

Supplementary Table 1. Proteins and peptide spectral matches (PSM) between *Acidovorax citrulli* (*Ac*) and *AcAppdaAc* in liquid chromatography-tandem mass spectrometry data

Strain	1st		2nd		3rd		shared proteins in 3 biological replicates
	Protein	PSM	Protein	PSM	Protein	PSM	
<i>Ac</i>	968	34,701	958	34,723	972	34,737	896
<i>AcAppdaAc</i>	1,022	41,212	1017	41,200	1007	41,222	947

Supplementary Table 2. Classification of more abundant (>2 fold) protein in *Acidovorax citrulli* (*Ac*) by clusters of ortholog groups (COG)

COG function	Accession no.	Gene function	Fold change	P-value	Included in other group
C (energy production and conversion)	ATG93227	Succinate dehydrogenase, cytochrome b556 subunit		*	
	ATG94293	FAD-dependent oxidoreductase	2.53	0.009	
	ATG93698	FAD-linked oxidase	2.18	0.001	
D (cell cycle control, cell division, chromosome partitioning)	ATG96877	Cell division protein ZapD		*	
E (amino acid metabolism and transport)	ATG95107	Threonine synthase		*	
	ATG95109	Pyridoxal phosphate-dependent aminotransferase		*	
	ATG95108	Homoserine dehydrogenase	9.17	0.0002	
	ATG95445	3-Deoxy-7-phosphoheptulonate synthase	3.85	0.0004	
F (nucleotide metabolism and transport)	ATG93517	Phosphoribosylglycinamide formyltransferase		*	
	ATG95028	dUTP diphosphatase		*	
	ATG97133	Serine/threonine protein kinase		*	
	ATG95436	Ribonucleotide-diphosphate reductase subunit beta	2.75	0.002	
	ATG96378	5-(Carboxyamino)imidazole ribonucleotide synthase	2.37	0.002	
	ATG94489	Glutamine-hydrolyzing GMP synthase	2.27	0.0004	
	ATG93720	Glutamate 5-kinase	2.25	0.001	
ATG95406	Bifunctional phosphoribosylaminoimidazolecarboxamide Formyltransferase/IMP cyclohydrolase PurH	2.04	0.005		
H (coenzyme transport and metabolism)	ATG94414	Bifunctional 3-demethylubiquinone 3-O-methyltransferase/2-octaprenyl-6-hydroxy phenol methylase		*	
	ATG95464	Phosphomethylpyrimidine synthase ThiC		*	
	ATG95670	tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA		*	
	ATG96398	Glutathione synthase		*	
	ATG95998	Methionine synthase	4.28	0.001	
	ATG94229	Sulfate adenylyltransferase	2.64	0.024	
	ATG96060	Phosphoenolpyruvate carboxykinase (GTP)	2.47	0.001	

I		ATG94499	Enoyl-CoA hydratase/isomerase family protein		*	
	(lipid metabolism)	ATG94311	Short-chain dehydrogenase		*	Q
J	(translation)	ATG93341	rRNA methyltransferase		*	
		ATG93713	Peptide chain release factor 1		*	
		ATG94046	TlyA family RNA methyltransferase		*	
		ATG94501	tRNA pseudouridine(55) synthase TruB		*	
		ATG96811	tRNA dihydrouridine(20/20a) synthase DusA		*	
		ATG94751	30S ribosomal protein S12 methylthiotransferase RimO	6.21	0.009	
		ATG94193	23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB	3.33	0.003	
		ATG93718	Proline--tRNA ligase	3.19	0.031	
		ATG96940	23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD	2.50	0.030	
		ATG94035	Tyrosine--tRNA ligase	2.43	0.020	
K	(transcription)	ATG93493	Ribosome maturation factor RimM	2.29	0.016	
		ATG93642	DNA-directed RNA polymerase subunit omega		*	
		ATG94791	Hypothetical protein CQB05_12740		*	
		ATG95292	BolA family transcriptional regulator		*	
		ATG93025	Fe-S cluster assembly transcriptional regulator IscR	2.17	0.011	
L	(replication and repair)	ATG93746	Single-stranded-DNA-specific exonuclease RecJ		*	
		ATG94382	Exodeoxyribonuclease I		*	
		ATG94483	Restriction endonuclease		*	
		ATG96450	ATP-dependent DNA helicase Rep		*	
		ATG96647	Holliday junction branch migration protein RuvA		*	
		ATG94385	DNA polymerase III subunit alpha	2.37	0.012	
		ATG93457	DNA polymerase I	2.19	0.015	
		ATG96158	Recombination-associated protein RdgC	2.19	0.004	
M	(cell wall/membrane/envelope biogenesis)	ATG96177	Chromosomal replication initiator protein DnaA	2.01	0.015	
		ATG92997	Penicillin-binding protein 1A		*	
		ATG94053	Hypothetical protein CQB05_08450		*	
		ATG94443	Energy transducer TonB		*	
		ATG94573	RIP metalloprotease RseP		*	
		ATG94999	RND transporter		*	
		ATG95001	MexE family multidrug efflux RND transporter periplasmic adaptor subunit		*	
		ATG95094	N-acetyltransferase		*	
		ATG95235	Hypothetical protein CQB05_15410		*	
		ATG96615	Carbohydrate porin		*	
		ATG97147	Hypothetical protein CQB05_24200		*	
N	(cell motility)	ATG95243	Methyl-accepting chemotaxis protein		*	T
		ATG97068	Hypothetical protein CQB05_19715		*	T
		ATG95386	Type II secretion system protein GspE		*	U
O	(post-translational modification, protein turnover, and chaperones)	ATG96285	Glutathione S-transferase		*	
		ATG95097	ATP-dependent chaperone ClpB	7.85	0.0004	
		ATG97035	Hsp70 family protein	3.73	0.003	
		ATG96611	Molecular chaperone HtpG	3.12	7.37E-05	
		ATG95120	Molecular chaperone DnaJ	2.50	0.050	
P	(inorganic ion transport and metabolism)	ATG93774	hsp70 family protein	2.17	0.031	
		ATG92932	Sulfate ABC transporter ATP-binding protein		*	
		ATG93388	Aromatic ring-hydroxylating dioxygenase subunit alpha		*	
		ATG93703	sn-glycerol-3-phosphate import ATP-binding protein UgpC		*	
		ATG94456	TonB-dependent receptor		*	
		ATG94583	Heavy metal translocating P-type ATPase		*	

	ATG94996	DUF4198 domain-containing protein		*
	ATG96084	Nitrate ABC transporter ATP-binding protein		*
	ATG96986	TonB-dependent siderophore receptor		*
	ATG94819	MetQ/NlpA family lipoprotein	4.50	0.001
	ATG97071	TonB-dependent siderophore receptor	3.87	0.014
	ATG92943	Methionine ABC transporter ATP-binding protein	2.79	0.0002
S	ATG92851	Nucleoid-associated protein, YbaB/EbfC family		*
(function un-	ATG93076	Hypothetical protein CQB05_02635		*
known)	ATG93690	FmdB family transcriptional regulator		*
	ATG93957	MoxR family ATPase		*
	ATG93975	5'-Nucleotidase		*
	ATG93994	Plasmid replication/partition related protein		*
	ATG94373	Hypothetical protein CQB05_10270		*
	ATG94374	Hypothetical protein CQB05_10275		*
	ATG94931	Hypothetical protein CQB05_13580		*
	ATG95863	DUF493 domain-containing protein		*
	ATG95958	Glycerate kinase		*
	ATG96156	DUF3297 domain-containing protein		*
	ATG96283	Hypothetical protein CQB05_21490		*
	ATG93161	Phosphoesterase	6.50	0.010
	ATG92987	ABC transporter	3.55	0.021
	ATG95746	Cluster of hypothetical protein CQB05_18345 (ATG95746)	2.09	0.036
U	ATG92916	MotA/TolQ/ExbB proton channel family protein		*
(intracellular traf-	ATG94445	Biopolymer transporter ExbD		*
ficking and secre-	ATG96309	Protein translocase subunit SecF		*
tion)				
V	ATG95000	AcrB/AcrD/AcrF family protein		*
(defense mecha-	ATG95294	ABC transporter ATP-binding protein		*
nisms)	ATG94482	SAM-dependent DNA methyltransferase	4.90	0.042

*indicates that the protein is unique to *Ac*.

Supplementary Table 3. Classification of more abundant (>2 fold) protein in *AcAppdaAc* by clusters of ortholog groups (COG)

COG function	Accession no.	Gene function	Fold change	P-value	Included in other group	
C (energy production and conversion)	ATG93913	Cytochrome c oxidase subunit II		*		
	ATG93956	Cytochrome c4		*		
	ATG94829	Aldo/keto reductase		*		
	ATG95651	Glycerol-3-phosphate dehydrogenase/oxidase		*		
	ATG95897	2Fe-2S ferredoxin		*		
	ATG96225	Methylmalonate-semialdehyde dehydrogenase (CoA acylating)		*		
	ATG96777	Isocitrate lyase		*		
	ATG96791	Aldehyde dehydrogenase		*		
	ATG94998	NAD-dependent succinate-semialdehyde dehydrogenase	2.06	0.001		
	ATG93258	Cluster of electron transfer flavoprotein subunit alpha	2.20	0.0001		
	ATG96994	NADH-quinone oxidoreductase subunit NuoE	2.24	0.011		
	ATG94438	D-Glycerate dehydrogenase	2.58	0.033		
	ATG94301	Electron transfer flavoprotein-ubiquinone oxidoreductase	2.73	0.018		
	ATG96692	4-Hydroxyphenylpyruvate dioxygenase	3.95	0.001		
	ATG96540	Isovaleryl-CoA dehydrogenase	4.16	0.041		
	ATG96066	D-Amino acid dehydrogenase	7.23	0.001		
	ATG93385	ABC transporter substrate-binding protein	9.24	0.0001		
		ATG94335	Oxidoreductase		*	H
		ATG97061	Redoxin		*	O
D (cell cycle control, cell division, chromosome partitioning)	ATG92830	ParA family protein		*		
	ATG96070	Cell division topological specificity factor		*		
E (amino acid metabolism and transport)	ATG93583	Allophanate hydrolase		*		
	ATG93673	ABC transporter substrate-binding protein		*		
	ATG94417	Phosphoserine aminotransferase		*		
	ATG95068	ABC transporter permease		*		
	ATG95220	OHCU decarboxylase		*		
	ATG95624	Low-specificity L-threonine aldolase		*		
	ATG95923	L-Serine ammonia-lyase		*		
	ATG96316	N-Formylglutamate amidohydrolase		*		
	ATG96572	Hypothetical protein CQB05_23270		*		
	ATG96931	ABC transporter substrate-binding protein		*		
	ATG96993	ABC transporter permease		*		
	ATG97076	Arginase		*		
	ATG93009	Oligopeptidase A	2.56	0.018		
	ATG95173	Ornithine carbamoyltransferase	2.75	0.003		
	ATG95459	ABC transporter substrate-binding protein	3.24	0.001		
	ATG94317	Branched-chain amino acid ABC transporter substrate-binding protein	3.25	0.002		
	ATG95282	1-(5-Phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	3.37	0.004		
	ATG95126	Aspartate-semialdehyde dehydrogenase	5.10	0.00001		
	ATG96182	ABC transporter substrate-binding protein	6.22	0.002		
	ATG95181	Kynureninase	7.36	0.0003		

	ATG96561	MFS transporter		*	GP
	ATG93176	Thiamine pyrophosphate-binding protein		*	H
	ATG95676	Type 1 glutamine amidotransferase	2.05	0.048	H
	ATG95916	Phosphoadenylylsulfate reductase	2.35	0.035	H
	ATG93452	Amino acid ABC transporter substrate-binding protein		*	T
	ATG97069	Amino acid ABC transporter substrate-binding protein		*	T
	ATG93787	ABC transporter substrate-binding protein	2.18	0.012	T
F	ATG95393	Bifunctional pyr operon transcriptional regulator/uracil phosphoribosyltransferase		*	
(nucleotide metabolism and transport)	ATG95658	Glycerol kinase		*	
	ATG96240	NUDIX hydrolase		*	
	ATG96383	HPr kinase/phosphorylase		*	
	ATG95365	Transaldolase	3.91	0.007	
G	ATG95652	Carbohydrate ABC transporter substrate-binding protein		*	
(carbohydrate metabolism and transport)	ATG96673	Alpha, alpha-trehalose-phosphate synthase (UDP-forming)		*	
	ATG94560	Fructose 1,6-bisphosphatase	2.40	0.018	
	ATG92717	Keto-deoxy-phosphogluconate aldolase	3.02	0.0005	
	ATG97016	Glucose-6-phosphate isomerase	3.69	0.003	
H	ATG93863	Quinolinate synthase NadA		*	
(coenzyme transport and metabolism)	ATG93864	3-Methyl-2-oxobutanoate hydroxymethyltransferase		*	
	ATG93872	Molybdopterin-synthase adenylyltransferase MoeB		*	
	ATG94239	Bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase		*	
	ATG95029	Bifunctional phosphopantothenoylecysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC		*	
	ATG95140	Pyridoxine 5'-phosphate synthase		*	
	ATG95805	Glutamate--cysteine ligase		*	
	ATG96846	Phosphoenolpyruvate carboxylase	2.89	0.031	
	ATG94885	Acetate--CoA ligase	4.72	0.003	
I	ATG92643	Acetyl-CoA C-acyltransferase		*	
(lipid metabolism)	ATG93582	Acetyl/propionyl-CoA carboxylase subunit alpha		*	
	ATG93950	3-Oxoadipyl-CoA thiolase		*	
	ATG96154	Acetyl-CoA C-acyltransferase		*	
	ATG96812	Class I poly(R)-hydroxyalkanoic acid synthase		*	
	ATG96632	3-Hydroxybutyryl-CoA dehydrogenase	3.07	0.045	
	ATG94289	CoA transferase subunit B	4.57	0.002	
	ATG94290	CoA transferase subunit A	11.43	9.7E-05	
	ATG96553	AMP-binding protein		*	Q
	ATG96368	Long-chain fatty acid--CoA ligase	2.70	0.028	Q
	ATG92653	3-Hydroxyacyl-CoA dehydrogenase	4.41	5.1E-05	Q
	ATG94809	3-Hydroxybutyrate dehydrogenase	4.54	0.001	Q
J	ATG94339	Ribonuclease		*	
(translation)	ATG94565	RNA methyltransferase		*	
K	ATG94059	LysR family transcriptional regulator		*	
(transcription)	ATG94645	XRE family transcriptional regulator		*	
	ATG95700	Hypothetical protein CQB05_18055		*	
	ATG96529	DNA-binding response regulator		*	
	ATG95456	IcIR family transcriptional regulator	2.17	0.008	
	ATG93007	DNA-binding response regulator	2.38	0.011	
	ATG94913	Protein kinase	2.35	0.010	LT

L (replication and repair)	ATG92823	Single-stranded DNA-binding protein			*	
	ATG93660	DNA repair protein RecN	2.35	0.046		
	ATG94340	ATP-dependent endonuclease	3.90	0.002		
M (cell wall/membrane/envelope biogenesis)	ATG93495	N-Acetyltransferase			*	
	ATG94568	Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase			*	
	ATG95133	Glycosyltransferase family 1 protein			*	
	ATG95207	Porin			*	
	ATG95216	Gamma-glutamyltransferase			*	
	ATG95353	Glycosyltransferase family 4 protein			*	
	ATG95474	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanine ligase			*	
	ATG95930	Rod shape-determining protein MreC			*	
	ATG96928	Peptidylprolyl isomerase			*	
	ATG97026	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase			*	
	ATG97102	OmpW family protein			*	
	ATG93871	S41 family peptidase	2.09	0.001		
	ATG94440	Gamma-glutamyltransferase	2.26	0.005		
	ATG96580	RND transporter			*	U
	N (cell motility)	ATG96515	Flagellar cap protein FliD			*
ATG96513		Flagellin	2.25	0.0003		
ATG93311		Chemotaxis protein			*	T
ATG95368		Methyl-accepting chemotaxis protein			*	T
ATG96536		Chemotaxis protein CheD			*	T
ATG96859		Methyl-accepting chemotaxis protein			*	T
ATG96534		Chemotaxis protein CheW	2.08	0.006		T
ATG95814		Methyl-accepting chemotaxis protein	2.15	0.029		T
ATG96440		Cluster of methyl-accepting chemotaxis protein	2.39	0.002		T
ATG93889		Methyl-accepting chemotaxis protein	2.61	0.005		T
ATG96597		Methyl-accepting chemotaxis protein	2.77	0.006		T
ATG96997		Hypothetical protein CQB05_14745	2.24	0.001		U
ATG95316		Pilus assembly protein PilM	2.31	0.039		U
ATG93728		Type II secretion system F family protein	2.68	0.002		U
ATG93727		Type IV-A pilus assembly ATPase PilB	3.11	0.014		U
ATG95626		Type IV pili twitching motility protein PilT	3.62	0.002		U
ATG95628		Twitching motility protein PilT	4.34	0.001		U
O (post-translational modification, protein turnover, and chaperones)	ATG95959	DNA repair protein Rada			*	
	ATG96373	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB			*	
	ATG97141	Glutathione S-transferase			*	
P (inorganic ion transport and metabolism)	ATG92889	Superoxide dismutase family protein			*	
	ATG93279	Nitrate ABC transporter substrate-binding protein			*	
	ATG93845	MFS transporter			*	
	ATG95656	ABC transporter ATP-binding protein			*	
	ATG95657	ABC transporter ATP-binding protein			*	
	ATG95664	DNA starvation/stationary phase protection protein	2.10	0.001		
Q (secondary structure)	ATG96708	Sulfurtransferase	2.39	0.008		
	ATG93447	Carboxymethylenebutenolidase			*	
	ATG93886	FAA hydrolase family protein			*	
	ATG95299	Outer membrane lipid asymmetry maintenance protein MlaD			*	

	ATG95301	ABC transporter ATP-binding protein		*
	ATG96303	Hypothetical protein CQB05_21595		*
	ATG92993	FAA hydrolase family protein	3.25	0.008
	ATG95907	Dienelactone hydrolase family protein	4.18	0.003
S	ATG92939	NADPH-dependent oxidoreductase		*
(function un-	ATG93943	Tripartite tricarboxylate transporter substrate binding protein		*
known)	ATG94187	C4-dicarboxylate ABC transporter substrate-binding protein		*
	ATG94237	Hypothetical protein CQB05_09480		*
	ATG94450	Hypothetical protein CQB05_10730		*
	ATG94530	Folate-binding protein YgfZ		*
	ATG94628	DUF2158 domain-containing protein		*
	ATG94721	Hypothetical protein CQB05_12360		*
	ATG94794	Hypothetical protein CQB05_12755		*
	ATG94883	Hypothetical protein CQB05_13265		*
	ATG94941	GTPase HflX		*
	ATG95192	BMP family ABC transporter substrate-binding protein		*
	ATG95254	MoxR family ATPase		*
	ATG95489	DUF484 domain-containing protein		*
	ATG95621	DNA-binding protein		*
	ATG95963	Tripartite tricarboxylate transporter substrate binding protein		*
	ATG95978	Cluster of type VI secretion system tip protein VgrG		*
	ATG96185	Hypothetical protein CQB05_20895		*
	ATG96761	Hypothetical protein CQB05_24355		*
	ATG97054	Hypothetical protein CQB05_18685		*
	ATG97072	Hypothetical protein CQB05_19925		*
	ATG97126	cys-tRNA(pro)/cys-tRNA(cys) deacylase		*
	ATG93175	Chromosome segregation protein SMC	2.01	0.005
	ATG92650	NADP-dependent oxidoreductase	2.01	0.002
	ATG95800	Hypothetical protein CQB05_18645	2.02	0.007
	ATG93579	Polyisoprenoid-binding protein	2.08	0.002
	ATG93665	Hypothetical protein CQB05_06150	2.15	0.023
	ATG95417	Peptidase M61	2.85	0.003
	ATG96710	Peptidoglycan-binding protein LysM	2.88	0.045
	ATG93441	Twin-arginine translocation pathway signal	2.91	0.031
	ATG94904	Type VI secretion system contractile sheath large subunit	3.09	0.002
	ATG94441	Phasin (PHA-granule associated protein)	3.56	5.1E-07
	ATG95846	LemA family protein	3.56	0.012
T	ATG93349	Two-component system response regulator		*
(signal transduc-	ATG93350	Hybrid sensor histidine kinase/response regulator		*
tion)	ATG93478	Sigma-54-dependent Fis family transcriptional regulator		*
	ATG94313	Universal stress protein		*
	ATG95433	Sigma-54-dependent Fis family transcriptional regulator		*
	ATG96273	FHA domain-containing protein		*
	ATG96532	Response regulator		*
	ATG96659	Carbon starvation protein A		*
	ATG95401	Response regulator	2.04	0.039
	ATG95397	Hybrid sensor histidine kinase/response regulator	2.09	0.029
U	ATG95380	Type II secretion system protein GspG		*
(intracellular				
trafficking and				
secretion)				

*indicates that the protein is unique to *AcAppdaAc*.