

Table 1: A list of reactions in the core *E. coli* network and associated chemical, genetic, and classification information.

Abbreviation	OfficialName	Equation	Subsystem	GeneDescription	Protein Description	Protein Class Description
ENO	enolase	[c] : 2pg $\leftrightarrow$ h2o + pep	Glycolysis/Gluconeogenesis	b2779	Eno	EC-4.2.1.11
FBA	fructose-bisphosphate aldolase	[c] : fdp $\leftrightarrow$ dhap + g3p	Glycolysis/Gluconeogenesis	b2925	FbaA	EC-4.1.2.13
FBP	fructose-bisphosphatase	[c] : fdp + h2o $\rightarrow$ f6p + pi	Glycolysis/Gluconeogenesis	b4232	Fbp	EC-3.1.3.11
GAPD	glyceraldehyde-3-phosphate dehydrogenase	[c] : g3p + nad + nad + pi $\leftrightarrow$ 13dpg + h + nadh	Glycolysis/Gluconeogenesis	b1779, b1416, b1417	GapA, GapC	EC-1.1.1.12
PDH	pyruvate dehydrogenase	[c] : coa + nad + pyr $\rightarrow$ accoa + co2 + nadh	Glycolysis/Gluconeogenesis	b0114, b0115, b0116	AceE	EC-undetermined
PFK	phosphofructokinase	[c] : atp + f6p $\rightarrow$ adp + f6p + h	Glycolysis/Gluconeogenesis	b3916, b1723	PfkA, PfkB	EC-2.7.1.11
PGI	glucose-6-phosphate isomerase	[c] : g6p $\leftrightarrow$ f6p	Glycolysis/Gluconeogenesis	b4025	Pgi	EC-5.3.1.9
PGK	phosphoglycerate kinase	[c] : 3pg + atp $\rightarrow$ 13dpg + adp	Glycolysis/Gluconeogenesis	b2926	Pgk	EC-2.7.2.3
PGM	phosphoglycerate mutase	[c] : 2pg $\leftrightarrow$ 3pg	Glycolysis/Gluconeogenesis	b4395, b0755	GpmB, GpmA	EC-5.4.2.1
PPS	phosphoenolpyruvate synthase	[c] : atp + h2o + pyr $\rightarrow$ amp + (2) h + pep + pi	Glycolysis/Gluconeogenesis	b1702	Ppsa	EC-2.7.9.2
PYK	pyruvate kinase	[c] : adp + h + pep $\rightarrow$ atp + pyr	Glycolysis/Gluconeogenesis	b1854, b1676	Pyka, Pykf	EC-2.7.1.40
TPI	triose-phosphate isomerase	[c] : dhap $\leftrightarrow$ g3p	Glycolysis/Gluconeogenesis	b3919	Tpi	EC-5.3.1.1
G6PDH2r	glucose 6-phosphate dehydrogenase	[c] : g6p + nadp $\leftrightarrow$ 6pgl + h + nadph	Pentose Phosphate Cycle	b1852	Zwf	EC-1.1.1.49
GND	phosphogluconate dehydrogenase	[c] : 6pgc + nadp $\rightarrow$ co2 + nadph + ru5p-D	Pentose Phosphate Cycle	b2029	Gnd	EC-1.1.1.44
PGL	6-phosphogluconolactonase	[c] : 6pgl + h2o $\rightarrow$ 6pgc + h	Pentose Phosphate Cycle	b3386	Rpeec	EC-3.1.1.31
RPE	ribulose 5-phosphate 3-epimerase	[c] : ru5p-D $\leftrightarrow$ xu5p-D	Pentose Phosphate Cycle	b2914, b4090	RpiA, RpiB	EC-5.3.1.3
RPI	ribose-5-phosphate isomerase	[c] : r5p $\leftrightarrow$ ru5p-D	Pentose Phosphate Cycle	b0008	TalB	EC-5.3.1.6
TALA	transaldolase	[c] : g3p + s7p $\leftrightarrow$ e4p + f6p	Pentose Phosphate Cycle	b2935, b2465	TktA, TktB	EC-2.2.1.2
TKT1	transketolase	[c] : r5p + xu5p-D $\leftrightarrow$ g3p + s7p	Pentose Phosphate Cycle	b2935, b2465	TktA, TktB	EC-2.2.1.1
TKT2	transketolase	[c] : e4p + xu5p-D $\leftrightarrow$ f6p + g3p	Pentose Phosphate Cycle	b2935, b2465	TktA, TktB	EC-2.2.1.1
ADKI	adenylate kinase	[c] : amp + atp $\leftrightarrow$ (2) adp	Oxidative phosphorylation	b0474	Adk	EC-2.7.4.3
ATPM	ATP maintenance requirement for one ATP	[c] : atp + h2o $\rightarrow$ adp + h + pi	Oxidative phosphorylation			
ATPS4r	ATP synthase (four protons)	adp[c] + (4) h[c] + pi[c] $\leftrightarrow$ atp[c] + (3) h[c] + h2o[c]	Oxidative phosphorylation	b3736, b3737, b3738, b3731, b3732, b3733, b0429, b0430, b0431, b0432	AtpF0, AtpF1, AtpI, CyoA	EC-3.6.3.14
CYTBD	cytochrome oxidase bd (ubiquinol-8: 2 protons)	(2) h[c] + h2o[c] + q8[c] $\rightarrow$ (2) h[c] + nadh[c] + q8h2[c]	Oxidative phosphorylation	b2276, b2277, b2278, b2279, b2280, b2281, b2282, b2283, b2284, b2285, b2286, b2287, b2288	Nuo	EC-1.10.2.2
NADH11	NADH dehydrogenase (ubiquinone-8 & 2 protons)	(2) h[c] + nad[c] + q8h2[c]	Oxidative phosphorylation			EC-1.6.5.3
SUCD4	succinate dehydrogenase	[c] : fadh2 + q8 $\leftrightarrow$ fad + q8h2	Oxidative phosphorylation	b0721, b0722, b0723, b0724	Sdh	EC-undetermined
NADTRHD	NAD transhydrogenase	[c] : nad + nadph $\rightarrow$ nadh + nadp	Oxidative phosphorylation	b1602, b1603	Pnt	EC-1.6.1.2
THD2	NAD(P) transhydrogenase	(2) h[c] + nadh[c] + nadp[c] $\rightarrow$ (2) h[c] + nad[c] + nadph[c]	Oxidative phosphorylation	b1602, b1603	Pnt	EC-1.6.1.1

Table 1: *Continued*

Abbreviation	OfficialName	Equation	Subsystem	GeneDescription	Protein Description	Protein Class Description
ACKr	acetate kinase	$[c] : ac + atp \rightarrow acp + adp$	Pyruvate metabolism	b2296	ACKr	EC-2.7.2.1
ADHER	Acetaldehyde dehydrogenase	$[c] : accoa + (2) h + (2) nadh \rightarrow coa + etoh + (2) nad$	Pyruvate metabolism	b1241	ADHE	EC-1.1.1.1, EC-1.1.1.10, EC-1.1.1.28
LDH-LD	D-lactate dehydrogenase	$[c] : lac-D + nad \rightarrow h + nadh + pyr$	Pyruvate metabolism	b1380	Ldh	EC-1.1.1.28
PFL	pyruvate formate lyase	$[c] : coa + pyr \rightarrow accoa + for$	Pyruvate metabolism	b3951, b3952	PFLC	EC-2.3.1.54
PYTA	phosphotransacetylase	$[c] : accoa + pi \rightarrow acp + coa$	Pyruvate metabolism	b2297	Pyta	EC-2.3.1.8
ICL	isocitrate lyase	$[c] : icit \rightarrow glx + succ$	Anaplerotic reactions	b4015	AcEA	EC-4.1.3.1
MALS	malate synthase	$[c] : accoa + glx + h_2o \rightarrow coa + h + mal-L$	Anaplerotic reactions	b4014, b2976	AcEB, GlcB	EC-4.1.3.2
ME1	malic enzyme (NAD)	$[c] : mal-L + nad \rightarrow co_2 + nadh + pyr$	Anaplerotic reactions	b1479	Sfc	EC-1.1.1.38
ME2	malic enzyme (NADP)	$[c] : mal-L + nadp \rightarrow co_2 + nadph + pyr$	Anaplerotic reactions	b2463	Mae	EC-1.1.1.40
PPC	phosphoenolpyruvate carboxylase	$[c] : co_2 + h_2o + pep \rightarrow h + oaa + pi$	Anaplerotic reactions	b3956	Ppc	EC-4.1.1.31
PPCK	phosphoenolpyruvate carboxykinase	$[c] : atp + oaa \rightarrow adp + co_2 + pep$	Anaplerotic reactions	b3403	Pck	EC-4.1.1.49
AKG12r	2-oxoglutarate reversible transport via symport	$akg[c] + h[c] \rightarrow akc[c] + h[c]$	Transport	b2587	KetPec	
CO2t	CO2 transporter via diffusion	$co_2[c] \leftrightarrow co_2[c]$	Transport			
D-LAC12	D-lactate transporter via proton symport	$h[c] + lac-D[c] \leftrightarrow h[c] + lac-D[c]$	Transport			
ETOH12r	ethanol reversible transport via proton symport	$etoh[h] + h[c] \leftrightarrow etoh[h] + h[c]$	Transport			
FORt	formate transport via diffusion	$for[c] \leftrightarrow for[c]$	Transport	b1101, b2415,	Pts	
GLCpts	D-glucose transport via PEP-Pyr PTS	$glc-D[e] + pep[c] \rightarrow g6p[c] + pyr[c]$	Transport	b2416, b2417		
H2O1	H2O transport via diffusion	$h_2o[c] \leftrightarrow h_2o[c]$	Transport			
AC12r	acetate reversible transport via proton symport	$ac[e] + h[e] \leftrightarrow ac[c] + h[c]$	Transport	b3528	DetA	
FUM122	Fumarate transport via proton symport (2 H)	$fun[e] + (2) h[e] \rightarrow fun[c] + (2) h[c]$	Transport	b0621	DetC	
SUCC12b	Succinate efflux via proton symport	$h[c] + succ[c] \rightarrow h[c] + succ[e]$	Transport			
PYR12r	pyruvate reversible transport via proton symport	$h[e] + pyr[e] \leftrightarrow h[c] + pyr[c]$	Transport	b3528	DetA	
SUCC122	succinate transport via proton symport (2 H)	$(2) h[e] + succ[e] \rightarrow (2) h[c] + succ[c]$	Transport			
PIt	Inorganic phosphate exchange, diffusion	$pi[c] \leftrightarrow pi[e]$	Transport			
O2t	o2 transport (diffusion)	$o_2[e] \leftrightarrow o_2[c]$	Transport	b1136	Icd	EC-1.1.1.42
ICDHyr	isocitrate dehydrogenase (NADP)	$[c] : icit + nadp \rightarrow akc + co_2 + nadph$	Citric Acid Cycle	b0720	GHA	EC-1.1.1.37
CS	citrate synthase	$[c] : accoa + h_2o + oaa \rightarrow cit + coa + h$	Citric Acid Cycle	b1611, b1612,	FumCec, FumA,	EC-4.2.1.2
FUM	fumarase	$[c] : fum + h_2o \rightarrow mal-L$	Citric Acid Cycle	b4122	FumB	EC-4.1.3.1
MDH	malate dehydrogenase	$[c] : mal-L + nad \rightarrow h + nadh + oaa$	Citric Acid Cycle	b3236	Mdh	EC-1.1.1.37
SUCD1i	succinate dehydrogenase	$[c] : fad + succ \rightarrow fadh_2 + fun$	Citric Acid Cycle	b0723, b0721,	Sdh	EC-1.3.99.1
AKGDH	2-Oxoglutarate dehydrogenase	$[c] : akc + coa + nad \rightarrow co_2 + nadh + succoa$	Citric Acid Cycle	b0722, b0724,	SucA	EC-Undetermined
SUCCOAS	succinyl-CoA synthetase (ADP-forming)	$[c] : atp + coa + succ \rightarrow adp + pi + succoa$	Citric Acid Cycle	b0116	SucC	EC-6.2.1.5
FRD	fumarate reductase	$[c] : fadh_2 + fun \rightarrow fad + succ$	Citric Acid Cycle	b0728, b0729,	FrD	EC-1.3.99.1
				b4154, b4153,		
				b4151, b4152,		
				b3117		
ACONT	aconitase	$[c] : cit \leftrightarrow icit$	Citric Acid Cycle	b0118, b1276	AcnB, AcnA	EC-4.2.1.3