



STRUCTURAL BIOLOGY
COMMUNICATIONS

Volume 72 (2016)

Supporting information for article:

Crystal structure of a thiolase from *Escherichia coli* at 1.8 Å resolution

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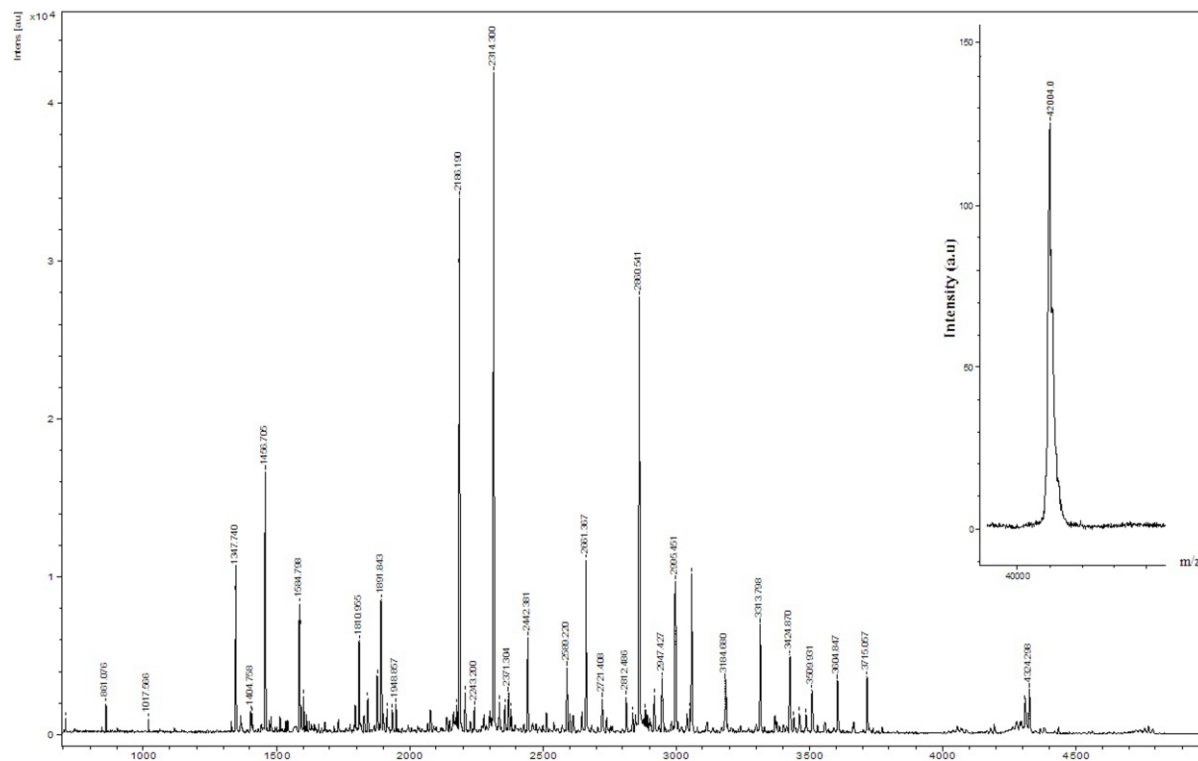


Figure S1 (a) MS spectrum for purified protein. (b) MALDI spectra for peptides of trypsin digested protein.

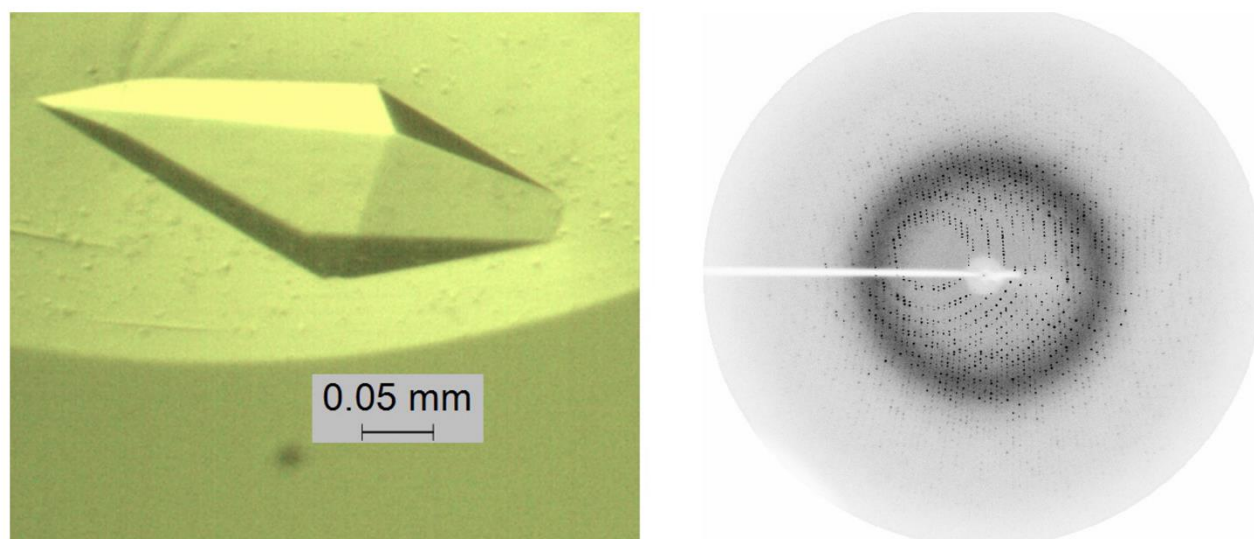


Figure S2 (a) A crystal of the *E. coli* thiolase obtained by co-crystallization in the presence of avetyl-CoA. (b) A typical oscillation diffraction image acquired using the home X-ray source.

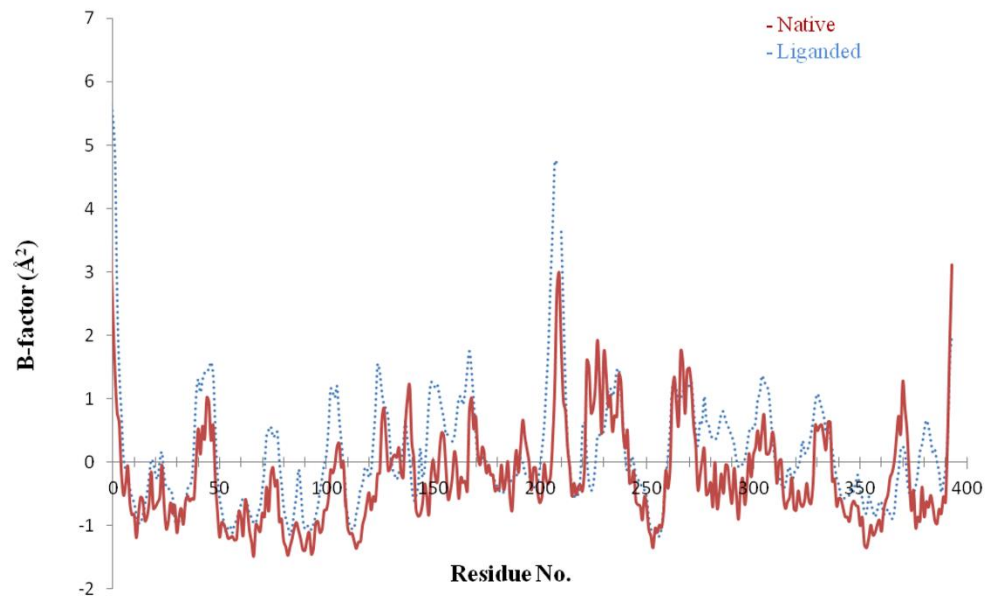


Figure S3 B-factor plot for the A-chain of both native and liganded (CoA bound) structures.

Table S1 Peptide mass fingerprinting of trypsin digested peptides and mass of individual peptides

S. No	Residue No.	Observed mass	Mr (Expt)	Mr (Calc)	Delta	Peptide sequence
1.	3 - 11	1017.57	1016.56	1016.54	0.02	NCVIVSAVR
2.	12 - 40	2834.54	2833.53	2833.52	0.01	TAIGSFNGSLASTSAIDLGATVIKAA IER
3.	41 - 67	2860.54	2859.53	2859.47	0.07	AKIDSQHVDEVIMGNVLQAGLGQNPA R
4.	43 - 67	2661.37	2660.36	2660.33	0.03	IDSQHVDEVIMGNVLQAGLGQNPAR
5.	94 - 128	3487.93	3486.93	3486.78	0.14	SVALAAQAIQAGQAOQSIVAGGMENMS LAPYLLDAK
6.	94 - 130	3715.06	3714.05	3713.92	0.13	SVALAAQAIQAGQAOQSIVAGGMENMS LAPYLLDAKAR
7.	131 - 146	1810.95	1809.95	1809.94	0.01	SGYRLGDGQVYDVILR
8.	135 - 146	1347.74	1346.73	1346.72	0.01	LGDGQVYDVILR
9.	135 - 167	3604.85	3603.84	3603.73	0.11	LGDGQVYDVILRDGLMCATHGYHMG I TAENVAK
10	147 - 173	2995.45	2994.44	2994.38	0.07	DGLMCATHGYHMGITAENVAKEYGIT R
11	168 - 185	2176.05	2175.04	2175.04	0.00	EYGITREMQDELALHSQR
12	174 - 185	1456.70	1455.70	1455.68	0.02	EMQDELALHSQR
13	174 - 186	1584.80	1583.79	1583.77	0.02	EMQDELALHSQRK
14	174 - 186	1600.85	1599.84	1599.77	0.07	EMQDELALHSQRK
15	187 - 208	2186.19	2185.18	2185.17	0.01	AAAAIESGAFTAEIVPVNVVTR
16	187 - 209	2314.30	2313.29	2313.27	0.02	AAAAIESGAFTAEIVPVNVVTRK
17	211 - 221	1344.67	1343.66	1343.64	0.02	TFVFSQDEFPPK
18	211 - 238	3057.60	3056.60	3056.52	0.07	TFVFSQDEFPPKANSTAEALGALRPAF DK
19	239 - 275	3424.87	3423.86	3423.77	0.10	AGTVTAGNASGINDGAAALVIMEESA ALAAGLTPLAR
20	330 - 357	2721.41	2720.40	2720.40	0.00	NLGFDFSEKVVNNGGAIALGHPIGASG AR
21	372 - 394	2357.26	2356.25	2356.26	-0.01	TLGLATLCIGGGQGIAMVIERLN