

Supplementary Material

Table S1. List of proteins identified in the *Beta vulgaris* leaf proteome during BNYVV infection of susceptible sugar beet via mass spectrometry.

Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
Photosynthesis and energy production								
Ribulose biphosphate carboxylase large chain	Q4PLI7	rbcL	53	3.50E-03	88	66%	x	x
ATP synthase subunit beta, chloroplastic	Q4PLI6	atpB	54	1.40E-03	39	85%	x	x
Ribulose biphosphate carboxylase small chain	P00870	RBCS	14	1.00E-03	6	51%	x	x
Rubisco activase	Q8L5T3	rca	48	7.80E-04	25	49%	x	x
ATP synthase subunit alpha, chloroplastic	P06450	atpA	55	6.20E-04	35	47%	x	x
Cytochrome b559 subunit alpha	Q2Z1Q5	psbE	9	4.00E-04	4	48%	x	x
Photosystem I iron-sulfur center	P10098	psaC	9	3.60E-04	8	83%	x	x
Photosystem I reaction center subunit IV, chloroplastic	P12354	PSAE-1	13	3.50E-04	4	35%	x	x
Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic	P12860	GAPB	48	3.30E-04	10	33%	x	x
Photosystem I reaction center subunit II, chloroplastic	P12353	psaD	23	3.20E-04	9	32%	x	x
Phosphoglycerate kinase, chloroplastic	P29409		46	3.10E-04	16	42%	x	x
Chlorophyll a/b-binding protein	O49812		28	3.10E-04	9	57%	x	x
Phosphoribulokinase, chloroplastic	P09559		45	2.90E-04	5	46%	x	x
Glycine decarboxylase subunit T	Q947L6	gdt	14	2.80E-04	7	78%	x	x
Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic	P19866	GAPA	43	2.70E-04	8	28%	x	x
Oxygen-evolving enhancer protein 1, chloroplastic	P12359	PSBO	35	2.60E-04	2	25%		x
ATP synthase subunit b, chloroplastic	P06453	atpF	21	2.00E-04	7	38%	x	x
23 kDa OEC protein	B0L802	PsbP	22	1.70E-04	4	15%	x	x

Table S1. Cont.

Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
Photosystem I reaction center subunit VI, chloroplastic	P22179	PSAH	15	1.60E-04	2	8.30%	x	x
Dihydrolipoamide dehydrogenase	Q947M1	dhl	18	1.60E-04	6	51%	x	x
V-type proton ATPase catalytic subunit A	Q39442		69	1.60E-04	27	54%	x	x
Chlorophyll a/b binding protein	Q7XAC6	cab11	28	1.40E-04	7	52%	x	x
Sedoheptulose-1,7-bisphosphatase, chloroplastic	O20252		42	1.20E-04	7	19%	x	x
Photosynthetic oxygen-evolving protein 16 kDa subunit	B0L6Y3	psbQ	25	1.20E-04	2	15%	x	x
Apocytochrome f	P16013	petA	35	1.10E-04	7	20%	x	x
Glycine decarboxylase subunit P	Q947L7	gdp	8	1.00E-04	5	40%		x
Photosystem II reaction center protein H	P05146	psbH	8	9.30E-05	2	29%	x	x
Cytochrome b6	P00165	petB	24	9.20E-05	3	21%	x	x
Triosephosphate isomerase, chloroplastic	P48496	TPIP1	34	8.90E-05	6	32%	x	x
Chloroplast ribose-5-phosphate isomerase	Q8RU73		31	8.80E-05	4	16%	x	x
ADP-ribosylation factor 1	H2EP74	ARF1	21	8.50E-05	8	46%	x	x
Fructose-1,6-bisphosphatase, chloroplastic	P22418		45	8.10E-05	4	13%	x	x
ATP-dependent Clp protease proteolytic subunit	Q9M3K5	clpP	22	6.90E-05	2	21%		x
ATP synthase subunit b', chloroplastic	P31853	ATPG	24	6.40E-05	2	9.00%	x	x
ATP synthase epsilon chain, chloroplastic	P00833	atpE	15	5.90E-05	2	16%	x	x
ATP synthase delta chain, chloroplastic	P11402	ATPD	28	5.70E-05	3	7.40%		x
Photosystem I reaction center subunit XI, chloroplastic	Q41385	PSAL	23	5.40E-05	2	12%	x	x

Table S1. Cont.

Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
V-type proton ATPase subunit E	Q41396	VATE	26	5.40E−05	9	48%	x	x
Photosystem II 22 kDa protein, chloroplastic	Q02060	PSBS	29	4.70E−05	4	20%	x	x
Photosystem II CP43 chlorophyll apoprotein	Q6EY72	psbC	46	4.60E−05	2	19%	x	x
Photosystem I reaction center subunit V, chloroplastic	P12357	PSAG	18	4.50E−05	3	10%	x	x
Ribulose-phosphate 3-epimerase, chloroplastic	Q43157	RPE	30	4.50E−05	2	15%		x
Photosystem II D2 protein	P06005	psbD	40	4.10E−05	3	9.10%	x	x
Cytochrome b6-f complex iron-sulfur subunit, chloroplastic	P08980	petC	24	4.00E−05	3	17%	x	x
Photosystem II CP43 chlorophyll apoprotein	P06003	psbC	52	3.60E−05	3	25%	x	x
Photosystem I reaction center subunit III, chloroplastic	P12355	PSAF	25	3.50E−05	4	20%	x	x
Photosystem Q(B) protein	P69565	psbA	39	1.90E−05	4	16%	x	x
Delta-aminolevulinic acid dehydratase, chloroplastic	P24493	HEMB	47	1.90E−05	3	18%	x	x
Photosystem I P700 chlorophyll a apoprotein A2	P06512	psaB	82	1.90E−05	5	9.80%	x	x
Oxygen-evolving enhancer protein 3, chloroplastic	P12301	PSBQ	25	1.70E−05	3	5.20%	x	x
Vacuolar proton pump ATPase subunit H	G4XKY2	VHA-H	53	1.50E−05	5	12%	x	x
Violaxanthin de-epoxidase, chloroplastic	Q9SM43	VDE1	54	1.40E−05	3	7.80%	x	x
Type III chlorophyll a/b-binding protein	Q9AVE9	cab3	17	9.90E−06	2	16%		x
NADPH-protochlorophyllide oxidoreductase 2	Q9AVF1	POR2	25	4.80E−06	3	20%		x
UDP-glucose:flavonoid-O-glucosyltransferase	Q5GIG8		54	4.00E−06	2	6.50%	x	

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Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
26S protease regulatory subunit 7	Q41365	RPT1	48	2.00E-06	2	6.60%		x
Photosystem I P700 chlorophyll a apoprotein A1	P06511	psaA	83	1.70E-06	2	2.30%		x
Metabolism and/or secondary metabolism								
Glyceraldehyde-3-phosphate dehydrogenase	A3FMH0		37	5.10E-04	19	79%	x	x
Glutamine synthetase	B2CZA8	GNL2	47	4.00E-04	20	56%	x	x
Malate dehydrogenase, cytoplasmic	Q9SML8	NR1	35	3.60E-04	16	64%	x	x
Serine hydroxymethyltransferase	Q947K8	sht	5	2.70E-04	2	32%	x	x
Fructose-bisphosphate aldolase, chloroplastic	P16096		42	2.50E-04	13	32%	x	x
Methionine synthase	Q4H1G2	BvMS1	88	2.30E-04	15	48%	x	x
50S ribosomal protein L12, chloroplastic	Q53WU1	Soc	20	2.30E-04	6	33%	x	x
Alpha tubulin	B5BT09	TUB	24	2.00E-04	6	56%	x	x
S-adenosylmethionine synthase 1	Q4H1G4	SAMS1	43	1.80E-04	22	68%	x	x
Adenosylhomocysteinase	Q4H1G1	BvSAHH1	53	1.70E-04	24	60%	x	x
Transketolase, chloroplastic	O20250		80	1.70E-04	13	21%	x	x
ClpC protease	O98447	clpC	99	1.60E-04	39	51%	x	x
Elongation factor 1-alpha	Q8H9A9	skef-1A	49	1.60E-04	19	38%	x	x
50S ribosomal protein L14, chloroplastic	P09596	rpl14	13	1.30E-04	5	51%	x	x
Carbonic anhydrase, chloroplastic	P16016		35	1.10E-04	3	13%	x	x
Elongation factor 2	O23755		94	1.10E-04	28	50%	x	x
Sal k 3 pollen allergen	C1KEU0		84	1.10E-04	2	22%	x	x
Choline monooxygenase, chloroplastic	O22553	CMO	50	1.00E-04	12	33%	x	x
Elongation factor 1-delta	O81918		25	1.00E-04	5	40%	x	x
Glutamate synthase	I6PD11		157	9.60E-05	46	42%	x	x
Carbonic anhydrase	Q947M3		14	9.30E-05	2	20%		x
30S ribosomal protein S17, chloroplastic	P82137	RPS17	4	9.00E-05	2	47%		x
Enolase	Q9LEE0	eno	48	8.40E-05	9	29%	x	x
Fructose-bisphosphate aldolase	Q6RSN7		39	7.10E-05	6	25%	x	x

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Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV- IV (C2) ³	BNYVV- IV (C3) ⁴
Glutamate								
1-semialdehyde aminotransferase	Q9AVF5	GSA-AT	33	7.10E-05	6	23%	x	x
Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic	P55232	AGPB1	54	6.60E-05	15	43%	x	x
30S ribosomal protein S11, chloroplastic	P06506	rps11	15	6.60E-05	3	24%	x	x
Pyruvate dehydrogenase E1alpha subunit	Q852S0	PDH E1a-1	44	6.50E-05	8	29%	x	x
30S ribosomal protein S4, chloroplastic	P13788	rps4	23	6.10E-05	8	39%	x	x
50S ribosomal protein L5, chloroplastic	P82192	RPL5	24	6.00E-05	2	12%	x	x
Plasma membrane intrinsic protein PIP1;1	C7DYC4		31	5.80E-05	6	36%	x	x
30S ribosomal protein S16, chloroplastic	P28807	rps16	10	5.80E-05	2	24%	x	x
50S ribosomal protein L2, chloroplastic	P06509	rpl2-A	30	5.60E-05	5	25%	x	x
Nucleoside diphosphate kinase 2, chloroplastic	Q01402	NDPK2	26	5.20E-05	3	15%	x	x
30S ribosomal protein S1, chloroplastic	P29344	RPS1	45	5.10E-05	8	17%	x	x
Fructose-1,6- bisphosphatase, cytosolic	Q42649		37	5.00E-05	3	25%	x	x
Isocitrate dehydrogenase	Q9SPH8	Icdh	28	4.80E-05	3	12%	x	x
Uroporphyrinogen decarboxylase	Q9AVF8	UROD	21	4.70E-05	4	26%	x	x
Proteasome subunit alpha type	I6U5E4	PAC1	27	4.60E-05	2	28%	x	x
Ferredoxin—NADP reductase, chloroplastic	P00455	PETH	41	4.60E-05	4	13%	x	x
Fructokinase	Q42645		35	4.10E-05	10	40%	x	x
Cysteine synthase	B5U9U9	CSase A	34	4.10E-05	4	20%	x	x
Nitrite reductase	E2JFE1	NiR	67	4.00E-05	8	30%	x	x
Glutamine synthetase	B0LSR3	GNL1	39	3.90E-05	6	32%	x	x
Ribosome-recycling factor, chloroplastic	P82231	RRF	30	3.50E-05	4	13%	x	x
Ketol-acid reductoisomerase, chloroplastic	Q01292	AHRI	64	3.50E-05	11	24%	x	x

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Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
Fructose-bisphosphate aldolase, cytoplasmic isozyme	P29356		38	3.30E−05	3	9.50%	x	x
Dehydroascorbate reductase	Q9FVE4	DHAR	30	3.30E−05	3	11%	x	x
30S ribosomal protein S13, chloroplastic	P82163	RPS13	16	3.20E−05	2	9.70%	x	x
40S ribosomal protein S25	Q94G66	RPS25	13	2.80E−05	2	21%	x	x
60S acidic ribosomal protein P0	P29764		34	2.70E−05	3	8.70%	x	x
30S ribosomal protein S9, chloroplastic	P82278	PRPS9	21	2.60E−05	3	23%	x	x
Peptidyl-prolyl cis-trans isomerase, chloroplastic	O49939	TLP40	50	2.40E−05	3	10%	x	x
30S ribosomal protein S5, chloroplastic	Q9ST69	rps5	34	2.40E−05	3	13%	x	x
Acyl-[acyl-carrier-protein] desaturase, chloroplastic	P28645		46	2.30E−05	4	13%	x	x
50S ribosomal protein L24, chloroplastic	P27683	RPL24	21	2.30E−05	2	10%	x	
Formate—tetrahydrofolate ligase	P28723		68	2.30E−05	6	14%	x	x
30S ribosomal protein S8, chloroplastic	P09597	rps8	16	2.10E−05	3	22%	x	x
rRNA N-glycosidase	B1VCR4		28	2.00E−05	3	14%	x	x
50S ribosomal protein L1, chloroplastic	Q9LE95	RPL1	39	2.00E−05	2	6.80%	x	x
Phosphoenolpyruvate carboxylase	B2MW80		110	1.90E−05	16	15%	x	x
Phosphoethanolamine N-methyltransferase	Q9M571	PEAMT	56	1.70E−05	4	8.30%		x
Coproporphyrinogen oxidase	Q9AVF7	COPROX	19	1.60E−05	2	12%		x
Sucrose synthase	Q6SJP5	SBSS2	92	1.60E−05	7	16%	x	x
40S ribosomal protein S11	Q1H8R1	rpS11	18	1.60E−05	2	15%	x	x
Fatty acid hydroperoxide lyase	E7E818	HPL	55	1.40E−05	5	13%	x	x
50S ribosomal protein L16, chloroplastic	P17353	rpl16	15	1.10E−05	2	16%	x	x

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Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
Granule bound starch synthase I	D6RSA2	GBSSI	67	1.10E−05	3	6.90%	x	
Malate dehydrogenase [NADP], chloroplastic	P52426	MDH	47	1.00E−05	2	6.40%		x
Proteasome subunit beta type-5	O24361		30	9.60E−06	2	8.50%	x	
30S ribosomal protein S19 alpha, chloroplastic	P06508	rps19	11	8.70E−06	2	33%		x
Phosphoserine aminotransferase, chloroplastic	P52877		47	8.70E−06	4	10.00%	x	x
30S ribosomal protein S3, chloroplastic	P09595	rps3	25	8.60E−06	5	23%		x
6-phosphogluconate dehydrogenase, decarboxylating 1	Q94KU1	pgdC	53	6.80E−06	3	12%	x	x
50S ribosomal protein L11, chloroplastic	P31164	rpl11	24	6.00E−06	2	14%	x	x
11S globulin seed storage protein	Q38712		57	5.90E−06	2	4.40%	x	x
Putative vacuolar processing enzyme	Q949L7		54	5.80E−06	3	8.60%	x	
UDP-sulfoquinovose synthase, chloroplastic	Q84KI6	SQD1	54	5.80E−06	2	7.70%	x	x
Delta 1-pyrroline-5-carboxylate synthetase	Q8LRT0	P5CS	24	4.00E−06	2	15%		x
Monodehydroascorbate reductase	Q94IB7		54	4.00E−06	2	6.40%	x	x
Myo-inositol-1-phosphate synthase	Q944C3	INPS	57	3.80E−06	2	6.10%		x
Hexokinase-1	Q9SEK3	HXK1	54	3.60E−06	2	8.00%		x
Cysteine synthase like protein	Q767A2	CSaseLP	36	3.30E−06	2	11%		x
Glucose-6-phosphate isomerase	O82058	GPIP	68	2.80E−06	2	4.00%	x	x
Glycylpeptide N-tetradecanoyltransferase	K4Q1D5		51	1.90E−06	2	7.80%		x
Glucose-1-phosphate adenylyltransferase large subunit, chloroplastic/amyloplastic	P55233	AGPS1	58	1.70E−06	2	4.00%	x	x

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Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
Signal transduction and/or transport								
33 kDa protein of the oxygen-evolving complex	B5BT06	OEE1	35	4.70E-04	7	56%	x	x
Non-specific lipid-transfer protein	Q7XZE0	AnLTP	12	4.30E-04	2	11%	x	
Beta-tubulin	A3FMG7		12	3.50E-04	6	60%	x	
Actin 1	E9P160		42	3.50E-04	20	64%	x	
Profilin	A8VT60		14	2.20E-04	3	24%	x	
Calmodulin	Q3UKW2	Calm1	22	1.50E-04	7	73%	x	
Voltage-dependent anion channel protein	Q41368	SVDAC1	30	1.50E-04	7	30%	x	
28 kDa ribonucleoprotein, chloroplastic	P28644		25	1.30E-04	6	30%	x	
Putative GTP binding protein	Q0MX58		23	9.40E-05	7	27%	x	
Luminal-binding protein	Q42434	HSC70	74	5.50E-05	11	26%	x	
Plasma membrane major intrinsic protein 2	Q39440		30	5.00E-05	9	41%	x	
20 kDa chaperonin, chloroplastic	Q02073	CPN21	27	4.80E-05	2	7.10%	x	
Calreticulin	O81919		48	4.00E-05	7	29%	x	
Chloroplast mRNA-binding protein CSP41	O24365		45	2.70E-05	3	6.70%	x	
Protein phosphatase 2A	H6VX93	PP2A	35	8.20E-06	3	21%		x
Protein translocase subunit SecA, chloroplastic	Q36795	secA	117	4.70E-06	2	3.40%		x
Response to stimulus (including plant defense response)								
Peroxisomal (S)-2-hydroxy-acid oxidase	P05414		40	3.40E-04	17	54%	x	x
Cytosolic heat shock 70 protein	O22664	HSC70	71	2.40E-04	25	45%	x	x
Peroxiredoxin Q, chloroplastic	Q6UBI3	PRXQ	24	2.30E-04	8	36%	x	x
Superoxide dismutase [Cu-Zn]	A7WTB6		22	2.20E-04	6	20%	x	x
Heat shock 70 protein	O50036	HSC70-9	76	1.90E-04	24	38%	x	x
Glucan endo-1,3-beta-D-glucosidase	Q9XFW8	Glu2	36	1.50E-04	14	63%	x	x
14-3-3-like protein	P29308		25	1.40E-04	9	28%	x	x
Ascorbate peroxidase	Q42459		28	1.30E-04	3	28%	x	x

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Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
Catalase	Q94EV9	CAT1	57	1.30E-04	9	23%	x	x
2-Cys peroxiredoxin BAS1, chloroplastic	O24364	BAS1	29	1.30E-04	5	25%	x	x
Cell wall peroxidase	O81266		9	7.70E-05	2	61%	x	x
Laccase-like protein	I3W7E6		51	7.50E-05	12	36%	x	x
Superoxide dismutase	H9BQP5	MnSOD	26	7.50E-05	4	25%	x	x
Thioredoxin M-type, chloroplastic	P07591		20	7.40E-05	3	10%	x	x
Thaumatin like protein	Q949L8		23	5.70E-05	3	20%	x	x
Peroxidase prx13	Q9M4Z4		36	5.40E-05	3	17%	x	x
Chitinase	Q9XFW7	Ch4	28	5.10E-05	7	44%	x	x
Heat shock protein 83	Q1H8M1	hsp83	40	4.60E-05	7	28%	x	x
Germin-like protein Kiel 1	Q84RC0	GLP-Ki1	22	4.40E-05	3	11%	x	x
Pathogenesis-related protein 1a	B5QTD3	pr1a	18	3.90E-05	3	32%	x	
Germin-like protein Wageningen 1	Q84V63	GLP-Wag1	22	3.50E-05	4	16%	x	
Betaine aldehyde dehydrogenase, chloroplastic	P28237		55	3.40E-05	12	29%	x	x
Salt tolerance protein 4	Q84LL8	sato4	22	2.90E-05	2	16%	x	x
Salt tolerance protein 2	Q711N3	sato2	38	2.70E-05	6	23%	x	x
Major latex like protein homolog	Q949M0		17	2.40E-05	4	27%	x	x
Peroxisomal ascorbate peroxidase	L0CTS4		31	2.30E-05	6	31%	x	x
Peroxidase	P93552	prxr8	36	2.20E-05	3	15%	x	
Catalase	Q941J0	cat2	33	2.00E-05	3	12%	x	x
Heat shock 70 protein	O49045	HSC70-10	72	1.90E-05	5	16%	x	x
Peroxidase	P93547	prxr3	38	1.80E-05	2	11%	x	
Acidic endochitinase SP2	P42820	SP2	30	1.70E-05	5	24%	x	
Salt tolerance protein 5	Q84LL6	sato5	33	1.50E-05	2	17%	x	x
Auxin-induced beta-glucosidase	Q7XJH8		83	1.40E-05	4	8.00%	x	x
Acidic endochitinase SE2	P36910	SE2	31	1.40E-05	2	11%	x	
Cationic peroxidase	Q1H8N1	cprx1	35	1.00E-05	4	25%	x	x
DnaJ protein homolog ANJ1	P43644		47	9.70E-06	2	8.90%	x	x
Chitinase	Q42421	Ch1	48	6.50E-06	3	13%	x	x
Stress-induced protein sti1-like protein	H9B3R7		51	1.40E-06	2	5.10%		x

Table S1. Cont.

Protein Name ¹	Uniprot Accession	Name	Mass kDa	NSAF ²	Number Unique Peptides	% Coverage	BNYVV-IV (C2) ³	BNYVV-IV (C3) ⁴
Unknown or other								
RS2 protein	Q9FNT2	Rs2	16	1.40E-04	7	33%	x	x
Putative uncharacterized protein	E2DN06		15	1.20E-04	2	16%	x	x
Histone H3.3C	P02301	H3f3c	15	9.80E-05	5	51%	x	x
Putative uncharacterized protein	E2DN04		15	3.40E-05	2	13%	x	
37 kDa inner envelope membrane protein, chloroplastic	P23525		39	1.70E-05	3	14%		x
Uncharacterized protein	K4PYU2		18	8.00E-06	2	13%		x

Footnotes: ¹ Proteins are organized based on GO terms and putative annotated function. ² NSAF: Normalized spectral abundance factors. ³ C2: Proteins that were identified from the susceptible sugar beet genotype (R30_rz1) infected with the resistance breaking BNYVV strain from the Rockwood 158 field, Imperial County, CA (BNYVV-IV). ⁴ C3: Proteins that were identified from the susceptible sugar beet genotype (R30_rz1) infected with A-type of BNYVV (BNYVV-A) strain. Proteins in **bold** lettering were previously identified in the study by Larson *et al.* [1].

References

1. Larson, R.L.; Hill, A.L.; Nunez, A. Characterization of protein changes associated with sugar beet (*Beta vulgaris*) resistance and susceptibility to *Fusarium oxysporum*. *J. Agric. Food Chem.* **2007**, *55*, 7905–7915.

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