

Supplemental Table 2: Gene changes at 60 minutes in adherent versus non-adherent samples

Affy_ID	Fold change	p-value	Realtime change	Annotation	Derivation of annotation
A4052_s_at	4.313332633	0.024012538	Increase_in_Adherent	trpE; anthranilate synthase component I (EC:4.1.3.27); K01657 anthranilate synthase component I [EC:4.1.3.27]	ecw:EcE24377A_1463
V1799_s_at	3.972247924	0.033307448	Increase_in_Adherent	hscB; co-chaperone HscB ; K04082 molecular chaperone HscB	sdv:SDY_2723
V0231_s_at	3.95580421	0.000284517	Increase_in_Adherent	ssb; single-stranded DNA-binding protein ; K03111 single-strand DNA-binding protein	sdv:SDY_4508
SB5_0275_s_at	3.893614168	1.07E-05	Increase_in_Adherent	hypothetical protein ; K02040 phosphate transport system substrate-binding protein	sbo:SBO_3421
K3820_x_at	3.763692747	7.60E-05	Increase_in_Adherent	putative holin protein	eqj:EC026_3693
O2CoV121_at	3.647435418	2.22E-05	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
SD1_2456_x_at	3.566304619	0.015156769	Increase_in_Adherent	putative fructose-like phosphotransferase EIIB subunit 3 ; K11202 PTS system, fructose-specific IIB-like component [EC:2.7.1.69]	sbv:SbBS512_E4440
SDY_4180_x_at	3.540687986	4.18E-05	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
D1328_s_at	3.533442346	0.004222188	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
A0552_s_at	3.51323466	0.019815913	Increase_in_Adherent	hscB; co-chaperone HscB ; K04082 molecular chaperone HscB	sdv:SDY_2723
b3350_s_at	3.455476842	0.000165312	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
V0624_x_at	3.388319399	0.000108353	Increase_in_Adherent	hypothetical protein ; K05521 ADP-ribosylglycohydrolase [EC:3.2.-.]	sdv:SDY_2272
EC869_7614_x_at	3.35904693	0.000329902	Increase_in_Adherent	iron-containing alcohol dehydrogenase ; K08317 putative oxidoreductase [EC:1.1.-.]	dze:Dd1591_2414
V6086_s_at	3.350223296	1.94E-05	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
SS5_1928_s_at	3.341423506	0.00016005	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
SD1_1765_at	3.27870319	0.000290704	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
SD1_0998_s_at	3.254654737	0.000313497	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
c0511_s_at	3.174120061	1.20E-05	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
S2121_x_at	3.162633479	0.000249231	Increase_in_Adherent	transposase (IS4 family)	sbv:SbBS512_E1691
SS5_3223_s_at	2.94619103	0.002054826	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
EC9_1238_s_at	2.862502378	4.07E-05	Increase_in_Adherent	hypothetical protein	ecw:EcE24377A_1340
EC869_7066_x_at	2.844254044	0.002132362	Increase_in_Adherent	ADP-ribosylglycohydrolase family protein ; K05521 ADP-ribosylglycohydrolase [EC:3.2.-.]	sbv:SbBS512_E1139
b4060_s_at	2.831107646	0.035196322	Increase_in_Adherent	ycjB; hypothetical protein	sdv:SDY_4507
SB5_0762_s_at	2.734698737	0.028542042	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
EC869_0252_s_at	2.702537684	0.000630605	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
EC869_3005_x_at	2.674321482	0.001711709	Increase_in_Adherent	phnK; phosphonate C-P lyase system protein PhnK ; K05781 putative phosphonate transport system ATP-binding protein	sbo:SBO_4123
EC869_2283_s_at	2.64745681	0.000183281	Increase_in_Adherent	metH; B12-dependent methionine synthase ; K00548 5-methyltetrahydrofolate-homocysteine methyltransferase [EC:2.1.1.13]	cko:CKO_03902
SBO_0242_s_at	2.596453763	1.65E-05	Increase_in_Adherent	prfH; peptide chain release factor-like protein ; K02839 peptide chain release factor RF-H	sdv:SDY_0481
A3217_s_at	2.487467147	0.001509214	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
b0113_s_at	2.421377298	0.006374488	Increase_in_Adherent	pdhR; transcriptional regulator PdhR ; K05799 GntR family transcriptional regulator, transcriptional repressor for pyruvate dehydrogenase complex	sdv:SDY_0143
L4020_s_at	2.383643228	7.90E-06	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
S1087_s_at	2.373402292	7.68E-06	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
ECP_4339_s_at	2.342157822	0.007839305	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
b0957_s_at	2.280984057	0.000577787	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
c3413_s_at	2.259757707	0.002000598	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
SDM_4211_x_at	2.258436431	0.000613156	Increase_in_Adherent	L(+)-tartarate dehydratase subunit beta ; K03780 L(+)-tartarate dehydratase beta subunit [EC:4.2.1.32]	cko:CKO_04452
AFFX-25srRnad_at	2.126497314	0.000254012	Increase_in_Adherent	hypothetical protein	ppp:PHYPADRAFT_103626
b0583_s_at	2.047777996	0.003577589	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
V1792_s_at	1.99677787	0.04885354	Increase_in_Adherent	cysteine desulfurase IscS (EC:2.8.1.7); K04487 cysteine desulfurase [EC:2.8.1.7]	dze:Dd1591_1104
EC536_1754_x_at	1.959771988	0.010888817	Increase_in_Adherent	phnK; phosphonate C-P lyase system protein PhnK ; K05781 putative phosphonate transport system ATP-binding protein	sbo:SBO_4123
EC869_5323_s_at	1.952182908	0.000404866	Increase_in_Adherent	mtr; tryptophan permease ; K03835 tryptophan-specific transport protein	sdv:SDY_3340
b3161_s_at	1.94089143	0.032547659	Increase_in_Adherent	mtr; tryptophan permease ; K03835 tryptophan-specific transport protein	sdv:SDY_3340
V0229_s_at	1.876626876	0.034084599	Increase_in_Adherent	ycjB; hypothetical protein	sdv:SDY_4507
b1531_s_at	1.875262525	0.015191741	Increase_in_Adherent	DNA-binding transcriptional activator MarA	cko:CKO_01552
F4980_s_at	1.860218382	0.000589014	Increase_in_Adherent	ferric iron reductase involved in ferric hydroxamate transport	edi:EcColC_3688
D4795_s_at	1.772324507	0.031390751	Increase_in_Adherent	ybl207; hypothetical protein	ebi:B21_03841
A1975_s_at	1.767655466	0.000857729	Increase_in_Adherent	hypothetical protein	cko:CKO_00114
A1802_s_at	1.750779417	0.000468091	Increase_in_Adherent	serine acetyltransferase (EC:2.3.1.30); K00640 serine O-acetyltransferase [EC:2.3.1.30]	ttu:TERTU_0669
ECP_3905_s_at	1.744024296	0.038819294	Increase_in_Adherent	rnP; ribonuclease P (EC:3.1.26.5); K03536 ribonuclease P protein component [EC:3.1.26.5]	sdv:SDY_4186
AFFX-18srRnaa_at	1.722622005	0.000894788	Increase_in_Adherent	hypothetical protein LOC769550	gga:G769550
D4794_s_at	1.660321085	0.00945824	Increase_in_Adherent	hypothetical protein	cef:CE1543
D4793_s_at	1.60084765	0.023643729	Increase_in_Adherent	hypothetical protein	lpr:pg2751
V1827_x_at	1.591600861	0.013900562	Increase_in_Adherent	pbpC; penicillin-binding protein 1C (EC:2.4.2.-); K05367 penicillin-binding protein 1C [EC:2.4.1.-]	sbv:SbBS512_E2894
D4792_s_at	1.542942674	0.042466788	Increase_in_Adherent	hypothetical protein	bnj:BMULJ_05092
V0550_s_at	1.536169695	0.015583986	Increase_in_Adherent	yegH; UPF0053 protein YegH	ctu:Clu_27600
M0299_x_at	1.528937614	0.035636063	Increase_in_Adherent	hypothetical protein ; K07090	sbv:SbBS512_E2705
EC536_6685_s_at	1.500206271	0.006728467	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
ECP_3198_s_at	1.432541687	0.032420828	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
ECP_0062_s_at	1.427598482	0.032340035	Increase_in_Adherent	araD; L-ribulose-5-phosphate 4-epimerase (EC:5.1.3.4); K01786 L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]	kpe:KPK_4682
G4660_at	1.346838003	0.02525556	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
V4037_s_at	1.344099221	0.005561907	Increase_in_Adherent	hypothetical protein ; K00117 quinoprotein glucose dehydrogenase [EC:1.1.5.2]	cko:CKO_03243
AFFX-25srRnad_at	1.340464038	0.001385801	Increase_in_Adherent	hypothetical protein	kla:KLLA0D17578g
pCoo036_x_at	1.242240393	0.002944779	Increase_in_Adherent	repA; replication protein	ecw:EcE24377A_C0025
Z2553_s_at	1.229243042	0.031559344	Increase_in_Adherent	yciG; hypothetical protein; K06884	sfv:SFV_1273
V0683_s_at	1.228525846	0.021110027	Increase_in_Adherent	ABC transporter, quaternary amine uptake (QAT) family, permease protein ; K05846 osmoprotectant transport system permease protein	sbv:SbBS512_E0843
A3232_s_at	1.214234501	0.037334567	Increase_in_Adherent	NO_KEGG_DATA	NO_KEGG_DATA
A3516_s_at	1.194956785	0.007234506	Increase_in_Adherent	hypothetical protein	sbv:SbBS512_E2502
c0262_x_at	1.178468014	0.000717211	Increase_in_Adherent	putative protein encoded within IS	sf:CP0086
V5493_x_at	1.176311235	0.001355963	Increase_in_Adherent	phosphoglycolate phosphatase ; K01091 phosphoglycolate phosphatase [EC:3.1.3.18]	cko:CKO_04806
EC869_0480_s_at	1.114666936	0.006253729	Increase_in_Adherent	zntA; zinc/cadmium/mercury/lead-transporting ATPase (EC:3.6.3.5); K01532 Cd2+-exporting ATPase [EC:3.6.3.5]; K01534 Zn2+-exporting ATPase [EC:3.6.3.5]	ssn:SSON_3707
D4740_at	1.078944025	6.73E-07	Increase_in_Adherent	hypothetical protein	smm:Smp_109290

SD1_3102_s_at	-6.427547052	0.008745703	Decrease_in_adherent metE; 5-methyltetrahydropteroylglutamate-homocysteine S-methyltransferase (EC:2.1.1.14); K00549 5-methyltetrahydropteroylglutamate-homocysteine methyltran	sdY:SDY_3914
A2032_s_at	-6.331052702	0.002545566	Decrease_in_adherent metE; 5-methyltetrahydropteroylglutamate-homocysteine S-methyltransferase (EC:2.1.1.14); K00549 5-methyltetrahydropteroylglutamate-homocysteine methyltran	ssn:SSON_4003
V4383_s_at	-5.83173624	0.003416839	Decrease_in_adherent pfb; formate acetyltransferase 1; K00656 formate C-acetyltransferase [EC:2.3.1.54]	sdY:SDY_2358
EC869_4008_s_at	-5.524484838	0.000841218	Decrease_in_adherent pfb; formate acetyltransferase 1; K00656 formate C-acetyltransferase [EC:2.3.1.54]	sdY:SDY_2358
A3028_s_at	-5.252314181	0.00058341	Decrease_in_adherent hypothetical protein	sdY:SDY_0367
A4188_s_at	-5.022479908	0.000901535	Decrease_in_adherent adhA; aldehyde dehydrogenase A (EC:1.2.1.22 1.2.1.21); K00138 lactaldehyde dehydrogenase [EC:1.2.1.22]; K07248 glycolaldehyde dehydrogenase [EC:1.2.1.21]	sbC:SbBS512_E1635
A1237_s_at	-4.961943713	0.00761433	Decrease_in_adherent glgS; glycogen synthesis protein GlgS	sdY:SDY_3228
A2373_s_at	-4.896160705	1.55E-05	Decrease_in_adherent adhE; fumarate reductase subunit D; K00247 fumarate reductase subunit D [EC:1.3.99.1]	sdY:SDY_4395
EC869_1970_s_at	-4.761558213	0.013450862	Decrease_in_adherent adhE; bifunctional acetaldehyde-CoA/alcohol dehydrogenase; K00001 alcohol dehydrogenase [EC:1.1.1.1]; K04072 acetaldehyde dehydrogenase [EC:1.2.1.10]	sdY:SDY_1295
SD1_3168_s_at	-4.728678396	0.01414552	Decrease_in_adherent adhE; bifunctional acetaldehyde-CoA/alcohol dehydrogenase; K00001 alcohol dehydrogenase [EC:1.1.1.1]; K04072 acetaldehyde dehydrogenase [EC:1.2.1.10]	sdY:SDY_1295
V0291_s_at	-4.563346142	0.001327638	Decrease_in_adherent malE; maltose ABC transporter periplasmic protein; K10108 maltose/maltodextrin transport system substrate-binding protein	ssn:SSON_4212
b4002_s_at	-4.527401431	0.001321476	Decrease_in_adherent zraP; zinc resistance protein; K07803 zinc resistance-associated protein	sbC:SbBS512_E4493
A3980_s_at	-4.483927867	0.010537802	Decrease_in_adherent adhE; bifunctional acetaldehyde-CoA/alcohol dehydrogenase; K00001 alcohol dehydrogenase [EC:1.1.1.1]; K04072 acetaldehyde dehydrogenase [EC:1.2.1.10]	sdY:SDY_1295
V0290_s_at	-4.471612231	6.16E-06	Decrease_in_adherent malE; maltose transport system periplasmic maltose-binding component; K10108 maltose/maltodextrin transport system substrate-binding protein	kpu:KPY_0275
G3995_s_at	-4.432274242	7.50E-05	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V2454_s_at	-4.432076442	0.020237987	Decrease_in_adherent dhaL; dihydroxyacetone kinase ADP-binding subunit (EC:2.7.1.-); K05879 dihydroxyacetone kinase, C-terminal domain [EC:2.7.1.-]	sbC:SbBS512_E1358
V7066_s_at	-4.417353118	0.005625045	Decrease_in_adherent hypothetical protein	ecx:EcHS_A1937
b1846_s_at	-4.368394178	0.013499171	Decrease_in_adherent hypothetical protein	ecx:EcHS_A1937
A2135_s_at	-4.361284236	0.004266081	Decrease_in_adherent hypothetical protein	sbC:SbBS512_E4404
V1509_s_at	-4.235920745	0.007730285	Decrease_in_adherent gapA; glyceraldehyde-3-phosphate dehydrogenase A; K00134 glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]	sdY:SDY_1488
A2229_s_at	-4.190485913	0.012703192	Decrease_in_adherent pepE; peptidase E (EC:3.4.13.21); K05995 dipeptidase E [EC:3.4.13.21]	sbC:SbBS512_E4515
A2136_s_at	-4.157487045	3.47E-05	Decrease_in_adherent yjiT; universal stress protein UspD	sdY:SDY_3821
V3051_s_at	-4.125072934	0.008770613	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b4189_s_at	-4.12289405	0.003552868	Decrease_in_adherent yjiF; hypothetical protein	sdY:SDY_4358
V4449_s_at	-4.117559516	0.010486473	Decrease_in_adherent dmsA; anaerobic dimethyl sulfoxide reductase subunit A; K07306 anaerobic dimethyl sulfoxide reductase subunit A [EC:1.8.99.-]	sbo:SBO_0827
ECs2489_s_at	-4.106340737	0.007322581	Decrease_in_adherent yeaD; hypothetical protein	etw:ECSP_2352
V0028_s_at	-4.089697338	0.003285994	Decrease_in_adherent frdA; fumarate reductase flavoprotein subunit (EC:1.3.99.1); K00244 fumarate reductase flavoprotein subunit [EC:1.3.99.1]	sdY:SDY_4398
SD1_3424_s_at	-4.081387034	0.013279759	Decrease_in_adherent asnB; asparagine synthetase B; K01953 asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]	spe:Spro_1222
p166897_140_s_at	-4.071235828	0.000934873	Decrease_in_adherent mok; modulator of post-segregation killing protein	ecv:APECO1_01CoBM20
V0033_s_at	-4.039025222	0.000679152	Decrease_in_adherent frdB; fumarate reductase iron-sulfur subunit (EC:1.3.99.1); K00245 fumarate reductase iron-sulfur protein [EC:1.3.99.1]	sbC:SbBS512_E4685
M3390_s_at	-4.032311351	0.001929966	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V0058_s_at	-4.031894473	0.000646269	Decrease_in_adherent aspA; aspartate ammonia-lyase (EC:4.3.1.1); K01744 aspartate ammonia-lyase [EC:4.3.1.1]	sdY:SDY_4444
V0242_s_at	-4.030291619	1.34E-05	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V5434_s_at	-4.02286197	0.016141102	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b2597_s_at	-3.999392341	0.000557263	Decrease_in_adherent hypothetical protein	eci:UT189_C2930
A3481_s_at	-3.973324861	0.002267151	Decrease_in_adherent ginQ; glutamine ABC transporter ATP-binding protein; K10038 glutamine transport system ATP-binding protein [EC:3.6.3.-]	sdY:SDY_0787
EC869_0982_s_at	-3.944039989	0.007779627	Decrease_in_adherent hypothetical protein	eci:UT189_C2580
SD1_0493_s_at	-3.907929882	0.006979332	Decrease_in_adherent malP; maltodextrin phosphorylase; K00688 starch phosphorylase [EC:2.4.1.1]	ssn:SSON_3549
A1692_s_at	-3.898379448	5.19E-05	Decrease_in_adherent hdeB; acid-resistance protein	sbC:SbBS512_E3907
EC869_0579_s_at	-3.896682023	0.035721537	Decrease_in_adherent slp; outer membrane protein induced after carbon starvation; K07285 outer membrane lipoprotein	sdY:SDY_3557
V0034_s_at	-3.896008722	8.98E-06	Decrease_in_adherent frdC; fumarate reductase subunit C; K00246 fumarate reductase subunit C [EC:1.3.99.1]	sbC:SbBS512_E4684
A0545_s_at	-3.863916517	0.000222016	Decrease_in_adherent sseA; 3-mercaptopyruvate sulfurtransferase; K01011 3-mercaptopyruvate sulfurtransferase [EC:2.8.1.2]	sko:CKO_00261
A2931_s_at	-3.857933932	0.004158454	Decrease_in_adherent yagJ; hypothetical protein; K08996 putative membrane protein	eqj:ECCO26_0322
A4639_s_at	-3.813534085	0.000208219	Decrease_in_adherent cold shock-like protein CspC; K03704 cold shock protein (beta-ribon, CspA family)	sdY:SDY_01152
ECP_4059_s_at	-3.800590664	0.000341897	Decrease_in_adherent fadB; multifunctional fatty acid oxidation complex subunit alpha (EC:5.3.3.8 5.1.2.3 1.1.1.35 4.2.1.17); K00022 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]; K01692	ecp:ECP_4059
A0068_at	-3.793681442	0.022719854	Decrease_in_adherent vipB; Vi polysaccharide biosynthesis protein VipB/TviC	ecw:EcE24377A_2324
A2210_s_at	-3.782552484	0.000306188	Decrease_in_adherent hupA; transcriptional regulator HU subunit alpha; K05787 DNA-binding protein HU-alpha	sdY:SDY_3726
EC869_6281_s_at	-3.773350917	0.001775501	Decrease_in_adherent eno; phosphopyruvate hydratase; K01689 enolase [EC:4.2.1.11]	sko:CKO_04134
F2023_at	-3.75828255	3.08E-05	Decrease_in_adherent hypothetical protein	sdY:SDY_1970
Sb5_4039_s_at	-3.755415548	0.005702743	Decrease_in_adherent ybeJ; glutamate and aspartate transporter subunit; K10001 glutamate/aspartate transport system substrate-binding protein	sdY:SDY_0592
A2825_s_at	-3.748276385	1.26E-06	Decrease_in_adherent hlpA; periplasmic chaperone; K06142 outer membrane protein	sdY:SDY_0194
Sb5_1437_s_at	-3.746594392	1.66E-05	Decrease_in_adherent dmsB1; anaerobic dimethyl sulfoxide reductase, B subunit	sbC:SbBS512_E1775
H4310_x_at	-3.744239716	0.004893524	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V6213_s_at	-3.729138072	5.89E-05	Decrease_in_adherent OsmC family protein; K04063 osmotically inducible protein OsmC	ent:Ent638_2041
SD1_0513_s_at	-3.719340718	0.008542829	Decrease_in_adherent pckA; phosphoenolpyruvate carboxykinase (EC:4.1.1.49); K01610 phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	sdY:SDY_3673
V5800_at	-3.715094779	0.00054037	Decrease_in_adherent yjiE; hypothetical protein	ssn:SSON_4117
A2220_s_at	-3.714431024	0.01150689	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b2579_s_at	-3.707169565	0.001031566	Decrease_in_adherent grcA; autonomous glycol radical cofactor GrcA; K06866 autonomous glycol radical cofactor	sbC:SbBS512_E2957
V7049_s_at	-3.705339235	2.55E-05	Decrease_in_adherent pykA; pyruvate kinase (EC:2.7.1.40); K00873 pyruvate kinase [EC:2.7.1.40]	sdY:SDY_1141
V3561_s_at	-3.689700401	0.001871911	Decrease_in_adherent purC; phosphoribosylaminoimidazole-succinocarboxamide synthase (EC:6.3.2.6); K01923 phosphoribosylaminoimidazole-succinocarboxamide synthase [EC:6.3.2.6]	sdY:SDY_2684
A1218_s_at	-3.689536177	0.000796254	Decrease_in_adherent hypothetical protein	eci:UT189_C3456
EC869_1963_s_at	-3.67228583	0.002183122	Decrease_in_adherent hns; global DNA-binding transcriptional dual regulator H-NS; K03746 DNA-binding protein H-NS	sdY:SDY_1289
V2862_s_at	-3.667745188	0.008385431	Decrease_in_adherent fba; fructose-bisphosphate aldolase (EC:4.1.2.13); K01624 fructose-bisphosphate aldolase, class II [EC:4.1.2.13]	sdY:SDY_3157
A3938_s_at	-3.660847826	0.041582479	Decrease_in_adherent dhaK; dihydroxyacetone kinase N-terminal domain containing protein; K05878 dihydroxyacetone kinase, N-terminal domain [EC:2.7.1.-]	eqj:ECCO26_1713
b1743_s_at	-3.622031493	0.002617798	Decrease_in_adherent hypothetical protein	eci:UT189_C1937
V4114_s_at	-3.608162723	0.017312418	Decrease_in_adherent glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]	sdY:SDY_2741
A1693_s_at	-3.601442092	7.43E-06	Decrease_in_adherent hdeA; acid-resistance protein	sdY:SDY_3543
V5859_s_at	-3.589647662	0.005985397	Decrease_in_adherent tpiA; triosephosphate isomerase (EC:5.3.1.1); K01803 triosephosphate isomerase (TIM) [EC:5.3.1.1]	sdY:SDY_3826
W4275_at	-3.582408116	0.000689605	Decrease_in_adherent putative cytoplasmic protein	stm:STM1872
EC869_5449_s_at	-3.570653976	0.025140527	Decrease_in_adherent nanA; N-acetylneuraminate lyase (EC:4.1.3.3); K01639 N-acetylneuraminate lyase [EC:4.1.3.3]	sdY:SDY_3400
ECs0981_s_at	-3.562107295	0.020916666	Decrease_in_adherent hypothetical protein; K07308 anaerobic dimethyl sulfoxide reductase subunit C (DMSO reductase anchor subunit)	sko:CKO_02174
ECs5340_s_at	-3.549261889	0.000231529	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b1376_s_at	-3.538222965	0.000649915	Decrease_in_adherent ynaF; stress-induced protein, ATP-binding protein	ebf:ECB_01347
b3339_s_at	-3.527237152	3.39E-06	Decrease_in_adherent tuFB; tuf; elongation factor Tu (EC:3.6.5.3); K02358 elongation factor EF-Tu [EC:3.6.5.3]	sdY:SDY_3748

A0189_s_at	-3.52576989	2.81E-05	Decrease_in_adherent	mgIB; galactose-binding transport protein ; K10540 methyl-galactoside transport system substrate-binding protein	sdv:SDY_2130
N4689_at	-3.519238199	0.001697785	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
D4441_s_at	-3.506924754	0.001330531	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
A4382_s_at	-3.503271392	2.49E-05	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
EC869_8900_s_at	-3.498335543	0.011239915	Decrease_in_adherent	hydrogenase 2 small subunit [EC:1.12.99.6]; K02682 hydrogenase small subunit [EC:1.12.99.6]	sdv:SDY_3076
ECs0987_s_at	-3.48464145	0.012143551	Decrease_in_adherent	foaA; formate transporter ; K06212 formate transporter	sdv:SDY_2357
V3949_s_at	-3.477995381	0.006731208	Decrease_in_adherent	NarL; transcriptional regulator NarL. ; K07684 two-component system, NarL family, nitrate/nitrite response regulator NarL	sdv:SDY_1275
A1081_at	-3.46637288	0.010833386	Decrease_in_adherent	phage integrase family protein	ecw:ECe24377A_3356
EC869_2220_s_at	-3.458930344	0.00441242	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
EC869_3973_s_at	-3.458833017	0.000228322	Decrease_in_adherent	transcriptional regulator, AsnC family	etr:ETA_E_2200
S55_4395_s_at	-3.452379282	0.001810673	Decrease_in_adherent	shiA; shikimate transporter ; K08172 MFS transporter, MHS family, shikimate and dehydroshikimate transport protein	sdv:SDY_2254
A4608_s_at	-3.450639994	0.001848097	Decrease_in_adherent	yeaQ; hypothetical protein	sdv:SDY_1695
A1694_s_at	-3.445041468	0.008409911	Decrease_in_adherent	acid-resistance membrane protein	sbcs:SBBS512_E3909
A3097_s_at	-3.444940261	0.000413357	Decrease_in_adherent	hupB; transcriptional regulator HU subunit beta ; K03530 DNA-binding protein HU-beta	sdv:SDY_0292
A3945_s_at	-3.440425628	0.001483255	Decrease_in_adherent	hypothetical protein	sbcs:SBBS512_E1369
c0238_s_at	-3.414534703	0.004304425	Decrease_in_adherent	metQ; DL-methionine transporter substrate-binding subunit; K02073 D-methionine transport system substrate-binding protein	ecc:c0238
EC869_2294_s_at	-3.408569994	0.013763863	Decrease_in_adherent	pepE; peptidase E (EC:3.4.13.21); K05995 dipeptidase E [EC:3.4.13.21]	sbcs:SBBS512_E4515
APeCO1_1866_s_at	-3.402803482	0.002998064	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
V3435_s_at	-3.400077294	2.48E-05	Decrease_in_adherent	ptsI; phosphoenolpyruvate-protein phosphotransferase (EC:2.7.3.9); K08483 phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]	sdv:SDY_2613
A4620_s_at	-3.395775429	0.000159738	Decrease_in_adherent	putative outer membrane protein ; K07285 outer membrane lipoprotein	sdv:SDY_1710
A3235_s_at	-3.395620059	0.023560039	Decrease_in_adherent	ybdH; hypothetical protein ; K08317 putative oxidoreductase [EC:1.1.-.-]	sdv:SDY_0531
V2453_s_at	-3.392179703	0.023940565	Decrease_in_adherent	dhaH; fused putative dihydroxyacetone-specific PTS enzymes: HPr component/El component; K05881 PTS hybrid protein	eah:ECO103_1300
EC869_5018_s_at	-3.37755348	0.003776332	Decrease_in_adherent	gltA; type II citrate synthase (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]	sdv:SDY_0658
D4819_s_at	-3.375631441	0.006405765	Decrease_in_adherent	putative transposase	ecw:ECe24377A_D0068
S2143_x_at	-3.374906608	0.016786314	Decrease_in_adherent	putative cell killing protein of prophage	sfk:S2143
F3184_s_at	-3.366783215	9.59E-05	Decrease_in_adherent	bgIA; 6-phospho-beta-glucosidase A, cryptic ; K01223 6-phospho-beta-glucosidase [EC:3.2.1.86]	ssn:SSON_3054
A2199_s_at	-3.35874889	0.009403221	Decrease_in_adherent	rpoC; DNA-directed RNA polymerase subunit beta' (EC:2.7.7.6); K03046 DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6]	sbo:SBO_4008
SB5_4158_s_at	-3.357818185	0.012369338	Decrease_in_adherent	phoH; hypothetical protein ; K06217 phosphate starvation-inducible protein PhoH and related proteins	sbcs:SBBS512_E2301
EC869_3914_s_at	-3.347070159	2.31E-06	Decrease_in_adherent	elongation factor Tu ; K02358 elongation factor EF-Tu [EC:3.6.5.3]	ckc:CKO_03011
UT189_C2497_s_at	-3.337285371	0.00041619	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
A4742_s_at	-3.328913365	0.000584013	Decrease_in_adherent	flhC; flagellin ; K02406 flagellin	ecw:ECe24377A_2158
S55_4352_s_at	-3.327116909	0.00435472	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
A2477_x_at	-3.324628654	0.000659823	Decrease_in_adherent	yjgD; hypothetical protein ; K09893 hypothetical protein	sdv:SDY_4277
pCoo074_at	-3.310493299	0.015588432	Decrease_in_adherent	fImC; modulator of post-segregation killing protein	ecz:PECS88_0057
K2723_at	-3.303754318	0.006015084	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
SD1_0481_s_at	-3.301229934	0.000431201	Decrease_in_adherent	gIpD; glycerol-3-phosphate dehydrogenase (EC:1.1.5.3); K00111 glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]	sbcs:SBBS512_E3808
A2345_s_at	-3.292004147	0.004757175	Decrease_in_adherent	yjJ; hypothetical protein ; K06975	sdv:SDY_4240
K4999_s_at	-3.287822398	0.006945346	Decrease_in_adherent	asparagine synthetase AsnA ; K01914 aspartate--ammonia ligase [EC:6.3.1.1]	ckc:CKO_00084
A2162_s_at	-3.282353946	0.000271763	Decrease_in_adherent	gIdA; glycerol dehydrogenase (EC:1.1.1.6); K00005 glycerol dehydrogenase [EC:1.1.1.6]	sdv:SDY_3780
c0897_s_at	-3.282216526	0.020634869	Decrease_in_adherent	hypothetical protein	ecc:c0897
A0334_s_at	-3.278547811	0.001330641	Decrease_in_adherent	ackA; acetate kinase (EC:2.7.2.1); K00925 acetate kinase [EC:2.7.2.1]	sbcs:SBBS512_E2672
b1094_s_at	-3.262998909	2.95E-06	Decrease_in_adherent	hypothetical protein	eci:UT189_C1219
EC536_2323_s_at	-3.255366346	0.000543615	Decrease_in_adherent	hypothetical protein	ecc:c3343
EC869_3589_s_at	-3.255125648	0.000119582	Decrease_in_adherent	dps; DNA starvation/stationary phase protection protein Dps ; K04047 starvation-inducible DNA-binding protein	sdv:SDY_0783
EC869_0979_s_at	-3.24962638	0.001210085	Decrease_in_adherent	acetate kinase ; K00925 acetate kinase [EC:2.7.2.1]	cko:CKO_00498
SD1_3595_s_at	-3.246995699	0.011083463	Decrease_in_adherent	gpmA; phosphoglyceromutase 1 ; K01834 phosphoglycerate mutase [EC:5.4.2.1]	sdv:SDY_0702
V5372_s_at	-3.24619394	0.011350687	Decrease_in_adherent	yhhA; hypothetical protein	sdv:SDY_3596
W4348_at	-3.238216707	0.006292619	Decrease_in_adherent	putative cytoplasmic protein	stm:STM4002
A0438_s_at	-3.236108374	0.001754326	Decrease_in_adherent	rrr; glucose-specific PTS system component (EC:2.7.1.-); K02777 PTS system, glucose-specific IIA component [EC:2.7.1.69]	kpe:KPK_1374
V2081_s_at	-3.231507685	0.003345516	Decrease_in_adherent	yjgR; putative NAD(P)-binding dehydrogenase	ej:ECO26_4190
EC869_5629_s_at	-3.226018867	0.000827318	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
F4521_s_at	-3.222714537	0.000957859	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
pCoo013_at	-3.211969793	0.000122787	Decrease_in_adherent	CS1 type fibrillar major subunit	spe:Spro_0216
EC869_5178_s_at	-3.20867063	0.000168135	Decrease_in_adherent	lpdA; dihydroliipoamide dehydrogenase (EC:1.8.1.4); K00382 dihydroliipoamide dehydrogenase [EC:1.8.1.4]	sdv:SDY_0146
A3684_s_at	-3.1951023	0.025896639	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
A2260_s_at	-3.183237696	0.007302389	Decrease_in_adherent	yjvJ; putative stress-response protein	sdv:SDY_4529
V2860_s_at	-3.180564108	0.001921992	Decrease_in_adherent	pgk; phosphoglycerate kinase ; K00927 phosphoglycerate kinase [EC:2.7.2.3]	cko:CKO_04296
b1854_s_at	-3.179703693	0.00213108	Decrease_in_adherent	ypbK; pyruvate kinase (EC:2.7.1.40); K00873 pyruvate kinase [EC:2.7.1.40]	sbcs:SBBS512_E2130
b1243_s_at	-3.173737311	0.002290454	Decrease_in_adherent	oppA; oligopeptide transporter subunit; K02035 peptide/nickel transport system substrate-binding protein	ecj:JW1235
EC869_0204_s_at	-3.171231525	1.74E-05	Decrease_in_adherent	fusA; elongation factor G ; K02355 elongation factor EF-G [EC:3.6.5.3]	sdv:SDY_3501
EC869_2217_s_at	-3.167852569	0.000232363	Decrease_in_adherent	did; D-lactate dehydrogenase (EC:1.1.1.28); K03777 D-lactate dehydrogenase [EC:1.1.1.28]	sdv:SDY_2155
M1976_x_at	-3.166446345	0.002804693	Decrease_in_adherent	lIdP; L-lactate permease ; K00427 L-lactate permease	eci:UT189_C4144
A3486_s_at	-3.163423673	0.000851311	Decrease_in_adherent	ompB; outer membrane protein X ; K11934 outer membrane protein X	sdv:SDY_0781
SD1_3403_s_at	-3.16212068	0.010856485	Decrease_in_adherent	glutamate and aspartate transporter subunit ; K10001 glutamate/aspartate transport system substrate-binding protein	cko:CKO_02507
V0312_s_at	-3.159323301	0.005975721	Decrease_in_adherent	pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]	sdv:SDY_4226
SDY_2364_s_at	-3.157635782	0.007744176	Decrease_in_adherent	hypothetical protein	cko:CKO_02173
A3388_s_at	-3.153091676	0.007739886	Decrease_in_adherent	gpmA; phosphoglyceromutase 1 ; K01834 phosphoglycerate mutase [EC:5.4.2.1]	sdv:SDY_0702
ECP_3241_s_at	-3.146192719	9.86E-06	Decrease_in_adherent	NO_KEGG_DATA	NO_KEGG_DATA
EC869_3598_s_at	-3.141116641	0.010503557	Decrease_in_adherent	glnQ; glutamine ABC transporter ATP-binding protein ; K10038 glutamine transport system ATP-binding protein [EC:3.6.3.-]	sdv:SDY_0787
EC869_4317_s_at	-3.135885155	0.004203558	Decrease_in_adherent	serA; D-3-phosphoglycerate dehydrogenase ; K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	sdv:SDY_3169
SD1_1464_s_at	-3.120934384	0.00147101	Decrease_in_adherent	rimJ; ribosomal-protein-S5-alanine N-acetyltransferase ; K03790 ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]	sdv:SDY_2086
V0313_s_at	-3.119967289	0.000724953	Decrease_in_adherent	pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]	sdv:SDY_4226
V0311_s_at	-3.116353775	0.001870409	Decrease_in_adherent	pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]	sdv:SDY_4226
V2562_s_at	-3.115754722	0.000176674	Decrease_in_adherent	gst; glutathione S-transferase ; K00799 glutathione S-transferase [EC:2.5.1.18]	sdv:SDY_1858

A1575_s_at	-3.112757658	0.049699826	Decrease_in_adherent pckA; phosphoenolpyruvate carboxykinase (EC:4.1.1.49); K01610 phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	eci:UT189_C3903
EC869_4095_s_at	-3.097023491	0.01666697	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0073_at	-3.093994222	0.002231165	Decrease_in_adherent rftA; dTDP-4-dehydrorhamnose 3,5-epimerase (EC:5.1.3.13); K01790 dTDP-4-dehydrorhamnose 3,5-epimerase [EC:5.1.3.13]	ecw:EcE24377A_2329
SB5_2457_s_at	-3.079714211	0.000931665	Decrease_in_adherent csaA; carbon starvation protein A; K06200 carbon starvation protein	sbcb:SbBS512_E0500
SD1_0444_s_at	-3.074179982	0.021271824	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_2476_s_at	-3.066676109	0.005150255	Decrease_in_adherent hypothetical protein	eci:UT189_C2016
SB5_0930_x_at	-3.058244053	0.012560339	Decrease_in_adherent relF; polypeptide destructive to membrane potential	sdj:SDY_1432
EC869_8291_s_at	-3.05678449	0.00804602	Decrease_in_adherent crr; glucose-specific PTS system component ; K02777 PTS system, glucose-specific IIA component [EC:2.7.1.69]	sdj:SDY_2614
A1938_s_at	-3.055581678	0.012300297	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_4248
SF0956_s_at	-3.053836256	0.020967704	Decrease_in_adherent ycbG; hypothetical protein ; K09911 hypothetical protein	sdj:SDY_0929
V4370_s_at	-3.051365341	0.000314248	Decrease_in_adherent gnxB; glutaredoxin 2 ; K03675 glutaredoxin 2	sbcb:SbBS512_E2262
EC869_4069_s_at	-3.0471044	0.004082414	Decrease_in_adherent mukB; cell division protein MukB ; K03632 chromosome partition protein MukB	cko:CKO_02144
V0287_s_at	-3.044122226	3.33E-05	Decrease_in_adherent malM; maltose regulon periplasmic protein MalM; K05775 maltose operon periplasmic protein	ej:ECO26_5152
b3928_s_at	-3.039224427	0.000385533	Decrease_in_adherent yilU; hypothetical protein ; K09892 hypothetical protein	sdj:SDY_3816
EC536_1048_s_at	-3.028276196	0.004909081	Decrease_in_adherent putative glutamate dehydrogenase	eci:UT189_C0015
SB5_2779_s_at	-3.021298061	0.023105837	Decrease_in_adherent ynhG; hypothetical protein	sbo:SBO_1452
N3879_s_at	-3.019997604	6.38E-05	Decrease_in_adherent qor; quinone oxidoreductase, NADPH-dependent ; K00344 NADPH2:quinone reductase [EC:1.6.5.5]	sdj:SDY_4523
A0061_x_at	-3.016837961	0.018034423	Decrease_in_adherent hisI; bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase protein (EC:3.6.1.31 3.5.4.19); K11755 phosphoribosyl-ATP pyrophosphatase	ssn:SSON_2097
A3367_s_at	-3.011194869	0.006755332	Decrease_in_adherent sucD; succinyl-CoA synthetase subunit alpha (EC:6.2.1.5); K01902 succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]	sbcb:SbBS512_E0648
SD1_0613_s_at	-3.002591853	0.018973322	Decrease_in_adherent did; D-lactate dehydrogenase (EC:1.1.1.28); K03777 D-lactate dehydrogenase [EC:1.1.1.28]	sdj:SDY_2155
b0786_s_at	-2.999584531	0.008769262	Decrease_in_adherent ybhL; hypothetical protein ; K06890	sdj:SDY_0817
F4838_s_at	-2.991059175	0.008665383	Decrease_in_adherent pyrI; aspartate carbamoyltransferase regulatory subunit ; K00610 aspartate carbamoyltransferase regulatory subunit	sbcb:SbBS512_E4839
A4701_s_at	-2.979556092	0.000386312	Decrease_in_adherent cheY; chemotaxis regulatory protein CheY ; K03413 two-component system, chemotaxis family, response regulator CheY	sbcb:SbBS512_E2175
EC869_5019_s_at	-2.970101674	0.008611184	Decrease_in_adherent gltA; type II citrate synthase (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]	sdj:SDY_0658
V0004_s_at	-2.966051402	0.010785249	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3296_s_at	-2.964698839	0.013321636	Decrease_in_adherent gltL; glutamate/aspartate ABC transporter, ATP-binding protein ; K10004 glutamate/aspartate transport system ATP-binding protein [EC:3.6.3.-]	sbcb:SbBS512_E0597
A2344_s_at	-2.96444859	0.009105682	Decrease_in_adherent hypothetical protein	sbo:SBO_4330
A1798_x_at	-2.961264085	0.006320292	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V4229_s_at	-2.95727031	0.004262507	Decrease_in_adherent clpB; protein disaggregation chaperone ; K03695 ATP-dependent Clp protease ATP-binding subunit ClpB	sdj:SDY_2835
EC869_6279_s_at	-2.952618217	0.001425049	Decrease_in_adherent eno; phosphopyruvate hydratase ; K01689 enolase [EC:4.2.1.11]	kpu:KP1_4395
V2524_s_at	-2.951003459	0.015019059	Decrease_in_adherent manA; mannose-6-phosphate isomerase [EC:5.3.1.8]	sdj:SDY_1829
ECP_4493_x_at	-2.949753041	0.001141587	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b0145_s_at	-2.944951987	0.003731501	Decrease_in_adherent dksA; DnaK suppressor protein; K06204 DnaK suppressor protein	ctu:CTU_07760
H3052_s_at	-2.944212219	0.019724533	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SB5_2069_s_at	-2.943952182	0.000202798	Decrease_in_adherent hypothetical protein	sbcb:SbBS512_E2723
V1345_s_at	-2.942364864	0.015295287	Decrease_in_adherent dnaK; chaperone protein DnaK; K04043 molecular chaperone DnaK	ctu:CTU_06390
A1966_s_at	-2.936621865	0.000180038	Decrease_in_adherent yifE; hypothetical protein ; K09897 hypothetical protein	sdj:SDY_3984
F2712_s_at	-2.935624865	0.002192354	Decrease_in_adherent ucpA; short chain dehydrogenase (EC:1.-.-.-)	sbcb:SbBS512_E2798
A3718_s_at	-2.928554316	0.009221589	Decrease_in_adherent yccJ; hypothetical protein	sdj:SDY_0979
S1023_s_at	-2.925947262	0.002203759	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A1281_s_at	-2.92579627	0.010562667	Decrease_in_adherent ygiU; serine/threonine transporter SstT ; K07862 serine/threonine transporter	sdj:SDY_3274
c4709_at	-2.920689014	0.001751487	Decrease_in_adherent hypothetical protein ; K00973 glucose-1-phosphate thymidyltransferase [EC:2.7.7.24]	cko:CKO_00130
V3798_x_at	-2.916281303	0.003659311	Decrease_in_adherent yahO; hypothetical protein	ej:ECO26_0367
V0414_s_at	-2.902840077	0.002081378	Decrease_in_adherent fusA; elongation factor G ; K02355 elongation factor EF-G [EC:3.6.5.3]	sdj:SDY_3501
EC869_1864_s_at	-2.901258773	0.014966731	Decrease_in_adherent tktA; transketolase (EC:2.2.1.1); K00615 transketolase [EC:2.2.1.1]	sbcb:SbBS512_E3367
V7054_s_at	-2.900567666	0.000298955	Decrease_in_adherent ynfJ; glucose-6-phosphate 1-dehydrogenase (EC:1.1.1.49); K00036 glucose-6-phosphate 1-dehydrogenase [EC:1.1.1.49]	sdj:SDY_1138
A4340_s_at	-2.891787392	0.012852865	Decrease_in_adherent ynfG; 3-hydroxy acid dehydrogenase ; K00540 [EC:1.-.-.-]	sdj:SDY_1586
b1717_s_at	-2.889806516	0.000791521	Decrease_in_adherent hypothetical protein	cko:CKO_01743
V3384_s_at	-2.886251945	0.014066382	Decrease_in_adherent phosphoenolpyruvate synthase ; K01007 pyruvate, water dikinase [EC:2.7.9.2]	cko:CKO_01725
APECO1_2795_at	-2.883641423	0.014309106	Decrease_in_adherent hypothetical protein	cko:CKO_05114
EC869_3591_s_at	-2.883223608	0.025881033	Decrease_in_adherent glnH; glutamine ABC transporter periplasmic protein ; K10036 glutamine transport system substrate-binding protein	sbo:SBO_0702
SDY_3461_x_at	-2.88041489	0.035985556	Decrease_in_adherent hypothetical protein ; K03747 Smg protein	cky:CKY_04697
A2678_s_at	-2.876786885	0.001355802	Decrease_in_adherent caiF; DNA-binding transcriptional activator CaiF ; K08277 transcriptional activator CaiF	sdj:SDY_0056
A0065_at	-2.867902275	0.002074908	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_2321
b3157_s_at	-2.866982651	0.000478096	Decrease_in_adherent yhbT; hypothetical protein	sdj:SDY_3336
V4616_s_at	-2.866127433	0.000849161	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A1402_s_at	-2.863123096	0.021987985	Decrease_in_adherent yhbH; putative sigma(54) modulation protein ; K05808 putative sigma-54 modulation protein	sdj:SDY_3384
b1256_s_at	-2.860881759	0.006358326	Decrease_in_adherent yoiD; outer membrane protein W ; K07275 outer membrane protein	sdj:SDY_1320
A3558_s_at	-2.859861099	0.006559641	Decrease_in_adherent clpA; ATP-dependent Clp protease ATP-binding subunit ; K03694 ATP-dependent Clp protease ATP-binding subunit ClpA	sdj:SDY_2379
A2977_s_at	-2.859789115	0.005637259	Decrease_in_adherent yahK; putative oxidoreductase, Zn-dependent and NAD(P)-binding	ecr:ECIAI1_0327
F4391_s_at	-2.85321169	0.010138216	Decrease_in_adherent yilM; hypothetical protein	eum:EUCUMN_4439
ECs2281_at	-2.850748666	0.004113936	Decrease_in_adherent hypothetical protein	eci:ECO111_1411
ECs5510_s_at	-2.849049156	0.002550214	Decrease_in_adherent hypothetical protein	ecp:ECP_2774
V4298_s_at	-2.847842938	0.002997493	Decrease_in_adherent TrpR binding protein WrbA ; K03809 Trp repressor binding protein	cko:CKO_02047
SB5_3624_s_at	-2.842851809	0.007626547	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A1088_at	-2.838928288	0.005533592	Decrease_in_adherent UvrD family helicase ; K03657 DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.1.-]	ecw:EcE24377A_3362
ECs2754_x_at	-2.836351318	0.026569048	Decrease_in_adherent putative prophage maintenance protein	ej:ECO26_1476
A4482_s_at	-2.834907293	0.000706639	Decrease_in_adherent lpp; murein lipoprotein ; K06078 murein lipoprotein	sdj:SDY_1908
A2355_s_at	-2.832467286	0.007652251	Decrease_in_adherent dcaA; anaerobic C4-dicarboxylate transporter ; K07791 anaerobic C4-dicarboxylate transporter DcuA	sdj:SDY_4443
SD1_2489_s_at	-2.823151239	0.008341555	Decrease_in_adherent hypothetical protein	ecv:APECO1_2541
F3644_x_at	-2.815481042	0.014266909	Decrease_in_adherent hypothetical protein ; K03747 Smg protein	cko:CKO_04697
b3024_s_at	-2.813347017	0.025968021	Decrease_in_adherent ygiW; hypothetical protein	sdj:SDY_3215
V3388_s_at	-2.808240806	0.009165315	Decrease_in_adherent ppsA; phosphoenolpyruvate synthase (EC:2.7.9.2); K01007 pyruvate, water dikinase [EC:2.7.9.2]	sbo:SBO_1427
b3612_s_at	-2.80722681	0.002403118	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA

SD1_2134_s_at	-2.639823105	0.017692996	Decrease_in_adherent vacJ; lipoprotein precursor ; K04754 lipoprotein	sdv:SDY_2550
SD1_2139_s_at	-2.639759078	0.046083148	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V2498_s_at	-2.639727895	0.001064606	Decrease_in_adherent mlc; putative NAGC-like transcriptional regulator	sdv:SDY_1562
SD1_1883_s_at	-2.638343429	0.001093768	Decrease_in_adherent lipA; lipoyl synthase ; K03644 lipoyl acid synthetase [EC:2.8.1.8]	sdv:SDY_0550
A1497_s_at	-2.63073317	0.003427909	Decrease_in_adherent hypothetical protein	eci:UTI89_C3763
b0426_s_at	-2.629886116	0.001508987	Decrease_in_adherent putative nucleotide-binding protein ; K09767 hypothetical protein	sbc:SbBS512_E0348
A3297_s_at	-2.62794598	0.014758828	Decrease_in_adherent gltK; glutamate/aspartate ABC transporter, permease protein GltK ; K10002 glutamate/aspartate transport system permease protein	ecw:EcE24377A_0681
b3303_s_at	-2.624436183	0.01208169	Decrease_in_adherent hypothetical protein	ecv:c4064
EC869_6406_s_at	-2.620166619	0.044180631	Decrease_in_adherent melF; 5,10-methylenetetrahydrofolate reductase (EC:1.5.1.20); K00297 methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]	ctu:Clu_01820
M2693_s_at	-2.6195252	0.013216977	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
AFFX-LysX_3_at	-2.618928454	0.000415299	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
EC869_6416_s_at	-2.618590333	0.002304387	Decrease_in_adherent melB; cystathionine gamma-synthase, PLP-dependent; K01739 cystathionine gamma-synthase [EC:2.5.1.48]	etw:ECSP_5009
A3035_s_at	-2.616545114	0.0175695	Decrease_in_adherent psiF; induced by phosphate starvation	sdv:SDY_0360
V6500_s_at	-2.616135394	0.002894896	Decrease_in_adherent fabI; enoyl-(acyl carrier protein) reductase (EC:1.3.1.10); K00208 enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9]	sdv:SDY_1368
EC869_6165_s_at	-2.61452371	0.001284896	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
AFFX-PheX_3_at	-2.613938914	0.000364308	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]	bsu:BSU27900
SD1_1375_s_at	-2.603734307	0.020491186	Decrease_in_adherent purL; phosphoribosylformylglycinamide synthase (EC:6.3.5.3); K01952 phosphoribosylformylglycinamide synthase [EC:6.3.5.3]	sbc:SbBS512_E2922
AFFX-r2-Bs-lys-5_at	-2.602691793	2.19E-05	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
b0865_s_at	-2.602588416	0.006055243	Decrease_in_adherent ybjP; putative lipoprotein	eqj:ECO26_0992
c1138_s_at	-2.601740979	0.002340162	Decrease_in_adherent hypothetical protein	ecc:c1138
A2889_s_at	-2.601712826	4.89E-05	Decrease_in_adherent ykE; C-lysozyme inhibitor	sdv:SDY_0246
V0315_s_at	-2.600069119	0.025261431	Decrease_in_adherent pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]	sdv:SDY_4226
EC869_5719_s_at	-2.598553022	0.005941658	Decrease_in_adherent pntB; pyridine nucleotide transhydrogenase (EC:1.6.1.2); K00325 NAD(P) transhydrogenase subunit beta [EC:1.6.1.2]	sdv:SDY_1551
V5399_s_at	-2.595907971	0.00256853	Decrease_in_adherent glgC; glucose-1-phosphate adenyllyltransferase (EC:2.7.7.27); K00975 glucose-1-phosphate adenyllyltransferase [EC:2.7.7.27]	sdv:SDY_3576
c2315_s_at	-2.590188942	4.17E-05	Decrease_in_adherent yecI; ferritin-like protein ; K02255 ferritin-like protein 2	sdv:SDY_1116
D2423_x_at	-2.585971656	0.001307666	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3985_s_at	-2.584409024	0.025662464	Decrease_in_adherent oppD; oligopeptide transporter ATP-binding component ; K02031 peptide/nickel transport system ATP-binding protein	sbc:SbBS512_E1415
SD1_2503_s_at	-2.580672611	0.00319687	Decrease_in_adherent pfkA; 6-phosphofructokinase (EC:2.7.1.11); K00850 6-phosphofructokinase [EC:2.7.1.11]	sdv:SDY_3831
SD1_1168_s_at	-2.58002785	0.000738907	Decrease_in_adherent ucpA; putative oxidoreductase	eqj:ECO26_3478
EC869_3855_s_at	-2.574389758	0.001234878	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b1136_s_at	-2.574148857	0.003312238	Decrease_in_adherent hypothetical protein	ecc:c1516
V0081_s_at	-2.572832213	0.011743747	Decrease_in_adherent dcuB; anaerobic C4-dicarboxylate transporter ; K07792 anaerobic C4-dicarboxylate transporter DcuB	sdv:SDY_4232
A4234_s_at	-2.571679318	0.005368689	Decrease_in_adherent pptA; 4-oxalocrotonate tautomerase; K01821 4-oxalocrotonate tautomerase [EC:5.3.2.-]	eci:ECO111_1852
b3472_s_at	-2.569013985	0.008393273	Decrease_in_adherent hypothetical protein	sdv:SDY_3623
EC869_3090_s_at	-2.567653978	0.007843366	Decrease_in_adherent acetyl-coenzyme A synthetase (EC:6.2.1.1); K01895 acetyl-CoA synthetase [EC:6.2.1.1]	sbc:SbBS512_E4588
EC869_7448_s_at	-2.56510116	0.00380562	Decrease_in_adherent nagB; glucosamine-6-phosphate deaminase (EC:3.5.99.6); K02564 glucosamine-6-phosphate deaminase [EC:3.5.99.6]	sbc:SbBS512_E0573
A4642_s_at	-2.56187326	0.002780863	Decrease_in_adherent putative regulator	ssn:SSON_1334
A2459_s_at	-2.557541198	0.042420365	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SD1_2927_s_at	-2.553977577	0.023715306	Decrease_in_adherent ydaA; universal stress protein UspE	sdv:SDY_1413
M0375_s_at	-2.553611258	0.002765463	Decrease_in_adherent ptsI; phosphoenolpyruvate-protein phosphotransferase (EC:2.7.3.9); K08483 phosphotransferase system, enzyme I, PtsI [EC:2.7.3.9]	sdv:SDY_2613
AFFX-r2-Bs-lys-M_a	-2.550653517	5.34E-09	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
b3236_s_at	-2.546471893	0.010317415	Decrease_in_adherent mdh; malate dehydrogenase (EC:1.1.1.37); K00026 malate dehydrogenase [EC:1.1.1.37]	sdv:SDY_3412
V3863_s_at	-2.545359328	0.003037445	Decrease_in_adherent ybgE; hypothetical protein	sdv:SDY_0683
A2847_s_at	-2.543983572	0.010864283	Decrease_in_adherent D-methionine transporter permease subunit ; K02072 D-methionine transport system permease protein	ent:Ent638_0736
APECO1_3736_s_at	-2.543490385	0.029734337	Decrease_in_adherent ygdH; hypothetical protein ; K06966	sbo:SBO_2676
SD1_2453_s_at	-2.542815722	5.96E-05	Decrease_in_adherent ppc; phosphoenolpyruvate carboxylase (EC:4.1.1.31); K01595 phosphoenolpyruvate carboxylase [EC:4.1.1.31]	ssn:SSON_4129
AFFX-r2-Bs-phe-M_i	-2.542761754	3.28E-05	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]	bsu:BSU27900
EC869_7770_x_at	-2.539109707	0.000878153	Decrease_in_adherent lplA; lipoate-protein ligase A (EC:6.3.2.-); K03800 lipoate-protein ligase A [EC:2.7.7.63]	sbc:SbBS512_E4933
b1881_s_at	-2.538490403	0.001829204	Decrease_in_adherent cheZ; chemotaxis regulator CheZ ; K03414 chemotaxis protein CheZ	sbc:SbBS512_E2174
AFFX-r2-Bs-phe-3_a	-2.537057096	0.000146353	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]	bsu:BSU27900
A1498_s_at	-2.536908246	0.000235181	Decrease_in_adherent rpsC; 30S ribosomal protein S3 ; K02982 small subunit ribosomal protein S3	cko:CKO_04729
A1915_s_at	-2.535116901	4.78E-07	Decrease_in_adherent NADPH-dependent FMN reductase	sbc:SbBS512_E4209
F1834_s_at	-2.531704673	0.005694942	Decrease_in_adherent transcriptional regulator SlyA ; K06075 MarR family transcriptional regulator, transcriptional regulator for hemolysin	cko:CKO_01654
EC869_1180_s_at	-2.527300432	0.007340837	Decrease_in_adherent glucose-specific PTS system IIBC components ; K02778 PTS system, glucose-specific IIB component [EC:2.7.1.69]; K02779 PTS system, glucose-specific IIC component	cko:CKO_01957
A4480_s_at	-2.526538977	0.012556603	Decrease_in_adherent hypothetical protein	sdv:SDY_1904
SD1_0883_s_at	-2.524504102	0.013694934	Decrease_in_adherent yncE; hypothetical protein	eci:ECO103_1583
AFFX-LysX_5_at	-2.51751688	0.000212034	Decrease_in_adherent lysA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	bsu:BSU23380
ECs1080_x_at	-2.517463769	0.018378288	Decrease_in_adherent prophage maintenance protein	ecs:ECs1080
b0623_s_at	-2.517401322	0.010546296	Decrease_in_adherent cspE; cold shock protein CspE ; K03704 cold shock protein (beta-ribbon, CspA family)	cko:CKO_02534
SBS_2639_s_at	-2.513153011	0.048315171	Decrease_in_adherent hypothetical protein ; K07180 serine protein kinase	cko:CKO_01806
A2361_s_at	-2.506915608	0.001350436	Decrease_in_adherent groEL; chaperonin GroEL ; K04077 chaperonin GroEL	sdv:SDY_4449
D0357_x_at	-2.505176011	0.000886361	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0066_at	-2.503729761	0.00269988	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_2322
c2930_s_at	-2.498497824	0.000691228	Decrease_in_adherent hypothetical protein	sbc:SbBS512_E2759
ECs5520_s_at	-2.496786433	0.002662207	Decrease_in_adherent hypothetical protein	ecv:ECSE_3407
EC536_4089_s_at	-2.494905582	0.008266137	Decrease_in_adherent pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]	sdv:SDY_4226
b4232_s_at	-2.492779392	0.006425263	Decrease_in_adherent fbp; fructose-1,6-bisphosphatase (EC:3.1.3.11); K03841 fructose-1,6-bisphosphatase I [EC:3.1.3.11]	sdv:SDY_4250
H4105_s_at	-2.491230648	0.03751976	Decrease_in_adherent aphA; acid phosphatase/phosphotransferase (EC:3.1.3.2); K03788 acid phosphatase (class B) [EC:3.1.3.2]	ecr:ECIAI_4287
V2352_s_at	-2.48910217	0.000859347	Decrease_in_adherent ppnK; inorganic polyphosphate/ATP-NAD kinase (EC:2.7.1.23); K00858 NAD+ kinase [EC:2.7.1.23]	efe:EFER_0458
N0912_s_at	-2.488734034	0.021740295	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_8209_s_at	-2.4887014	0.002377852	Decrease_in_adherent transketolase (EC:2.2.1.1); K00615 transketolase [EC:2.2.1.1]	ecs:ECs327
F2636_s_at	-2.485409956	0.01377796	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SD1_2776_s_at	-2.48389082	7.07E-05	Decrease_in_adherent nadE; NH(3)-dependent Nad(+) synthetase	elf:LF82_1436
A2908_s_at	-2.483544008	0.011616657	Decrease_in_adherent crl; DNA-binding transcriptional regulator Crl ; K11926 sigma factor-binding protein Crl	sdv:SDY_0477

pCoo004_s_at -2.480522655 0.005935204 Decrease_in_adherent hypothetical protein
H1841_x_at -2.477265522 6.14E-05 Decrease_in_adherent hypothetical protein
SD1_2578_s_at -2.474591669 0.004023435 Decrease_in_adherent polA; DNA polymerase I [EC:2.7.7.7]; K02335 DNA polymerase I [EC:2.7.7.7]
A0020_s_at -2.474580588 0.00526998 Decrease_in_adherent hypothetical protein
V5964_s_at -2.474158199 0.046250179 Decrease_in_adherent glnG; nitrogen regulation protein NR(I); K07712 two-component system, NtrC family, nitrogen regulation response regulator GlnG
ECs1520_x_at -2.473976443 0.033421352 Decrease_in_adherent mtkP; putative cell killing protein encoded within cryptic prophage CP-933P
SD1_3096_s_at -2.471034945 0.001276722 Decrease_in_adherent hypothetical protein
EC869_8742_s_at -2.466961678 0.017145993 Decrease_in_adherent ppsA; phosphoenolpyruvate synthase (EC:2.7.9.2); K01007 pyruvate, water dikinase [EC:2.7.9.2]
EC869_2608_s_at -2.460294001 0.043243698 Decrease_in_adherent flhD; DNA-binding transcriptional dual regulator with FlhC; K02403 flagellar transcriptional activator FlhD
EC869_4578_s_at -2.4519848 0.027538844 Decrease_in_adherent gloB; hydroxyacylglutathione hydrolase (EC:3.1.2.6); K01069 hydroxyacylglutathione hydrolase [EC:3.1.2.6]
b1508_s_at -2.446660857 0.044270717 Decrease_in_adherent hipB; DNA-binding transcriptional regulator HipB
A3719_s_at -2.446248232 0.013597291 Decrease_in_adherent wrbA; TrpR binding protein WrbA; K03809 Trp repressor binding protein
b2926_s_at -2.444700641 0.00060472 Decrease_in_adherent pgk; phosphoglycerate kinase (EC:2.7.2.3); K00927 phosphoglycerate kinase [EC:2.7.2.3]
b3916_s_at -2.43734698 0.007284209 Decrease_in_adherent pfkA; 6-phosphofructokinase (EC:2.7.1.11); K00850 6-phosphofructokinase [EC:2.7.1.11]
V3541_s_at -2.430314047 0.020684538 Decrease_in_adherent acrD; aminoglycoside/multidrug efflux system; K03296 hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family
SD1_2474_s_at -2.428472523 0.008153833 Decrease_in_adherent methionine repressor, MetJ; K03764 transcriptional repressor of met regulon (beta-ribbon, MetJ family)
EC869_5640_s_at -2.411121009 0.011353368 Decrease_in_adherent cpdB; bifunctional 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'-nucleotidase periplasmic precursor protein; K01119 2',3'-cyclic-nucleotide 2'-phosphodiesterase [EC:3.1.1.11]
V4568_s_at -2.408195269 0.019874977 Decrease_in_adherent anaerobic ribonucleoside triphosphate reductase (EC:1.17.4.2); K00527 ribonucleoside-triphosphate reductase [EC:1.17.4.2]
A0712_s_at -2.406160608 0.001773851 Decrease_in_adherent ygaG; S-ribosylhomocysteine lyase; K07173 S-ribosylhomocysteine lyase [EC:4.4.1.21]
V7336_s_at -2.406096903 1.85E-06 Decrease_in_adherent hypothetical protein
AFFX-LysX-M_at -2.403903818 0.000287411 Decrease_in_adherent ysaA; diaminopimelate decarboxylase (EC:4.1.1.20); K01586 diaminopimelate decarboxylase [EC:4.1.1.20]
SD1_3346_s_at -2.402186196 0.029408389 Decrease_in_adherent ycbB; hypothetical protein
c3307_s_at -2.399795175 0.009711536 Decrease_in_adherent RNA polymerase sigma factor RpoS; K03087 RNA polymerase nonessential primary-like sigma factor
b2572_s_at -2.399010771 0.0136524 Decrease_in_adherent rseA; anti-RNA polymerase sigma factor SigE; K03597 sigma-E factor negative regulatory protein RseA
D3045_s_at -2.396157237 0.009291479 Decrease_in_adherent NO_KEGG_DATA
SBO_3336_s_at -2.392690115 0.034307982 Decrease_in_adherent yhfA; hypothetical protein; K07397 putative redox protein
V3865_s_at -2.391886985 0.002084674 Decrease_in_adherent hypothetical protein
AFFX-r2-Bs-thr-3_s_ -2.387019069 0.000153193 Decrease_in_adherent thrB; homoserine kinase (EC:2.7.1.39); K00872 homoserine kinase [EC:2.7.1.39]
V3386_s_at -2.382721808 0.007767569 Decrease_in_adherent ppsA; phosphoenolpyruvate synthase (EC:2.7.9.2); K01007 pyruvate, water dikinase [EC:2.7.9.2]
V5379_s_at -2.381844155 0.001788655 Decrease_in_adherent yhhX; putative dehydrogenase
A2811_s_at -2.380012901 0.01769734 Decrease_in_adherent yaeH; hypothetical protein
b1676_s_at -2.378695389 0.014626141 Decrease_in_adherent pykF; pyruvate kinase (EC:2.7.1.40); K00873 pyruvate kinase [EC:2.7.1.40]
A4644_s_at -2.377656647 0.014642896 Decrease_in_adherent htpX; heat shock protein HtpX; K03799 heat shock protein HtpX [EC:3.4.24.-]
V4294_s_at -2.376901484 0.004467681 Decrease_in_adherent NO_KEGG_DATA
SFV_2948_s_at -2.376386907 0.023149163 Decrease_in_adherent yqfB; hypothetical protein; K09900 hypothetical protein
F3660_s_at -2.37570042 0.001666666 Decrease_in_adherent NO_KEGG_DATA
b3409_s_at -2.374369893 8.05E-05 Decrease_in_adherent feoB; ferrous iron transport protein B; K04759 ferrous iron transport protein B
A4412_s_at -2.373758154 0.014291091 Decrease_in_adherent ydgA; hypothetical protein
N1415_x_at -2.366559575 1.12E-06 Decrease_in_adherent yjgD; hypothetical protein; K09893 hypothetical protein
A1819_s_at -2.366583868 0.008142245 Decrease_in_adherent waaW; lipopolysaccharide 1,2-galactosyltransferase; K12985 (galactosyl)LPS 1,2-glucosyltransferase [EC:2.4.1.-]
SF3597_s_at -2.363840347 0.000552015 Decrease_in_adherent yhlV; putative transport system permease protein; K03296 hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family
ECP_3075_s_at -2.363624669 0.003565199 Decrease_in_adherent hypothetical protein; K11209 GST-like protein
A0436_s_at -2.362326206 0.000812695 Decrease_in_adherent ptsH; phosphocarrier protein HPr (EC:2.7.1.69 2.7.3.9); K02784 phosphocarrier protein HPr
A2371_s_at -2.362166787 0.030348948 Decrease_in_adherent bci; outer membrane lipoprotein Blc; K03098 outer membrane lipoprotein Blc
V1199_s_at -2.358902381 0.005311381 Decrease_in_adherent ycbB; hypothetical protein
EC869_6407_s_at -2.357332562 0.024940913 Decrease_in_adherent metF; 5,10-methylenetetrahydrofolate reductase (EC:1.5.1.20); K00297 methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]
c0735_s_at -2.353416461 0.034567272 Decrease_in_adherent rihA; ribonucleoside hydrolase 1 (EC:3.2.2.-); K01250 pyrimidine-specific ribonucleoside hydrolase [EC:3.2.-.-]
SD1_1706_s_at -2.35243886 0.011785003 Decrease_in_adherent secF; preprotein translocase subunit SecF; K03074 preprotein translocase subunit SecF
EC869_7314_s_at -2.346540842 0.003698716 Decrease_in_adherent tsx; nucleoside channel; K05517 nucleoside-specific channel-forming protein
V5386_s_at -2.343627029 0.000197993 Decrease_in_adherent NO_KEGG_DATA
V3441_x_at -2.336184765 0.00694572 Decrease_in_adherent yfeK; hypothetical protein
SF1458_s_at -2.335421738 0.003139214 Decrease_in_adherent hypothetical protein
A2648_s_at -2.331993499 0.006902087 Decrease_in_adherent NO_KEGG_DATA
ECP_1632_s_at -2.330303518 0.014179316 Decrease_in_adherent hypothetical protein
EC869_2830_s_at -2.330300248 0.001047846 Decrease_in_adherent purA; adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]
A4547_s_at -2.328898179 0.02491143 Decrease_in_adherent osmE; DNA-binding transcriptional activator OsmE; K04064 osmotically inducible lipoprotein OsmE
b0880_s_at -2.326835958 0.026988106 Decrease_in_adherent cspD; stationary phase/starvation inducible regulatory protein CspD; K03704 cold shock protein (beta-ribbon, CspA family)
V1193_s_at -2.325627223 0.002354577 Decrease_in_adherent aromatic amino acid aminotransferase; K00813 aspartate aminotransferase [EC:2.6.1.1]
A0302_s_at -2.317398738 0.011917654 Decrease_in_adherent menB; naphthoate synthase (EC:4.1.3.36); K01661 naphthoate synthase [EC:4.1.3.36]
AFFX-PheX-5_at -2.317219127 9.36E-05 Decrease_in_adherent pheB; hypothetical protein; K06209 chorismate mutase [EC:5.4.99.5]
A0306_s_at -2.313833603 0.03676709 Decrease_in_adherent eiaB; hypothetical protein; K05594 EiaB protein
b3609_s_at -2.309074641 5.82E-05 Decrease_in_adherent secB; preprotein translocase subunit SecB; K03071 preprotein translocase subunit SecB
b0965_s_at -2.308863277 0.001658987 Decrease_in_adherent hypothetical protein; K06929
A4534_s_at -2.306487819 0.016407944 Decrease_in_adherent hypothetical protein
V2075_s_at -2.305342833 0.013541815 Decrease_in_adherent yglJ; serine/threonine transporter SstT; K07862 serine/threonine transporter
F2998_s_at -2.305255633 0.001497602 Decrease_in_adherent hypB; hydrogenase nickel incorporation protein HypB; K04652 hydrogenase nickel incorporation protein HypB
ECP_1856_at -2.304933751 0.001055333 Decrease_in_adherent hypothetical protein
SFV_4273_s_at -2.298581703 0.029576602 Decrease_in_adherent cysQ; adenosine-3'(2'),5'-bisphosphate nucleotidase; K03677 CysQ protein
EC869_5670_s_at -2.296499837 0.000315677 Decrease_in_adherent luxS; S-ribosylhomocysteine lyase; K07173 S-ribosylhomocysteine lyase [EC:4.4.1.21]
EC869_1014_s_at -2.296435843 5.55E-06 Decrease_in_adherent purF; amidophosphoribosyltransferase (EC:2.4.2.14); K00764 amidophosphoribosyltransferase [EC:2.4.2.14]
b0876_s_at -2.2963891 0.022983195 Decrease_in_adherent hypothetical protein; K07459 putative ATP-dependent endonuclease of the OLD family
EC869_8934_s_at -2.295921448 0.006752962 Decrease_in_adherent yihI; hypothetical protein; K09894 hypothetical protein
A3442_s_at -2.294717757 0.009068283 Decrease_in_adherent putative kinase inhibitor protein; K06910
AFFX-ThrX-3_at -2.294306671 4.18E-05 Decrease_in_adherent thrB; homoserine kinase (EC:2.7.1.39); K00872 homoserine kinase [EC:2.7.1.39]

ecw:EcE24377A_D0044
ecx:EcHS_A1898
sbc:SbBS512_E4337
ssn:SSON_2055
sbc:SbBS512_E4344
etw:ECCSP_2125
ecc:c4772
sbc:SbBS512_E1905
etw:ECCSP_2466
sbc:SbBS512_E0208
ssn:SSON_1613
sdy:SDY_0980
sbo:SBO_3067
sdy:SDY_3831
ssn:SSON_2550
dze:Dd1591_0119
sbc:CKO_03616
ppr:PBPB0442
sdy:SDY_2884
eti:UTI89_C3749
bsu:BSU23380
sdy:SDY_2332
sfi:SF2764
sdy:SDY_2813
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sdy:SDY_3518
ecc:c0813
bsu:BSU32240
sdy:SDY_1794
ssn:SSON_3682
sdy:SDY_0181
sbc:SbBS512_E1877
sdy:SDY_1977
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sdy:SDY_3181
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sbc:SbBS512_E3790
ssn:SSON_1546
sdy:SDY_4277
sbc:SbBS512_E4051
sdy:SDY_3537
ecc:ECP_3075
ctu:CTu_30130
ssn:SSON_4335
sdy:SDY_2332
spe:Spro_4784
ecc:ECS88_0686
eti:ETA_E0962
sdy:SDY_0323
NO_KEGG_DATA
sbo:SBO_2445
sbc:SbBS512_E2020
NO_KEGG_DATA
sdy:SDY_1673
sdy:SDY_4412
sdy:SDY_1541
sdy:SDY_2381
cko:CKO_02139
efe:EFER_0906
bsu:BSU27910
sdy:SDY_2462
sbc:SbBS512_E4037
sdy:SDY_0940
sdy:SDY_1818
sbc:SbBS512_E3150
ecc:ECP_1856
sfv:SFV_4273
sbo:SBO_3634
sbc:SbBS512_E2690
sbc:SbBS512_E2452
sdy:SDY_3877
sbc:SbBS512_E2579
bsu:BSU32240

V0714_s_at	-2.294018113	0.005100374	Decrease_in_adherent mglB; galactose-binding transport protein ; K10540 methyl-galactoside transport system substrate-binding protein	sdv:SDY_2130
A0547_s_at	-2.290970138	0.033779565	Decrease_in_adherent sseB; enhanced serine sensitivity protein SseB	sbv:SBBS512_E2897
A4633_s_at	-2.288385293	0.002767441	Decrease_in_adherent manX; PTS system, mannose-specific IIB component [EC:2.7.1.69]; K02793 PTS system, mannose-specific IIA component [EC:2.7.1.69]; K02794 PTS system, mannose-specific IIC component [EC:2.7.1.69]	sbv:SBBS512_E2083
Z6074_s_at	-2.286913114	0.006964522	Decrease_in_adherent hypothetical protein	eqj:EC026_2665
A0371_s_at	-2.286786585	0.021382582	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
AFFX-PheX-M_at	-2.285173313	5.18E-05	Decrease_in_adherent pheA; prephenate dehydratase (EC:4.2.1.51); K04518 prephenate dehydratase [EC:4.2.1.51]	bsu:BSU27900
SD1_1948_s_at	-2.285066332	0.010339558	Decrease_in_adherent htpG; heat shock protein 90 ; K04079 molecular chaperone HtpG	sdv:SDY_0446
V5329_s_at	-2.282472362	0.017873657	Decrease_in_adherent hypothetical protein	cko:CKO_04902
A4021_at	-2.279124017	0.005903997	Decrease_in_adherent hypothetical protein	ecw:EC24377A_1430
A2395_s_at	-2.276758918	0.001217195	Decrease_in_adherent purA; adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]	sdv:SDY_4412
EC869_5658_s_at	-2.274800806	3.01E-05	Decrease_in_adherent fklB; peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K03773 FKBP-type peptidyl-prolyl cis-trans isomerase FklB [EC:5.2.1.8]	sdv:SDY_4377
SD1_0131_s_at	-2.273423467	0.000402844	Decrease_in_adherent secB; preprotein translocase subunit SecB ; K03071 preprotein translocase subunit SecB	sdv:SDY_4042
SB5_0712_s_at	-2.271681459	3.11E-05	Decrease_in_adherent qor; quinone oxidoreductase, NADPH-dependent (EC:1.6.5.5); K00344 NADPH2:quinone reductase [EC:1.6.5.5]	ect:ECIAI39_4471
A4727_s_at	-2.271235179	0.018748189	Decrease_in_adherent yecA; hypothetical protein ; K07039	sbv:SBBS512_E0654
EC869_4316_s_at	-2.268362471	0.001091541	Decrease_in_adherent serA; D-3-phosphoglycerate dehydrogenase ; K00058 D-3-phosphoglycerate dehydrogenase [EC:1.1.1.95]	sdv:SDY_3169
A2158_s_at	-2.268149858	0.044065762	Decrease_in_adherent metF; 5,10-methylenetetrahydrofolate reductase (EC:1.5.1.20); K00297 methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]	sdv:SDY_3776
SBO_0104_s_at	-2.267983949	0.013189412	Decrease_in_adherent aceF; dihydrolipoamide acetyltransferase ; K00627 pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	sbv:SBBS512_E0987
V5833_s_at	-2.267441021	0.006541497	Decrease_in_adherent hslV; ATP-dependent protease peptidase subunit ; K01419 ATP-dependent HslUV protease, peptidase subunit HslV [EC:3.4.25.-]	sdv:SDY_3805
V5769_s_at	-2.267077402	0.008721154	Decrease_in_adherent psv; phosphoenolpyruvate carboxylase (EC:4.1.1.31); K01595 phosphoenolpyruvate carboxylase [EC:4.1.1.31]	sdv:SDY_3791
A4713_s_at	-2.264228914	0.037879967	Decrease_in_adherent yecG; universal stress protein UspC	sbv:SBBS512_E0987
SB5_4462_at	-2.263758166	0.025388053	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A1592_s_at	-2.262458072	0.002381101	Decrease_in_adherent transcriptional regulator MalT; K03556 LuxR family transcriptional regulator, maltose regulon positive regulatory protein	ect:EC0295
V0314_s_at	-2.262123673	0.003878772	Decrease_in_adherent pgi; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-6-phosphate isomerase [EC:5.3.1.9]	sdv:SDY_4226
V6990_s_at	-2.25855193	0.025887116	Decrease_in_adherent tar; methyl-accepting chemotaxis protein II ; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor	ssn:SSON_1231
A2739_s_at	-2.253983143	0.000703878	Decrease_in_adherent hypothetical protein	sbv:SBBS512_E0987
c5607_at	-2.25246795	0.000803258	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V4234_s_at	-2.247664589	0.01434001	Decrease_in_adherent kgtP; alpha-ketoglutarate transporter ; K03761 MFS transporter, MHS family, alpha-ketoglutarate permease	sdv:SDY_2830
b1603_s_at	-2.245963717	0.002833183	Decrease_in_adherent pntA; NAD(P) transhydrogenase subunit alpha (EC:1.6.1.2); K00324 NAD(P) transhydrogenase subunit alpha [EC:1.6.1.2]	ect:EC027
A0626_s_at	-2.24531629	0.005130379	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_8287_x_at	-2.243951488	0.001438273	Decrease_in_adherent yfeK; hypothetical protein	sbv:SBBS512_E0654
A3372_s_at	-2.242364871	0.00771712	Decrease_in_adherent cydA; cytochrome d ubiquinol oxidase, subunit I (EC:1.10.3.-); K00425 cytochrome bd-I oxidase subunit I [EC:1.10.3.-]	ect:EC011_2259
A4557_s_at	-2.23995664	0.001787585	Decrease_in_adherent ascC; succinylornithine transaminase AscC, PLP-dependent; K00840 succinylornithine aminotransferase [EC:2.6.1.81]	etw:ECSP_0113
ECs0116_s_at	-2.237163275	0.008675374	Decrease_in_adherent aroP; aromatic amino acid transporter; K11734 aromatic amino acid transport protein AroP	ssn:SSON_1445
A4519_s_at	-2.236788538	0.000174994	Decrease_in_adherent pheT; phenylalanyl-tRNA synthetase subunit beta (EC:6.1.1.20); K01890 phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]	sbv:SBBS512_E0987
SB5_4552_s_at	-2.235855946	0.009488944	Decrease_in_adherent shikimate transporter ; K08172 MFS transporter, MHS family, shikimate and dehydroshikimate transport protein	sdv:SDY_4050
EC869_4486_s_at	-2.234594068	0.00043652	Decrease_in_adherent kbl; 2-amino-3-ketobutyrate coenzyme A ligase (EC:2.3.1.29); K00639 glycine C-acetyltransferase [EC:2.3.1.29]	sdv:SDY_1674
V3343_s_at	-2.234207402	0.009935076	Decrease_in_adherent hypothetical protein	etw:ECSP_0727
EC869_7445_s_at	-2.23419518	0.010154365	Decrease_in_adherent glnS; glutamyl-tRNA synthetase; K01886 glutamyl-tRNA synthetase [EC:6.1.1.18]	sbv:SBBS512_E3479
A1232_s_at	-2.230872347	0.009612505	Decrease_in_adherent hypothetical protein ; K09806 hypothetical protein	cko:CKO_02010
A3772_s_at	-2.224044342	0.046278932	Decrease_in_adherent hypothetical protein	sdv:SDY_0175
A2807_s_at	-2.220303086	0.013692084	Decrease_in_adherent pfs; 5-methylthioadenosine/S-adenosylhomocysteine nucleosidase (EC:3.2.2.9); K01243 S-adenosylhomocysteine/5-methylthioadenosine nucleosidase [EC:3.2.2.9]	ebr:ECB_03475
H3672_s_at	-2.218674828	0.004339211	Decrease_in_adherent kbi; 2-amino-3-ketobutyrate coenzyme A ligase (EC:2.3.1.29); K00639 glycine C-acetyltransferase [EC:2.3.1.29]	bsu:BSU27910
AFFX-r2-Bs-phe-5_a	-2.214337778	1.88E-06	Decrease_in_adherent pheB; hypothetical protein; K06209 chorismate mutase [EC:5.4.99.5]	ssn:MS1295
V4112_s_at	-2.212304276	0.048397158	Decrease_in_adherent glyA; serine hydroxymethyltransferase (EC:2.1.2.1); K00600 glycine hydroxymethyltransferase [EC:2.1.2.1]	sbv:SBBS512_E4486
c3026_s_at	-2.211433087	0.005700834	Decrease_in_adherent guaA; GMP synthase (EC:6.3.5.2); K01951 GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]	ssn:SSON_2589
F4472_s_at	-2.211426547	0.027690676	Decrease_in_adherent rsd; anti-RNA polymerase sigma 70 factor ; K07740 regulator of sigma D	sbv:SBBS512_E3780
K1746_s_at	-2.209411247	0.000541676	Decrease_in_adherent hypothetical protein	ecc:c0640
F0588_s_at	-2.205606006	0.000352087	Decrease_in_adherent hypothetical protein	ecw:EC24377A_2330
A0074_x_at	-2.203332052	0.001488634	Decrease_in_adherent rfbA1; glucose-1-phosphate thymidyltransferase (EC:2.7.7.24); K00973 glucose-1-phosphate thymidyltransferase [EC:2.7.7.24]	NO_KEGG_DATA
V1009_s_at	-2.202471319	0.004993735	Decrease_in_adherent NO_KEGG_DATA	sdv:SDY_0957
SD1_1646_s_at	-2.202427162	0.000986848	Decrease_in_adherent yocC; cryptic autophosphorylating protein tyrosine kinase EtK ; K00903 protein-tyrosine kinase [EC:2.7.10.-]	sdv:SDY_0665
A3365_s_at	-2.202326204	0.019408085	Decrease_in_adherent sucB; dihydrolipoamide succinyltransferase (EC:2.3.1.61); K00658 2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]	sbv:SBBS512_E3752
b3375_s_at	-2.201620896	0.001117919	Decrease_in_adherent friR; DNA-binding transcriptional regulator FriR ; K10711 GntR family transcriptional regulator, friABCD operon transcriptional regulator	sdv:SDY_1343
A4059_s_at	-2.200979309	0.024696877	Decrease_in_adherent yciN; hypothetical protein	sdv:SDY_4049
c4443_s_at	-2.198371816	0.01023511	Decrease_in_adherent tdh; L-threonine 3-dehydrogenase (EC:1.1.1.103); K00060 threonine 3-dehydrogenase [EC:1.1.1.103]	sdv:SDY_4263
A2468_s_at	-2.195961245	0.026486753	Decrease_in_adherent pyrI; aspartate carbamoyltransferase regulatory subunit (EC:2.1.3.2); K00610 aspartate carbamoyltransferase regulatory subunit	ssn:SSON_1385
ECs2487_s_at	-2.194261737	0.019661169	Decrease_in_adherent yeaA; methionine sulfoxide reductase B (EC:1.8.4.11); K07305 peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12]	NO_KEGG_DATA
c1317_at	-2.187786551	0.040867901	Decrease_in_adherent NO_KEGG_DATA	ecw:EC24377A_0981
A3579_s_at	-2.185602224	0.002107252	Decrease_in_adherent phage integrase family site specific recombinase	ssn:SSON_1305
F2040_s_at	-2.183616381	0.005222892	Decrease_in_adherent hypothetical protein	bsu:BSU2250
AFFX-r2-Bs-thr-5_s	-2.183326989	5.76E-07	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	ecw:EC24377A_1707
A4299_at	-2.178407872	0.016463377	Decrease_in_adherent hypothetical protein	sbv:SBBS512_E0985
A0011_s_at	-2.17833082	0.000284958	Decrease_in_adherent hypothetical protein	sdv:SDY_2476
EC869_0940_s_at	-2.175803917	0.001502869	Decrease_in_adherent nuoJ; NADH dehydrogenase subunit J (EC:1.6.5.3); K00339 NADH dehydrogenase I subunit J [EC:1.6.5.3]	sdv:SDY_0141
A2755_s_at	-2.172792566	1.30E-05	Decrease_in_adherent ampE; regulatory protein AmpE ; K03807 AmpE protein	ebr:ECB_02319
H2460_x_at	-2.170589279	0.010716214	Decrease_in_adherent yfeK; hypothetical protein	ect:ECIAI39_2181
H1026_s_at	-2.169712535	0.001781355	Decrease_in_adherent hypothetical protein	sdv:SDY_1288
A3975_s_at	-2.167869848	0.007478185	Decrease_in_adherent galU; UTP--glucose-1-phosphate uridylyltransferase subunit GalU ; K00963 UTP--glucose-1-phosphate uridylyltransferase [EC:2.7.7.9]	sdv:SDY_2049
A3817_s_at	-2.166264681	0.006454934	Decrease_in_adherent ptsG; glucose-specific PTS system IIC components ; K02778 PTS system, glucose-specific IIB component [EC:2.7.1.69]; K02779 PTS system, glucose-specific IIC component [EC:2.7.1.69]	efl:LF82_p210
ECP_1297_s_at	-2.162691308	0.038248535	Decrease_in_adherent hypothetical protein YciY	ebr:ECB_03926
b4054_s_at	-2.158303067	0.000527716	Decrease_in_adherent tyrB; tyrosine aminotransferase, tyrosine-repressible, PLP-dependent (EC:2.6.1.57); K00832 aromatic-amino-acid transaminase [EC:2.6.1.57]	sdv:SDY_0567
A3285_s_at	-2.15729387	0.033019818	Decrease_in_adherent ybeL; hypothetical protein	sbv:SBBS512_E3723
A1518_s_at	-2.155504077	0.000285119	Decrease_in_adherent slyD; FKBP-type peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K03775 FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [EC:5.2.1.8]	bsu:BSU2250
AFFX-ThrX-M_at	-2.155223181	0.000129375	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	

A2623_s_at	-2.154049828	0.022062724	Decrease_in_adherent deoA; thymidine phosphorylase (EC:2.4.2.4); K00758 thymidine phosphorylase [EC:2.4.2.4]	sdv:SDY_4642
EC869_3291_s_at	-2.151826174	0.000937614	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0656_at	-2.151575098	0.000300598	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_2912
A1480_s_at	-2.149568354	0.005114298	Decrease_in_adherent DNA-directed RNA polymerase subunit alpha ; K03040 DNA-directed RNA polymerase subunit alpha [EC:2.7.7.6]	cko:CKO_04708
A1089_at	-2.141349484	0.012476879	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_3363
ECs2809_s_at	-2.13848414	0.004737465	Decrease_in_adherent hypothetical protein ; K09802 hypothetical protein	sb:SBBS512_E1230
A3862_at	-2.137449892	0.01970285	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_1265
S55_1846_x_at	-2.135027298	0.022496323	Decrease_in_adherent sbcB; exonuclease I (EC:3.1.11.1); K01141 exodeoxyribonuclease I [EC:3.1.11.1]	sdv:SDY_2231
b4406_s_at	-2.133654593	0.009944194	Decrease_in_adherent yaeP; hypothetical protein	sdv:SDY_0208
A3853_s_at	-2.130534296	0.019082469	Decrease_in_adherent hypothetical protein	ef:ECH74115_2279
A1499_s_at	-2.129979925	0.008702559	Decrease_in_adherent hypothetical protein	sec:SC3369
b2908_s_at	-2.128737379	0.028529899	Decrease_in_adherent pepP; proline aminopeptidase P II ; K01262 X-Pro aminopeptidase [EC:3.4.11.9]	sdv:SDY_3173
V6077_s_at	-2.127674134	0.036973646	Decrease_in_adherent ddl; D-alanyl-alanine synthetase A (EC:6.3.2.4); K01921 D-alanine-D-alanine ligase [EC:6.3.2.4]	sb:SBBS512_E0298
A4533_s_at	-2.127488793	0.027534785	Decrease_in_adherent hypothetical protein	sdv:SDY_1817
A1805_s_at	-2.126915507	0.000178381	Decrease_in_adherent grxC; glutaredoxin 3 ; K03676 glutaredoxin 3	sdv:SDY_4043
A2197_s_at	-2.12369759	0.005680133	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_4526
A1500_s_at	-2.123683909	0.003549665	Decrease_in_adherent rpsS; 30S ribosomal protein S19 ; K02965 small subunit ribosomal protein S19	cko:CKO_04732
A3414_s_at	-2.120024057	0.000183551	Decrease_in_adherent regulatory protein C1 from bacteriophage origin	eum:ECUMN_0588
SD1_3571_s_at	-2.11781967	0.015732883	Decrease_in_adherent yaeO; Rho-binding antiterminaltor	sdv:SDY_0207
EC869_5211_s_at	-2.114917747	0.013664451	Decrease_in_adherent hypothetical protein	sbo:SBO_0084
D4749_s_at	-2.109359754	0.033652715	Decrease_in_adherent relaxosome component	seh:SeHA_A0073
SD1_0741_s_at	-2.107879507	0.00162837	Decrease_in_adherent ribosomal protein S1 ; K02945 small subunit ribosomal protein S1	dze:Di1591_2339
b0839_s_at	-2.105315951	0.028184071	Decrease_in_adherent dacC; D-alanyl-D-alanine carboxypeptidase fraction C (EC:3.4.16.4); K07258 D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6) [EC:3.4.16.4]	sb:SBBS512_E2506
V6499_s_at	-2.103603656	0.000106271	Decrease_in_adherent fabI; enoyl-(acyl carrier protein) reductase (EC:1.3.1.10); K00208 enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9]	sdv:SDY_1368
V4232_s_at	-2.102790087	0.045794204	Decrease_in_adherent kgtP; alpha-ketoglutarate transporter ; K03761 MFS transporter, MHS family, alpha-ketoglutarate permease	sdv:SDY_2830
A0621_s_at	-2.102509784	0.021073797	Decrease_in_adherent clpB; protein disaggregation chaperone ; K03695 ATP-dependent Clp protease ATP-binding subunit ClpB	sb:SBBS512_E2973
AFFX-r2-Bs-thr-M_s	-2.099396963	7.92E-05	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	bsu:BSU32250
V3344_s_at	-2.098621838	0.01803193	Decrease_in_adherent ydiJ; putative oxidase ; K06911	sdv:SDY_1675
c2650_at	-2.096996049	0.006335032	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
H2063_s_at	-2.096082576	0.006061959	Decrease_in_adherent putative Aida-I adhesin-like protein	eqj:ECO26_3415
V3698_x_at	-2.092646925	0.037150796	Decrease_in_adherent cri; DNA-binding transcriptional regulator Cri ; K11926 sigma factor-binding protein Cri	sdv:SDY_0477
b2741_s_at	-2.08470163	0.002808824	Decrease_in_adherent hypothetical protein	eci:UT189_C3110
A3783_s_at	-2.084482021	6.82E-05	Decrease_in_adherent rimJ; ribosomal-protein-S5-alanine N-acetyltransferase ; K03790 ribosomal-protein-alanine N-acetyltransferase [EC:2.3.1.128]	sdv:SDY_2086
A2271_s_at	-2.080377605	0.015563231	Decrease_in_adherent yjgQ; hypothetical protein	ssn:SSON_4236
V6896_s_at	-2.076536176	0.000545595	Decrease_in_adherent pnuC; required for MNM transport ; K03811 nicotinamide mononucleotide transporter	sdv:SDY_0695
A1987_s_at	-2.07616387	0.020910632	Decrease_in_adherent rffG; dTDP-glucose 4,6-dehydratase RffG; K01710 dTDP-glucose 4,6-dehydratase [EC:4.2.1.46]	eqj:ECO26_4798
A3266_s_at	-2.073711758	7.14E-07	Decrease_in_adherent tatE; twin arginine translocase protein E ; K03425 sec-independent protein translocase protein TatE	sdv:SDY_0549
AFFX-ThrX_5_at	-2.070667476	7.94E-06	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	bsu:BSU32250
A0485_s_at	-2.070490263	2.48E-05	Decrease_in_adherent yfjB; hypothetical protein	sdv:SDY_2655
A3809_s_at	-2.066778427	0.00026515	Decrease_in_adherent fabG; 3-ketoacyl-(acyl-carrier-protein) reductase (EC:1.1.1.100); K00059 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	sb:SBBS512_E2231
EC536_5493_s_at	-2.064940809	0.004510456	Decrease_in_adherent hypothetical protein	eci:UT189_C0464
EC869_2599_s_at	-2.064890904	0.008002202	Decrease_in_adherent tra; methyl-accepting chemotaxis protein II; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor	ent:ECSP_2460
A3430_s_at	-2.062346661	0.036035897	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b2796_s_at	-2.058964961	0.000333136	Decrease_in_adherent hypothetical protein	ec:3363
b0435_s_at	-2.057625501	0.04138362	Decrease_in_adherent bolA; transcriptional regulator BolA ; K05527 BolA protein	sdv:SDY_0298
V3521_s_at	-2.055571762	0.000468228	Decrease_in_adherent transketolase (EC:2.2.1.1); K00615 transketolase [EC:2.2.1.1]	ent:Ent638_2960
A0009_s_at	-2.054393989	0.027906134	Decrease_in_adherent amn; AMP nucleosidase ; K01241 AMP nucleosidase [EC:3.2.2.4]	elf:LF82_0084
F3392_s_at	-2.053672877	0.015393013	Decrease_in_adherent mdaB; modulator of drug activity B ; K03923 modulator of drug activity B	sb:SBBS512_E3461
V5378_s_at	-2.051904395	0.002473194	Decrease_in_adherent putative dehydrogenase	cko:CKO_04859
V4816_s_at	-2.048948792	0.011061704	Decrease_in_adherent yieE; hypothetical protein	sdv:SDY_4201
V5011_s_at	-2.047845722	0.02814671	Decrease_in_adherent lld; L-lactate dehydrogenase (EC:1.1.2.3); K00101 L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]	sdv:SDY_4038
A2172_at	-2.047508062	8.38E-05	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0072_at	-2.045977041	0.03603949	Decrease_in_adherent glycosyl transferase group 2 family protein (EC:2.4.1.-)	ecw:EcE24377A_2328
b4142_s_at	-2.045542076	0.000971534	Decrease_in_adherent hypothetical protein	ecc:c5225
SDY_0383_s_at	-2.042982338	0.002584217	Decrease_in_adherent cof; hypothetical protein ; K11938 HMP-PP phosphatase [EC:3.6.1.-]	sdv:SDY_0383
D4444_s_at	-2.041093128	0.007545752	Decrease_in_adherent rpsD; 30S ribosomal protein S4 ; K02986 small subunit ribosomal protein S4	cko:CKO_04709
EC869_8298_x_at	-2.040160897	0.022752044	Decrease_in_adherent cysK; cysteine synthase A ; K01738 cysteine synthase A [EC:2.5.1.47]	sdv:SDY_2611
F0652_s_at	-2.040079562	0.003895205	Decrease_in_adherent cstA2; carbon starvation protein, predicted membrane protein; K06200 carbon starvation protein	etr:ETAE_2509
K2158_s_at	-2.039166185	0.025522889	Decrease_in_adherent 6-phosphofructokinase 2 ; K00850 6-phosphofructokinase [EC:2.7.1.11]	ecy:ECSE_1892
EC869_8425_s_at	-2.035046542	2.10E-05	Decrease_in_adherent pheT; phenylalanyl-tRNA synthetase subunit beta ; K01890 phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]	cko:CKO_01740
V4193_s_at	-2.032085095	0.025847278	Decrease_in_adherent DNA-binding transcriptional activator CafF ; K08277 transcriptional activator CafF	cko:CKO_03349
SD1_0310_s_at	-2.029133085	0.002674329	Decrease_in_adherent gadA; glutamate decarboxylase isozyme	sdv:SDY_3532
G1262_s_at	-2.026505241	0.009101596	Decrease_in_adherent trg; methyl-accepting chemotaxis protein III ; K05876 methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor	ssn:SSON_1721
b0605_s_at	-2.024422848	0.047331742	Decrease_in_adherent ahpC; alkyl hydroperoxide reductase subunit C (EC:1.11.1.15); K03386 peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]	sb:SBBS512_E0519
EC869_5106_s_at	-2.023006516	0.034098979	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b3936_s_at	-2.02254373	0.00994075	Decrease_in_adherent rpmE; 50S ribosomal protein L31 ; K02909 large subunit ribosomal protein L31	sdv:SDY_3801
A4157_s_at	-2.020377131	0.002804573	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_4082_s_at	-2.01802406	0.003345904	Decrease_in_adherent ompF; outer membrane protein F ; K09476 outer membrane pore protein F	sdv:SDY_2328
EC536_4168_s_at	-2.01666082	0.009930436	Decrease_in_adherent pdxH; pyridoxine 5'-phosphate oxidase; K00275 pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]	etw:ECSP_2203
V0844_s_at	-2.016343123	0.041957317	Decrease_in_adherent hfq; RNA-binding protein Hfq ; K03666 host factor-I protein	sbo:SBO_4284
V3467_s_at	-2.015679846	0.001459825	Decrease_in_adherent hypothetical protein ; K07223 putative iron-dependent peroxidase	sdv:SDY_2629
V6065_s_at	-2.013413115	0.039234333	Decrease_in_adherent proC; pyrroline-5-carboxylate reductase (EC:1.5.1.2); K00286 pyrroline-5-carboxylate reductase [EC:1.5.1.2]	sdv:SDY_0356
EC869_1986_s_at	-2.012180045	0.02552691	Decrease_in_adherent yciB; intracellular septation protein A ; K06190 intracellular septation protein	sdv:SDY_1318
SD1_1093_s_at	-2.009059628	0.013477225	Decrease_in_adherent putative oxidoreductase	sbo:SBO_1510

A3557_s_at	-2.008494928	0.045615357	Decrease_in_adherent cIpS; ATP-dependent Clp protease adaptor protein ClpS ; K06891 ATP-dependent Clp protease adaptor protein ClpS	sdv:SDY_2380
A3042_s_at	-2.001414886	0.012312459	Decrease_in_adherent hypothetical protein ; K09913 hypothetical protein	sbv:SbBS512_E0308
A0057_s_at	-2.001290312	8.59E-05	Decrease_in_adherent hisB; imidazoleglycerol-phosphate dehydratase/histidinol-phosphate phosphatase ; K10189 imidazoleglycerol-phosphate dehydratase / histidinol-phosphate [EC:4.2.1.]	kpu:KP1_3683
V5495_s_at	-1.996439247	0.005867051	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
S55_4421_s_at	-1.995584186	0.022578387	Decrease_in_adherent yfbT; putative phosphatase	sdv:SDY_2489
G0937_x_at	-1.992818767	0.004863351	Decrease_in_adherent rraB; uncharacterized protein YjgD ; K09893 hypothetical protein	efl:LF82_1990
EC869_7371_s_at	-1.991932173	0.006207632	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V4311_s_at	-1.9907023	0.001461165	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3624_s_at	-1.988149991	5.63E-05	Decrease_in_adherent aspC; aromatic amino acid aminotransferase (EC:2.6.1.57); K00813 aspartate aminotransferase [EC:2.6.1.1]	sdv:SDY_2329
S85_4324_s_at	-1.985356028	0.011107679	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2849_s_at	-1.983905339	0.032024625	Decrease_in_adherent yaeD; D,D-heptose 1,7-bisphosphate phosphatase ; K03273 D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.-]	ssn:SSON_0214
b3103_s_at	-1.981849619	0.023907064	Decrease_in_adherent putative inner membrane protein YnhH	sbv:SbBS512_E3258
S85_1453_s_at	-1.978145379	0.036230097	Decrease_in_adherent gadC; glutamate:gamma aminobutyrate antiporter	sbv:SbBS512_E1755
APECO1_3321_at	-1.978079246	0.039193975	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V3693_s_at	-1.977473123	0.014803446	Decrease_in_adherent pepD; aminoacyl-histidine dipeptidase (peptidase D) (EC:3.4.13.3); K01270 aminoacylhistidine dipeptidase [EC:3.4.13.3]	ebr:ECB_00232
A0654_at	-1.976647067	0.022558958	Decrease_in_adherent putative type I restriction-modification system, S subunit ; K01154 type I restriction enzyme, S subunit [EC:3.1.21.3]	ecw:EcE24377A_2910
A1821_s_at	-1.975326232	0.001505356	Decrease_in_adherent rfaJ; lipopolysaccharide 1,2-glucosyltransferase (EC:2.4.1.58); K03276 UDP-glucose/galactose:(glucosyl)1,2-galactose-1,2-glucosyl/galactosyltransferase [EC:2.4.1.-]	sbv:SbBS512_E4053
V5680_s_at	-1.970294548	0.028738935	Decrease_in_adherent glnP; glutamine ABC transporter permease protein ; K10037 glutamine transport system permease protein	sdv:SDY_0786
A2627_s_at	-1.965847786	0.01931171	Decrease_in_adherent lplA; lipotein-protein ligase A (EC:6.3.2.-); K03800 lipotein-protein ligase A [EC:2.7.7.63]	sbv:SbBS512_E4933
V3697_s_at	-1.962382641	0.036293373	Decrease_in_adherent frsA; hydrolase FrsA; K11750 esterase FrsA [EC:3.1.-.1]	eqj:EC026_0295
A0363_at	-1.961674563	0.042362249	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V1944_x_at	-1.959760289	0.023568047	Decrease_in_adherent hypothetical protein	cko:CKO_04557
A0633_s_at	-1.958482082	0.000218122	Decrease_in_adherent rplS; 50S ribosomal protein L19 ; K02884 large subunit ribosomal protein L19	sdv:SDY_2780
A0833_s_at	-1.955785687	0.02902406	Decrease_in_adherent rplS; 50S ribosomal protein L19 ; K02884 large subunit ribosomal protein L19	cko:CKO_04145
V3518_s_at	-1.955113995	0.019637767	Decrease_in_adherent talI; transaldolase A (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2]	sbv:SbBS512_E2830
A1822_s_at	-1.951842666	0.000292741	Decrease_in_adherent waaO; rfaI; UDP-glucose:(glucosyl) LPS alpha1,3-glucosyltransferase WaaO ; K03275 UDP-glucose:(glucosyl)LPS alpha-1,3-glucosyltransferase [EC:2.4.1.-]	ebr:ECB_03486
b4032_s_at	-1.950742516	0.000150009	Decrease_in_adherent malG; maltose transporter permease ; K10110 maltose/maltodextrin transport system permease protein	ssn:SSON_4210
A3916_s_at	-1.946863375	0.000408906	Decrease_in_adherent hypothetical protein	sbv:SbBS512_E1335
A1431_s_at	-1.946509014	0.022100536	Decrease_in_adherent argR; arginine repressor ; K03402 transcriptional regulator of arginine metabolism	sdv:SDY_3413
A3910_s_at	-1.945077514	0.00105214	Decrease_in_adherent minD; cell division inhibitor MinD ; K03609 septum site-determining protein MinD	sdv:SDY_1206
SDY_4021_s_at	-1.942344195	0.021870371	Decrease_in_adherent hypothetical protein	sdv:SDY_PA07
pCo0005_at	-1.937586104	0.047926871	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_D0041
c2804_s_at	-1.936646276	0.000664102	Decrease_in_adherent menC; O-succinylbenzoate synthase (EC:4.2.1.-); K02549 O-succinylbenzoate synthase [EC:4.2.1.113]	sbv:SbBS512_E2640
A2738_s_at	-1.933650327	0.011285171	Decrease_in_adherent ftsA; cell division protein FtsA ; K03590 cell division protein FtsA	cko:CKO_03281
A0365_s_at	-1.933308548	0.01455889	Decrease_in_adherent hypothetical protein	sdv:SDY_2524
V5387_s_at	-1.930551822	0.002404904	Decrease_in_adherent asd; aspartate-semialdehyde dehydrogenase (EC:1.2.1.11); K00133 aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	sdv:SDY_3579
EC869_7476_s_at	-1.929414078	0.034096228	Decrease_in_adherent PhoH family protein	ddc:dds66_1152
b2665_s_at	-1.927631801	0.043486428	Decrease_in_adherent ynfJ; LysM domain/BON superfamily protein	sdv:SDY_2855
A2145_s_at	-1.925369237	0.001179251	Decrease_in_adherent hslU; ATP-dependent protease ATP-binding subunit HslU ; K03667 ATP-dependent HslUV protease ATP-binding subunit HslU	sbv:SbBS512_E4413
V5396_s_at	-1.922181035	0.036838781	Decrease_in_adherent glgX; glycogen debranching enzyme ; K02438 glycogen operon protein GlgX [EC:3.2.1.-]	sdv:SDY_3577
A1479_s_at	-1.922146232	0.000451349	Decrease_in_adherent rplQ; 50S ribosomal protein L17 ; K02879 large subunit ribosomal protein L17	sdv:SDY_3470
A1631_s_at	-1.922105764	0.000222431	Decrease_in_adherent livM; leucine/isoleucine/valine transporter permease subunit ; K01998 branched-chain amino acid transport system permease protein	sbv:SbBS512_E3866
V1007_s_at	-1.91995555	0.04051981	Decrease_in_adherent purB; adenylosuccinate lyase (EC:4.3.2.2); K01756 adenylosuccinate lyase [EC:4.3.2.2]	pmr:PM10886
SD1_3331_s_at	-1.919036107	0.039748589	Decrease_in_adherent pflA; pyruvate formate lyase-activating enzyme 1 (EC:1.97.1.4); K04069 pyruvate formate lyase activating enzyme [EC:1.97.1.4]	sdv:SDY_2359
SD1_2172_s_at	-1.917482096	0.000143045	Decrease_in_adherent fabB; 3-oxoacyl-(acyl carrier protein) synthase I (EC:2.3.1.41); K00647 3-oxoacyl-(acyl-carrier-protein) synthase I [EC:2.3.1.41]	sdv:SDY_2522
A1478_s_at	-1.915199246	0.045729676	Decrease_in_adherent yhdN; hypothetical protein	sdv:SDY_3469
EC869_0563_s_at	-1.912556131	0.003383062	Decrease_in_adherent priC; oligopeptidase A ; K01414 oligopeptidase A [EC:3.4.24.70]	sdv:SDY_3564
A4455_s_at	-1.91239256	0.042114763	Decrease_in_adherent ydhD; hypothetical protein ; K07390 monothiol glutaredoxin	sdv:SDY_1880
EC869_7364_s_at	-1.912328544	0.012298315	Decrease_in_adherent cIpX; ATP-dependent protease ATP-binding subunit ClpX ; K03544 ATP-dependent Clp protease ATP-binding subunit ClpX	sdv:SDY_0294
W4306_s_at	-1.911141159	0.006366983	Decrease_in_adherent hypothetical protein	sec:SC2696
AFfX-DapX-5_at	-1.909050309	3.54E-05	Decrease_in_adherent dapB; dihydrodipicolinate reductase (EC:1.3.1.26); K00215 dihydrodipicolinate reductase [EC:1.3.1.26]	bsu:BSU22490
EC869_3959_s_at	-1.908037065	0.017980771	Decrease_in_adherent putative phage repressor protein CI	eqj:EC026_2664
A2072_s_at	-1.907275548	0.041770539	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3909_s_at	-1.906213517	0.001516365	Decrease_in_adherent minE; cell division topological specificity factor MinE ; K03608 cell division topological specificity factor	sdv:SDY_1205
V0042_s_at	-1.904843947	0.000246075	Decrease_in_adherent efp; elongation factor P ; K02356 elongation factor EF-P	sdv:SDY_4390
SD1_1682_s_at	-1.90265131	0.00157377	Decrease_in_adherent apbA; 2-dehydropantoate 2-reductase (EC:1.1.1.169); K00077 2-dehydropantoate 2-reductase [EC:1.1.1.169]	sdv:SDY_0305
A4101_s_at	-1.902416403	0.004490277	Decrease_in_adherent pspB; phage shock protein B ; K03970 phage shock protein B	sdv:SDY_1939
AFfX-DapX-3_at	-1.901869767	9.08E-06	Decrease_in_adherent ypfJ; hypothetical protein	bsu:BSU22470
b2905_s_at	-1.89975366	0.027464489	Decrease_in_adherent govT; glycine cleavage system aminomethyltransferase T (EC:2.1.2.10); K00605 aminomethyltransferase [EC:2.1.2.10]	sdv:SDY_3176
SD1_0336_s_at	-1.894335542	0.00017397	Decrease_in_adherent priC; oligopeptidase A (EC:3.4.24.70); K01414 oligopeptidase A [EC:3.4.24.70]	sbv:SbBS512_E3824
V4544_x_at	-1.892977551	0.010030505	Decrease_in_adherent argI; ornithine carbamoyltransferase subunit I (EC:2.1.3.3); K00611 ornithine carbamoyltransferase [EC:2.1.3.3]	sbo:SBO_4188
A0951_s_at	-1.890879541	0.013199604	Decrease_in_adherent fIdB; flavodoxin FIdB ; K03840 flavodoxin II	sdv:SDY_3187
F3193_s_at	-1.890431726	0.040116213	Decrease_in_adherent ygfB; hypothetical protein ; K09895 hypothetical protein	sdv:SDY_3172
A4769_s_at	-1.888083714	0.018612167	Decrease_in_adherent hypothetical protein	ecv:APECO1_991
A4154_s_at	-1.886639171	0.019529717	Decrease_in_adherent idhA; D-lactate dehydrogenase (EC:1.1.1.28); K03778 D-lactate dehydrogenase [EC:1.1.1.28]	sbv:SbBS512_E1618
A2905_s_at	-1.88471812	0.016452586	Decrease_in_adherent pepD; aminoacyl-histidine dipeptidase ; K01270 aminoacylhistidine dipeptidase [EC:3.4.13.3]	sdv:SDY_0480
AFfX-r2-Bs-dap-3_a	-1.884404137	6.09E-06	Decrease_in_adherent ypfJ; hypothetical protein	bsu:BSU22470
EC869_0457_s_at	-1.883027235	0.007756656	Decrease_in_adherent livK; high-affinity leucine-specific transport system; periplasmic binding protein ; K01999 branched-chain amino acid transport system substrate-binding protein	sdv:SDY_3607
V2537_s_at	-1.882316822	0.017524654	Decrease_in_adherent hdhA; 7-alpha-hydroxysteroid dehydrogenase (EC:1.1.1.159); K00076 7-alpha-hydroxysteroid dehydrogenase [EC:1.1.1.159]	sdv:SDY_1838
BF3598_s_at	-1.878979192	0.002485018	Decrease_in_adherent yhiV; putative transport system permease protein; K03296 hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family	svf:SCV_3986
b0078_s_at	-1.866630775	0.004830591	Decrease_in_adherent livH; acetylactate synthase small subunit (EC:2.2.1.6); K01653 acetylactate synthase IIII small subunit [EC:2.2.1.6]	ebr:ECB_00080
V3520_s_at	-1.865872974	5.00E-05	Decrease_in_adherent talI; transaldolase A (EC:2.2.1.2); K00616 transaldolase [EC:2.2.1.2]	sbv:SbBS512_E2830
F3748_s_at	-1.865654707	0.019888733	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V6747_s_at	-1.861998408	0.012007552	Decrease_in_adherent tas; putative aldo-keto reductase	sdv:SDY_3051

EC869_4322_s_at	-1.860449969	0.03810349	Decrease_in_adherent chromosome replication initiation inhibitor protein ; K05596 LysR family transcriptional regulator, chromosome initiation inhibitor	cko:CKO_04281
ECs1050_s_at	-1.860091267	0.018833184	Decrease_in_adherent hypothetical protein	eci:UTI89_C1032
V0296_s_at	-1.860018925	0.006632577	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
AFFX-r2-Bs-dap-M_i	-1.858852322	0.000203468	Decrease_in_adherent mgsA; methylglyoxal synthase (EC:4.2.3.3); K01734 methylglyoxal synthase [EC:4.2.3.3]	bsu:BSU22480
EC869_0354_s_at	-1.858621149	0.007233325	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
F1227_s_at	-1.856839944	0.047292118	Decrease_in_adherent cupin family protein	sb:SBBS512_E1306
UTI89_C4861_x_at	-1.852629098	0.003241474	Decrease_in_adherent rraB; uncharacterized protein YjgD ; K09893 hypothetical protein	elf:LF82_1990
b2276_s_at	-1.851322564	0.001976012	Decrease_in_adherent nuoN; NADH dehydrogenase subunit N (EC:1.6.5.3); K00343 NADH dehydrogenase I subunit N [EC:1.6.5.3]	sdv:SDY_2472
A1433_s_at	-1.851099154	0.024610425	Decrease_in_adherent hypothetical protein ; K03623 ribonuclease inhibitor	sb:SBBS512_E3537
V6718_s_at	-1.848806721	0.023691629	Decrease_in_adherent fruR; DNA-binding transcriptional regulator FruR ; K03435 LacI family transcriptional regulator, fructose operon transcriptional repressor	sb:SBBS512_E0073
AFFX-r2-Bs-dap-5_a	-1.847002518	1.35E-06	Decrease_in_adherent dapB; dihydrodipicolinate reductase (EC:1.3.1.26); K00215 dihydrodipicolinate reductase [EC:1.3.1.26]	bsu:BSU22490
SD1_2880_s_at	-1.844764107	0.026230687	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b4255_x_at	-1.844351284	0.000965942	Decrease_in_adherent yjgD; hypothetical protein ; K09893 hypothetical protein	sdv:SDY_4277
A1823_s_at	-1.843508611	0.016897149	Decrease_in_adherent waaP; putative LPS biosynthesis enzyme ; K02848 heptose (I) phosphotransferase [EC:2.7.1.-]	sdv:SDY_4060
A2625_s_at	-1.843357263	0.023594162	Decrease_in_adherent deoD; purine nucleoside phosphorylase (EC:2.4.2.1); K03784 purine-nucleoside phosphorylase [EC:2.4.2.1]	sdv:SDY_4644
A2643_s_at	-1.843067577	0.031379224	Decrease_in_adherent two-component response regulator ; K07773 two-component system, OmpR family, aerobic respiration control protein ArcA	cko:CKO_03387
A3820_s_at	-1.839974619	0.01916657	Decrease_in_adherent hinT; similar to histidine triad-like protein ycf of escherichia coli ; K12150 HIT-like protein HinT	pay:PAU_01712
A3606_s_at	-1.839739658	0.002656523	Decrease_in_adherent rpsA; 30S ribosomal protein S1 ; K02945 small subunit ribosomal protein S1	cko:CKO_02162
AFFX-DapX-M_at	-1.839397903	5.47E-05	Decrease_in_adherent mgsA; methylglyoxal synthase (EC:4.2.3.3); K01734 methylglyoxal synthase [EC:4.2.3.3]	bsu:BSU22480
A2717_s_at	-1.837776658	0.024663005	Decrease_in_adherent leuC; isopropylmalate isomerase large subunit (EC:4.2.1.33); K01703 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [EC:4.2.1.33]	sdv:SDY_0099
EC869_0211_s_at	-1.837713604	0.02823655	Decrease_in_adherent fkpA; FKBP-type peptidyl-prolyl cis-trans isomerase ; K03772 FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]	sbo:SB0_3327
A1527_s_at	-1.837333241	0.036284637	Decrease_in_adherent crp; cAMP-regulatory protein ; K10914 CRP/FNR family transcriptional regulator, cyclic AMP receptor protein	ecw:EcE24377A_3827
EC869_3856_s_at	-1.836405122	0.005097565	Decrease_in_adherent purH; bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase (EC:2.1.3.3.5.4.10); K00602 phosphoribosylaminoimidazolecarboxamide	sb:SBBS512_E4498
S55_2236_x_at	-1.83602427	0.026825191	Decrease_in_adherent yfeK; hypothetical protein	ssn:SSON_2509
A1294_s_at	-1.834585201	0.039892927	Decrease_in_adherent yqjD; hypothetical protein	sdv:SDY_3285
S85_4325_s_at	-1.827067918	0.006239764	Decrease_in_adherent livI; acetolactate synthase 3 catalytic subunit [EC:2.2.1.6]; K01652 acetolactate synthase I/II/III large subunit [EC:2.2.1.6]	sdv:SDY_0107
V3848_s_at	-1.826649855	0.012708125	Decrease_in_adherent tolC; outer membrane channel protein ; K12340 outer membrane channel protein TolC	sdv:SDY_3205
SDM_4222_s_at	-1.826522773	2.56E-05	Decrease_in_adherent hypothetical protein ; K07567 TdcF protein	sb:SBBS512_E3244
A2272_s_at	-1.826164479	0.000808723	Decrease_in_adherent hypothetical protein	cko:CKO_03844
A2897_s_at	-1.824709864	0.022326014	Decrease_in_adherent putative HicB	ej:ECO26_0244
V7071_s_at	-1.818909612	8.23E-07	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2646_s_at	-1.818038274	0.046441115	Decrease_in_adherent thrB; homoserine kinase (EC:2.7.1.39); K00872 homoserine kinase [EC:2.7.1.39]	sdv:SDY_0003
LH0125_s_at	-1.817647433	0.019801941	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_2285_s_at	-1.815869502	0.005010258	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SD1_1220_s_at	-1.815496239	0.009477433	Decrease_in_adherent hypothetical protein	sdv:SDY_2649
SD1_3015_x_at	-1.814786595	0.011276718	Decrease_in_adherent yjgD; hypothetical protein ; K09893 hypothetical protein	sdv:SDY_4277
A1482_s_at	-1.814195217	0.008967887	Decrease_in_adherent rpsK; 30S ribosomal protein S11 ; K02948 small subunit ribosomal protein S11	sdv:SDY_3473
V6469_s_at	-1.811971157	0.00057232	Decrease_in_adherent pspA; phage shock protein PspA ; K03969 phage shock protein A	sdv:SDY_1940
A4625_s_at	-1.810994467	0.02401527	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V6006_s_at	-1.810469675	0.005846246	Decrease_in_adherent tsx; nucleoside channel ; K05517 nucleoside-specific channel-forming protein	sdv:SDY_0323
ECP_2591_s_at	-1.810218149	0.039020178	Decrease_in_adherent transposase	sb:SBBS512_E1228
SF1462_s_at	-1.807603698	0.005101874	Decrease_in_adherent gdhA; glutamate dehydrogenase (EC:1.4.1.4); K00262 glutamate dehydrogenase (NADP+) [EC:1.4.1.4]	sfl:SF1462
A1048_at	-1.804865649	0.036794241	Decrease_in_adherent DNA methylase N-4/N-6 (EC:2.1.1.72)	eck:EC55989_3268
b0917_s_at	-1.789359816	0.001626753	Decrease_in_adherent ycaR; hypothetical protein ; K09791 hypothetical protein	sdv:SDY_2341
b2293_s_at	-1.788549686	0.014129132	Decrease_in_adherent yfbT; putative phosphatase	sdv:SDY_2489
V2687_s_at	-1.78572374	0.006289373	Decrease_in_adherent hybB; putative hydrogenase 2 b cytochrome subunit	sdv:SDY_3078
b1215_s_at	-1.78484718	0.043087595	Decrease_in_adherent kdsA; 2-dehydro-3-deoxyphosphoacetate aldolase (EC:2.5.1.55); K01627 2-dehydro-3-deoxyphosphoacetate aldolase (KDO 8-P synthase) [EC:2.5.1.55]	sdv:SDY_1264
A1971_s_at	-1.783912917	6.77E-07	Decrease_in_adherent ilvD; dihydroxy-acid dehydratase (EC:4.2.1.9); K01687 dihydroxy-acid dehydratase [EC:4.2.1.9]	ssn:SSON_3942
EC869_4308_x_at	-1.777625416	0.00695166	Decrease_in_adherent pepP; proline aminopeptidase P II (EC:3.4.11.9); K01262 X-Pro aminopeptidase [EC:3.4.11.9]	sb:SBBS512_E3329
EC869_8306_s_at	-1.775930838	0.030196996	Decrease_in_adherent ypeH; putative cytochrome oxidase	sdv:SDY_2606
ECs1680_s_at	-1.771638273	0.000687796	Decrease_in_adherent dsbB; disulfide bond formation protein B ; K03611 disulfide bond formation protein DsbB	sdv:SDY_1222
A3025_s_at	-1.771232293	0.001295228	Decrease_in_adherent hypothetical protein	ecr:ECIAI1_0372
c0999_s_at	-1.770278701	0.014909924	Decrease_in_adherent hypothetical protein	sdv:SDY_2397
A1262_s_at	-1.769669401	0.002140515	Decrease_in_adherent aer; aerotaxis sensor receptor, flavoprotein ; K03776 aerotaxis receptor	ssn:SSON_3210
A4635_s_at	-1.768343276	0.017860619	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A4535_s_at	-1.76713122	0.009917053	Decrease_in_adherent hypothetical protein	sdv:SDY_1819
V6704_s_at	-1.7652869	0.048103559	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V3875_s_at	-1.763956437	0.028567595	Decrease_in_adherent sucC; succinyl-CoA synthetase subunit beta (EC:6.2.1.5); K01903 succinyl-CoA synthetase beta subunit [EC:6.2.1.5]	sdv:SDY_0666
EC869_5206_s_at	-1.762874037	0.01635129	Decrease_in_adherent secA; azi, div; preprotein translocase subunit SecA ; K03070 preprotein translocase subunit SecA	sdv:SDY_0128
SF1693_s_at	-1.762697595	0.003875127	Decrease_in_adherent IS-10 transposase	aci:ACL_0003
A2740_s_at	-1.762436263	0.024992087	Decrease_in_adherent lpxC; UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase ; K02535 UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [EC:3.5.1.-]	sdv:SDY_0126
S55_4713_s_at	-1.761466878	0.029817542	Decrease_in_adherent tsr; methyl-accepting chemotaxis protein I ; K05874 methyl-accepting chemotaxis protein I, serine sensor receptor	sb:SBBS512_E4893
b3186_s_at	-1.757190613	0.014158069	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_3672
A1013_s_at	-1.755370307	0.013608217	Decrease_in_adherent metK; S-adenosylmethionine synthetase (EC:2.5.1.6); K00789 S-adenosylmethionine synthetase [EC:2.5.1.6]	sdv:SDY_3130
A2146_s_at	-1.755133796	0.011858478	Decrease_in_adherent hslV; ATP-dependent protease peptidase subunit ; K01419 ATP-dependent HslUV protease, peptidase subunit HslV [EC:3.4.25.-]	sdv:SDY_3805
b1777_s_at	-1.753706363	0.035395632	Decrease_in_adherent yeaC; hypothetical protein ; K09916 hypothetical protein	ebw:BWG_1590
EC536_4973_s_at	-1.750538223	0.007757055	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V1769_s_at	-1.750493798	0.00048698	Decrease_in_adherent pepN; aminopeptidase N ; K01256 aminopeptidase N [EC:3.4.11.2]	sdv:SDY_2325
M3860_s_at	-1.748822248	0.024211773	Decrease_in_adherent parM; plasmid segregation protein ParM	ecw:EcE24377A_D0013
b3305_s_at	-1.746890375	0.018375607	Decrease_in_adherent rplF; 50S ribosomal protein L6 ; K02933 large subunit ribosomal protein L6	sdv:SDY_3481
EC869_4279_s_at	-1.746689033	0.00262448	Decrease_in_adherent channel protein, hemolysin III family ; K11068 hemolysin III	sb:SBBS512_E3320
EC869_1120_s_at	-1.743127825	0.001018431	Decrease_in_adherent hypothetical protein	ecc:c1337
K4295_at	-1.740063711	0.033069276	Decrease_in_adherent thrC; threonine synthase (EC:4.2.3.1); K01733 threonine synthase [EC:4.2.3.1]	af:AFE_0474
A1678_s_at	-1.739395196	0.041281348	Decrease_in_adherent gor; glutathione reductase (EC:1.8.1.7); K00383 glutathione reductase (NADPH) [EC:1.8.1.7]	sdv:SDY_3562

A1495_s_at	-1.737698826	0.015675347	Decrease_in_adherent rpsQ; 30S ribosomal protein S17; K02961 small subunit ribosomal protein S17	ctu:ctu_38380
F3897_s_at	-1.737342394	0.048284675	Decrease_in_adherent mdtE; multidrug efflux system protein MdtE	eum:ECUMN_4014
A4654_s_at	-1.737221273	0.030599896	Decrease_in_adherent hypothetical protein	sdv:SDY_1125
V2361_s_at	-1.73472973	0.017974573	Decrease_in_adherent fliY; cystine transporter subunit ; K02424 cystine transport system substrate-binding protein	sbv:SbBS512_E1048
EC869_5213_s_at	-1.733122336	0.005583259	Decrease_in_adherent hypothetical protein	sbo:SBO_0084
A3683_s_at	-1.72886288	0.04421857	Decrease_in_adherent yccA; hypothetical protein ; K06890	sdv:SDY_0945
c0823_s_at	-1.727414561	0.003871711	Decrease_in_adherent hypothetical protein	ecc:c0824
A3915_s_at	-1.726160304	0.00297597	Decrease_in_adherent hypothetical protein ; K09902 hypothetical protein	sbv:SbBS512_E1334
D4092_s_at	-1.725015115	0.047008508	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A3838_s_at	-1.724342691	0.017630465	Decrease_in_adherent cobB; NAD-dependent deacetylase ; K12410 NAD-dependent deacetylase [EC:3.5.1.-]	sdv:SDY_2030
A1818_s_at	-1.72186077	0.002644632	Decrease_in_adherent glycosyl transferase, group 2 family protein (EC:2.4.1.-); K12983 UDP-glucose:(glucosyl)LPS beta-1,3-glucosyltransferase [EC:2.4.1.-]	sbv:SbBS512_E4050
A1510_s_at	-1.720459628	0.025536226	Decrease_in_adherent rpsG; 30S ribosomal protein S7; K02992 small subunit ribosomal protein S7	ctu:ctu_38550
b3963_s_at	-1.719422105	0.008028911	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_4522
N4246_s_at	-1.718394226	0.01861146	Decrease_in_adherent gpmB; phosphoglycerate mutase (EC:5.4.2.1); K01834 phosphoglycerate mutase [EC:5.4.2.1]	ssn:SSON_4545
EC536_6355_s_at	-1.717203224	0.015113682	Decrease_in_adherent trpS; tryptophanyl-tRNA synthetase (EC:6.1.1.2); K01867 tryptophanyl-tRNA synthetase [EC:6.1.1.2]	sdv:SDY_3695
A4012_at	-1.716624053	0.040068154	Decrease_in_adherent putative phage repressor protein CI	eoh:ECO103_1364
A1577_s_at	-1.714712065	0.017653884	Decrease_in_adherent two component transcriptional regulator, winged helix family ; K07659 two-component system, OmpR family, phosphate regulon response regulator OmpR	dze:DD1591_0244
S55_4357_s_at	-1.713309399	0.042639031	Decrease_in_adherent yciR; RNase II stability modulator	sbo:SBO_1779
A3569_s_at	-1.713276958	0.022187305	Decrease_in_adherent serS; seryl-tRNA synthetase (EC:6.1.1.11); K01875 seryl-tRNA synthetase [EC:6.1.1.11]	sbo:SBO_0826
A0889_s_at	-1.711528261	0.001915644	Decrease_in_adherent tas; putative aldo-keto reductase	sdv:SDY_3051
A1226_s_at	-1.71074424	0.004658954	Decrease_in_adherent hypothetical protein	sbv:SbBS512_E3469
SVF_3790_s_at	-1.709052244	0.000562954	Decrease_in_adherent yieJ; hypothetical protein; K09925 hypothetical protein	svf:SVF_3790
EC52343_s_at	-1.708520082	0.020105645	Decrease_in_adherent tppB; putative tripeptide transporter permease ; K03305 proton-dependent oligopeptide transporter, POT family	sbv:SbBS512_E1824
A3314_s_at	-1.708155766	0.02294441	Decrease_in_adherent nagE; N-acetyl glucosamine specific PTS system components IIABC (EC:2.7.1.69); K02802 PTS system, N-acetylglucosamine-specific IIA component [EC:2.7.1.69]; K00	sbv:SbBS512_E0571
A2049_s_at	-1.707971342	0.04032529	Decrease_in_adherent pepG; proline dipeptidase ; K01271 X-Pro dipeptidase [EC:3.4.13.9]	sdv:SDY_3898
V3830_s_at	-1.706342879	0.032157174	Decrease_in_adherent cytosine deaminase ; K01485 cytosine deaminase [EC:3.5.4.1]	set:SEN3167
F1880_s_at	-1.705394008	0.001909387	Decrease_in_adherent putative inner membrane protein	sdv:SDY_1676
F0889_s_at	-1.704970495	0.004905372	Decrease_in_adherent hypothetical protein ; K01993 HlyD family secretion protein	sdv:SDY_0808
A3983_s_at	-1.704576983	0.000423539	Decrease_in_adherent oppB; oligopeptide transporter permease ; K02033 peptide/nickel transport system permease protein	sbc:SbBS1823
D3362_x_at	-1.70288442	0.027146805	Decrease_in_adherent tkfA; transketolase (EC:2.2.1.1); K00615 transketolase [EC:2.2.1.1]	sbv:SbBS512_E3367
V3434_s_at	-1.702646006	0.018131005	Decrease_in_adherent cysK; cysteine synthase A (EC:2.5.1.47); K01738 cysteine synthase A [EC:2.5.1.47]	sbv:SbBS512_E2766
A1492_s_at	-1.702445341	0.017621213	Decrease_in_adherent rpiE; 50S ribosomal protein L5 ; K02931 large subunit ribosomal protein L5	kpu:KPI_5029
A4380_s_at	-1.700481343	0.029013181	Decrease_in_adherent speG; spermidine N1-acetyltransferase (EC:2.3.1.57); K00657 diamine N-acetyltransferase [EC:2.3.1.57]	efe:EFER_1522
V1005_s_at	-1.699519123	0.00802323	Decrease_in_adherent phoP; DNA-binding transcriptional regulator PhoP ; K07660 two-component system, OmpR family, response regulator PhoP	sdv:SDY_2022
A1296_s_at	-1.699186499	0.030391573	Decrease_in_adherent hypothetical protein	sbv:SbBS512_E3261
pCoo049_x_at	-1.690049743	0.010339596	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_E0058
V6012_s_at	-1.676650985	0.042379986	Decrease_in_adherent secF; preprotein translocase subunit SecF ; K03074 preprotein translocase subunit SecF	sdv:SDY_0325
V1254_s_at	-1.674883019	0.001296897	Decrease_in_adherent osmY; periplasmic protein ; K04065 hyperosmotically inducible periplasmic protein	sdv:SDY_4526
A4418_s_at	-1.670569339	0.015858537	Decrease_in_adherent himA; integration host factor alpha subunit ; K04764 integration host factor subunit alpha	kpu:KPI_3278
A0342_s_at	-1.670188935	0.008729221	Decrease_in_adherent NAD-binding domain-containing protein ; K07071	ecw:EcE24377A_2598
V5400_s_at	-1.670154781	0.029807069	Decrease_in_adherent glgC; glucose-1-phosphate adenyltransferase (EC:2.7.7.27); K00975 glucose-1-phosphate adenyltransferase [EC:2.7.7.27]	sdv:SDY_3576
A1196_s_at	-1.667538409	0.007773938	Decrease_in_adherent yghA; oxidoreductase ; K00540 [EC:1.-.-.-]	ssn:SSON_3147
F4396_s_at	-1.66553788	0.00520734	Decrease_in_adherent cpxP; periplasmic repressor CpxP ; K06006 periplasmic protein CpxP	ecm:ECMS35_4306
A4684_s_at	-1.66457765	0.043499133	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
APECO1_4078_s_at	-1.662837246	0.018768759	Decrease_in_adherent govR; glycine cleavage system transcriptional repressor ; K03567 glycine cleavage system transcriptional repressor	sdv:SDY_2668
b3984_s_at	-1.661343836	0.028468684	Decrease_in_adherent rplA; 50S ribosomal protein L1 ; K02863 large subunit ribosomal protein L1	sdv:SDY_3744
A2860_s_at	-1.660606553	0.034304115	Decrease_in_adherent dnaQ; DNA polymerase III subunit epsilon ; K02342 DNA polymerase III subunit epsilon [EC:2.7.7.7]	sdv:SDY_0234
b2495_s_at	-1.660176873	0.018793628	Decrease_in_adherent putative oxidoreductase ; K00537 arsenate reductase [EC:1.20.4.1]	sdv:SDY_2684
EC869_4790_s_at	-1.652659921	0.030456522	Decrease_in_adherent frr; ribosome recycling factor ; K02838 ribosome recycling factor	sdv:SDY_0188
A1496_s_at	-1.649927954	0.006473173	Decrease_in_adherent rpmC; 50S ribosomal protein L29 ; K02904 large subunit ribosomal protein L29	sbv:SbBS512_E3697
A0319_s_at	-1.648243579	0.00186106	Decrease_in_adherent nuoJ; NADH dehydrogenase subunit I (EC:1.6.9.5); K00338 NADH dehydrogenase I subunit I [EC:1.6.5.3]	sbv:SbBS512_E2657
A3463_s_at	-1.646884328	0.003998547	Decrease_in_adherent ybhF; fused putative transporter subunits of ABC superfamily; ATP-binding components	eoh:ECO103_0830
EC869_3558_s_at	-1.646477528	0.013250556	Decrease_in_adherent ybiK; L-asparaginase ; K13051 beta-aspartyl-peptidase (threonine type) [EC:3.4.19.5]	sbo:SBO_0718
A2456_s_at	-1.643800629	0.043460056	Decrease_in_adherent mpl; UDP-N-acetylmuramate-L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase; K02558 UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate	eqj:EC026_5400
c0827_s_at	-1.64344264	0.00298906	Decrease_in_adherent hypothetical protein; K03295 cation efflux system protein, CDF family	ecc:c0827
V3607_s_at	-1.64199898	0.009626584	Decrease_in_adherent hypothetical protein	sdv:SDY_2683
EC869_0939_s_at	-1.641897636	0.015231576	Decrease_in_adherent NADH dehydrogenase subunit K ; K00340 NADH dehydrogenase I subunit K [EC:1.6.5.3]	cko:CKO_00517
A1018_s_at	-1.641578359	0.015790553	Decrease_in_adherent gshB; glutathione synthetase (EC:6.3.2.3); K01920 glutathione synthase [EC:6.3.2.3]	ssn:SSON_3101
A2040_s_at	-1.640824428	0.028016348	Decrease_in_adherent tsaB; twin arginine translocase protein A ; K03116 sec-independent protein translocase protein TsaA	sdv:SDY_3907
V5388_s_at	-1.639835903	0.001289259	Decrease_in_adherent asd; aspartate-semialdehyde dehydrogenase (EC:1.2.1.11); K00133 aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]	sbv:SbBS512_E3891
V2945_s_at	-1.639605229	0.034531355	Decrease_in_adherent ygdP; dinucleoside polyphosphate hydrolase ; K06311 putative (di)nucleoside polyphosphate hydrolase [EC:3.6.1.-]	sdv:SDY_3047
V3168_s_at	-1.639068669	0.00744064	Decrease_in_adherent nuoL; NADH:ubiquinone oxidoreductase, membrane subunit L ; K00341 NADH dehydrogenase I subunit L [EC:1.6.5.3]	eqj:EC026_3266
SDY_2200_s_at	-1.639027288	0.007821037	Decrease_in_adherent hypothetical protein	sdv:SDY_2200
A2631_s_at	-1.637981709	0.006741756	Decrease_in_adherent nmpR; nicotinamide-nucleotide adenyltransferase (EC:2.7.7.1); K00952 nicotinamide-nucleotide adenyltransferase [EC:2.7.7.1]; K06210 ribosylnicotinamide kinase	sbv:SbBS512_E4937
S55_2456_s_at	-1.637671106	0.007244861	Decrease_in_adherent sadA; hypothetical protein ; K06186 small protein A	sdv:SDY_2790
SD1_3251_s_at	-1.633291994	0.00187194	Decrease_in_adherent tyrS; tyrosyl-tRNA synthetase (EC:6.1.1.1); K01866 tyrosyl-tRNA synthetase [EC:6.1.1.1]	sdv:SDY_1860
V6884_s_at	-1.630586981	0.028966892	Decrease_in_adherent visC; hypothetical protein	sdv:SDY_3175
A2716_s_at	-1.628467841	0.024876342	Decrease_in_adherent leuD; isopropylmalate isomerase small subunit (EC:4.2.1.33); K01704 3-isopropylmalate/(R)-2-methylmalate dehydratase [EC:4.2.1.33]	sbv:SbBS512_E0065
F1141_s_at	-1.627461808	6.53E-05	Decrease_in_adherent hypothetical protein	ecc:c1317
EC536_5731_s_at	-1.62676711	0.027296643	Decrease_in_adherent ycgR; hypothetical protein	sdv:SDY_1233
A3063_s_at	-1.625451342	0.00036009	Decrease_in_adherent yajD; hypothetical protein	sdv:SDY_0324
V7379_s_at	-1.625431337	0.034998557	Decrease_in_adherent putative 5-methylcytosine-specific restriction enzyme with GTPase activity (EC:3.1.21.-)	efe:EFER_3105
EC869_0561_x_at	-1.620945162	0.046831121	Decrease_in_adherent yhiQ; putative methyltransferase	ecw:APECO1_2956
V0207_s_at	-1.620246915	0.010707431	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA

SD1_0307_s_at	-1.618824902	0.002112564	Decrease_in_adherent tref; trehalase [EC:3.2.1.28]; K01194 alpha,alpha-trehalase [EC:3.2.1.28]	sbcsbBS512_E3922
V4574_s_at	-1.615711834	0.016828519	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
F1250_s_at	-1.614756871	0.022446867	Decrease_in_adherent ycgJ; hypothetical protein	ect:ECIAI39_1896
EC869_0750_s_at	-1.613928965	0.019775783	Decrease_in_adherent yhjL; putative oxidoreductase subunit	sbo:SBO_3529
SDY_3666_x_at	-1.611179373	0.013121289	Decrease_in_adherent yhgG; hypothetical protein; K07490 ferrous iron transport protein C	sdysDY_3666
S3180_s_at	-1.610551158	0.012360849	Decrease_in_adherent reverse transcriptase-like protein	sfx:S3180
L1644_s_at	-1.608944878	0.047583691	Decrease_in_adherent mvpT; putative post-segregational killing toxin	eqj:ECO26_3521
A1581_s_at	-1.607631668	0.000117617	Decrease_in_adherent feoA; ferrous iron transport protein A; K04758 ferrous iron transport protein A	cko:CKO_04830
V4620_s_at	-1.602980588	0.007642838	Decrease_in_adherent htrA; serine endoprotease; K04771 serine protease Do [EC:3.4.21.107]	sdysDY_0178
EC536_0055_s_at	-1.598889469	0.002910206	Decrease_in_adherent galactokinase; K00849 galactokinase [EC:2.7.1.6]	cko:CKO_02378
A0182_s_at	-1.594864655	0.001786827	Decrease_in_adherent odd; cytidine deaminase [EC:3.5.4.5]; K01489 cytidine deaminase [EC:3.5.4.5]	sbcsbBS512_E0828
SB5_1853_s_at	-1.592131549	0.003154844	Decrease_in_adherent tkb; transketolase [EC:2.2.1.1]; K00615 transketolase [EC:2.2.1.1]	sfx:S2658
D3279_s_at	-1.584015188	0.000629456	Decrease_in_adherent DNA-binding transcriptional repressor AIIr; K10973 IclR family transcriptional regulator, negative regulator of allantoin and glyoxylate utilization operons	ecy:ECSE_0532
A1959_s_at	-1.574342741	0.0406893871	Decrease_in_adherent rbsB; D-ribose transporter subunit RbsB; K10439 ribose transport system substrate-binding protein	efe:EFER_4050
F4817_s_at	-1.573817653	0.032808649	Decrease_in_adherent ppa; inorganic pyrophosphatase [EC:3.6.1.1]; K01507 inorganic pyrophosphatase [EC:3.6.1.1]	sdysDY_4462
A3247_s_at	-1.57347258	0.011952844	Decrease_in_adherent rna; ribonuclease I [EC:3.1.27.6]; K01169 ribonuclease I (enterobacter ribonuclease) [EC:3.1.27.6]	ebr:ECB_00579
V1601_s_at	-1.573302778	0.012362428	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_3950_s_at	-1.570580555	0.004100288	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V7152_s_at	-1.570445107	0.006795561	Decrease_in_adherent nfnB; dihydropteridine reductase [EC:1.5.1.34]; K10679 nitroreductase / dihydropteridine reductase [EC:1.5.1.34]	sdysDY_0491
EC869_3782_s_at	-1.56922404	0.024451685	Decrease_in_adherent rplD; 50S ribosomal protein L4; K02926 large subunit ribosomal protein L4	cko:CKO_04737
A0318_s_at	-1.566668235	7.13E-05	Decrease_in_adherent nuoJ; NADH dehydrogenase subunit J [EC:1.6.5.3]; K00339 NADH dehydrogenase I subunit J [EC:1.6.5.3]	sdysDY_2476
V7078_s_at	-1.566444587	0.0446761	Decrease_in_adherent yebZ; putative inner membrane protein; K07245 putative copper resistance protein D	eqj:ECO26_2678
EC869_8837_s_at	-1.564933419	0.013311508	Decrease_in_adherent glx; glutamyl-tRNA synthetase [EC:6.1.1.17]; K01885 glutamyl-tRNA synthetase [EC:6.1.1.17]	sdysDY_2600
A4682_s_at	-1.563538727	0.02056037	Decrease_in_adherent aspS; aspartyl-tRNA synthetase [EC:6.1.1.12]; K01876 aspartyl-tRNA synthetase [EC:6.1.1.12]	sbcsbBS512_E1106
M2167_x_at	-1.563230134	0.000105127	Decrease_in_adherent endopeptidase; K01423 [EC:3.4.-.-]	sfv:SFV_0211
SD1_2278_s_at	-1.562644161	0.001438625	Decrease_in_adherent lysA; diaminopimelate decarboxylase [EC:4.1.1.20]; K01586 diaminopimelate decarboxylase [EC:4.1.1.20]	ssn:SSON_2998
F1202_s_at	-1.562611776	0.023097768	Decrease_in_adherent ycfM; hypothetical protein; K07337 hypothetical protein	sdysDY_2045
V2049_s_at	-1.557026845	0.044372267	Decrease_in_adherent yqjE; hypothetical protein	sdysDY_3286
b3790_s_at	-1.55405187	0.000342611	Decrease_in_adherent wecD; TDP-fucosamine acetyltransferase	sdysDY_3958
A0673_at	-1.553787164	0.00353486	Decrease_in_adherent hypothetical protein	ecw:EC24377A_2927
A1031_s_at	-1.553122467	0.0010645	Decrease_in_adherent yggL; hypothetical protein; K09923 hypothetical protein	sdysDY_3113
SB5_0774_s_at	-1.552329206	0.029086134	Decrease_in_adherent hypothetical protein	ecw:EC24377A_4522
A1489_s_at	-1.550311605	0.032378708	Decrease_in_adherent rplR; 50S ribosomal protein L18; K02881 large subunit ribosomal protein L18	cko:CKO_04717
UT189_C1546_s_at	-1.549705743	0.025794832	Decrease_in_adherent hypothetical protein	ecz:ECSS8_1415
V2162_s_at	-1.54565621	0.048811663	Decrease_in_adherent lldD; protease TldD; K03568 TldD protein	ssn:SSON_3386
EC869_1162_s_at	-1.545442845	0.014010044	Decrease_in_adherent fabG; 3-oxoacyl-(acyl-carrier-protein) reductase [EC:1.1.1.100]; K00059 3-oxoacyl-(acyl-carrier protein) reductase [EC:1.1.1.100]	sdysDY_2057
c3048_s_at	-1.541308841	0.028353638	Decrease_in_adherent pepB; peptidase B; K07751 PepB aminopeptidase [EC:3.4.11.23]	efl:LF8_1612
A3801_s_at	-1.538598788	0.002038787	Decrease_in_adherent rme; RNase E; endoribonuclease for rRNA processing and mRNA degradation; K08300 ribonuclease E [EC:3.1.26.12]	hde:HDEF_0352
EC869_5510_s_at	-1.535793921	0.039951071	Decrease_in_adherent accD; acetyl-CoA carboxylase biotin carboxylase subunit [EC:6.4.1.2]; K01946 biotin carboxylase [EC:6.3.4.14]; K01961 acetyl-CoA carboxylase, biotin carboxylase subunit	sdysDY_3433
A0328_s_at	-1.53577289	0.037978916	Decrease_in_adherent aminotransferase AlaT; K10907 aminotransferase [EC:2.6.1.-]	sbcsbBS512_E2666
EC536_2685_s_at	-1.535636951	0.032191106	Decrease_in_adherent hypothetical protein	ecc:c0222
b2021_s_at	-1.53517466	0.0131934	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V4101_s_at	-1.517120241	0.012831768	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A1555_s_at	-1.515672113	0.034084815	Decrease_in_adherent gph; phosphoglycolate phosphatase [EC:3.1.3.18]; K01091 phosphoglycolate phosphatase [EC:3.1.3.18]	ecw:EC24377A_3854
A1014_s_at	-1.512656986	3.42E-05	Decrease_in_adherent galP; galactose-proton symport of transport system; K08137 MFS transporter, SP family, galactose:H+ symporter	sdysDY_3129
SF0484_s_at	-1.512613447	0.009793291	Decrease_in_adherent iso-1S10R ORF	sfi:SF0484
SD1_1427_x_at	-1.51200961	0.003420286	Decrease_in_adherent rne; fused ribonucleaseE: endoribonuclease/RNA-binding protein/RNA degradosome binding protein; K08300 ribonuclease E [EC:3.1.26.12]	ebw:BWG_0932
V5454_s_at	-1.511963768	0.001216156	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SB5_0443_s_at	-1.505323053	0.008964842	Decrease_in_adherent rrdG; anaerobic ribonucleotide reductase-activating protein; K04068 anaerobic ribonucleoside-triphosphate reductase activating protein [EC:1.97.1.4]	sdysDY_4256
b1207_s_at	-1.503362575	0.001230121	Decrease_in_adherent prsA; ribose-phosphate pyrophosphokinase [EC:2.7.6.1]; K00948 ribose-phosphate pyrophosphokinase [EC:2.7.6.1]	sdysDY_1256
D4502_s_at	-1.503128248	0.040351391	Decrease_in_adherent putative relaxase/mobilization nuclease domain protein	seh:SeHA_A0074
A2816_s_at	-1.499793395	0.029358933	Decrease_in_adherent hypothetical protein	ecv:APEC01_1817
G3295_s_at	-1.499699747	0.047939484	Decrease_in_adherent prc; carboxy-terminal protease [EC:3.4.21.102]; K03797 carboxyl-terminal processing protease [EC:3.4.21.102]	sdysDY_1978
G1166_s_at	-1.499641713	0.009425926	Decrease_in_adherent hypothetical protein	ecz:ECSS8_1415
b2217_s_at	-1.496938981	0.018232624	Decrease_in_adherent transcriptional regulator RcsB; K07687 two-component system, NarL family, captular synthesis response regulator RcsB	cko:CKO_00553
SFV_2319_s_at	-1.496934695	0.015199342	Decrease_in_adherent competence damage-inducible protein A; K03742 competence/damage-inducible protein ClnA	ssn:SSON_2310
A0802_s_at	-1.492762397	0.006715908	Decrease_in_adherent cysH; phosphoadenosine phosphosulfate reductase [EC:1.8.4.8]; K00390 phosphoadenosine phosphosulfate reductase [EC:1.8.4.8]	sfx:S2971
A0900_s_at	-1.489741478	0.042506358	Decrease_in_adherent acetyl-CoA acetyltransferase [EC:2.3.1.-]; K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	ecw:EC24377A_3166
A3788_s_at	-1.488068149	0.031033762	Decrease_in_adherent flgM; anti-sigma28 factor FlgM; K02398 negative regulator of flagellin synthesis FlgM	sdysDY_2081
A1490_s_at	-1.487594768	0.039986565	Decrease_in_adherent hypothetical protein	ecti:UTI89_C3754
V0964_s_at	-1.486493736	0.017878764	Decrease_in_adherent hypothetical protein	sbcsbBS512_E3562
H3457_x_at	-1.486301116	0.013044112	Decrease_in_adherent yhgG; hypothetical protein; K07490 ferrous iron transport protein C	sfv:SFV_3415
V1302_s_at	-1.482902183	0.003892638	Decrease_in_adherent putative ABC transporter ATP-binding protein	cko:CKO_03395
V3622_x_at	-1.481767453	0.000542033	Decrease_in_adherent purN; phosphoribosylglycinamide formyltransferase [EC:2.1.2.2]; K1175 phosphoribosylglycinamide formyltransferase 1 [EC:2.1.2.2]	sdysDY_2689
SD1_3080_s_at	-1.48160651	0.048184272	Decrease_in_adherent proline dipeptidase; K10271 X-Pro dipeptidase [EC:3.4.13.9]	cko:CKO_00190
A2772_s_at	-1.480144803	0.000330759	Decrease_in_adherent yadH; hypothetical protein; K09686 antibiotic transport system permease protein	sdysDY_0037
SB5_0350_s_at	-1.47770482	0.01261471	Decrease_in_adherent ppiA; peptidyl-prolyl cis-trans isomerase A (rotamase A); K03767 peptidyl-prolyl cis-trans isomerase A (cyclophilin A) [EC:5.2.1.8]	sdysDY_3525
A2392_s_at	-1.476684965	0.045619405	Decrease_in_adherent hflC; FtsH protease regulator HflC [EC:3.4.-.-]; K04087 membrane protease subunit HflC [EC:3.4.-.-]	sbcsbBS512_E4706
V1059_s_at	-1.476004659	2.13E-05	Decrease_in_adherent acrB; acridine efflux pump; K03296 hydrophobic/ampiphilic exporter-1 (mainly G-bacteria), HAE1 family	sbo:SBO_0362
EC869_8432_s_at	-1.474526348	0.013634391	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0419_s_at	-1.470270858	0.002334464	Decrease_in_adherent glk; glucokinase [EC:2.7.1.2]; K00845 glucokinase [EC:2.7.1.2]	sdysDY_2587
A1747_s_at	-1.469933919	0.011867449	Decrease_in_adherent glyS; glycyl-tRNA synthetase subunit beta [EC:6.1.1.14]; K01879 glycyl-tRNA synthetase beta chain [EC:6.1.1.14]	sbcsbBS512_E3966
M4990_s_at	-1.469123938	0.005769444	Decrease_in_adherent trxB; thioredoxin reductase; K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]	sdysDY_2373
V5015_s_at	-1.467849712	0.000840522	Decrease_in_adherent lldR; DNA-binding transcriptional repressor LldR	sdysDY_4037

ECs4252_x_at	-1.466875815	0.021817694	Decrease_in_adherent yhgG; hypothetical protein ; K07490 ferrous iron transport protein C	sdv:SDY_3666
A1609_s_at	-1.466437685	0.045707056	Decrease_in_adherent glgB; glycogen branching enzyme (EC:2.4.1.18); K00700 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	ssn:SSON_3672
C4081_s_at	-1.460249079	0.0173055029	Decrease_in_adherent hypothetical protein	sec:SC3369
V2948_x_at	-1.458680255	0.000358291	Decrease_in_adherent hchA; chaperone protein HchA ; K05523 molecular chaperone HchA (Hsp31)	sb:SBBS512_E0916
A0983_s_at	-1.45543652	0.034056859	Decrease_in_adherent mscS; mechanosensitive channel MscS ; K03442 small conductance mechanosensitive ion channel, MscS family	sb:SBBS512_E3349
ECP_0709_s_at	-1.455034748	0.005808913	Decrease_in_adherent pgm; phosphoglucomutase ; K01835 phosphoglucomutase [EC:5.4.2.2]	efl:LF82_1632
V4600_s_at	-1.449635547	0.022731442	Decrease_in_adherent ppa; inorganic pyrophosphatase (EC:3.6.1.1); K01507 inorganic pyrophosphatase [EC:3.6.1.1]	sdv:SDY_4462
V0762_s_at	-1.449488602	0.03972489	Decrease_in_adherent pepG; proline dipeptidase ; K01271 X-Pro dipeptidase [EC:3.4.13.9]	sdv:SDY_3898
SS5_2237_x_at	-1.436151886	0.019050038	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
EC869_4066_s_at	-1.435257927	0.000489539	Decrease_in_adherent mukB; cell division protein MukB ; K03632 chromosome partition protein MukB	sdv:SDY_2334
V3982_s_at	-1.433665134	0.001818027	Decrease_in_adherent trpB; tryptophan synthase subunit beta (EC:4.2.1.20); K01696 tryptophan synthase beta chain [EC:4.2.1.20]	sfv:SFV_1275
V6739_s_at	-1.431673195	0.023568372	Decrease_in_adherent murC; UDP-N-acetylmuramate-L-alanine ligase; K01924 UDP-N-acetylmuramate-alanine ligase [EC:6.3.2.8]	eci:EcoIC_3566
b2185_s_at	-1.430873445	0.027531619	Decrease_in_adherent rplY; 50S ribosomal protein L25 ; K02897 large subunit ribosomal protein L25	sdv:SDY_0894
A1637_s_at	-1.429790984	0.004630401	Decrease_in_adherent hypothetical protein	eci:ECIAI1_3605
V1006_s_at	-1.428956047	0.038981148	Decrease_in_adherent purB; adenylosuccinate lyase (EC:4.3.2.2); K01756 adenylosuccinate lyase [EC:4.3.2.2]	pha:PSHAA1692
UT189_C1474_x_at	-1.423761073	0.025354675	Decrease_in_adherent putative cell killing protein encoded within cryptic prophage CP-933M	eci:UT189_C1474
A0055_x_at	-1.420576362	0.006661997	Decrease_in_adherent hisD; histidinol dehydrogenase (EC:1.1.1.23); K00013 histidinol dehydrogenase [EC:1.1.1.23]	ebi:ECB_01922
EC869_5557_x_at	-1.41825009	0.019302237	Decrease_in_adherent argI; ornithine carbamoyltransferase subunit I (EC:2.1.3.3); K00611 ornithine carbamoyltransferase [EC:2.1.3.3]	sbo:SBO_4188
A0826_s_at	-1.417853609	0.034427831	Decrease_in_adherent chpR; antitoxin MazE ; K07172	sdv:SDY_3000
V1239_s_at	-1.414461334	6.96E-05	Decrease_in_adherent ribosomal protein S1 ; K02945 small subunit ribosomal protein S1	dze:Dd1591_2339
V4019_s_at	-1.413029343	0.015329926	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
b2431_s_at	-1.408537822	0.000325019	Decrease_in_adherent ybi110; hypothetical protein	ebi:B21_02292
V1149_s_at	-1.407658168	0.019037174	Decrease_in_adherent purK; phosphoribosylaminoimidazole carboxylase ATPase subunit (EC:4.1.1.21); K01589 5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]	sdv:SDY_0274
SS5_3158_x_at	-1.406770266	0.002876811	Decrease_in_adherent yhgG; hypothetical protein ; K07490 ferrous iron transport protein C	ssn:SSON_3541
UT189_C2914_x_at	-1.401255607	0.002160836	Decrease_in_adherent hypothetical protein	eci:UT189_C2914
V1262_s_at	-1.396509388	0.008070028	Decrease_in_adherent FadR; fatty acid metabolism regulator ; K03603 GntR family transcriptional regulator, negative regulator for Fad regulon and positive regulator of fabA	sdv:SDY_1224
V3422_s_at	-1.394840204	0.005760149	Decrease_in_adherent kefG; glutathione-regulated potassium-efflux system ancillary protein KefG ; K11748 glutathione-regulated potassium-efflux system ancillary protein KefG	efe:EFER_3322
EC869_4608_x_at	-1.394020095	0.000802993	Decrease_in_adherent pgm; phosphoglucomutase (EC:5.4.2.2); K01835 phosphoglucomutase [EC:5.4.2.2]	sdv:SDY_0628
EC869_1169_s_at	-1.391775867	0.008386427	Decrease_in_adherent fabF; 3-oxoacyl-(acyl carrier protein) synthase ; K00458 3-oxoacyl-(acyl-carrier-protein) synthase II [EC:2.3.1.179]	kpu:KP1_2084
D3528_s_at	-1.387158144	0.010391819	Decrease_in_adherent predicted hydrolase	ech:ECO103_p46
SFV_3581_s_at	-1.384897698	0.038346051	Decrease_in_adherent cpxR; DNA-binding transcriptional regulator CpxR ; K07662 two-component system, OmpR family, response regulator CpxR	sdv:SDY_3834
V6992_s_at	-1.381446465	0.037470992	Decrease_in_adherent hypothetical protein ; K05875 methyl-accepting chemotaxis protein II, aspartate sensor receptor	cko:CKO_01066
EC869_0400_s_at	-1.379860992	0.030307901	Decrease_in_adherent yhcG; glutathione branching enzyme ; K00700 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	cko:CKO_04851
A1375_s_at	-1.378988349	0.001189673	Decrease_in_adherent glmM; phosphoglucoamine mutase (EC:5.4.2.10); K03431 phosphoglucoamine mutase [EC:5.4.2.10]	sb:SBBS512_E3594
F4327_s_at	-1.377559528	7.52E-05	Decrease_in_adherent hypothetical protein	bmi:BMULJ_05092
A0497_s_at	-1.376358846	0.024269837	Decrease_in_adherent bcp; thioredoxin-dependent thiol peroxidase (EC:1.11.1.7); K03564 peroxiredoxin Q/BPC [EC:1.11.1.15]	sdv:SDY_2669
A3580_at	-1.375927391	7.59E-05	Decrease_in_adherent Cl; bacteriophage CI repressor protein	yen:YE0854
EC869_5021_s_at	-1.374536213	0.018790494	Decrease_in_adherent sdhD; succinate dehydrogenase cytochrome b556 small membrane subunit (EC:1.3.5.1); K00242 succinate dehydrogenase hydrophobic membrane anchor protein [EC:1.3.5.1]	sdv:SDY_0660
V4970_s_at	-1.367880322	0.033697774	Decrease_in_adherent rfaG; lipopolysaccharide core biosynthesis protein RfaG ; K02844 UDP-glucose:(heptosyl)lPS alpha-1,3-glucosyltransferase [EC:2.4.1.-]	sb:SBBS512_E4056
A3498_s_at	-1.366841776	2.65E-06	Decrease_in_adherent moeB; molybdopterin biosynthesis protein MoeB; K03751 molybdopterin biosynthesis protein MoeB	eci:ECIAI1_0865
EC869_5202_s_at	-1.36535142	0.025559543	Decrease_in_adherent secA, azi, div; preprotein translocase subunit SecA ; K03070 preprotein translocase subunit SecA	sdv:SDY_0128
c5600_s_at	-1.36506866	0.002361873	Decrease_in_adherent ybi4; hypothetical protein	ebi:B21_00199
b3231_s_at	-1.363362691	0.04746774	Decrease_in_adherent rplM; 50S ribosomal protein L13; K02871 large subunit ribosomal protein L13	sfv:SFV_3258
V1915_s_at	-1.362847507	0.042974055	Decrease_in_adherent hflB; ATP-dependent metalloprotease (EC:3.4.24.-); K03798 cell division protease FtsH [EC:3.4.24.-]	sb:SBBS512_E3592
SFV_1321_x_at	-1.359732447	0.000646949	Decrease_in_adherent pspD; peripheral inner membrane phage-shock protein; K03971 phage shock protein D	sfv:SFV_1321
V1240_s_at	-1.357029198	0.01851577	Decrease_in_adherent ribosomal protein S1 ; K02945 small subunit ribosomal protein S1	dze:Dd1591_2339
V3161_s_at	-1.353179025	0.001248454	Decrease_in_adherent nuoH; NADH dehydrogenase subunit H (EC:1.6.5.3); K00337 NADH dehydrogenase I subunit H [EC:1.6.5.3]	sdv:SDY_2478
F0029_s_at	-1.352976214	0.000519044	Decrease_in_adherent lrpA; lipoprotein signal peptidase ; K03101 signal peptidase II [EC:3.4.23.36]	cko:CKO_03365
A4488_s_at	-1.347928361	0.04337477	Decrease_in_adherent ynhE; cysteine desulfurase activator complex subunit SufB ; K09014 Fe-S cluster assembly protein SufB	sbo:SBO_1447
F2472_s_at	-1.347633567	0.004372622	Decrease_in_adherent yejK; nucleoid-associated protein NdpA ; K06899	sdv:SDY_0893
A0051_s_at	-1.341481933	0.048258759	Decrease_in_adherent NAD dependent epimerase/dehydratase family protein	sb:SBBS512_E1216
A0351_s_at	-1.336885598	0.038534518	Decrease_in_adherent cvpA; colicin V production protein ; K03558 membrane protein required for colicin V production	sdv:SDY_2512
K0352_x_at	-1.332610653	0.002205339	Decrease_in_adherent pspD; peripheral inner membrane phage-shock protein; K03971 phage shock protein D	sfv:SFV_1321
S3181_s_at	-1.329085313	0.043404387	Decrease_in_adherent reverse transcriptase-like protein	sfx:SC3181
b3724_s_at	-1.328972427	0.016432199	Decrease_in_adherent PhoU; transcriptional regulator PhoU ; K02039 phosphate transport system protein	sdv:SDY_4026
EC869_2084_s_at	-1.320832723	0.011951317	Decrease_in_adherent dsbE; disulfide oxidoreductase ; K02199 cytochrome c biogenesis protein CcmG, thiol:disulfide interchange protein DsbE	eci:EC026_1059
SD1_3598_s_at	-1.319774457	0.000886451	Decrease_in_adherent galM; aldose 1-epimerase (EC:5.1.3.-); K01785 aldose 1-epimerase [EC:5.1.3.3]	sb:SBBS512_E0677
SBO_3496_s_at	-1.318700453	2.23E-05	Decrease_in_adherent prfC; oligopeptidase A (EC:3.4.24.70); K01414 oligopeptidase A [EC:3.4.24.70]	sb:SBBS512_E3824
A1046_s_at	-1.318693895	0.002082045	Decrease_in_adherent conserved hypothetical protein, putative ATPase	eci:EC55989_3266
b3410_x_at	-1.306944873	0.035894927	Decrease_in_adherent yhgG; hypothetical protein ; K07490 ferrous iron transport protein C	sdv:SDY_3666
b0932_s_at	-1.306762313	0.006666602	Decrease_in_adherent pepN; aminopeptidase N; K01256 aminopeptidase N [EC:3.4.11.2]	sdv:SDY_4532
b2701_s_at	-1.305840898	0.004214056	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A2257_s_at	-1.302553983	0.031326228	Decrease_in_adherent dgkA; diacylglycerol kinase ; K00901 diacylglycerol kinase [EC:2.7.1.107]	sdv:SDY_4532
c5177_x_at	-1.296694604	0.049308095	Decrease_in_adherent transposase ORF A, IS629	eum:ECUMN_3344
A4704_s_at	-1.293289749	0.031506872	Decrease_in_adherent tap; methyl-accepting protein IV ; K05877 methyl-accepting chemotaxis protein IV, peptide sensor receptor	eci:EC55989_2064
A0425_s_at	-1.289034515	0.038075711	Decrease_in_adherent yfeC; hypothetical protein	sdv:SDY_2596
V3565_s_at	-1.287184317	0.044534512	Decrease_in_adherent lipoprotein ; K07287 lipoprotein-34	cko:CKO_00310
V4999_s_at	-1.278108993	0.005619417	Decrease_in_adherent gpsA; NAD(P)H-dependent glycerol-3-phosphate dehydrogenase (EC:1.1.1.94); K00057 glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94]	sdv:SDY_4041
EC869_5075_s_at	-1.276111271	0.022987137	Decrease_in_adherent ybgF; tol-pal system protein YbgF	sdv:SDY_0690
A1830_s_at	-1.274969161	0.030880942	Decrease_in_adherent rpmB; 50S ribosomal protein L28 ; K02902 large subunit ribosomal protein L28	kpu:KP1_5329
V0699_s_at	-1.274175671	0.003017889	Decrease_in_adherent odd; cytidine deaminase (EC:3.5.4.5); K01489 cytidine deaminase [EC:3.5.4.5]	sdv:SDY_2144
A3567_s_at	-1.272593596	0.024739197	Decrease_in_adherent loaA; outer-membrane lipoprotein carrier protein ; K03634 outer membrane lipoproteins carrier protein	sdv:SDY_2370
SD1_2877_s_at	-1.270011878	2.99E-05	Decrease_in_adherent ndh; NADH dehydrogenase ; K03885 NADH dehydrogenase [EC:1.6.99.3]	efl:LF82_1473
A2005_x_at	-1.269957705	0.006571728	Decrease_in_adherent cyaY; frataxin-like protein ; K06202 CyaY protein	sdv:SDY_3938

A1483_s_at	-1.266537953	0.048495492	Decrease_in_adherent rpsM; 30S ribosomal protein S13 ; K02952 small subunit ribosomal protein S13	sdv:SDY_3474
V2172_s_at	-1.266170259	0.037382652	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A1502_s_at	-1.266108751	0.038820682	Decrease_in_adherent rplD; 50S ribosomal protein L4 ; K02926 large subunit ribosomal protein L4	cko:CKO_04737
LH0104_s_at	-1.26564423	0.009265475	Decrease_in_adherent hypothetical protein	ssn:SSON_2657
A2762_s_at	-1.257837263	0.038059153	Decrease_in_adherent acnB; bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase (EC:4.2.1.3) ; K01682 aconitate hydratase 2 [EC:4.2.1.3]	ecv:APECO1_1867
A2012_s_at	-1.244440644	0.047570622	Decrease_in_adherent dapF; diaminopimelate epimerase ; K01778 diaminopimelate epimerase [EC:5.1.1.7]	cko:CKO_00151
V3621_s_at	-1.243691155	0.030401882	Decrease_in_adherent purM; phosphoribosylaminoimidazole synthetase (EC:6.3.3.1) ; K01933 phosphoribosylformylglycinamide cyclo-ligase [EC:6.3.3.1]	sdv:SDY_2688
V5728_s_at	-1.24293349	0.00322537	Decrease_in_adherent ybhQ; cardiolipin synthase 2 ; K06132 putative cardiolipin synthase [EC:2.7.8.-]	ssn:SSON_0768
V1348_s_at	-1.240402883	0.000157893	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
A0075_s_at	-1.24031424	0.030839293	Decrease_in_adherent rfdD; dTDP-4-dehydrodihydroxymose reductase (EC:1.1.1.133) ; K00067 dTDP-4-dehydrodihydroxymose reductase [EC:1.1.1.133]	sdv:SDY_2205
V6893_s_at	-1.239795762	0.00927362	Decrease_in_adherent proline aminopeptidase P II ; K01262 X-Pro aminopeptidase [EC:3.4.11.9]	spe:Spro_3919
A2812_s_at	-1.235755121	0.016728941	Decrease_in_adherent dapD; 2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase (EC:2.3.1.117) ; K00674 2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase [EC:2.3.1.117]	ssn:SSON_0178
V4018_s_at	-1.235716075	0.000910819	Decrease_in_adherent aceE; pyruvate dehydrogenase subunit E1 ; K00163 pyruvate dehydrogenase E1 component [EC:1.2.4.1]	sdv:SDY_0144
V2140_s_at	-1.23439664	0.026424179	Decrease_in_adherent glnE; fused deadenylyltransferase/adenylyltransferase for glutamine synthetase (EC:2.7.7.42) ; K00982 glutamate-ammonia-ligase adenylyltransferase [EC:2.7.7.42]	ebr:ECB_02923
A2419_s_at	-1.233505856	0.024756835	Decrease_in_adherent ribosomal protein S18 ; K02963 small subunit ribosomal protein S18	dze:Dd1591_0776
S3755_s_at	-1.232185082	0.00979944	Decrease_in_adherent cpxP; periplasmic repressor CpxP ; K06006 periplasmic protein CpxP	sdv:SDY_3833
SF0983_s_at	-1.228504688	0.001380453	Decrease_in_adherent yccK; cryptic autophosphorylating protein tyrosine kinase Etk; K00903 protein-tyrosine kinase [EC:2.7.10.-]	svf:SFV_0990
EC869_5429_x_at	-1.227827603	0.001898147	Decrease_in_adherent gltB; glutamate synthase subunit alpha (EC:1.4.7.1) ; K00265 glutamate synthase (NADPH/NADH) large chain [EC:1.4.1.13 1.4.1.14]	spe:Spro_4344
A0426_s_at	-1.227353622	0.018615751	Decrease_in_adherent hypothetical protein	sko:SbBS512_E2780
A2277_s_at	-1.226740079	0.004625819	Decrease_in_adherent soxS; DNA-binding transcriptional regulator SoxS	sbk:SbBS512_E4580
pCoo054_at	-1.225311047	0.001701831	Decrease_in_adherent EAL domain-containing protein	ecw:EcE24377A_E0053
V4379_s_at	-1.221016158	0.006201903	Decrease_in_adherent serC; phosphoserine aminotransferase (EC:2.6.1.52) ; K00831 phosphoserine aminotransferase [EC:2.6.1.52]	sdv:SDY_2354
V5274_s_at	-1.220174611	0.017042977	Decrease_in_adherent hypothetical protein	ecy:ECSE_3781
EC869_8838_s_at	-1.219412421	0.001321564	Decrease_in_adherent gltX; glutamyl-tRNA synthetase (EC:6.1.1.17) ; K01885 glutamyl-tRNA synthetase [EC:6.1.1.17]	sdv:SDY_2600
A3348_s_at	-1.218449509	0.007152863	Decrease_in_adherent putative carboxylase	ecy:ECSE_0771
EC869_8932_s_at	-1.217801171	1.50E-05	Decrease_in_adherent yihA; GTP-binding protein; K03978 GTP-binding protein	etw:ECSP_4917
c3479_s_at	-1.212392537	0.015891651	Decrease_in_adherent ygfZ; tRNA-modifying protein YgfZ ; K06980	efl:LF82_3181
V3098_s_at	-1.207095442	0.027877656	Decrease_in_adherent folC; bifunctional folypolyglutamate synthase/dihydrofolate synthase ; K11754 dihydrofolate synthase / folypolyglutamate synthase [EC:6.3.2.12 6.3.2.17]	sdv:SDY_2514
EC536_3670_s_at	-1.202731057	0.006785392	Decrease_in_adherent ynfJ; F0F1 ATP synthase subunit gamma (EC:3.6.3.14) ; K02115 F-type H+-transporting ATPase subunit gamma [EC:3.6.3.14]	sdv:SDY_4015
V3992_s_at	-1.201626798	0.009137986	Decrease_in_adherent trpD; bifunctional glutamine amidotransferase/anthranilate phosphoribosyltransferase (EC:4.1.1.48 2.4.2.18) ; K00766 anthranilate phosphoribosyltransferase [EC:2.4.2.18]	sdv:SDY_1331
V1968_s_at	-1.198305789	0.004807236	Decrease_in_adherent yraO; DnaA initiator-associating protein DiaA ; K12961 DnaA initiator-associating protein	sdv:SDY_3328
F0177_s_at	-1.196157086	0.006704544	Decrease_in_adherent map; methionine aminopeptidase (EC:3.4.11.18) ; K01265 methionyl aminopeptidase [EC:3.4.11.18]	sdv:SDY_0184
A2731_s_at	-1.192647391	0.03145615	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
D4754_at	-1.190980951	0.016605047	Decrease_in_adherent eltA; heat-labile enterotoxin A ; K10928 cholera enterotoxin subunit A [EC:2.4.2.36]	ecw:EcE24377A_F0200
ECP_3142_s_at	-1.190335155	2.95E-06	Decrease_in_adherent glnE; bifunctional glutamine-synthetase adenylyltransferase/deadenyltransferase (EC:2.7.7.42) ; K00982 glutamate-ammonia-ligase adenylyltransferase [EC:2.7.7.42]	ecm:ECMS35_3345
SD1_2241_s_at	-1.18889751	0.046653711	Decrease_in_adherent accD; acetyl-CoA carboxylase subunit beta (EC:6.4.1.2) ; K01963 acetyl-CoA carboxylase carboxyl transferase subunit beta [EC:6.4.1.2]	efe:EFER_0847
M3184_s_at	-1.184283739	0.01143769	Decrease_in_adherent gloA; glyoxalase I (EC:4.4.1.5) ; K01759 lactoylglutathione lyase [EC:4.4.1.5]	sdv:SDY_1877
A3128_s_at	-1.184105354	0.008183777	Decrease_in_adherent hypothetical protein	ecw:EcE24377A_0508
V6095_s_at	-1.181472555	0.010079964	Decrease_in_adherent hemB; delta-aminolevulinic acid dehydratase (EC:4.2.1.24) ; K01698 porphobilinogen synthase [EC:4.2.1.24]	sdv:SDY_0501
V4772_s_at	-1.179706204	0.024580595	Decrease_in_adherent hypothetical protein	ecc:c4661
EC869_2594_s_at	-1.176373753	0.04202338	Decrease_in_adherent tap; methyl-accepting protein IV ; K05877 methyl-accepting chemotaxis protein IV, peptide sensor receptor	sbk:SbBS512_E2178
V4146_s_at	-1.175757998	0.049824802	Decrease_in_adherent atpG; pyridoxine 5'-phosphate synthase ; K03474 pyridoxine 5-phosphate synthase [EC:2.6.99.2]	sdv:SDY_2805
A4706_s_at	-1.175649191	0.001084471	Decrease_in_adherent cheW; purine-binding chemotaxis protein ; K03408 purine-binding chemotaxis protein CheW	ssn:SSON_1230
L1795_s_at	-1.174698994	0.033124164	Decrease_in_adherent hypothetical protein	sbk:SbBS512_E3978
ECs2438_s_at	-1.158262929	0.038440527	Decrease_in_adherent katE; hydroperoxidase II (EC:1.11.1.6) ; K03781 catalase [EC:1.11.1.6]	ssn:SSON_1426
SD1_3011_s_at	-1.14985724	0.004130394	Decrease_in_adherent valS; valyl-tRNA synthetase (EC:6.1.1.9) ; K01873 valyl-tRNA synthetase [EC:6.1.1.9]	sdv:SDY_4282
SSO_3777_s_at	-1.149655133	0.003579688	Decrease_in_adherent waaP; putative LPS biosynthesis enzyme ; K02848 heptose (I) phosphotransferase [EC:2.7.1.-]	sdv:SDY_4060
A1670_s_at	-1.147302178	0.034678732	Decrease_in_adherent pyridine nucleotide-disulfide oxidoreductase family protein ; K07007	sbk:SbBS512_E3830
A0521_s_at	-1.142859492	0.001667926	Decrease_in_adherent purM; phosphoribosylaminoimidazole synthetase (EC:6.3.3.1) ; K01933 phosphoribosylformylglycinamide cyclo-ligase [EC:6.3.3.1]	sfz:S2692
EC869_1425_s_at	-1.139709873	0.037882686	Decrease_in_adherent ileS; isoleucyl-tRNA synthetase ; K01870 isoleucyl-tRNA synthetase [EC:6.1.1.5]	etw:ECSP_0027
A3821_s_at	-1.129238706	0.041689874	Decrease_in_adherent ycfL; hypothetical protein	ssn:SSON_1124
V5768_s_at	-1.127503983	0.00163158	Decrease_in_adherent ppc; phosphoenolpyruvate carboxylase (EC:4.1.1.31) ; K01595 phosphoenolpyruvate carboxylase [EC:4.1.1.31]	sdv:SDY_3791
V7305_s_at	-1.126382572	0.027733243	Decrease_in_adherent ycfQ; hypothetical protein	sdv:SDY_2039
SD1_1241_s_at	-1.125200375	0.002482889	Decrease_in_adherent dapA; dihydrodipicolinate synthase (EC:4.2.1.52) ; K01714 dihydrodipicolinate synthase [EC:4.2.1.52]	sbk:SbBS512_E2850
EC869_4505_s_at	-1.123788959	0.02349134	Decrease_in_adherent gpsA; NAD(P)H-dependent glycerol-3-phosphate dehydrogenase (EC:1.1.1.94) ; K00057 glycerol-3-phosphate dehydrogenase (NAD(P)+) [EC:1.1.1.94]	sdv:SDY_4041
V6221_s_at	-1.113975903	0.036602418	Decrease_in_adherent sfcA; malate dehydrogenase (EC:1.1.1.38) ; K00027 malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]	sbk:SbBS512_E1742
V5243_s_at	-1.107345451	0.044757195	Decrease_in_adherent putative ribonuclease ; K07058	sbk:SbBS512_E3927
J2890_s_at	-1.106794638	0.043520429	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
SFV_4186_s_at	-1.09285492	0.004952808	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
ECs4628_s_at	-1.092842741	0.014910755	Decrease_in_adherent hypothetical protein	sbk:SbBS512_E4231
A4379_s_at	-1.073183017	0.039722084	Decrease_in_adherent hypothetical protein	svf:SFV_1561
V2732_s_at	-1.071647334	0.005376436	Decrease_in_adherent glcB; malate synthase G ; K01638 malate synthase [EC:2.3.3.9]	eqj:EC026_4076
EC869_8661_s_at	-1.071215154	0.002807762	Decrease_in_adherent mutY; adenine DNA glycosylase ; K03575 A/G-specific adenine glycosylase [EC:3.2.2.-]	sdv:SDY_3111
c4182_s_at	-1.069136084	0.002660764	Decrease_in_adherent hypothetical protein	eci:UTI89_C3906
b1888_s_at	-1.062311544	0.010994281	Decrease_in_adherent CheA signal transduction histidine kinase ; K03407 two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3]	ebd:ECBD_1750
EC869_6920_x_at	-1.061030752	0.047938789	Decrease_in_adherent hisD; histidinol dehydrogenase (EC:1.1.1.23) ; K00013 histidinol dehydrogenase [EC:1.1.1.23]	sdv:SDY_2221
c5616_s_at	-1.056611508	0.002523634	Decrease_in_adherent cell-wall-associated hydrolase	bnj:BMULJ_05090
A0054_s_at	-1.054719384	0.004737493	Decrease_in_adherent hisG; ATP phosphoribosyltransferase (EC:2.4.2.17) ; K00765 ATP phosphoribosyltransferase [EC:2.4.2.17]	sbk:SbBS512_E1213
A1943_s_at	-1.049828382	0.003888365	Decrease_in_adherent F0F1 ATP synthase subunit C ; K02110 F-type H+-transporting ATPase subunit C [EC:3.6.3.14]	cko:CKO_00077
A1366_s_at	-1.049193552	0.003364984	Decrease_in_adherent rpsO; 30S ribosomal protein S15 ; K02956 small subunit ribosomal protein S15	sdv:SDY_3344
V4694_s_at	-1.048021915	0.045914199	Decrease_in_adherent wecF; putative common antigen polymerase ; K02853 4-alpha-L-fucosyltransferase [EC:2.4.1.-]	sdv:SDY_3954
EC869_0326_s_at	-1.046209808	0.048565499	Decrease_in_adherent envZ; osmolarity sensor protein; K07638 two-component system, OmpR family, osmolarity sensor histidine kinase EnvZ [EC:2.7.13.3]	etr:ETA_E_3278
c4454_s_at	-1.045579005	0.037909991	Decrease_in_adherent waaP; putative LPS biosynthesis enzyme ; K02848 heptose (I) phosphotransferase [EC:2.7.1.-]	sdv:SDY_4060
AFFX-18srRnac_at	-1.044832375	0.048021148	Decrease_in_adherent SORBIIDRAFT_1180s002020; hypothetical protein	sbi:SORBI_1180s002020

S1440_x_at	-1.036189081	0.004300838	Decrease_in_adherent NO_KEGG_DATA	NO_KEGG_DATA
V4048_s_at	-1.033956136	0.033841079	Decrease_in_adherent panD; aspartate alpha-decarboxylase (EC:4.1.1.11); K01579 aspartate 1-decarboxylase [EC:4.1.1.11]	sdY:SDY_0041
V4930_s_at	-1.012955618	0.011934188	Decrease_in_adherent yicE; putative transport protein	ssn:SSON_3751
SB5_0656_s_at	-1.006461186	0.037737665	Decrease_in_adherent phnA; hypothetical protein ; K06193 phosphonoacetate hydrolase [EC:3.11.1.2]	sdY:SDY_4109
V6732_s_at	-1.006087327	0.00541329	Decrease_in_adherent murD; UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase (EC:6.3.2.9); K01925 UDP-N-acetylmuramoylalanine--D-glutamate ligase [EC:6.3.2.9]	sdY:SDY_0118
V3104_s_at	-1.003712382	0.010162377	Decrease_in_adherent cvpA; colicin V production protein ; K03558 membrane protein required for colicin V production	sdY:SDY_2512
A3607_s_at	-1.000125606	0.000710167	Decrease_in_adherent ihfB; integration host factor subunit beta ; K05788 integration host factor subunit beta	sdY:SDY_2346