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Research article

Proteomic and transcriptomic analyses of *Cutibacterium acnes* biofilms and planktonic cultures in presence of epinephrine

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Supplementary

Table S1. Proteomic changes in *C. acnes* in control biofilms in comparison with control planktonic cultures. Red color indicates downregulated proteins. Green color indicates upregulated proteins.

Accession #	Accession # on STRING	Protein name	Difference	SE of difference	t ratio	df	q value	Fold change
A0A085B0S7	ALT34593.1	Inorganic pyrophosphatase	-2.895	0.6159	4.701	4834	0.000147	0.12
A0A9Q4C1B0	ALT36376.1	Oxidoreductase, NAD-binding domain protein	-6.287	0.6159	10.21	4834	<0.000001	0.02
Q6A5D5	ALT36290.1	Ribose 5-phosphate isomerase	-4.736	0.5509	8.597	4834	<0.000001	0.04
A0A9N7ATH9	ALT34452.1	Nitrite reductase, copper-dependent	-4.513	0.5509	8.192	4834	<0.000001	0.04
Q6AAK0	ALT34771.1	Sugar phosphate isomerase/epimerase	-4.408	0.5509	8.003	4834	<0.000001	0.05
Q6A8V2	ALT35257.1	Ribonuclease D	-3.898	0.5509	7.076	4834	<0.000001	0.07
E6D3P8	ALT34776.1	Oxidoreductase, NAD-binding domain protein	-4.234	0.6159	6.875	4834	<0.000001	0.07
A0A828SGK0	ALT35727.1	Aminopeptidase N	-3.574	0.5509	6.489	4834	<0.000001	0.08
A0A9Q4GDG5	ALT34531.1	Penicillin-binding protein, transpeptidase domain protein	-2.587	0.6159	4.201	4834	0.001144	0.09
A0A371N860	AOG29170.1	ADP/GDP-polyphosphate phosphotransferase	-3.582	0.6159	5.817	4834	<0.000001	0.09
A0A9Q4BZN0	ALT34464.1	67 kDa Myosin-crossreactive antigen family protein	-3.82	0.6159	6.203	4834	<0.000001	0.10
A0A9N7AVS8	ALW21_06360	Oxoglutarate dehydrogenase (Succinyl-transferring), E1 component	-3.26	0.5509	5.919	4834	<0.000001	0.10
A0A9Q4BZZ3	ALT36368.1	Hyaluronate lyase	-2.364	0.6159	3.839	4834	0.00418	0.12
A0A9Q4BXX9	ALT36531.1	Bacterial extracellular solute-binding protein	-3.065	0.5509	5.563	4834	0.000003	0.12
Q6ABE1	ALT34514.1	Iron-sulfur protein	-3.008	0.5509	5.461	4834	0.000005	0.12
A0A9N7G0V0	ALT34913.1	Amidino transferase	-2.944	0.5509	5.344	4834	0.000008	0.13
A0A9Q4C050	ALT35200.1	Carbamoyl-phosphate synthase large chain	-2.843	0.5509	5.16	4834	0.00002	0.14
A0A9N7G2Y2	ALT36409.1	Bifunctional glutamine synthetase adenylyltransferase/adenylyl-removing enzyme	-2.817	0.5509	5.113	4834	0.000025	0.14
Q6AAJ0	ALT34781.1	Conserved protein, putative helicase of DeaD/DeaH box family	-2.779	0.5509	5.044	4834	0.000033	0.15
Q6ABE2	ALT34513.1	Conserved protein	-2.766	0.5509	5.021	4834	0.000036	0.15

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Accession #	Accession # on STRING	Protein name	Difference	SE of difference	t ratio	df	q value	Fold change
A0A8B2VQT6	ALT34454.1	N-acetyltransferase	-2.68	0.5509	4.864	4834	0.000075	0.16
E6D4M0	ALT36128.1	DEAD/DEAH box helicase	-2.643	0.5509	4.798	4834	0.0001	0.16
A0A828SLV1	ALT36244.1	Alanine dehydrogenase	-2.614	0.5509	4.744	4834	0.000124	0.16
A0A9N7B064	AOG29020.1	Pyridine nucleotide-disulfide oxidoreductase	-2.373	0.6159	3.853	4834	0.004135	0.17
Q6ABF6	ALT34501.1	NADH dehydrogenase	-2.543	0.5509	4.616	4834	0.000212	0.17
Q6AAL0	ALT34763.1	Transaldolase	-2.432	0.5509	4.415	4834	0.000523	0.19
A0A9N7AN67	ALT35430.1	DoxX family protein	-2.371	0.5509	4.304	4834	0.000835	0.19
A0A9Q4GGK6	ALT35136.1	ATP-dependent DNA helicase, RecQ family	-2.333	0.5509	4.236	4834	0.001081	0.20
A0A9N7FZU1	ALT34959.1	cAMP factor (Cfa)	-2.326	0.5509	4.223	4834	0.001081	0.20
A0A9N7AS59	ALT34440.1	Succinate-semialdehyde dehydrogenase	-2.326	0.5509	4.222	4834	0.001081	0.20
A0A9N7G3U9	ALT36182.1	NAD(P)H quinone oxidoreductase, PIG3 family	-2.227	0.5509	4.043	4834	0.00219	0.21
A0A9N7AN74	ALT36099.1	Triacylglycerol lipase	-2.161	0.5509	3.923	4834	0.003403	0.22
Q6A5I5	ALT36248.1	Citrate synthase	-2.156	0.5509	3.914	4834	0.003437	0.22
Q6AAQ4	ALT34727.1	Zinc-binding dehydrogenase	-2.145	0.5509	3.893	4834	0.003636	0.23
A0A9Q4C152	ALT36123.1	Oxidoreductase, aldo/keto reductase family protein	-2.12	0.5509	3.848	4834	0.004135	0.23
A0A9N7AP39	ALT34844.1	Uncharacterized protein	-2.09	0.5509	3.794	4834	0.004641	0.23
Q6A5L5	ALT36226.1	Zinc-type alcohol dehydrogenase-like protein	-2.085	0.5509	3.784	4834	0.004714	0.24
Q6A790	ALT35738.1	ABC transporter	-2.074	0.5509	3.765	4834	0.004975	0.24
Q6ABB7	ALT34536.1	Aminoglycoside phosphotransferase domain-containing protein	-2.046	0.5509	3.714	4834	0.005953	0.24
A0A9N7AY85	ALT36455.1	Trehalose 6-phosphate phosphatase	-2.04	0.5509	3.702	4834	0.006001	0.24
A0A9N7ALH2	ALW21_11825	D-alanine--D-alanine ligase	-2.038	0.5509	3.7	4834	0.006001	0.24
Q6A8U7	ALT35262.1	Tryptophanase	-1.997	0.5509	3.626	4834	0.00785	0.25
Q6A5D7	ALT36288.1	Conserved L-arabinose operon protein, hydrolase	-1.994	0.5509	3.621	4834	0.00785	0.25
Q6ABU7	ALT34429.1	Glycosyl hydrolase	-1.979	0.5509	3.592	4834	0.008577	0.25
Q6A5D9	ALT36286.1	L-arabinose utilization protein, glycerol dehydrogenase	-1.966	0.5509	3.568	4834	0.009209	0.26

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Accession #	Accession # on STRING	Protein name	Difference	SE of difference	t ratio	df	q value	Fold change
Q6A850	ALT35472.1	RecBCD enzyme subunit RecB	-2.354	0.6159	3.822	4834	0.004249	0.26
Q6ABL2	ALW21_00020	DNA replication and repair protein RecF	-1.955	0.5509	3.549	4834	0.009714	0.26
Q6A5V1	ALT36621.1	Peptide ABC transporter, ATP-binding protein	-2.583	0.6747	3.829	4834	0.004243	0.35
Q6A7V7	ALT35548.1	Biotin synthase	3.695	0.6159	6	4834	<0.000001	3.60
Q6A7C5	ALT35709.1	Conserved phage-associated protein	2.441	0.6159	3.963	4834	0.002971	5.44
Q6A8V6	ALT35254.1	Amino acid permease / DNA binding protein	3.433	0.5509	6.231	4834	<0.000001	10.80

Table S2. Proteomic changes in *C. acnes* in 5 nM epinephrine biofilms in comparison with in 5 nM epinephrine planktonic cultures. Yellow labeling means the proteins which were affected in control samples. Red color indicates downregulated proteins. Green color indicates upregulated proteins.

Accession #	Accession # on STRING	Protein name	Difference	SE of difference	t ratio	df	q value	Fold change
A0A085B0S7	ALT34593.1	Ribose 5-phosphate isomerase	-4.419	0.5347	8.265	4702	<0.000001	0.01
Q6A5D5	ALT36290.1	Anaerobic ribonucleoside-triphosphate reductase	3.553	0.8021	4.43	4702	0.000831	0.05
Q6A945	ALT35173.1	ATP-dependent dethiobiotin synthetase BioD	-4.156	0.5347	7.773	4702	<0.000001	0.06
A0A9Q4C1B0	ALT36376.1	Metallophosphoesterase	-3.064	0.5978	5.125	4702	0.000033	0.08
A0A828UFF1	AOH45217.1	Aminooxidase	-2.836	0.5347	5.304	4702	0.000015	0.09
A0A9N7AVS8	ALW21_06360	Ribulokinase	-3.555	0.5978	5.947	4702	<0.000001	0.11
A0A9Q4GER7	ALT35781.1	SPFH/Band 7/PHB domain protein	2.472	0.6549	3.775	4702	0.008047	0.11
Q6A5Z8	ALT36102.1	cAMP factor 3	-2.749	0.5978	4.598	4702	0.000405	0.11
A0A828UK58	ALT36285.1	Myo-inositol catabolism protein	-3.175	0.5978	5.311	4702	0.000015	0.11
A0A9N7G0V0	ALT34913.1	Tat pathway signal sequence domain protein	-2.152	0.5347	4.025	4702	0.003744	0.11
Q6AAK0	ALT34771.1	AP endonuclease, family 2	-3.058	0.5347	5.719	4702	0.000002	0.12
A0A9Q4BYX8	ALT35629.1	ABC transporter, solute-binding protein	-2.355	0.5347	4.404	4702	0.000879	0.12
A0A828SG38	ALT35236.1	ADP/GDP-polyphosphate phosphotransferase	-2.844	0.5978	4.757	4702	0.000201	0.14
A0A9Q4BXX9	ALT36531.1	Amidinotransferase	-3.166	0.5347	5.92	4702	<0.000001	0.20

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Accession #	Accession # on STRING	Protein name	Difference	SE of difference	t ratio	df	q value	Fold change
Q6ABE0	ALT34515.1	LUD domain-containing protein	-2.275	0.5347	4.255	4702	0.001528	0.21
A0A9Q4GGK6	ALT35136.1	30S ribosomal protein S13	-2.061	0.5347	3.854	4702	0.006339	0.22
A0A371N860	AOG29170.1	Succinate CoA transferase	-2.011	0.5347	3.761	4702	0.008188	0.22
A0A9N7FZU1	ALT34959.1	Oxoglutarate dehydrogenase (Succinyl-transferring), E1 componen	-3.237	0.5347	6.054	4702	<0.000001	0.22
Q6AAL0	ALT34763.1	Transaldolase	-2.09	0.5347	3.909	4702	0.005781	0.23
Q6ABE2	ALT34513.1	Cysteine-rich domain protein	-2.083	0.5347	3.896	4702	0.005825	0.24
Q6A8U7	ALT35262.1	Tryptophanase	-2.076	0.5347	3.883	4702	0.005876	0.24
A0A9Q4GEX3	ALT35364.1	Glycosyltransferase family 2 protein	-3.155	0.5978	5.278	4702	0.000016	0.24
Q6AAK3	ALT34770.1	Methylmalonate-semialdehyde dehydrogenase (Acylating)	-2.055	0.5347	3.844	4702	0.006346	0.24
A0A085B1W8	ALT36064.1	Inorganic pyrophosphatase	-4.837	0.7562	6.396	4702	<0.000001	0.25
A0A9Q4GGS6	ALT36130.1	ATP-dependent DNA helicase, RecQ family	-2.19	0.5347	4.096	4702	0.002908	3.00
A0A9Q4GEK0	ALT35999.1	Oxidoreductase, NAD-binding domain protein	-5.095	0.7562	6.737	4702	<0.000001	4.24
Q6A7U4	ALT35559.1	ACR, COG1399	2.312	0.5347	4.324	4702	0.00119	4.97

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