

Table S1				
Bb induced enzymes involved in general metabolism of silkworm by KEGG prediction				
Gene	Pvalue	Enzyme code	Enzyme	Typical Reaction
Pyrimidine metabolism				
BGIBMGA013054 BGIBMGA010234 BGIBMGA006292 BGIBMGA011753 BGIBMGA005739 BGIBMGA005469 BGIBMGA004913 BGIBMGA004994 BGIBMGA001898	6.00E-06	EC 2.7.7.6	RNA uridylyltransferase	UTP + RNA <=> Diphosphate + RNA
BGIBMGA010642	6.00E-06	EC 2.4.2.3	phosphate alpha-D-ribosyltransferase	Uridine + Orthophosphate <=> Uracil + alpha-D-Ribose 1-phosphate
BGIBMGA005628	6.00E-06	EC 2.4.2.10	Orotidine-5'-ppospho-alpha-D-ribosyl-transferase	Orotidine 5'-phosphate + Diphosphate <=> Orotate +5-Phospho-alpha-D-ribose 1-diphosphate
BGIBMGA001137	6.00E-06	EC 2.1.1.45	dUMP C-methyltransferase	dUMP + 5,10-Methylenetetrahydrofolate <=> Dihydrofolate + dTMP
BGIBMGA010291	6.00E-06	EC 3.1.3.5	Thymidylate 5'-phosphohydrolase	dTMP + H2O <=> Thymidine + Orthophosphate
BGIBMGA007367	6.00E-06	EC 2.7.4.6	CDP phosphotransferase	ATP + CDP <=> ADP + CTP
BGIBMGA011887	6.00E-06	EC1.3.3.1	oxygen oxidoreductase	(S)-Dihydroorotate + Oxygen <=> Orotate + H2O2
BGIBMGA003377 BGIBMGA006931 BGIBMGA009495 BGIBMGA005991	6.00E-06	EC 2.7.7.7	DNA deoxynucleotidyltransferase (DNA-directed)	dCTP + DNA <=> Diphosphate + DNA
BGIBMGA007005	6.00E-06	EC 3.6.1.5	CTP phosphohydrolase	CTP + H2O <=> CDP + Orthophosphate
BGIBMGA006816	6.00E-06	EC 2.1.3.2	L-aspartate carbamoyltransferase	Carbamoyl phosphate + L-Aspartate <=> Orthophosphate +N-Carbamoyl-L-aspartate
BGIBMGA005717	6.00E-06	EC 3.5.2.2	5,6-Dihydrouracil amidohydrolase	5,6-Dihydrouracil + H2O <=> 3-Ureidopropionate
Purine metabolism				
BGIBMGA001333	1.90E-05	EC 1.7.3.3	oxygen oxidoreductase	Urate + Oxygen + H2O <=> 5-Hydroxyisourate + H2O2
BGIBMGA002462	1.90E-05	EC 2.1.2.3	5'-phosphoribosyl-5-amino-4-imidazolecarboxamide formyltransferase	10-Formyltetrahydrofolate +1-(5'-Phosphoribosyl)-5-amino-4-imidazolecarboxamide <=> Tetrahydrofolate +1-(5'-Phosphoribosyl)-5-formamido-4-imidazolecarboxamide
BGIBMGA000807	1.90E-05	EC3.5.4.6	AMP aminohydrolase	AMP + H2O <=> IMP + NH3
BGIBMGA014227 BGIBMGA010637 BGIBMGA010177 BGIBMGA002654 BGIBMGA012772 BGIBMGA005168 BGIBMGA010715	1.90E-05	EC 3.6.1.3	ATP phosphohydrolase	ATP + H2O <=> ADP + Orthophosphate
BGIBMGA007835	1.90E-05	EC 3.6.1.15	nucleoside-triphosphatase	NTP + H2O = NDP + phosphate
BGIBMGA010377	1.90E-05	EC 1.17.1.4	NAD+ oxidoreductase	Hypoxanthine + NAD+ + H2O <=> Xanthine + NADH + H+
BGIBMGA007935	1.90E-05	EC 6.3.2.6	Ligases	ATP + 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate +L-aspartate = ADP + phosphate +(S)-2-[5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido]succinate
BGIBMGA001278	1.90E-05	EC 3.5.4.4	adenosine deaminase;deoxyadenosine deaminase	adenosine + H2O = inosine + NH3
BGIBMGA006812	1.90E-05	EC 3.5.2.5	allantoinase	(S)-allantoin + H2O = allantoate
BGIBMGA010291	1.90E-05	EC 3.1.3.5	5'-ribonucleotide phosphohydrolase	a 5'-ribonucleotide + H2O = a ribonucleoside + phosphate

BGIBMGA005485	1.90E-05	EC 3.6.1.13	ADP-ribose ribophosphohydrolase	ADP-ribose + H ₂ O = AMP + D-ribose 5-phosphate
BGIBMGA007367	1.90E-05	EC 2.7.4.6	nucleoside-diphosphate phosphotransferase	ATP + nucleoside diphosphate = ADP + nucleoside triphosphate
BGIBMGA003330	1.90E-05	EC 3.2.2.1	purine-nucleoside ribohydrolase	a purine nucleoside + H ₂ O = D-ribose + a purine base
BGIBMGA001898 BGIBMGA004913 BGIBMGA004994 BGIBMGA005469 BGIBMGA005739 BGIBMGA011753 BGIBMGA006292 BGIBMGA010234 BGIBMGA013054	1.90E-05	EC 2.7.7.6	RNA uridylyltransferase	UTP + RNA <=> Diphosphate + RNA
BGIBMGA006931 BGIBMGA005991 BGIBMGA003377 BGIBMGA009495	1.90E-05	EC 2.7.7.7	DNA deoxynucleotidyltransferase (DNA-directed)	dCTP + DNA <=> Diphosphate + DNA
BGIBMGA001570	1.90E-05	EC 2.7.6.1	ribose-phosphate pyrophosphokinase	ATP + D-ribose 5-phosphate = AMP + 5-phospho-α-D-ribose 1-diphosphate
BGIBMGA000060 BGIBMGA009962	1.90E-05	EC 3.1.4.17	3',5'-cyclic-nucleotide phosphodiesterase	nucleoside 3',5'-cyclic phosphate + H ₂ O = nucleoside 5'-phosphate
BGIBMGA007005	1.90E-05	EC 3.6.1.5	diphosphoinositol-polyphosphate diesterase	ATP + 2 H ₂ O = AMP + 2 phosphate
BGIBMGA001068	1.90E-05	EC 4.1.1.-	lyases	a lot of
BGIBMGA010715	1.90E-05	EC 3.6.1.3	adenosinetriphosphatase	ATP + H ₂ O = ADP + phosphate
Pentose and glucuronate interconversions				
BGIBMGA004965	0.001236	2.4.1.17	glucuronosyltransferase	UDP-glucuronate + acceptor = UDP + acceptor beta-D-glucuronoside
BGIBMGA005500	0.001236	EC 3.2.1.31	beta-D-glucuronoside glucuronosohydrolase	a beta-D-glucuronoside + H ₂ O = D-glucuronate + an alcohol
BGIBMGA014453	0.001236	EC 1.1.1.21	NAD(P)+ 1-oxidoreductase	alditol + NAD(P)+ = aldose + NAD(P)H + H+
BGIBMGA007258	0.001236	EC 1.1.1.10	NADP+ 4-oxidoreductase	xylitol + NADP+ = L-xylulose + NADPH + H+
BGIBMGA006727	0.001236	EC 2.7.1.16	L(or D)-ribulose 5-phosphotransferase	ATP + L(or D)-ribulose = ADP + L(or D)-ribulose 5-phosphate
Citrate cycle (TCA cycle)				
BGIBMGA011412	0.006392	EC 1.1.1.41	NAD+ oxidoreductase	isocitrate + NAD+ = 2-oxoglutarate + CO ₂ + NADH
BGIBMGA003815	0.006392	EC 2.3.1.61	enzyme-N6-(dihydrolipoyl)lysine S-succinyltransferase	succinyl-CoA + enzyme N6-(dihydrolipoyl)lysine = CoA + enzyme N6-(S-succinyldihydrolipoyl)lysine
BGIBMGA007783 BGIBMGA012780	0.006392	EC 6.2.1.5	CoA ligase	ATP + succinate + CoA = ADP + phosphate + succinyl-CoA
BGIBMGA007121	0.006392	EC 4.2.1.3	citrate(isocitrate) hydro-lyase	citrate = isocitrate
BGIBMGA004276	0.006392	EC 4.1.1.32	oxaloacetate carboxy-lyase	GTP + oxaloacetate = GDP + phosphoenolpyruvate + CO ₂
BGIBMGA004130	0.006392	EC 1.1.1.37	NAD+ oxidoreductase	(S)-malate + NAD+ = oxaloacetate + NADH + H+
BGIBMGA012226	0.006392	EC 1.3.99.1	acceptor oxidoreductase	succinate + acceptor = fumarate + reduced acceptor
BGIBMGA008442	0.006392	EC 6.4.1.1	carbon-dioxide ligase	ATP + pyruvate + HCO ₃ ⁻ = ADP + phosphate + oxaloacetate
BGIBMGA000672	0.006392	EC 2.3.3.1	oxaloacetate C-acetyltransferase	acetyl-CoA + H ₂ O + oxaloacetate = citrate + CoA
Pyruvate metabolism				
BGIBMGA002750	0.010729	EC 1.2.4.1	Oxidoreductases	pyruvate + [dihydrolipoyllysine-residue acetyltransferase] lipoyllysine = [dihydrolipoyllysine-residue acetyltransferase] S-acetyldihydrolipoyllysine + CO ₂
BGIBMGA001966	0.010729	EC 1.2.1.3	NAD+ oxidoreductase	an aldehyde + NAD+ + H ₂ O = an acid + NADH + H+
BGIBMGA006419	0.010729	EC 1.1.1.40	NADP+ oxidoreductase	(S)-malate + NADP+ = pyruvate + CO ₂ + NADPH
BGIBMGA004276	0.010729	EC 4.1.1.32	oxaloacetate carboxy-lyase	GTP + oxaloacetate = GDP + phosphoenolpyruvate + CO ₂

BGIBMGA014453	0.010729	EC 1.1.1.21	NAD(P)+ 1-oxidoreductase	alditol + NAD(P)+ = aldose + NAD(P)H + H+
BGIBMGA004130	0.010729	EC 1.1.1.37	NAD+ oxidoreductase	(S)-malate + NAD+ = oxaloacetate + NADH + H+
BGIBMGA008983	0.010729	EC 2.3.1.12	Transferases	acetyl-CoA + enzyme N6-(dihydrolipoyl)lysine = CoA + enzyme N6-(S-acetyldihydrolipoyl)lysine
BGIBMGA007508	0.010729	EC 1.1.2.3	ferricytochrome-c 2-oxidoreductase	(S)-lactate + 2 ferricytochrome c = pyruvate + 2 ferrocytochrome c + 2 H+
BGIBMGA001068	0.010729	EC 4.1.1.-	Lyases	Pyruvate + CO2 <=> 2-Hydroxyethylenedicarboxylate
BGIBMGA008442	0.010729	EC 6.4.1.1	carbon-dioxide ligase	ATP + pyruvate + HCO3- = ADP + phosphate + oxaloacetate
Pentose phosphate pathway				
BGIBMGA008096	0.019729	EC 1.1.1.47	NAD(P)+ 1-oxidoreductase	beta-D-glucose + NAD(P)+ = D-glucono-1,5-lactone + NAD(P)H + H+
BGIBMGA001570	0.019729	EC 2.7.6.1	D-ribose-5-phosphate diphosphotransferase	ATP + D-ribose 5-phosphate = AMP + 5-phospho-alpha-D-ribose 1-diphosphate
BGIBMGA014211 BGIBMGA009156	0.019729	EC 2.2.1.1	D-glyceraldehyde-3-phosphate glycolaldehydetransferase	sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate
BGIBMGA000936	0.019729	EC 5.3.1.6	D-ribose-5-phosphate aldose-ketose-isomerase	D-ribose 5-phosphate = D-ribulose 5-phosphate
BGIBMGA000926	0.019729	EC 2.2.1.2	D-glyceraldehyde-3-phosphate glyceronetransferase	sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate
BGIBMGA008478	0.019729	EC 2.7.1.15	D-ribose 5-phosphotransferase	ATP + D-ribose = ADP + D-ribose 5-phosphate
Butanoate metabolism				
BGIBMGA002750	0.03102	EC 1.2.4.1	acetyltransferase-lipoyllysine 2-oxidoreductase	pyruvate + [dihydrolipoyllysine-residue acetyltransferase] lipoyllysine = [dihydrolipoyllysine-residue acetyltransferase]S-acetyldihydrolipoyllysine + CO2
BGIBMGA007408 BGIBMGA008621 BGIBMGA001929	0.03102	EC 1.1.1.35	NAD+ oxidoreductase	(S)-3-hydroxyacyl-CoA + NAD+ = 3-oxoacyl-CoA + NADH + H+
BGIBMGA001966	0.03102	EC 1.2.1.3	NAD+ oxidoreductase	an aldehyde + NAD+ + H2O = an acid + NADH + H+
BGIBMGA004001	0.03102	EC 2.3.3.10	acetoacetyl-CoA C-acetyltransferase	acetyl-CoA + H2O + acetoacetyl-CoA = (S)-3-hydroxy-3-methylglutaryl-CoA + CoA
BGIBMGA004229 BGIBMGA008633 BGIBMGA014599	0.03102	EC 3.1.1.-	Hydrolases	4-Sulfolactone + HO- <=> HSO3- + 2-Maleylacetate
BGIBMGA004489	0.03102	EC 4.2.1.17	(3S)-3-hydroxyacyl-CoA hydro-lyase	(3S)-3-hydroxyacyl-CoA = trans-2(or 3)-enoyl-CoA + H2O
BGIBMGA012226	0.03102	EC 1.3.99.1	acceptor oxidoreductase	succinate + acceptor = fumarate + reduced acceptor
Tryptophan metabolism				
BGIBMGA007408 BGIBMGA008621 BGIBMGA001929	0.001744	EC 1.1.1.35	(S)-3-hydroxyacyl-CoA:NAD+ oxidoreductase	(S)-3-hydroxyacyl-CoA + NAD+ = 3-oxoacyl-CoA + NADH + H+
BGIBMGA001966	0.001744	EC 1.2.1.3	NAD+ oxidoreductase	an aldehyde + NAD+ + H2O = an acid + NADH + H+
BGIBMGA004776 BGIBMGA007842	0.001744	EC 2.1.1.-	Transferases	L-Histidine + S-Adenosyl-L-methionine <=> N(pi)-Methyl-L-histidine + S-Adenosyl-L-homocysteine
BGIBMGA005733	0.001744	EC 6.3.2.-	Ligases	ATP + 2,3-Dihydroxybenzoate <=> Diphosphate + (2,3-Dihydroxybenzoyl)adenylate
BGIBMGA001068	0.001744	EC 4.4.1.-	Lyases	S-(Indolylmethylthiohydroximoyl)-L-cysteine + H2O <=> Indolylmethylthiohydroximate + Pyruvate + NH3
BGIBMGA007424 BGIBMGA012866	0.001744	EC 3.5.1.4	acylamide amidohydrolase	a monocarboxylic acid amide + H2O = a monocarboxylate + NH3
BGIBMGA007146	0.001744	EC 3.7.1.3	L-kynurenine hydrolase	L-kynurenine + H2O = anthranilate + L-alanine
BGIBMGA004489	0.001744	EC 4.2.1.17	(3S)-3-hydroxyacyl-CoA hydro-lyase	(3S)-3-hydroxyacyl-CoA = trans-2(or 3)-enoyl-CoA + H2O
BGIBMGA002958	0.001744	EC 4.1.1.28	aromatic-L-amino-acid carboxy-lyase	3,4-dihydroxy-L-phenylalanine = dopamine + CO2
Histidine metabolism				
BGIBMGA001966	0.005648	EC 1.2.1.3	NAD+ oxidoreductase	an aldehyde + NAD+ + H2O = an acid + NADH + H+

BGIBMGA004776 BGIBMGA007842	0.005648	EC 2.1.1.-	Transferases	L-Histidine + S-Adenosyl-L-methionine <=> N(pi)-Methyl-L-histidine + S-Adenosyl-L-homocysteine
BGIBMGA002958 BGIBMGA003199	0.005648	EC 4.1.1.28	aromatic-L-amino-acid carboxy-lyase	3,4-dihydroxy-L-phenylalanine = dopamine + CO2
Valine, leucine and isoleucine degradation				
BGIBMGA007408 BGIBMGA008621 BGIBMGA001929	0.025613	EC 1.1.1.35	(S)-3-hydroxyacyl-CoA:NAD+ oxidoreductase	(S)-3-hydroxyacyl-CoA + NAD+ = 3-oxoacyl-CoA + NADH + H+
BGIBMGA001966	0.025613	EC 1.2.1.3	NAD+ oxidoreductase	an aldehyde + NAD+ + H2O = an acid + NADH + H+
BGIBMGA014181	0.025613	EC 2.3.1.16	acetyl-CoA C-acyltransferase	acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA
BGIBMGA004001	0.025613	EC 2.3.3.10	acetoacetyl-CoA C-acetyltransferase	acetyl-CoA + H2O + acetoacetyl-CoA =(S)-3-hydroxy-3-methylglutaryl-CoA + CoA
BGIBMGA001237	0.025613	EC 2.6.1.42	2-oxoglutarate aminotransferase	L-leucine + 2-oxoglutarate = 4-methyl-2-oxopentanoate + L-glutamate
BGIBMGA004489	0.025613	EC 4.2.1.17	(3S)-3-hydroxyacyl-CoA hydro-lyase	(3S)-3-hydroxyacyl-CoA = trans-2(or 3)-enoyl-CoA + H2O
BGIBMGA007497	0.025613	EC 6.4.1.4	carbon-dioxide ligase	ATP + 3-methylcrotonoyl-CoA + HCO3- = ADP + phosphate +3-methylglutaconyl-CoA
Urea cycle and metabolism of amino group				
BGIBMGA001966	0.038333	EC 1.2.1.3	NAD+ oxidoreductase	an aldehyde + NAD+ + H2O = an acid + NADH + H+
BGIBMGA007424 BGIBMGA012866	0.038333	EC 3.5.1.4	acylamide amidohydrolase	a monocarboxylic acid amide + H2O = a monocarboxylate + NH3
BGIBMGA011001	0.038333	EC 3.5.1.14	N-acyl-L-amino-acid amidohydrolase	an N-acyl-L-amino acid + H2O = a carboxylate + an L-amino acid
BGIBMGA007716	0.038333	EC 3.5.3.1	L-arginine amidinohydrolase	L-arginine + H2O = L-ornithine + urea
Aminophosphonate metabolism				
BGIBMGA011813	0.02516	EC 2.7.7.14	ethanolamine-phosphate cytidyltransferase	CTP + ethanolamine phosphate = diphosphate + CDP-ethanolamine
BGIBMGA004776 BGIBMGA007842	0.02516	EC 2.1.1.-	Transferases	L-Histidine + S-Adenosyl-L-methionine <=> N(pi)-Methyl-L-histidine + S-Adenosyl-L-homocysteine
Nitrogen metabolism				
BGIBMGA014491 BGIBMGA006507 BGIBMGA013477	0.025926	EC 1.4.1.3	NAD(P)+oxidoreductase	L-glutamate + H2O + NAD(P)+ = 2-oxoglutarate + NH3 + NAD(P)H + H+
BGIBMGA002647	0.025926	EC 4.2.1.1	carbonate hydro-lyase	H2CO3 = CO2 + H2O
BGIBMGA007111	0.025926	EC 1.4.1.13	NADP+ oxidoreductase	2 L-glutamate + NADP+ = L-glutamine + 2-oxoglutarate + NADPH + H+
BGIBMGA007025	0.025926	EC 3.5.1.1	L-asparagine amidohydrolase	L-asparagine + H2O = L-aspartate + NH3
BGIBMGA006703	0.025926	EC 6.3.1.2	ammonia ligase	ATP + L-glutamate + NH3 = ADP + phosphate + L-glutamine
2,4-Dichlorobenzoate degradation				
BGIBMGA004229 BGIBMGA008633 BGIBMGA014599	0.011242	EC 3.1.1.-	Hydrolases	a lot of
BGIBMGA003842	0.011242	EC 1.13.11.8	oxygen 4,5-oxidoreductase	protocatechuate + O2 = 4-carboxy-2-hydroxymuconate semialdehyde
Benzoate degradation via hydroxylation				
BGIBMGA014181	0.019888	EC 2.3.1.16	acyl-CoA:acetyl-CoA C-acyltransferase	acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA
BGIBMGA003655	0.019888	EC 5.1.2.2	mandelate racemase	(S)-mandelate = (R)-mandelate
BGIBMGA001068	0.019888	EC 4.1.1.-	Lyases	a lot of
BGIBMGA003842	0.019888	EC 1.13.11.8	oxygen 4,5-oxidoreductase	protocatechuate + O2 = 4-carboxy-2-hydroxymuconate semialdehyde
Styrene degradation				

BGIBMGA007424 BGIBMGA012866	0.044869	EC 3.5.1.4	acylamide amidohydrolase	a monocarboxylic acid amide + H2O = a monocarboxylate + NH3
BGIBMGA005064	0.044869	EC 5.2.1.2	4-maleylacetoacetate cis-trans-ison	4-maleylacetoacetate = 4-fumarylacetoacetate
Porphyrin and chlorophyll metabolism				
BGIBMGA004965	0.005202	EC 2.4.1.17	glucuronosyltransferase	UDP-glucuronate + acceptor = UDP + acceptor beta-D-glucuronoside
BGIBMGA009964	0.005202	EC 4.4.1.17	Lyases	holocytochrome c = apocytochrome c + heme
BGIBMGA000937	0.005202	EC 4.1.1.37	uroporphyrinogen-III carboxy-lyase	uroporphyrinogen III = coproporphyrinogen III + 4 CO2
BGIBMGA005500	0.005202	EC 3.2.1.31	Hydrolases	a beta-D-glucuronoside + H2O = D-glucuronate + an alcohol
BGIBMGA013998	0.005202	EC 1.14.99.3	Oxidoreductases	heme + 3 AH2 + 3 O2 = biliverdin + Fe2+ + CO + 3 A + 3 H2O
BGIBMGA007912	0.005202	EC 1.3.1.33	NADP+ 7,8-oxidoreductase	chlorophyllide a + NADP+ = protochlorophyllide + NADPH + H+
BGIBMGA003440	0.005202	EC 6.1.1.17	tRNA ^{Glu} ligase (AMP-forming)	ATP + L-glutamate + tRNA ^{Glu} = AMP + diphosphate + L-glutamyl-tRNA ^{Glu}
BGIBMGA002540	0.005202	EC 1.3.3.4	oxygen oxidoreductase	protoporphyrinogen IX + 3 O2 = protoporphyrin IX + 3 H2O2
Pantothenate and CoA biosynthesis				
BGIBMGA002243 BGIBMGA005508	0.010427	EC 2.7.1.24	3'-dephospho-CoA 3'-phosphotransferase	ATP + 3'-dephospho-CoA = ADP + CoA
BGIBMGA001237	0.010427	EC 2.6.1.42	2-oxoglutarate aminotransferase	L-leucine + 2-oxoglutarate = 4-methyl-2-oxopentanoate + L-glutamate
BGIBMGA001340	0.010427	EC 2.7.1.33	(R)-pantothenate 4'phosphotransferase	ATP + (R)-pantothenate = ADP + (R)-4'-phosphopantothenate
BGIBMGA005717	0.010427	EC 3.5.2.2	5,6-dihydropyrimidine amidohydrolase	5,6-dihydrouracil + H2O = 3-ureidopropanoate
One carbon pool by folate				
BGIBMGA004950	0.031689	EC 6.3.4.3	tetrahydrofolate ligase	ATP + formate + tetrahydrofolate = ADP + phosphate +10-formyltetrahydrofolate
BGIBMGA001137	0.031689	EC 2.1.1.45	dUMP C-methyltransferase	5,10-methylenetetrahydrofolate + dUMP = dihydrofolate + dTMP
BGIBMGA002462	0.031689	EC 2.1.2.3	Transferases	10-formyltetrahydrofolate +5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide = tetrahydrofolate +5-formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide