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## Appendices

### Appendix A: Global regulators and their regulated genes

#### ArcA/B:

+: *pfl*, *cydAB*

–: *aceBAK*, *aceEF*, *acnA*, *fumAC*, *gltA*, *icdA*, *lpdA*, *mdh*, *ptsG*, *sdhCDAB*, *cyo*

#### pdhR:

+: *aceEF*, *ndh*, *yfiD*

–: *cyoABCD*

#### Fur:

+: *hmp*

–: *cyoABCD*, *ompF*

#### Cra:

+: *aceA*, *acnA*, *fbp*, *icdA*, *pckA*, *ppsA*, *cydB*

–: *acnB*, *eda*, *edd*, *eno*, *gapA*, *pfkA*, *ptsHI*, *pykF*

#### Crp/Cya:

+: *mlc*, *aceEF*, *acnAB*, *crr*, *fumA*, *gltA*, *mdh*, *pckA*, *ptsG*, *ptsHI*, *sdhABCD*, *sucABCD*, *tpiA*, *ompF*, *rpoS*

–: *lpdA*, *aceBAK*, *acnA*, *cyoA*, *gdhA*, *glnAL*, *gltA*, *mdh*, *sdhCDAB*, *sodA*, *sucABCD*, *ugpA*,

#### Fnr:

+: *frd*, *pfl*, *ackA*, *ndh*, *nuoA*, *pstSCAB-phoU*, *yfiD*

–: *acnA*, *fumAC*, *icdA*, *lpdA*, *ptsG*, *sdhCDAB*, *talA*, *cyoABCD*, *cydAB*

#### PhoB:

+: *phoBR*, *phoA-psiF*, *asr*, *pstSCAB-phoU*

–: *phoH*, *phnCHN*, *ugpA*, *argP*

**RpoS:**

+: *gadA, gadB, osmB, sodC, talA, tktB, acs, poxB, acnA, fumC*

**SoxR/S:**

+: *sodA, zwf, rpoD, rpoS, fumC, tolC, micF, marA*

- : *rob*

**Mlc**

+: *ldhA*

- : *crr, ptsG, ptsH1, manXYZ, malT*

**GadE**

+: *gadE, gadXW*

- : *cyoABCDE, gltB*

## Appendix B: Metabolic pathway reactions and the corresponding enzymes and genes

	enzyme	gene	reactions
PTS			Glc+PEP→PYR+G6P
	El	<i>ptsI</i>	
	HPr	<i>ptsH</i>	
	EIIA	<i>crr</i>	
	EIICB	<i>ptsG</i>	
Glk	Glk	<i>glk</i>	
Glycolysis			
	Pgi	<i>pgi</i>	G6P↔F6p
	Pfk	<i>pfkA,B</i>	F6P+ATP⇒F16BP+ADP
	Fbp	<i>fbp</i>	F16BP+Pi⇒F6P
	Fba	<i>fba</i>	F16BP↔GAP+DHAP
	Tpi	<i>tpi</i>	GAP↔DHAP
	GAPDH	<i>gapA,C</i>	GAP+Pi+NAD+⇒13BPG+NADH
	Pgk	<i>pgk</i>	13BPG+ADP↔3PG+ATP
	Pgm	<i>pgm</i>	3PG↔2PG
	Eno	<i>eno</i>	2PG↔PEP
	Pyk	<i>pykF,A</i>	PEP+ADP⇒PYR+ATP
	PDH	<i>AceE,F,lpdA</i>	PYR+CoA+NAD+⇒AcCoA+CO <sub>2</sub> +NADH
	Ppc	<i>ppc</i>	PEP+CO <sub>2</sub> ⇒OAA+Pi
	Pck	<i>pckA</i>	OAA+ATP⇒PEP+CO <sub>2</sub> +ADP
	Pps	<i>ppsA</i>	PYR+ATP⇒PEP+AMP+Pi

## PP pathway

G6PDH	<i>zwf</i>	$G6P + NADP^+ \Rightarrow 6PGL + NADPH$
6Pgl	<i>pgl</i>	$6PGL \Rightarrow 6PG$
6PGDH	<i>gnd</i>	$6PG + NADP^+ \Rightarrow RU5P + NADPH + CO_2$
Rpi	<i>rpiA,B</i>	$Ru5P \Leftrightarrow R5P$
Rpe	<i>rpe</i>	$Ru5P \Leftrightarrow X5P$
Tkt1	<i>tktA</i>	$R5P + X5P \Leftrightarrow GAP + S7P$
Tal	<i>talA,B</i>	$GAP + S7P \Leftrightarrow E4P + F6P$
Tkt2	<i>tktB</i>	$X5P + E4P \Leftrightarrow F6P + GAP$

## ED pathway

	<i>edd</i>	$6PG \Rightarrow KDPG$
KDPG	<i>eda</i>	$KDPG \Rightarrow GAP + PYR$

## Fermentative pathway

LDH	<i>ldhA</i>	$PYR + NADH \Leftrightarrow NAD + Lac$
ADH	<i>adhE</i>	$AcAld + NADH \Leftrightarrow NAD + ETOH$
AcAldDH	<i>adhE</i>	$Ace + NADH \Leftrightarrow NAD + AcAld$
Pfl	<i>pflABCD,foc</i>	$PYR + CoA \Rightarrow AcCoA + formic\ acid$
Fhl	<i>fhl</i>	$HCOOH \Rightarrow CO_2$
Pta	<i>pta</i>	$AcCoA + Pi \Leftrightarrow AcP + CoA$
Ack	<i>ackA</i>	$AcP + ADP \Leftrightarrow ATP + Ace$

## TCA cycle

CS	<i>glcA</i>	$AcCoA + OAA \Rightarrow Citrate$
Acn	<i>acnA,B</i>	$CIT \Rightarrow ICIT$
ICDH	<i>icdA</i>	$ICIT + NAD \Rightarrow CO_2 + NAD(P)H + \alpha KG$
$\alpha$ KGDH	<i>sucA,B</i>	$\alpha KG + NAD + CoA \Rightarrow CO_2 + NADH + SucCoA$
SCS	<i>sucC,D</i>	$SucCoA + GDP(ADP) + Pi \Leftrightarrow GTP(ATP) + CoA + SUC$
SDH	<i>sdhCDAB</i>	$SUC + FAD \Rightarrow FADH_2 + FUM$
Frd	<i>frd</i>	$FUM + FADH_2 \Rightarrow SUC + FAD$
Fum	<i>fumA,B,C</i>	$FUM \Leftrightarrow MAL$
MDH	<i>mdh</i>	$MAL + NAD \Leftrightarrow NADH + OAA$
Mez	<i>medB</i>	$MAL + NADP \Rightarrow CO_2 + NADPH + PYR$
Sfc	<i>sfc</i>	$MAL + NAD \Rightarrow CO_2 + NADH + PYR$
Icl	<i>aceA</i>	$ICIT \Rightarrow GOX + SUC$
MS	<i>aceB</i>	$AcCoA + GOX \Rightarrow CoA + MAL$

## Appendix C: A table of genes and their associated functions

### (a) Global regulatory genes

Gene names	Description (function as encoded protein)
<i>arcA</i>	Anoxic redox control
<i>cra</i>	Catabolite repressor activator
<i>crp</i>	cAMP receptor protein
<i>fnr</i>	Fumarate and nitrate reductase
<i>rpoS</i>	RNA polymerase sigma factor
<i>rpoD</i>	RNA polymerase, sigma 70 subunit
<i>soxS</i>	Dual transcriptional activator
<i>soxR</i>	Superoxide response protein
<i>mlc</i>	Making large colonies protein

### (b) PhoB regulatory genes

Gene names	Description (function as encoded protein)
<i>phoB</i>	Dual transcription regulator
<i>phoR</i>	Sensor kinase of the PhoRB two component signal transduction pathway
<i>phoA</i>	Alkaline phosphatase precursor
<i>phoE</i>	Outer-membrane pore protein
<i>phoH</i>	PhoH protein (phosphate starvation inducible protein PsiH)
<i>phnC</i>	ATP binding component of the alkylphosphonate ABC transporter
<i>pstS</i>	Subunit of phosphate ABC transporter
<i>ugpB</i>	Subunit of glycerol-3-P ABC transporter
<i>phoU</i>	Phosphate transport system regulatory protein
<i>phoM(creC)</i>	Sensor histidine kinase of the CreCB two-component signal transduction system

### (c) Metabolic pathway genes

Gene names	Description (function as encoded protein)
<i>ptsH</i>	Phosphohistidinoprotein-hexose phosphotransferase
<i>ptsG</i>	Glucose phosphotransferase enzyme IIBC[Glc]
<i>pfkA</i>	6-phosphofructokinase
<i>pykF</i>	Pyruvate kinase
<i>lpdA</i>	Lipoamide dehydrogenase
<i>gltA</i>	Citrate synthase
<i>icdA</i>	Isocitrate dehydrogenase
<i>sucA</i>	$\alpha$ -ketoglutarate dehydrogenase
<i>sdhC</i>	Succinate dehydrogenase

<i>mdh</i>	Malate dehydrogenase
<i>zwf</i>	Glucose 6-phosphate-1-dehydrogenase
<i>gnd</i>	6-phosphogluconate dehydrogenase
<i>tktA</i>	Transketolase I
<i>tktB</i>	Transketolase II
<i>talA</i>	Transaldolase A
<i>talB</i>	Transaldolase B
<i>edd</i>	6-phosphogluconate dehydratase
<i>eda</i>	Entner-Doudoroff aldolase
<i>ldhA</i>	D-lactate dehydrogenase
<i>yfiD</i>	Stress-induced alternate pyruvate formate-lyase subunit
<i>asr</i>	Acid shock RNA
<i>gadA</i>	Glutamate decarboxylase A
<i>ackA</i>	Acetate kinase
<i>pta</i>	Phosphate acetyltransferase

#### (d) Nitrogen regulatory genes

Gene names	Description (function as encoded protein)
<i>rpoN</i>	RNA polymerase, sigma 54 (sigma N) factor
<i>gdhA</i>	Glutamate dehydrogenase
<i>gltB</i>	Glutamate synthase, large subunit
<i>gltD</i>	Glutamate synthase, small subunit
<i>glnA</i>	Glutamine synthetase
<i>glnB</i>	Protein PII-control the level and activity of glutamine synthetase
<i>glnD</i>	Uridylyltransferase/uridylyl-removing enzyme
<i>glnE</i>	Glutamine synthetase adenylyltransferase [multifunctional]
<i>glnG</i>	NtrC transcriptional dual regulator
<i>glnK</i>	Nitrogen regulatory protein
<i>glnL</i>	NtrB sensory histidine kinase
<i>nac</i>	Nac DNA-binding transcriptional dual regulator

#### (e) Respiratory chain genes

Gene names	Description (function as encoded protein)
<i>cyoA</i>	Cytochrome <i>bo</i> terminal oxidase subunit II
<i>cydB</i>	Cytochrome <i>bd-I</i> terminal oxidase subunit II
<i>atpA</i>	ATP synthase $\alpha$ -subunit
<i>ndh</i>	Ubiquinone oxidoreductase II
<i>nuoA</i>	NADH: ubiquinone oxidoreductase
<i>sodA</i>	Superoxide dismutase (Mn)

## Appendix D: Gene names

Gene	Product
Sugar uptake	
PEP-carbohydrate phosphotransferase system	
<i>ptsG</i>	PTS system, glucose-specific IIBC component
<i>ptsH</i>	PTS system protein HPr
<i>ptsI</i>	PEP-protein phosphotransferase system enzyme I
<i>crr</i>	PTS system, glucose-specific IIA component
<i>fruR</i>	transcriptional repressor of <i>fru</i> operon and global regulator
<i>fruB</i>	PTS system, fructose-specific IIA/fpr component
<i>fruK</i>	fructose-1-phosphate kinase
<i>fruA</i>	PTS system, fructose-specific transport protein
<i>manA</i>	mannose-6-phosphate isomerase
<i>manX</i>	PTS enzyme IAB, mannose-specific
<i>manY</i>	PTS enzyme IIC, mannose-specific
<i>manZ</i>	PTS enzyme IID, mannose-specific
<i>malI</i>	repressor of <i>malX</i> and <i>Y</i> genes
<i>malX</i>	PTS system, maltose and glucose-specific II ABC
<i>malY</i>	enzyme that may degrade or block biosynthesis of endogenous <i>mal</i> inducer, probably aminotransferase
<i>malZ</i>	maltodextrin glucosidase
<i>nagE</i>	PTS system, <i>N</i> -acetylglucosamine-specific enzyme II ABC
<i>nagB</i>	glucosamine-6-phosphate deaminase
<i>nagA</i>	<i>N</i> -acetylglucosamine-6-phosphate deacetylase
<i>nagC</i>	transcriptional repressor of <i>nag</i> operon
<i>nagD</i>	<i>N</i> -acetylglucosamine metabolism
<i>bglX</i>	$\beta$ -D-glucoside glucohydrolase, periplasmic
<i>bglA</i>	6-phospho- $\beta$ -glucosidase A
<i>bglB</i>	phospho- $\beta$ -glucosidase B
<i>bglF</i>	PTS system $\beta$ -glucosides, enzyme II
<i>bglG</i>	positive regulation of <i>bgl</i> operon
<i>bglJ</i>	2-component transcriptional regulator

Sugar-H <sup>+</sup> symport and phosphorylation	
<i>glk</i>	glucokinase
<i>galM</i>	galactose-1-epimerase (mutarotase)
<i>galK</i>	galactokinase
<i>galT</i>	galactose-1-phosphate uridylyltransferase
<i>galE</i>	UDP-galactose-4-epimerase
<i>galF</i>	homolog of Salmonella UTP-glucose-1-P uridylyltransferase, probably a UDP-gal transferase
<i>galU</i>	glucose-1-phosphate uridylyltransferase
<i>galS</i>	mgI repressor, galactose operon inducer
<i>galR</i>	repressor of galETK operon
<i>galP</i>	galactose-proton symport of transport system
<i>xylB</i>	xylulokinase
<i>xylA</i>	D-xylulose isomerase
<i>xylF</i>	xylose binding protein transport system
<i>xylG</i>	putative ATP-binding protein of xylose transport system
<i>xylH</i>	putative xylose transport, membrane component
<i>xylR</i>	putative regulator of xyl operon
<i>xylE</i>	xylose-proton symport
<i>fucP</i>	fucose permease
<i>fucO</i>	L-1,2-propanediol oxidoreductase
<i>fucA</i>	L-fuculose-1-phosphate aldolase
<i>fucI</i>	L-fucose isomerase
<i>fucK</i>	L-fuculokinase
<i>fucU</i>	protein of fucose operon
<i>fucR</i>	positive regulator of the fuc operon
<i>araD</i>	L-ribulose-5-phosphate 4-epimerase
<i>araD</i>	L-ribulose-5-phosphate 4-epimerase
<i>araA</i>	L-arabinose isomerase
<i>araB</i>	L-ribulokinase
<i>araC</i>	transcriptional regulator for ara operon
<i>araH</i>	high-affinity L-arabinose transport system membrane protein

(Continued)

Gene	Product
Sugar-H <sup>+</sup> symport and phosphorylation	
<i>araG</i>	ATP-binding component of high-affinity L-arabinose transport system
<i>araF</i>	L-arabinose-binding periplasmic protein
<i>araE</i>	low-affinity L-arabinose transport system proton symport protein
<i>rhaD</i>	rhamnulose-phosphate aldolase
<i>rhaA</i>	L-rhamnose isomerase
<i>rhaB</i>	rhamnulokinase
<i>rhaS</i>	positive regulator for <i>rhaBAD</i> operon
<i>rhaR</i>	positive regulator for <i>rhaRS</i> operon
<i>rhaT</i>	rhamnose transport
Direct glucose oxidation and gluconate uptake	
<i>gcd</i>	glucose dehydrogenase
<i>pqqA</i>	PQQ precursor
<i>pqqB</i>	coenzyme PQQ synthesis protein B
<i>pqqC</i>	coenzyme PQQ synthesis protein C
<i>pqqD</i>	coenzyme PQQ synthesis protein D
<i>pqqE</i>	coenzyme PQQ synthesis protein E
<i>pqqF</i>	coenzyme PQQ synthesis protein F
<i>gnl</i>	gluconolactonase
	annotated as gluconolactonase precursor
<i>gntT</i>	high-affinity gluconate permease
<i>gntR</i>	repressor for both <i>gntT</i> and <i>gntK-gntU</i>
<i>gntK</i>	thermoresistant gluconate kinase
<i>gntU</i>	low-affinity gluconate permease
Glycolysis and gluconeogenesis	
Embden-Meyerhof-Parnas pathway	
<i>pgm</i>	Glucose6P-Glucose1P
<i>fruK</i>	fructose-1-phosphate kinase
<i>pgi</i>	phosphoglucose isomerase
<i>pfkA</i>	6-Phosphofructokinase-I



<i>pfkB</i>	6-Phosphofructokinase-II
<i>fbp</i>	fructose-1,6-bisphosphatase
<i>fba</i>	fructose biphosphate aldolase
<i>tpi</i>	triose phosphate isomerase
<i>gapA</i>	Glyceraldehyde-3P dehydrogenase-A complex
<i>pgk</i>	phosphoglycerate kinase
<i>gpmA</i>	phosphoglycerate mutase
<i>gpmB</i>	phosphoglycerate mutase
<i>eno</i>	enolase
<i>pykA</i>	pyruvate kinase
<i>pykF</i>	pyruvate kinase
<i>ppsA</i>	phosphoenolpyruvate synthetase
<i>pckA</i>	PEP carboxykinase
<i>sfcA</i>	malic enzyme
<i>maeB</i>	malic enzyme
Penthouse phosphate pathway	
<i>zwf</i>	glucose-6-phosphate dehydrogenase
<i>pzwf</i>	glucose-6-phosphate dehydrogenase
<i>ybhE</i>	6-phosphogluconolactonase
<i>gnd</i>	6-phosphogluconate dehydrogenase
<i>rpiA</i>	Ribulose-5P isomerase
<i>rpiB</i>	Ribulose-5P isomerase
<i>rpe</i>	ribulose phosphate 3-epimerase
<i>tktA</i>	transketolase
<i>tktB</i>	transketolase
<i>talA</i>	transaldolase
<i>talB</i>	transaldolase
Entner-Doudoroff pathway	
<i>edd</i>	phosphogluconate dehydratase
<i>eda</i>	multifunctional 2-keto-3-deoxygluconate 6-phosphate aldolase and oxaloacetate decarboxylase
TCA cycle, glyoxylate shunt and ammonia assimilation	
<i>ppc</i>	PEP carboxylase

(Continued)

Gene	Product
<i>pycA</i>	pyruvate carboxylase
<i>gltA</i>	citrate synthase
<i>acnA</i>	aconitate hydratase 1
<i>acnB</i>	aconitate hydratase 2
<i>icdA</i>	isocitrate dehydrogenase
<i>sucA</i>	2-ketoglutarate dehydrogenase
<i>sucB</i>	2-ketoglutarate dehydrogenase
<i>sucC</i>	succinate thiokinase
<i>sucD</i>	succinate thiokinase
<i>lpdA</i>	lipoamide dehydrogenase (NADH); component of 2-oxodehydrogenase and pyruvate complexes; L-protein of glycine cleavage complex
<i>sdhC</i>	succinate dehydrogenase, cytochrome b556
<i>sdhD</i>	succinate dehydrogenase, hydrophobic subunit
<i>sdhA</i>	succinate dehydrogenase, flavoprotein subunit
<i>sdhB</i>	succinate dehydrogenase, iron sulfur protein
<i>fumA</i>	fumarase A = fumarate hydratase Class I
<i>fumC</i>	fumarase C = fumarate hydratase Class II, isozyme, oxygen-stable
<i>mdh</i>	malate dehydrogenase
<i>frdA</i>	fumarate reductase, anaerobic, flavoprotein
<i>frdB</i>	fumarate reductase, anaerobic, iron-sulfur protein subunit
<i>frdC</i>	fumarate reductase, anaerobic, membrane anchor polypeptide
<i>frdD</i>	fumarate reductase, anaerobic, membrane anchor polypeptide
<i>aceA</i>	isocitrate lyase
<i>aceB</i>	malate synthase
<i>aceK</i>	isocitrate dehydrogenase kinase/phosphatase
<i>iclR</i>	repressor of the aceBAK operon
<i>glnA</i>	glutamine synthetase
<i>gltB</i>	glutamate synthase, large subunit (putative)
<i>gltD</i>	glutamate synthase, small subunit
<i>gdhA</i>	NAD <sup>+</sup> /NADP <sup>+</sup> -glutamate dehydrogenase
<i>aspC</i>	aspartate aminotransferase
<i>tyrB</i>	aromatic amino acids aminotransferase, tyrosine repressible

Acetate and fermentative metabolism	
<i>poxB</i>	pyruvate oxidase
<i>ackA</i>	acetate kinase
<i>pta</i>	phosphotransacetylase
<i>acs</i>	acetyl-CoA synthetase
<i>ldhA</i>	fermentative D-lactate dehydrogenase, NAD-dependent
<i>adhE</i>	CoA-linked acetaldehyde dehydrogenase and iron-dependent alcohol dehydrogenase
<i>adhP</i>	alcohol dehydrogenase
<i>mhpF</i>	acetaldehyde dehydrogenase
<i>yjgB</i>	Zn-dependent alcohol dehydrogenase
<i>dhaT</i>	1,3-propanediol dehydrogenase
	Iron-dependent alcohol dehydrogenase
<i>budR</i>	transcriptional regulator
<i>budA</i>	alpha-acetolactate decarboxylase
<i>budB</i>	catabolic acetolactate synthase
<i>budC</i>	acetoin(diacetyl) reductase

# Appendix E: Precursor requirements (μmol/g DW) for biomass synthesis of *E. coli*

Table. Precursor requirements (μmol/g DW) for biomass synthesis of *E. coli*

Precursor	Amount	Stoichiometry														
		G6P	F6P	R5P	E4P	GAP	3PG	PEP	PYR	ACoA	OAA	AKG	CO2	NADPH	ATP	NADH
Ala	488								1					1		
Arg	281											1	1	4	7	-1
Asn	229										1			1	3	
Asp	229										1			1		
Cys	87						1							5	3	-1
Gln	250											1		1	1	
Glu	250											1		1		
Gly	582						1							1		-1
His	90			1										1	4	-2
Ile	276								1		1		-1	5	2	
Leu	428								2	1			-2	2		-1
Lys	326								1		1		-1	4	2	
Met	146										1			8	6	-1
Phe	176				1			2					-1	2	1	
Pro	210											1		3	1	
Ser	205						1							1		-1
Thr	241										1			3	2	
Trp	54			1	1			1					-1	2	4	-2
Tyr	131				1			2					-1	1	1	

Val	402							2					-1		2				
Protein						144	361	874		668	2750	428	1447	991	-1940	11338	27144	-2017	
RNA	630					630	368							262	368	1163	6540	-1366	
DNA	100					100	50							50	50	274.6	1001.6	-200	
Lipids	129					161	97				1842				-97	2821	2100	64	
LPS	8.4	34	25	76	17					302				-17	521	462	-42		
Peptidoglycan	27							27	81	54	27	27			189	270	27		
Glycogen	154	154															154		
Polyamines	41													41	-41	123	82		
Precursor		G6P	F6P	R5P	E4P	GAP	3PG	PEP	PYR	ACoA	OAA	AKG	CO2	NADPH	ATP	NADH			
Total		188	79	950	361	161	1406	695	2831	2626	1786	1059	-1677	16429	37754	-3534			