Supporting Information

Biosynthesis of the Antibiotic Tropodithietic Acid by the Marine Bacterium *Phaeobacter inhibens*

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Identification of 1 and 2:

Both compounds tropodithietic acid (1) and hydroxytropodithietic acid (2) were obtained from the commercial supplier Bioviotica Naturstoffe GmbH, 37127 Dransfeld, Germany. These compounds were used as standards for the identification of 1 and 2 in all culture extracts of *Phaeobacter inhibens* obtained during the course of this work.

Compounds 1 and 2 were isolated in the group of Prof. Axel Zeeck (University of Göttingen). The structure elucidation, full spectroscopic data for 1 and 2, and the evaluation of their bioactivities are given in:

Lanfang Liang, PhD thesis, University of Göttingen, 2003.

This thesis can be downloaded from:

http://ediss.uni-goettingen.de/bitstream/handle/11858/00-1735-0000-0006-B0BB-4/liang.pdf?sequence=1

EGV41540	MSNHVDIVP	SYLOGOWV	RPENPSRIVDV	ADASTC	EIVARVSSEGI	DIHGALD	YARTV
NP 415905	MOOLA	SFLSGTWO	SGRGRSRLI	HHAISC	EALWEVTSEGI	DMAAAROI	FAIEK
NP 745413	MSAAPTLQ	∽ Sfiagr <mark>w</mark> l	GQHG-AQAL	RSALD	HVLAYSHEERE	- DFAEAVD	YARAR
NP 947071	MTAILO	SLACDRWE	TPATGLVDI	PSAID	RVVARASSAGI	DFAAIAR	HAROV
YP_001105742	MAALR	SFVNGD <mark>w</mark> h	VPSEDGAPL	HDAVTG	EEVARISSAGI	DIAGALE	YGRÂR
YP_001335130	MOOLA	Sylsgawo	TGRGRARTI	HHAITG	AALWEVTSEGI	DMAOARRI	FAIER
YP_001542038	MSLLDVQ	∽ SFAAGHWI	APDADARMI	AHAVTC	APLARAGNGAI	DVQAMLD	YARDT
YP_612432	MCPKDVA	SFAAGEWI	APDHSAREI	ASAITC	EVIARAGNATI	DVQAMLDI	HARDT
WP 007118518	MRDIQ	SFAAGEWL	APGAGARNI	ASAITC	DVIAQAGNDAI	DVQAMLGI	FARDH
WP 009073845	MVLLR	SYVSGG <mark>w</mark> h	TAPGEGVPL	HDAATC	EEVARISSEGI	DFAAALD	YGRKV
YP_006574071	MSLLDVS	SFAAGQ <mark>w</mark> i	APGAGARSI	ASAITG	APLAQAGNDAI	DVQGMLD	YARTV
YP_006575081	MTDHVKRPRFLQ	SLIAERWD	HCGAQTQVF	'AD <mark>A</mark> ATN	IQPNAVLAYGSI	DGIQAVDI	FARAV
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EGV41540	G QKN <mark>L</mark> KALT F HE	RALKI <mark>k</mark> el	aly <mark>l</mark> nehkdvl	YQLAMC	SGANKR <mark>D</mark> NFVI	ID <mark>G</mark> GISTN	MFTFS
NP 415905	GAPALRAMTFIE	RAAML <mark>K</mark> AV	AKH <mark>L</mark> LSEKERF	YALSAÇ	TGATRADSWVI	IE <mark>G</mark> GIGTI	LFTYA
NP 745413	GLAS <mark>L</mark> MGMD F QQ	RAQRL <mark>K</mark> AL	aly <mark>l</mark> aeckeql	YALSHH	ISGATRADSWII	IE <mark>G</mark> GNATI	LFSYA
NP_947071	G GPK L RAMT F HQ	RADMLKAL	GAYLGERKEQL	YALAAC)T <mark>GA</mark> NRR <mark>D</mark> NAII	ID <mark>G</mark> SLVTI	LAAFA
YP_001105742	G GPV L GELT F HQ	RAALL <mark>K</mark> VL	ASHLEHREEL	YALSAR	RTGATLG <mark>D</mark> SKFI	ID <mark>G</mark> GIGVI	LFGYS
YP_001335130	GGKALQAMTFIE	RSAML <mark>K</mark> AV	AKH <mark>L</mark> LEQKDQF	YAISAÇ	TGATRADSWVI	IE <mark>G</mark> GIGTI	LFTYA
YP_001542038	- GGPALRALT F HD	RARML <mark>K</mark> AL	ALHLGAHKQAL	YDLSFA	TGATQADHLII	ID <mark>G</mark> GIGT	VFVFA
YP_612432	g gpa l ramt f hd	RARML <mark>K</mark> AL	AQH <mark>L</mark> DAHKQEL	YDQSFE	TGATOKDHLII	VD <mark>G</mark> GIGTV	VFVFA
WP 007118518	g gpa l ramt f hd	RARML <mark>K</mark> AL	ALHIMEHKQAL	YDLSYD	TGATLSDHKII	VD <mark>G</mark> GIGTN	MLVFA
WP 009073845	g gpa <mark>l</mark> rklt f hq	RAALLKSL	ASH L REHREEL	YALSAR	RTGATLG <mark>D</mark> SKFI	ID <mark>G</mark> GIGVI	LFSYG
YP_006574071	GGPSLRKLT F HD	RARML <mark>K</mark> AL	agh <mark>l</mark> nohkoal	YDLSFN	ITGATQSDHMII	ID <mark>G</mark> GIGTN	MFVFA
YP 006575081	<mark>g</mark> gpa <mark>l</mark> ralg f qd	RAQQLRAV	ARILKDNRAAL	YRESLT	IGATRHDCALI	VD <mark>G</mark> GIARI	LSALA
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EGV41540	SK <mark>G</mark> RRELPNTNV	IVDGPPEV	FAKDSS <mark>F</mark> QGQ <mark>H</mark>	IYTTLI	GVAVQINAFNE	'PVWGMLEI	KFAPS
EGV41540 NP 415905	SK <mark>GRRE</mark> LPNTNV SLGSRELPDDTL	IVDGPPEV WPEDELIP	FAKDSS <mark>F</mark> QGQH LSKEGG F AARH	IYTTLI LLTSKS	GVAVQINAFNE GVAVHINAFNE	PVWGMLEI PCWGMLEI	KFAPS KLAPT
EGV41540 NP_415905 NP 745413	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL	IVDGPPEV WPEDELIP VHEGPAIP	FAKDSS <mark>F</mark> QGQH LSKEGGFAARH LGKQGHFAGSH	IYTTLI LLTSKS ILVPRA	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE	'PVWGMLEI 'PCWGMLEI 'PIWGMLEI	KFAPS KLAPT KFAPT
EGV41540 NP_415905 NP_745413 NP_947071	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH	IYTTLI LLTSKS ILVPRA ILTPLH	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE	'PVWGMLEI 'PCWGMLEI 'PIWGMLEI 'PCWGLLEI	KFAPS KLAPT KFAPT KLAPA
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LGKGGTFVGQH	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLR	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE	'PVWGMLEI 'PCWGMLEI 'PIWGMLEI 'PCWGLLEI 'PVWGPLEI	KFAPS KLAPT KFAPT KLAPA KFAPA
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LGKGGTFVGQH LSKQGGFAARH	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLR VLTSKS	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE GVAVHINAFNE	'PVWGMLEI 'PCWGMLEI 'PIWGMLEI 'PCWGLLEI 'PVWGPLEI 'PCWGMLEI	KFAPS KLAPT KFAPT KLAPA KFAPA KLAPT
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LGKGGTFVGQH LSKQGGFAARH LSRTGTFLGQH	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLR VLTSKS IATPLQ	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE	'PVWGMLEI 'PCWGMLEI 'PIWGMLEI 'PCWGLLEI 'PCWGPLEI 'PCWGMLEI 'PVWGMLEI	KFAPS KLAPT KFAPT KLAPA KFAPA KLAPT KLAPT
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038 YP_612432	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDSTV	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YTDGAVEQ	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LGKGGTFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLR VLTSKS IATPLQ ICTSLF	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE	'PVWGMLEI 'PCWGMLEI 'PIWGMLEI 'PCWGLLEI 'PCWGPLEI 'PCWGMLEI 'PVWGMLEI 'PVWGMLEI	KFAPS KLAPT KFAPT KLAPA KFAPA KLAPT KLAPT KLAPT
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038 YP_612432 WP_007118518	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDSTV SKGRREMPDAHV	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YTDGAVEQ YLDGAPEQ	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LGREGQFMGRH	IYTTLT LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE	'PVWGMLEI 'PCWGMLEI 'PIWGMLEI 'PCWGLLEI 'PCWGPLEI 'PCWGMLEI 'PVWGMLEI 'PVWGMLEI 'PVWGMLEI	KFAPS KLAPT KLAPA KLAPA KLAPT KLAPT KLAPT KLAPT
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038 YP_612432 WP_007118518 WP_009073845	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDSTV SKGRREMPDAHV SKGRREMPDAHV	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YTDGAVEQ YLDGAPEQ YVEGAVEP	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LGKGGTFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LGREGQFMGRH LSRGGTFVAQH	IYTTLT LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ IATPLQ	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAIQINAFNE	'PVWGMLEI 'PCWGMLEI 'PCWGLLEI 'PCWGPLEI 'PCWGMLEI 'PVWGMLEI 'PVWGMLEI 'PVWGMLEI 'PVWGMLEI 'PVWGPLEI	KFAPS KLAPT KLAPT KLAPA KLAPT KLAPT KLAPT KLAPT KFAPA
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EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_01542038 YP_612432 WP_007118518 WP_009073845 YP_006574071 YP_006575081	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV GQALKSLPNAPV	IVDGPPEV WPEDELIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YTDGAVEQ YLDGAPEQ YVEGAVEP YLDGDIEQ LHLEDG	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LGKGGTFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LGREGQFMGRH LSRGGTFVAQH LSRNGTFLGQH IGPGSTTGRQQ	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ ICTPLQ ILAPLS	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVALIQINAFNE GVALHVTALDN	'PVWGMLEI 'PCWGMLEI 'PCWGLLEI 'PCWGPLEI 'PVWGMLEI 'PVWGMLEI 'PVWGMLEI 'PVWGMLEI 'PVWGPLEI 'PVWGMLEI 'PVWGMLEI	KFAPS KLAPT KFAPT KLAPA KLAPT KLAPT KLAPT KFAPA KLAPT QIAPA
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EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038 YP_612432 WP_007118518 WP_009073845 YP_006574071 YP_006575081 EGV41540	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV GQALKSLPNAPV FIAGMPTIVKPA	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YLDGAPEQ YLDGAPEQ LHLEDG TPTGYITA	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LSRGGTFVAQH LSRNGTFLGQH IGPGSTTGRQQ EAVRLMVE <mark>S</mark> GI	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLR VLTSKS IATPLQ ICTSLF ICTPLQ ILATPLQ ILAPLS	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE GVAVUNAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVALUNTAFNE GVALLINTALDN	PVWGMLEI PCWGMLEI PCWGLLEI PVWGPLEI PVWGPLEI PVWGMLEI PVWGMLEI PVWGMLEI PVWGMLEI PVWGMLEI	KFAPS KLAPT KLAPA KLAPT KLAPT KLAPT KLAPT KLAPT QLAPT QLAPA
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038 YP_612432 WP_007118518 WP_009073845 YP_006574071 YP_006575081 EGV41540 NP_415905	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV GQALKSLPNAPV FIAGMPTIVKPA WLGGMPAIIKPA	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YLDGAVEQ YLDGAPEQ YLDGAIEQ LHLEDG IPTGYITA TATAQLTQ	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LSRGGTFVAQH LSRNGTFLGQH IGPGSTTGRQQ EAVRLMVESGI AMVKSIVDSGL	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ ILAPLS LPEGSI VPEGAI	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVUINAFNE GVAVUINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVALHVTALDN LQLISGSVGDLI SLICGSAGDLI	PVWGMLE PCWGMLE PCWGLLE PCWGLLE PCWGPLE PCWGMLE PVWGMLE PVWGMLE PVWGMLE PVWGMLE PVWGMLE PVWGMLE PVWGMLE DVWGMLE	KFAPS KLAPT KFAPA KFAPA KLAPT KLAPT KLAPT KLAPT KFAPA KLAPT QIAPA
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038 YP_612432 WP_007118518 WP_009073845 YP_006574071 YP_006575081 EGV41540 NP_415905 NP_745413	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV GQALKSLPNAPV FIAGMPTIVKPA WLGGMPAIIKPA FLAGMPCIVKPA	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YLDGAVEQ YLDGAPEQ YLEGAVEP YLDGDIEQ LHLEDG TPTGYITA TATAQLTQ TSTSYLTE	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LSRGGTFVAQH LSRGGTFVAQH IGPGSTTGRQQ EAVRLMVESGI AVVKSIVDSGL AVVRLMNASGL	IYTTLT LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ ILAPLS LPEGSI LPEGSI LPEGSI	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVALHVTALDN LQLISGSVGDLI SLICGSAGDLI LQLVIGSTGDLI	PVWGMLEI PCWGMLEI PCWGLLEI PCWGPLEI PCWGMLEI PVWGMLEI PVWGMLEI PVWGMLEI PVWGMLEI PVWGMLEI PVSGLLE DHLDSQD DHLDSQD	KFAPS KLAPT KFAPA KLAPT KLAPT KLAPT KLAPT KLAPT KLAPT VTFT VVTFT VVTFT
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_01542038 YP_612432 WP_007118518 WP_009073845 YP_006574071 YP_006575081 EGV41540 NP_415905 NP_745413 NP_947071	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV GQALKSLPNAPV FIAGMPTIVKPA WLGGMPAIIKPA FLAGMPCIVKPA LLAGVPVIAKPA	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YLDGAVEQ YLDGAPEQ YLDGDIEQ LHLEDG TPTGYITA TATAQLTQ ISTSYLTE TATAYVAE	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LSRGGTFVAQH LSRGGTFVAQH IGREGQFMGRH LSRGGTFVAQH IGPGSTTGRQQ EAVRLMVESGI AVVRLMNASGL ALVKMIDESKL	IYTTLT LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ ILATPLQ ILAPLS VPEGAI LPEGSI LPEGSI LPEGSI	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVQINAFNE GVAVHINAFNE QVAVHINAFNE QVAVHINAFNE QVAVHINAFNE GVALHVTALDN LQLISGSVGDLI LQLVIGSTGDLI LQLVCGGLGDLI	PVWGMLEI PCWGMLEI PCWGLLEI PCWGLLEI PCWGPLEI PVWGMLEI PVWGMLEI PVWGMLEI PVWGMLEI PVWGPLEI PVWGPLEI DVWGPLEI DVWGPLEI DVWGPLEI DVUGQLEI DHLDSQD DRLQGQD	KFAPS KLAPT KFAPA KFAPA KLAPT KLAPT KLAPT KLAPT QIAPA HVAFT VVTFT VVTFT VIAFT
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EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_01542038 YP_612432 WP_007118518 WP_009073845 YP_006574071 YP_006575081 EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038 YP_612432	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV GQALKSLPNAPV FIAGMPTIVKPA WLGGMPAIIKPA FLAGMPCIVKPA LLAGMPAIIKPA LLAGMPAIVKPA LLAGMPAIVKPA	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGEVEQ YTDGAVEQ YLDGAPEQ YLDGAPEQ YLDGDIEQ LHLEDG IPTGYITA IATAQLTQ ISTSYLTE IATAYVAE SQTAYLTH IATAQLTQ IASCYVTE IATCYVTE	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LGKGGTFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LSRHGSFMGQH LSRGGTFVAQH LSRGGTFVAQH IGPGSTTGRQQ EAVRLMVESGI AVVRLMNASGL ALVKMIDESKL RLVELIVESGV AMVKAIVDSGL KAVRIILDSGI AAVRLMLDSGL	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ ILTPLQ ILAPLS LPEGSI LPEGSI LPEGSI VPEGAI LPAGAI LPAGAI	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVALHVTALDN QUAVGGLGDLI QLVCGGLGDLI QLVCGGLGDLI QLVCGGLGDMI QLVSGGLGDMI	PVWGMLEH PCWGMLEH PCWGMLEH PCWGLLEH PVWGPLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVSGLLE DHLDSQDY DHLDSQDY DHLTQQD DHLDSQDY DHLDSQDY	KFAPS KLAPT KFAPA KFAPA KLAPT KLAPT KLAPT KLAPT KLAPT VIAFT VVTFT VVTFT VVTFT VVTFT VVSFT VVSFT
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EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_01542038 YP_612432 WP_007118518 WP_009073845 YP_006574071 YP_006575081 EGV41540 NP_415905 NP_745413 NP_947071 YP_001335130 YP_001542038 YP_612432 WP_007118518 WP_009073845	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPNAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV GQALKSLPNAPV FIAGMPTIVKPA WLGGMPAIIKPA FLAGMPCIVKPA LLAGVPVIAKPA LLAGVPAIVKPA LLAGVPAIVKPA LLAGVPAIVKPA LLAGVPAIVKPA FLAGVPSLIKPA	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGAVEQ YTDGAVEQ YLDGAPEQ YLDGDIEQ LHLEDG TPTGYITA IATAQLTQ ISTSYLTE IATAYVAE SQTAYLTH IATAQLTQ IASCYVTE IATCYVTE SQTAYLTA	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LGKGGTFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LSRHGSFMGQH LSRHGSFMGQH LSRGGTFVAQH LSRNGTFLGQH IGPGSTTGRQQ EAVRLMVESGI AVVRLMNASGL ALVKMIDESKL RLVELIVESGI AAVRLMLDSGL AAVRLMLDSGL RLVELIVESGI	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ ILTPLQ ILAPLS LPEGSI LPEGSI LPEGSI LPEGAI LPEGAI LPEGAI LPEGAI LPAAV	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVALHVTALDN QUVIGSTGDLI QLVCGGLGDLI QLVCGGLGDLI QLVCGGLGDLI QLVSGGLGDMI QLVSGGLGDMI QLVSGGLGDMI QLVSGGLGDMI	PVWGMLEH PCWGMLEH PCWGMLEH PCWGLLEH PCWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH DVWGMLEH DVUGGLEQ DULDSQDY DHLDSQDY DHLDSQDY DHLDSQDY DHLTCQDY DHLTCQDY	KFAPS KLAPT KFAPA KFAPA KLAPT KLAPT KLAPT KLAPT KLAPT VTFT VVTFT VVTFT VVTFT VVTFT VVTFT VVTFT VVTFT VVSFT VVSFT AVAFT
EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_01542038 YP_612432 WP_007118518 WP_009073845 YP_006574071 YP_006575081 EGV41540 NP_415905 NP_745413 NP_947071 YP_001105742 YP_001335130 YP_001542038 YP_612432 WP_007118518 WP_009073845 YP_006574071	SKGRRELPNTNV SLGSRELPDDTL GIGSRELPSGNL SRGRRELPDAGF GKGRREMPDAKV GLGSRELPDDIL SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV SKGRREMPDAHV GQALKSLPNAPV FIAGMPTIVKPA WLGGMPAIIKPA FLAGMPCIVKPA LLAGVPVIAKPA LLAGVPAIVKPA LLAGVPAIVKPA LLAGVPAIVKPA LLAGVPSLIKPA LLAGVPAIVKPA	IVDGPPEV WPEDELIP VHEGPAIP ITEGEVEA YVDGAVEP WPEDELIP YLDGAVEQ YTDGAVEQ YLDGAPEQ YLDGAPEQ YLDGDIEQ LHLEDG TPTGYITA IATAQLTQ ISTSYLTE IATAYVAE SQTAYLTH IATAQLTQ TASCYVTE IATCYVTE SQTAYLTA	FAKDSSFQGQH LSKEGGFAARH LGKQGHFAGSH LSKRGSFVGQH LSKQGGFAARH LSRTGTFLGQH LSRHGSFMGQH LSRHGSFMGQH LSRHGSFMGQH LSRHGSFMGQH LSRNGTFLGQH IGPGSTTGRQQ EAVRLMVESGI AVVRLMNASGL AVVRLMNASGL AVVRLMNASGL AVVRLMLDSGL RAVRILDSGL RLVELIVESGI LAVRLMLESGI	IYTTLI LLTSKS ILVPRA ILTPLH ICTPLF VLTSKS IATPLQ ICTSLF ICTPLQ ILTPLQ ILAPLS VPEGAI LPEGSI LPEGSI LPEGAI LPEGAI LPEGAI LPAAV LPEGAI	GVAVQINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVAVHINAFNE GVALHVTALDN GULVSGLADN GVAGSVGDLI QLVSGLADN	PVWGMLEH PCWGMLEH PCWGMLEH PCWGLLEH PCWGMLEH PCWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH PVWGMLEH DVWGMLEH DVUGQLEQ DHLDSQD DHLDSQD DHLDSQD DHLDQD DHLTQD DHLDCQD DHLDCQD DHLDCQD DHLTQD	KFAPS KLAPT KFAPA KFAPA KLAPT KLAPT KLAPT KLAPT KLAPT VAFT VVTFT VVTFT VVTFT VVTFT VVTFT VVSFT VVSFT LVSFT LVSFT

Figure 1. Alignment of amino acid sequences of PaaZ from a selection of bacteria (EGV41540: *Corynebacterium glutamicum*, NP_415905: *Escherichia coli*, NP_745413: *Pseudomonas putida*, NP_947071: *Rhodopseudomonas palustris*, YP_001105742: *Saccharopolyspora erythraea*, YP_001335130: *Klebsiella pneumoniae*, YP_001542038: *Dinoroseobacter shibae*, YP_612432: *Ruegeria* sp., WP_007118518: *Oceanibulbus indolifex*, WP_009073845: *Streptomyces* sp., YP_006574071: *Phaeobacter inhibens* PaaZ1). Consensus of *P. inhibens* PaaZ2 (YP_006575081) to the highly conserved (black) residues is in the ECH-domain 52% (75/143) and in the ALDH-domain 86% (38/44).

EGV41540	GSAKTADTILRNLPKVRENGVRFSAEADSLNAAILGPDASVDTPEFEAYTKMLFAEMTSKA
NP 415905	GSAATGQM <mark>lr</mark> vQPnivaksipftm <mark>c</mark> adslnccvlgedvtpdqpefalfirevvr <mark>emt</mark> tka
NP 745413	GSADTAAK <mark>LR</mark> VTPNLIRNSVPFTAEADSLNCAILGPDVSPDSEEFDLYIKEVVREMTTKA
NP 947071	GSLETSEKLRAHPNVARHSIRFIAERDSLNAAVLGPDIKPADPEFDLFAHEIVREMTAKA
YP_001105742	GSAATGORLRAHPNVAARSVRFNVEADSLNCSVLGPDAAPGTDEFDLFVKOLVTEMTVKA
YP_001335130	GSAATGOOLRAHPNLVAKSIPFTMEADSLNCCVLGEDVTPEOPEFALFIREVVREMTAKA
YP_001542038	GSADUALRIRAAPHLLRNAVREVADODSINASIIGPDAVPGTPEFDLFIREVAREMUAKA
YP 612432	GSAATALKLROTPALVENSVREVADODSLNASTLGPDAAPGSAEEDLELKEVOREMTTKA
WP_007118518	GSADDALKLRSNDVLLONSVRETSDODSLNASVLGPDATPGTPEEDLEVKEVOREMTAKA
WP_009073845	CSA STAOKLRAHDA TURNSVRENAFADSINCSTI A DDARDSTDEEDI. FUKOLTTEMTUKA
VP 00657/071	
VP 006575081	
11_000075001	
EGV41540	GQKCTAIRRAIVPHGLIDNVAQALKQRLDDKVTVGDPRDASATMGPLVSVEQAEDVEGAV
NP 415905	GOKCTAIRRIIVPOALVNAVSDALVARLO-KVVVGDPAQEGVKMGALVNAEORADVOEKV
NP 745413	GOKCTAIRRAIVPARHLDAVATRLRERLS-KVVVGDPSLEGVRMGALASHDOORDVGERV
NP 947071	GOKCTATRRVLVPRAOEAAVIEALKARLA-DVKLGDPRRDDKAMGPLVSRGOREAVRAAI
YP_001105742	GOKCTATERALVPAGEVDDVVOAASEELS-KVVVGNPASPEVEMGALASLEOREEVERSI.
YP_001335130	GOKCTATERITVPLACINAWSDALTSRUH-KVTVCDPACEGVKMGAUVNSEORODVCESV
YP_001542038	GOKCTATERILAPOAOVDGWIAALGARIA-KTVIGDPRDTATTMGALVSNGOKEDWLAKA
VP 612432	COKCTATERITUPDA OVNAWIDCI.SA AIA - KITICDPRA DSTRMCALVSA AOKRDWLEGA
WD 007118518	
WP_000072045	
WP_009073043	
IP_006574071	
IP_006575081	GORRHAVERILLERHREAEVLADLSVILA-DIIVGVEDDAAIQMGALVSRGHLEIVQAAL
EGV41540	EKLIAAG G QVVTGGTVE <mark>GA</mark> FFA <mark>P</mark> TILTFADAYAER-I <mark>H</mark> DT <mark>EAFGPV</mark> VSLI
NP 415905	NILLAAGCEIRL <mark>G</mark> QQADLSAA <mark>GA</mark> FFP <mark>P</mark> TLLYCPQPDETPAVHATEAFGPVATLM
NP 745413	RSLLOS-CDOLF G ASDGFAPRGEGVAE <mark>CA</mark> FFA P TLLOARDPHAEGGAHDIEAFGPVSTLM
NP 947071	ATLOSEAEIVF-GDPNVCEAEGIDTOAGAYMSPVLLRAREPMOASHVHATEAFGPVATVL
YP 001105742	KALLAAGTLVH-GDPERVEVAGADAERGAFLPPMLVRCDDPDRAE-PHEVEAFGPVSTIM
YP 001335130	NKLIAAGCEVLLGGEADLSAAGAFFPPTLLYCSOPDETPAVHATEAFGPVATLM
YP_001542038	RVIATEAERVE-GDPEAETVHGADARTGAEI.PPMLI.HCADPDAAORI.HDTEAEGPVSTVM
VP 612432	DKIATEATRVE-COPONETVECADKOKCAEVODMLEHCADODAARHVHOTEAECOVSTVM
WP 007118518	ALL SAFAFRUE-CODDNETUKCADKOKCAFI DDMI FICADDOKAFRUHDTEAFCDUSTIM
WD 000073845	
WP_006574071	
IP_000574071 VD_006575091	
IP_006575081	DELRHGAEFVSDPIITPVETGGAFLSPVLLHCARPANTPDVHQTFVQGPVATAM
EGV41540	GYGDIDEAIELAAL <mark>G</mark> K <mark>GSI</mark> VASVATHDPATTARVAAGIAAH HGR LHFIDREDAKTS TGHG
NP 415905	PAONORHALOLACAGGESTAGTLVTADPOTAROFTADAARTHGRIOTLNEESAKESTGHG
NP 745413	AYDDLDEALALAARGKCSLVATLVTADRSVAAKATPVAAAWHGRLLVLDSOAAKESTGHG
NP 947071	AYDDVAOAVELVRRGECSLVASLFTYDDVVAEOMTLGLAPFHGRLLTVDRDDAAESTGHG
VP 001105742	
VD 001335130	
VD 0015/2020	
11_UUIJ42U30	GINDLDHAVALVINGAGOTVASLIINDELVARQVALGAGAFIGKLIINDRDSMGEAIGHG
IF_UIZ43Z	
	GYRDLSHASELANRGOGSLVASLITADPVVAREVTLNIAAFHGRVYINNATSMKESTGHG
WI_000110010	GYRDLSHASELANRGQGSLVASLITADPVVAREVTLNIAAFHGRVYINNATSMKESTGHG PYRDLPHASALLNRGQGSLVASIITNDGEVARELTIGSAAFHGRLYFNNRTSMKEATGHG
WP_009073845	GYRDLSHASELANRGQGSLVASLITADPVVAREVTLNIAAFHGRVYINNATSMKESTGHG PYRDLPHASALLNRGQGSLVASIITNDGEVARELTIGSAAFHGRLYFNNRTSMKEATGHG PYTSVKQVIEFAARGGGSLAGSVVTGDPVFAREIVLGVAPYHGRLLVLDSEDAKESTGHG
WP_009073845 YP_006574071	GYRDLSHASELANRGQGSLVASLITADPVVAREVTLNIAAFHGRVYINNATSMKESTGHG PYRDLPHASALLNRGQGSLVASIITNDGEVARELTIGSAAFHGRLYFNNRTSMKEATGHG PYTSVKQVIEFAARGGGSLAGSVVTGDPVFAREIVLGVAPYHGRLLVLDSEDAKESTGHG GYHDLDHAITLANRGEGSLVASVITHDTEVAREVALGAGAYHGRLYFNNRDSMKESTGHG

Figure 1. Alignment of amino acid sequences of PaaZ from a selection of bacteria (EGV41540: *Corynebacterium glutamicum*, NP_415905: *Escherichia coli*, NP_745413: *Pseudomonas putida*, NP_947071: *Rhodopseudomonas palustris*, YP_001105742: *Saccharopolyspora erythraea*, YP_001335130: *Klebsiella pneumoniae*, YP_001542038: *Dinoroseobacter shibae*, YP_612432: *Ruegeria* sp., WP_007118518: *Oceanibulbus indolifex*, WP_009073845: *Streptomyces* sp., YP_006574071: *Phaeobacter inhibens* PaaZ1). Consensus of *P. inhibens* PaaZ2 (YP_006575081) to the highly conserved (black) residues is in the ECH-domain 52% (75/143) and in the ALDH-domain 86% (38/44).

NP_415905SPLPQLVHG-GPGRAGGGEELGGLRAVKHYMQRTAVQGSPTMLAXNP_745413SPLPQLKHG-GPGRAGGGEELGGLRAVKHYLQRAAVQGSPSMLTXNP_947071TPLPALLHG-GPGRAGGGEELGGLRSVYHYMQRTAIQCSPRRLAMYP_001105742SPLPALVHG-GPGRAGGGEELGGLRSVYHYMQRTAVQADPDTLTXYP_001335130SPLPQLVHG-GPGRAGGGEELGGLRSVKHYMQRTAVQGSPTMLAXYP_001542038APLPHMIHG-GPGRAGGGEELGGVRGVMHYMQRTAIQGSPDMLTXYP_612432SPLPMWYHG-GPGRAGGGEELGGVRAVKHYMORTAVQGSPELLSX	AISKQWVRGA AVTGEYVRGG RLTGTWTRGA
NP_745413SPLPQLKHG-GPGRAGGGEELGGLRAVKHYLQRAAVQGSPSMLTZNP_947071TPLPALLHG-GPGRAGGGEELGGLRSVYHYMQRTAIQCSPRRLAHYP_001105742SPLPALVHG-GPGRAGGGEELGGLRSVKHYMQRTAVQADPDTLTZYP_001335130SPLPQLVHG-GPGRAGGGEELGGLRSVKHYMQRTAVQGSPTMLASYP_001542038APLPHMIHG-GPGRAGGGEELGGVRGVMHYMQRTAIQGSPDMLTZYP_612432SPLPMWHG-GPGRAGGGEELGGVRAVKHYMORTAVQGSPEILSZ	AVTGEYVR <mark>G</mark> G RLTGTWTRGA
NP_947071TPLPALLHG-GPGRAGGGEELGGLRSVYHYMQRTAIQCSPRRLAIYP_001105742SPLPALVHG-GPGRAGGGEEMGGVRGVLHHMQRTAVQADPDTLTAYP_001335130SPLPQLVHG-GPGRAGGGEELGGLRSVKHYMQRTAVQGSPTMLASYP_001542038APLPHMIHG-GPGRAGGGEELGGVRGVMHYMQRTAIQGSPDMLTAYP_612432SPLPHMVHG-GPGRAGGGEELGGVRAVKHYMORTAVQGSPEILGS	RLTGTWTR <mark>G</mark> A
YP_001105742 SPLPALVHG-GPGRAGGGEEMGGVRGVLHHMQRTAVQADPDTLTZ YP_001335130 SPLPQLVHG-GPGRAGGGEELGGLRSVKHYMQRTAVQGSPTMLAS YP_001542038 APLPHMIHG-GPGRAGGGEELGGVRGVMHYMQRTAIQGSPDMLTZ YP_612432 SPLPHMVHG-GPGRAGGGEELGGVRAVKHYMQRTAVQGSPEILGZ	
YP_001335130SPLPQLVHG-GPGRAGGGEELGGLRSVKHYMQRTAVQGSPTMLA: YP_001542038APLPHMIHG-GPGRAGGGEELGGVRGVMHYMQRTAIQGSPDMLTA YP_612432SPLPHMVHG-GPGRAGGGEELGGVBAVKHYMORTAVQGSPEILS3	AVTGQWVP <mark>g</mark> s
YP_001542038 APLPHMIHG-GPGRAGGGEELGGVRGVMHYMORTAIOGSPDMLT2 YP_612432 SPLPHMVHG-GPGRAGGGEELGGVBAVKHYMORTAVOGSPEILS2	FIGQQWVR <mark>G</mark> A
	AIGGKWVP <mark>G</mark> A
	AITGKWVP <mark>G</mark> G
WP 007118518 SPLPHMVHG-GPGRAGGGEELGGTRGVMHYMORTAVOGSPDTLT	ATGKOWVPGA
WP 009073845 SPMPOLVHG-GPGRAGGGEEMGGTRGVLHHMORTAVOGSPKVLG	AVTGRWVEG
YP 006574071 SPLPHMVHG-GPGRAGGGEELGGVBGVKHYMORTATOGSPDTLS	ATGEOWVPGG
YP 006575081 PDPSVPRLFAATHHAOVCGADDIR-HAVAAYMMRTETHAPPOLUT	ALTGRWVEGA
EGV41540 VTRAEVEAGTAE HPP RKDLATLKI G DOFASEL R EVTMGEIOA F AEE'	IGDTFYAHVNEEAA
NP 415905KVEEDRIHPERKYFEELOPGDSLLTPRETMTEADIVNEACL	SGDHFYAHMDKTAA
NP 745413EVIETEVHPERRYFEOLRVGESLLTHRETVTEADLVNEGCL	SGDHFYMHFDETAA
NP 947071PAPAAEVHPEKLNYNOLEIGOSIETASBPITLDDIEHEAHE	TGDTFYAHMDEAAA
YP 001105742 GRSVTDVHPERKHLEDLRVGDTVMAGPBAVTLEDVEHEAEF	TGDTFYAHTDEEAA
YP 001335130OVNEDRIHPERKYFEETOPGDSLLTPRBTLTEADIVNEACL	SGDHFYAHMDKTAA
YP = 0.01542038 =TETPAPAHPETRGEPALRIGETLHTPAROVTLADIEHEAAF	TGDTFYAHMDDAAA
	IGDTFYAHMDDAAA
WP 007118518OFTTORDHPETERFTELDLCETEVSKSREISLDDTETEANET	TGDTFYAHMDDEAA
WD = 0.00738/5 = -CPRVFC = -FHPERKSIAFISICDERTIFICATION CONTRACTOR	IGDIFIANMDEAAA ICDIFYAHTDEAAA
	TODII IMII DDMMA TODTEVAHMDDEAA
	TGDVFVAHMDRFAA
EGV41540 MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIOP	VTYG <mark>D</mark> SIRVE LT AK
EGV41540 MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPV NP 415905 AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPV	VTYG <mark>D</mark> SIRVE <mark>LT</mark> AK VKPGDTIOVRLTCK
EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-OFGKRIAHGYFVLSAAAGLEVSPGAGPVLANYGLDTLRFINP	VTYG <mark>D</mark> SIRVE <mark>LT</mark> AK VKPGDTIQVRLTCK VGIGDTIOARLTCK
EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPY	VTYG <mark>D</mark> SIRVE <mark>LT</mark> AK VKPGDTIQVRLTCK VGIGDTIQARLTCK VSPDDSIKVKLTVK
EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVSFAAGLFVEPSPGPVLANYGLENLRFLTP	VTYGDSIRVELTAK VKPGDTIQVRLTCK VGIGDTIQARLTCK VSPDDSIKVKLTVK FYPGDELTVTLTAK
EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVSFAAGLFVEPSPGPVLANYGLENLRFLTPYP_001335130AES-IFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEP	VTYGDSIRVELTAK VKPGDTIQVRLTCK VGIGDTIQARLTCK VSPDDSIKVKLTVK IYPGDELTVTLTAK VKPGDTIOVRLTCK
EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVVSFAAGLFVEPSPGPVLANYGLENLRFLTPYP_001335130AES-IFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEPYP_001542038ABNPFFPGRVAHGYLLLSFAAGLFVDPEGPVLANTGLDSLRFLKP	VTYGDSIRVELTAK VKPGDTIQVRLTCK VGIGDTIQARLTCK VSPDDSIKVKLTVK IYPGDELTVTLTAK VKPGDTIQVRLTCK VAPGDSLKARLTVK
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EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVVSFAAGLFVDPAPGPVLANYGLENLRFIEPYP_001335130AES-IFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEPYP_01542038ARNPFFPGRVAHGYLLLSFAAGLFVDPDEGPVLANTGLDSLRFLKPYP_612432ERNPFFPGRVAHGYLLLSFAAGMFVEPNEGPVLANTGLDNLRFMKPWP_007118518AANPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFLEPWP_009073845AANPLFGGTVAHGYLVVSFAAGLFVSPEPGPVLANYGLENLRFLTP	VTYGDSIRVELTAK VKPGDTIQVRLTCK VSPDDSIKVKLTVK TYPGDELTVTLTAK VKPGDTIQVRLTCK VAPGDSIKVRLTVK VVPGDSIKVRLTVK VVPGDSIKVRLTVK
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EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVVSFAAGLFVEPSPGPVLANYGLENLRFLTPYP_001335130AES-IFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEPYP_01542038ARNPFFPGRVAHGYLLLSFAAGLFVDPDEGPVLANTGLDSLRFLKPYP_612432ERNPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFMKPWP_007118518AANPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFLEPYP_006574071ARNPFFPGRVAHGYLLISFAAGLFVQPDGPVLANTGLDNLRFLEPYP_006574071ARNPFFPGRVAHGYLLISFAAGLFVQPDGPVLANTGLDNLRFLEPYP_006575081RSHPFFDDRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKP	VTYGDSIRVELTAK VKPGDTIQVRLTCK VSPDDSIKVKLTVK IYPGDELTVTLTAK VKPGDTIQVRLTCK VAPGDSLKARLTVK VVPGDSIKVRLTVK VSAGDSMKVRLTVK VKVDDQLTVTLTAK VSAGDSIKVRLTVK
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EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVVSFAAGLFVEPSPGPVLANYGLENLRFLTPYP_001335130AES-IFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEPYP_01542038ARNPFFPGRVAHGYLLLSFAAGLFVDPDEGPVLANTGLDNLRFMKPYP_612432ERNPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFLEPWP_007118518AANPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFLEPWP_009073845AANPLFGGIVAHGYLLVSFAAGLFVSPEPGPVLANTGLDNLRFMKPYP_006574071ARNPFFPGRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006575081RSHPFFDDRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006575081RITPRVTDEYGEVAWDTVLYNQDDEIVAAYDVLTLVEKVNT*NP 415905RKTLKKORSAEEKPTGVVEWAVEVFNOHOTPVALYSILTLVAROHGI	VTYGDSIRVELTAK VKPGDTIQVRLTCK VSPDDSIKVKLTVK IYPGDELTVTLTAK VKPGDTIQVRLTCK VAPGDSIKVRLTVK VVPGDSIKVRLTVK VSAGDSMKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VYFGDCLHVRVTCK
EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVVSFAAGLFVEPSPGPVLANYGLENLRFLTPYP_001335130AES-IFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEPYP_001542038ARNPFFPGRVAHGYLLLSFAAGLFVDPDEGPVLANTGLDSLRFLKPYP_612432ERNPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFMKPWP_007118518AANPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFLEPYP_006574071ARNPFFPGRVAHGYLLLSFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006574071ARNPFFPGRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006575081RSHPFFDDRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006575081RITPRVTDEYGEVAWDTVLYNQDDEIVAAYDVLTLVEKVNTNP_415905RKTLKKQRSAEEKPTGVVEWAVEVFNQHQTPVALYSILTLVARQHGINP_745413RKIDOGKTSPLGOPOGVVAWDVEVTNOLGELVASYDILTLVLKKPA	VTYGDSIRVELTAK VKPGDTIQVRLTCK VSPDDSIKVKLTVK TYPGDELTVTLTAK VKPGDTIQVRLTCK VAPGDSIKVRLTVK VVPGDSIKVRLTVK VSAGDSMKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VYFGDCLHVRVTCK
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EGV41540MRNPFFPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVVSFAAGLFVEPSPGPVLANYGLENLRFIEPYP_001335130AES-IFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEPYP_01542038ARNPFFPGRVAHGYLLLSFAAGLFVDPDEGPVLANTGLDSLRFLKPYP_0118518AANPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFMKPWP_009073845AANPFFPGRVAHGYLLLSFAAGLFVQPDFGPVLANTGLDNLRFLKPYP_006574071ARNPFFPGRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006575081RSHPFFDDRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006575081RITPRVTDEYGEVAWDTVLYNQDDEIVAAYDVLTLVEKVNT*NP_415905RKTLKKQRSAEEKPTGVVEWAVEVFNQHQTPVALYSILTLVARQHGINP_745413RKIDQGKTSPLGQPQGVVAWDVEVTNQLGELVASYDILTLVLKKPA-NP_947071QKSPARRPEYGEVRWDVEVVNQNGEPVARYDLLTMSARPAA-YP_001105742QITPRVNAEHGEVRWDADVTNOVGESVAKYDVLTLVAKRPEN	VTYGDSIRVELTAK VKPGDTIQVRLTCK VSPDDSIKVKLTVK TYPGDELTVTLTAK VKPGDTIQVRLTCK VAPGDSIKVRLTVK VVPGDSIKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VFGDCLHVRVTCK TYANDQKAEELAGV
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EGV41540MRNPFEPRRVAHGYLLVSWAAGLFVEPAPGPVLANYGLENLRFIQPNP_415905AES-IFGERVVHGYFVLSAAAGLFVDAGVGPVIANYGLESLRFIEPNP_745413KAS-QFGKRIAHGYFVLSAAAGLFVSPGAGPVLANYGLDTLRFINPNP_947071KANPFFPGRVAHGYLILAFAAGLFVDPAPGPLLANYGLDNLRFLKPYP_001105742KANPFFEGRVAHGYLVVSFAAGLFVEPSPGPVLANYGLENLRFLTPYP_001335130AES-IFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEPYP_001542038ARNPFFPGRVAHGYLLLSFAAGLFVDPDEGPVLANTGLDSLRFLKPYP_018518AANPFFPGRVAHGYLLLSFAAGLFVQPDPGPVLANTGLDNLRFMKPWP_009073845AANPFFPGRVAHGYLLLSFAAGLFVQPDFGPVLANTGLDNLRFLEPYP_006574071ARNPFFPGRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006575081RSHPFFDDRVAHGYLLISFAAGLFVQPDEGPVLANTGLDNLRFMKPYP_006575081RSHPFFDDRVAHGQLVVSFANGLLVDPAPGPVLANIGSDNLRFHAPEGV41540RITPRVTDEYGEVAWDTVLYNQDDEIVAAYDVLTLVEKVNT?NP_415905RKTLKKQRSAEEKPTGVVEWAVEVFNOHQTPVALYSILTLVARQHGINP_947071QKSPARRPEYGEVRWDDVEVVNQNGEPVARYDLLTWKRAPAYP_001105742QITPRVNAEHGEVRWDADVTNQVGESVAKYDVLTLVAKRPENYP_001335130RKTVKRQRSADEKATGVVEWAVEIFNOHQQAVALYSILTLVARQGGIYP_01142038HKTPRNDAYGEVRWHVSLTNCEDDLVAEYELLTMIAYAAYP612432AKTPRNEEYGEVRWHVSLTNODDELVAEYDLLTWAF	VTYGDSIRVELTAK VKPGDTIQVRLTCK VGIGDTIQARLTCK VSPDDSIKVKLTVK IYPGDELTVTLTAK VKPGDTIQVRLTCK VAPGDSIKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VYFGDCLHVRVTCK IYANDQKAEELAGV DFVD
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EGV41540MRNPFEPRRVAHGYLLVSWAAGLEVEPAPGPVLANYGLENLREIQPNP_415905AES-IFGERVVHGYFVLSAAAGLEVDAGVGPVIANYGLESLREIEPNP_745413KAS-QEGKRIAHGYFVLSAAAGLEVDPAGPULANYGLDTLREINPNP_947071KANPFEPGRVAHGYLILAFAAGLEVDPAPGPULANYGLDNLRELKPYP_001105742KANPFEGRVAHGYLVVSFAAGLEVEPSPGPVLANYGLENLREITPYP_001335130AES-IFGERVVHGYFLISAAAGLEVDPAGPULANYGMENLREIEPYP_001542038ARNPFEPGRVAHGYLLLSFAAGLEVDPDEGPVLANTGLDNLREMKPYYP_01542038ARNPFEPGRVAHGYLLLSFAAGLEVQPDPGPVLANTGLDNLREMKPYYP_00574071AANPFEPGRVAHGYLLLSFAAGLEVQPDGPVLANTGLDNLREMKPYYP_006574071ARNPFEPGRVAHGYLLSFAAGLEVQPDGPVLANTGLDNLREMKPYYP_006575081RSHPFEDDRVAHGYLLSFAAGLEVQPDEGPVLANTGLDNLREMKPYYP_006575081RSHPFEDDRVAHGYLLSFAAGLEVQPDEGPVLANTGLDNLREMKPYYP_001105742QKSPAVTDEYGEVAWDTVLYNQDDEIVAAYDVLTLVEKVNT7NP_415905RKTLKKQRSAEEKPTGVEWAVEVFNQHQTPVALYSILTLVARQHGINP_947071QKSPARRPEYGEVRWDAVEVTNQLGELVASYDITLVARAPAYP_001105742QITPRVNAEHGEVRWDADVTNQVGESVAKYDVLTLVARAPAYP_011335130RKTVKRQRSADEKATGVEWAVEIFNQHQQAVALYSILTLVARQGIYP_01135130RKTVKRQRSADEKATGVEWAVEIFNQHQAVALYSILTLVARQAFYP_0118518HKTPRNEEYGEVRWHVTLTNQDDELVAEYDLTMNALWP_009073845OITPRRNEEYGEVRWHVTLTNQREEAVAEYDLTMNAL	VTYGDSIRVELTAK VKPGDTIQVRLTCK VGIGDTIQARLTCK VSPDDSIKVKLTVK TYPGDELTVTLTAK VKPGDTIQVRLTCK VAPGDSIKVRLTVK VVPGDSIKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VSAGDSIKVRLTVK VYFGDCLHVRVTCK IYANDQKAEELAGV DFVD
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Figure 1. Alignment of amino acid sequences of PaaZ from a selection of bacteria (EGV41540: *Corynebacterium glutamicum*, NP_415905: *Escherichia coli*, NP_745413: *Pseudomonas putida*, NP_947071: *Rhodopseudomonas palustris*, YP_001105742: *Saccharopolyspora erythraea*, YP_001335130: *Klebsiella pneumoniae*, YP_001542038: *Dinoroseobacter shibae*, YP_612432: *Ruegeria* sp., WP_007118518: *Oceanibulbus indolifex*, WP_009073845: *Streptomyces* sp., YP_006574071: *Phaeobacter inhibens* PaaZ1). Consensus of *P. inhibens* PaaZ2 (YP_006575081) to the highly conserved (black) residues is in the ECH-domain 52% (75/143) and in the ALDH-domain 86% (38/44).

EGV41540	
NP_415905	
NP_745413	
NP_947071	
YP_001105742	
YP_001335130	
YP_001542038	
YP_612432	
WP_007118518	
WP_009073845	
YP_006574071	
YP_006575081	HTAATPHRAQDPVQQPAE

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Figure 2. Amino acid sequence alignment of PaaZ from *E. coli* with PaaZ1 and PaaZ2 from *P. inhibens*. A) C-terminal ECH-domains, B) N-terminal ALDH-domains. Asterisks mark essential residues of the ECH-domain while arrows highlight Cys-295 and Glu-256 of *E. coli* PaaZ which are essential for functional ALDH-domains as discussed in the main text.



Figure 3. Incorporation of the ³⁴S-labeling into TDA (1). A) *P. inhibens* control; B) after feeding of 1 mM [³⁴S]Cys; C) after feeding of 1 mM Na₂³⁴SSO₃; D) after feeding of 1 mM NaH³⁴SO₄; E) after feeding of 0.5 mM [³⁴S₂]cystine.



Figure 4. HPLC chromatograms (mass range m/z = 210.5-211.5) of culture extracts from *P*. *inhibens*. A) wild type, B) strain CP58, C) strain NB01. Tropodithietic acid (1) elutes at 7.4 min.



Figure 5. Incorporation of the ³⁴S-labeling into hydroxytropodithietic acid (**2**). A) *P. inhibens* control; B) after feeding of 1 mM [³⁴S]Cys; C) after feeding of 1 mM Na₂³⁴SSO₃; D) after feeding of 1 mM NaH³⁴SO₄; E) after feeding of 0.5 mM [³⁴S₂]cystine.



Figure 6. Feeding experiments with [*phenol*-¹⁷O]-L-tyrosine and ¹⁸O₂ and incorporation of labeling into hydroxytropodithietic acid (**2**). A) *P. inhibens* control; B) after feeding of 1 mM [¹⁷O]-L-Tyr; C) after incubation in an atmosphere with synthetic air containing ¹⁸O₂.



Figure 7. Mass spectra of tropone hydrate (24). A) *P. inhibens* control; B) *P. inhibens* after incubation in an atmosphere with synthetic air containing ¹⁸O₂.

Gene	Predicted function	Locus Tag ^[a]	Accession no. ^[b]
tdaA	Transcriptional regulator	PGA1_262p00980	YP_006575099
tdaB	Glutathione-S-transferase	PGA1_262p00970	YP_006575098
tdaC	Prephenate dehydratase-like protein	PGA1_262p00960	YP_006575097
tdaD	Thioesterase	PGA1_262p00950	YP_006575096
tdaE	Acyl-CoA dehydrogenase	PGA1_262p00940	YP_006575095
tdaF	Phosphopantothenoylcysteine decarboxylase	PGA1_262p00810	YP_006575082

Table 1. Bioinformatic analysis of the TDA gene cluster of *P. inhibens* DSM 17395.

[a] Locus tags of the targeted genes. [b] Accession number of the targeted proteins.

 Table 2. Oligonucleotide primers used in this study.

Primer	Sequence
NB064f_patB-LA_KpnI	CGCCTCCATGGTACCGATCATGTCCTGCC
NB064r_patB-LA_BamHI	CTCCCGTGGATCCCGGGCGAAGCTAAC
NB065f_patB-RA_BamHI	GCGATCGGATCCGCAACGCCTTCTC
NB065r_patB-RA_HindIII	GTCCTCAAGCTTGCCGGTGATCTCG
NB033f_pBBR1MCS1-5_BamHI	GGTCATAGCTGGATCCTGTGTGAAATTG
NB033r_pBBR1MCS1-5_BamHI	GCGCACGGATCCCCGAAAAGTG

Experimental Procedures and Spectral Data

Bacterial strains, plasmids, growth conditions and feeding experiments. Phaeobacter inhibens DSM17395, strain CP58¹, and strain NB01 were grown in half strength Marine Broth (MB 2216, Roth) and shaking (160 rpm) or on corresponding solid agar medium (20 g/L agar) at 28°C. When required, the medium was spiked after autoclavation with gentamycin sulfate (25 µg/mL) or kanamycin sulfate (60 µg/mL). Escherichia coli strains were grown in 2YT medium (16 g/L tryptone, 10 g/L yeast extract, 5 g/L NaCl, pH = 7.2) at 37°C with shaking (200 rpm) or on corresponding solid agar medium (20 g/L agar). When required, the medium was spiked after autoclavation with ampicillin (100 µg/mL) or kanamycin sulfate (50 µg/mL). For the feeding experiments, half strength MB liquid medium (50 mL) was spiked after autoclavation with 1 mM Na2³⁴SSO3 · 5 H2O, NaH³⁴SO4 (50% ³⁴S-enchrichment), [³⁴S]-Lcysteine hydrochloride, [*phenol*-¹⁷O]-L-tyrosine (35–40% ¹⁷O-enchrichment), or 0.5 mM [34 S₂]-L-cystine dihydrochloride, respectively. The flasks were inoculated with 1 mL of the preculture and incubated for 16 h at 28°C. For the feeding experiment with ¹⁸O₂, synthetic air was prepared from N₂ (790 mL) and ${}^{18}O_2$ (97.1% enrichment, 210 mL) in a balloon and connected to an inoculated flask. The culture flask volume (300 mL) diminished the effective labeling to ca. 75%. After 16 h, each culture was acidified with aqueous HCl (2 M, 5 mL), extracted with an equal volume of ethyl acetate, dried with MgSO₄, and concentrated in vacuo. The residue was taken up in methanol (2 mL) and analyzed via HPLC-MS. Collection of volatiles was done with a CLSA as reported previously.²

Construction of *P. inhibens* **mutant strains.** Primers used in this study are listed in Table 2. For deletion of *patB*, primers were designed to amplify chromosomal fragments upstream and downstream of the gene. The amplified upstream region was cloned into the *KpnI* and *Bam*HI sites of pUC-19. The amplified downstream region was cloned into the *Bam*HI and *Hin*dIII sites of the previously obtained plasmid carrying the respective upstream region. The kanamycin resistance gene (amplified from pBBR1MCS-2 and digested with *Bam*HI was cloned into the or *Bam*HI site of the respective plasmid that already carried the upstream and downstream regions. *P. inhibens* DSM 17395 was transformed by electroporation with this plasmid, leading to the strain NB01 ($\Delta patB::kan$).

HPLC-MS analyses. HPLC-MS analyses were carried out on a Thermo LTQ XL system with a C₁₈ column (Hypersil GOLD, 3 μ m, 150 × 2.1 mm). MS-Conditions were as follows: source type: HESI, capillary temperature: 275 °C, source heater temperature: 40 °C, sheath gas flow: 15, aux gas flow: 10, negative polarity, source voltage: 4 kV. The LC was programmed as follows:

Time (min)	Water	Acetonitrile	Methanol/water 1:1 + 2% formic acid
0.0	0.925	0.025	0.050
1.5	0.925	0.025	0.050
8.0	0.025	0.925	0.050
15.0	0.025	0.925	0.050
17.0	0.925	0.025	0.050
22.0	0.925	0.025	0.050

Commercially available tropodithietic acid (1) eluted at 7.4 min and hydroxytropodithietic acid (2) at 6.7 min.

General Synthetic Methods. Chemicals were purchased from Acros Organics (Geel, Belgium) or Sigma-Aldrich Chemie GmbH (Steinheim, Germany), and used without further purification. ³⁴S₈ (99.93% enriched) was purchased from Campro Scientific GmbH (Berlin, Germany). ¹⁸O₂ (97.1% enriched) and [*phenol*-¹⁷O]-L-tyrosine (35–40% enriched) were purchased from Euriso-Top GmbH (Saarbrücken, Germany). Solvents were purified by distillation, and dried according to standard methods. Oxygen and/or moisture sensitive reactions were carried out under inert atmosphere (N_2) in vacuum-heated flasks with dried solvents. Thin-layer chromatography (SiO₂, TLC) was performed on 0.20 mm Macherey-Nagel silica gel plates (Polygram SIL G/UV₂₅₄). Column chromatography was performed on Merck silica gel 60 (0.040 - 0.063 mm) using standard flash chromatographic methods. The NMR spectra were recorded on Bruker AV II-300 (300 MHz), DRX-400 (400 MHz) or AV III-400 (400 MHz) spectrometers, and were referenced against TMS or TMSP ($\delta = 0.00$ ppm) for ¹H-NMR and CHCl₃ ($\delta = 77.01$ ppm) for ¹³C-NMR. Multiplicities are abbreviated as follows: s = singlet, d = doublet, t = triplet, q =quartet, m = multiplet, br. = broad. Infrared spectra were recorded on a Bruker Tensor 27 ATR spectrometer. UV spectra were recorded on a Varian Cary 100 Bio spectrometer. Specific rotations were measured using a Dr. Kernchen Propol Digital Automatic Polarimeter. GC-MS analyses for the synthetic compounds were carried out on a HP6890 GC system connected to a HP5973 Mass Selective Detector fitted with a BPX-5 fused silica capillary column (25 m x 0.22 mm i.d., 0.25 µm film, SGE Inc., Melbourne, Australia). Conditions were as follows: inlet pressure: 77.1 kPa, He 23.3 mL min⁻¹; injection volume: 1 µL; injector: 250 °C; transfer line: 300 °C; electron energy: 70 eV. The GC was programmed as follows: 50 °C (5 min isothermic), increasing at 10 °C min⁻¹ to 320 °C, and operated in split mode; carrier gas (He): 1.0 mL min⁻¹ ¹. Retention indices were determined from a homologous series of *n*-alkanes (C_8-C_{32}).

K³⁴SCN: Elemental ³⁴S₈ (0.189 g, 5.56 mmol, 1.0 equiv.) was added to a solution of KCN (0.362 g, 5.56 mmol, 1.0 equiv.) in water (22 mL) and was stirred under reflux until the sulfur was consumed (48 h). Filtration and concentration in vacuo gave K³⁴SCN (0.546 g, 5.52 mmol, 99%) as a colorless solid. ¹³C-NMR (75 MHz, D₂O): δ = 136.1 (C_q) ppm.

Methyl N-(tert-butoxycarbonyl)-O-tosyl-L-serinate (13):³ To a solution of methyl N-(tertbutoxycarbonyl)-L-serinate (5.96 g, 27.2 mmol, 1.0 equiv.) in dry pyridine (50 mL) was added 4-toluenesulfonyl chloride (7.28 g, 38.1 mol, 1.4 equiv.) at -10 °C. After stirring at -10 °C overnight, the reaction was quenched with water, the mixture extracted with ethyl acetate, dried with MgSO₄, and concentrated in vacuo. The residue was purified by column chromatography on silica gel (hexane/ethyl acetate = 2:1) to give **13** (7.26 g, 19.5 mmol, 72%) as a colorless oil. TLC (hexane/ethyl acetate 2:1, $R_f = 0.42$). ¹H-NMR (400 MHz, CDCl₃, TMS): $\delta = 7.76$ (d, ${}^{3}J(H,H) = 8.4 \text{ Hz}, 2H, 2 \text{ CH}), 7.36 \text{ (d, }{}^{3}J(H,H) = 8.2 \text{ Hz}, 2H, 2 \text{ CH}), 5.32 \text{ (d, }{}^{3}J(H,H) = 8.1 \text{ Hz},$ 1H, NH), 4.51 (dt, ${}^{3}J(H,H) = 8.2$ Hz, ${}^{3}J(H,H) = 3.1$ Hz, 1H, CH), 4.40 (dd, ${}^{2}J(H,H) = 10.1$ Hz, ${}^{3}J(H,H) = 3.1 \text{ Hz}, 1H, CH_{2}, 4.29 \text{ (dd, }{}^{2}J(H,H) = 10.1 \text{ Hz}, {}^{3}J(H,H) = 3.1 \text{ Hz}, 1H, CH_{2}, 3.70 \text{ (s,})$ 3H, CH₃), 2.45 (s, ${}^{1}J(C,H) = 127.4$ Hz, 3H, CH₃), 1.42 (s, 9H, 3 CH₃) ppm. ${}^{13}C$ -NMR (100) MHz, CDCl₃): $\delta = 168.9$ (C_q), 154.9 (C_q), 145.1 (C_q), 132.3 (C_q), 129.9 (2 CH), 128.0 (2 CH), 80.4 (C_a), 69.5 (CH₂), 52.90 (CH), 52.85 (CH₃), 28.2 (3 CH₃), 21.6 (CH₃) ppm. IR (ATR): $\tilde{\nu}$ = 3399 (m), 2891 (w), 2927 (w), 1739 (s), 1704 (s), 1597 (w), 1510 (s), 1444w), 1370 (w), 1343 (s), 1243 (s), 1211 (m), 1155 (s), 1098 (m), 1058 (s), 1035 (w), 993 (s), 938 (s), 889 (s), 862 (m), 839 (m), 812 (s), 780 (s), 759 (m), 732 (s), 705 (w), 667 (s), 637 (m), 553 (s), 534 (s) cm⁻ ¹. UV/Vis (CH₂Cl₂): λ_{max} (ε , L mol⁻¹ cm⁻¹) = 273 (475), 262 (608), 231 (7980) nm.

[³⁴S]Methyl *N*-(*tert*-butoxycarbonyl)-*S*-cyano-L-cysteinate (14):⁴ A suspension of 13 (1.81 g, 4.85 mmol, 1.0 equiv.) and $K^{34}SCN$ (0.506 g, 5.11 mmol, 1.05 equiv.) in dry acetonitrile (20 mL) was stirred under reflux overnight. After concentration in vacuo, the residue was purified by column chromatography on silica gel (hexane/ethyl acetate = 3:1) to give 14 (0.399 g, 1.52

mmol, 32%) as a pale yellow oil. TLC (hexane/ethyl acetate 3:1, $R_f = 0.27$). GC (BPX-5): I = 1753. $[\alpha]^{22}_D = +95.1$ (*c* 1.67 in CHCl₃). ¹H-NMR (400 MHz, CDCl₃, TMS): $\delta = 5.57$ (d, ³*J*(H,H) = 7.0 Hz, 1H, NH), 4.69 (m, 1H, CH), 3.84 (s, ¹*J*(C,H) = 148.5 Hz, 3H, CH₃), 3.55 (dd, ²*J*(H,H) = 14.0 Hz, ³*J*(H,H) = 4.6 Hz, 1H, CH₂), 3.45 (dd, ²*J*(H,H) = 14.0 Hz, ³*J*(H,H) = 4.5 Hz, 1H, CH₂), 1.46 (s, ¹*J*(C,H) = 126.8 Hz, 9H, 3 CH₃) ppm. ¹³C-NMR (100 MHz, CDCl₃): $\delta = 169.2$ (C_q), 154.8 (C_q), 111.3 (C_q), 80.9 (C_q), 53.3 (CH), 53.1 (CH₃), 36.3 (CH₂), 28.2 (3 CH₃) ppm. MS (EI, 70 eV): m/z (%) = 262 (<1) [M]⁺, 203 (1), 188 (1), 145 (3), 128 (2), 103 (19), 88 (6), 57 (100), 41 (53). IR (ATR): $\tilde{\nu} = 3367$ (w), 2979 (w), 2157 (w), 1745 (m), 1703 (s), 1503 (m), 1438 (w), 1393 (w), 1366 (m), 1349 (m), 1317 w), 1247 (m), 1216 (m), 1158 (s), 1054 (m), 1013 (m), 914 (w), 857 (w), 779 (w), 731 (s), 647 (w) cm⁻¹. UV/Vis (CH₂Cl₂): λ_{max} (ε , L mol⁻¹ cm⁻¹) = 268 (269), 228 (289) nm.

[³⁴S]Methyl N-(tert-butoxycarbonyl)-L-cysteinate (15):⁵ To a solution of 14 (1.32 g, 5.04 mmol, 1.0 equiv.) and water (2.99 g, 166 mmol, 33 equiv.) in dry THF (111 mL) was added SmI₂ (4.48 g, 11.1 mol, 2.2 equiv.) at room temperature. After stirring for 5 min, the reaction was quenched with a saturated aqueous NH₄Cl solution, the mixture extracted with diethyl ether, dried with MgSO₄, and concentrated in vacuo. The residue was purified by column chromatography on silica gel (hexane/ethyl acetate = 3:1) to give **15** (0.855 g, 3.61 mmol, 72%) as a colorless oil. TLC (hexane/ethyl acetate 3:1, $R_f = 0.47$). GC (BPX-5): I = 1539. ¹H-NMR (400 MHz, CDCl₃, TMS): $\delta = 5.42$ (d, ³*J*(H,H) = 7.3 Hz, 1H, NH), 4.61 (m, 1H, CH), 3.79 (s, ${}^{1}J(C,H) = 147.9 \text{ Hz}, 3H, CH_{3}), 3.00 \text{ (ddd, } {}^{2}J(H,H) = 14.1 \text{ Hz}, {}^{3}J(H,H) = 9.2 \text{ Hz}, {}^{3}J(H,H) = 4.6 \text{ Hz}, 3.00 \text{ (ddd, } {}^{2}J(H,H) = 14.1 \text{ Hz}, 3.00 \text{ (ddd$ Hz, 1H, CH₂), 2.96 (ddd, ${}^{2}J(H,H) = 13.9$ Hz, ${}^{3}J(H,H) = 9.0$ Hz, ${}^{3}J(H,H) = 4.6$ Hz, 1H, CH₂), 1.46 (s, 9H, 3 CH₃) 1.40 (t, ${}^{3}J(H,H) = 8.9$ Hz, 1H, SH) ppm. ${}^{13}C$ -NMR (100 MHz, CDCl₃): $\delta =$ 170.8 (Cq), 155.1 (Cq), 80.3 (Cq), 54.8 (CH), 52.6 (CH₃), 28.3 (3 CH₃), 27.3 (CH₂) ppm. MS $(EI, 70 \text{ eV}): m/z \ (\%) = 237 \ (<1) \ [M]^+, 181 \ (10), 164 \ (5), 136 \ (6), 120 \ (25), 104 \ (8), 88 \ (19), 78$ (18), 57 (100), 41 (53). IR (ATR): $\tilde{\nu} = 3367$ (w), 2978 (w), 2568 (w), 1744 (m), 1704 (s), 1501 (m), 1438 (w), 1392 (w), 1366 (m), 1349 (m), 1249 (m), 1212 (m), 1159 (s), 1061 (m), 1025 (m), 910 (w), 858 (w), 800 (w), 780 (w), 733 (m) cm⁻¹. UV/Vis (CH₂Cl₂): λ_{max} (ε , L mol⁻¹ cm⁻¹ 1) = 228 (191) nm.

[³⁴S]-L-Cysteine hydrochloride (16):³ A solution of 15 (0.211 g, 0.89 mmol, 1.0 equiv.) in aqueous HCl (1 M, 10 mL) was stirred under reflux for 3 h. After concentrating in vacuo, the residue was purified by ion-exchange column chromatography (Dowex® 50-8, elution with 1 M HCl) to give 16 (0.107 g, 0.67 mmol, 75%) as a pale yellow solid. [α]²²_D = -24.5 (*c* 0.99 in H₂O, pH = 1.89). ¹H-NMR (400 MHz, D₂O, TMSP): δ = 4.29 (dd, ³*J*(H,H) = 5.6 Hz, ³*J*(H,H) = 4.3 Hz, 1H, CH), 3.17 (dd, ²*J*(H,H) = 15.1 Hz, ³*J*(H,H) = 5.6 Hz, 1H, CH₂), 3.11 (dd, ²*J*(H,H) = 15.1 Hz, ³*J*(H,H) = 4.3 Hz, 1H, CH₂) ppm. ¹³C-NMR (100 MHz, D₂O): δ = 173.4 (C_q), 57.5 (CH), 26.8 (CH₂) ppm. HRMS (ESI) [M – HCl + H⁺]/*z* calcd. 124.02282, found 124.02284.

[³⁴S₂]-L-Cystine dihydrochloride (17):⁶ [³⁴S]-L-cysteine hydrochloride (16, 11.9 mg, 74.4 μmol, 1 equiv.) was added to 0.15 mL of a solution of sodium iodide (11.2 mg, 74.7 μmol, 0.01 equiv.) in water (14.8 mL) and aqueous H₂O₂ (30%, 0.8 mL) at room temperature. After stirring at room temperature for 30 min, the reaction mixture was filtered, washed with water, and dried in vacuo to give **17** (9.5 mg, 30.0 μmol, 81%) as a colorless solid. $[\alpha]^{22}_{D} = -86.9$ (*c* 1.01 in 3% NaOH-H₂O, pH = 13.30). ¹H-NMR (300 MHz, 3%NaOD-D₂O, TMSP): δ = 3.57 (dd, ³*J*(H,H) = 7.5 Hz, ³*J*(H,H) = 4.7 Hz, 1H, CH), 3.11 (dd, ²*J*(H,H) = 13.6 Hz, ³*J*(H,H) = 4.7 Hz, 1H, CH₂), 2.91 (dd, ²*J*(H,H) = 13.6 Hz, ³*J*(H,H) = 7.6 Hz, 1H, CH₂) ppm. ¹³C-NMR (75 MHz, 3% NaOD-D₂O): δ = 183.5 (C_q), 57.5 (CH), 46.3 (CH₂) ppm.

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220	210	200	190	180	170	160	150	140	130	120	110	100	90	80	70	60	50	40	30	20	10	0 ppm









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