

Supporting materials

article title: Steroid Metabolism in Thermophilic Actinobacteria *Saccharopolyspora hirsuta*

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author names: Tatyana Lobastova, Victoria Fokina, Sergey Tarlachkov, Andrey Shutov, Eugeny Bragin, Alexey Kazantsev, Marina Donova

***Correspondence:** 2vvfokina@gmail.com

Supplementary Table S6. Result of BLAST search for the 29 protein sequences from the *M. tuberculosis* steroid catabolism enzymes in the *Geobacillus kaustophilus* HTA426 and *Parageobacillus thermoglucosidasius* DSM 2542 genomes.

No.	Protein	<i>Geobacillus kaustophilus</i> HTA426. BA000043.1			<i>Parageobacillus thermoglucosidasius</i> DSM 2542. CP012712.1		
		Query cover (%)	Number of identical amino-acids	% of identical amino-acids	Query cover (%)	Number of identical amino-acids	% of identical amino-acids
1	ChoD	6.7	16	2.7	5.7	16	2.7
2	Ltp4	6.5	12	3.4	9.6	12	3.4
3	Ltp3	22.1	24	6.0	18.5	24	6.1
4	Hsd4A	50.1	75	23.6	49.5	68	21.4

5	FadE26	73.0	101	25.2	73.0	95	23.7
6	FadE27	76.1	83	22.2	76.1	82	22.0
7	FadD17	87.8	125	24.9	70.3	106	21.1
8	EchA19	92.0	92	35.0	92.0	83	31.6
9	KshA	11.4	18	4.7	19.7	22	5.7
10	HsaF	25.1	27	7.8	93.9	167	48.3
11	HsaE	27.6	24	9.2	96.5	109	41.8
12	KstD	0	0	0	0	0	0
13	FadE29	85.2	113	29.2	89.1	111	28.7
14	FadE28	91.4	97	28.6	98.5	88	26.0
15	Cyp125	9.0	15	3.4	12.2	18	4.2
16	FadA5	95.9	184	47.1	96.2	177	45.3
17	EchA20	78.5	70	28.3	93.9	69	27.9
18	FadE30	83.6	105	27.3	85.7	103	26.7
19	FadD3	98.4	178	35.1	98.4	172	33.9
20	HsaB	80.7	55	29.4	78.6	52	27.8
21	HsaC	86.3	74	24.7	28.7	26	8.7
22	HsaD	86.6	71	24.4	92.8	91	31.2
23	HsaA	84.0	79	20.0	82.7	83	21.1

24	KshB	54.2	63	17.6	60.0	73	20.4
25	IpdB	6.0	32	12.8	15.2	14	5.6
26	ChsH1	12.4	46	35.7	25.6	15	11.6
27	ChsH2	31.5	28	9.0	21.9	25	8.0
28	FadD19	87.2	161	29.3	87.6	166	30.2
29	Hsd4B	31.8	27	9.4	31.8	26	9.1