0.57	27.10 %	203
58	170732	Triticum aestivum	38.79 %	30of411	0.51	40.30 %	77
59	170730	Triticum aestivum	38.79 %	30of411	0.48	40.30 %	77
60	21930	Triticum turgidum subsp. durum	37.50 %	27of411	0.96	26.10 %	180
61	75219081	Triticum aestivum	37.46 %	26of411	0.81	40.50 %	74
62	21926	Triticum turgidum subsp. durum	37.46 %	25of411	1.2	40.50 %	74
63	625509333	Triticum aestivum	36.24 %	9of411	11	36.70 %	79

Full-length FASTA matches for Oleosin S2-2

NCBI-GI	opt	bits	E(2233)	%_id	%_sim	alen
49617323	571	164.7	1.80E-42	0.525	0.873	158
113200509	530	153.3	5.20E-39	0.462	0.784	171
52001239	522	151.1	2.10E-38	0.523	0.819	149
10834827	440	128.2	1.80E-31	0.459	0.783	157
71040655	323	95.7	9.20E-22	0.438	0.727	128
29170509	323	95.6	9.50E-22	0.41	0.769	117
198250343	323	95.6	9.90E-22	0.409	0.727	132
5381321	321	95.1	1.50E-21	0.409	0.727	132
122218540	316	93.7	3.60E-21	0.399	0.71	138
52001241	313	92.8	8.10E-21	0.382	0.715	144

Matches with 80-mer FASTA for Oleosin S2-2

Hit #	NCBI-gi	Species	Best %ID	# Hits > 35%	Full-align E-val	Full-align %ID	Full-align len
1	49617323	Corylus avellana	70.01 %	109of109	1.80E-42	52.50 %	158
2	113200509	Arachis hypogaea	64.98 %	104of109	5.20E-39	46.20 %	171

3	52001239	Arachis hypogaea	64.98 %	106of109	2.10E-38	52.30 %	149
4	10834827	Sesamum indicum	62.50 %	103of109	1.80E-31	45.90 %	157
5	71040655	Arachis hypogaea	55.00 %	74of109	9.20E-22	43.80 %	128
6	5381321	Sesamum indicum	53.80 %	78of109	1.50E-21	40.90 %	132
7	198250343	Sesamum indicum	53.80 %	78of109	9.90E-22	40.90 %	132
8	122218540	Arachis hypogaea	53.80 %	71of109	3.60E-21	39.90 %	138
9	291705009	Corylus avellana	50.00 %	68of109	9.50E-22	41.00 %	117
10	52001241	Arachis hypogaea	45.10 %	77of109	8.10E-21	38.20 %	144

Full-length FASTA matches for Napin-3

NCBI-GI	opt	bits	E(2233)	%_id	%_sim	alen
75107016	907	95.9	4.70E-22	1	1	125
32363444	835	89.3	4.60E-20	0.891	0.953	129
1009438	592	67.1	2.50E-13	0.819	0.847	144
1009440	590	67	2.80E-13	0.826	0.854	144
1009436	590	67	2.80E-13	0.826	0.854	144
1009442	588	66.8	3.20E-13	0.813	0.847	144
51338758	582	66.2	4.70E-13	0.826	0.847	144
1009434	579	65.9	5.70E-13	0.813	0.84	144
17697	552	63.6	3.50E-12	0.809	0.858	141
26985163	408	50	2.60E-08	0.532	0.757	111
110349081	245	35.3	0.00096	0.348	0.705	112
28207731	222	33.2	0.0041	0.322	0.678	115
31321942	217	32.8	0.0059	0.324	0.667	111
1794252	210	32.1	0.0086	0.306	0.667	111
226437844	198	31	0.019	0.352	0.63	108
13183175	196	30.9	0.022	0.336	0.588	119
209165427	194	30.7	0.025	0.336	0.58	119
68564970	181	29.4	0.055	0.31	0.612	116
112754	181	29.4	0.056	0.235	0.574	115
24473800	171	28.5	0.1	0.348	0.652	115
5381323	160	27.5	0.21	0.283	0.593	113
21068	163	28.2	0.23	0.349	0.688	109
158121995	150	26.7	0.42	0.254	0.569	130

Matches with 80-mer FASTA for Napin-3

Hit #	NCBI-gi	Species	Best %ID	# Hits > 35%	Full-align E-val	Full-align %ID	Full-align len
1	75107016	Brassica napus	100.00 %	46of46	4.70E-22	100.00 %	125
2	32363444	Brassica juncea	92.70 %	46of46	4.60E-20	89.10 %	129
3	1009436	Sinapis alba	91.60 %	46of46	2.80E-13	82.60 %	144
4	1009438	Sinapis alba	91.60 %	46of46	2.50E-13	81.90 %	144
5	51338758	Sinapis alba	91.60 %	46of46	4.70E-13	82.60 %	144
6	1009440	Sinapis alba	91.60 %	46of46	2.80E-13	82.60 %	144
7	1009442	Sinapis alba	90.40 %	46of46	3.20E-13	81.30 %	144
8	17697	Brassica rapa	90.00 %	46of46	3.50E-12	80.90 %	141
9	1009434	Sinapis alba	89.20 %	46of46	5.70E-13	81.30 %	144
10	26985163	Brassica napus	55.00 %	46of46	2.60E-08	53.20 %	111
11	110349081	Pistacia vera	38.76 %	18of46	0.00096	34.80 %	112
12	21068	Ricinus communis	38.71 %	17of46	0.23	34.90 %	109
13	13183175	Sesamum indicum	37.52 %	12of46	0.022	33.60 %	119
14	209165427	Sesamum indicum	37.52 %	12of46	0.025	33.60 %	119
15	208605348	Triticum aestivum	36.60 %	2of46	4.3	28.20 %	131
16	208605346	Triticum aestivum	36.60 %	2of46	3.8	28.20 %	131
17	31321942	Juglans nigra	36.29 %	7of46	0.0059	32.40 %	111
18	226437844	Corylus avellana	36.27 %	5of46	0.019	35.20 %	108
19	288860106	Triticum aestivum	36.20 %	4of46	11	36.20 %	80
20	28207731	Carya illinoinensis	36.20 %	1of46	0.0041	32.20 %	115
21	170738	Triticum aestivum	35.80 %	6of46	11	27.60 %	127
22	886967	Triticum aestivum	35.20 %	4of46	27	31.50 %	127
23	244738000	Anacardium occidentale	35.00 %	3of46	0.1	34.80 %	115
24	283476402	Triticum aestivum	35.00 %	7of46	4.7	32.10 %	109

Full-length FASTA matches for Squalene monooxygenase 1,2

No sequences from FARRP allergenic protein database were found matching Squalene monooxygenase 1,2 (ERG12_BRANA) with FASTA E-value < 1 criterion.

Matches with 80-mer FASTA for Squalene monooxygenase 1,2

No sequences from FARRP allergenic protein database were found matching Squalene monooxygenase 1,2 (ERG12_BRANA) using the sliding window 80-mer FASTA search with identity > 35 %.

3.7 Sequence matches from FARRP Celiac Disease database

There were no exact peptide matches for any of the query sequences from Table 1 in the FARRP Celiac Disease 1013 peptide dataset.

Some matches were found with the full-length FASTA search against the 72 protein sequences in the Celiac Disease dataset of the FARRP database. However, none of the matches had the required sequence identity (> 45 %) or E-value (< 10^{-16}) needed for labelling the proteins as having potential to elicit Celiac Disease.

Full-length FASTA matches for Cruciferin CRU4

NCBI-GI	opt	z-sc	E(72)	%_id	%_sim	alen
118772075	145	95.6	0.12	0.294	0.504	228
146261040	150	87.3	0.34	0.282	0.512	209

Full-length FASTA matches for Cruciferin CRU1

NCBI-GI	opt	z-sc	E(72)	%_id	%_sim	alen
117650782	264	118.5	0.0061	0.341	0.52	223
146261040	260	116.9	0.0076	0.331	0.5	272
294719862	258	115.3	0.0093	0.315	0.516	254
736319	258	115.1	0.0095	0.336	0.528	214
146261042	251	113.4	0.012	0.335	0.533	227
114842970	251	111.6	0.015	0.329	0.516	219
118772075	211	108.8	0.021	0.314	0.51	245
21751	231	105.2	0.034	0.305	0.492	266
7209265	188	94.8	0.13	0.288	0.481	243
7209261	178	90.4	0.23	0.299	0.549	144
21765	179	89.2	0.27	0.291	0.474	234
73912496	186	88	0.31	0.29	0.484	217
7209263	168	85.8	0.41	0.274	0.525	179
7209259	168	85.7	0.41	0.272	0.539	180
26185821	169	85.7	0.42	0.273	0.57	172
7209247	168	85.5	0.43	0.283	0.527	184
7209257	166	84.4	0.49	0.303	0.549	142
147883552	160	80.8	0.77	0.283	0.5	180

Full-length FASTA matches for Cruciferin BnC1

NCBI-GI	opt	z-sc	E(72)	%_id	%_sim	alen
736319	207	101	0.059	0.3	0.529	227
117650782	200	97.8	0.088	0.333	0.519	156
118772075	152	92.3	0.18	0.364	0.533	165
146261042	174	85.9	0.41	0.304	0.571	217
294719862	168	80.9	0.76	0.333	0.549	162
114842970	168	80.7	0.78	0.311	0.541	183
262070686	134	79.6	0.9	0.395	0.579	76

Full-length FASTA matches for Oleosin S2-2

No full-length FASTA matches from the FARRP Celiac Disease protein dataset were found with the E-value < 1 criterion were found.

Full-length FASTA matches for Napin-3

NCBI-GI	opt	z-sc	E(72)	%_id	%_sim	alen
166557	138	82.2	0.65	0.297	0.532	111
75107166	132	80.8	0.77	0.32	0.53	100

Full-length FASTA matches for Squalene monooxygenase 1,2

No full-length FASTA matches from the FARRP Celiac Disease protein dataset were found with the E-value < 1 criterion were found.

3.8 BLASTP matches from the NCBI-NR database

For all the query sequences together, there were 447 distinct NCBI protein hits found with the E-value < 0.05 criterion. Of these, ten proteins were part of the FARRP allergenic protein database and were already found in during the searches against the FARRP database (NCBI Accession numbers: AAX77383.1, AAX77384.1, CAA62908.1, CAA62909.1, CAA62910.1, CAA62911.1, CAA62912.1, P15322.2, P80207.1, and P80208.1). Of the rest of the 437 NCBI proteins that were homologous to the query proteins, majority were hypothetical proteins, or proteins without a known function assigned. In particular, the BLAST search results against NCBI did not find associations with any allergens not already found in the search against the FARRP database.

Query sequence	Hit (NCBI) Accession	Percent identity	E-value	NCBI Gene Title	Update date
2SS3_BRANA	CAG7884491.1	63.281	7.16E-45	unnamed protein product [Brassica rapa]	13/07/2021
2SS3_BRANA	CAG7887786.1	87.234	4.58E-78	unnamed protein product [Brassica rapa]	13/07/2021
2SS3_BRANA	CAG7887789.1	82.979	8.23E-66	unnamed protein product [Brassica rapa]	13/07/2021
2SS3_BRANA	CAG7887791.1	77.857	1.18E-58	unnamed protein product [Brassica rapa]	13/07/2021
2SS3_BRANA	CAG7898617.1	55.97	1.56E-38	unnamed protein product [Brassica rapa]	13/07/2021
2SS3_BRANA	P15322.2	81.944	2.86E-62	RecName: Full=Allergen Sin a 1; AltName: Full=Allergen Sin a I; AltName: Allergen=Sin a 1; Contains: RecName: Full=Allergen Sin a 1 small chain; Contains: RecName: Full=Allergen Sin a 1 large chain; Flags: Precursor	02/06/2021
2SS3_BRANA	P38057.1	84.496	3.47E-59	RecName: Full=Trypsin inhibitor; AltName: Full=TISA; Contains: RecName: Full=Trypsin inhibitor small chain; Contains: RecName: Full=Trypsin inhibitor large chain	02/06/2021
2SS3_BRANA	P80207.1	82.171	1.76E-49	RecName: Full=Allergen Bra j 1-E; AltName: Full=Allergen Bra j I; AltName: Allergen=Bra j 1-E; Contains: RecName: Full=Allergen Bra j 1-E small chain; Contains: RecName: Full=Allergen Bra j 1-E large chain	02/06/2021
2SS3_BRANA	WP_159188241.1	79.104	1.54E-56	alpha-amylase inhibitor/seed storage family protein, partial [Klebsiella pneumoniae]	16/05/2021
2SS3_BRANA	P01091.1	74.627	2.29E-52	RecName: Full=Napin-1; AltName: Full=1.7S seed storage protein; Contains: RecName: Full=Napin-1 small chain; Contains: RecName: Full=Napin-1 large chain; Flags: Precursor	07/04/2021
2SS3_BRANA	P80208.1	100	6.35E-82	RecName: Full=Napin-3; AltName: Full=1.7S seed storage protein; AltName: Full=Napin BnIII; AltName: Full=Napin nIII; Contains: RecName: Full=Napin-3 small chain; Contains: RecName: Full=Napin-3 large chain	07/04/2021
2SS3_BRANA	KAG5414099.1	77.372	5.09E-60	hypothetical protein IGI04_001666 [Brassica rapa subsp. trilocularis]	30/03/2021
2SS3_BRANA	KAG5414099.1	80.469	7.53E-59	hypothetical protein IGI04_001666 [Brassica rapa subsp. trilocularis]	30/03/2021
2SS3_BRANA	KAG5414099.1	84.722	1.84E-71	hypothetical protein IGI04_001666 [Brassica rapa subsp. trilocularis]	30/03/2021
2SS3_BRANA	KAG5414331.1	80.142	1.48E-62	hypothetical protein IGI04_001898 [Brassica rapa subsp. trilocularis]	30/03/2021
2SS3_BRANA	CAF2150198.1	77.465	2.60E-59	unnamed protein product [Brassica napus]	05/03/2021
2SS3_BRANA	CAF2245202.1	55.97	2.15E-38	unnamed protein product [Brassica napus]	05/03/2021
2SS3_BRANA	KAG2248443.1	78.417	2.81E-59	hypothetical protein Bca52824_088071 [Brassica carinata]	29/01/2021
2SS3_BRANA	KAG2248447.1	84.722	1.10E-75	hypothetical protein Bca52824_088075 [Brassica carinata]	29/01/2021
2SS3_BRANA	KAG2248450.1	86.525	3.30E-77	hypothetical protein Bca52824_088078 [Brassica carinata]	29/01/2021
2SS3_BRANA	KAG2248451.1	77.477	9.02E-42	hypothetical protein Bca52824_088079 [Brassica carinata]	29/01/2021
2SS3_BRANA	KAG2248453.1	82.883	2.27E-52	hypothetical protein Bca52824_088081 [Brassica carinata]	29/01/2021
2SS3_BRANA	KAG2319316.1	62.308	2.91E-42	hypothetical protein Bca52824_012529 [Brassica carinata]	29/01/2021
2SS3_BRANA	KAG2239066.1	78.014	6.99E-62	hypothetical protein Bca52824_089926 [Brassica carinata]	28/01/2021

2SS3_BRANA	KAG2245378.1	73.427	2.46E-55	hypothetical protein Bca52824_092802 [Brassica carinata]	28/01/2021
2SS3_BRANA	KAG2245379.1	72.917	1.30E-56	hypothetical protein Bca52824_092803 [Brassica carinata]	28/01/2021
2SS3_BRANA	KAG2245382.1	75	4.16E-58	hypothetical protein Bca52824_092806 [Brassica carinata]	28/01/2021
2SS3_BRANA	XP_009131634.2	73.427	1.54E-53	napin embryo-specific [Brassica rapa]	07/12/2020
2SS3_BRANA	XP_009137640.1	63.281	3.30E-44	napin-B-like [Brassica rapa]	07/12/2020
2SS3_BRANA	XP_009143128.1	86.525	1.34E-77	napin [Brassica rapa]	07/12/2020
2SS3_BRANA	XP_009143139.1	77.622	3.81E-59	napin-like [Brassica rapa]	07/12/2020
2SS3_BRANA	XP_009143149.2	84.722	1.48E-75	napin-like [Brassica rapa]	07/12/2020
2SS3_BRANA	XP_009143159.1	82.979	9.60E-66	napin-like [Brassica rapa]	07/12/2020
2SS3_BRANA	XP_009143171.2	82.979	7.06E-66	napin-like [Brassica rapa]	07/12/2020
2SS3_BRANA	XP_009145761.1	80.851	1.35E-62	napin-B [Brassica rapa]	07/12/2020
2SS3_BRANA	XP_033133133.1	55.97	1.04E-38	napin-B-like [Brassica rapa]	07/12/2020
2SS3_BRANA	P09893.1	65.517	4.17E-47	RecName: Full=Napin embryo-specific; AltName: Full=1.7S seed storage protein; Contains: RecName: Full=Napin embryo-specific small chain; Contains: RecName: Full=Napin embryo-specific large chain; Flags: Precursor	02/12/2020
2SS3_BRANA	KAF8093902.1	76.429	1.20E-59	hypothetical protein N665_0375s0019 [Sinapis alba]	22/10/2020
2SS3_BRANA	KAF8094368.1	60.769	7.81E-45	hypothetical protein N665_0365s0054 [Sinapis alba]	22/10/2020
2SS3_BRANA	KAF8114599.1	78.472	9.06E-62	hypothetical protein N665_0036s0123 [Sinapis alba]	22/10/2020
2SS3_BRANA	KAF8114601.1	77.778	1.28E-60	hypothetical protein N665_0036s0125 [Sinapis alba]	22/10/2020
2SS3_BRANA	KAF8114602.1	82.639	1.20E-64	hypothetical protein N665_0036s0126 [Sinapis alba]	22/10/2020
2SS3_BRANA	KAF8114603.1	81.25	1.63E-64	hypothetical protein N665_0036s0127 [Sinapis alba]	22/10/2020
2SS3_BRANA	KAF8114604.1	77.193	2.22E-40	hypothetical protein N665_0036s0128 [Sinapis alba]	22/10/2020
2SS3_BRANA	KAF8114606.1	81.944	4.07E-65	hypothetical protein N665_0036s0130 [Sinapis alba]	22/10/2020
2SS3_BRANA	KAF3489542.1	85.496	2.30E-68	hypothetical protein F2Q69_00052222 [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF3501402.1	94.444	1.21E-64	hypothetical protein F2Q69_00041762, partial [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF3505652.1	77.477	1.89E-40	hypothetical protein F2Q69_00008109 [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF3533809.1	79.433	1.09E-59	hypothetical protein DY000_02038913 [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF3533809.1	71.942	3.11E-49	hypothetical protein DY000_02038913 [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF3540886.1	84.028	3.37E-74	hypothetical protein F2Q69_00019398 [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF3543628.1	71.918	6.01E-50	hypothetical protein DY000_02000764 [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF3601452.1	82.27	1.48E-64	hypothetical protein F2Q69_00034152 [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF3601461.1	76.429	6.05E-62	hypothetical protein F2Q69_00034154 [Brassica cretica]	24/03/2020
2SS3_BRANA	KAF2550171.1	95.455	1.92E-50	hypothetical protein F2Q68_00033573 [Brassica cretica]	21/02/2020

2SS3_BRANA	P01090.2	80.282	4.57E-63	RecName: Full=Napin-2; AltName: Full=1.7S seed storage protein; Contains: RecName: Full=Napin-2 small chain; Contains: RecName: Full=Napin-2 large chain; Flags: Precursor	11/12/2019
2SS3_BRANA	P27740.1	78.723	1.54E-61	RecName: Full=Napin-B; AltName: Full=1.7S seed storage protein; Contains: RecName: Full=Napin-B small chain; Contains: RecName: Full=Napin-B large chain; Flags: Precursor	11/12/2019
2SS3_BRANA	VDC75280.1	82.979	1.44E-65	unnamed protein product [Brassica rapa]	16/11/2018
2SS3_BRANA	VDD49875.1	80.42	5.91E-62	unnamed protein product [Brassica oleracea]	16/11/2018
2SS3_BRANA	VDD49877.1	80.42	5.97E-62	unnamed protein product [Brassica oleracea]	16/11/2018
2SS3_BRANA	RID78909.1	80.702	1.02E-50	hypothetical protein BRARA_A01689 [Brassica rapa]	13/09/2018
2SS3_BRANA	XP_013681845.1	72.603	4.76E-51	napin embryo-specific-like [Brassica napus]	04/10/2017
2SS3_BRANA	XP_013688210.1	80.282	5.39E-63	napin-2 [Brassica napus]	04/10/2017
2SS3_BRANA	XP_013708806.1	55.97	1.70E-38	napin-B-like [Brassica napus]	04/10/2017
2SS3_BRANA	XP_013729988.1	72.603	7.45E-51	napin embryo-specific [Brassica napus]	04/10/2017
2SS3_BRANA	XP_013738176.1	63.281	7.46E-45	napin-B-like [Brassica napus]	04/10/2017
2SS3_BRANA	XP_013742722.1	76.429	1.26E-61	napin-like [Brassica napus]	04/10/2017
2SS3_BRANA	XP_013743463.1	79.433	1.54E-61	napin-B [Brassica napus]	04/10/2017
2SS3_BRANA	CDY29278.1	78.723	1.12E-63	BnaC01g19300D [Brassica napus]	12/07/2017
2SS3_BRANA	CDY29280.1	80.142	1.22E-64	BnaC01g19320D [Brassica napus]	12/07/2017
2SS3_BRANA	CDY29281.1	77.857	2.48E-62	BnaC01g19330D [Brassica napus]	12/07/2017
2SS3_BRANA	XP_018453699.1	76.642	4.07E-57	PREDICTED: napin-2 [Raphanus sativus]	04/10/2016
2SS3_BRANA	XP_018469054.1	74.815	2.37E-59	PREDICTED: napin-like [Raphanus sativus]	04/10/2016
2SS3_BRANA	XP_018469273.1	74.126	1.82E-56	PREDICTED: napin-like [Raphanus sativus]	04/10/2016
2SS3_BRANA	XP_018469298.1	79.412	3.51E-59	PREDICTED: napin-like [Raphanus sativus]	04/10/2016
2SS3_BRANA	XP_018469309.1	74.648	1.71E-56	PREDICTED: napin [Raphanus sativus]	04/10/2016
2SS3_BRANA	XP_018469312.1	75.735	3.09E-60	PREDICTED: napin-like [Raphanus sativus]	04/10/2016
2SS3_BRANA	XP_018481895.1	76.119	3.35E-55	PREDICTED: napin-like [Raphanus sativus]	04/10/2016
2SS3_BRANA	CAA62908.1	78.472	2.45E-60	allergen sin a 1.0108, partial [Sinapis alba]	14/07/2016
2SS3_BRANA	CAA62909.1	80.556	6.86E-61	allergen sin a 1.0104, partial [Sinapis alba]	14/07/2016
2SS3_BRANA	CAA62910.1	81.944	7.76E-64	allergen sin a 1.0105, partial [Sinapis alba]	14/07/2016
2SS3_BRANA	CAA62911.1	79.167	7.17E-61	allergen sin a 1.0106, partial [Sinapis alba]	14/07/2016
2SS3_BRANA	CAA62912.1	81.944	1.37E-63	allergen sin a 1.0107, partial [Sinapis alba]	14/07/2016
2SS3_BRANA	XP_013588759.1	75.714	4.59E-61	PREDICTED: napin-like [Brassica oleracea var. oleracea]	25/08/2015
2SS3_BRANA	XP_013589349.1	81.119	7.52E-62	PREDICTED: napin-like [Brassica oleracea var. oleracea]	25/08/2015

2SS3_BRANA	XP_013592507.1	86.525	3.09E-77	PREDICTED: napin [Brassica oleracea var. oleracea]	25/08/2015
2SS3_BRANA	XP_013621452.1	80.142	3.25E-62	PREDICTED: napin-2 [Brassica oleracea var. oleracea]	25/08/2015
2SS3_BRANA	XP_013623354.1	72.414	4.09E-51	PREDICTED: napin embryo-specific [Brassica oleracea var. oleracea]	25/08/2015
2SS3_BRANA	CAA32653.1	78.873	3.90E-61	unnamed protein product [Brassica napus]	18/04/2005
2SS3_BRANA	CAA46171.1	78.723	5.66E-61	2S storage protein [Brassica rapa]	18/04/2005
2SS3_BRANA	CAA46172.1	78.723	1.20E-60	2S storage protein [Brassica oleracea]	18/04/2005
2SS3_BRANA	CAA46173.1	75.887	7.71E-62	2S storage protein [Brassica nigra]	18/04/2005
2SS3_BRANA	CAA52813.1	84.173	1.89E-58	2S storage prepropeptide [Brassica carinata]	18/04/2005
2SS3_BRANA	AAS68184.1	86.517	8.56E-38	napin 1.7S, partial [Brassica napus var. napus]	24/03/2004
2SS3_BRANA	AAB37413.1	88.636	1.75E-37	napin large chain L1a=calmodulin antagonist/calcium-dependent protein kinase substrate [Brassica napus=kohlrabi, rapifera, seeds, Peptide, 86 aa]	03/12/1996
2SS3_BRANA	AAB37414.1	82.558	2.88E-37	napin large chain L1B=calmodulin antagonist/calcium-dependent protein kinase substrate [Brassica napus=kohlrabi, rapifera, seeds, Peptide, 88 aa]	03/12/1996
2SS3_BRANA	AAB37416.1	97.727	9.28E-52	napin large chain L2A=calmodulin antagonist/calcium-dependent protein kinase substrate [Brassica napus=kohlrabi, rapifera, seeds, Peptide, 88 aa]	03/12/1996
2SS3_BRANA	AAA63470.1	78.832	1.94E-56	storage protein, partial [Raphanus sativus]	07/03/1995
2SS3_BRANA	AAA63471.1	72.028	4.67E-52	storage protein, partial [Raphanus sativus]	07/03/1995
2SS3_BRANA	AAA63472.1	74.126	3.40E-56	storage protein, partial [Raphanus sativus]	07/03/1995
2SS3_BRANA	AAA32998.1	72.727	9.81E-54	napin [Brassica rapa subsp. oleifera]	12/08/1993
2SS3_BRANA	CAA46174.1	78.873	1.02E-61	2S storage protein [Brassica juncea]	06/08/1992
2SS3_BRANA	AAA33006.1	80.282	5.51E-63	napin prepropeptide [Brassica napus]	07/11/1984
CRU1_BRANA	CAG78733300.1	97.143	0	unnamed protein product [Brassica rapa]	13/07/2021
CRU1_BRANA	CAG78945591.1	88.98	0	unnamed protein product [Brassica rapa]	13/07/2021
CRU1_BRANA	KAG7591037.1	69.388	0	Cupin 1 [Arabidopsis thaliana x Arabidopsis arenosa]	13/07/2021
CRU1_BRANA	KAG7604853.1	79.01	0	RmlC-like cupin domain superfamily [Arabidopsis thaliana x Arabidopsis arenosa]	13/07/2021
CRU1_BRANA	KAG7612221.1	79.283	0	Cupin 1 [Arabidopsis suecica]	13/07/2021
CRU1_BRANA	KAG7652970.1	68.367	0	RmlC-like cupin domain superfamily [Arabidopsis suecica]	13/07/2021
CRU1_BRANA	KAG7532809.1	77.014	0	Cupin 1 [Arabidopsis thaliana x Arabidopsis arenosa]	12/07/2021
CRU1_BRANA	KAG7536518.1	76.654	0	RmlC-like cupin domain superfamily [Arabidopsis suecica]	12/07/2021
CRU1_BRANA	P11090.1	98.776	0	RecName: Full=Cruciferin; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin subunit alpha; Contains: RecName: Full=Cruciferin subunit beta; Flags: Precursor	02/06/2021
CRU1_BRANA	P33522.1	69.002	0	RecName: Full=Cruciferin CRU4; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin	02/06/2021

				CRU4 alpha chain; Contains: RecName: Full=Cruciferin CRU4 beta chain; Flags: Precursor	
CRU1_BRANA	P33523.2	100	0	RecName: Full=Cruciferin BnC1; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin BnC1 subunit alpha; Contains: RecName: Full=Cruciferin BnC1 subunit beta; Flags: Precursor	02/06/2021
CRU1_BRANA	P33524.2	86.29	0	RecName: Full=Cruciferin BnC2; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin BnC2 subunit alpha; Contains: RecName: Full=Cruciferin BnC2 subunit beta; Flags: Precursor	02/06/2021
CRU1_BRANA	Q02498.1	55.645	1.73E-180	RecName: Full=Cruciferin PGCRURSE5; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin PGCRURSE5 alpha chain; Contains: RecName: Full=Cruciferin PGCRURSE5 beta chain; Flags: Precursor	02/06/2021
CRU1_BRANA	KAG5374765.1	67.835	0	hypothetical protein IGI04_039361 [Brassica rapa subsp. trilocularis]	30/03/2021
CRU1_BRANA	KAG5395280.1	97.551	0	hypothetical protein IGI04_025243 [Brassica rapa subsp. trilocularis]	30/03/2021
CRU1_BRANA	KAG5411171.1	81.02	0	hypothetical protein IGI04_007490 [Brassica rapa subsp. trilocularis]	30/03/2021
CRU1_BRANA	CAF2091563.1	97.551	0	unnamed protein product [Brassica napus]	05/03/2021
CRU1_BRANA	CAF2310147.1	67.629	0	unnamed protein product [Brassica napus]	05/03/2021
CRU1_BRANA	CAE5956469.1	68.367	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021
CRU1_BRANA	CAE6221440.1	76.163	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021
CRU1_BRANA	CAE6221461.1	77.912	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021
CRU1_BRANA	KAG2262042.1	90.816	0	hypothetical protein Bca52824_069121 [Brassica carinata]	29/01/2021
CRU1_BRANA	KAG2267406.1	68.79	0	hypothetical protein Bca52824_061961 [Brassica carinata]	29/01/2021
CRU1_BRANA	KAG2301891.1	88.163	0	hypothetical protein Bca52824_030542 [Brassica carinata]	29/01/2021
CRU1_BRANA	XP_009101736.1	97.143	0	cruciferin BnC1 [Brassica rapa]	07/12/2020
CRU1_BRANA	XP_009119353.1	67.629	0	cruciferin CRU4 [Brassica rapa]	07/12/2020
CRU1_BRANA	XP_009123931.2	88.391	0	cruciferin BnC2 [Brassica rapa]	07/12/2020
CRU1_BRANA	3KGL_A	99.358	0	Chain A, Cruciferin	01/12/2020
CRU1_BRANA	KAF8093127.1	87.551	0	hypothetical protein N665_0390s0034 [Sinapis alba]	22/10/2020
CRU1_BRANA	KAF8104437.1	90.447	0	hypothetical protein N665_0172s0067 [Sinapis alba]	22/10/2020
CRU1_BRANA	KAF8111721.1	69.492	0	hypothetical protein N665_0073s0077 [Sinapis alba]	22/10/2020
CRU1_BRANA	CAD5333907.1	78.812	0	unnamed protein product [Arabidopsis thaliana]	11/09/2020
CRU1_BRANA	KAF3486646.1	90.403	0	hypothetical protein F2Q69_00055158 [Brassica cretica]	24/03/2020
CRU1_BRANA	KAF3596484.1	98.98	0	hypothetical protein DY000_02024393 [Brassica cretica]	24/03/2020
CRU1_BRANA	KAF2534322.1	98.876	0	hypothetical protein F2Q70_00031286 [Brassica cretica]	21/02/2020

CRU1_BRANA	KAF2549000.1	69.002	0	hypothetical protein F2Q70_00019310 [Brassica cretica]	21/02/2020
CRU1_BRANA	KAF2550280.1	99.235	0	hypothetical protein F2Q68_00035701 [Brassica cretica]	21/02/2020
CRU1_BRANA	CAA7017480.1	82.653	0	unnamed protein product [Microthlaspi erraticum]	18/01/2020
CRU1_BRANA	CAA7017481.1	83.806	0	unnamed protein product [Microthlaspi erraticum]	18/01/2020
CRU1_BRANA	CAA0407416.1	78.854	0	unnamed protein product [Arabidopsis thaliana]	12/12/2019
CRU1_BRANA	VYS69229.1	78.812	0	unnamed protein product [Arabidopsis thaliana]	12/11/2019
CRU1_BRANA	VVA89872.1	69.043	0	unnamed protein product [Arabis nemorensis]	06/08/2019
CRU1_BRANA	VVB07153.1	76.846	0	unnamed protein product [Arabis nemorensis]	06/08/2019
CRU1_BRANA	NP_001289907.1	81.174	0	uncharacterized protein LOC104725055 precursor [Camelina sativa]	05/05/2019
CRU1_BRANA	NP_001289908.1	68.367	0	12S seed storage protein CRB precursor [Camelina sativa]	05/05/2019
CRU1_BRANA	NP_001289909.1	67.959	0	uncharacterized protein LOC104754510 precursor [Camelina sativa]	05/05/2019
CRU1_BRANA	NP_171884.1	68.367	0	cruciferin 2 [Arabidopsis thaliana]	14/02/2019
CRU1_BRANA	NP_199225.1	78.812	0	RmlC-like cupins superfamily protein [Arabidopsis thaliana]	14/02/2019
CRU1_BRANA	NP_851128.1	77.556	0	RmlC-like cupins superfamily protein [Arabidopsis thaliana]	14/02/2019
CRU1_BRANA	VDD24973.1	90.657	0	unnamed protein product [Brassica oleracea]	16/11/2018
CRU1_BRANA	RID60621.1	97.347	0	hypothetical protein BRARA_F03764 [Brassica rapa]	13/09/2018
CRU1_BRANA	RID75743.1	82.041	0	hypothetical protein BRARA_B02771 [Brassica rapa]	13/09/2018
CRU1_BRANA	XP_006403137.1	82.317	0	cruciferin BnC1 isoform X3 [Eutrema salsugineum]	26/02/2018
CRU1_BRANA	XP_006403138.1	80.612	0	cruciferin BnC1 isoform X1 [Eutrema salsugineum]	26/02/2018
CRU1_BRANA	XP_006418193.1	68	0	12S seed storage protein CRB [Eutrema salsugineum]	26/02/2018
CRU1_BRANA	XP_024013253.1	81.837	0	cruciferin BnC1 isoform X2 [Eutrema salsugineum]	26/02/2018
CRU1_BRANA	XP_006279075.1	80.285	0	12S seed storage protein CRA1 isoform X1 [Capsella rubella]	02/02/2018
CRU1_BRANA	XP_006281468.1	80.285	0	12S seed storage protein CRA1 [Capsella rubella]	02/02/2018
CRU1_BRANA	XP_006282361.1	79.878	0	12S seed storage protein CRA1 [Capsella rubella]	02/02/2018
CRU1_BRANA	XP_006303676.1	68.776	0	12S seed storage protein CRB [Capsella rubella]	02/02/2018
CRU1_BRANA	XP_023634754.1	80.081	0	12S seed storage protein CRA1 isoform X2 [Capsella rubella]	02/02/2018
CRU1_BRANA	XP_013703356.1	87.903	0	cruciferin BnC2 [Brassica napus]	04/10/2017
CRU1_BRANA	XP_013706380.1	97.143	0	cruciferin [Brassica napus]	04/10/2017
CRU1_BRANA	XP_013734592.1	56.653	9.59E-180	cruciferin CRU1-like [Brassica napus]	04/10/2017
CRU1_BRANA	XP_022557043.1	99.388	0	cruciferin BnC1 [Brassica napus]	04/10/2017
CRU1_BRANA	CDY14908.1	86.735	0	BnaA02g22500D [Brassica napus]	12/07/2017
CRU1_BRANA	CDY18193.1	67.728	0	BnaC05g02160D [Brassica napus]	12/07/2017
CRU1_BRANA	CDY22309.1	93.265	0	BnaA06g36310D [Brassica napus]	12/07/2017

CRU1_BRANA	CDY38381.1	55.04	1.12E-179	BnaC01g09900D [Brassica napus]	12/07/2017
CRU1_BRANA	XP_002889479.1	68.571	0	12S seed storage protein CRB [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU1_BRANA	XP_020889541.1	78.02	0	12S seed storage protein CRA1 [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU1_BRANA	XP_020889551.1	74.038	0	LOW QUALITY PROTEIN: 12S seed storage protein CRA1-like [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU1_BRANA	XP_010441951.1	81.174	0	PREDICTED: 12S seed storage protein CRA1 [Camelina sativa]	29/11/2016
CRU1_BRANA	XP_010457405.1	68.98	0	PREDICTED: 12S seed storage protein CRB isoform X1 [Camelina sativa]	29/11/2016
CRU1_BRANA	XP_010481774.1	79.837	0	PREDICTED: 12S seed storage protein CRA1-like [Camelina sativa]	29/11/2016
CRU1_BRANA	XP_010482688.1	64.95	0	PREDICTED: 12S seed storage protein CRB-like [Camelina sativa]	29/11/2016
CRU1_BRANA	XP_010522580.1	66.004	0	PREDICTED: 12S seed storage protein CRB-like [Tarenaya hassleriana]	18/11/2016
CRU1_BRANA	XP_010556853.2	64.741	0	PREDICTED: 12S seed storage protein CRA1-like [Tarenaya hassleriana]	18/11/2016
CRU1_BRANA	XP_018449576.1	69.133	0	PREDICTED: cruciferin CRU4 [Raphanus sativus]	04/10/2016
CRU1_BRANA	XP_018469192.1	56.653	0	PREDICTED: cruciferin PGCRURSE5 [Raphanus sativus]	04/10/2016
CRU1_BRANA	XP_018484881.1	92.857	0	PREDICTED: cruciferin BnC1 isoform X1 [Raphanus sativus]	04/10/2016
CRU1_BRANA	XP_018484882.1	90.204	0	PREDICTED: cruciferin BnC1 isoform X2 [Raphanus sativus]	04/10/2016
CRU1_BRANA	XP_018484883.1	89.388	0	PREDICTED: cruciferin BnC1 isoform X3 [Raphanus sativus]	04/10/2016
CRU1_BRANA	ABD14346.1	97.089	0	cruciferin-like protein, partial [Brassica napus]	26/07/2016
CRU1_BRANA	CAA40980.1	68.119	0	cruciferin cru4 subunit, partial [Brassica napus]	26/07/2016
CRU1_BRANA	BAC80213.1	94.433	0	cruciferin, partial [Brassica napus]	25/07/2016
CRU1_BRANA	OAO92112.1	79.01	0	CRU1 [Arabidopsis thaliana]	25/05/2016
CRU1_BRANA	XP_013585668.1	69.002	0	PREDICTED: cruciferin CRU4 [Brassica oleracea var. oleracea]	25/08/2015
CRU1_BRANA	XP_013596349.1	99.184	0	PREDICTED: cruciferin BnC1 [Brassica oleracea var. oleracea]	25/08/2015
CRU1_BRANA	KFK29566.1	79.125	0	hypothetical protein AALP_AA7G151400 [Arabis alpina]	21/08/2014
CRU1_BRANA	KFK31664.1	74.903	0	hypothetical protein AALP_AA6G142800 [Arabis alpina]	21/08/2014
CRU1_BRANA	KFK42731.1	67.635	0	hypothetical protein AALP_AA1G032400 [Arabis alpina]	21/08/2014
CRU1_BRANA	AFQ32289.1	80.972	0	12S seed storage protein [Camelina sativa]	27/08/2012
CRU1_BRANA	AFQ32291.1	80.567	0	12S seed storage protein [Camelina sativa]	27/08/2012
CRU1_BRANA	AFQ32292.1	80.769	0	12S seed storage protein [Camelina sativa]	27/08/2012
CRU1_BRANA	AAA32777.1	78.812	0	12S storage protein CRA1 [Arabidopsis thaliana]	06/08/1990
CRU1_BRANA	AAA32778.1	68.163	0	12S storage protein CRB [Arabidopsis thaliana]	06/08/1990
CRU1_BRANA	AAA32988.1	99.184	0	cruciferin precursor [Brassica napus]	15/03/1989
CRU3_BRANA	CAG787330 0.1	58.599	1.43E-179	unnamed protein product [Brassica rapa]	13/07/2021
CRU3_BRANA	CAG789459 1.1	56.4	4.44E-179	unnamed protein product [Brassica rapa]	13/07/2021

CRU3_BRANA	CAG7898569.1	84.54	0	unnamed protein product [Brassica rapa]	13/07/2021
CRU3_BRANA	KAG7604853.1	54	0	RmlC-like cupin domain superfamily [Arabidopsis thaliana x Arabidopsis arenosa]	13/07/2021
CRU3_BRANA	KAG7612221.1	53.8	0	Cupin 1 [Arabidopsis suecica]	13/07/2021
CRU3_BRANA	KAG7536518.1	54.812	1.21E-176	RmlC-like cupin domain superfamily [Arabidopsis suecica]	12/07/2021
CRU3_BRANA	KAG7541137.1	82.812	0	RmlC-like cupin domain superfamily [Arabidopsis thaliana x Arabidopsis arenosa]	12/07/2021
CRU3_BRANA	KAG7545843.1	81.238	0	Cupin 1 [Arabidopsis suecica]	12/07/2021
CRU3_BRANA	P33523.2	58.686	3.08E-180	RecName: Full=Cruciferin BnC1; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin BnC1 subunit alpha; Contains: RecName: Full=Cruciferin BnC1 subunit beta; Flags: Precursor	02/06/2021
CRU3_BRANA	P33525.1	100	0	RecName: Full=Cruciferin CRU1; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin CRU1 alpha chain; Contains: RecName: Full=Cruciferin CRU1 beta chain; Flags: Precursor	02/06/2021
CRU3_BRANA	Q02498.1	89.412	0	RecName: Full=Cruciferin PGCRURSE5; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin PGCRURSE5 alpha chain; Contains: RecName: Full=Cruciferin PGCRURSE5 beta chain; Flags: Precursor	02/06/2021
CRU3_BRANA	KAG5395280.1	59.023	1.15E-180	hypothetical protein IGI04_025243 [Brassica rapa subsp. trilocularis]	30/03/2021
CRU3_BRANA	KAG5413258.1	99.411	0	hypothetical protein IGI04_000825 [Brassica rapa subsp. trilocularis]	30/03/2021
CRU3_BRANA	CAF2091563.1	58.599	5.31E-180	unnamed protein product [Brassica napus]	05/03/2021
CRU3_BRANA	CAF2148186.1	99.804	0	unnamed protein product [Brassica napus]	05/03/2021
CRU3_BRANA	CAF2244408.1	84.344	0	unnamed protein product [Brassica napus]	05/03/2021
CRU3_BRANA	CAE6171351.1	82.012	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021
CRU3_BRANA	CAE6221440.1	55.932	1.67E-180	unnamed protein product [Arabidopsis arenosa]	12/02/2021
CRU3_BRANA	KAG2256511.1	79.924	0	hypothetical protein Bca52824_075805 [Brassica carinata]	29/01/2021
CRU3_BRANA	KAG2301891.1	55.2	1.17E-180	hypothetical protein Bca52824_030542 [Brassica carinata]	29/01/2021
CRU3_BRANA	KAG2319363.1	88.845	0	hypothetical protein Bca52824_012576 [Brassica carinata]	29/01/2021
CRU3_BRANA	XP_009101736.1	56.175	0	cruciferin BnC1 [Brassica rapa]	07/12/2020
CRU3_BRANA	XP_009109088.1	84.344	0	cruciferin PGCRURSE5 [Brassica rapa]	07/12/2020
CRU3_BRANA	XP_009123931.2	56.2	4.92E-179	cruciferin BnC2 [Brassica rapa]	07/12/2020
CRU3_BRANA	XP_009129556.1	97.642	0	cruciferin CRU1 [Brassica rapa]	07/12/2020
CRU3_BRANA	3KGL_A	58.65	5.69E-179	Chain A, Cruciferin	01/12/2020
CRU3_BRANA	KAF8093127.1	55.8	5.59E-178	hypothetical protein N665_0390s0034 [Sinapis alba]	22/10/2020
CRU3_BRANA	KAF8094326.1	84.825	0	hypothetical protein N665_0365s0013 [Sinapis alba]	22/10/2020
CRU3_BRANA	KAF8104437.1	59.873	7.36E-179	hypothetical protein N665_0172s0067 [Sinapis alba]	22/10/2020

CRU3_BRANA	KAF8114478.1	85.88	0	hypothetical protein N665_0036s0013 [Sinapis alba]	22/10/2020
CRU3_BRANA	CAD5333907.1	53.8	0	unnamed protein product [Arabidopsis thaliana]	11/09/2020
CRU3_BRANA	KAF3486646.1	55.556	1.12E-177	hypothetical protein F2Q69_00055158 [Brassica cretica]	24/03/2020
CRU3_BRANA	KAF3528743.1	93.883	0	hypothetical protein DY000_02037184, partial [Brassica cretica]	24/03/2020
CRU3_BRANA	KAF3570360.1	77.104	0	hypothetical protein F2Q69_00060459 [Brassica cretica]	24/03/2020
CRU3_BRANA	KAF3596484.1	58.439	8.73E-179	hypothetical protein DY000_02024393 [Brassica cretica]	24/03/2020
CRU3_BRANA	KAF2540365.1	95.294	0	hypothetical protein F2Q68_00029333 [Brassica cretica]	21/02/2020
CRU3_BRANA	KAF2586251.1	93.732	0	hypothetical protein F2Q70_00034448, partial [Brassica cretica]	21/02/2020
CRU3_BRANA	KAF2591500.1	84.736	0	hypothetical protein F2Q70_00039788 [Brassica cretica]	21/02/2020
CRU3_BRANA	CAA7017480.1	54.224	1.35E-178	unnamed protein product [Microthlaspi erraticum]	18/01/2020
CRU3_BRANA	CAA7017481.1	53.2	2.88E-178	unnamed protein product [Microthlaspi erraticum]	18/01/2020
CRU3_BRANA	CAA7050133.1	76.667	0	unnamed protein product [Microthlaspi erraticum]	18/01/2020
CRU3_BRANA	CAA0407416.1	55.417	1.48E-180	unnamed protein product [Arabidopsis thaliana]	12/12/2019
CRU3_BRANA	VYS69229.1	53.438	0	unnamed protein product [Arabidopsis thaliana]	12/11/2019
CRU3_BRANA	VVA89834.1	81.437	0	unnamed protein product [Arabis nemorensis]	06/08/2019
CRU3_BRANA	NP_001289907.1	55.208	0	uncharacterized protein LOC104725055 precursor [Camelina sativa]	05/05/2019
CRU3_BRANA	NP_194581.1	85	0	cruciferin 3 [Arabidopsis thaliana]	14/02/2019
CRU3_BRANA	NP_199225.1	53.242	0	RmlC-like cupins superfamily protein [Arabidopsis thaliana]	14/02/2019
CRU3_BRANA	RID50768.1	83.645	0	hypothetical protein BRARA_H01475, partial [Brassica rapa]	13/09/2018
CRU3_BRANA	RID60621.1	56.773	0	hypothetical protein BRARA_F03764 [Brassica rapa]	13/09/2018
CRU3_BRANA	RID78004.1	98.625	0	hypothetical protein BRARA_A00867 [Brassica rapa]	13/09/2018
CRU3_BRANA	XP_006412944.1	79.846	0	cruciferin PGCRURSE5 [Eutrema salsugineum]	26/02/2018
CRU3_BRANA	XP_024010080.1	89.381	0	LOW QUALITY PROTEIN: cruciferin CRU1 [Eutrema salsugineum]	26/02/2018
CRU3_BRANA	XP_006282820.1	81.25	0	12S seed storage protein CRC [Capsella rubella]	02/02/2018
CRU3_BRANA	XP_013656366.1	84.736	0	cruciferin CRU1-like [Brassica napus]	04/10/2017
CRU3_BRANA	XP_013696793.1	99.607	0	cruciferin CRU1 [Brassica napus]	04/10/2017
CRU3_BRANA	XP_013703356.1	56.859	5.24E-179	cruciferin BnC2 [Brassica napus]	04/10/2017
CRU3_BRANA	XP_013706380.1	58.386	9.37E-180	cruciferin [Brassica napus]	04/10/2017
CRU3_BRANA	XP_013734582.1	94.499	0	cruciferin CRU1-like [Brassica napus]	04/10/2017
CRU3_BRANA	XP_013734592.1	94.695	0	cruciferin CRU1-like [Brassica napus]	04/10/2017
CRU3_BRANA	XP_022557043.1	58.65	8.64E-179	cruciferin BnC1 [Brassica napus]	04/10/2017
CRU3_BRANA	CDY14908.1	54	3.13E-179	BnaA02g22500D [Brassica napus]	12/07/2017
CRU3_BRANA	CDY22309.1	56.476	3.09E-178	BnaA06g36310D [Brassica napus]	12/07/2017

CRU3_BRANA	CDY35196.1	96.071	0	BnaA01g08350D [Brassica napus]	12/07/2017
CRU3_BRANA	CDY38381.1	91.945	0	BnaC01g09900D [Brassica napus]	12/07/2017
CRU3_BRANA	XP_002869496.1	85.546	0	12S seed storage protein CRC isoform X1 [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU3_BRANA	XP_020874599.1	85.546	0	12S seed storage protein CRC isoform X2 [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU3_BRANA	XP_020889541.1	56.809	0	12S seed storage protein CRA1 [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU3_BRANA	XP_010433207.1	78.937	0	PREDICTED: 12S seed storage protein CRC [Camelina sativa]	29/11/2016
CRU3_BRANA	XP_010441951.1	54.812	1.84E-180	PREDICTED: 12S seed storage protein CRA1 [Camelina sativa]	29/11/2016
CRU3_BRANA	XP_010447969.1	79.452	0	PREDICTED: 12S seed storage protein CRC-like [Camelina sativa]	29/11/2016
CRU3_BRANA	XP_010481774.1	53.586	0	PREDICTED: 12S seed storage protein CRA1-like [Camelina sativa]	29/11/2016
CRU3_BRANA	XP_019087322.1	76.641	0	PREDICTED: 12S seed storage protein CRC-like [Camelina sativa]	29/11/2016
CRU3_BRANA	XP_010522580.1	57.265	0	PREDICTED: 12S seed storage protein CRB-like [Tarenaya hassleriana]	18/11/2016
CRU3_BRANA	XP_010555095.1	65.121	0	PREDICTED: cruciferin PGCRURSE5 [Tarenaya hassleriana]	18/11/2016
CRU3_BRANA	XP_010556853.2	55.446	0	PREDICTED: 12S seed storage protein CRA1-like [Tarenaya hassleriana]	18/11/2016
CRU3_BRANA	XP_018469192.1	91.961	0	PREDICTED: cruciferin PGCRURSE5 [Raphanus sativus]	04/10/2016
CRU3_BRANA	XP_018484881.1	57.325	7.63E-178	PREDICTED: cruciferin BnC1 isoform X1 [Raphanus sativus]	04/10/2016
CRU3_BRANA	XP_018484882.1	56.263	6.13E-177	PREDICTED: cruciferin BnC1 isoform X2 [Raphanus sativus]	04/10/2016
CRU3_BRANA	XP_018484883.1	55.839	6.89E-178	PREDICTED: cruciferin BnC1 isoform X3 [Raphanus sativus]	04/10/2016
CRU3_BRANA	ABD14346.1	58.599	2.65E-178	cruciferin-like protein, partial [Brassica napus]	26/07/2016
CRU3_BRANA	BAC80213.1	58.686	4.78E-177	cruciferin, partial [Brassica napus]	25/07/2016
CRU3_BRANA	AAK07609.1	94.303	0	cruciferin subunit [Brassica napus]	14/07/2016
CRU3_BRANA	OAO92112.1	53.438	0	CRU1 [Arabidopsis thaliana]	25/05/2016
CRU3_BRANA	OAO99762.1	85	0	CRU3 [Arabidopsis thaliana]	25/05/2016
CRU3_BRANA	XP_013585447.1	94.706	0	PREDICTED: cruciferin CRU1 [Brassica oleracea var. oleracea]	25/08/2015
CRU3_BRANA	XP_013596349.1	58.65	5.17E-179	PREDICTED: cruciferin BnC1 [Brassica oleracea var. oleracea]	25/08/2015
CRU3_BRANA	XP_013603560.1	81.676	0	PREDICTED: cruciferin CRU1-like isoform X1 [Brassica oleracea var. oleracea]	25/08/2015
CRU3_BRANA	XP_013603561.1	81.8	0	PREDICTED: cruciferin CRU1-like isoform X2 [Brassica oleracea var. oleracea]	25/08/2015
CRU3_BRANA	ESQ37783.1	85.546	0	hypothetical protein EUTSA_v10029458mg [Eutrema salsugineum]	23/03/2015
CRU3_BRANA	KFK29566.1	55.556	1.73E-176	hypothetical protein AALP_AA7G151400 [Arabis alpina]	21/08/2014
CRU3_BRANA	AFQ32289.1	54.812	1.20E-180	12S seed storage protein [Camelina sativa]	27/08/2012
CRU3_BRANA	AFQ32291.1	55.864	1.76E-180	12S seed storage protein [Camelina sativa]	27/08/2012
CRU3_BRANA	AFQ32292.1	54.812	1.20E-180	12S seed storage protein [Camelina sativa]	27/08/2012
CRU3_BRANA	AAX77383.1	86.301	0	11S globulin precursor [Sinapis alba]	24/01/2006
CRU3_BRANA	AAX77384.1	91.765	0	11S globulin precursor [Sinapis alba]	24/01/2006

CRU3_BRANA	AAL91248.1	85	0	AT4g28520/F20O9_210 [Arabidopsis thaliana]	24/03/2002
CRU3_BRANA	AAA32989.1	99.601	0	cruciferin precursor, partial [Brassica napus]	15/09/1990
CRU3_BRANA	AAA32777.1	53.438	0	12S storage protein CRA1 [Arabidopsis thaliana]	06/08/1990
CRU4_BRANA	CAG787 3300.1	69.723	0	unnamed protein product [Brassica rapa]	13/07/2021
CRU4_BRANA	CAG789 4591.1	70.103	0	unnamed protein product [Brassica rapa]	13/07/2021
CRU4_BRANA	KAG759 1037.1	84.749	0	Cupin 1 [Arabidopsis thaliana x Arabidopsis arenosa]	13/07/2021
CRU4_BRANA	KAG760 4853.1	70.921	0	RmlC-like cupin domain superfamily [Arabidopsis thaliana x Arabidopsis arenosa]	13/07/2021
CRU4_BRANA	KAG761 2221.1	71.579	0	Cupin 1 [Arabidopsis suecica]	13/07/2021
CRU4_BRANA	KAG765 2970.1	84.532	0	RmlC-like cupin domain superfamily [Arabidopsis suecica]	13/07/2021
CRU4_BRANA	KAG753 2809.1	68.856	0	Cupin 1 [Arabidopsis thaliana x Arabidopsis arenosa]	12/07/2021
CRU4_BRANA	KAG753 6518.1	68.553	0	RmlC-like cupin domain superfamily [Arabidopsis suecica]	12/07/2021
CRU4_BRANA	KAG754 1137.1	54.397	3.24E-164	RmlC-like cupin domain superfamily [Arabidopsis thaliana x Arabidopsis arenosa]	12/07/2021
CRU4_BRANA	P11090.1	68.565	0	RecName: Full=Cruciferin; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin subunit alpha; Contains: RecName: Full=Cruciferin subunit beta; Flags: Precursor	02/06/2021
CRU4_BRANA	P33522.1	100	0	RecName: Full=Cruciferin CRU4; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin CRU4 alpha chain; Contains: RecName: Full=Cruciferin CRU4 beta chain; Flags: Precursor	02/06/2021
CRU4_BRANA	P33523.2	68.987	0	RecName: Full=Cruciferin BnC1; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin BnC1 subunit alpha; Contains: RecName: Full=Cruciferin BnC1 subunit beta; Flags: Precursor	02/06/2021
CRU4_BRANA	P33524.2	67.886	0	RecName: Full=Cruciferin BnC2; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin BnC2 subunit alpha; Contains: RecName: Full=Cruciferin BnC2 subunit beta; Flags: Precursor	02/06/2021
CRU4_BRANA	Q02498.1	54.957	4.68E-165	RecName: Full=Cruciferin PGCRURSE5; AltName: Full=11S globulin; AltName: Full=12S storage protein; Contains: RecName: Full=Cruciferin PGCRURSE5 alpha chain; Contains: RecName: Full=Cruciferin PGCRURSE5 beta chain; Flags: Precursor	02/06/2021
CRU4_BRANA	KAG537 4765.1	97.849	0	hypothetical protein IGI04_039361 [Brassica rapa subsp. trilocularis]	30/03/2021
CRU4_BRANA	KAG539 5280.1	70.149	0	hypothetical protein IGI04_025243 [Brassica rapa subsp. trilocularis]	30/03/2021
CRU4_BRANA	KAG541 1171.1	62.733	0	hypothetical protein IGI04_007490 [Brassica rapa subsp. trilocularis]	30/03/2021
CRU4_BRANA	CAF2091 563.1	69.723	0	unnamed protein product [Brassica napus]	05/03/2021
CRU4_BRANA	CAF2310 147.1	97.634	0	unnamed protein product [Brassica napus]	05/03/2021
CRU4_BRANA	CAE5956 469.1	84.532	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021

CRU4_BRANA	CAE6221440.1	68.191	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021
CRU4_BRANA	CAE6221461.1	69.247	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021
CRU4_BRANA	KAG2262042.1	72.21	0	hypothetical protein Bca52824_069121 [Brassica carinata]	29/01/2021
CRU4_BRANA	KAG2267406.1	99.14	0	hypothetical protein Bca52824_061961 [Brassica carinata]	29/01/2021
CRU4_BRANA	KAG2301891.1	72.211	0	hypothetical protein Bca52824_030542 [Brassica carinata]	29/01/2021
CRU4_BRANA	XP_009101736.1	69.023	0	cruciferin BnC1 [Brassica rapa]	07/12/2020
CRU4_BRANA	XP_009119353.1	97.634	0	cruciferin CRU4 [Brassica rapa]	07/12/2020
CRU4_BRANA	XP_009123931.2	69.815	0	cruciferin BnC2 [Brassica rapa]	07/12/2020
CRU4_BRANA	3KGL_A	69.528	0	Chain A, Cruciferin	01/12/2020
CRU4_BRANA	KAF8093127.1	71.667	0	hypothetical protein N665_0390s0034 [Sinapis alba]	22/10/2020
CRU4_BRANA	KAF8104437.1	69.895	0	hypothetical protein N665_0172s0067 [Sinapis alba]	22/10/2020
CRU4_BRANA	KAF8111721.1	87.361	0	hypothetical protein N665_0073s0077 [Sinapis alba]	22/10/2020
CRU4_BRANA	CAD5333907.1	71.13	0	unnamed protein product [Arabidopsis thaliana]	11/09/2020
CRU4_BRANA	KAF3486646.1	66.735	0	hypothetical protein F2Q69_00055158 [Brassica cretica]	24/03/2020
CRU4_BRANA	KAF3596484.1	69.556	0	hypothetical protein DY000_02024393 [Brassica cretica]	24/03/2020
CRU4_BRANA	KAF2549000.1	98.925	0	hypothetical protein F2Q70_00019310 [Brassica cretica]	21/02/2020
CRU4_BRANA	KAF2550280.1	69.565	0	hypothetical protein F2Q68_00035701 [Brassica cretica]	21/02/2020
CRU4_BRANA	CAA7017480.1	68.344	0	unnamed protein product [Microthlaspi erraticum]	18/01/2020
CRU4_BRANA	CAA7017481.1	70.878	0	unnamed protein product [Microthlaspi erraticum]	18/01/2020
CRU4_BRANA	CAA0407416.1	70.815	0	unnamed protein product [Arabidopsis thaliana]	12/12/2019
CRU4_BRANA	VYS69229.1	70.921	0	unnamed protein product [Arabidopsis thaliana]	12/11/2019
CRU4_BRANA	VVA89872.1	85.313	0	unnamed protein product [Arabis nemorensis]	06/08/2019
CRU4_BRANA	VVB07153.1	71.215	0	unnamed protein product [Arabis nemorensis]	06/08/2019
CRU4_BRANA	NP_001289907.1	72.185	0	uncharacterized protein LOC104725055 precursor [Camelina sativa]	05/05/2019
CRU4_BRANA	NP_001289908.1	84.052	0	12S seed storage protein CRB precursor [Camelina sativa]	05/05/2019
CRU4_BRANA	NP_001289909.1	82.826	0	uncharacterized protein LOC104754510 precursor [Camelina sativa]	05/05/2019
CRU4_BRANA	NP_171884.1	84.096	0	cruciferin 2 [Arabidopsis thaliana]	14/02/2019
CRU4_BRANA	NP_199225.1	70.921	0	RmlC-like cupins superfamily protein [Arabidopsis thaliana]	14/02/2019
CRU4_BRANA	NP_851128.1	72.222	0	RmlC-like cupins superfamily protein [Arabidopsis thaliana]	14/02/2019
CRU4_BRANA	RID60621.1	69.647	0	hypothetical protein BRARA_F03764 [Brassica rapa]	13/09/2018
CRU4_BRANA	RID75743.1	63.975	0	hypothetical protein BRARA_B02771 [Brassica rapa]	13/09/2018
CRU4_BRANA	XP_006403137.1	73.895	0	cruciferin BnC1 isoform X3 [Eutrema salsugineum]	26/02/2018
CRU4_BRANA	XP_006403138.1	69.502	0	cruciferin BnC1 isoform X1 [Eutrema salsugineum]	26/02/2018

CRU4_BRANA	XP_006418193.1	84.701	0	12S seed storage protein CRB [Eutrema salsugineum]	26/02/2018
CRU4_BRANA	XP_024013253.1	70.208	0	cruciferin BnC1 isoform X2 [Eutrema salsugineum]	26/02/2018
CRU4_BRANA	XP_006279075.1	71.619	0	12S seed storage protein CRA1 isoform X1 [Capsella rubella]	02/02/2018
CRU4_BRANA	XP_006281468.1	71.492	0	12S seed storage protein CRA1 [Capsella rubella]	02/02/2018
CRU4_BRANA	XP_006282361.1	71.175	0	12S seed storage protein CRA1 [Capsella rubella]	02/02/2018
CRU4_BRANA	XP_006303676.1	84.13	0	12S seed storage protein CRB [Capsella rubella]	02/02/2018
CRU4_BRANA	XP_023634754.1	71.492	0	12S seed storage protein CRA1 isoform X2 [Capsella rubella]	02/02/2018
CRU4_BRANA	XP_013703356.1	69.309	0	cruciferin BnC2 [Brassica napus]	04/10/2017
CRU4_BRANA	XP_013706380.1	69.444	0	cruciferin [Brassica napus]	04/10/2017
CRU4_BRANA	XP_013734592.1	54.219	6.49E-164	cruciferin CRU1-like [Brassica napus]	04/10/2017
CRU4_BRANA	XP_022557043.1	69.345	0	cruciferin BnC1 [Brassica napus]	04/10/2017
CRU4_BRANA	CDY14908.1	74.348	0	BnaA02g22500D [Brassica napus]	12/07/2017
CRU4_BRANA	CDY18193.1	97.419	0	BnaC05g02160D [Brassica napus]	12/07/2017
CRU4_BRANA	CDY22309.1	73.378	0	BnaA06g36310D [Brassica napus]	12/07/2017
CRU4_BRANA	CDY35196.1	54.219	1.06E-163	BnaA01g08350D [Brassica napus]	12/07/2017
CRU4_BRANA	CDY38381.1	54.741	5.04E-166	BnaC01g09900D [Brassica napus]	12/07/2017
CRU4_BRANA	XP_002889479.1	84.967	0	12S seed storage protein CRB [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU4_BRANA	XP_020889541.1	70.64	0	12S seed storage protein CRA1 [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU4_BRANA	XP_020889551.1	65.361	0	LOW QUALITY PROTEIN: 12S seed storage protein CRA1-like [Arabidopsis lyrata subsp. lyrata]	11/05/2017
CRU4_BRANA	XP_010441951.1	71.93	0	PREDICTED: 12S seed storage protein CRA1 [Camelina sativa]	29/11/2016
CRU4_BRANA	XP_010457405.1	84.348	0	PREDICTED: 12S seed storage protein CRB isoform X1 [Camelina sativa]	29/11/2016
CRU4_BRANA	XP_010481774.1	70.69	0	PREDICTED: 12S seed storage protein CRA1-like [Camelina sativa]	29/11/2016
CRU4_BRANA	XP_010482688.1	79.749	0	PREDICTED: 12S seed storage protein CRB-like [Camelina sativa]	29/11/2016
CRU4_BRANA	XP_010522580.1	71.824	0	PREDICTED: 12S seed storage protein CRB-like [Tarenaya hassleriana]	18/11/2016
CRU4_BRANA	XP_010556853.2	69.099	0	PREDICTED: 12S seed storage protein CRA1-like [Tarenaya hassleriana]	18/11/2016
CRU4_BRANA	XP_018449576.1	91.435	0	PREDICTED: cruciferin CRU4 [Raphanus sativus]	04/10/2016
CRU4_BRANA	XP_018469192.1	55.437	3.15E-165	PREDICTED: cruciferin PGCRURSE5 [Raphanus sativus]	04/10/2016
CRU4_BRANA	XP_018484881.1	71.674	0	PREDICTED: cruciferin BnC1 isoform X1 [Raphanus sativus]	04/10/2016
CRU4_BRANA	XP_018484882.1	73.111	0	PREDICTED: cruciferin BnC1 isoform X2 [Raphanus sativus]	04/10/2016
CRU4_BRANA	XP_018484883.1	74.33	0	PREDICTED: cruciferin BnC1 isoform X3 [Raphanus sativus]	04/10/2016
CRU4_BRANA	ABD14346.1	69.528	0	cruciferin-like protein, partial [Brassica napus]	26/07/2016
CRU4_BRANA	CAA40980.1	99.516	0	cruciferin cru4 subunit, partial [Brassica napus]	26/07/2016

CRU4_BRANA	BAC80213.1	70.021	0	cruciferin, partial [Brassica napus]	25/07/2016
CRU4_BRANA	OAO92112.1	70.711	0	CRU1 [Arabidopsis thaliana]	25/05/2016
CRU4_BRANA	XP_013585668.1	99.355	0	PREDICTED: cruciferin CRU4 [Brassica oleracea var. oleracea]	25/08/2015
CRU4_BRANA	XP_013596349.1	69.345	0	PREDICTED: cruciferin BnC1 [Brassica oleracea var. oleracea]	25/08/2015
CRU4_BRANA	KFK29566.1	66.467	0	hypothetical protein AALP_AA7G151400 [Arabis alpina]	21/08/2014
CRU4_BRANA	KFK31664.1	62.016	0	hypothetical protein AALP_AA6G142800 [Arabis alpina]	21/08/2014
CRU4_BRANA	KFK42731.1	83.26	0	hypothetical protein AALP_AA1G032400 [Arabis alpina]	21/08/2014
CRU4_BRANA	AFQ32289.1	71.93	0	12S seed storage protein [Camelina sativa]	27/08/2012
CRU4_BRANA	AFQ32291.1	71.586	0	12S seed storage protein [Camelina sativa]	27/08/2012
CRU4_BRANA	AFQ32292.1	71.93	0	12S seed storage protein [Camelina sativa]	27/08/2012
CRU4_BRANA	AAA32777.1	70.502	0	12S storage protein CRA1 [Arabidopsis thaliana]	06/08/1990
CRU4_BRANA	AAA32778.1	83.878	0	12S storage protein CRB [Arabidopsis thaliana]	06/08/1990
CRU4_BRANA	AAA32988.1	68.71	0	cruciferin precursor [Brassica napus]	15/03/1989
ERG12_BRANA	CAG78600213.1	75.723	0	unnamed protein product [Brassica rapa]	13/07/2021
ERG12_BRANA	CAG78701996.1	97.683	0	unnamed protein product [Brassica rapa]	13/07/2021
ERG12_BRANA	CAG78905948.1	81.042	0	unnamed protein product [Brassica rapa]	13/07/2021
ERG12_BRANA	KAG76003285.1	77.756	0	FAD/NAD(P)-binding domain superfamily [Arabidopsis thaliana x Arabidopsis arenosa]	13/07/2021
ERG12_BRANA	KAG76003287.1	76.062	0	FAD/NAD(P)-binding domain superfamily [Arabidopsis thaliana x Arabidopsis arenosa]	13/07/2021
ERG12_BRANA	KAG76100230.1	77.95	0	Squalene epoxidase [Arabidopsis suecica]	13/07/2021
ERG12_BRANA	KAG76100231.1	76.357	0	FAD/NAD(P)-binding domain superfamily [Arabidopsis suecica]	13/07/2021
ERG12_BRANA	KAG75506303.1	77.907	0	Squalene epoxidase [Arabidopsis suecica]	12/07/2021
ERG12_BRANA	KAG53801978.1	75.483	0	hypothetical protein IGI04_033448 [Brassica rapa subsp. trilocularis]	30/03/2021
ERG12_BRANA	KAG54000491.1	74.808	0	hypothetical protein IGI04_015098 [Brassica rapa subsp. trilocularis]	30/03/2021
ERG12_BRANA	KAG54102143.1	76.731	0	hypothetical protein IGI04_008462 [Brassica rapa subsp. trilocularis]	30/03/2021
ERG12_BRANA	KAG54102145.1	80.084	0	hypothetical protein IGI04_008464, partial [Brassica rapa subsp. trilocularis]	30/03/2021
ERG12_BRANA	CAF2016249.1	99.807	0	unnamed protein product [Brassica napus]	05/03/2021
ERG12_BRANA	CAF2036590.1	75.869	0	unnamed protein product [Brassica napus]	05/03/2021
ERG12_BRANA	CAF2088798.1	96.935	0	unnamed protein product [Brassica napus]	05/03/2021
ERG12_BRANA	CAF2144762.1	79.769	0	unnamed protein product [Brassica napus]	05/03/2021
ERG12_BRANA	CAE6117831.1	77.593	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021
ERG12_BRANA	CAE6117855.1	75.769	0	unnamed protein product [Arabidopsis arenosa]	12/02/2021
ERG12_BRANA	KAG23001244.1	78.835	0	hypothetical protein Bca52824_029895 [Brassica carinata]	29/01/2021
ERG12_BRANA	KAG23001245.1	75.816	0	hypothetical protein Bca52824_029896 [Brassica carinata]	29/01/2021

ERG12_BRANA	KAG2316712.1	77.22	0	hypothetical protein Bca52824_019834 [Brassica carinata]	29/01/2021
ERG12_BRANA	KAG2325894.1	74.038	0	hypothetical protein Bca52824_008622 [Brassica carinata]	29/01/2021
ERG12_BRANA	KAG2239599.1	96.388	0	hypothetical protein Bca52824_091557 [Brassica carinata]	28/01/2021
ERG12_BRANA	KAG2240200.1	90.734	0	hypothetical protein Bca52824_090961 [Brassica carinata]	28/01/2021
ERG12_BRANA	NP_001302760.1	74.324	0	squalene monooxygenase 1,1 [Brassica napus]	10/12/2020
ERG12_BRANA	XP_009130083.1	76.731	0	squalene epoxidase 5-like [Brassica rapa]	07/12/2020
ERG12_BRANA	XP_009130084.1	76.525	0	squalene epoxidase 5 isoform X1 [Brassica rapa]	07/12/2020
ERG12_BRANA	XP_009130085.1	79.769	0	squalene epoxidase 5 isoform X2 [Brassica rapa]	07/12/2020
ERG12_BRANA	XP_009130086.1	77.49	0	squalene monooxygenase 1,1 isoform X3 [Brassica rapa]	07/12/2020
ERG12_BRANA	XP_009139532.2	75.385	0	squalene monooxygenase 1,1-like [Brassica rapa]	07/12/2020
ERG12_BRANA	XP_009141944.1	76.062	0	squalene monooxygenase 1,1 [Brassica rapa]	07/12/2020
ERG12_BRANA	XP_009150944.1	97.876	0	squalene monooxygenase 1,2 isoform X1 [Brassica rapa]	07/12/2020
ERG12_BRANA	O65726.1	100	0	RecName: Full=Squalene monooxygenase 1,2; AltName: Full=Squalene epoxidase 1,2; Short=SE 1,2	02/12/2020
ERG12_BRANA	KAF8089972.1	92.471	0	hypothetical protein N665_0493s0027 [Sinapis alba]	22/10/2020
ERG12_BRANA	KAF8097127.1	73.654	0	hypothetical protein N665_0294s0029 [Sinapis alba]	22/10/2020
ERG12_BRANA	KAF8097128.1	77.237	0	hypothetical protein N665_0294s0030 [Sinapis alba]	22/10/2020
ERG12_BRANA	KAF8119094.1	74.808	0	hypothetical protein N665_0001s0146 [Sinapis alba]	22/10/2020
ERG12_BRANA	NP_001302490.2	98.842	0	squalene monooxygenase 1,2 [Brassica napus]	10/10/2020
ERG12_BRANA	CAD5332533.1	76.596	0	unnamed protein product [Arabidopsis thaliana]	11/09/2020
ERG12_BRANA	CAD5332534.1	76.596	0	unnamed protein product [Arabidopsis thaliana]	11/09/2020
ERG12_BRANA	CAD5332535.1	77.597	0	unnamed protein product [Arabidopsis thaliana]	11/09/2020
ERG12_BRANA	KAF3488871.1	98.225	0	hypothetical protein F2Q69_00056431 [Brassica cretica]	24/03/2020
ERG12_BRANA	KAF3559921.1	75.385	0	hypothetical protein F2Q69_00015658 [Brassica cretica]	24/03/2020
ERG12_BRANA	KAF3579688.1	75.192	0	hypothetical protein DY000_02033007 [Brassica cretica]	24/03/2020
ERG12_BRANA	KAF3590675.1	96.139	0	hypothetical protein DY000_02026156 [Brassica cretica]	24/03/2020
ERG12_BRANA	KAF2566527.1	75.385	0	hypothetical protein F2Q68_00026558 [Brassica cretica]	21/02/2020
ERG12_BRANA	KAF2572294.1	75.337	0	hypothetical protein F2Q70_00000426 [Brassica cretica]	21/02/2020
ERG12_BRANA	KAF2595852.1	76.154	0	hypothetical protein F2Q68_00012368 [Brassica cretica]	21/02/2020
ERG12_BRANA	CAA7023367.1	78.035	0	unnamed protein product [Microthlaspi erraticum]	18/01/2020
ERG12_BRANA	CAA0404507.1	77.8	0	unnamed protein product [Arabidopsis thaliana]	12/12/2019
ERG12_BRANA	VYS67761.1	77.563	0	unnamed protein product [Arabidopsis thaliana]	12/11/2019
ERG12_BRANA	VYS67763.1	77.8	0	unnamed protein product [Arabidopsis thaliana]	12/11/2019

ERG12_BRANA	VVB17403.1	73.694	0	unnamed protein product [Arabis nemorensis]	06/08/2019
ERG12_BRANA	NP_001031935.1	77.871	0	FAD/NAD(P)-binding oxidoreductase family protein [Arabidopsis thaliana]	14/02/2019
ERG12_BRANA	NP_197803.1	77.563	0	FAD/NAD(P)-binding oxidoreductase family protein [Arabidopsis thaliana]	14/02/2019
ERG12_BRANA	NP_197804.1	76.448	0	squalene monooxygenase 6 [Arabidopsis thaliana]	14/02/2019
ERG12_BRANA	VDC67882.1	72.621	0	unnamed protein product [Brassica rapa]	16/11/2018
ERG12_BRANA	VDC92827.1	80	0	unnamed protein product [Brassica rapa]	16/11/2018
ERG12_BRANA	VDD10599.1	74.904	0	unnamed protein product [Brassica oleracea]	16/11/2018
ERG12_BRANA	VDD11459.1	75.096	0	unnamed protein product [Brassica rapa]	16/11/2018
ERG12_BRANA	VDD27101.1	75.869	0	unnamed protein product [Brassica oleracea]	16/11/2018
ERG12_BRANA	VDD28326.1	74.857	0	unnamed protein product [Brassica oleracea]	16/11/2018
ERG12_BRANA	RID65464.1	73.654	0	hypothetical protein BRARA_D00655 [Brassica rapa]	13/09/2018
ERG12_BRANA	RID76744.1	76.923	0	hypothetical protein BRARA_B03698 [Brassica rapa]	13/09/2018
ERG12_BRANA	XP_006394673.1	78.42	0	squalene monooxygenase 1,1 [Eutrema salsugineum]	26/02/2018
ERG12_BRANA	XP_006287518.1	75.337	0	squalene epoxidase 5 [Capsella rubella]	02/02/2018
ERG12_BRANA	XP_006290055.2	74.903	0	squalene epoxidase 5 [Capsella rubella]	02/02/2018
ERG12_BRANA	XP_013643445.1	97.683	0	squalene monooxygenase 1,2-like isoform X1 [Brassica napus]	04/10/2017
ERG12_BRANA	XP_013661011.1	76.255	0	squalene monooxygenase 1,1 isoform X1 [Brassica napus]	04/10/2017
ERG12_BRANA	XP_013675367.1	76.062	0	squalene epoxidase 5-like [Brassica napus]	04/10/2017
ERG12_BRANA	XP_013688661.1	75.385	0	squalene monooxygenase 1,1-like [Brassica napus]	04/10/2017
ERG12_BRANA	XP_013700582.1	76.923	0	squalene epoxidase 5-like [Brassica napus]	04/10/2017
ERG12_BRANA	XP_013700587.1	79.769	0	squalene epoxidase 5-like isoform X1 [Brassica napus]	04/10/2017
ERG12_BRANA	XP_013700590.1	79.576	0	squalene epoxidase 5-like isoform X2 [Brassica napus]	04/10/2017
ERG12_BRANA	XP_013700593.1	81.042	0	squalene epoxidase 5-like isoform X3 [Brassica napus]	04/10/2017
ERG12_BRANA	XP_013724652.1	75.915	0	squalene monooxygenase 1,1-like [Brassica napus]	04/10/2017
ERG12_BRANA	XP_022562768.1	99.035	0	squalene monooxygenase 1,2 [Brassica napus]	04/10/2017
ERG12_BRANA	XP_002874173.1	77.132	0	squalene epoxidase 5 [Arabidopsis lyrata subsp. lyrata]	11/05/2017
ERG12_BRANA	XP_002874174.1	76.493	0	squalene epoxidase 6 [Arabidopsis lyrata subsp. lyrata]	11/05/2017
ERG12_BRANA	XP_010421226.1	75.577	0	PREDICTED: squalene epoxidase 5-like isoform X1 [Camelina sativa]	29/11/2016
ERG12_BRANA	XP_010421228.1	75.676	0	PREDICTED: squalene epoxidase 5 [Camelina sativa]	29/11/2016
ERG12_BRANA	XP_010421231.1	77.071	0	PREDICTED: squalene epoxidase 5-like [Camelina sativa]	29/11/2016
ERG12_BRANA	XP_010454706.1	75.385	0	PREDICTED: squalene epoxidase 5 [Camelina sativa]	29/11/2016
ERG12_BRANA	XP_010454707.1	76.062	0	PREDICTED: squalene epoxidase 5-like [Camelina sativa]	29/11/2016
ERG12_BRANA	XP_010454708.1	76.493	0	PREDICTED: squalene epoxidase 5-like [Camelina sativa]	29/11/2016

ERG12_BRANA	XP_010493554.1	76.108	0	PREDICTED: squalene epoxidase 5-like [Camelina sativa]	29/11/2016
ERG12_BRANA	XP_010493555.1	75.962	0	PREDICTED: squalene epoxidase 5 [Camelina sativa]	29/11/2016
ERG12_BRANA	XP_018439095.1	76.923	0	PREDICTED: squalene epoxidase 5-like isoform X1 [Raphanus sativus]	04/10/2016
ERG12_BRANA	XP_018452101.1	76.879	0	PREDICTED: squalene monooxygenase 1,1 [Raphanus sativus]	04/10/2016
ERG12_BRANA	XP_018478606.1	92.278	0	PREDICTED: squalene monooxygenase 1,2 [Raphanus sativus]	04/10/2016
ERG12_BRANA	CAA06772.1	77.476	0	squalene epoxidase homologue, partial [Arabidopsis thaliana]	25/07/2016
ERG12_BRANA	OAO93702.1	76.789	0	hypothetical protein AXX17_AT5G23810 [Arabidopsis thaliana]	25/05/2016
ERG12_BRANA	XP_013599338.1	98.263	0	PREDICTED: squalene monooxygenase 1,2 [Brassica oleracea var. oleracea]	25/08/2015
ERG12_BRANA	XP_013612157.1	76.311	0	PREDICTED: squalene monooxygenase 1,1 [Brassica oleracea var. oleracea]	25/08/2015
ERG12_BRANA	XP_013618804.1	76.062	0	PREDICTED: squalene epoxidase 5-like [Brassica oleracea var. oleracea]	25/08/2015
ERG12_BRANA	XP_013634115.1	75	0	PREDICTED: squalene monooxygenase 1,1-like [Brassica oleracea var. oleracea]	25/08/2015
ERG12_BRANA	EOA22953.1	74.806	0	hypothetical protein CARUB_v10003690mg [Capsella rubella]	21/03/2015
ERG12_BRANA	KFK23559.1	74.038	0	hypothetical protein AALP_AAs41881U000500 [Arabis alpina]	21/08/2014
ERG12_BRANA	KFK27698.1	75	0	hypothetical protein AALP_AA8G416900 [Arabis alpina]	21/08/2014
OLES2_BRANA	CAG7902573.1	60	2.79E-60	unnamed protein product [Brassica rapa]	13/07/2021
OLES2_BRANA	CAG7906574.1	73.881	1.50E-56	unnamed protein product [Brassica rapa]	13/07/2021
OLES2_BRANA	KAG7632810.1	80	6.13E-86	Oleosin [Arabidopsis suecica]	13/07/2021
OLES2_BRANA	KAG7548662.1	67.045	3.08E-59	Oleosin [Arabidopsis suecica]	12/07/2021
OLES2_BRANA	KAG7559003.1	81.915	2.37E-87	Oleosin [Arabidopsis thaliana x Arabidopsis arenosa]	12/07/2021
OLES2_BRANA	KAG7563801.1	82.447	7.43E-89	Oleosin [Arabidopsis suecica]	12/07/2021
OLES2_BRANA	KAG7575559.1	59.236	1.33E-57	Oleosin [Arabidopsis thaliana x Arabidopsis arenosa]	12/07/2021
OLES2_BRANA	KAG7580235.1	57.595	8.32E-55	Oleosin [Arabidopsis suecica]	12/07/2021
OLES2_BRANA	QUV72339.1	53.254	4.58E-50	oleosin [Anacardium occidentale]	12/05/2021
OLES2_BRANA	KAG5411806.1	86.559	1.57E-92	hypothetical protein IGI04_008125 [Brassica rapa subsp. trilocularis]	30/03/2021
OLES2_BRANA	CAF1859148.1	77.5	3.03E-50	unnamed protein product [Brassica napus]	05/03/2021
OLES2_BRANA	CAF2166809.1	59.487	6.83E-60	unnamed protein product [Brassica napus]	05/03/2021
OLES2_BRANA	CAE5965745.1	58.599	3.36E-56	unnamed protein product [Arabidopsis arenosa]	12/02/2021
OLES2_BRANA	CAE6203907.1	67.045	6.90E-59	unnamed protein product [Arabidopsis arenosa]	12/02/2021
OLES2_BRANA	KAG2278807.1	91.772	9.45E-86	hypothetical protein Bca52824_061362 [Brassica carinata]	29/01/2021
OLES2_BRANA	KAG2278809.1	90.244	4.49E-86	hypothetical protein Bca52824_061364 [Brassica carinata]	29/01/2021
OLES2_BRANA	KAG2301498.1	83.871	7.01E-89	hypothetical protein Bca52824_030149 [Brassica carinata]	29/01/2021
OLES2_BRANA	KAG2307752.1	78.125	1.55E-57	hypothetical protein Bca52824_027500 [Brassica carinata]	29/01/2021
OLES2_BRANA	KAG2316322.1	93.158	2.23E-104	hypothetical protein Bca52824_019444 [Brassica carinata]	29/01/2021

OLES2_BRANA	XP_009111581.1	100	6.37E-132	oleosin S2-2 [Brassica rapa]	07/12/2020
OLES2_BRANA	XP_009125136.1	59.184	6.45E-59	oleosin 21.2 kDa [Brassica rapa]	07/12/2020
OLES2_BRANA	XP_009129400.1	87.097	2.72E-93	oleosin S2-2 [Brassica rapa]	07/12/2020
OLES2_BRANA	XP_009140003.1	74.627	2.38E-57	oleosin 21.2 kDa [Brassica rapa]	07/12/2020
OLES2_BRANA	KAF8408284.1	56.329	1.64E-50	hypothetical protein HHK36_007433 [Tetracentron sinense]	30/10/2020
OLES2_BRANA	KAF8049616.1	90.206	1.45E-100	hypothetical protein N665_2169s0006 [Sinapis alba]	22/10/2020
OLES2_BRANA	KAF8051909.1	61.856	6.69E-63	hypothetical protein N665_1651s0001 [Sinapis alba]	22/10/2020
OLES2_BRANA	KAF8075440.1	61.78	3.85E-62	hypothetical protein N665_1093s0001 [Sinapis alba]	22/10/2020
OLES2_BRANA	KAF8088404.1	83.77	1.18E-97	hypothetical protein N665_0543s0014 [Sinapis alba]	22/10/2020
OLES2_BRANA	KAF8096465.1	79.528	4.06E-57	hypothetical protein N665_0308s0039 [Sinapis alba]	22/10/2020
OLES2_BRANA	KAF3519872.1	59.487	1.14E-56	hypothetical protein DY000_02060986 [Brassica cretica]	24/03/2020
OLES2_BRANA	KAF3522921.1	60	1.19E-58	hypothetical protein F2Q69_00048590 [Brassica cretica]	24/03/2020
OLES2_BRANA	KAF3556567.1	59.677	5.89E-58	hypothetical protein F2Q69_00016176 [Brassica cretica]	24/03/2020
OLES2_BRANA	KAF3580851.1	75.373	1.61E-58	hypothetical protein DY000_02033714 [Brassica cretica]	24/03/2020
OLES2_BRANA	KAF2538068.1	97.872	1.81E-129	hypothetical protein F2Q68_00018699 [Brassica cretica]	21/02/2020
OLES2_BRANA	KAF2564614.1	91.743	4.43E-66	hypothetical protein F2Q70_00018402 [Brassica cretica]	21/02/2020
OLES2_BRANA	KAF2598922.1	82.447	1.05E-89	hypothetical protein F2Q68_00011720 [Brassica cretica]	21/02/2020
OLES2_BRANA	WP_162721329.1	63.846	3.99E-50	hypothetical protein [Escherichia coli]	21/02/2020
OLES2_BRANA	CAA7046599.1	80.412	1.74E-84	unnamed protein product [Microthlaspi erraticum]	18/01/2020
OLES2_BRANA	CAA7055248.1	56.281	1.59E-58	unnamed protein product [Microthlaspi erraticum]	18/01/2020
OLES2_BRANA	WP_157782993.1	100	1.47E-84	hypothetical protein, partial [Dickeya zeae]	21/12/2019
OLES2_BRANA	NP_001302485.1	59.487	2.94E-57	oleosin 21.2 kDa-like [Brassica napus]	27/11/2019
OLES2_BRANA	NP_001302696.1	59.162	1.10E-57	oleosin 21.2 kDa-like [Brassica napus]	27/11/2019
OLES2_BRANA	NP_001302798.1	73.881	1.99E-56	oleosin 21.2 kDa-like [Brassica napus]	27/11/2019
OLES2_BRANA	NP_001303224.1	58.854	1.07E-59	oleosin 21.2 kDa-like [Brassica napus]	27/11/2019
OLES2_BRANA	KAD7479554.1	52.326	2.80E-50	hypothetical protein E3N88_02690 [Mikania micrantha]	28/10/2019
OLES2_BRANA	KAE8021493.1	55.944	2.09E-51	hypothetical protein FH972_007378 [Carpinus fangiana]	28/10/2019
OLES2_BRANA	TXG54705.1	55.215	8.61E-52	hypothetical protein EZV62_019961 [Acer yangbiense]	19/08/2019
OLES2_BRANA	VVB04243.1	77.128	3.52E-85	unnamed protein product [Arabis nemorensis]	06/08/2019
OLES2_BRANA	VVB09373.1	65.426	8.13E-62	unnamed protein product [Arabis nemorensis]	06/08/2019
OLES2_BRANA	XP_028772353.1	52.632	1.01E-53	P24 oleosin-like [Prosopis alba]	24/04/2019
OLES2_BRANA	NP_001326794.1	79.474	2.02E-85	oleosin 4 [Arabidopsis thaliana]	14/02/2019
OLES2_BRANA	NP_186806.1	57.692	9.05E-55	Oleosin family protein [Arabidopsis thaliana]	14/02/2019

OLES2_BRANA	NP_198858.1	64.674	3.47E-61	oleosin 2 [Arabidopsis thaliana]	14/02/2019
OLES2_BRANA	XP_004493360.1	54.857	9.37E-49	P24 oleosin-like [Cicer arietinum]	14/12/2018
OLES2_BRANA	VDD26315.1	81.915	5.41E-89	unnamed protein product [Brassica oleracea]	16/11/2018
OLES2_BRANA	VDD61652.1	77.311	3.17E-53	unnamed protein product [Brassica oleracea]	16/11/2018
OLES2_BRANA	RID65892.1	74.627	2.12E-57	hypothetical protein BRARA_D01064 [Brassica rapa]	13/09/2018
OLES2_BRANA	AVI16670.1	52.299	6.22E-50	oleosin 17.5 kDa protein [Paeonia ostii]	04/03/2018
OLES2_BRANA	XP_006405494.1	60.847	7.08E-58	oleosin 21.2 kDa [Eutrema salsugineum]	26/02/2018
OLES2_BRANA	XP_006408525.1	54.14	1.50E-51	oleosin S1-2 [Eutrema salsugineum]	26/02/2018
OLES2_BRANA	XP_010108818.1	55.28	1.48E-50	oleosin 18.2 kDa [Morus notabilis]	26/02/2018
OLES2_BRANA	XP_024007352.1	86.702	4.26E-85	oleosin S2-2 [Eutrema salsugineum]	26/02/2018
OLES2_BRANA	XP_006285841.1	63.212	1.47E-57	oleosin 21.2 kDa [Capsella rubella]	02/02/2018
OLES2_BRANA	XP_006293022.1	79.474	4.99E-86	oleosin 20.3 kDa [Capsella rubella]	02/02/2018
OLES2_BRANA	XP_023641329.1	54.023	1.87E-55	oleosin 5 [Capsella rubella]	02/02/2018
OLES2_BRANA	PHT57115.1	49.704	1.06E-48	Oleosin [Capsicum baccatum]	27/10/2017
OLES2_BRANA	XP_013677557.1	81.915	6.11E-89	oleosin S2-2-like [Brassica napus]	04/10/2017
OLES2_BRANA	XP_013710504.1	88.889	2.11E-68	oleosin S2-2-like [Brassica napus]	04/10/2017
OLES2_BRANA	XP_022565510.1	83.511	3.72E-105	oleosin S2-2-like [Brassica napus]	04/10/2017
OLES2_BRANA	CDY11685.1	63.243	2.64E-60	BnaC06g12930D [Brassica napus]	12/07/2017
OLES2_BRANA	CDY50118.1	77.5	1.60E-50	BnaC04g32530D [Brassica napus]	12/07/2017
OLES2_BRANA	XP_020874719.1	64.13	8.33E-59	oleosin 21.2 kDa [Arabidopsis lyrata subsp. lyrata]	11/05/2017
OLES2_BRANA	XP_020882520.1	81.915	5.95E-88	oleosin 20.3 kDa [Arabidopsis lyrata subsp. lyrata]	11/05/2017
OLES2_BRANA	XP_020887463.1	58.599	4.05E-56	oleosin 5 [Arabidopsis lyrata subsp. lyrata]	11/05/2017
OLES2_BRANA	XP_010425544.1	78.534	2.19E-85	PREDICTED: oleosin 20.3 kDa-like [Camelina sativa]	29/11/2016
OLES2_BRANA	XP_010435635.1	57.325	4.62E-54	PREDICTED: oleosin 5 [Camelina sativa]	29/11/2016
OLES2_BRANA	XP_010435899.1	65.946	3.11E-61	PREDICTED: oleosin 21.2 kDa [Camelina sativa]	29/11/2016
OLES2_BRANA	XP_010496295.1	54.023	3.68E-54	PREDICTED: oleosin 5-like [Camelina sativa]	29/11/2016
OLES2_BRANA	XP_010502771.1	79.581	2.37E-86	PREDICTED: oleosin 20.3 kDa [Camelina sativa]	29/11/2016
OLES2_BRANA	XP_010514477.1	78.01	3.62E-85	PREDICTED: oleosin 20.3 kDa-like [Camelina sativa]	29/11/2016
OLES2_BRANA	XP_010524296.1	54.217	3.70E-55	PREDICTED: oleosin 5 [Tarenaya hassleriana]	18/11/2016
OLES2_BRANA	XP_010528231.1	63.975	3.97E-53	PREDICTED: oleosin 21.2 kDa-like [Tarenaya hassleriana]	18/11/2016
OLES2_BRANA	XP_018437931.1	86.559	1.76E-94	PREDICTED: oleosin S2-2 [Raphanus sativus]	04/10/2016
OLES2_BRANA	XP_018454714.1	94.681	4.35E-109	PREDICTED: oleosin S2-2 [Raphanus sativus]	04/10/2016
OLES2_BRANA	XP_018462556.1	80.469	6.42E-60	PREDICTED: oleosin 21.2 kDa-like [Raphanus sativus]	04/10/2016

OLES2_BRANA	XP_018483926.1	79.688	1.40E-59	PREDICTED: oleosin 21.2 kDa [Raphanus sativus]	04/10/2016
OLES2_BRANA	EFH58432.1	58.228	3.86E-56	glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	25/07/2016
OLES2_BRANA	OAP01778.1	87.05	9.50E-70	OLEO4 [Arabidopsis thaliana]	25/05/2016
OLES2_BRANA	XP_013610159.1	97.34	8.42E-129	PREDICTED: oleosin S2-2 [Brassica oleracea var. oleracea]	25/08/2015
OLES2_BRANA	XP_013619214.1	81.915	1.39E-88	PREDICTED: oleosin S2-2 [Brassica oleracea var. oleracea]	25/08/2015
OLES2_BRANA	XP_013631623.1	76.119	1.38E-58	PREDICTED: oleosin 21.2 kDa-like [Brassica oleracea var. oleracea]	25/08/2015
OLES2_BRANA	ESQ32696.1	87.209	1.07E-83	hypothetical protein EUTSA_v10005366mg [Eutrema salsugineum]	23/03/2015
OLES2_BRANA	KFK33105.1	60.309	6.84E-56	hypothetical protein AALP_AA6G331800 [Arabis alpina]	21/08/2014
OLES2_BRANA	KFK33678.1	78.378	1.50E-84	hypothetical protein AALP_AA5G045600 [Arabis alpina]	21/08/2014
OLES2_BRANA	KFK33679.1	76.63	4.57E-78	hypothetical protein AALP_AA5G045700 [Arabis alpina]	21/08/2014
OLES2_BRANA	ACG69503.1	87.097	1.32E-93	oleosin S2-1 [Brassica napus]	18/03/2013
OLES2_BRANA	ABQ57396.1	55.901	4.66E-51	oleosin H-isoform [Ficus pumila var. awkeotsang]	28/05/2008
OLES2_BRANA	AAM63098.1	78.421	1.09E-83	oleosin isoform [Arabidopsis thaliana]	27/01/2006
OLES2_BRANA	CAA63011.1	79.474	2.97E-85	oleosin type4 [Arabidopsis thaliana]	03/10/1996
OLES2_BRANA	CAA63022.1	61.979	1.17E-60	oleosin type2 [Arabidopsis thaliana]	06/12/1995

4. Conclusions and summary

The presence of cruciferin and napin proteins was confirmed on a peptide level in all Raptein™30 samples. The samples may have contained very little, if any, of the intact protein but a relatively complex set of proteoforms was observed. Both cruciferin and napin do exist as several proteoforms [1, 2]. Raptein™30 does not solubilize to salt buffer, but is solubilized with strong denaturant (8 M urea).

The sequence searches with FARRP allergen protein database version 21 provided several hits characterizing the possible allergenic effects of the proteins found in Raptein™30. The full-length FASTA search results should we be interpreted with > 35 % as the minimum identity threshold to an allergenic protein to infer any indication of possible allergenic cross-reactivity, although typically a minimum of > 50 % sequence identity may be required for a reliable allergenic indication. Likewise, the sequence similarity found in 80-mer FASTA searches may need to be interpreted in combination with the full-length FASTA searches. The BLASTP searches against the NCBI protein database found 467 sequences homologous to the query sequences, but did not include

any new allergenic proteins apart from ten that were already found during the FARRP database searches.

The Raptein™30 proteins did not match any peptides using the word search against the CD peptide dataset, which the primary tool to indicate elicitation of CD search. Likewise, the full-length FASTA search against the CD protein dataset also did not indicate high sequence similarity with the Raptein™90 proteins with the criteria of E-value < 10^{-15} and identity > 45 %. This result indicates that the Raptein™30 proteins are unlikely to elicit CD.

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GRAS NOTICE OF

CANOLA CONCENTRATE (RAPESEED CONCENTRATE)

Appendix 5

GMP+ certificate
of the rapeseed press cake supplier

Prozess

ZERTIFIKAT

Die Zertifizierungsstelle

DAkkS Deutsche Akkreditierungsstelle D-ZE-16087-01-00

AGRIZERT Zertifizierungs GmbH
Siebenmorgenweg 6-8
53229 Bonn

(akkreditiert nach DIN EN 17065
GMP+ International Reg.-Nr.: CI000033)

bestätigt, dass berechtigterweise davon auszugehen ist, dass die Prozesse

der Herstellung von Einzelfuttermitteln

beim Teilnehmer

Teutoburger Ölmühle GmbH
Gutenbergstraße 16a
49479 Ibbenbüren

den zutreffenden Anforderungen und Voraussetzungen aus dem Standard

GMP+ B2
Herstellung von Futtermittelinhaltsstoffen

des GMP+ FC scheme (basierend auf GMP+ C6) der GMP+ International (www.gmpplus.org) entsprechen.

Zertifikat-Registrier-Nr.:	GMPAGZ0550
Zertifikatsgültigkeit:	01.12.2020 – 30.11.2023
GMP+ International Reg.-Nr.:	GMP027298

Bonn, 24.11.2020

Zertifizierungsstelle

Dieses Zertifikat ist Eigentum der Zertifizierungsstelle und muss auf Nachfrage zurückgegeben werden.

CB registration code: CI000020

BUREAU VERITAS
Certification

Process Certificate

Awarded to

Grupa Wilmar Marek Wilczyński S.K.A.

Al. Niepodległości 2E 55-020 Żórawina, Poland
Registration-code: GMP052235

Bureau Veritas Inspection and Certification The Netherlands B.V. declares that there is justifiable confidence that Grupa Wilmar Marek Wilczyński S.K.A. meets the applicable requirements and conditions for Production of feed materials GMO Controlled. Therefore Grupa Wilmar Marek Wilczyński S.K.A. is certified for the standard(s) GMP+ MI105 GMO Controlled, of the GMP+ FC scheme (based on GMP+ C6) of GMP+ International.

Standard(s)

GMP+ MI105 GMO Controlled

GMO Controlled

Original cycle start date: **18 February 2020**

Certification / Recertification cycle start date: **18 February 2020**

Subject to the continued satisfactory operation of the organization's Feed Responsibility Assurance, this certificate is valid until: **17 February 2023**

Certificate No. **NL022094** Version: **01** Revision date: **18 February 2020**

Sebastiaan ter Horst
Director Certification

Issuing office: Bureau Veritas Inspection & Certification The Netherlands B.V.
Computerweg 2, 3821 AB Amersfoort, The Netherlands
Bureau Veritas Inspection and Certification The Netherlands B.V. is registered under CI000020

Feed Responsibility FRA Assurance

MIX Paper from responsible sources FSC® C074440

GRAS NOTICE OF

CANOLA CONCENTRATE (RAPESEED CONCENTRATE)

Appendix 6

Use of canola concentrate as a functional ingredient as extender in sausage meat product

Use of canola concentrate as a functional ingredient as extender in sausage meat product

Objectives

The objectives of this study were to evaluate the quality characteristics of sausages containing 2% Raptein™ 30 canola concentrate as a partial replacement of soy protein concentrate in a sausage link product.

Materials and Methods

Boston Butts-1/4" grind and mechanically separated turkey 18% fat were obtained from Von Hansen's Meats, Minneapolis, MN. Soy protein concentrate was obtained from DuPont, Wilmington, DE. Raptein™ 30 was provided by Napiferyn Biotech, Lodz, Poland. Raptein™ 30 is a canola concentrate product with a composition of 40.5% total protein and 55.9% total fiber. Two treatments were formulated shown in Table 1. One control treatment using soy protein concentrate and 1 test treatment using canola concentrate.

Sausages were formulated with 3.5% soy protein concentrate as meat extender ingredient as the control and 1.5% soy protein concentrate and 2.0% canola concentrate.

Table 1. Sausage Link Formulation

	Control	Test
Boston Butts-1/4" grind	42.50%	42.50%
Mechanically Separated Turkey-18% fat	42.50%	42.50%
Soy Protein Concentrate	3.50%	1.50%
Canola Concentrate	0.0%	2.00%
Salt	1.50%	1.50%
Water	10.00%	10.00%
Total	100.00%	100.00%

Evaluations

Cooked yield

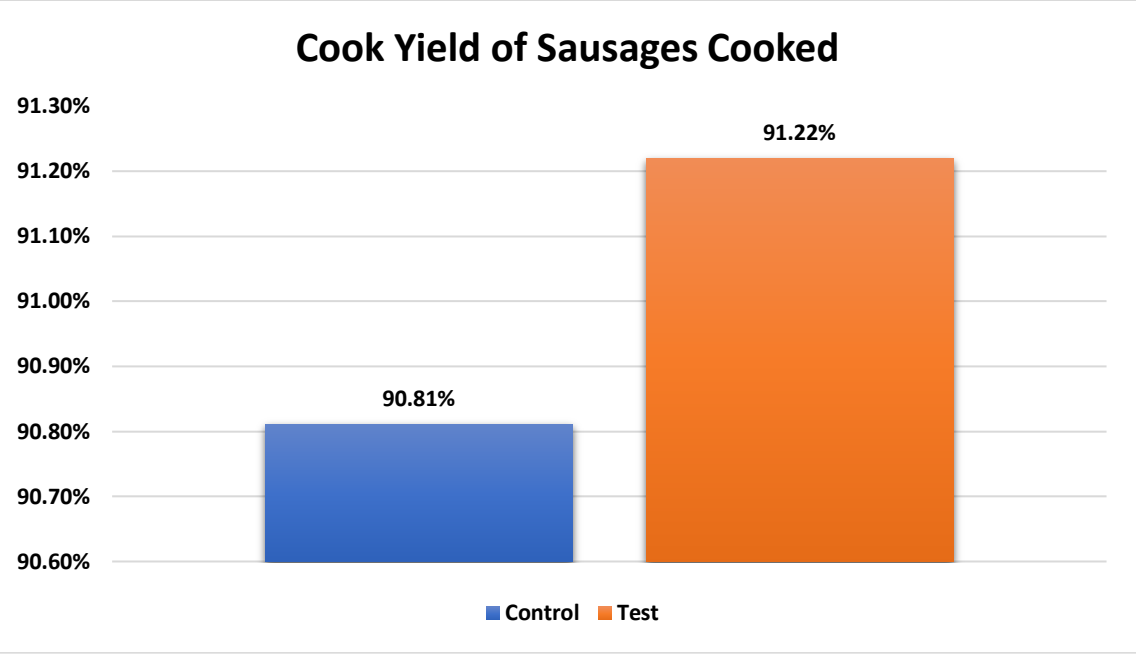
For each individual treatment, product cooked yield was calculated by dividing the chilled product weight 24h by the uncooked product weight (cooked product weight/uncooked product weight x 100). Cooked yield, therefore, represented product weight losses that occurred primarily during thermal processing and chilling. Comparison yields are shown in Chart 1 and individual yield values for control and test product are shown in Tables 2 and 3, respectively.

Texture Analysis

Texture analysis was conducted using Stable Microsystems TA.TX.plus texture analyzer measuring. Texture analysis comparison data are shown in Chart 2 and individual texture values for control and test and shown in Table 4.

Results and Discussion

Chart 1. Cook Yield



No significant difference was observed between the soy control compared to the canola concentrate test sausages for cooked yield.

Table 2. Control Yields

Control	Pre-cook weight g	Post cook weight g	% yield
Test 1	273.4	239.00	87.42%
Test 2	277.20	255.30	92.10%
Test 3	263.40	241.20	91.57%
Test 4	272.8	251.4	92.16%
		AVG	90.81%

Table 3. Test Yields

Canola Concentrate	Pre-cook weight g	Post cook weight g	% yield
Test 1	264.4	238.8	90.32%
Test 2	261.7	239.1	91.36%
Test 3	258.2	236.3	91.52%
Test 4	264.4	242.4	91.68%
		AVG	91.22%

Chart 2. Texture Analysis

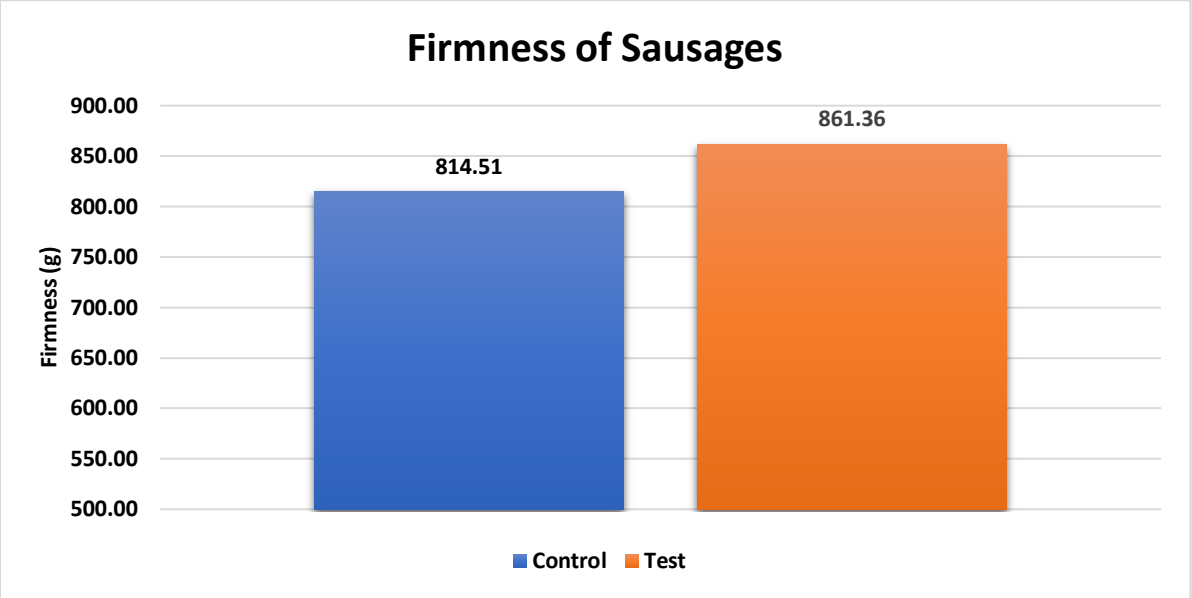
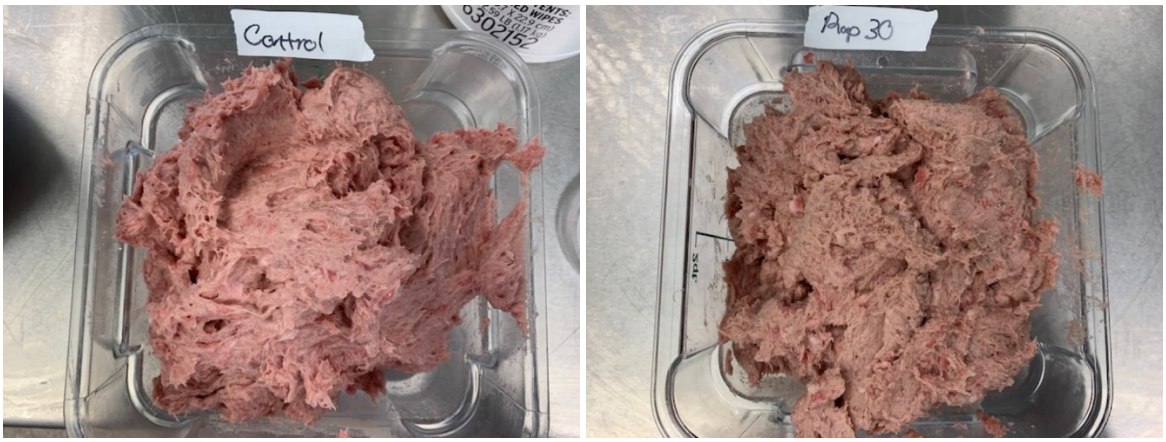


Table 4. Texture Analysis

	Control	Test
#1	878.106	745.692
#2	818.139	809.532
#3	671.709	1058.69
#4	832.3	902.738
#5	859.086	925.798
#6	-	861.959
Average	814.51	861.36

Sausages formulated with canola concentrate had a trend toward higher cooked yield (non-significant) compared to the control.

Figure 1. Pre-formed blend



The pre-formed canola concentrate test samples appeared slightly more dark and brown in color than the soy control.

Figure 2. Formed and Cooked Product

The canola concentrate test product had more structure and appeared dryer on the surface than the control. Small particulates of canola concentrate were visible on the surface.

Conclusions

The canola concentrate performed very similar to soy protein concentrate. Post-cook yield averages were between 90.8%-91.2% for both variables with no significant difference. Texture analysis shows firmness is similar for the canola concentrate samples compared to the soy control. The canola concentrate sausages were slightly dryer than the soy protein concentrate control. No major off notes or flavors were detected in the canola concentrate sausages. There were no significant differences between the test and control sausages in terms of flavor.

GRAS NOTICE OF

CANOLA CONCENTRATE (RAPESEED CONCENTRATE)

Appendix 7

Protein separation by SDS PAGE

Laboratory Industrial Biotechnology

93-465 Lodz, 114/116 Dubois Str.
e-mail: biuro@bionanopark.pl

№:B21/20/159A

REPORT

Sample	Description of the study	
1.1. Company name Napiferyn BioTech sp. z o.o.	2.1. Type of the study (tittle): Protein separation by SDS PAGE	
1.2. Name of the sample R-03#35, 1 mg/ml, koncentrat błonnikowo-białkowy - B21/20/001 R-06#60, 1 mg/ml, koncentrat błonnikowo-białkowy - B21/20/002 R-09#41, 1 mg/ml, koncentrat błonnikowo-białkowy - B21/20/003 R-13#60, 1 mg/ml, koncentrat błonnikowo-białkowy - B21/20/004 R-15#66, 1 mg/ml, koncentrat błonnikowo-białkowy - B21/20/005 R-08#64, 1 mg/ml, koncentrat błonnikowo-białkowy - B21/20/006 R-03#57, 1 mg/ml, izolat białkowy - B21/20/007 R-06#35, 1 mg/ml, izolat białkowy - B21/20/008 R-08#57, 1 mg/ml, izolat białkowy - B21/20/009 R-12#52, 1 mg/ml, izolat białkowy - B21/20/010 R-15#59, 1 mg/ml, izolat białkowy - B21/20/011		
1.3. Sample delivery date: 2021-09-13	2.2. Constructor of research: (name and surname) Martyna Leszczewicz, Natalia Broncel	2.3. Experimental completion date: 2021-09-28

RESULTS

3.1.Description

Protein electrophoresis in polyacrylamide gel under denaturing conditions (SDS-PAGE) was performed according to the Laemmli method (Laemmli U. Cleavage of structural proteins during the assembly of the head of bacteriophage T4. Nature 227, 680–685 (1970). http://doi.org/10.1038/227680a0). The analysis was carried out in a 20% polyacrylamide gel. Samples separations were performed under reducing (with β-mercaptoethanol, BME) and non-reducing conditions (without BME). The molecular weight (MW) of proteins were estimated based on molecular weight markers (11-245 kDa).

3.2. Results

The SDS-PAGE analysis of proteins isolates and concentrates were performed according to the method developed in Industrial Biotechnology Laboratory. The results are presented in Figures 1-2 and Table 1-2.

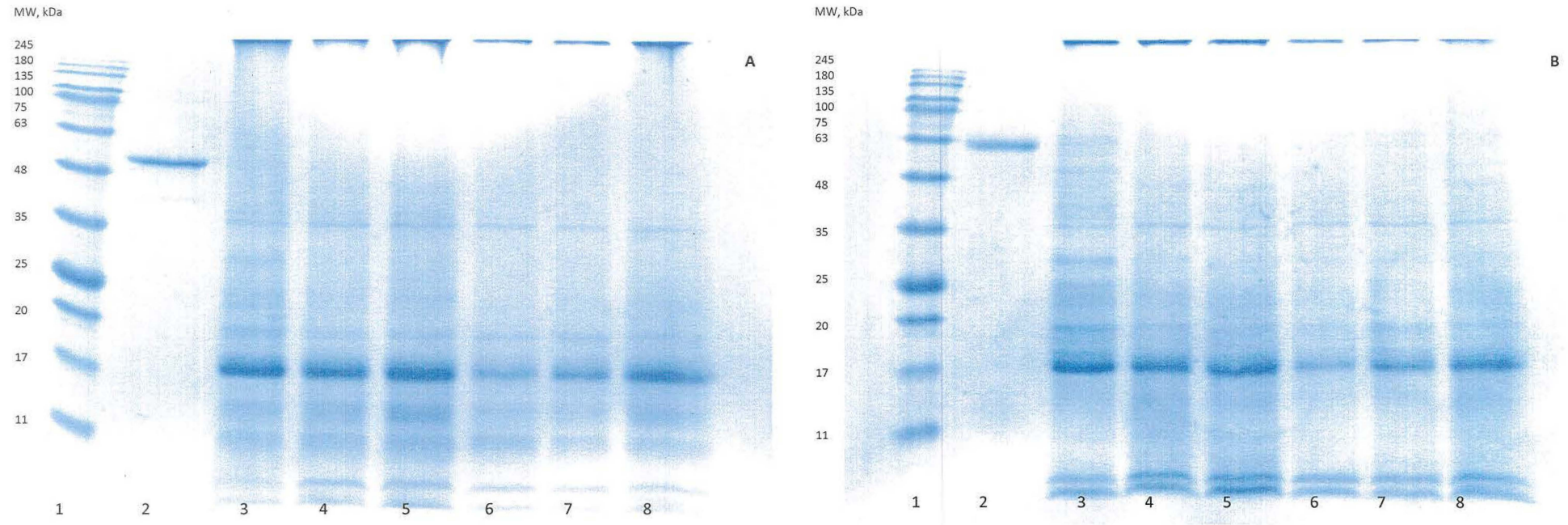


Figure 1 SDS-PAGE of protein-fibre concentrates in A - non-reducing and B - reducing conditions; 1 - molecular weight marker, 2 - bovine serum albumin standard 1 µg, 3 - R-03#35, 4 - R-06#60, 5 - R-09#41, 6 - R-13#60, 7 - R-15#66, 8 - R-08#64

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№:B21/20/159A

Table 1 Molecular weight, banding range, number of protein bands and the total number of bands in protein-fibre concentrates

Molecular weight range [kDa]	Non-reducing conditions						Reducing conditions					
	Line No.											
	3	4	5	6	7	8	3	4	5	6	7	8
	No. of protein bands											
<11	3	3	3	3	3	3	2	2	2	2	2	2
11-17	1	1	1	1	1	1	nd	1	1	nd	1	1
17-20	2	2	2	2	2	2	4	3	3	3	3	3
20-25	2	1	1	nd	nd	1	3	2	2	nd	nd	2
25-35	1	nd	nd	nd	nd	nd	1	nd	nd	nd	nd	nd
35-48	2	2	3	2	2	2	3	2	2	2	2	3
48-63	nd	nd	nd	nd	nd	nd	3	1	1	1	3	1
63-245	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
>245	1	1	1	1	1	1	1	1	1	1	1	1
Total bands	12	10	11	9	9	10	17	12	12	9	12	13

nd – not detected

The protein profiles of concentrates are similar in reducing and non-reducing conditions. In non-reducing conditions, we observed from 9 to 12 bands (Fig. 1 A). Their molecular weight has been estimated and detailed in Table 1. However, the highest intensity in each sample was showed by a protein of approximately 17 kDa. In reducing conditions, every sample contained from 9 to 17 different proteins (Fig. 1B, Table 1). The most intensive bands were observed for proteins with molecular weight around 17 kDa and lower than 11 kDa. The samples columns in both SDS-PAGE results contain intensive bands at the beginning of the separation gel (> 245 kDa). This phenomenon might be the result of the migration of fibre-bound protein which is too large and not sufficiently charged to migrate freely in the gel.

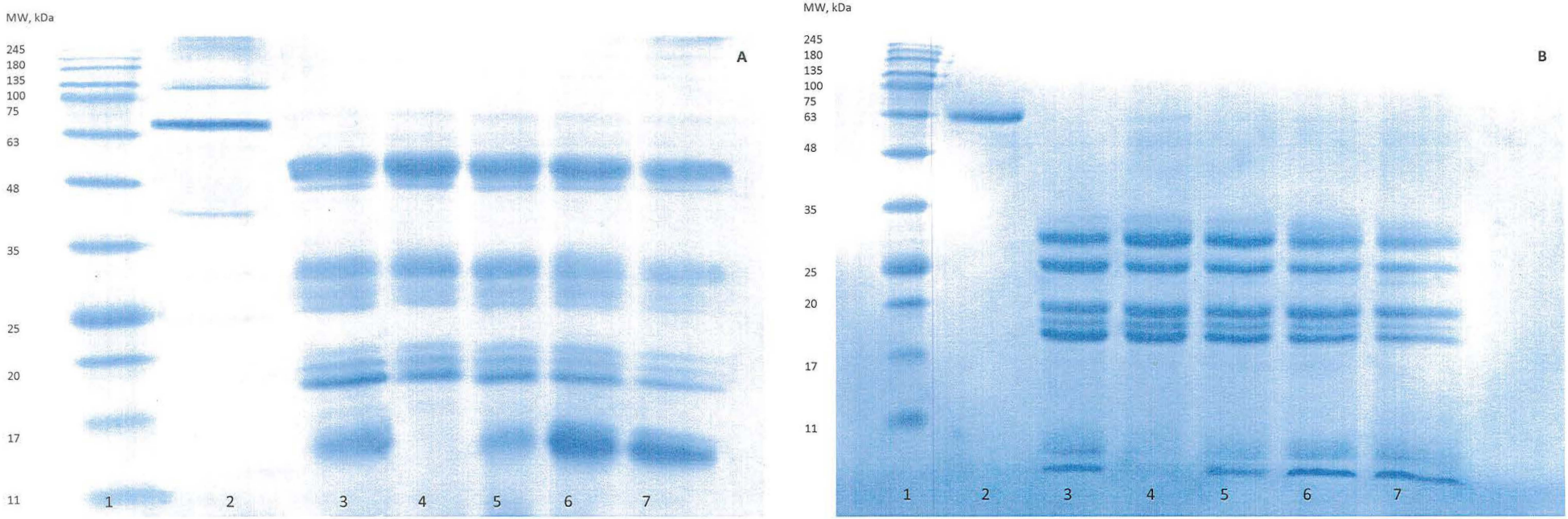

Figure 2 SDS-PAGE of protein isolates in A - non-reducing and B - reducing conditions; 1 - molecular weight marker, 2 - bovine serum albumin standard 1 µg, 3 - R-03#57, 4 - R-06#35, 5 - R-08#57, 6 - R-12#52, 7 - R-15#59

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№:B21/20/159A

Table 2 Molecular weight, banding range, number of protein bands and the total number of bands in protein isolates

Molecular weight range [kDa]	Non-reducing conditions					Reducing conditions				
	Line No.									
	3	4	5	6	7	3	4	5	6	7
	No. of protein bands									
<11	nd	nd	nd	nd	nd	2	nd	2	2	2
11-17	1	nd	1	1	1	1	1	1	1	nd
17-20	2	2	2	2	2	4	4	4	3	3
20-25	1	1	1	1	1	nd	nd	1	1	1
25-35	3	3	3	3	3	3	3	3	3	3
35-48	1	1	1	1	1	nd	1	nd	nd	nd
48-63	1	2	2	2	1	nd	1	nd	nd	nd
63-75	1	1	1	1	1	nd	nd	nd	nd	1
75-100	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
100-135	1	1	1	1	1	nd	nd	nd	nd	nd
135-180	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
180-245	1	1	1	1	1	nd	nd	nd	nd	nd
Total bands	12	12	13	13	12	10	10	11	10	10

nd – not detected

The profiles of proteins found in isolates, obtained in reducing and non-reducing conditions, presented slightly different characteristics. In non-reducing conditions in each line, we observed 12 or 13 bands (Fig. 2 A). In most cases, there were 4 major bands with the highest intensities that corresponded to proteins with molecular weight in the range of 11-17, 17-20, 25-35 and 48-63 kDa. Line 4 showed a lack of proteins smaller than 17 kDa. In the presence of a reducing agent, in each sample, we detected from 10 to 11 proteins (Fig. 2B, Table 2). The most intensive bands were observed in the range of 17-20 and 25-35 kDa. Additionally, in lines 3, 5, 6 and 7 fractions below 11 kDa were presented.

3.3. List of attachments

B21_20 koncentrat – nieredukujące, B21_20 koncentrat – redukujące, B21_20 izolat – nieredukujące, B21_20 izolat – redukujące

Confirmation of report

4.1. Date of develop	4.2. Developed by:	4.3. Date of approval:	4.4. Approved by:
05-10-2021	[redacted]	2021-10-11	[redacted]

Consensus Statement Concerning the Generally Recognized as Safe (GRAS) Status of the Proposed Uses of NapiFeryn's Canola Concentrate (Rapeseed Concentrate) (Raptein™30)

22 November 2021

INTRODUCTION

Bioresco, at the request of NapiFeryn BioTech, convened an expert panel of independent scientists qualified by their scientific training and national and international experience in evaluating the safety of food ingredients, to conduct a critical and comprehensive evaluation of the publicly available data and information on Raptein™30 and other Canola proteins. The charge to this panel of experts ("GRAS Panel") was to determine whether Raptein™30 would be GRAS under the proposed conditions of use as a food ingredient (protein and fiber source). The GRAS Panel consisted of the below-signed qualified scientific experts: Joseph F. Borzelleca, Ph.D., Robert J. Nicolosi, Ph.D. and Michael W. Pariza, Ph.D.

The GRAS Panel, independently and collectively, critically evaluated a comprehensive package of publicly available scientific information compiled and summarized by Bioresco and submitted to the GRAS Panel as GRAS Notice, "Canola Concentrate (Rapeseed Concentrate) for Use as an Ingredient in Human Food". The information contained therein was summarized by Bioresco following its comprehensive search of the scientific literature through September 2021. The GRAS Panel also evaluated other information deemed appropriate or necessary. The information evaluated by the GRAS Panel included history of use and regulatory status of Raptein™30, the method of manufacture and product specifications including stability, intended levels of use and estimated consumption, specified food products, consumption estimates from all intended uses, safety data, and comprehensive literature review of Raptein™30 and related approved ingredients.

Following independent critical evaluation of such data and information and following a teleconference (22 November 2021), the GRAS Panel unanimously concluded that under the conditions of intended use as a food ingredient (protein and fiber source) Raptein™30 meeting appropriate food-grade specifications and manufactured consistent with current Good Manufacturing Practice (cGMP), is GRAS based on scientific procedures.

SOURCE, PROCESSING AND SPECIFICATIONS

The raw material for production of Raptein™30 canola concentrate (rapeseed concentrate) is the press cake which is a by-product of oil production from the seeds of *Brassica* species: *Brassica napa*, *Brassica juncea* and *Brassica rapa*.

Raptein™30 is prepared by aqueous and solvent extraction of cold-pressed rapeseed cake (*Brassica napa* and/or *Brassica juncea* and/or *Brassica rapa*) that remains from the production of Canola oil. Residual slurry after extraction is subjected to a solid-liquid separation step followed by solvent wash and drying. The canola concentrate, Raptein™30, is mainly composed of protein (30-45% dry matter) and dietary fiber (40-70% dry matter).

Raptein™30 contains on average 62.4 % dry matter of total dietary fiber (TDF), 58.9 % dry matter of insoluble dietary fiber (IDF) and approximately 3.5 % dry matter of soluble dietary fiber (SDF).
The fiber content is further characterized as: neutral detergent fiber (36.0 % dry matter), acid detergent fiber (24.6 % dry matter), acid detergent lignin (4.2 % dry matter). Batch analyses confirm the production of a product that meets the established food grade specifications. All processing aids are approved for their specific use. The product is stable under the recommended storage conditions.

ESTIMATED DAILY INTAKES BASED ON PROPOSED USES

Raptein™30 will be used as a substitute for other approved protein sources, and as a fiber source and for functional purposes. Daily protein intake should not be increased. The fiber intake will not be increased significantly.

SAFETY ASSESSMENT

Since the use of Canola proteins as food ingredients has already been approved by the US FDA (e.g., GRAS Notice 000683, 2011) and since the Canola proteins in Raptein™30 are chemically similar to other approved Canola proteins, an extensive discussion is not necessary.

Canola proteins have a long history of safe ingestion which supports their use as a dietary protein. There are no data on the ingestion of fiber from Canola but the intake from Raptein™30 is unlikely to increase fiber intake significantly (the dietary intake is generally lower than the amount recommended by health authorities).

CONCLUSION

We, the undersigned members of the GRAS Panel, have independently and collectively, critically evaluated the information in the GRAS Notice presented by Bioresco. We unanimously conclude that the proposed use as a source of protein and fiber of Raptein™30 , produced consistent with cGMP and meeting appropriate food-grade specifications as presented in the GRAS Notice, is safe.

We unanimously conclude that the proposed use of Raptein™30 as a source of protein and fiber, produced consistent with cGMP and meeting appropriate food-grade specifications presented in the GRAS Notice, is GRAS based on scientific procedures.

It is our professional opinion that other qualified experts would also concur with these conclusions.

[redacted] 25 November 2021

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