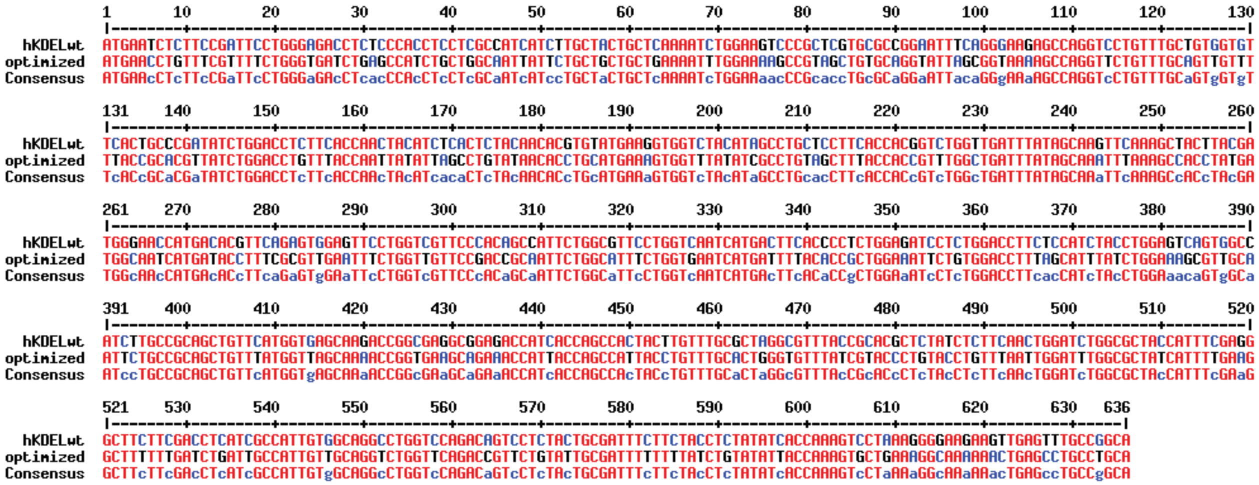
Supplementary data

Supplementary figure 1. Alignment of the cDNA derived and for *E. coli* expression optimised hKDEL genes.

Alignment of the cDNA derived gene encoding hKDEL (KDELR1 ERD 2.1) and for expression in *E. coli* optimised version as desigened by Geneart (www.geneart.com). The figure was created using the program multalin (Corpet, F. (1988). Multiple sequence alignment with hierarchical clustering. *Nucleic Acids Res* **16**, 10881-90)**.** The stop codon is missing since in this study the gene encoding hKDEL is fused through a linker to *gfp* (see “Material and Methods”).



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          1       10        20        30        40        50        60        70        80        90        100       110       120       130
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  hKDELwt ATGAATCTCTTCCGATTCCTGGGAGACCTCTCCCACCTCCTCGCCATCATCTTGCTACTGCTCAAAATCTGGAAGTCCCGCTCGTGCGCCGGAATTTCAGGGAAGAGCCAGGTCCTGTTTGCTGTGGTGT
optimized ATGAACCTGTTTCGTTTTCTGGGTGATCTGAGCCATCTGCTGGCAATTATTCTGCTGCTGCTGAAAATTTGGAAAAGCCGTAGCTGTGCAGGTATTAGCGGTAAAAGCCAGGTTCTGTTTGCAGTTGTTT
Consensus ATGAAcCTcTTcCGaTTcCTGGGaGAcCTcacCCAcCTcCTcGCaATcATccTGCTaCTGCTcAAAATcTGGAAaacCCGcaccTGcGCaGGaATTacaGGgAAaAGCCAGGTcCTGTTTGCaGTgGTgT

          131     140       150       160       170       180       190       200       210       220       230       240       250       260
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  hKDELwt TCACTGCCCGATATCTGGACCTCTTCACCAACTACATCTCACTCTACAACACGTGTATGAAGGTGGTCTACATAGCCTGCTCCTTCACCACGGTCTGGTTGATTTATAGCAAGTTCAAAGCTACTTACGA
optimized TTACCGCACGTTATCTGGACCTGTTTACCAATTATATTAGCCTGTATAACACCTGCATGAAAGTGGTTTATATCGCCTGTAGCTTTACCACCGTTTGGCTGATTTATAGCAAATTTAAAGCCACCTATGA
Consensus TcACcGCaCGaTATCTGGACCTcTTcACCAAcTAcATcacaCTcTAcAACACcTGcATGAAaGTGGTcTAcATaGCCTGcacCTTcACCACcGTcTGGcTGATTTATAGCAAaTTcAAAGCcACcTAcGA

          261     270       280       290       300       310       320       330       340       350       360       370       380       390
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  hKDELwt TGGGAACCATGACACGTTCAGAGTGGAGTTCCTGGTCGTTCCCACAGCCATTCTGGCGTTCCTGGTCAATCATGACTTCACCCCTCTGGAGATCCTCTGGACCTTCTCCATCTACCTGGAGTCAGTGGCC
optimized TGGCAATCATGATACCTTTCGCGTTGAATTTCTGGTTGTTCCGACCGCAATTCTGGCATTTCTGGTGAATCATGATTTTACACCGCTGGAAATTCTGTGGACCTTTAGCATTTATCTGGAAAGCGTTGCA
Consensus TGGcAAcCATGAcACcTTcaGaGTgGAaTTcCTGGTcGTTCCcACaGCaATTCTGGCaTTcCTGGTcAATCATGAcTTcACaCCgCTGGAaATcCTcTGGACCTTcacCATcTAcCTGGAaacaGTgGCa

          391     400       410       420       430       440       450       460       470       480       490       500       510       520
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------|
  hKDELwt ATCTTGCCGCAGCTGTTCATGGTGAGCAAGACCGGCGAGGCGGAGACCATCACCAGCCACTACTTGTTTGCGCTAGGCGTTTACCGCACGCTCTATCTCTTCAACTGGATCTGGCGCTACCATTTCGAGG
optimized ATTCTGCCGCAGCTGTTTATGGTTAGCAAAACCGGTGAAGCAGAAACCATTACCAGCCATTACCTGTTTGCACTGGGTGTTTATCGTACCCTGTACCTGTTTAATTGGATTTGGCGCTATCATTTTGAAG
Consensus ATccTGCCGCAGCTGTTcATGGTgAGCAAaACCGGcGAaGCaGAaACCATcACCAGCCAcTACcTGTTTGCaCTaGGcGTTTAcCGcACcCTcTAcCTcTTcAAcTGGATcTGGCGCTAcCATTTcGAaG

          521     530       540       550       560       570       580       590       600       610       620       630   636
          |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+---------+-----|
  hKDELwt GCTTCTTCGACCTCATCGCCATTGTGGCAGGCCTGGTCCAGACAGTCCTCTACTGCGATTTCTTCTACCTCTATATCACCAAAGTCCTAAAGGGGAAGAAGTTGAGTTTGCCGGCA
optimized GCTTTTTTGATCTGATTGCCATTGTTGCAGGTCTGGTTCAGACCGTTCTGTATTGCGATTTTTTTTATCTGTATATTACCAAAGTGCTGAAAGGCAAAAAACTGAGCCTGCCTGCA
Consensus GCTTcTTcGAcCTcATcGCCATTGTgGCAGGcCTGGTcCAGACaGTcCTcTAcTGCGATTTcTTcTAcCTcTATATcACCAAAGTcCTaAAaGGcAAaAAacTGAGccTGCCgGCA
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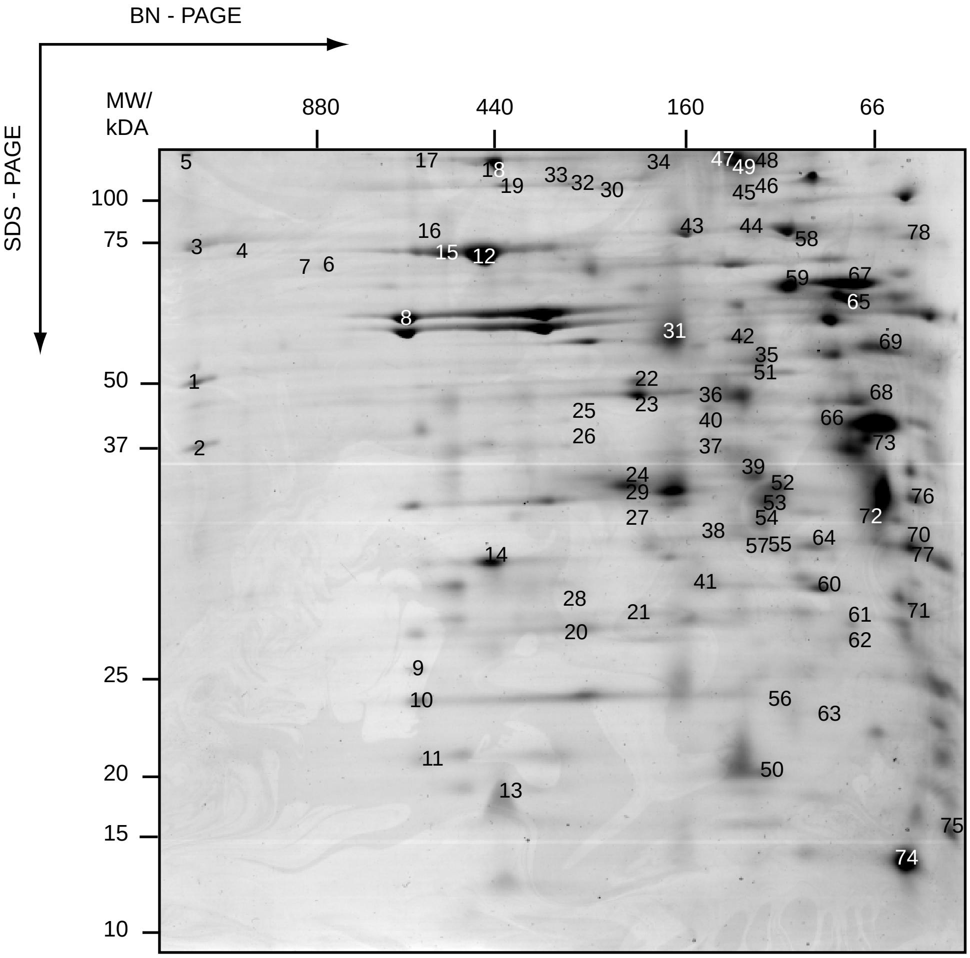
-Supplementary Figure 1-

Supplementary figure 2. 2D BN/ SDS gel of cytoplasmic membranes of C43(DE3) cells not overexpressing hKDEL-GFP.

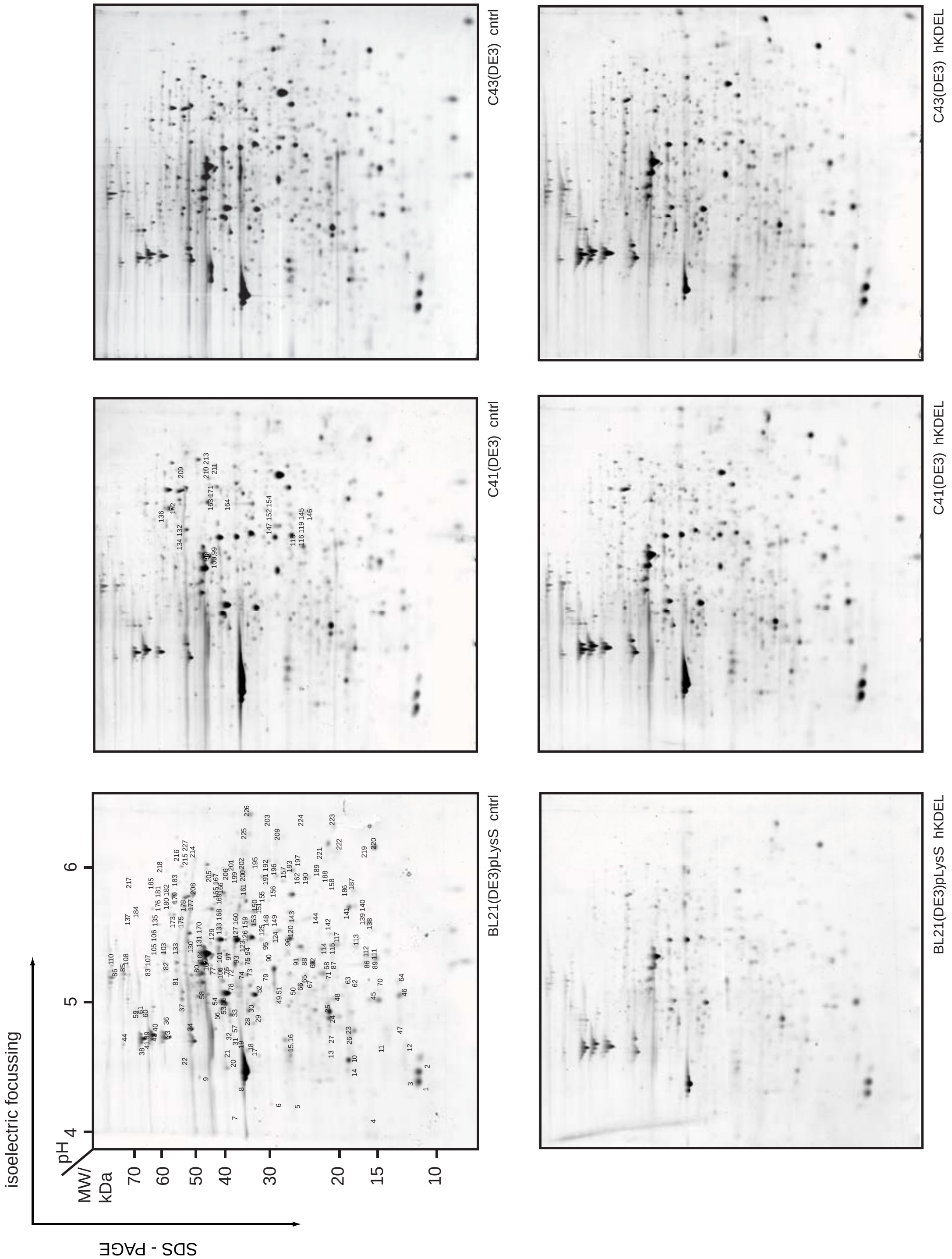
Cytoplasmic membrane fractions of cells expressing hKDEL-GFP and non-expressing control cells were isolated and analysed using 2D BN/ SDS-PAGE combined with colloidal Coomassie staining as described in “Material and Methods”. A representative gel of C43(DE3) control membranes is shown here. The numbers in the gel refer to the numbers in supplementary table 1.



-Supplementary Figure 2-

Supplementary figure 3. 2D SDS gels of whole cell lysates of BL21(DE3)pLysS, C41(DE3) and C43(DE3) cells overexpressing hKDEL-GFP and controls by 2D gel electrophoresis.

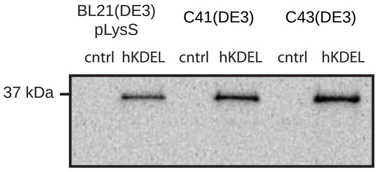
Whole cell samples of cells expressing hKDEL-GFP and control cells were cultured and prepared for 2D SDS-PAGE as described in “Material and Methods”. Each condition was run in quadruplet; each of the four representing a biologically independent sample. The gels were stained by colloidal Coomassie. Quantification data and results of the ANOVA analysis are presented in supplementary table 2. The numbers in the gel in the upper corner on the left refer to the numbers in supplementary table 2.



-Supplementary Figure 3-

Supplementary figure 4. Immuno-blot analysis of BL21(DE3)pLysS, C41(DE3) and C43(DE3) cells expressing hKDEL-GFP and control cells with a GFP antibody.

After 4 h of induction proteins of whole cell lysates of BL21(DE3)pLysS, C41(DE3) and C43(DE3) cells with the empty control vector and overexpressing hKDEL-GFP were separated by means of SDS-PAGE and subsequently subjected to immuno-blotting analysis with an antibody against GFP (see “Material and Methods”). The hKDEL-GFP bands represent the fluorescent bands shown in figure 1C.



-Supplementary Figure 4-

Supplementary Table 1: Relative quantification and mass spectrometry identification of spots from 2D BN/ SDS gels of cytoplasmic membranes of cells overexpressing hKDEL-GFP and control cells.
2D BN/ SDS gels of cytoplasmic membranes were analysed as described by Klepsch et al. (Klepsch, M., Schlegel, S., Wickstrom, D., Friso, G., van Wijk, K. J., Persson, J. O., de Gier, J. W. & Wagner, S. (2008). Immobilization of the first dimension in 2D blue native/ SDS-PAGE allows the relative quantification of membrane proteomes. Methods 46, 48-53). For each spot a two-way ANOVA with treatment (i.e., hKDEL-GFP overexpression) and strain as factors was performed on log transformed data, resulting in a p-value for each spot. Spots with missing data in all replicates, for some combination of treatment and strain, were excluded from the ANOVA-analysis. The effect of those 43 spots was “qualitative”. Significant effects for “treatment”, “strain”, “treatment and strain” (no interaction), and “interaction” were found for 35 spots. Non-identifiable proteins were excluded from the data set. In the end, 80 proteins in 78 spots remained. A grouping of the spots on the kind of effect was done. The effects were “treatment”, “strain”, “Treatment and strain (no interaction)” and “interaction”. Furthermore, matrix and/ or auto-proteolytic trypsin fragments were removed by the software Peak Eraser v2.01 (Lighthouse data). Gray coloring groups proteins belonging to the same complex.

Abbreviations: acc., accession; quant., quantitation.

						ANOVA						BL21(DE3)pLysS				C41(DE3)				C43(DE3)			
spot Nr. (a)	gene name (b)	UniProt acc.	predicted MW (kDa) (precursor/ mature) (c)	observed MW (kDa) (d)	observed mass in complex (d)	p-value model	p-value treatment	p-value strain	p-value interaction	effect	standard deviation	quant. value (control) (e)	CV (control) (f)	quant. value (KDEL-OE) (e)	CV (KDEL-OE) (f)	quant. value (control) (e)	CV (control) (f)	quant. value (KDEL-OE) (e)	CV (KDEL-OE) (f)	quant. value (control) (e)	CV (control) (f)	quant. value (KDEL-OE) (e)	CV (KDEL-OE) (f)
1	hflK	P0ABC7	45.5	40.87	1142	0.003538	0.00657	0.002028	0.749241	beh and strain	0.740499	303.4	61.40%	650.8	16.10%	1478.4	46.60%	6284.1	27.30%	1631.1	110.00%	3593.9	63.80%
2	hflC	P0ABC3	37.7	37.7	1130	0.012375	0.287844	0.098255	0.005041	interaction	0.657169	2054.9	29.50%	493.2	17.70%	1271.6	80.80%	5024.6	27.00%	912.3	90.90%	1972	61.30%
3	hflB	P0AAI3	70.7	72.12	1100	0.000395	9.32E-01	0.002459	0.000324	interaction	0.456884	5602.4	35.50%	1270.7	62.70%	1834.2	11.20%	7778.7	27.90%	1130.3	48.20%	1287.6	36.20%
4	nuoCD	P33599	68.7	68.39	1036	0.022801	0.547257	0.006196	0.205216	strain only	0.553653	655.4	44.40%	321.8	62.80%	706.4	28.20%	891.1	82.90%	183.2	47.10%	231.3	8.50%
5	nsrR	P0AF63	15.6	124	1200	0.000145	0.942593	1.93E-05	0.250627	strain only	0.455391	1100	41.20%	599.2	20.50%	3000.7	32.60%	3783	28.20%	367.5	67.50%	412.1	36.40%
6	nuoCD	P33599	68.7	63.45	829					qualitative		299.3	49.00%		0.00%	1032.7	46.00%	2278.3	55.00%	89	62.30%	226.4	59.70%
7	nuoCD	P33599	68.7	63.12	877					qualitative		98.1	17.80%		0.00%	121.6	63.10%	2701.4	162.50%	8.6	131.00%	45.8	60.90%
8	atpA	P0ABB0	55.2	48.32	634	0.006748	0.067	0.001875	0.417535	strain only	0.290311	17556.4	46.40%	17153.9	9.00%	9608.4	11.50%	15831.7	13.80%	24522.9	39.80%	32241.2	30.80%
9	atpH	P0ABA4	19.3	22.02	612	2.47E-06	0.129317	2.18E-07	0.508966	strain only	0.502353	207	27.50%	243.7	70.20%	4053.1	38.90%	7829.5	49.80%	327	55.60%	495.7	14.60%
10	atpF	P0ABA0	17.3	19.95	604	1.68E-06	0.047375	1.65E-07	0.308945	beh and strain	0.438448	622.5	6.80%	663	46.10%	8895.3	54.10%	16193.4	1.00%	782.8	45.40%	1467.8	43.70%
11	atpC	P0A6E6	15.1	16.5	592					qualitative			0.00%	7756.3	29.20%	4298.9	17.40%	11260.8	20.60%	7213.5	85.60%	313	64.30%
12	sdhA	P0AC41	64.4	68.39	447	6.39E-04	3.13E-01	0.000741	0.002731	interaction	0.256781	65448	55.10%	137739.8	18.60%	71216.9	7.40%	44231.2	24.90%	117559	6.50%	124406.6	14.20%
13	sdhC	P69054	14.3	14.77	411	3.65E-03	2.86E-01	0.000891	0.128126	strain only	1.385731	50556.4	86.30%	952.6	91.50%	63536.4	22.90%	84704.8	35.80%	1266.4	8.10%	1798	27.90%
14	sdhB	P07014	26.8	31.3	430	0.001806	0.774697	0.000523	0.040427	interaction	0.374502	5019.8	78.70%	8523.6	20.50%	24940.4	9.20%	15068	35.90%	8753.8	31.00%	8540.6	14.50%
14	manZ	P69805	31.3	31.3	430	0.001806	0.774697	0.000523	0.040427	interaction	0.374502	5019.8	78.70%	8523.6	20.50%	24940.4	9.20%	15068	35.90%	8753.8	31.00%	8540.6	14.50%
15	nuoCD	P33599	68.7	68.87	539	0.000705	0.075022	0.000132	0.254171	strain only	0.319349	31093.4	33.10%	18192.4	16.50%	10613.7	14.00%	7335.4	45.00%	23375.4	30.00%	24917.8	20.90%
16	fdoH	P0AAJ5	33.1	78.5	574					qualitative			0.00%	356.8	36.60%	390.2	15.30%		0.00%		0.00%		0.00%
17	fdoG	P32176	112.5	116.93	596					qualitative		384.5	26.20%	102	32.10%		0.00%		0.00%	155.4	52.60%	306.5	54.50%
18	acrB	P31224	113.574	113.55	423	0.001206	0.70138	0.000668	0.009937	interaction	0.388026	30437.5	35.80%	10755.2	16.50%	4004.3	17.80%	7660.1	38.60%	10863.2	33.00%	13943.3	50.70%
19	yrbD	P64604	19.6/16.5	105.07	408					qualitative			0.00%		0.00%	899.6	3.80%	1425.4	59.20%		0.00%		0.00%
20	atpB	P0AB98	30.3	25.06	280					qualitative		618.8	54.00%	470.7	45.30%		0.00%	420.2	22.70%	453.8	23.40%	556.5	22.80%
21	malG	P68183	32.2	26.37	230	0.017697	0.076149	0.025559	0.051178	strain only	0.66711	792.5	46.20%	798	19.70%	598.8	44.50%	127.5	79.70%	479.2	57.70%	407.9	43.70%
22	malF	P02916	57	40.97	237	0.003052	0.114783	0.003229	0.014893	interaction	0.353692	2273.1	35.30%	2927.1	18.20%	1956.7	28.90%	726.7	50.10%	1262.9	22.50%	1175.5	15.20%
23	malK	P68187	41	40.19	238	0.000969	0.046543	0.006158	0.001413	interaction	0.268324	7394.1	8.60%	10676.7	8.00%	8474.4	12.20%	3060	49.50%	6284.8	26.20%	5552.9	3.90%
24	arnC	P77757	36.3	35.39	244	8.09E-04	8.45E-01	9.84E-05	0.293888	strain only	0.838344	717.4	35.10%	341.9	28.10%	8409	41.30%	33981.3	87.60%	3011.9	79.50%	1780.5	20.50%
25	yfgL	P77774	41.9	39.01	301	0.003505	9.29E-01	0.001504	0.028595	interaction	0.803313	1832.4	19.20%	361.3	33.40%	153.8	73.90%	594.4	108.60%	96.3	73.50%	137.6	95.10%
26	nlpB	P0A903	36.8	37.75	303	0.001345	0.542013	0.001216	0.005629	interaction	0.640397	1602.4	26.40%	268.2	16.50%	207.8	85.50%	709.3	92.80%	123.6	59.00%	104	15.50%
27	yhbG	P0A9V1	26.8	32.4	251					qualitative			0.00%		0.00%	1041.5	17.10%	902.7	43.00%		0.00%		0.00%
28	mscS	P0C0S1	30.9	28.18	279	0.014781	0.340582	0.003325	0.299331	strain only	0.397178	451.3	16.20%	370.1	31.50%	973.6	4.50%	674.9	60.70%	250.1	11.80%	326.1	44.90%
29	nlpB	P0A903	36.8	34.49	247					qualitative			0.00%		0.00%	3327	52.70%	3100.5	45.50%		0.00%		0.00%
30	pnp	p05055	77.1	99.72	258	7.83E-03	4.00E-01	0.003874	0.046738	interaction	0.426665	584.6	40.40%	1038.8	22.70%	3026.7	31.80%	1751.6	65.90%	1963.9	35.70%	1185.8	34.90%
31	cyoB	P0ABI8	74.4	44.61	210	2.07E-07	6.32E-01	1.58E-08	0.457104	strain only	0.402559	130074.8	28.80%	108380.6	29.00%	4160.3	23.10%	5083.3	70.10%	49514.3	39.20%	74088.4	34.20%
32	yaeT	P0A940	90.6	102.12	295	0.000409	0.586262	0.000104	0.023437	interaction	0.686764	6785.1	21.20%	2385.5	28.60%	370.6	84.10%	1517.2	96.40%	346.3	39.90%	371.9	35.60%
33	yrbD	P64604	19.6	105.89	315					qualitative			0.00%		0.00%	503.5	30.40%	1218.9	66.50%	303.9	108.50%	127.1	68.50%
34	nuoG	P33602	100.2	124.69	228					qualitative		885	21.70%	1128.3	72.90%	2031	73.20%		0.00%	3723.6	109.30%	5944.4	158.60%
35	cydA	P0ABJ9	58.2	42.12	146	0.000013	1.53E-02	6.44E-06	0.001416	interaction	0.39045	827.5	23.30%	5432.7	62.00%	9919.3	34.20%	6966.2	32.60%	1129.9	12.20%	1393.5	41.50%
36	dppF	P37313	37.9	39.56	181					qualitative			0.00%	289.3	70.70%		0.00%		0.00%	712.9	67.00%	695.4	77.40%
37	dppD	P0AAG0	35.8	38.01	182					qualitative			0.00%	265.4	109.70%		0.00%		0.00%	510.3	69.50%	379.1	19.90%
38	dppB	P0AEF8	37.5	32.69	180					qualitative		1381.1	8.20%		0.00%		0.00%		0.00%	298.1	23.10%	452.5	49.20%
39	gatC	P69831	48.4	35.91	147					qualitative			0.00%	14187.6	54.60%	18644	21.30%	4980.7	77.90%	4576.7	98.80%	2696.7	112.50%
40	oppD	P76027	37.2	38.91	183					qualitative			0.00%	426.4	37.30%	2957.7	24.80%	16127.3	81.80%	410.4	36.00%	221.7	61.80%
41	oppB	P0AFH2	33.4	28.7	182					qualitative			0.00%		0.00%	1225.9	56.90%	449.1	71.40%	617.8	86.00%	327.9	80.60%
42	pntA	P07001	54.9	43.57	161	9.20E-06	0.8638	2.74E-06	0.001073	interaction	0.295906	856.9	29.90%	1976.5	7.50%	8092.5	23.70%	3435.5	21.40%	1416.6	38.40%	1256.8	27.50%
43	ppiD	P0ADY1	68.1	77.01	200	9.97E-03	5.25E-03	0.040996	0.110086	beh and strain	0.445697	677.2	23.90%	2615.6	16.40%	2095.9	21.70%	3874.9	31.70%	2054.3	68.30%	2473.6	54.70%
44	frdA	P00363	66	79.42	156					qualitative			0.00%	361.9	34.70%	3706.9	26.70%	6966.8	138.60%	241.9	20.00%	319.2	11.00%
45	atmA	P0ABB8	99.5	112.41	165					qualitative			0.00%		0.00%		0.00%	10298.9	85.80%		0.00%		0.00%

46	atmA	P0ABB8	99.5	114.99	156					qualitative		2492	72.90%	133549	35.70%	315276.5	12.40%		0.00%	322346.2	85.70%	156008.5	172.70%
47	atmA	P0ABB8	99.5	121.09	163					qualitative		762.4	60.80%	1008.1	32.20%		0.00%	53581.1	92.90%	940.3	124.70%	1257.6	68.70%
48	atmA	P0ABB8	99.5	127.18	167					qualitative			0.00%		0.00%		0.00%	10318.5	127.40%		0.00%		0.00%
49	atmA	P0ABB8	99.5	121.56	169					qualitative			0.00%		0.00%		0.00%	20061.4	68.60%		0.00%		0.00%
50	yhcB	P0ADW3	15	15.86	139	6.38E-06	0.081442	9.91E-07	0.018427	interaction	0.512626	13012.5	50.50%	2490.6	10.10%	13635.4	61.70%	17228.7	26.40%	839.9	49.60%	740.7	63.80%
51	zipA	P77173	36.5	41.34	133					qualitative		683.7	35.60%	706.8	26.30%		0.00%		0.00%	752	74.80%	1029	70.80%
52	gntT	P39835	46	35.4	129					qualitative			0.00%	557.3	89.30%	2276.9	59.10%	1285.4	75.50%	518.4	103.30%	789.7	65.30%
53	ompA	P0A910	37.3/35.2	34.43	135					qualitative			0.00%	1511.3	59.80%	2528.3	30.60%	3657.9	75.30%	844.3	38.60%	1004	17.80%
54	sdaC	P0AAD6	46.9	33.14	142					qualitative			0.00%	3452.5	57.10%	2729	71.70%	1936	27.70%	371.8	31.80%	519.2	47.50%
55	glnQ	P10346	26.7	31.88	129					qualitative			0.00%	604.2	20.60%	927.7	67.80%	295.2	8.80%	478.2	54.50%	605.6	28.30%
56	glnP	P0AEQ6	24.4	19.94	128					qualitative			0.00%	52	60.30%	315.8	31.90%	4578.7	168.60%	93.9	50.50%	105.4	30.30%
57	cydB*	P0ABK2	42.5	32.95	142					qualitative			0.00%		0.00%	1188.7	3.00%		0.00%	646.1	24.40%	767.9	0.00%
58	nuoCD	P33599	68.7	74.68	110	0.009955	0.031074	0.011588	0.083093	beh and strain	0.522522	789.1	46.40%	3221.1	40.60%	3481.3	7.90%	3348.5	28.00%	1251.3	76.10%	1521.2	23.00%
59	yijP	P32678	66.6	58.04	121	1.36E-02	9.54E-01	5.26E-03	0.074926	strain only	0.685217	12584.9	58.00%	3643.9	5.00%	16762.4	38.00%	21483.9	27.50%	4595.1	125.80%	6293.2	54.80%
60	nuoB	P0AFC7	25.1	28.71	97	0.000725	0.428715	0.000159	0.054308	strain only	0.490202	627	60.90%	862.9	31.00%	6074.5	26.70%	2377.6	58.40%	2723.4	31.50%	2826.9	32.30%
61	dsbA	P0AEG4	23.1	25.58	87					qualitative		362.9	10.80%		0.00%		0.00%	389.2	25.50%	190.3	0.00%	185.8	89.40%
62	moaB	P0AEZ9	18.7	24.37	87					qualitative		280.4	45.90%		0.00%		0.00%	430.4	24.90%	238.8	0.00%	214.2	84.00%
63	ygaU	P0ADE6	16.1	19.12	89					qualitative			0.00%	244.5	39.70%	369	9.10%	6479.9	168.40%	96.4	18.80%	164	9.00%
64	psd	P0A8K1	35.9	32.05	100	3.26E-07	0.000804	1.46E-07	0.000178	interaction	0.358411	26910.8	23.00%	3325.3	33.20%	1257.2	23.30%	778.6	64.70%	889.3	20.70%	1430.4	38.20%
65	rbsA	P04983	55	53.51	87	9.29E-06	0.112411	2.85E-05	3.25E-05	interaction	0.226002	4449.3	1.70%	15794	19.60%	7250.3	4.50%	3857.6	2.70%	14786.9	16.10%	14792.2	53.50%
66	putP	P07117	54.3	38.75	89					qualitative			0.00%		0.00%	1169.6	24.40%		0.00%		0.00%		0.00%
67	secD	P0AG90	66.6	58.65	88	0.014113	0.621092	0.002092	0.563324	strain only	0.415405	28553.9	31.40%	22978.9	8.20%	9011.6	12.00%	10746.4	24.80%	28446.6	91.80%	31354.4	30.90%
68	dacA	P0AEB2	44.4	40.09	86					qualitative			0.00%	6457.3	42.90%		0.00%	2021.5	44.00%		0.00%	1687	11.20%
69	dld	P06149	64.6	42.61	85					qualitative		4579.7	26.90%	285.1	60.90%		0.00%		0.00%	7706.4	129.10%	600.5	145.30%
69	dadA	P0A6J5	47.6	42.61	85					qualitative		4579.7	26.90%	285.1	60.90%	7706.4	129.10%	600.5	145.30%		0.00%		0.00%
70	ompA	P0A910	37.3/35.2	33.44	84	0.003947	0.248471	0.001706	0.046384	interaction	0.899917	1226.2	64.70%	9680.9	70.70%	1447.5	141.00%	343.7	40.60%	5482.5	72.60%	5149.5	39.50%
71	rpoE	P0AGB6	21.7	25.69	83					qualitative			0.00%	269.1	42.70%	277.7	43.40%	570.1	29.50%	234.8	13.40%	909.3	36.50%
72	ompA	P0A910	37.3/35.2	33.61	85					qualitative			0.00%	2501.2	75.80%	154.3	121.40%		0.00%	3482.3	31.70%	18488.1	139.20%
73	wzzB	P35272	36.3	38.04	86					qualitative		684	21.80%		0.00%		0.00%	1234	10.30%	8725.1	25.50%	1908.6	44.20%
74	yajC	P0ADZ7	11.9	11.9	83	0.008964	0.411648	0.001129	0.920366	strain only	0.619902	11296.2	18.00%	12770.1	20.60%	15219.3	118.90%	16517.6	57.00%	49434.6	7.60%	66377.4	46.10%
75	ygaU	P0ADE6	16.1	13.02	0.7					qualitative			0.00%		0.00%	1490.5	98.00%	830.4	20.80%	17763.8	65.10%	9599.1	95.30%
76	atpG	P0ABA6	31.6	34.72	0.7					qualitative		2454.1	13.50%	557.5	31.90%	1165.6	130.00%	1703.7	55.10%		0.00%	903.1	13.20%
77	metQ	P28635	29.4	31.55	69	1.78E-05	4.97E-02	2.70E-06	0.064064	beh and strain	0.272838	8047.3	9.30%	4353.3	19.80%	1203.1	33.80%	1841	40.10%	7067.3	6.30%	4804.3	19.20%
78	oppA	P23843	60.9	75.42	0.68					qualitative		336.4	51.40%	545.7	18.20%	273.1	67.70%	385.7	7.90%	385.7	28.40%		0.00%

(a) The numbering corresponds to the spots in 2D gel images of Supplementary figure 2.

(b) Gene name and synonyms extracted from the Swiss Prot database v54.6 for *E. coli* (release 12/04/07, http://www.expasy.org). "*" indicates these identities are only tentative.

(c) Protein sizes (in kDa) predicted from amino acid sequence. Two sizes are given for secretory proteins, the first size corresponds to the mature form of the protein after signal sequence processing, and the second size corresponds to the precursor form including the signal sequence.

(d) Size of proteins calculated from the spot position on the 2D gels used for the analysis.

(e) The average spot intensity of all gels in one replicate group after normalization calculated by PDQuest. The values are based on the area under a Gaussian distribution constructed from spots in the filtered 2D gel images.

(f) Coefficient of variation of spot intensities within a replicate group.

Supplementary Table 2: Comparative analysis and mass spectrometry identification of spots from 2D gels of whole cell lysates of membrane protein-overexpressing cells and control cells.

Coomassie stained 2D maps of whole cell lysates (Supplementary figure 3) For each spot a two-way ANOVA was performed on log transformed data as described previously (Supplementary table 1; Klepsch, M., Schlegel, S., Wickstrom, D., Friso, G., van Wijk, K. J., Persson, J. O., de Gier, J. W. & Wagner, S. (2008). Immobilization of the first dimension in 2D blue native/SDS-PAGE allows the relative quantification of membrane proteomes. Methods 46, 48-53; Wagner, S., Klepsch, M. M., Schlegel, S., Appel, A., Draheim, R., Tarry, M., Hogbom, M., van Wijk, K. J., Slotboom, D. J., Persson, J. O. & de Gier, J. W. (2008). Tuning Escherichia coli for membrane protein overexpression. Proc Natl Acad Sci U S A 105, 14371-6), with treatment and strain as factors. Significance was determined using a two-way ANOVA with treatment (i.e., hKDEL-GFP overexpression) and strain as factors, resulting in a p-value for each spot. Spots with missing data in all replicates, for some combination of treatment and strain, were excluded from the ANOVA-analysis. The effect of those 75 spots was “qualitative”. Significant effects for “treatment”, “strain”, “treatment and strain” (no interaction), and “interaction”

were found for 154 spots. Non-identifiable proteins were excluded from the data set. In the end, 257 significantly changed proteins in 227 spots remained. A grouping of the spots on the kind of effect was done.

The effects were “treatment”, “strain”, “treatment and strain (no interaction)” and “interaction”.

Furthermore, matrix and/or auto-proteolytic trypsin fragments were removed by the software Peak Eraser v2.01 (Lighthouse data). Shown are only spots that could be identified by MS.

Abbreviations: acc., accession; seq., sequence; pep., peptides; quant., quantitation.

spot Nr. (a)	gene name(s) (b)	Swiss Prot acc.	ID ref. (c)	MALDI-TOF MS				predicted MW (kDa) (precursor/ mature) (h)	predicted pI (precursor/ mature) (i)	observed MW (kDa) (j)	observed pI (k)	ANOVA						BL21(DE3)pLysS				C41(DE3)				C43(DE3)			
				mascot score (d)	% seq. cover (e)	Nr. of matched pep. (f)	Nr. of unmatched pep. (g)					p-value model	p-value treatment	p-value strain	p-value interaction	effect	standard deviation	quant. value (control) (l)	CV (control) (m)	quant. value (KDEL-OE) (l)	CV (KDEL-OE) (m)	quant. value (control) (l)	CV (control) (m)	quant. value (KDEL-OE) (l)	CV (KDEL-OE) (m)	quant. value (control) (l)	CV (control) (m)	quant. value (KDEL-OE) (l)	CV (KDEL-OE) (m)
1	rplL	P0A7K2		76	71	6	27	12.3	4.60	11.92	4.42	0.0176029	0.0132792	0.0197125	0.62139	treat + strain	0.4481	25086	2.20%	39567.6	13.60%	13492.4	52.50%	29767.1	49.50%	13272.2	40.50%	18658.5	35.80%
2	rplL	P0A7K2		64	43	5	27	12.3	4.6	11.82	4.51	0.0029188	0.0005539	0.0554637	0.401196	treat	0.5143	22050.4	5.80%	40774.7	50.00%	9043.1	53.70%	33138.8	46.40%	9420.2	46.10%	26565.1	41.40%
3	rpsJ	P0A7R5		58	47	5	19	11.7	9.68	12.35	4.35					qualitatitve			0.00%	3735.3	34.70%		0.00%	88.1	66.10%		0.00%	1362.4	66.20%
4	fldA	P61949		69	39	4	14	19.7	4.21	20.32	4.35					qualitatitve			0.00%	245.9	110.40%		0.00%	433.6	130.80%	171.5	106.90%	1290.9	13.70%
5	rplC	P60438		68	42	6	20	22.2	9.9	24.21	4.32	0.0037942	0.0440551	0.0012795	0.335613	treat + strain	1.2073	90.7	103.70%	282.3	29.30%	21.7	93.30%	312.8	114.80%	579.9	34.80%	693.3	6.80%
6	atpB	P0ABB5	OE(1)					50.2	4.90	28.64	4.35	4.46E-06	2.54E-07	0.0039422	0.809972	treat + strain	0.17	1260	23.30%	2245.5	9.80%	825	14.20%	1653.4	22.40%	1048.6	19.50%	1857.4	8.40%
7	rpoA	P0A7Z4		71	20	6	13	36.5	4.98	36.18	4.29	0.0073359	0.76289	0.0108283	0.023961	interaction	0.655	59.8	70.50%	262.9	81.40%	415.4	28.70%	159.4	77.10%	478.3	1.80%	454.3	47.40%
8	yfgL	P77774		86	29	9	23	41.9/39.9	4.72/4.61	36.02	4.4	0.0000127	2.59E-06	0.0008081	0.03479	interaction	0.1814	483.3	29.40%	1167.4	25.70%	891.6	4.80%	1325.3	16.10%	941.3	9.80%	1400.4	22.60%
9	hemX	P09127	2					42.9	4.68	47.19	4.46	0.0000216	0.0005211	0.0000586	0.204164	treat + strain	0.2121	1578.7	19.80%	1204	11.90%	1020.9	10.80%	772.5	32.30%	926	23.20%	485.1	22.90%
10	crr	P69783		109	58	6	14	18.3	4.73	19.59	4.6	0.0019989	0.9378253	0.0003864	0.324994	strain	0.3647	12752	1.40%	9215.6	16.70%	4790.8	33.20%	6498.8	28.90%	4078.8	60.60%	3664.1	10.80%
11	nifU	P0ACD4		61	42	5	22	13.8	4.82	15.45	4.69	0.0117079	0.0020946	0.3805878	0.037552	interaction	0.5676	419.5	122.30%	1541.4	20.20%	611	50.70%	1134.3	13.30%	924.4	30.80%	1004.7	21.70%
12	ompX	P0A917		82	57	6	21	16.6/16.4	6.56/5.3	12.93	4.76	8.77E-06	6.07E-06	0.0000613	0.701524	treat + strain	0.3068	1544.1	56.10%	4208.1	46.10%	3615.3	7.90%	7706.6	20.90%	4103.7	15.80%	9905.2	37.40%
13	crr	P69783		79	43	7	13	18.119	4.73	22.1	4.63	0.0008539	0.0910952	0.0002013	0.00479	interaction	0.6041	518.6	67.70%	53.5	2.10%	618.8	34.60%	1061.6	37.50%	780.5	23.40%	988.8	57.70%
13	pal	P0A912		58	38	5	13	18.8/16.6	6.29/5.59	22.1	4.63	0.0008539	0.0910952	0.0002013	0.00479	interaction	0.6041	518.6	67.70%	53.5	2.10%	618.8	34.60%	1061.6	37.50%	780.5	23.40%	988.8	57.70%
14	crr	P69783		72	34	6	26	18.119	4.73	19.69	4.51	0.0167197	0.0152975	0.0133357	0.330609	treat + strain	0.7023	1189	14.60%	3364.4	10.80%	483.5	89.50%	1346.9	35.10%	543.4	52.40%	716.3	59.70%
15	metQ	P28635		120	47	9	15	29.4/27.3	5.13/4.93	25.73	4.62					qualitatitve		4263.9	63.80%	10560.1	61.90%		0.00%		0.00%	2423.5	62.40%	1474.9	43.30%
16	metQ	P28635		137	63	9	19	29.4/27.2	5.13/4.93	25.96	4.67	0.0187016	0.5343686	0.0023213	0.822008	strain	0.713	2374.8	67.80%	3302.5	129.90%	7929.3	7.20%	8511.4	8.20%	6712.2	9.60%	5441	45.00%
17	potD	P0AFK9		128	40	11	8	38.9/36.5	5.24/4.86	31.52	4.64					qualitatitve			0.00%		0.00%		0.00%		0.00%	173.1	26.10%	16.6	40.70%
17	nlpB	P0A903		100	36	9	8	36.8/34.4	5.34/4.96	31.52	4.64					qualitatitve			0.00%		0.00%		0.00%		0.00%	173.1	26.10%	16.6	40.70%
18	rplU	P0AG48		164	57	9	4	11.6	9.85	32.47	4.67	0.0157358	0.0101306	0.5871317	0.009415	interaction	0.0157	2986.1	76.00%	430.6	130.60%	1007.4	35.10%	947.5	52.50%	1117.3	34.10%	1102	10.30%
19	atpA	P0ABB0		158	30	15	18	55.2	5.8	36.17	4.71					qualitatitve		437.8	81.20%		0.00%	365	64.00%	83	32.70%	335.1	8.50%	185.9	102.20%
20	ftsZ	P0A9A6		146	40	12	9	40.3	4.65	38.31	4.53	0.0201161	0.8516622	0.0044683	0.242281	strain	0.4124	2340.5	37.30%	2803.6	22.00%	999.4	41.70%	1347.2	41.90%	2413.8	23.50%	1732.2	39.30%
20	sucC	P0A836		51	18	6	9	41.4	5.37	38.31	4.53	0.0201161	0.8516622	0.0044683	0.242281	strain	0.4124	2340.5	37.30%	2803.6	22.00%	999.4	41.70%	1347.2	41.90%	2413.8	23.50%	1732.2	39.30%
21	groL	P0A6F5		117	18	10	5	57.2	4.85	38.61	4.76	0.0000148	5.38E-06	0.0252	0.003922	interaction	0.1948	855.3	24.10%	923.8	24.20%	543.8	18.50%	1048	11.20%	423.4	18.80%	991.6	16.80%
22	atpA	P0ABB0		70	20	8	20	55.2	5.8	54.6	4.61	0.0035041	0.013333	0.0018408	0.741058	treat + strain	0.5808	551.7	2.60%	876.8	22.60%	233.1	136.60%	274.6	49.90%	165.4	23.20%	430.7	31.30%
23	dps	P0ABT2		107	62	9	29	18.7	5.72	20.01	4.81	0.0105015	0.0362913	0.0044085	0.447256	treat + strain	0.8387	262.6	48.90%	1023	50.40%	2260.3	35.80%	2670.1	13.60%	719.6	86.80%	1408.4	77.50%
23	pal	P0A912		63	50	6	32	18.8/16.6	6.29/5.59	20.01	4.81	0.0105015	0.0362913	0.0044085	0.447256	treat + strain	0.8387	262.6	48.90%	1023	50.40%	2260.3	35.80%	2670.1	13.60%	719.6	86.80%	1408.4	77.50%
23	bfr	P0ABD3		57	47	7	31	18.5	4.69	20.01	4.81	0.0105015	0.0362913	0.0044085	0.447256	treat + strain	0.8387	262.6	48.90%	1023	50.40%	2260.3	35.80%	2670.1	13.60%	719.6	86.80%	1408.4	77.50%
24	appA	P0A7A9		104	42	8	18	19.7	5.03	21.35	4.84	0.0036903	0.7869355	0.0005432	0.287343	strain	0.2913	2600.6	20.10%	2143.8	28.80%	1185.6	20.70%	1586.8	13.60%	1079.5	23.60%	1155.3	38.90%
24	ahpC	P0AE08		57	34	5	21	20.8	5.03	21.35	4.84	0.0036903	0.7869355	0.0005432	0.287343	strain	0.2913	2600.6	20.10%	2143.8	28.80%	1185.6	20.70%	1586.8	13.60%	1079.5	23.60%	1155.3	38.90%
25	potD	P0AFK9		105	38	10	17	38.9/36.5	5.24/4.86	21.78	4.93					qualitatitve			0.00%		0.00%		0.00%	193.3	122.50%	924.2	101.20%	1129.7	26.10%
25	nlpB	P0A903		75	31	8	17	36.8/34.4	5.34/4.96	21.78	4.93					qualitatitve			0.00%		0.00%		0.00%	193.3	122.50%	924.2	101.20%	1129.7	26.10%
26	yfgM	P76576		86	50	8	36	22.2	5.07	20.48	4.73					qualitatitve			0.00%	758.4	67.00%	21.8	115.50%	504.4	78.50%	104.4	53.70%	820.3	9.90%
27	pal	P0A912		93	48	6	11	18.8/16.6	6.29/5.59	21.95	4.75					qualitatitve			0.00%		0.00%	114.9	64.20%	307.9	32.00%	171.3	62.60%	288.5	61.20%
27	crr	P69783		79	41	5	11	18.119	4.73	21.95	4.75					qualitatitve			0.00%		0.00%	114.9	64.20%	307.9	32.00%	171.3	62.60%	288.5	61.20%
27	ftnA	P0A998		71	29	5	11	29.4	4.77	21.95	4.75					qualitatitve			0.00%		0.00%	114.9	64.20%	307.9	32.00%	171.3	62.60%	288.5	61.20%
28	talB	P0A870		91	36	8	12	35.1	5.11	32.65	4.81					qualitatitve			0.00%		0.00%	462.5	26.10%	455	36.10%	376.8	45.60%	247.1	64.70%
28	tpx	P0A862		79	58	6	12	17.7	4.75	32.65	4.81					qualitatitve			0.00%		0.00%	462.5	26.10%	455	36.10%	376.8	45.60%	247.1	64.70%
29	tsf	P0A6P1		62	21	6	12	30.4	5.22	30.75	4.86	0.0007618	0.0002589	0.1668056	0.056584	treat	0.1392	2555.6	16.20%	2695.7	24.80%	1822.3	5.60%	2847.8	9.00%	1875.3	12.20%	2714.9	16.20%
30	tsf	P0A6P1	OE(21)					30.4	5.22	31.16	4.91	3.29E-07	1.07E-08	0.0207642	0.128023	treat + strain	0.4157	1142.4	43.90%	5533.3	28.60%	528.5	48.00%	2848.6	13.70%	455.7	48.90%	4938.6	22.90%
31	rpiB	P37351		67	42	3	5	16.1	6.58	40.09	4.8	0.0055556	0.4630584	0.0005158	0.802696	strain	0.4639	259.6	54.80%	200.8	69.90%	474.1	6.30%	395.7	8.80%	611.7	28.60%	621.9	20.00%
32	engD	P0ABU2	18					40	4.87	41.45	4.81	0.0103297	0.012111	0.0116556	0.380783	treat + strain	0.2412	1822.7	31.70%	2116.1	27.50%	1011.3	28.70%	1609.1	19.50%	1293.5	8.80%	1589.4	3.90%
33	mdtE	P37636	OE(18)					41.2/38.9	5.73/5.12	36.65	4.92	0.0081796	0.0114868	0.0065475	0.586048	treat + strain	0.4063	4715.9	41.50%	5985.2	32.10%	1927.2	29.10%	3198.2	42.90%	2163.6	39.80%	4450.2	52.50%
34	tig	P0A850		194	46	18	15	48.1	4.8	49.45	4.81	0.0016199	0.000486	0.0245741	0.281967	treat + strain	0.7976	6039.5	43.70%	9195.4	13.30%	3153.3	62.00%	5039.8	25.60%	7845	49.40%	8480.7	34.20%
35	tig	P0A850	7					48.1	4.8	49.26	4.73	0.000236	0.0002738	0.1320622	0.000103	interaction	0.226	20431.3	37.00%	74304.4	6.20%	28018	3.60%	32860.6	27.50%	31627.1	22.10%	29109.8	18.40%
36	groL	P0A6F5		92	21	8	23	57.3	4.85	59.3	4.86					qualitatitve		101	102.00%	57.2	53.60%		0.00%	111	96.40%	355	9.50%	706.3	35.50%
37	ydaA	P77804	OE(20)					54.7/53.2	5.07/5.01	52.94	4.95	0.0143754	0.0243319	0.0062162	0.853801	treat + strain	0.3531	1199.4	21.50%	1550.3	16.80%	599.6	19.30%	1015.6	46.70%	691.6	63.80%	900.8	31.30%
38	yraM	P45464		133	29	17	33	72.8	5.26	72	4.65					qualitatitve			0.00%		0.00%	77.4	59.50%		0.00%	68.1	0.00%	341.1	85.10%
39	dnaK	P0A6Y8	OE(120)					69	4.83	71.3	4.74	9.75E-08	1.62E-09	0.032713	0.314269	treat + strain	0.1914	50597.4	34.10%	160738	16.10%	42104.7	9.20%	108192	9.90%	55719.2	21.90%	131851	7.30%
40	rpsA	P0AG67	8					61.2	4.89	66.63	4.78	5.34E-07	2.62E-08	0.1657632	0.000136	interaction	0.1565	35316.5	12.90%	140742	22.50%	61762.6	16.10%	95734.3	12.40%	69544.8	23.20%	102630	7.00%
41	yraM	P45464		87	14	9	10	72.8	5.26	70.45	4.68					qualitatitve		441.8	43.40%		0.00%	564.9	7.80%	448.7	64.10%	535.9	0.00%	1010.8	54.40%
42	dnaK	P0A6Y8		76	12	8	10	69.1	4.83	57.95	4.68	0.0000315	0.0001413	0.0000467	0.675993	treat + strain	0.4735	192.6	25.70%	409.2	14.80%	46.6	30.20%	152.5	74.60%	39.9	75.80%	112.8	18.90%
43	groL	P0A6F5	OE(121)					57.2	4.85	60.99	4.78	6.39E-10	7.72E-11	1.35E-07	0.03957	interaction	0.1529	38259.4	10.10%	132546	11.80%	19238.4	5.30%	44724.8	7.50%	27411.4	23.70%	93274.7	20.10%
44	yeaT	P76250		199	31	20	7	34.6	6.21	82.43	4.72	0.0047739	0.0022699	0.4359888	0.015896	interaction	0.3458	12694	76.40%	15037.6	16.70%	6078.8	37.20%	18410.7	18.30%	12028.5	19.70%	12772	10.50%
44	fusA	P0A6M8		60	18	9	7	77.5	5.24	82.43	4.72	0.0047739	0.0022699	0.4359888	0.015896	interaction	0.3458	12694	76.40%	15037.6	16.70%	6078.8	37.20%	18410.7	18.30%	12028.5	19.70%	12772	10.50%
45	ibpB	P0C058		86	50	6	14	16.08	5.19	16.51	5.05	0.0026688	0.0747063	0.0006367	0.124052	strain	0.3772	4218.2	20.70%	8316.6	16.00%	2569.1	10.90%	2637.7	50.90%	2338.3	7.10%	3441.4	23.90%
45	risH	P61714		69	41	5	15	16.15	5.15	16.51	5.05	0.0026688	0.0747063	0.0006367	0.124052	strain	0.3772	4218.2	20.70%	8316.6	16.00%	2569.1	10.90%	2637.7	50.90%	2338.3	7.10%	3441.4	23.90%
46	groS	P0A6F9	27					10.4	5.15	13.33	5.08	0.0003458	0.0005658	0.0006076	0.331067	treat + strain	0.3667	9928.9	5.40%	24639.8	10.30%	4955.5	7.10%	12558.4	63.00%	5160.1	11.30%	8074.2	55.50%
47	ftnA	P0A998		64	36	6	25	19.4	4.77	13.33	4.89	0.0017372	0.0004894	0.0094164	0.3432	treat + strain	1.1129	123.1	53.70%	2560.2	23.70%	169.1	67.50%	1088.6	66.90%	62.7	93.40%	300.1	131.40%
47	bfr	P0ABD3		58	43	6	25	18.5	4.69	13.33	4.89	0.0017372	0.0004894	0.0094164	0.3432	treat + strain	1.1129	123.1	53.70%	2560.2	23.70%	169.1	67.50%	1088.6	66.90%	62.7	93.40%	300.1	131.40%
48	luxS	P45578	OE(27)					19.4	5.18	20.69	5.05	0.0003983	0.000073	0.995743	0.003011	interaction	0.3597	5098.5	19.60%	1116.6	55.50%	2410	17.50%	2089.2	33.40%	2826.8	11.60%	1768.5	37.50%
49	tsf	P0A6P1		165	55	13	13	30.4	5.22	30.7	5.01	5.76E-07	3.59E-08	0.0017664	0.232777	treat + strain	0.1607	3085.3	20.80%	5218.4	35.90%	1759.7	3.40%	4003.8	9.70%	2035	11.20%	4372.3	18.40%
50	argT	P09551	OE(25)					28.0/25.8	5.62/5.22	25.33	5.04	8.13E-06	1.18E-07	0.3413721	0.656306	treat	0.141	2243.9	16.90%	1088	9.80%	2284	15.10%	1305.8	14.10%	2065.2	19.30%	1149.7	23.50%
51	yhaH	P64590		66	52	3	7	14.3	9.72	27.32	5.05					qualitatitve		142.3	60.10%		0.00%	512.2	19.30%	387.8	46.00%	430.7	14.10%	325.1	15.70%
52	tsf	P0A6P1		73	21	21	18	30.291	5.22	30.09	5.08	0.0000839	0.0024762	0.0002239	0.379095	treat + strain	0.3622	8796	62.10%	18105.3	7.50%	26270.9	12.00%	38127.3	4.80%	24445.6	21.00%	36753.7	5.10%
53	pgk	P0A799		196	50	14	10	41.1	5.08	39.62	4.97	0.0051932	0.2163995	0.0009945	0.496297	strain	0.1736	2574	26.10%	2467.1	13.70%	1602	7.00%	1958.5	13.60%	1618.4	18.60%	1794.6	15.90%
54	pgk	P0A799		127	40	11	20	41.1	5.08	41.43	5.01	0.0190069	0.0638928	0.0059565	0.772842	strain	0.4643	1386.1	31.10%	1658.3	24.70%	576.1	55.60%	856.6	26.40%	1089.3	42.50%	1591.9	32.30%
55	pgk	P0A799	17					41.1	5.08	38.56	5.03	7.75E-06	0.4388868	0.0000917	6.06E-05	interaction	0.447	1867.9	69.50%	9484.9	4.40%	22520.4	17.30%	10042.9	40.70%	15569.9	49.40%	8609.9	19.90%
56	pgk	P0A799	19					41.1	5.08	40.12	4.9	5.39E-13	1.33E-14	5.18E-07	0.006359	interaction	0.1616	600.8	19.30%	2616	17.20%	291.2	9.10%	1245.4	12.30%	284.7	17.20%	2085.9	20.60%
57	pgk	P0A799	20					41.1	5.08	40.2	4.87	0.0007616	0.0003511	0.0035772	0.244123	treat + strain	0.6192	258.6	42.10%	997.4	39.60%	123.8	60.10%	260.5	59.50%	164.7	23.90%	797.6	27.90%
58	deoA	P07650		83	28	9	18	47.2	5.21	46.5	5.06	6.82E-08	2.33E-09	0.0064288	2.99E-05	interaction	0.3078	2865.4	23.30%	148.6	26.30%	1454.8	18.40%	566.9	46.50%	1978.8	37.90%	786.9	13.90%
59	pnp	P05055	25					77.1	5.11	78.93	4.98	0.0109186	0.0071017	0.05139	0.190571	treat	0.577	161.5	39.20%	276	85.70%	224	15.60%	556.4	17.40%	145.4	18.10%	507.6	34.60%
60	pnp	P05055		88	19	12	20	77.1	5.11	76.86	5.02	0.000161	0.0000204	0.0163335	0.318747	treat + strain	0.5244	84.1	33.50%	323.4	38.20%	113	34.30%	293.5	56.40%	181	63.70%	791.1	21.60%
61	pnp	P05055	24					77.1	5.11	78.51	5.03	0.0000697	0.0009571	0.0003378	0.01396	interaction	0.4556	240.2	11.50%	278.9	64.80%	595.5	9.30%	1250	9.80%	316.3	74.20%	1285.5	17.10%

62	rpsF	P02358	28					15.7	4.93	18.49	5.11	0.0006322	0.2359284	0.0001131	0.094653	strain	0.7083	469.7	58.10%		0.00%	855.1	11.30%	212.2	121.20%	566.2	32.50%	155.4	118.70%
63	ompX	P0A917	29					18.6/16.4	6.56/5.3	19.25	5.14	0.0084198	0.0017285	0.586634	0.039482	interaction	1.2165	263.4	144.60%	5467.7	14.00%	993.4	80.00%	2681.6	72.10%	1242.1	71.70%	3042.3	67.70%
63	pal	P0A912	29					18.7/16.6	6.29/5.59	19.25	5.14	0.0084198	0.0017285	0.586634	0.039482	interaction	1.2165	263.4	144.60%	5467.7	14.00%	993.4	80.00%	2681.6	72.10%	1242.1	71.70%	3042.3	67.70%
64	yigF	P0AF94	38					13.5	5.36	13.45	5.17	0.0018785	0.0001323	0.1153499	0.182939	treat	0.4792	2893.3	13.10%	1021.7	116.90%	3084.7	11.60%	1932.6	30.60%	2931.2	23.30%	1025.4	36.40%
65	rpsD	P0A7V8		119	48	10	4	23.5	10.05	23.73	5.09	0.0002019	0.0109212	0.0003548	0.283522	treat + strain	0.5553	208.9	129.00%	446.3	21.10%	759.4	26.10%	1101.1	29.60%	851.6	14.00%	1321.1	20.70%
65	sspA	P0ACA3		71	41	6	4	24.3	5.22	23.73	5.09	0.0002019	0.0109212	0.0003548	0.283522	treat + strain	0.5553	208.9	129.00%	446.3	21.10%	759.4	26.10%	1101.1	29.60%	851.6	14.00%	1321.1	20.70%
65	rplC	P60438		56	37	5	4	22.2	9.9	23.73	5.09	0.0002019	0.0109212	0.0003548	0.283522	treat + strain	0.5553	208.9	129.00%	446.3	21.10%	759.4	26.10%	1101.1	29.60%	851.6	14.00%	1321.1	20.70%
66	yggG	P25894		82	42	7	20	26.8	5.75	24.42	5.09	0.0120406	0.0021102	0.1456306	0.08956	treat	0.8706	1735.8	35.40%	340.5	98.10%	1231.3	8.40%	489.6	65.20%	1428	6.20%	1091.1	41.40%
67	artI	P30859	OE(37)					26.9/25.0	5.79/5.32	24.05	5.14	2.70E-07	7.90E-08	0.0695586	3.14E-05	interaction	0.1881	4844.4	20.50%	1199.2	23.00%	2317.6	11.50%	1947.9	16.00%	2465.9	21.00%	1440.9	19.20%
68	dps	P0ABT2		97	58	8	23	18.6	5.72	21.32	5.18	0.0000334	5.17E-07	0.2831929	0.993743	treat	0.2029	1035.5	19.10%	2042.8	31.40%	926.6	21.70%	1800.1	15.60%	871.1	16.50%	1673	15.60%
69	apt	P69503		144	75	8	5	19.9	5.26	22.63	5.2	1.14E-06	3.42E-08	0.0026112	0.994825	treat + strain	0.2074	1573	31.60%	3483.5	18.70%	971.3	12.10%	2248.5	21.40%	1120.6	10.90%	2516.1	7.70%
70	ndk	P0A763		90	44	6	6	15.3	5.55	15.37	5.19					qualitatitve		113.9	2.50%		0.00%	679.9	44.20%	835.6	74.30%	139.2	139.00%	79.3	73.40%
70	rplQ	P0AG44		64	29	6	6	14.4	11.05	15.37	5.19					qualitatitve		113.9	2.50%		0.00%	679.9	44.20%	835.6	74.30%	139.2	139.00%	79.3	73.40%
71	yrdA	P0A9W9		145	66	10	15	20.2	5.26	21.67	5.14					qualitatitve		1530.4	54.30%		0.00%	671.8	25.20%		0.00%	531.2	48.80%	110.6	101.00%
72	trxB	P0A9P4		80	28	7	14	34.5	5.3	34.67	5.16	0.0009718	0.0060978	0.0004077	0.836241	treat + strain	0.4649	1525.8	37.30%	2408.2	24.60%	437.9	38.40%	881.9	55.60%	861.1	13.10%	2054.5	50.80%
73	tsf	P0A6P1		167	45	11	5	30.4	5.22	30.7	5.16	0.0000815	6.18E-06	0.0167327	0.505566	treat + strain	0.2729	1595.9	45.30%	2614.6	3.00%	937.5	24.00%	2186.5	6.10%	752.8	13.90%	1938.9	24.40%
74	pfkB	P06999		183	63	16	24	32.5	5.25	32.91	5.21	0.0047353	0.0471011	0.1170659	0.004843	interaction	0.3111	3378.6	60.20%	1221.7	46.40%	1287.1	6.30%	1569.7	5.30%	1326.4	15.10%	1260.9	6.50%
75	pfkB	P06999						32.5	5.25	31.96	5.21	0.0063579	0.0011663	0.0573708	0.776219	treat	0.5566	3841.3	57.30%	1303.3	29.00%	1781.2	10.60%	882.4	65.70%	1583.8	14.60%	816.9	26.60%
76	malE	P0AEX9		236	51	18	17	43.4/40.7	5.53/5.22	38.27	5.17	0.005323	0.0304548	0.0033387	0.459852	treat + strain	0.382	3894.2	10.40%	2081.1	17.20%	2204.4	23.10%	2001.5	34.80%	1594.6	30.50%	1240.6	55.60%
77	agp	P19926	OE(41)					46.0/43.6	5.48/5.38	42.02	5.22	2.58E-06	0.0000259	6.91E-06	0.450603	treat + strain	0.3031	2004.9	18.50%	1128.6	17.30%	963.3	12.90%	567.1	65.40%	809.1	30.60%	308.7	24.50%
78	malE	P0AEX9	OE(35)					43.4/40.7	5.53/5.22	37.93	5.09	2.03E-13	2.10E-15	0.0461396	0.000389	interaction	0.1434	81795.9	4.50%	11088.6	18.20%	69198.9	19.10%	19738	16.30%	72746.1	15.20%	14385.8	8.20%
79	deoB	P0A6K6	OE(26)					44.7	5.11	32.01	5.04	0.000355	9.95E-06	0.2511171	0.202743	treat	0.6554	575.4	58.80%	3066	0.20%	470.5	82.40%	1343.1	18.90%	237.3	78.40%	2489.2	25.90%
80	degQ	P39099		66	25	9	29	46.2/43.4	5.75/5.37	46.73	5.1	7.13E-06	0.4933341	0.0000745	0.000365	interaction	0.6261	697	25.60%	194.1	82.70%	19.6	46.20%	210	109.30%	663.7	41.10%	216.9	52.40%
81	atpD	P0ABA4		162	54	14	7	50.2	4.9	52.97	5.14	0.0003383	0.0000128	0.2702232	0.188798	treat	0.4637	493.9	87.50%	1089.3	16.20%	334.3	33.30%	725.2	27.10%	192	31.40%	1040.2	39.80%
81	lpdA	P0A9P0		145	32	14	7	50.6	5.79	52.97	5.14	0.0003383	0.0000128	0.2702232	0.188798	treat	0.4637	493.9	87.50%	1089.3	16.20%	334.3	33.30%	725.2	27.10%	192	31.40%	1040.2	39.80%
82	treA, osmA	P13482	OE(44)					63.6/60.5	4.60/5.36	59.43	5.23	0.0002675	0.000023	0.1509465	0.321576	treat	0.6681	1359.8	17.90%	209.2	10.50%	744.7	12.20%	108.8	74.90%	702.2	29.70%	336.2	87.60%
83	cpdB	P08331	OE(45)					70.9/68.9	5.45/5.38	68.46	5.19	0.0074092	0.002718	0.0797857	0.175186	treat	0.3749	569.2	23.90%	218.1	12.60%	284.8	9.10%	258.4	42.50%	292.1	29.10%	187.2	44.50%
84	acnB	P36683		181	25	18	12	93.5	5.24	88.35	5.16	1.13E-06	0.8058622	7.07E-08	0.402628	strain	0.2221	9052.2	14.60%	7695.5	28.90%	19801.2	18.80%	22788.5	22.90%	27116.5	14.10%	27191	28.70%
85	fusA, far, fus	P0A6M8	51					77.7	5.24	81.65	5.2	0.0021374	0.0003698	0.1066184	0.018326	interaction	1.0251	7734.1	17.80%	67016.6	65.20%	12889.2	38.50%	18777.7	75.00%	2709.6	98.60%	42693.8	53.50%
86	gatA	P69828		53	39	4	15	16.9	5.15	16.95	5.31	4.72E-06	1.01E-07	0.2265235	0.069532	treat	0.6709	4791.8	13.30%	89.9	85.00%	3363	9.00%	544.7	71.80%	2913	17.20%	202.6	56.90%
87	osmY	P0AFH8	OE(34)					21.1/18.2	6.32/5.42	21.6	5.23	3.09E-06	2.00E-07	0.0371847	0.005994	interaction	0.5483	6603	4.20%	607.7	126.10%	3337.2	14.30%	1490.6	29.10%	2835.6	36.30%	429.8	64.10%
88	kad	P69441		132	44	10	15	23.6	5.55	24.52	5.33	0.000671	0.0000463	0.0225214	0.423545	treat + strain	0.4336	2467.7	41.40%	8307.3	24.60%	1814.5	13.60%	5136.1	32.80%	1543.3	17.60%	3670.1	66.10%
89	hns	P0ACF8		85	56	8	26	15.4	5.44	15.82	5.32					qualitatitve		389.8	165.70%		0.00%	765.2	46.50%	1109.8	97.00%	1235.7	65.00%	1012	29.70%
90	pfkB	P06999		168	55	14	22	32.5	5.25	29.82	5.34					qualitatitve		75.6	143.70%		0.00%	206.9	29.40%	180.5	37.50%	230.3	96.30%	137.5	96.80%
91	pspA	P0AFM6		105	33	7	11	25.5	5.39	24.9	5.3					qualitatitve		257.3	99.10%		0.00%	225.5	53.40%	395.4	109.70%	368	54.40%	1379.8	106.10%
92	osmY	P0AFH8		73	48	7	8	21.1	6.32	21.74	5.26					qualitatitve			0.00%		0.00%	426.4	67.80%	1919.2	26.10%	727.6	9.20%	2225.7	23.70%
92	rpoE	P0AGB6		59	36	6	8	21.7	5.38	21.74	5.26					qualitatitve			0.00%		0.00%	426.4	67.80%	1919.2	26.10%	727.6	9.20%	2225.7	23.70%
92	ssB	P0AGE0		57	34	6	8	19	5.44	21.74	5.26					qualitatitve			0.00%		0.00%	426.4	67.80%	1919.2	26.10%	727.6	9.20%	2225.7	23.70%
93	mdh	P61889		96	38	10	33	32.3	5.61	34.5	5.3	0.004835	0.1633048	0.0007001	0.619563	strain	0.4273	7108.2	8.90%	9100.5	10.40%	2300.1	19.80%	3823.7	34.70%	4838.4	95.30%	3733.4	15.50%
93	hldD	P67910		82	35	9	34	34.9	4.8	34.5	5.3	0.004835	0.1633048	0.0007001	0.619563	strain	0.4273	7108.2	8.90%	9100.5	10.40%	2300.1	19.80%	3823.7	34.70%	4838.4	95.30%	3733.4	15.50%
94	mdh	P61889		182	44	11	4	32.3	5.61	31.42	5.33	0.0000559	0.0020139	0.0001102	0.056813	treat + strain	0.1981	3499.1	19.80%	1921.7	21.70%	1669.3	14.00%	1558.4	17.20%	1679.3	21.60%	1334.2	24.10%
95	yehZ	P33362		81	32	9	26	32.6/30.2	5.82/5.56	28.8	5.4					qualitatitve			0.00%		0.00%	268.7	11.60%	135.6	97.30%	106.5	28.00%	57.1	72.80%
95	dapD	P0A9D8		74	32	8	26	29.9	5.56	28.8	5.4					qualitatitve			0.00%		0.00%	268.7	11.60%	135.6	97.30%	106.5	28.00%	57.1	72.80%
96	tpiA	P0A858		95	33	8	17	27	5.64	25.38	5.44					qualitatitve		744.8	156.80%		0.00%	1687.1	33.40%	668.4	67.70%	415.1	147.00%	967.9	35.90%
97	gcsT	P27248		81	19	6		40	5.36	37.15	5.24	0.0015064	0.0151529	0.2377147	0.000451	interaction	0.4949	1844.2	29.70%	335.8	107.60%	753.3	17.20%	829.4	46.20%	856.4	29.00%	1245.3	26.80%
98	eno	P0A6P9		180	39	12	4	45.5	5.32	41.66	5.28	0.0029195	0.286164	0.0003771	0.888447	strain	0.3069	1630.1	34.70%	1456.5	37.40%	820.9	28.90%	641.6	18.60%	819.1	38.00%	724.8	23.00%
99	agp	P19926	58					46.0/43.6	5.48/5.38	41.42	5.34	4.34E-07	0.0000334	0.0000283	0.018976	interaction	0.2142	4445.9	13.50%	4163.1	0.00%	2800.8	24.20%	1116.1	27.00%	2909.4	22.70%	1173.6	12.70%
100	sucC	P0A836		226	54	19	17	41.4	5.37	39.09	5.3					qualitatitve			0.00%	3089.7	17.30%		0.00%	1471.8	26.80%	183.5	94.70%	2776.4	29.20%
101	add	P22333		106	42	8	10	36.4	5.36	32.58	5.3					qualitatitve			0.00%		0.00%		0.00%		0.00%		0.00%	278.2	11.90%
102	agp	P19926		67	19	7	24	46.0/43.6	5.48/5.38	41.82	5.25					qualitatitve			0.00%	336.9	0.00%	269.4	59.10%	155.7	76.10%	363.3	3.00%	232.4	45.50%
103	tnaA	P0A853		59	18	8	26	52.8	5.88	52.86	5.29					qualitatitve			0.00%		0.00%	121.3	49.50%	278.9	70.90%	115.9	49.20%	366.1	60.00%
104	eno	P0A6P9		55	29	7	39	44.9	5.31	44.06	5.3	0.0012776	0.0003315	0.042424	0.020121	interaction	0.1477	61856.3	7.80%	36930.5	23.00%	60994.1	17.10%	47392.9	15.70%	60427.4	14.70%	57312.2	10.40%
105	treA	P13482		92	27	12	34	63.6/60.5	5.6/5.36	62.09	5.28	0.0003645	0.0001302	0.0755138	0.014764	interaction	0.1729	778	18.40%	388.4	23.00%	540.6	7.80%	434.3	11.00%	476.3	24.20%	405.9	14.40%
106	pckA	P22259		103	22	8	5	59.6	5.46	57.56	5.33					qualitatitve			0.00%		0.00%	273.8	30.20%	258.2	31.30%	193.2	70.40%	184.9	60.30%
107	cpdB	P08331	49					70.9/68.9	5.45/5.38	67.9	5.25	0.0003709	0.0000203	0.1984716	0.205651	treat	0.2089	1532.5	29.30%	727	31.00%	1074.9	15.40%	719.4	7.80%	1029.2	16.70%	696.6	16.90%
108	fecA	P13036	50					85.3/81.7	5.59/5.36	78.3	5.26	0.0008932	0.0001698	0.1022814	0.089353	treat	0.3196	747.6	43.30%	1015.9	41.40%	855	19.10%	1427.7	20.80%	703.7	32.40%	2009.7	14.70%
109	cpdB	P08331		73	15	7	8	70.9/68.9	5.45/5.38	78.82	5.38	0.0001649	0.0000982	0.0795709	0.004579	interaction	0.4071	161.3	34.50%	230.5	34.50%	48.5	53.90%	281.5	18.40%	112.6	13.00%	207.8	46.40%
110	clpB, htpM	P63284	52					95.7	5.37	88.28	5.27	7.20E-09	2.42E-10	0.7011611	0.000352	interaction	0.3019	2774.6	19.60%	6834.1	45.90%	1628.1	37.70%	13278.4	25.60%	1437.4	22.20%	16891	31.40%
111	ibpA, hslT, htpN	P0C054	OE(57)					15.8	5.57	15.69	5.36	0.0203668	0.003706	0.4506197	0.151366	treat	0.2715	10395.8	8.30%	13220.3	14.50%	7013	40.80%	14322.9	25.30%	9622.7	27.90%	11999.4	20.10%
112	osmC	P0C0L2	OE(47)					15.1	5.56	16.65	5.38	0.0008471	0.0000285	0.2388433	0.766986	treat	0.8956	5279.8	11.10%	771.8	54.50%	3723.6	4.60%	444.9	95.20%	2654.4	8.30%	524.1	103.10%
113	atpF	P0ABA0		167	68	14	32	13.4	7.83	17.95	5.48					qualitatitve			0.00%		0.00%	2954.1	4.50%	4317.5	28.40%	2402.9	45.20%	3528.7	9.80%
114	ssb	P0AGE0		90	39	8	24	19	5.44	21.76	5.37					qualitatitve		1069	47.90%		0.00%	1646.8	15.10%	1475.1	70.20%	1399	63.80%	774	40.90%
115	sodF	P0AGD3		99	38	6	7	21.3	5.58	20.77	5.44					qualitatitve		4169.8	51.60%		0.00%	3381.7	26.70%	3399.4	31.40%	4653.3	27.40%	3727.9	18.00%
116	adk	P69441		125	54	11	16	23.6	5.55	24.1	5.45	0.001557	0.5259498	0.0019757	0.017375	interaction	0.244	10586.4	23.60%	6092.1	13.30%	4682	9.40%	5908.8	14.90%	4802.1	40.60%	5048.6	18.20%
117	atpF	P0ABA0		99	51	8	19	17.3	5.99	20.21	5.46	2.66E-06	4.50E-07	0.000301	0.031619	interaction	0.1349	3797	18.60%	7740.5	8.00%	3629.7	6.10%	5324.3	16.00%	3152.5	16.20%	4310.2	11.20%
118	lolA, lplA, yzzV	P61316		68	26	4	9	22.5/20.3	6.28/5.55	22.03	5.48	0.0131409	0.1667097	0.0049642	0.161861	strain	0.9295	202.8	69.70%	132.6	156.60%	460.5	52.70%	646.4	6.10%	584	11.30%	357.8	79.80%
119	rpsD	P0A7V8		100	41	10	21	23.3	10.05	23.57	5.49					qualitatitve			0.00%		0.00%	308.8	66.30%	504.4	41.20%	493.7	23.50%	682.4	41.60%
120	tpiA	P0A858		178	53	14	16	27	5.64	25.25	5.52	0.0099641	0.0039191	0.0288306	0.837461	treat + strain	0.4251	13884.1	17.30%	8786.3	18.30%	9820.9	26.40%	5926.2	54.40%	9118.7	46.10%	4354.3	49.50%
121	tpiA	P0A858		10	30	8	11	27	5.64	25.46	5.4	0.0152817	0.2962003	0.0027711	0.789195	strain	0.7632	2981.6	35.50%	1524.6	30.70%	613.1	58.80%	519.9	86.00%	1377.4	65.60%	1278	65.60%
122	nadE	P18843		90	35	8	18	30.6	5.41	30.26	5.46					qualitatitve			0.00%		0.00%	297.2	33.00%	451.6	29.90%	219.4	71.40%	429.5	13.70%
123	nadE	P18843		100	44	10	12	30.6	5.41	29.71	5.49					qualitatitve		162.2	130.50%		0.00%	127	117.80%		0.00%	924.6	12.30%	121.3	71.50%
123	tnaA	P0A853		80	22	10	12	52.8	5.88	29.71	5.49					qualitatitve		162.2	130.50%		0.00%	127	117.80%		0.00%	924.6	12.30%	121.3	71.50%
124	ompA	P0A910		150	33	9	2	37.2/35.2	5.99/5.6	27.3	5.5	0.0003746	0.4182526	0.000115	0.008399	interaction	1.0279	1839.3	32.20%	576.3	147.70%	6414.2	62.50%	6272	54.90%	5894.2	71.60%	22803.9	52.10%
125	yggE	P0ADS6		61	29	6	21	26.6	6.1	28.82	5.5	9.26E-06	0.0009605	2.89E-06	0.655079	treat + strain	0.1337	2353.9	6.90%	2790.7	20.80%	1251.5	8.70%	1711.9	20.60%	1393.3	14.30%	1783.8	7.70%
126	accA	P0ABD5		189	54	24	21	35.1	5.76	31.73	5.46					qualitatitve		155.5	89.60%		0.00%	476.3	12.50%	151.4	69.10%	537.8	18.60%	319.4	40.50%
127	ompA	P0A910		138	33	11	12	37.2/35.2	5.99/5.6	34.14	5.5	0.0022456	0.0585816	0.0034277	0.039956	interaction	0.4096	10098.4	28.50%	26902.7	48.80%	30922.1	21.40%	45650.5	34.60%	26603.8	39.80%	21723.2	49.30%
128	gcvT	P27248	OE(49)					40.1	5.36	36.8	5.36	0.000164	0.0018039	0.0011317	0.016758	interaction	0.1771	4705.2	13.70%	2515.8	0.50%	2906.5	4.70%	2535.8	15.90%	2421.1	29.90%	2192	5.30%
129	ompF	P02931		110	35	10	20	39.3/37.1	4.76/4.64	39.16	5.42	0.0029712	0.0030205	0.5476519	0.003396	interaction	0.238	4673.9	27.60%	1902.5	34.10%	2636.5	28.00%	2698.2	16.40%	3252.1	15.60%	2714.9	6.30%
130	lpdA	P0A9P0		63	13	5	4	50.9	5.79	51.5	5.39					qualitatitve		506.8	22.40%		0.00%	515.8	33.40%	129.1	74.10%	378.8	16.10%	193	20.90%
131	melA, mel7	P06720	70					51.3	5.52	49.64	5.48	0.0004059	0.0001811	0.0080859	0.181449	treat + strain	0.8689	3903.5	22.80%	598.4	0.20%	1133.2	30.30%	96.3	115.40%	1114.2	87.00%	283.4	66.90%
131	tnaA, ind	P0A853	70					53.1	5.88	49.64	5.48	0.0004059	0.0001811	0.0080859	0.181449	treat + strain	0.8689	3903.5	22.80%	598.4	0.20%	1133.2	30.30%	96.3	115.40%	1114.2	87.00%	283.4	66.90%
132	treA	P13482		84	21	10	23	60.7/57.6	5.51/5.28	53.56	5.48					qualitatitve			0.00%	1878.5	33.70%		0.00%	306.9	47.80%		0.00%	1116.7	59.00%
133	fimC	P31697		70	25	5	6	26.7/22.7	9.36/9.22	42.86	5.55	0.0133474	0.0024398	0.1764373	0.363301	treat	1.1256	125.6	146.00%	869.3	2.80%	76.7	83.50%	222.1	54.10%	173.2	30.80%	675.1	28.80%
134	ahpF	P35340		62	16	9	32	56.2	5.47	57.67	5.43	0.0030842	0.6517783	0.0004007	0.582863	strain	0.1762	1206.5	26.50%	1120.1	24.90%	703.9	12.30%	793.2	15.50%	753.9	12.00%	798	7.90%
135	atpA	P0ABB0	OE(68)					55.4	5.8	53.93	5.45	3.93E-06	6.31E-08	0.337481	0.289927	treat	0.5279	280.2	82.40%	2057	24.50%	221.1	8.40%	1009.9	13.80%	253.4	37.20%	2043.2	6.60%
135	cpdB	P08331		217	42	22	25	60.3/58.4	5.5/5.42	64.86	5.51					qualitatitve			0.00%		0.00%	107.2	48.90%	91.6	60.10%	124.6	29.40%	455	57.40%
136	guaB	P0ADG7	104					52.3	6.02	55.51	5.73	4.65E-06	1.34E-07	0.0205513	0.795591	treat + strain	0.4576	87.2	43.70%	569.4	8.30%	60.1	61.90%	242.3	31.80%	77.9	20.40%	438	13.70%
137	fusA	P0A6M8		269	52	24	12	77.6	5.24	83.25	5.5					qualitatitve		403.2	34.60%		0.00%	397	33.80%	272.7	56.00%	569.1	35.20%	389.1	112.80%
138	ibpA	P0C054								16.31	5.59	0.020084	0.0013973	0.6239353	0.146607	treat	1.2136	599.2	163.20%	3930.5	10.20%	924.6	33.30%	1791	22.90%	609.1	67.30%	1963.4	8.90%
139	ygaU	P0ADE6	OE(88)					15.9	5.72	16.76	5.65	6.58E-06	1.91E-07	0.2062643	0.007279	interaction	0.7317	5002.4	8.00%	138.4	139.90%	2875.3	12.00%	503.8	66.50%	2401.3	14.20%	454.3	67.90%
140	dps	P0ABT2		238	76	14	7	18.6	5.7	19.59	5.77	0.0000112	1.57E-06	0.0020156	0.021705	interaction	0.2762	8018.3	8.00%	2053	16.00%	5027.8	34.90%	3129	17.90%	3739.3	41.60%	1531.2	6.70%
141	dps	P0ABT2		219	79	15	19	18.6	5.7	18.59	5.77					qualitatitve		1955.6	23.50%	1675.5	69.10%	25.7	74.40%		0.00%	2214.2	14.90%	2502.1	15.40%
142	rplF	P0AG55		141	49	11	28	18.8	9.71	21.07	5.56	7.74E-07	2.10E-07	0.0000649	0.302978	treat + strain	0.1575	2186.9	6.80%	3693.6	17.20%	1200.4	21.40%	2476.5	15.80%	1508.6	16.50%	2480.9	10.10%
143	cysQ	P22255		67	35	6	21	27.2	5.59	25.26	5.57	0.0000467	7.50E-06	0.6106714	0.001497	interaction	0.318	1614.5	18.20%	336.3	60.50%	704.8	26.10%	528.1	32.80%	791.5	10.70%	465	29.00%
144	ribA	P0A717		68	47	6	25	21.8	5.6	21.94	5.62					qualitatitve			0.00%		0.00%	551.5	20.20%	651.2	64.90%	608	43.40%	710.9	63.60%
145	gpmA	P62707		58	34	7	30	28.4	5.86	24.96	5.63					qualitatitve		416.7	79.70%		0.00%	843.1	21.20%	884.8	32.20%	765	27.20%	697	10.70%
146	ribE	P0AFU8		108	53	9	25	23.4	5.64	22.67	5.64	5.71E-07	0.000254	6.30E-07	0.013539	interaction	0.6587	34.2	62.80%	308.8	63.70%	154.6	74.10%	615.8	44.30%	1473.1	12.20%	1514.7	12.90%
147	garR	P0ABQ2	65					30.5	5.58	28.41	5.55	0.0000636	0.019827	0.1256818	4.79E-06	interaction	0.3893	1226.2	9.10%	148.7	95.70%	415	32.80%	779.4	20.00%	470.7	24.50%	720.1	30.10%
148	fabI	P0AEK4		120	41	7	3	27.7	5.58	29.26	5.58					qualitatitve		1178.8	25.20%		0.00%	765.5	30.90%	315.3	63.30%	690.8	35.70%	275.3	58.80%

149	ydfG	P39831		65	32	6	21	27.2	5.65	27.01	5.58	6.42E-07	1.40E-06	5.89E-07	0.000238	interaction	0.3732	1965.8	25.10%	178.8	81.70%	3652.1	20.30%	2150.6	42.80%	3962.2	34.40%	2273.4	16.10%
150	yhbG	P0A9V1		94	34	7	10	26.7	5.64	26.68	5.58	0.000287	0.0001648	0.0153862	0.083335	treat + strain	0.4014	2796	30.20%	3535.3	36.00%	1492.1	71.40%	3844.6	23.70%	845.3	47.00%	2838.3	23.30%
151	cysQ	P22255		78	43	8	14	27.2	5.59	25.52	5.59					qualitatitve		594.8	36.60%		0.00%	641.6	11.90%	534.6	61.10%	631.6	19.90%	551.9	22.40%
152	cysQ	P22255		62	39	6	34	27.2	5.59	27.73	5.62					qualitatitve		214.6	52.90%		0.00%	325.2	47.80%	376	55.40%	268.8	60.90%	379.4	22.50%
153	ytfQ	P39325	OE(75)					64.4/32.1	6.67/5.77	30.5	5.64	3.76E-07	1.61E-08	0.0093116	0.2578	treat + strain	0.5067	6783.7	12.10%	644.1	21.20%	3073.9	15.10%	315.6	54.10%	2275.6	52.80%	497.8	55.20%
154	ydfG	P39831		111	44	10	27	27.2	5.65	27.28	5.66					qualitatitve			0.00%		0.00%	238.6	86.40%	192.8	114.10%	780.3	21.90%	473.2	76.20%
155	ampM	P07906		103	37	9	16	29.3	5.64	28.53	5.69	0.0004335	0.0001169	0.0234452	0.178631	treat + strain	0.1986	1977.7	41.30%	2302	23.00%	1105.4	13.50%	2062.6	12.00%	1192	9.50%	1982	9.30%
156	xthA	P09030		172	53	15	17	30.1	5.8	27.31	5.77					qualitatitve			0.00%		0.00%	328	74.30%	368.7	28.40%	234	80.30%	1120.4	93.20%
157	artJ	P30860		86	41	8	30	26.8/24.9	6.83/5.97	24.5	6.05					qualitatitve		146.1	87.10%		0.00%	331.1	82.00%	74.6	29.00%	290.7	35.10%	184.7	10.90%
158	tesA	P0ADA1		58	32	5	18	23.2/20.0	7.99/6.15	21.2	5.89					qualitatitve		207.2	101.30%		0.00%	163.1	73.20%	133.7	42.60%	196.1	85.50%	210.8	73.00%
159	yhdH	P26646		53	15	4	13	34.7	5.63	32.23	5.54					qualitatitve		739.2	87.20%		0.00%	652.7	24.80%	1035.9	18.90%	501.3	28.20%	831	7.30%
160	cysK	P0ABK5		237	60	16	11	34.5	5.83	33.37	5.6	0.0006438	0.100147	0.0003924	0.050005	strain	0.6581	893.3	16.50%	748.6	44.20%	287.1	16.50%	130.9	136.10%	427	28.70%	533.4	30.30%
160	gapA	P0A9B2		63	26	7	13	35.5	6.61	33.37	5.6	0.0006438	0.100147	0.0003924	0.050005	strain	0.6581	893.3	16.50%	748.6	44.20%	287.1	16.50%	130.9	136.10%	427	28.70%	533.4	30.30%
161	proX, proU	P0AFM2	87					36.1/33.7	5.90/5.65	31.5	5.77	0.0059375	0.0003108	0.3177188	0.742184	treat	0.2902	981.1	42.10%	1346.9	12.20%	803.7	9.00%	1545.4	15.10%	1020.1	20.60%	1819.6	21.30%
162	gpmA	P62707		197	55	10	9	28.6	5.85	25.96	5.85	0.0162588	0.5985811	0.0965381	0.026503	interaction	0.5634	3639.6	21.30%	1812.2	95.20%	758.8	40.70%	1945.6	59.10%	988.4	42.40%	1843.5	66.30%
163	ompR	P0AA16		94	48	9	9	27.4	6.04	42.12	5.69	0.0000352	0.0173611	0.0000157	0.048235	interaction	0.4839	818.8	29.70%	636.8	31.20%	89.6	46.50%	239.3	51.60%	286.5	53.90%	607.8	23.20%
164	yebZ	P0A9K3	90					39.1	5.71	37.17	5.7	0.008697	0.0354642	0.0063558	0.116455	treat + strain	0.3937	767.9	21.40%	763.4	7.70%	358.2	11.70%	511.9	49.20%	273.8	57.30%	579.5	6.10%
165	trpB	P0A879		101	25	10	19	43.0	5.71	41.69	5.73	0.0000967	0.1013143	0.0000109	0.06823	strain	0.5446	305.6	45.90%	116.3	89.30%	771	26.30%	910.7	66.10%	1010.3	39.70%	984.8	44.70%
165	ackA	P0A6A3		81	27	8	21	43.3	5.85	41.69	5.73	0.0000967	0.1013143	0.0000109	0.06823	strain	0.5446	305.6	45.90%	116.3	89.30%	771	26.30%	910.7	66.10%	1010.3	39.70%	984.8	44.70%
166	kbl	P0AB77		125	32	11	15	43.1	5.64	40.48	5.75					qualitatitve		343.8	30.50%		0.00%	467.1	15.90%	223.4	74.40%	250.4	52.60%	235.9	65.10%
167	ackA	P0A6A3	98					43.6	5.85	41.66	5.78	0.0000403	0.0005119	0.0000262	0.407977	treat + strain	0.1874	1880.7	14.80%	2387.1	5.50%	984.8	13.70%	1309.8	19.60%	1242	29.70%	1980.3	15.90%
168	ompA	P0A910	91					37.3/35.2	5.99/5.60	34.64	5.76	0.0003169	0.0046595	0.0001134	0.878908	treat + strain	0.8103	3022.9	47.80%	9842.3	50.90%	681.4	26.20%	1823.9	48.80%	368.1	84.60%	849.6	51.30%
169	gapA	P0A9B2		118	35	10	12	35.4	6.58	34.06	6.03					qualitatitve			0.00%	1305	102.60%	1861.9	37.00%	2553.5	18.00%	312.7	35.90%	2056.5	26.40%
169	rsmC	P39406		53	19	6	12	37.5	6	34.06	6.03					qualitatitve			0.00%	1305	102.60%	1861.9	37.00%	2553.5	18.00%	312.7	35.90%	2056.5	26.40%
170	melA	P06720	OE(67)					51.3	5.52	49.25	5.54	3.10E-06	7.05E-08	0.1238187	0.003177	interaction	0.5206	5256.1	28.90%	128.3	48.60%	3312.4	33.30%	713	36.40%	3737.9	67.10%	620.3	27.40%
171	pyrG	P0A7E5		185	29	17	16	60.4	5.63	47.82	5.66					qualitatitve		57.5	106.70%		0.00%	157.8	29.90%	227.1	70.00%	300	77.90%	199.5	77.50%
172	lpdA	P0A9P0	OE(88)					50.6	5.79	51.83	5.72	1.91E-06	0.000074	1.09E-06	0.422087	treat + strain	0.2403	2151.8	12.60%	2995.4	5.60%	769.8	25.50%	1345.9	21.50%	786.9	35.00%	1493	22.30%
173	ddpA	P76128	74					57.6/54.9	6.29/5.64	54.91	5.54	0.0000674	2.73E-06	0.4193372	0.190615	treat	0.4321	351.8	22.10%	115	8.90%	376.9	10.30%	70.2	71.50%	306	15.00%	98.3	51.40%
174	dppA	P23847		78	19	9	15	60.3/57.4	6.21/5.75	57.68	5.56					qualitatitve			0.00%		0.00%	295.5	44.40%	134.8	121.90%	164.5	40.60%	146.7	32.30%
175	lpdA	P0A9P0	OE(70)					50.9	5.79	52.71	5.58	2.75E-12	8.51E-14	1.46E-07	0.347143	treat + strain	0.1823	761	14.80%	3692.1	9.00%	312.2	15.10%	1493.4	19.60%	398	11.70%	2489.6	25.70%
176	pyrG	P0A7E5	76					60.3	5.63	61.86	5.61	0.0213852	0.1461446	0.0079285	0.351595	strain	0.4171	994.2	24.70%	0.41711	16.10%	464.7	27.20%	637	52.40%	378	26.20%	694.1	13.80%
177	lpdA	P0A9P0		194	32	18	20	50.6	5.79	52.78	5.63	0.0020598	0.0488764	0.0007996	0.257367	treat + strain	0.622	1132.1	25.20%	1148.8	31.30%	194.4	78.70%	421.7	17.00%	417.1	51.60%	685	52.80%
178	atpA	P0ABB0		66	11	3	0	55.2	5.8	53.27	5.65	0.0067991	0.0023854	0.0717494	0.156934	treat	0.6243	960.7	14.80%	1319.3	28.60%	388.9	53.20%	903.5	44.00%	374	78.40%	1260.5	18.40%
179	dppA	P23847	OE(84)					60.3/57.4	6.21/5.75	55.97	5.69	9.33E-07	6.51E-06	1.32E-06	0.070059	treat + strain	0.5844	2069.5	27.70%	278.1	79.50%	12818.7	57.90%	3112.1	13.00%	1495.7	19.40%	549.7	17.90%
180	oppA	P23843	OE(89)					61.0/58.4	6.05/5.85	57.56	5.69	0.00067	0.0000137	0.6974971	0.502352	treat	0.5257	1742.6	14.80%	452.3	44.60%	2251.2	8.50%	637.5	66.30%	1732.4	16.10%	671.9	32.50%
181	atpA	P0ABB0		217	43	18	14	55.2	5.8	61.25	5.72					qualitatitve			0.00%	103.4	33.20%	551.6	50.50%	585.5	42.80%	634.5	32.80%	615.7	28.30%
182	oppA	P23843	OE(90)					61.0/58.4	6.05/5.85	57.69	5.73	0.0001678	6.00E-06	0.1534965	0.063264	treat	0.6202	594	29.20%	85.1	132.60%	463	7.40%	130.7	59.10%	513.1	19.50%	202.2	53.10%
183	oppA	P23843	OE(112)					61.0/58.4	6.05/5.85	55.64	5.82	6.16E-07	3.66E-08	0.0008336	0.112925	treat + strain	0.2497	5189.5	22.60%	1881.6	19.30%	10908.9	31.50%	3004.5	11.90%	5679.3	34.70%	2751.7	23.10%
184	bglX	P33363	79					83.5781.4	5.85/5.77	80.54	5.56	0.0019249	0.6224205	0.0004076	0.249158	strain	0.2359	246.6	23.20%	186.2	2.30%	129.9	17.30%	125.3	26.20%	113.3	18.50%	137.2	32.70%
185	sdhA	P0AC41		176	32	15	10	64.4	5.85	68.91	5.73					qualitatitve		95.4	54.30%		0.00%	87.2	67.60%	124.5	7.60%	187.8	54.00%	105.9	50.00%
186	rplI	P0A7R1		152	69	11	20	15..8	6.17	18.49	5.88					qualitatitve		410.5	19.20%		0.00%	2661.4	18.30%	3182.2	30.10%	1153.4	45.50%	774.6	56.10%
187	hslV	P0A7B8/P0A8E7	OE(92)	58	31	4	20	19.0	5.95	19.37	5.89	0.0028146	0.0026151	0.0761703	0.006679	interaction	0.6623	2586.6	10.90%	520	147.70%	1963.4	26.90%	1542.7	31.10%	1464.5	21.60%	1177.8	16.70%
188	ycgM	P76004		120	49	10	27	23.7	5.88	23.08	5.86					qualitatitve		1167.9	16.40%		0.00%	863.9	13.60%	390.6	11.50%	923.1	17.50%	422.9	43.30%
189	tufA, tufB	P0A6N1		55	19	6	16	43.3	5.30	22.56	5.97	0.000512	0.0000572	0.014766	0.210439	treat+strain	0.6714	398.5	45.60%	89.7	56.50%	299.2	9.40%	35.5	94.70%	518.1	16.30%	237.7	89.30%
190	gpmA, gpm, pgm, pgmA	P62707		154	43	11	12	28.6	5.85	25.65	5.85	0.0025433	0.0193812	0.0045405	0.1567	treat+strain	0.3053	9324.3	15.60%	8615.3	21.50%	5930.3	35.10%	4775.1	42.70%	6980.9	22.50%	3403.6	27.70%
191	sucD	P0AGE9		159	57	12	16	29.9	6.31	28.56	5.85	0.0125267	0.2981716	0.0710454	0.013185	interaction	0.1896	922	14.70%	716.6	32.10%	543.3	11.30%	783.8	13.70%	582.4	13.20%	701.9	21.70%
192	sucD	P0AGE9	OE(98)					29.9	6.31	28.35	5.91	0.0002695	0.9164441	0.000019	0.740453	strain	0.6324	171.8	96.70%	85.7	54.60%	474.6	22.60%	576.2	36.30%	624.8	9.90%	799.6	42.20%
193	rbsB, prlB, rbsP	P02925	88					30.9/28.5	6.85/5.99	26.62	5.94	1.53E-11	2.84E-08	2.84E-12	0.006713	interaction	0.5187	2490	31.90%	145	113.80%	87051.6	39.20%	23336.8	53.70%	114101	17.30%	22089.8	15.90%
194	artJ	P30860		90	34	6	17	26.8/24.9	6.83/5.97	28.31	5.96					qualitatitve			0.00%		0.00%	526.2	22.60%	667.9	26.00%	740.1	26.90%	800.2	15.90%
195	yeaD	P39173		94	29	8	16	32.7	5.89	29.87	5.98	0.0013704	0.0017796	0.005651	0.305172	treat + strain	0.1744	2217.4	14.70%	1474.7	28.40%	1405.8	8.70%	1242.4	20.80%	1510.3	14.50%	1179.5	15.70%
196	dkgA	Q46857	OE(101)					31.1	6.00	27.84	5.98	8.02E-06	2.51E-07	0.0810711	0.454987	treat	0.2753	2443.4	7.90%	849	45.10%	1462.3	8.20%	710.6	40.20%	1710.1	21.10%	672.4	20.30%
197	udp	P12758		135	45	11	15	27.0	5.81	25.88	6.03	9.22E-06	0.4115053	5.63E-07	0.816457	strain	0.1447	4443.1	18.60%	4841.2	26.10%	2417.2	9.20%	2405.5	5.30%	2767.6	14.40%	2982.2	5.50%
198	dapA	P0A6L2		105	40	10	30	31.3	5.98	28.59	6.06	0.0037118	0.1787432	0.010795	0.008629	interaction	0.7133	28.2	7.30%	535.5	0.00%	206.2	71.10%	145.9	73.80%	706	41.40%	355.7	46.40%
199	pheS	P08312	OE(79)					36.9	5.79	34.66	5.82	0.0016532	0.0000589	0.1406575	0.84681	treat	0.4559	765.5	50.70%	2341.2	64.50%	456.2	17.00%	1141	30.30%	531.1	53.00%	1537.7	20.90%
200	manX	P69797		87	29	10	20	35	5.7	33.26	5.85					qualitatitve			0.00%	825.9	1.50%	247.4	0.20%	345.2	41.60%	386.4	61.00%	337.4	59.60%
201	kbl	P0AB77		190	45	17	24	43.1	5.64	34.68	5.88					qualitatitve		619.2	16.30%		0.00%	2397.5	30.20%	266.7	64.80%	1321.2	41.80%	321.2	50.10%
202	gatD	P0A9S3	116					37.8	5.9	33.66	5.99	1.55E-07	0.0006651	3.02E-07	2.01E-05	interaction	0.5264	1480.9	41.80%	7951.9	33.10%	489.5	19.40%	219.4	68.50%	430.6	22.80%	3707.9	29.20%
202	gapA	P0A0B2	116					35.7	6.6	33.66	5.99	1.55E-07	0.0006651	3.02E-07	2.01E-05	interaction	0.5264	1480.9	41.80%	7951.9	33.10%	489.5	19.40%	219.4	68.50%	430.6	22.80%	3707.9	29.20%
203	kdsA	P0A715		106	39	9	17	30.8	6.3	29.9	6.31					qualitatitve		1011.7	18.10%	267.5	88.60%	601.7	25.90%	369.7	28.50%		0.00%		0.00%
204	yahK	P75691	OE(83)					38.5	5.80	38.77	5.83	0.0089062	0.0014311	0.2729493	0.356768	treat	0.8386	1494.2	26.40%	364.7	42.00%	1028	11.70%	218.4	67.50%	645.8	25.10%	285.8	18.40%
205	carA	P0A6F1		68	24	7	19	41.4	5.91	42.05	5.91	0.001831	0.6980655	0.0017508	0.023206	interaction	0.1482	1944.8	17.90%	1461.5	10.60%	1109.4	15.70%	1338.8	8.90%	1306	12.60%	1329.8	17.80%
206	tonB	P02929		64	19	7	21	26.1	9.62	38.22	5.95	0.0038134	0.0004897	0.0488231	0.746298	treat + strain	0.4502	244	73.20%	486.2	46.20%	182	46.80%	440.6	22.70%	354.4	31.10%	655.3	11.60%
207	gapA	P0A9B2		60	22	6	16	35.4	6.58	33.44	6.13					qualitatitve		382.6	25.10%	919	96.20%	113.8	32.60%	334.5	0.00%	83.7	116.10%	366.9	70.00%
208	tnaA	P0A853		256	56	21	15	52.8	5.88	48.94	5.84	0.0005742	0.0000624	0.0284161	0.867537	treat + strain	0.5867	6790.4	24.20%	2268.9	31.00%	3712.3	56.10%	947.1	61.80%	8054	92.10%	1480.1	12.20%
209	lpdA, lpd	P0A9P0	124					50.9	5.79	52.02	5.92	0.0004039	0.0002049	0.0018892	0.499096	treat + strain	0.3914	522.1	37.20%	844.4	3.50%	206	43.00%	421.6	23.00%	230.2	60.60%	549.4	16.70%
210	ugpB	P0AG80		262	52	21	16	48.4/46.1	6.29/5.98	45.56	5.95	7.32E-07	0.0481626	1.68E-07	0.017136	interaction	0.1648	1081.9	18.50%	904.5	17.80%	381.5	24.40%	511.8	14.00%	521.9	14.30%	707.1	6.10%
211	ugpB	P0AG80	OE(107)					48.4/46.1	6.29/5.98	43.19	5.98	2.80E-08	4.62E-10	0.4695996	0.016077	interaction	0.2551	2318.4	18.40%	384.1	42.90%	1320.3	10.20%	464.7	34.10%	1480.3	16.80%	489.6	25.10%
212	glyA	P0A825		150	33	14	16	45.3	6.03	44.6	6.07	0.0043711	0.567381	0.0011948	0.226043	strain	0.2012	5218	19.30%	4009.2	13.50%	3234.3	29.20%	3160	21.50%	2753.2	16.50%	3095.4	15.00%
213	fumC	P05042	OE(109)					50.9	6.12	48.63	6.13	0.0012324	0.000066	0.0606328	0.478705	treat	0.2581	1341.5	34.80%	693.8	29.50%	1657.4	16.00%	876.5	34.20%	1582.1	10.40%	1077.7	7.00%
214	oppA	P23843		227	36	15	2	60.9/58.4	6.05/5.85	55.03	5.92	0.0000155	0.0009336	4.96E-06	0.621279	treat + strain	0.1674	718.7	25.10%	843.5	7.90%	358	16.50%	494.1	20.20%	400.3	14.50%	561.3	7.70%
215	oppA	P23843		136	26	14	11	60.9/58.4	6.05/5.85	53.15	5.99	0.0001826	0.0094511	0.0000326	0.57159	treat + strain	0.3001	880.8	24.00%	1380.7	13.10%	568.7	30.40%	950.9	37.30%	371.7	46.00%	423.3	17.50%
216	fumA	P0AC33		136	22	11	6	60.3	6.11	56.58	6.17					qualitatitve			0.00%	123.9	85.40%		0.00%		0.00%	55.5	66.40%	306.6	7.40%
217	glcB	P37330	130					80.8	5.79	79.12	5.84	0.0035191	0.0015336	0.3561938	0.166549	treat	0.5783	171.8	36.30%	126.4	0.00%	207.8	40.20%	47.9	48.30%	209.1	32.50%	42.9	69.60%
218	fumA	P0AC33		76	14	6	4	60.2	6.11	66.08	5.9	0.0115443	0.0442271	0.0026616	0.837475	treat + strain	0.2181	291.1	29.50%	371.3	16.30%	231.6	17.00%	287.3	26.20%	192	19.40%	218.2	19.70%
219	rplI	P0A7R1		173	63	9	2	15..8	6.17	17.13	6.13	0.0044389	0.0350194	0.0036674	0.26869	treat + strain	0.8579	102.9	142.20%	247.1	99.20%	272.1	30.20%	924.1	61.00%	560.1	26.50%	629.5	46.20%
220	rplI	P0A7R1		251	82	16	18	15..8	6.17	16.92	6.22	0.0001948	0.0000541	0.0029734	0.550226	treat + strain	0.3456	11338.7	10.70%	23636	17.90%	6392.7	29.10%	13141.2	46.60%	5082.3	48.90%	13596.2	25.80%
221	adk	P69441								22.31	6.13	0.016544	0.2589909	0.0093853	0.495158	strain	1.2204	215.7	181.60%	245.6	26.40%	807.5	61.60%	948	69.10%	1153.6	38.80%	1675.9	56.80%
222	nusG	P0AFG0		129	63	9	18	20.5	6.34	21.27	6.15					qualitatitve		177.9	0.00%		0.00%	263.7	54.70%	50.6	132.90%	386.1	14.30%	143.8	70.90%
223	lexA	P0A7C2		56	32	6	34	22.4	6.23	22.1	6.27	0.0023706	0.2871272	0.0048826	0.010887	interaction	0.2905	6975.6	11.00%	4495	14.70%	4680.6	9.50%	6080.9	15.30%	2862.4	57.30%	4480.2	9.60%
224	gapA	P0A9B2		163	50	12	10	35.4	6.58	26.87	6.3	0.0031209	0.0067589	0.0010001	0.206371	treat + strain	0.9266	1214.7	80.40%	102.9	117.80%	3036	17.70%	1698.8	61.00%	2793.9	35.60%	1621.9	42.50%
225	gapA	P0A9B2		118	29	10	8	35.4	6.58	34.36	6.16					qualitatitve		1032.3	45.10%		0.00%	693.2	23.90%	967.2	103.80%	819.4	30.60%	883.1	34.10%
226	dacA	P0AEB2		76	15	6	5	44.4/41.3	8.31/6.68	33.89	-1					qualitatitve			0.00%	3620.7	35.70%	73.1	111.90%	3835.8	23.60%	421	78.10%	423.4	44.70%
227	tnaA	P0A853		142	26	12	7	52.8	5.88	50.08	6.16					qualitatitve		146.8	109.20%		0.00%	237.8	34.30%	327.7	11.00%	299.7	27.40%	257.9	63.40%
227	fumC	P05042		43	10	5	12	50.5	6.12	50.08	6.16					qualitatitve		146.8	109.20%		0.00%	237.8	34.30%	327.7	11.00%	299.7	27.40%	257.9	63.40%

(a) The numbering corresponds to the spots in 2D gel images of Supplementary figure 3.

(b) Gene name and synonyms extracted from the Swiss Prot database v54.6 for *E. coli* (release 12/04/07, http://www.expasy.org).

(c) In case an ID reference is given, the identification is based on the matching of spots to a published reference gel by PDQuest 7.3 (Bio-Rad). OE referes to Figure 8 and Suppl. table 3 of Wagner et al. (2007) Mol. Cell. Proteomics 6,1527-1550.

(d) Mascot MOWSE protein score.

(e) Coverage by the matching peptides to the protein sequence in the Swiss Prot database v54.6.

(f) Number of matching peptides at mass accuracy of 25 ppm, without allowing missed cleavages.

(g) Number of not matching peptides.

(h) Protein sizes (in kDa) predicted from amino acid sequence. Two sizes are given for secretory proteins, the first size corresponds to the mature form of the protein after signal sequence processing, and the second size corresponds to the precursor form including the signal sequence.

(i) Size of proteins calculated from the spot position in the 2D gels used for the analysis.

(j) pI of proteins predicted from amino acid sequence. Two pIs are given for secretory proteins, the first pI corresponds to the mature form of the protein after signal sequence processing, and the second pI corresponds to the precursor form including the signal sequence.

(k) pI of proteins calculated from the spot position on the 2D gels used for the analysis.

(l) The average spot intensity of all gels in one replicate group after normalization calculated by PDQuest. The values are based on the area under a Gaussian distribution constructed from spots in the filtered 2D images.

(m) Coefficient of variation of spot intensities within a replicate group.