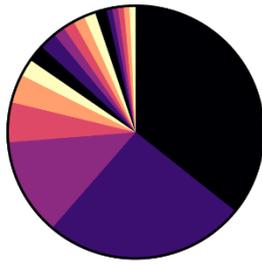


FigS1– Effect of pectin concentration on Flavobacteria colony expansion. (A) Schematic representation of PY2 agar plates streaked with 0.5, 1, 2, 4% pectin as indicated. (B) Wild type (WT) or gliding mutant (Δ gldJ) of *F. johnsoniae*, sp. F52, flavobacteria strains were inoculated in the center of PY2 plates streaked with lines of various pectin concentrations (as indicated in A.) or PY2 agar plates streaked with DDW as a control. Bacteria were grown for 48hr at 30^oC and the distance of the bacterial colony from the center outwards was measured using Fiji. $p < 0.05$ by Tukey HSD. N=4. (C) Distance of WT *F. johnsoniae*, *Flavobacterium* sp. F52 strains from the plate center outwards measured on PY2 agar covered with the indicated concentration of pectin. Presented bars show mean and SE values. $p < 0.05$ by Tukey HSD.

A.

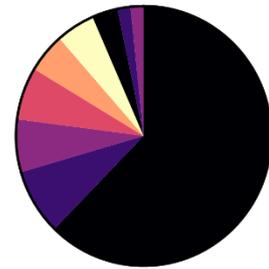
KEGG-Significantly upregulated proteins



Total=137

- Not assigned
- Enzyme families
- Carbohydrate metabolism
- Membrane transport
- Metabolism of cofactors and vitamins
- Drug resistance
- Signal transduction
- Translation
- Energy metabolism
- Lipid metabolism
- Metabolism of other amino acids
- Replication and repair
- Biosynthesis of other secondary metabolites
- Transcription
- Amino acid metabolism
- Cell growth and death
- Glycan biosynthesis and metabolism
- Transport and catabolism

KEGG-Significantly downregulated proteins

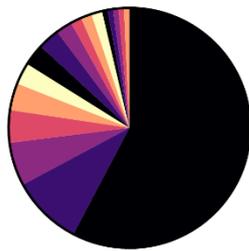


Total=61

- Not assigned
- Enzyme families
- Folding, sorting and degradation
- Carbohydrate metabolism
- Amino acid metabolism
- Translation
- Transport and catabolism
- Replication and repair
- Signaling molecules and interaction

B.

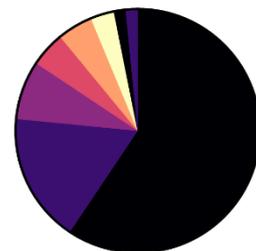
SEED-Significantly upregulated proteins



Total=137

- Not assigned
- D-Galacturonate and D-Glucuronate Utilization
- Nitric oxide synthase
- L-Arabinose CS
- Branched-Chain Amino Acid Biosynthesis
- Galactose degradation in plants
- L-rhamnose utilization
- Proteasome bacterial
- CoA Pantothenate HMP
- B12 Biosynthesis (Tavares copy1)
- Ribosome LSU bacterial
- Terminal cytochrome C oxidases
- Cobalt-zinc-cadmium resistance
- Alanine biosynthesis
- Arginine/arginine deiminase pathways in Streptococci
- Copper homeostasis: copper tolerance
- Multidrug Resistance Efflux Pumps

SEED-Significantly downregulated proteins

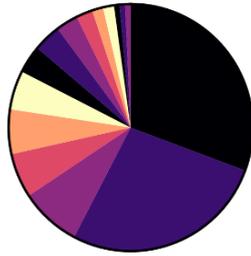


Total=64

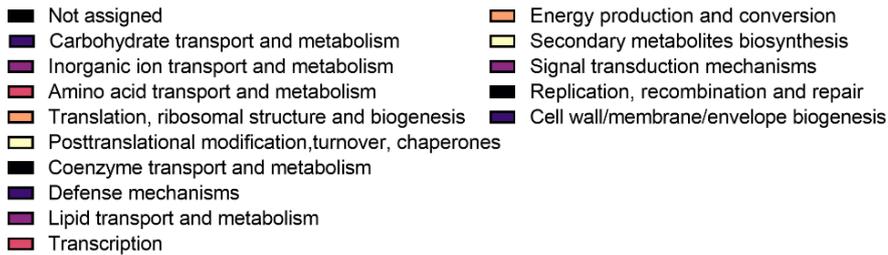
- Not assigned
- Photorespiration (oxidative C2 cycle)
- Arginine Biosynthesis extended
- Ethylmalonyl-CoA pathway of C2 assimilation
- Ribosome LSU bacterial
- Citrate Metabolism KE4
- Campylobacter Iron Metabolism
- Listeria surface proteins: Internalin-like pr

C.

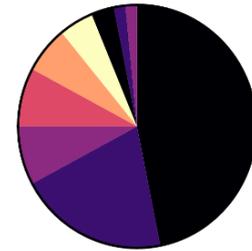
EggNOG-Significantly upregulated proteins



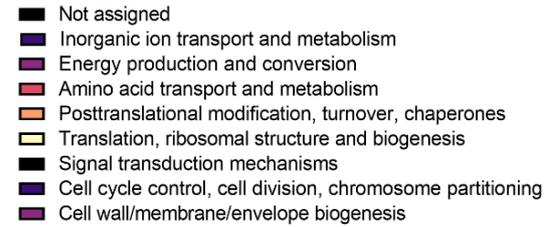
Total=137



EggNOG-Significantly downregulated proteins



Total=64



FigS2– Annotation of proteins upregulated and down regulated in response to pectin in *F. johnsoniae*

Proteins that were significantly altered and had fold change higher then 2 (left panel) or lower then 0.5 (right panel) between flavobacteria grown on PY2 with pectin or DDW were annotated using either: (A) KEGG (B) Seed (C) EggNog.

Supplementary Materials and Methods

Functional annotation of significantly induced and repressed proteins

Proteins showing at least two-fold increase or decrease in PY2 media amended with pectin relative to the PY2 media amended with DDW (control) were screened against the non-redundant (nr) NCBI protein database using DIAMOND v0.9.24.125 (Buchfink et al., 2015) to assign functional annotations. Results were then uploaded to MEGAN Ultimate edition software v6.15.2 (Buchfink et al., 2014). For functional annotation, the Kyoto Encyclopedia of Genes and Genomes (KEGG), SEED (Overbeek et al., 2014), and EggNOG (Based on Clusters of Orthologous groups – COG extension) databases were used.

Operon mapping of TonB-associated gene cluster

A TonB gene cluster that was significantly upregulated in the pectin samples (peg4455-4469 by RAST, WP_044048002.1-OXE95634.1 by NCBI annotation, bases 5125269-5130351 in *F. johnsoniae* UW101, complete genome Sequence ID: CP000685.1) was screened for the presence of operons using two independent tools: Operon mapper (Taboada et al., 2018), and FGENESB Suite of Bacterial Operon-Softberry Inc. (Tyson et al., 2004).

Table S1A- Significantly upregulated proteins of *F. johnsoniae* grown on PY2 covered with pectin vs. DDW

NCBI annotation	gene_number (RAST annotation)	Pectin/DDW: P-Value	Pectin/DDW: Fold change	DNA seq	RAST functional annotation
WP_012024292.1	2323	0.00669	585.7	atgaaaaaatcaattctattctatttaccagcttt	hypothetical protein
WP_012022292.1	192	0.00148	203.9	atgaaagcaaatatatttagaggactaatagccgt	hypothetical protein
WP_012023625.1	1618	0.01686	128.9	atgttgggattaaaattagctacagaccctcgctgggtt	tRNA-(ms[2]io[6]A)-hydroxylase (EC 1.-.-)
WP_012024113.1	2127	0.04239	84.3	atgttacaactaaaaatcaaaaaacagccattattttg	Beta-glucosidase (EC 3.2.1.21)
WP_012025397.1	3584	0.00002	38.6	atgaaagaatgtaactatcaaatgtagcagctctgtatt	Alkaline phosphatase (EC 3.1.3.1)
WP_012023204.1	1170	0.00388	29.9	atgaaaaattatgtcatagattagactcggaaacaga	Ribulokinase (EC 2.7.1.16)
WP_012023111.1	1074	0.00438	26.7	atgtcaattaatcgatagcagcaaaagatttgcocg	putative auxin-regulated protein
WP_012023206.1	1172	0.00564	25.8	atgatagatatactcaaaaagaagtgtgttagtag	L-arabinose isomerase (EC 5.3.1.4)
WP_012024544.1	2583	0.00180	23.1	atgaaactaaatcttaaaatcaattgcaactgcttggat	SciB protein
WP_012022294.1	194	0.00139	22.1	atgaaatllaaagatttataaacaaggagcaaatcgt	TonB family protein / TonB-dependent receptor
WP_012022711.1	646	0.04622	19.3	atgaaacaataataaactatactattcttctctca	hypothetical protein
WP_012022637.1	570	0.00997	14.4	atgaaaaatcaattttaaattcgttacagttgttctt	FIG00649626: hypothetical protein
WP_012025446.1	3634	0.02934	12.9	atgatttttcttaattataccagtgataatcgtccagatg	Glycosyltransferase
WP_012023596.1	1589	0.00918	12.8	atgaaaaaatgctactattcttctgcatgtcagttttggc	FIG00657157: hypothetical protein
WP_012022876.1	819	0.00389	12.1	atgctagacgaaaccccaaacgattgatagaattgt	transcriptional regulator, putative
SHH12854.1	4459	0.00449	11.9	atgttaggaatgattgtacaagcttaagtctgcagca	RagB/SusD domain protein
WP_012023313.1	1287	0.00123	11.4	atgaaaaaaacctacttttctgactatgcttcaattgc	Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8)
WP_012026225.1	4456	0.01930	11.2	atgataagaaaagccattttggttcccaatcatgc	Rhamnolacturonides degradation protein RhiN
WP_012022957.1	905	0.01684	10.1	atgagaaactgctctgaatgctctgaaaaactgtaggc	FIG00930353: hypothetical protein
WP_012026229.1	4460	0.00035	8.4	atgaacattcaaaaatcattaagaaaaataaaat	TonB family protein / TonB-dependent receptor
WP_012022293.1	193	0.00954	8.4	atgaaacataaataataatagcaggattgataattca	putative outer membrane protein, probably involved in nutrient binding
WP_012026233.1	4464	0.00003	7.7	atggaaaaaataacagatcaaatcagagtttcaaa	Altronate oxidoreductase (EC 1.1.1.58)
WP_012026234.1	4465	0.00005	6.8	atggcaaaaattcaagaatagaggtgcgcagacaa	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)
WP_012026236.1	4467	0.00006	6.4	atgagcgcgcaaatcattacacgcacaatttttattag	Uronate isomerase (EC 5.3.1.12)
WP_012022307.1	209	0.03901	6.1	atgtcagatacaatcgaaaaaataatgccttatatag	Thioredoxin reductase (EC 1.8.1.9)
WP_012026223.1	4454	0.00058	6.0	atgaaaaatataaaaatcgttattctctcttccgttttc	Beta-xylosidase (EC 3.2.1.37)
WP_011921584.1	72	0.03454	5.9	atggtaaaattggatatacaattttgactgtgaagacg	related lyases
WP_012026232.1	4463	0.00037	5.7	atggcagcgcgaaaaaattgataaaagtccaccad	Altronate hydrolase (EC 4.2.1.7)
SHL59770.1	2398	0.02051	5.5	atgtcacaataatatacttttaacaacaggaacata	Regulator of nucleoside diphosphate kinase
WP_012026691.1	4957	0.01793	5.5	atggaaaaatggaacaaaatcaatcgccgcaattct	TonB-dependent receptor, putative
WP_089477413.1	4508	0.04171	5.2	atgaagaaaatagcatgtattgctttagcttactatt	hypothetical protein
OXE95634.1	4469	0.00400	4.8	atgacaaaatagttcaagatagcgtcaagtcage	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)
WP_012026094.1	4323	0.04956	4.7	atgaaatlaactcgttttgagaatcggaagaaagaaa	5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase (EC 4.1.1.68)
WP_012026239.1	4470	0.00163	4.6	atgagtcaaaccgatgctgttacagtaaatcaaccgt	Hexuronate transporter
WP_044048002.1	4455	0.00000	4.6	atgtcggtttattagttgctgaatggcttaacaggctg	Rhamnolacturonides degradation protein RhiN
WP_012026071.1	4300	0.00094	4.4	atgaaaaagaacatcatatctcttattcttcaac	Putative glycosyl hydrolase of unknown function (DUF1680)
WP_012023778.1	1772	0.00746	4.3	atgaactacgtaagaatttaaaatttgcatacaag	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)
WP_044047683.1	2297	0.01650	4.1	atgagagaaaatgacatgttagaaaaagagagatt	FIG00655294: hypothetical protein
WP_012023203.1	1169	0.00112	4.0	atgaaaaaacactactactattgtttacaattgtat	Alpha-N-arabinofuranosidase 2 (EC 3.2.1.55)
WP_012023735.1	1729	0.00019	3.8	atggaaatgacattaacaacaagtgatgacaggtaa	Alternative cytochrome c oxidase polypeptide CoxO (EC 1.9.3.1); Cytochrome c oxidase, subunit III (EC 1.9.3.1)

WP_091490394.1	1180	0.00210	3.8	atggcctttgaattaccacaattacctatgcatcacgatgc	Manganese superoxide dismutase (EC 1.15.1.1)
WP_044048511.1	4466	0.00013	3.8	atgagtagagtagtggcattggagaaatcatgctgcggt	2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)
WP_012026231.1	4462	0.00004	3.7	atgagcggaaaaagtaaccatttatgatattgccgaaaa	Hexuronate utilization operon transcriptional repressor ExuR
WP_012026237.1	4468	0.01289	3.5	atgacaaactatttgacataaaaggaaaagttgccctt	2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)
WP_012024354.1	2387	0.02187	3.4	atgttcagaaaaattactctttaacgctgtattagctgct	hypothetical protein
WP_012026430.1	4683	0.04473	3.3	atgacaatgtattcattcagatataaaaaataaaaaccg	Probable Co/Zn/Cd efflux system membrane fusion protein
WP_012024436.1	2473	0.00884	3.2	atgaaaatacaagattcaggcaattcaattattgctg	oligoribonuclease A, Bacillus type
WP_052295191.1	3036	0.04623	3.2	atgaaaaatataaaaaaaccttcattatttgggtgat	Putative outer membrane protein, probably involved in nutrient binding
WP_044047803.1	3435	0.01612	3.1	atgtcaagcaaaagaagcatataaaaggtgacttctgatac	FIG01101450: hypothetical protein
WP_012026188.1	4419	0.00004	3.1	atgataatcggatcaaacatattgaatctcataacgag	Predicted L-rhamnose isomerase RhaI (EC 5.3.1.14)
WP_012025223.1	3406	0.00852	3.0	atgagcattaaaaacaattctttctctctatttatcac	Probable RND efflux membrane fusion protein
WP_012026482.1	4737	0.00920	2.9	atgagaatcatttcaggaaaaatacaaggcgccggg	16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171)
WP_012026068.1	4297	0.02085	2.9	atgaaaaacaaaatttaataatataatcactgacactt	putative outer membrane protein, probably involved in nutrient binding
WP_012026259.1	4490	0.00199	2.8	atgaatttaatacgttttgactccgcaaacccatttccat	RND multidrug efflux transporter; Acriflavin resistance protein
WP_012025845.1	4060	0.01054	2.7	atgacagtagacataatattccaatggatacctgagt	Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8)
WP_012026180.1	4411	0.04757	2.6	atgaaaaatttagttatttattagcagttgcaattcagttac	Copper homeostasis protein CutF precursor / Lipoprotein NlpE involved in surface adhesion
SEP16691.1	568	0.04429	2.6	ttgctattatgaaaaaaacacaaactaagattttatagt	Response regulator receiver: Transcriptional regulatory protein, C- terminal
SHF95927.1	1833	0.02412	2.5	ttgccaactgaaaatctgaaaaatgatcatccaaaa	Methionine aminopeptidase (EC 3.4.11.18)
WP_011921605.1	94	0.00879	2.5	atgagccatttagacgatataaaaaatcacgccgga	Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21)
WP_012025858.1	4074	0.00397	2.5	atgaaacgatataattttgaaatataataggatctgt	RagB/SusD domain protein
WP_012023590.1	1583	0.00139	2.4	atgaaacaagaagaactacaagccatagcctctcaat	Biotin synthesis protein BioC
WP_012022472.1	385	0.04716	2.4	atgttgcaattaaatgtaagaacgaaacatctaggctt	NG, NG-dimethylarginine dimethylaminohydrolase 1 (EC 3.5.3.18)
WP_012026165.1	4396	0.00089	2.3	atggaaacaaacattaagatggttcggaccaaatgatcc	Mannonate dehydratase (EC 4.2.1.8)
WP_012026655.1	4918	0.00377	2.3	atgaatacagcagattttactacaacaatactgtgagc	hypothetical protein
WP_012024856.1	2932	0.00615	2.3	atgaataccaaaaatagaccatcagctagaaactta	Cysteine desulfurase (EC 2.8.1.7)
WP_012023797.1	1792	0.03633	2.2	atgagaaaacttgagaatagcgaattagaagaagaaa	TRNA/rRNA methyltransferase
WP_012022623.1	556	0.01067	2.2	atgccatttcagaattttgataacgaattcaacaaaa	FIG00651957: hypothetical protein
WP_012026675.1	4939	0.02216	2.2	atgaaaaaatctactcttaattgcattattctgcaccgt	hypothetical protein
WP_012023198.1	1163	0.03806	2.2	atgaaaaatttgacattaacgaagatccacacagacc	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)
WP_012025504.1	3697	0.03226	2.1	atgattagaattcagttttatttttagctttttagttgt	hypothetical protein
WP_012022715.1	651	0.00014	2.1	atgaaaaataaaactatacgcctttctacagttcttcgc	hypothetical protein
WP_012025247.1	3431	0.01325	2.1	atgtcgttttaacatcattaacagtagcaggaaaagatt	hypothetical protein
WP_012024304.1	2335	0.00569	2.1	atgattcatttctgagctcaaaaaataaatacagccat	Aminotransferase
WP_012026057.1	4285	0.02152	2.1	atgggattgaaaaataaaataactgcgattgtttggaa	putative large secreted protein
WP_012024919.1	3003	0.00072	2.1	atggcaaatatttcaacacactaccacttagattacaat	Ketol-acid reductoisomerase (EC 1.1.1.86)
WP_012025852.1	4068	0.00074	2.1	atgaaagtactctataacactattagcagatttttaattcta	glycoside hydrolase, family 43
WP_044047537.1	1189	0.02710	2.0	atggcattaaggcaggtgtgttaacaggattaggtgca	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41)
WP_012026676.1	4940	0.02970	2.0	atgtcaacagcaaaaaagattataaaagaatcacag	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
WP_012022972.1	922	0.03873	2.0	atgaaaaaagttatcatcacattatttttagtattcttg	hypothetical protein
WP_012026682.1	4946	0.03967	2.0	atgaaattagacatattagccttggcgcacatccggat	LMBE-RELATED PROTEIN

WP_012026316.1	4551	0.04159	2.0	atgaaaaaaatagttgaataccgcaagttactaaacgt	chaperone with DnaK; heat shock protein
WP_007803649.1	405	0.02033	2.0	atgggtacaacaagaatcaagactaaaagtagcagat	LSU ribosomal protein L14p (L23e)

Table S1B- Significantly downregulated proteins of *F. johnsoniae* grown on PY2 covered with pectin vs. DDW

NCBI annotation	gene number (RAST annotation)	Pectin/DDW: P-Value	Pectin/DDW: Fold change	DNA seq	RAST functional annotation
WP_011921578.1	2219	0.01329	0.0	atggattcagaattaattcgaagtcactcgcaggaa	Possible Galanin
WP_012022355.1	1796	0.01684	0.0	atgaaaaaagtatttttaagtttagctgtgtgttttaa	hypothetical protein
WP_012022481.1	2768	0.00263	0.1	atgaaaaatacagaacaaaaataactaaagatac	protein of unknown function DUF892
WP_012022486.1	2790	0.02104	0.1	atgaaaacagatacaaaagggaaccagcgcaggaa	hypothetical protein
WP_073099567.1	2317	0.00190	0.1	atgaaaaagtattattatacagcaaacgtactactat	Erk/YbiS/YcfS/YnhG family protein
WP_012022550.1	3180	0.01144	0.2	atggagccactatttattatccgactttgagccgcaad	hypothetical protein
WP_012023095.1	3303	0.00112	0.2	atgaaaaatttcagatgaaaagcagcagatctgt	Catalase (EC 1.11.1.6)
WP_012023270.1	4631	0.01186	0.2	atgaatcttataaaagaaacggaagccatgtccggc	Small heat shock protein
WP_012022355.1	263	0.00189	0.2	atgaaaaaaaattctaaaacttccgttttagcactatt	hypothetical protein
WP_044048264.1	1817	0.00385	0.2	atgatacatacagatgaaaccacacaagaagctgta	hypothetical protein
WP_012023815.1	2422	0.01124	0.2	atgactccaatatcgaataatctcccgaacttaaaa	Non-specific DNA-binding protein Dps / Iron-binding ferritin-like antioxidant protein / Ferroxidase (EC 1.16.3.1)
WP_012023822.1	3937	0.00564	0.2	atgaatcttatcaaaagaaatgcaaacagcatcgtg	Small heat shock protein
WP_012023992.1	1243	0.02321	0.2	ttgacacagttaaactgtctaaaaacagagctttaacc	Internalin-like protein (LPXTG motif) Lmo0331 homolog
WP_012024192.1	3531	0.00304	0.2	atgggagatcataaagaccttactgaagaattgctgtc	Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)
WP_012024286.1	5085	0.00000	0.3	atggaatacaaaagtagtaccattcgtagctcaatcgt	hypothetical protein
N/A	5088	0.00065	0.3	ttggaggaaattgtttgcaactggagctttggctggat	hypothetical protein
WP_012024386.1	3238	0.02224	0.3	atggaacacgcaacacagcagattcaaaagaggta	protein of unknown function DUF305
WP_012024486.1	3304	0.02676	0.3	atgaaaaattcagaaaaacaaataatacaaaagct	protein of unknown function DUF892
WP_012024493.1	5084	0.04047	0.3	atgtttaaaaaagtaataattgctgaagatcgcagca	hypothetical protein
WP_012024711.1	4786	0.02762	0.3	atgaaagtaataattgattgtttgtttttcggctgtttt	hypothetical protein
WP_012024727.1	1809	0.00592	0.3	atgaaaaaccaattgaaataccgaaacggcaatg	Malate synthase (EC 2.3.3.9)
WP_012025066.1	4223	0.00011	0.3	atgaaactatacaaaacttttactttgtctttttacaatg	hypothetical protein
SHK65708.1	2530	0.00116	0.3	atgaaaaataaactctgttttttagctgtttcactgttc	Mechanosensitive ion channel family protein
WP_012025127.1	3541	0.00945	0.3	atgaaaaagatactattagccagtaaagcaatttagg	putative exported protein
WP_012025128.1	1810	0.01642	0.3	atgaaaaacaacagaaagcagaattcaggaattgata	Isocitrate lyase (EC 4.1.3.1)
WP_012025137.1	5248	0.00410	0.3	atgagaatataaaaatagctgcccagttacattata	hypothetical protein
WP_012025282.1	407	0.01798	0.3	atgaaacaatcagaataaaagatctttctgcagcgg	LSU ribosomal protein L29p (L35e)
WP_012025337.1	476	0.01318	0.3	atgagttccaccattctcagataaaaagaatcattac	Ferric siderophore transport system, periplasmic binding protein TonB
WP_012025345.1	66	0.03714	0.3	atgaaattatacaaaatagcaaccgttcaatgtaaat	Cell division inhibitor
WP_073409277.1	437	0.03784	0.4	atgtctgaaattgccttattcagctagaaaaaccga	Magnesium and cobalt efflux protein CorC
WP_012025413.1	3314	0.01428	0.4	atggcaacaacttcaaaaacgctggagtatatgtgta	Phage tail sheath protein FI
WP_012025418.1	3606	0.01249	0.4	atgaaaaagtagtattagcttatagcggaggattaga	Argininosuccinate synthase (EC 6.3.4.5)
WP_012025595.1	2414	0.01205	0.4	atgaaagcatctagcacaatttagtttgcagcagcg	Gas vesicle protein
WP_012025730.1	4990	0.00398	0.4	atgcataatttagaaacaaattaaaaattgaaacta	hypothetical protein
WP_012026000.1	1058	0.01935	0.4	atggcattggaagatgagagaaaaactgaaaaaa	FIG00654500: hypothetical protein
WP_012026385.1	3793	0.00828	0.4	atgagttagggtattttccagacaactctgaaagaag	hypothetical protein
WP_012026531.1	4860	0.01204	0.5	atggaaaaaaaaccgaagaataactcctgagaaa	Low-complexity acidic protein, XCC2875 type
WP_089477404.1	3601	0.02595	0.5	atgaactacatctcaataaaagatcgcactcattaca	Ornithine carbamoyltransferase (EC 2.1.3.3)
ABQ07757.1	2523	0.00426	0.5	atgaaaaaaagtactaacactaacgcccctgtttttag	hypothetical protein
WP_012026811.1	1992	0.00004	0.5	atgaaaaaattattatcgcagcaatgtttttgtggaat	hypothetical protein
WP_044048134.1	3524	0.02029	0.5	atgaatgtaactttaaagaatctgctataagttcatt	Signal transduction histidine kinase
WP_012026814.1	3466	0.00608	0.5	atgataaaatacagcccacaaaactttaaagcctg	Antifreeze protein
WP_012026963.1	397	0.01510	0.5	atggctaattattagtaaaacaagtaagaagcaaga	LSU ribosomal protein L30p (L7e)

Table S2- Fold change of proteins related to *F. johnsoniae* gliding machinery in pectin vs. DDW

Protein	NCBI annotation	Gene Sequence	# unique peptides	Pectin/DDW: P-Value	Pectin/DDW: Fold change	Annotation by RAST
RemC	WP_012022324.1	atgaaaagaaaaatacttttcttgg	2	0.08363	13.0	Glycosyltransferase (EC 2.4.1.-)
Wzc	WP_012022466.1	atgttagatataaaagattttccatt	19	0.38789	0.9	Tyrosine-protein kinase Wzc (EC 2.7.10.2)
Wza	WP_012022467.1	atgacaaaaaatagctttatatac	5	0.14301	1.2	Polysaccharide export outer membrane protein
SprF	WP_012023064.1	atgatgttatctaaaaaattattac	4	0.06417	1.2	FIG00654737: hypothetical protein
SprB	ABL60886.1	atgaaaaaacctactattttaagaa	27	0.00858	1.3	internalin, putative
SprD	WP_012023066.1	atgaagaaaattttactattcataac	28	0.06564	0.6	ToIA protein
SprC	WP_012023067.1	atgattcaaaaaactactttatcttt	7	0.62616	0.9	FIG00654018: hypothetical protein
RemG	WP_012023069.1	atgaaaaaaattactcaaatgatc	6	0.19823	1.1	FIG00653638: hypothetical protein
RemF	WP_012023070.1	atgaaagggaaaatttttatttag	1	0.25834	0.7	FIG00655764: hypothetical protein
GldE	WP_012023105.1	atgaaaatttcgataggaacgac	7	0.09691	0.7	Ribose 5-phosphate isomerase B (EC 5.3.1.6)
SprE	WP_012023137.1	ttgtataatggaggcttgacttga	13	0.06601	0.8	TPR domain protein
SprT	WP_012023545.1	atgagaaaaattgtaatcgctattt	4	0.49504	1.1	PorT protein
GldA	WP_012023594.1	atgtcगतagaagtaaacagtata	4	0.54640	1.1	ABC transporter, ATP-binding protein
GldD	WP_012023616.1	atgttaaaaaaatccttcagtaa	2	0.25781	1.6	GldD
PorV	WP_012023631.1	atgaaaaaaatatcgcttctatta	15	0.19036	1.4	FIG00650346: hypothetical protein
SprA	WP_012023729.1	atggagttagaaaatcctccaagc	28	0.03250	1.1	FIG00648977: hypothetical protein
RemB	WP_012023733.1	gtgaataagttattttatctttatcat	4	0.10729	2.1	FIG00654784: hypothetical protein
GldB	WP_012023869.1	atgaaaatgtatcgctttagtggt	6	0.07962	2.7	GldB
GldC	WP_012023870.1	atgtcaaatacaataaaatcagaa	1	0.83912	0.9	GldC
GldJ	WP_012023929.1	atgaagaagtttattgcatttgcagc	19	0.05145	0.9	GldJ
GldL	WP_012023930.1	atggcattattaagtaaaaaagtta	23	0.27486	1.1	FIG00648934: hypothetical protein
GldM	WP_012023931.1	atgtatctggtttcatcgcaatgta	53	0.00280	1.1	FIG00649784: hypothetical protein
GldN	WP_012023932.1	atgaaagtaagaaatttttaatagc	15	0.96310	1.0	GldN
GldO	WP_012023933.1	atgaaagtaaggaatttttaattgc	15	0.02686	0.7	GldN
GldI	WP_012024435.1	atgaactactaaaaatcagcattt	4	0.47280	1.0	GldI
GldG	WP_012024782.1	atgaaagcatctaataaattaaatc	11	0.64396	1.0	gliding motility protein GldG
RemI (RemG-paralog)	WP_012025180.1	atgattgtttactgctgacagctgc	7	0.34787	1.8	FIG00653638: hypothetical protein

Table S3- Pectin induced TonB regulated gene clusters

Cluster 1

NCBI annotation	# unique peptides	Pectin/DDW: P-Value	Pectin/DDW: Fold change	Gene Sequence	Signal Peptide?	RAST annotaion
WP_012026221.1	1	0.05681	18.2	atgaaatatttacttctattattaatttctctatgtttcatttgctcagcaaaataatttccaagagcaaa	Y	Polygalacturonase (EC 3.2.1.15)
WP_012026223.1	5	0.00058	6	atgaaaaatataaaaatcggtattcttctcctttccggtttttctttcaaaaaatacggcacaagcc	Y	Beta-xylosidase (EC 3.2.1.37)
WP_044048002.1	11	0	4.6	atgtcggttttattagtttgcgtaatggcttaacaggctgtaaagtaactcacaagaaacggcaaa	Y	Rhamnogalacturonides degradation protein RhiN
WP_012026225.1	5	0.0193	11.2	atgataaagaaaagccatftttagtttgcccaaatcatgcttataagatgatgctgttttcattgaat	Y	Rhamnogalacturonides degradation protein RhiN
WP_012026226.1	2	0.08763	7.4	atgaactataaaaaaacagtcctttgcatftttctgtgtacagcatftttactgttaggtcagaacaat	Y	Rhamnogalacturonides degradation protein RhiN
SHH12854.1	7	0.00449	11.9	atgtaggaatgattgttacaagcttaagttctgcagcaattatatagaggaggaaagttatcaa	N	RagB/SusD domain protein
WP_012026229.1	28	0.00035	8.4	atgaacattcaaaaatcattaaagaaaaataaaatacaatctgtattttttctgaattttc	Y	TonB family protein / TonB-dependent receptor
WP_012026230.1	2	0.13578	2.8	ttgactatatcatgctcaaaaaaattactcctgaagctgaaactgatccgtggaaaactatgga	N	Polygalacturonase (EC 3.2.1.15)
WP_012026231.1	6	0.00004	3.7	atgagcgaaaaagtaaccattatgatattgccgaaaaactaaatcactgcagctactgtttcc	N	Hexuronate utilization operon transcriptional
WP_012026232.1	12	0.00037	5.7	atggcagcgcagaaaaaattgataaaagttcacccaaccgacaatgtagcggttgctttggtgg	N	Altronate hydrolase (EC 4.2.1.7)
WP_012026233.1	14	0.00003	7.7	atggaaaaattaacagatcaaattcagagttttcaaacaggctccaattaaaattgtacaattt	N	Altronate oxidoreductase (EC 1.1.1.58)
WP_012026234.1	3	0.00005	6.8	atggcaaatattcaagaatagaggttgcgcagacaatgaaagataacggaatggtgccgttg	N	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-
WP_044048511.1	6	0.00013	3.8	atgagtagagtagttgcatttgagaaatcatgctgcgtttatcgacagaaagacatttacgttttc	N	deoxygluconate kinase (EC 2.7.1.15)
WP_012026236.1	15	0.00006	6.4	atgagcgcgaaatacattcatacagacaatttttattagaaaataaatacgcgtgaagagtatat	N	Uronate isomerase (EC 5.3.1.12)
WP_012026237.1	11	0.01289	3.5	atgacaaaactatttgacataaaaggaaaagttgcccttattacaggaagtacgcacggactgg	N	2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.175)
OXE95634.1	7	0.004	4.8	atgacaaaatagttcaagatacgcgtcaagtccagaagctgtaaaaaatgatcacaca	N	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)
WP_012026239.1	3	0.00163	4.6	atgagtcaaaccgatgctgttacagtaaatcaaaccgtaagtccgcaggaagatatcgttgga	N	Hexuronate transporter
WP_012026240.1	5	0.73526	1	ttgaaaaacacaaaaaccctttatttactcactgtcctgtttttcaggaattgtattacattcaagt	Y	Xylanase

Cluster 2

NCBI annotation	# unique peptides	Pectin/DDW: P-Value	Pectin/DDW: Fold change	Gene Sequence	Signal Peptide?	RAST annotaion
WP_012022292.1	10	0.00148	203.9	cgtaacagagattttagttcagccaggtaataataacccacaccataacagcagaagaaaaag	Y	hypothetical protein
WP_012022293.1	15	0.00954	8.4	ttaaagcatggggtgatgttcctgctcgtttgaacctatcactacagcaactttatattgcctaaat	Y	putative outer membrane protein, probably involved in nutrient binding
WP_012022294.1	34	0.00139	22.1	gtaacatcagcagagggttcgcctgatgccgatatacgaattagagttcgtggaggaggatcat	Y	TonB family protein / TonB-dependent receptor

Cluster 3

NCBI annotation	# unique peptides	Pectin/DDW: P-Value	Pectin/DDW: Fold change	Gene Sequence	Signal Peptide?	RAST annotaion
WP_012022634.1	3	0.10566	1.8	atgaaaatcaattttaaaaaacgtacaaattgctataaaatcggcattgtatcagcttttctc	N	Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)
SEP16691.1	3	0.04429	2.6	ttgctatttataaaaaaacacaaactaagattttattagttgacgacgaaccggatatctagaa	N	Response regulator receiver:Transcriptional regulatory protein, C-terminal
WP_012022636.1	30	0.05111	3.6	atgaacaatgatccgttgccttttgcctttgcaaatgtttagttaaagggtacaaacattagcgtaaataccg	N	TonB-dependent receptor
WP_012022637.1	22	0.00997	14.4	atgaaaaaatcaattttaaattcgttacagttgtgtcttatcaggagggttacttacaagctgtcta	Y	FIG00649626: hypothetical protein
WP_012022639.1	1	0.00753	47.1	ttgattacagccagcgatatattacaattcaagccataaacaattgaaaaaacagcattaaa	N	Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19)

Cluster 4

NCBI annotation	# unique peptides	Pectin/DDW: P-Value	Pectin/DDW: Fold change	Gene Sequence	Signal Peptide?	RAST annotaion
WP_012026068.1	5	0.02085	2.9	atgaaaacaaaatttaataaatatatactcagcacttttacttattgtaggtgcttcgtgcagcga	Y	putative outer membrane protein, probably involved in nutrient binding
WP_012026069.1	5	0.05904	5.4	atgaaacaagcacttttaagagatgtagtttctttgttgcactgatgagtgtaattacttatgctc	Y	TonB family protein / TonB-dependent receptor
WP_012026070.1				atgaaatacattctaacctatttttaataacaacactttcaatatcagcccaaacgcttgataacaaattgacattaa		rhamnogalacturonan acetylsterase

WP_012026071.1	2	0.00094	4.4	atgaaaagaacatcatcatatcctcttatttcttcaaccgtaatcttgcgagaacaagggtt	Y	Putative glycosyl hydrolase of unknown function (DUF1680)
WP_012026072.1	7	0.18079	2.5	atgataaagaattaataagcggtgctgtttgtccttgcttggaccacaaacggacaagcaca	Y	COG3866 Pectate lyase

*Validated by qPCR

Table S4- Pectin induced up regulated SusC/D proteins in *F. johnsoniae*

SusC-like protein				
NCBI annotation	DNA seq.	fold change	p-Value	Predicted substrate
WP_012022294.1	atgaatttaaagattattaacaaaggagca	22.12	0.00139	
WP_012026069.1	atgaaacaagcactttaagagatgtagtttc	5.38	0.05904	pectins
WP_012026168.1	atgtgtacagaccgaaaaatcaaatcgttaaa	102.43	0.00484	
WP_012026229.1	atgaacattcaaaaatcattaaagaaaaaat	8.39	0.00035	pectins

SusD-like protein				
NCBI annotation	DNA seq.	fold change	p-Value	Predicted substrate
WP_012022293.1	atgaaacataaattaataatagcaggattgata	8.36	0.00954	
WP_012024115.1	atgaaatatagtttaaaataaaaacattaggag	11.61	0.03876	
WP_052295191.1	atgaaaaatataaaaataacactttcattattatt	3.22	0.04623	peptides
WP_012025858.1	atgaaacgatatatttttagaaatttaataatagg	2.46	0.00397	hemicelluloses
WP_012026068.1	atgaaaacaaaatttaataaatatatactactgg	2.87	0.02085	pectins
SHH12854.1	atgtaggaatgattgttacaagcttaagttcttgc	11.86	0.00449	pectins

TableS5- List of primers for qPCR

Primer name	NCBI accession number	RAST annotation	Forward primer	Reverse primer	Tm	Amplicon length
Target genes						
TonB_445	WP_012022294	TonB family protein / TonB-dependent receptor	GGGTATAGACTGCCTCCTGTAA	TCCTCCTCCACGAACTCTAAT	62	92
Transcript_regul YafY family	WP_012022876	transcriptional regulator, putative	GGGTATAGACTGCCTCCTGTAA	GCGTAGTGTGTTCCCAAAGA	63/62	110
auxin_regulated protein	WP_012023111	putative auxin-regulated protein	ACAGCGGGTACCAACATTGTAA	CGTGGTACGGCAGTCCATT	58	79
SusD_73	SHH12854.1	RagB/SusD domain protein	CCTGCCGATGCAACCTATAA	AACCACGGATTTCTCCATAAA	62	98
TonB_260	WP_012026229	TonB family protein / TonB-dependent receptor	GCTTTCAAACGCAGGAAGTAAG	GAACCGTATCCTACAACCACTAC	62	106
TonB_2144	WP_012026069	TonB family protein / TonB-dependent receptor	GGCGCTGGCTTGTCTTTAT	TGATTGTTGCATCCCATTTAATATCT	58/59	132
Pectate-lyase	WP_012026072	COG3866 Pectate lyase	AACTGACGGAGGAGCAAAC	ACCTTCGTGTTGTGCATTTAAG	62	100
RemA_847	WP_012022896	internalin, putative RemA	GGAGAGACAAATAGCGGTACAA	ATGGCCTATCCAGGTGTTATTT	62	102
Reference genes						
Electron transfer flavoprotein, alpha subunit- ETF	WP_012023552	Electron transfer flavoprotein, alpha subunit, Threonine synthase	TTTAACCCGACACTTGGAGAC	CGATATCAGCATCGGCAATAGA	62	94
DNA gyrase subunit B (EC 5.99.1.3) -GyrB	WP_012024321	DNA gyrase subunit B	GAGAGGTTGTATCTCCGGTTTC	GAGCCTGAGCTGCTAAGATTAC	62	117
16S rRNA		16S rRNA	CGGCAACGAGCGCAACCC	CCATTGTAGCACGTGTGTAGCC	55	130

Table S6 - Predicted operons in TonB related cluster 1

Tool 1-

Operon Mapper: Bacterial Operon Prediction

Operon	NCBI annotation	Sequence	gene function	start	end	Strand	Operon mapper annotation
1	OXE95634.1	atgacaaaa	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)	215	1054	+	5-keto 4-deoxyuronate isomerase
1	WP_012026237.1	atgacaaac	2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)	1059	1850	+	R] Dehydrogenases with different specificities
1	WP_012026236.1	atgagcgca	Uronate isomerase (EC 5.3.1.12)	1875	3278	+	Glucuronate isomerase
1	WP_044048511.1	atgagtaga	2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	3432	4478	+	Sugar kinases, ribokinase family
1	WP_012026234.1	atggcaaaa	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyg	4491	5159	+	2-keto-3-deoxy-6-phosphogluconate aldolase
1	WP_012026233.1	atggaaaaa	Altronate oxidoreductase (EC 1.1.1.58)	5333	6817	+	Mannitol-1-phosphate/altronate dehydrogenases
1	OXE95634.1	atgacaaaa	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)	6856	8478	+	Altronate dehydratase
2	WP_012026231.1	atgagcgaa	Hexuronate utilization operon transcriptional repressor ExuR	8719	9747	-	Transcriptional regulators
3	WP_012026230.1	ttgactatc	Polygalacturonase (EC 3.2.1.15)	10038	11465	+	Endopolygalacturonase
3	WP_012026229.1	atgaacattc	TonB family protein / TonB-dependent receptor	11511	14615	+	
3	SHH12854.1	atgtaggaa	RagB/SusD domain protein	14628	16301	+	
4	WP_012026227.1	ttgatttaatg	Pectinesterase (EC 3.1.1.11)	16406	17362	+	Hydrolases of the alpha/beta superfamily
4	WP_012026226.1	atgaactata	Rhamnogalacturonides degradation protein RhiN	17383	18603	+	Predicted unsaturated glucuronyl hydrolase
4	WP_012026225.1	atgataaaga	Rhamnogalacturonides degradation protein RhiN	18616	19821	+	Predicted unsaturated glucuronyl hydrolase
4	WP_044048002.1	atgctggttta	Rhamnogalacturonides degradation protein RhiN	19871	21064	+	Predicted unsaturated glucuronyl hydrolase

Tool 2-

FGENESB: Bacterial Operon and Gene Prediction

Operon	NCBI annotation	Sequence	gene function	start	end	Strand	score
1	OXE95634.1	atgacaaaa	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)	215	1054	+	470
1	WP_012026237.1	atgacaaac	2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)	1059	1850	+	587
1	WP_012026236.1	atgagcgca	Uronate isomerase (EC 5.3.1.12)	1875	3278	+	725
2	WP_044048511.1	atgagtaga	2-dehydro-3-deoxygluconate kinase (EC 2.7.1.45)	3456	4478	+	687
2	WP_012026234.1	atggcaaaa	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyg	4491	5159	+	422
3	WP_012026233.1	atggaaaaa	Altronate oxidoreductase (EC 1.1.1.58)	5369	6817	+	1054
3	WP_012026233.1	atggaaaaa	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)	6856	8478	+	1196
4	WP_012026231.1	atgagcgaa	Hexuronate utilization operon transcriptional repressor ExuR	8719	9747	-	651
5	WP_012026230.1	ttgactatc	Polygalacturonase (EC 3.2.1.15)	10038	11465	+	717
5	WP_012026229.1	atgaacattc	TonB family protein / TonB-dependent receptor	11511	14615	+	1667
5	SHH12854.1	atgtaggaa	RagB/SusD domain protein	14646	16301	+	1049
6	WP_012026227.1	ttgatttaatg	Pectinesterase (EC 3.1.1.11)	16406	17362	+	335
6	WP_012026226.1	atgaactata	Rhamnogalacturonides degradation protein RhiN	17383	18603	+	872
6	WP_012026225.1	atgataaaga	Rhamnogalacturonides degradation protein RhiN	18616	19821	+	799
6	WP_044048002.1	atgctggttta	Rhamnogalacturonides degradation protein RhiN	19871	21062	+	848

*Validated by qPCR