

Supplementary Information 1

Table S1- Details on the metabolites found in the analysed metabolic footprints.

Metabolite	Abbv	Pathway	KEGG ID	MetaCyc ID
1. 2-isopropylmalate	3c3hmp	Leucine biosynthesis	C02504	3-CARBOXY-3-HYDROXY-ISOCAPROATE
2. 2-phenylglycine	2paac			D-PHENYLGLYCINE
3. Benzoate	bnz	Aromatic compound degradation (<i>Pseudomonas</i>)	C00180	BENZOATE
4. Carbamate	cbm	Cyanate degradation	C01563	CARBAMATE
5. <i>cis</i> -Aconitate	acon-C	TCA cycle	C00417	CIS-ACONITATE
6. Citrate	cit	TCA cycle	C00158	CIT
7. Fumarate	fum	TCA cycle	C00122	FUM
8. Glycine	gly	Glycine biosynthesis	C00037	GLY
9. 4-hydroxybenzoate	4hbz	Ubiquinone biosynthesis	C00156	4-hydroxybenzoate
10. Itaconate	itcon	Itaconate biosynthesis (<i>Aspergillus</i>)	C00490	ITACONATE
11. Asparagine	asn	Asparagine biosynthesis	C00152	ASN
12. Aspartate	asp	Aspartate biosynthesis	C00049	ASPARTATE
13. Glutamate	glu	Glutamate biosynthesis	C00025	GLT
14. Isoleucine	ile	Isoleucine biosynthesis	C00407	ILE
15. Lactate	lac	L-lactaldehyde degradation	C00186	LACTATE
16. Leucine	leu	Leucine biosynthesis	C00123	LEU
17. Malate	mal	TCA cycle	C00149	MAL
18. Phenylalanine	phe	Phenylalanine biosynthesis	C00079	PHE
19. Malonate	mlt		C00383	MALONATE
20. Tetradecanoate	ttdca	Fatty acid biosynthesis	C06424	CPD-7836
21. Acetyl-L-glutamate	acglu	Ornithine biosynthesis	C00624	ACETYL-GLU
22. Octadecanoate	ocdca	Fatty acid biosynthesis	C01530	STEARIC_ACID
23. Octadecenoate	ocdcea	Fatty acid biosynthesis	C00712	OLEATE-CPD
24. Succinate	succ	TCA cycle	C00042	SUC

In this work, metabolites secreted into the culture broth during fed-batch cultures were identified by GC-MS. Most of these metabolites were found to be participants of the central carbon metabolism such as tricarboxylic acid (TCA) cycle, amino and fatty acid biosynthesis and other energy generating pathways.

Among the detected amino acids, four are produced from TCA cycle intermediaries. **Asparagine**, **aspartate acid** and **isoleucine** are derived from oxaloacetate and L-glutamate from α -ketoglutarate. The formation of aspartate involves the transamination of oxaloacetate from L-glutamate, yielding a molecule of α -ketoglutarate. Aspartate serves as a precursor for the synthesis of L-asparagine using either L-glutamine or ammonia as the amino group donor. Isoleucine is synthesized from L-threonine (derived from L-aspartate) with the expense of L-glutamate as an amino group donor yielding a molecule of α -ketoglutarate. The **leucine** biosynthesis involves several enzymatic decarboxylation reactions converting pyruvate (glycolytic intermediary) into 2-keto-isovalerate (L-valine precursor), and a last transamination step that generates α -ketoglutarate from L-glutamate.

Other glycolytic intermediary, 3-phosphoglycerate, is involved in the synthesis of **glycine** that is converted from another amino acid (L-serine) by transferring a methyl group to tetrahydrofolate forming 5,10-methylene-tetrahydrofolate. Finally, **phenylalanine** is derived from the condensation of phosphoenolpyruvate (glycolytic intermediary) and D-erythrose-4-phosphate (pentose phosphate pathway intermediary). The last step of biosynthesis is also catalysed by an aminotransferase that convert L-glutamate into α -ketoglutarate.

Several TCA cycle intermediaries (carboxylic acids) were also found in the extracellular medium. The excretion of such metabolites requires unique physiological circumstances, since they are key players in energy supplying via aerobic oxidation and some are nodes that connect the central carbon metabolism to the anabolic biosynthetic pathways [1]. Metabolic imbalance between glycolysis and the carbon flux through the TCA cycle has been attributed to a limitation of enzymes activity that may lead to the accumulation of some of these organic acids [2].

Other metabolites were also detected in the extracellular medium, such as **carbamate**, an intermediate of the cyanate degradation pathway necessary to prevent the depletion of the intracellular bicarbonate pool; **4-hydroxybenzate**, an aromatic compound that is a metabolic participant and regulator of the ubiquinone biosynthesis pathway; **2-isopropylmalate**, an intermediary of the L-leucine biosynthesis; **acetyl-L-glutamate**, involved in the L-ornithine biosynthesis that is an important intermediate in many metabolic pathways, such as the urea cycle and the biosynthesis of several compounds (L-arginine, L-proline and putrescine); and the **benzoate** synthesised by an acylphosphatase encoded by the *yccX* gene that is also a competitive

inhibitor of the *N*-methyltryptophan oxidase [3;4], which catalyzes the oxidative demethylation of *N*-methyl amino acids.

Unexpectedly, other metabolites were identified in the extracellular medium, but no enzymatic activity has been reported in *E. coli*. **2-Phenylglycine** has no reported biosynthetic pathway to produce it in nature [5], though several actinomycete peptide antibiotics contain this compound (or derivatives). Itaconate and malonate acids are known enzymatic inhibitors of the *E. coli* isocitrate lyase [6] that participates in the glyoxylate bypass. **Itaconate** can be synthesized in *Aspergillus terreus* [7] through the decarboxylation of *cis*-aconitate, which is produced in the TCA cycle, and **malonate** was reported to be synthesized by the degradation of pyrimidines in microorganisms [8], but this is still not fully elucidated. Malonate is also well known as a competitive inhibitor of other TCA enzymes: fumarate dehydrogenase [9] and succinate dehydrogenase [9].

Three different fatty acids were identified in the media (**tetradecanoate**, **octadecanoate** and **octadecenoate**). Fatty acids comprise a major fraction of the cellular dry weight of *E. coli* and are found in phospholipids and lipid A. Bacterial cells are able to adapt to changes in their membrane fluidity mainly by modifying their membrane fatty acid composition (ratio between saturated and unsaturated fatty acids), whether they need to increase membrane permeability to facilitate metabolite exchanges or to protect cells against toxic chemicals in the medium [10]. Generally, the metabolism of fatty acids is comprised of anabolic and catabolic processes, both of which are tightly regulated at transcriptional and post-transcriptional levels [11]. Fatty acid accumulation would therefore, require significant re-engineering of cellular metabolism.

The next figure details the accumulation of several metabolites, such as phenylalanine (phe), isoleucine (ile), leucine (leu), acetyl-L-glutamate (acglu) and octadecenoate (ocdcea) in the $\Delta relA$ mutant culture shortly after acetate consumption has started.

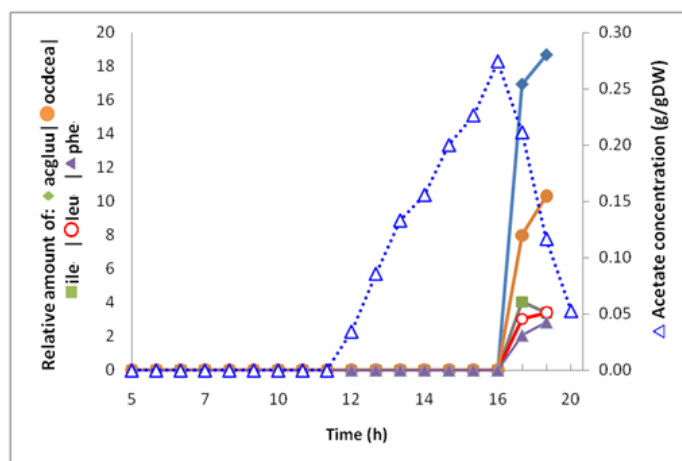


Figure S1- Details on the accumulation of several metabolites that occurred immediately after the acetate consumption by the $\Delta relA$ mutant strain.

References:

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Metabolites	A-1-relA	A-2-relA	A-3.1-relA	A-3.2-relA	A-3.3-relA	A-4.1-relA	A-4.2-relA
2paac	82.098	75.097	68.863	61.158	67.001	72.059	74.065
3c3hmp	0.000	0.000	0.000	0.000	0.000	0.000	0.000
4hbz	0.000	0.000	0.000	0.000	0.000	0.000	0.000
acglu	0.000	0.000	0.000	0.000	0.000	0.000	0.000
acon-C	0.000	0.000	0.000	0.000	0.000	0.000	0.000
asn-L	0.000	0.000	0.000	0.000	0.000	0.000	0.000
asp-L	0.000	0.000	0.000	0.000	0.000	0.000	0.000
bnz	99.271	237.233	111.863	105.574	75.710	72.984	124.376
cbm	6242.487	5025.131	6033.502	5078.917	5270.677	6051.396	5776.773
cit	0.000	0.000	0.000	0.000	0.000	0.000	0.000
fum	60.782	84.099	76.564	54.454	52.867	50.044	64.802
glu-L	0.000	0.000	0.000	0.000	0.000	0.000	0.000
gly	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ile-L	0.000	0.000	0.000	0.000	0.000	0.000	0.000
itcon	0.000	0.000	0.000	0.000	0.000	0.000	0.000
lac-L	0.000	0.000	0.000	0.000	0.000	0.000	0.000
leu-L	0.000	0.000	0.000	0.000	0.000	0.000	0.000
mal-L	0.000	0.000	0.000	0.000	0.000	0.000	0.000
mlt	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ocdca	35.976	26.642	43.935	18.426	31.552	0.000	0.000
ocdcea	0.000	0.000	0.000	0.000	0.000	0.000	0.000
phe-L	0.000	0.000	0.000	0.000	0.000	0.000	0.000
succ	91.126	70.379	80.437	44.775	61.615	59.104	61.112
ttdca	0.000	0.000	0.000	0.000	0.000	0.000	0.000

A-4.3-relA	A-5.1-relA	A-5.2-relA	A-5.3-relA	B-1.1-relA	B-1.2-relA	B-1.3-relA	B-2.1-relA
56.648	46.945	45.777	65.636	32.467	36.662	42.188	29.877
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	19.562	17.464	20.340	17.441
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
51.179	59.614	53.340	95.997	230.158	104.371	83.134	162.297
4205.814	5041.486	3447.709	4165.414	3471.099	2938.932	3493.454	3314.092
0.000	66.912	74.419	95.606	78.676	81.137	81.714	91.419
21.329	0.000	0.000	0.000	73.714	35.709	19.772	47.040
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	88.981	33.681	21.529	66.111
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	47.377	41.738	39.881	59.376
0.000	0.000	0.000	0.000	22.043	17.153	16.524	10.767
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
20.610	0.000	0.000	0.000	88.981	33.681	21.529	86.611
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

B-2.2-relA	B-2.3-relA	B-3.1-relA	B-3.2-relA	B-3.3-relA	B-4.1-relA	B-4.2-relA	B-4.3-relA	B-5.1-relA
34.211	28.039	32.863	30.406	29.830	26.849	29.635	28.293	30.772
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
22.003	14.789	23.526	20.165	27.678	23.913	21.063	24.183	32.498
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
130.599	40.709	40.587	44.854	159.813	35.122	70.722	54.765	127.906
2393.862	1965.274	1968.771	2305.564	2364.291	1365.229	2037.051	1730.810	1632.551
110.379	78.328	105.018	53.889	74.879	101.337	122.483	122.400	205.075
59.512	7.933	9.591	36.995	79.621	19.071	34.617	43.421	55.357
0.000	0.000	16.883	12.940	14.461	21.679	26.801	22.972	38.754
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	5.815	6.600	7.101	6.775
51.017	17.536	19.792	29.882	84.632	20.426	22.173	26.859	44.511
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
49.701	20.212	23.920	37.011	65.294	21.539	31.618	31.549	45.998
12.842	11.675	12.309	11.654	12.612	10.891	10.839	11.323	7.763
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
53.382	8.123	13.288	40.393	139.433	21.483	33.378	39.159	48.951
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

B-5.2-relA	B-5.3-relA	C-1.1-relA	C-1.2-relA	C-1.3-relA	C-2.1-relA	C-2.2-relA	C-2.3-relA	C-3.1-relA
32.601	25.167	11.707	15.413	13.625	5.757	4.977	5.686	6.041
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
28.206	23.359	31.019	42.815	30.810	47.455	41.097	42.739	44.669
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	304.169
68.703	60.210	36.945	68.194	39.477	32.178	74.824	18.107	33.524
1359.645	1373.215	1181.545	1507.013	1459.784	1050.775	1224.236	854.719	805.242
178.156	128.459	286.755	376.356	320.997	496.379	396.948	450.828	619.542
29.435	50.172	57.143	83.367	75.395	45.343	133.044	49.483	77.183
38.161	30.232	41.320	49.777	48.498	21.542	19.225	21.340	22.325
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	18.308
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
5.731	6.710	4.375	6.428	4.660	4.225	5.933	3.937	5.818
20.904	21.939	242.297	417.783	335.346	235.813	834.165	386.210	334.947
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
33.448	27.681	18.424	28.957	21.381	12.219	30.275	10.498	16.019
9.296	9.333	7.779	12.943	8.659	5.729	4.274	6.506	4.505
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
29.923	44.366	175.528	242.998	228.802	153.070	567.842	240.619	340.528
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

C-3.2-relA	C-3.3-relA	C-4.1-relA	C-4.2-relA	C-4.3-relA	D-1.1-relA	D-1.2-relA	D-1.3-relA	D-2.1-relA
6.662	6.955	4.636	5.839	5.133	7.767	6.825	5.223	13.994
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	10.036
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	41.781
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
48.618	66.794	46.737	50.862	50.350	56.730	53.197	42.076	41.343
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	11.672
316.953	385.996	350.046	431.367	417.192	552.920	626.275	518.992	463.233
17.958	58.756	35.795	44.396	20.011	48.045	31.392	41.640	24.230
806.422	829.976	655.952	829.787	629.245	758.924	919.660	800.148	555.776
736.965	924.201	737.337	872.217	763.014	1034.479	993.238	913.555	856.788
36.214	124.219	41.968	66.385	41.600	70.142	57.509	43.762	69.139
24.938	27.131	16.924	28.406	20.606	33.862	31.340	24.340	94.449
18.109	17.013	20.534	18.824	23.844	21.968	21.217	23.546	9.207
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
3.698	9.111	5.374	4.511	4.353	8.094	3.923	5.088	4.368
158.990	594.613	320.155	314.090	308.629	370.590	390.222	319.173	200.466
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
10.479	26.644	16.307	24.211	12.250	24.556	17.007	15.433	12.671
5.829	4.452	4.313	6.104	4.488	5.363	6.397	4.091	7.336
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
144.345	568.227	338.683	357.839	299.458	481.580	479.488	398.699	343.489
0.000	0.000	0.000	0.000	0.000	17.977	19.701	14.485	28.095

D-2.2-relA	D-2.3-relA	D-3.1-relA	D-3.2-relA	D-3.3-relA	D-4.1-relA	D-4.2-relA	D-4.3-relA	A-1.1
14.894	15.702	16.523	19.098	20.331	23.354	25.365	27.289	0.000
10.572	9.718	9.368	10.912	10.688	10.476	9.273	8.962	0.000
39.460	40.226	34.656	40.015	39.397	35.504	40.246	46.637	0.000
0.000	0.000	15.184	17.779	17.895	17.646	18.788	19.646	0.000
47.711	41.238	40.715	47.517	43.968	43.637	42.587	54.112	0.000
8.405	12.193	9.673	14.308	12.355	11.845	14.031	11.024	0.000
430.735	445.252	428.770	459.670	468.614	467.139	509.806	608.351	0.000
24.347	27.779	17.759	14.103	8.487	8.378	17.982	13.417	96.684
568.311	632.054	597.552	563.727	463.168	516.662	700.701	572.772	6303.445
847.613	891.585	816.892	862.192	759.639	829.542	898.713	943.878	0.000
69.105	110.964	47.947	38.396	20.648	19.374	33.629	28.830	295.205
84.149	101.023	62.055	81.762	73.851	71.176	78.184	78.618	0.000
9.504	7.849	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	3.556	4.838	3.746	3.280	3.266	3.674	0.000
4.401	4.544	4.701	3.978	3.635	5.083	4.326	5.391	0.000
196.953	227.435	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	2.565	3.315	3.218	2.791	3.586	3.879	0.000
0.000	0.000	30.040	33.169	23.337	17.179	5.814	20.794	232.192
12.291	23.702	12.567	10.777	6.370	7.617	16.850	12.203	0.000
12.759	8.102	10.778	10.556	8.585	13.158	16.217	18.364	0.000
0.000	0.000	7.489	8.105	8.402	9.698	9.783	11.497	0.000
0.000	0.000	1.767	2.383	2.100	2.411	2.833	3.354	0.000
315.055	386.185	236.325	218.462	127.496	153.498	158.894	194.961	161.788
33.301	31.762	41.075	38.967	45.315	45.461	51.874	54.561	0.000

A-1.2	A-1.3	A-2.1	A-2.2	A-3.1	A-3.2	A-3.3	A-4.1	A-4.2
0.000	0.000	0.000	0.000	45.522	49.866	53.691	46.130	44.073
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
131.662	91.655	122.782	45.516	47.503	40.614	112.855	50.899	48.652
4005.143	4561.215	2461.527	3391.769	4499.449	3585.476	3518.736	2760.108	2762.325
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
288.195	296.074	239.732	99.189	139.025	94.432	157.895	121.162	98.029
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
268.453	185.207	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	16.928	40.478	32.354	30.829	21.252	35.671	25.910
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
168.333	89.819	207.200	82.121	106.451	78.782	114.617	63.729	31.633
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

A-4.3	A-5.1	A-5.2	A-5.3	B-1.1	B-1.2	B-1.3	B-2.1	B-2.2
41.405	45.756	39.746	46.817	30.006	25.948	24.106	27.141	25.839
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	40.081	22.571	32.228	35.513	35.804
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
38.653	33.772	68.373	91.913	85.919	88.639	85.928	66.103	116.552
2645.864	2773.250	3070.701	2273.157	2932.566	2278.596	2810.932	1827.308	2570.034
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
57.313	42.559	107.520	132.426	101.561	93.974	116.690	99.260	141.648
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	62.830	59.762	53.521	52.831	66.644
26.874	18.189	20.049	13.727	16.992	15.368	9.998	11.309	11.053
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
19.450	19.397	110.269	68.440	66.243	57.912	67.808	59.077	130.807
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

B-3.1	B-3.2	B-3.3	B-4.1	B-4.2	B-4.3	B-5.1	B-5.2	B-5.3
29.410	34.012	31.713	20.262	27.169	34.215	15.587	20.159	19.835
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	16.513	21.389	17.140	19.472	19.796	17.036
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
44.261	39.925	50.131	33.044	39.184	39.565	36.907	54.851	38.901
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	118.934	191.507	131.954
50.073	36.539	27.562	32.226	44.518	70.342	24.313	46.180	24.016
1929.814	1786.991	1826.776	1700.887	1500.030	1807.413	595.767	1301.570	1366.005
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
49.700	47.383	32.865	27.099	38.063	74.905	27.892	39.379	17.692
25.451	28.815	30.357	23.521	30.622	21.950	15.409	25.202	21.189
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	5.693	9.267	6.942	10.088	10.836	7.963
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
30.312	31.167	26.945	21.517	24.432	39.234	16.613	28.947	21.405
14.855	16.265	21.699	12.358	13.285	14.109	11.613	14.663	13.495
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
31.016	32.728	19.498	13.328	35.859	76.151	26.650	52.918	25.746
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

C-1.1	C-1.2	C-1.3	C-2.1	C-2.2	C-2.3	C-3.1	C-3.2	C-3.3
12.498	13.858	12.515	7.985	8.145	6.832	7.360	6.004	6.122
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
21.801	21.519	25.170	21.416	26.584	24.994	43.227	33.321	39.922
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
51.881	56.196	69.736	73.986	85.339	74.983	95.269	85.092	81.725
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
224.802	274.729	285.994	387.159	463.466	497.192	754.426	557.055	524.061
48.349	67.875	65.223	32.588	53.242	53.532	26.000	20.673	19.544
1040.987	1071.210	867.750	1039.265	1084.896	1257.850	1183.180	916.113	832.172
669.344	668.378	650.379	575.869	835.102	834.667	1624.326	1076.150	1101.924
67.684	97.089	77.310	193.160	255.176	149.674	143.215	156.495	84.608
44.280	44.181	42.824	28.517	29.630	31.586	43.387	26.994	31.283
13.215	12.629	13.524	13.471	12.769	14.756	18.946	20.736	22.455
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
6.917	10.186	10.997	12.652	14.212	10.701	9.594	8.882	7.256
261.734	437.776	381.078	640.273	756.460	585.242	524.198	407.691	284.136
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
16.702	23.299	17.724	29.728	50.486	26.420	23.030	20.459	10.455
11.554	10.190	11.619	6.651	9.060	9.259	7.556	6.985	5.954
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
126.667	245.233	177.711	393.756	593.454	394.321	367.207	474.509	335.531
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

C-4.1	C-4.2	C-4.3	D-1.1	D-1.2	D-1.3	D-2.1	D-2.2	D-2.3
4.252	5.220	3.751	4.319	3.632	5.152	11.230	9.526	11.439
8.589	9.086	9.101	14.116	11.871	11.992	10.688	10.135	14.233
36.139	31.091	32.687	33.595	32.639	36.122	32.255	23.508	32.724
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
68.349	55.959	65.559	46.507	32.850	51.211	37.622	25.357	39.587
0.000	0.000	0.000	0.000	0.000	0.000	7.698	8.700	8.307
527.765	348.783	516.795	380.078	392.153	404.678	366.278	394.603	396.488
42.437	28.349	33.216	11.300	23.916	17.127	9.496	12.737	9.657
721.334	629.264	752.973	434.357	507.308	497.156	300.487	327.243	330.524
1040.227	956.423	1230.194	796.384	740.747	905.867	627.350	516.884	644.601
101.276	75.533	169.188	37.575	37.723	65.256	40.776	32.852	46.920
21.727	19.599	20.258	24.640	23.475	27.322	55.905	53.027	69.777
25.324	24.593	22.421	13.111	11.234	13.615	5.668	5.796	6.680
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
11.028	9.655	6.710	4.922	4.240	5.078	4.602	2.295	4.808
493.758	445.892	699.165	170.672	191.700	254.957	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	44.478	31.473	36.235
21.608	14.245	20.943	6.755	7.015	9.804	7.647	5.161	6.954
8.476	5.326	5.422	5.770	6.174	8.107	8.228	8.163	7.442
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
545.218	450.797	688.967	202.747	274.231	311.226	151.147	135.841	160.100
0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

D-3.1	D-3.2	D-3.3	D-4.1	D-4.2	D-4.3
12.522	14.506	19.076	29.976	27.966	27.469
11.936	13.752	18.062	18.705	13.137	16.625
27.101	31.745	48.164	49.309	61.133	50.323
0.000	0.000	0.000	0.000	0.000	0.000
44.793	35.421	71.451	61.628	55.650	50.774
6.516	12.289	25.047	0.000	0.000	0.000
582.565	538.352	641.020	806.447	513.245	529.431
27.899	17.210	29.954	20.080	19.278	10.238
585.703	642.898	745.131	739.120	525.852	519.777
757.456	894.985	1096.857	1328.600	923.070	961.324
88.922	41.474	47.191	33.636	28.219	19.364
39.941	57.280	73.313	118.783	116.862	111.010
6.339	7.102	8.311	6.965	5.714	5.888
0.000	0.000	0.000	0.000	0.000	0.000
8.233	5.188	10.552	7.140	8.649	4.841
0.000	0.000	0.000	0.000	0.000	0.000
7.140	8.324	11.058	15.532	16.929	15.580
18.007	25.830	39.812	0.000	0.000	0.000
23.802	11.379	14.429	25.887	18.429	9.410
12.138	10.971	12.934	11.150	8.998	9.426
0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000	0.000
204.491	189.200	229.281	153.008	203.618	119.293
0.000	0.000	0.000	0.000	0.000	0.000