

Table S1. List of genes and their products with antioxidant functionality of bifidobacteria

The product encoded by the gene	Antioxidant functionality	Gene	Strain	Reference
Ferroxidase	Iron chelation activity	BL01563	<i>B. longum</i> NCC2705	[Kwak et al.,2016, Kot et al., 1994]
Glutaredoxin Glutaredoxin-like NrdH	Reduce dehydroascorbate, peroxiredoxins, and methionine sulfoxide reductase. Reduced non-enzymatically by glutathione.	<i>grxA</i> ,, <i>grx1</i> , <i>grxC2</i> , <i>nrdH</i> , BBMN68_1397,	<i>B. longum</i> BBMN68,	[Elias et al., 2008, Xiao et al., 2011, Kwak et al.,2016]
Peroxideroxin (alkyl hydroperoxide reductase subunit C)	Reduces H ₂ O ₂ , organic peroxides and peroxyxynitrite	<i>ahpC</i> , BL0615	<i>B. longum</i> NCC2705	[Xiao et al., 2011, Zuo et al., 2014, Klijn et al., 2005]
Peroxideroxin OsmC family	Peroxidase activity with a strong preference for organic hydroperoxides	BLI010_09070	<i>B. infantis</i> JCM 7010	[Dubbs et al., 2007]
Peroxiredoxin Q/BCP	Protein reduces and detoxifies hydroperoxides, shows substrate selectivity toward fatty acid hydroperoxides.	LTBL16_000976, BL0615	<i>B. longum</i> LTBL16, <i>B. longum</i> NCC2705,	[Kwak et al.,2016, Oberg, et al., 2016, Huang et al., 2020]
Thioredoxin	Reduction of disulfide bonds of other proteins by cysteine thiol-disulfide exchange	<i>trxA</i> , <i>B</i> , BBMN68_991, BLD 0988	<i>B. longum</i> BBMN68, <i>B. longum</i> NCC2705	[Kwak et al.,2016, Lu et al.,2014, Xiao et al., 2011, Serata et al., 2012, Jia et al.,2017]
Thioredoxin reductase	Reduction of oxidized thioredoxins and glutaredoxin -like NrdH protein .	<i>trxB</i> , BL0164	<i>B. longum</i> BBMN68, <i>B. longum</i> LTBL16, <i>B. longum</i> NCC2705, <i>B. animalis lactis</i>	[Oberg, et al., 2016, Lu et al., 2014, Xiao et al., 2011, Klijn et al., 2005, Huang et al., 2020, Jia et al.,2017]
NAD(P)H oxidase	Source of cellular reactive oxygen species, transfer electrons from NADPH to oxygen molecule.	<i>nox</i> , LTBL16_001911	<i>B. longum</i> LTBL16,	[O'Callaghan et al.,2016, Lu et al., 2014, Xiao et al., 2011, Serata et al., 2012, Jia et al.,2017]
Dihydroorotate oxidase	Generates H ₂ O ₂ -forming NADH	<i>pyrK</i> ,	<i>B. bifidum</i> CNCMI-4319	[Kawasaki et al.,2009, Jia

	oxidase activity and indirect production of H ₂ O ₂ .	CNCMI_0917, <i>pyrD</i> CNCMI_0378		et al.,2017]
Oxygen-dependent coproporphyrinogen III oxidase	Involved in detoxifying molecular oxygen and/or H ₂ O ₂		<i>B. animalis lactis</i>	[Ruiz et al., 2012]
Possible Class I pyridine nucleotide-disulfideoxidoreductase (PNDR)	Involve in the cellular oxidative stress response	BL1626,	<i>B. longum</i> NCC 2705, <i>B. longum</i> BBMN68,	[Xiao et al., 2011, Delcardayre et al., 1998]
P-type ATPase	Transport of manganese to the bacterial cell	<i>mntP</i> , zntA1 BBMN68_1149	<i>B. longum</i> BBMN68	[Xiao et al., 2011, Jia et al.,2017]
Ferritin; ferroxidase; DNA starvation/stationary phase protection protein	Enzymes catalyzes the oxidation of Fe ²⁺ ions by hydrogen peroxide, which prevents hydroxyl radical production by the Fenton reaction	<i>dps</i> ,	<i>B. longum</i> NCC2705	[Klijn et al., 2005, Zhai,et al., 2019]
DsbA family oxidoreductase	Catalyzes intrachain disulfide bond formation as peptides emerge into the cell's periplasm	<i>dsbA</i> ,	<i>B. longum</i> MCC00353	[Zhai,et al., 2019] BioCyc
Ribonucleotide reductase	DNA oxidative damage-protective protein	<i>nrdA</i> , BL1752	<i>B. longum</i> BBMN68, <i>B. longum</i> D2957	[Xiao et al., 2011, Oberg, et al., 2016]
Nucleotide triphosphate pyrophosphohydrolases	DNA oxidative damage-protective proteins	<i>mutT1</i>	<i>B. longum</i> BBMN68	[Xiao et al., 2011]
NAD-dependent protein deacetylase of SIR2 family	Involved in the response to oxidative stress. NAD ⁺ -dependent deacetylation of σ^H and transcription factor FOXO3a. Improve foxo-dependent transcription of antioxidant enzymes and reduce ROS levels in cells	<i>sir2</i> , LTBL16_002010	<i>B. longum</i> LTBL16	[Halsey et al., 2004, Guo et al., 2017]

Linoleic acid isomerase	Participates in linoleic acid metabolism. Conjugated linoleic acid metabolites exhibit the ability to protect cells from oxidative effects.	<i>lai</i> , CNCMI4319_0491	<i>B. bifidum</i> CNCM I-4319	[Macdonald et al., 2000]
Cyclopropane-fatty-acyl-phospholipid synthase	Catalyzes cyclopropane fatty acid (cell-surface component) biosynthesis	BBMN68_1705,	<i>B. longum</i> BBMN68,	[Xiao et al., 2011]
Hydroxycinnamic acid esterase	Release of hydroxycinnamates from plant-based dietary sources	<i>caeA</i>	<i>B. longum</i>	[Kelly et al., 2018]
S-adenosylhomocysteinase, S-ribosylhomocysteinase	Synthesizes cysteine from methionine using homocysteine as an intermediate	<i>ahcY</i> , <i>luxS</i> , FC12_GL001705	<i>Bifidobacterium</i> spp.,	[Wada et al., 2021]
Subtilisin-like serine protease, cell envelope protease	Catalyzes the cleavage of peptide bonds	<i>aprE</i> , <i>cep</i>	<i>B. longum</i> KACC91563	[Chang et al., 2013]

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Table S2. Catalog the orthologs antioxidant genes of *B. longum*

Enzyme name	Number of orthologs
Alkyl hydroperoxide reductase AhpC	6
Alkyl hydroperoxide reductase AhpF	6
Class I pyridine nucleotide-disulfide oxidoreductase	3
Cobalamin-independent methionine synthase II	9
DSBA oxidoreductase	9
Dihydroorotate dehydrogenase	9
Glutaredoxin grxC2 (nrdH)	7
Glutathione import ATP-binding protein GsiA	8
Hydroxycinnamic acid esterase CaeA - carboxylesterase A	4
Linoleic acid isomerase	5
NADH oxidase	11
Oxygen-dependent coproporphyrinogen III oxidase	9
P-type ATPase	9
Peptidase O pepO	9
Permease	5
Peroxiredoxin	5
Polyphosphate kinase Ppk	9
Pyrophosphohydrolase MutT1	9
Ribonucleotide reductase NrdA	6
Subtilisin-like serine protease	2
Superoxide dismutase SodB	12
Superoxide dismutase SodC	11
Thioredoxin	4
Thioredoxin domain protein	9
Thioredoxin peroxidase	7
Thioredoxin reductase	14
Thioredoxin reductase-like protein	6

Table S3. Distribution genes of antioxidant functionality in the genomes of *B. longum*

[illegible]

<i>B. longum</i> subsp. <i>longum</i> strain AH1206	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain BORI	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain CCUG30698	+	+	+	+	+	+	+	-	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 11340	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 11341	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 11342	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 11343	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 7050	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 7052	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 7053	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain KCTC 3128	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain KCTC 3421	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain KCTC 5914	+	+	+	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain NCIMB8809	+	+	+	+	+	+	+	+	+	+

Table S3 (Continued). Distribution genes of antioxidant functionality in the genomes of *B. longum*

Strain	Permease	Peroxi redoxin	Subtilisin-like serine protease	Thioredoxin domain protein	Thioredoxin peroxidase	Thioredoxin reductase	Thioredoxin reductase-like protein
<i>B. longum</i> DJO10A	-	+	+	+	+	+	+
<i>B. longum</i> isolate MGYG-HGUT-01292	+	+	-	+	+	+	+
<i>B. longum</i> NCC2705	-	+	+	+	+	+	+
<i>B. longum</i> strain 105-A	-	+	+	+	+	+	+
<i>B. longum</i> strain 35624	-	+	+	+	+	+	+
<i>B. longum</i> strain 51A	-	+	+	+	+	+	+
<i>B. longum</i> strain BAMA-B05	-	+	+	+	+	+	+
<i>B. longum</i> strain BG7	-	+	+	+	+	+	+
<i>B. longum</i> strain BIM B-813D	-	+	+	+	+	+	+
<i>B. longum</i> strain BXY01	-	+	-	+	-	+	+

<i>B. longum</i> strain CACC 517	-	+	+	+	+	+	+
<i>B. longum</i> strain HN001	-	+	+	+	+	+	+
<i>B. longum</i> strain Jih1	-	+	+	+	+	+	+
<i>B. longum</i> strain JSRL02	-	+	+	+	+	+	+
<i>B. longum</i> K15	-	+	+	+	+	+	+
<i>B. longum</i> strain K5	-	+	+	+	+	+	+
<i>B. longum</i> strain LC67	-	+	+	+	+	+	+
<i>B. longum</i> strain LTBL16	-	+	+	+	+	+	+
<i>B. longum</i> strain NCTC11818	-	+	+	+	+	+	+
<i>B. longum</i> strain ZJ1	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> BBMN68	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> GT15	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> JCM 1217	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> JDM301	-	+	-	+	-	+	+
<i>B. longum</i> subsp. <i>longum</i> KACC 91563	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain AH1206	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain BORI	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain CCUG30698	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 11340	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 11341	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 11342	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 11343	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 7050	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 7052	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain JCM 7053	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain KCTC 3128	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain KCTC 3421	+	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain KCTC 5914	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain NCIMB8809	-	+	+	+	+	+	+
<i>B. longum</i> subsp. <i>longum</i> strain YS108R	-	+	+	+	+	+	+

Table S4. Parameters of the analyzed transcriptomic samples

Sample name	Raw samples		Trimmed samples	
	Size, mln reads	Size, blnb.p.	Size, mln reads	Size, blnb.p.
BL1	30.0	3.0	28.7	2.5
BL2	32.2	3.2	30.7	2.7
BL3	26.6	2.7	24.5	2.3
BL4	30.5	3.1	29.1	2.6
BL5	30.4	3.1	29.2	2.6

Table S5. The total number of upregulated transcripts in cells of *B. longum* GT15 under the action of a certain oxidative stress factor

Total transcripts*	Response to H₂O₂	Response to O₂ 2 h	Response to O₂ 4 h
Response to H ₂ O ₂	190	52	52
Response to O ₂ 2 h	58	117	52
Response to O ₂ 4 h	72	99	177

* results are expressed as more 2-fold change after oxidative stress compared to control (untreated) cells

Table S6. The total number of detected proteins in increased level in cells of *B. longum* GT15 under the action of a certain oxidative stress factor

Total proteins*	Response to H₂O₂	Response to O₂ 2 h	Response to O₂ 4 h
Response to H ₂ O ₂	13	5	3
Response to O ₂ 2 h	5	19	13
Response to O ₂ 4 h	3	13	14

* results are expressed as more 2-fold change after oxidative stress compared to control (untreated) cells

Table S7. The total number of common transcripts and proteins in increased level in cells of *B. longum* GT15 under the action of a certain oxidative stress factor

Total proteins/transcripts*	Response to H₂O₂	Response to O₂ 2 h	Response to O₂ 4 h
Response to H ₂ O ₂	8	2	3
Response to O ₂ 2 h	2	14	10
Response to O ₂ 4 h	3	10	13

* results are expressed as more 2-fold change after oxidative stress compared to control (untreated) cells

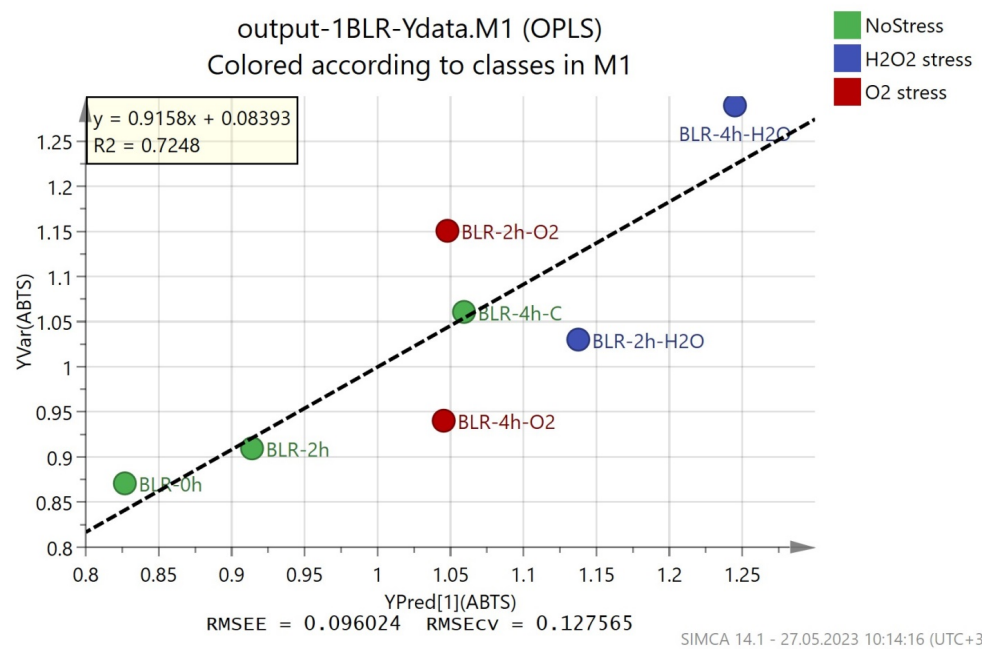


Figure S1. OPLS regression models on metabolic fingerprints of *B. longum* GT15 cells and their antioxidant activity (ABTS•+ method).

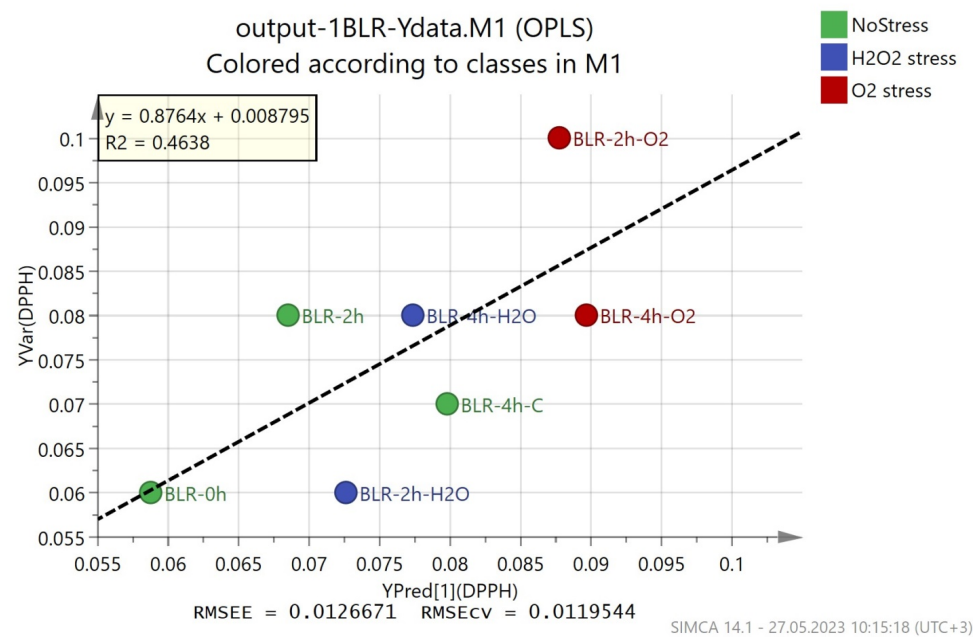


Figure S2. OPLS regression models on metabolic fingerprints of *B. longum* GT15 cells and their antioxidant activity (DPPH• method).

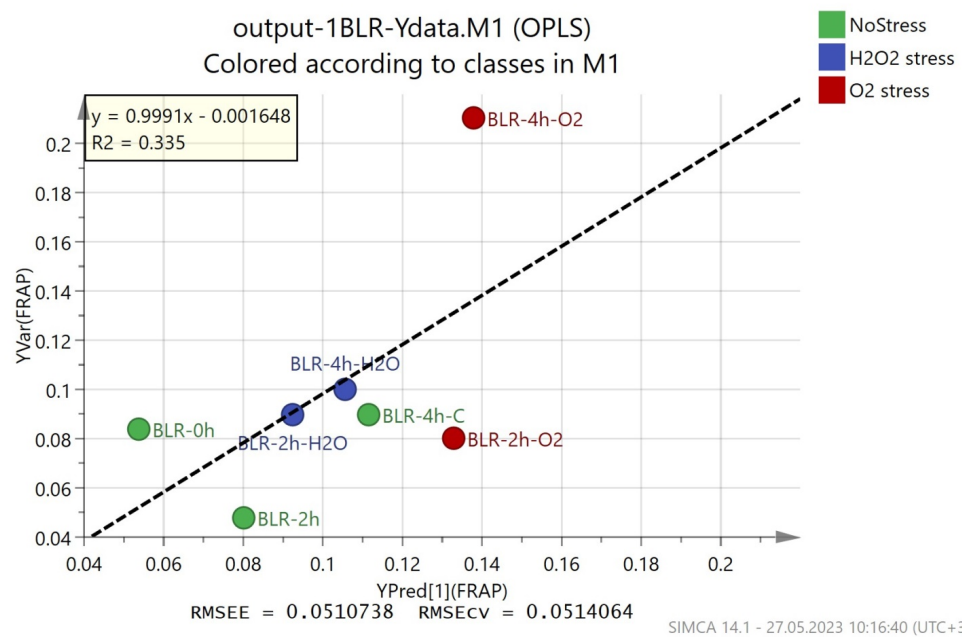


Figure S3. OPLS regression models on metabolic fingerprints of *B. longum* GT15 cells and their antioxidant activity (FRAP method).