

Supporting Information

Nocathioamides, Uncovered by a Tunable Metabologenomic Approach, Define a Novel Class of Chimeric Lanthipeptides

Hamada Saad, Saefuddin Aziz, Matthias Gehringer, Markus Kramer, Jan Straetener, Anne Berscheid, Heike Brötz-Oesterhelt, and [Harald Gross*](http://orcid.org/0000-0002-0731-821X)

anie_202102571_sm_miscellaneous_information.pdf

Author Contributions

- H.S. Conceptualization: Lead; Gene cluster analysis: Lead; Methodology & HRMS analysis: Lead; Structural elucidation: Lead; Writing: Original draft: Lead; Writing: Review & Editing: Lead
- S.A. Experimental: Preliminary bioassays: Supporting
- M.G. Experimental: Chemical transformations and computer modeling: Lead
- M.K. Experimental: (special) NMR measurements: Lead; Review & Editing: Supporting
- J.S. Experimental: Antibacterial and cytotoxicity assays: Lead
- A.B. Experimental: Antifungal assays: Lead
- H.B.O Funding acquisition: Lead; Methodology & Antimicrobial tests: Lead; Writing: Review & Editing: Supporting
- H.G. Funding acquisition: Lead; Conceptualization: Supporting; Gene cluster analysis: Supporting; Structural elucidation: Supporting; Writing: Review & Editing: Lead

Table of Contents

1. Experimental Procedures

2. Results and discussion

3. Supplemental References

1. Experimental Procedures

1.1 General experimental procedures

Solvents employed were all HPLC grade. Chemical reagents and standards were purchased from Sigma Aldrich unless indicated otherwise. The isotopically labeled substrates [(¹⁵NH₄)₂SO₄, L-leucine (D10, 98%), and L-proline (D7, 97-98%)] were purchased from Cambridge Isotope Laboratories. Optical rotation values were measured on a Jasco P-2000 polarimeter, using a 3.5 mm × 10 mm cylindrical quartz cell. UV spectra were recorded on a PerkinElmer Lambda 25 UV/vis spectrometer. Infrared spectra were obtained by employing a Jasco FT/IR 4200 spectrometer, interfaced with a MIRacle ATR device (ZnSe crystal).

For Liquid Chromatography/High-resolution Electron Spray Ionization Mass Spectrometry (LC/HRESI-MSMS) measurements, an Ultimate 3000 HPLC (Thermo Fisher Scientific) system united with MaXis-4G instrument (Bruker Daltonics, Bremen, Germany) was used. The developed HPLC-method was (0.1% FA in H₂O as solvent A and MeOH as solvent B), a gradient of 10% B to 100% B in 40 min ending with 100% B for an additional 15 min, with a flow rate of 0.3 ml/min, 5 μl injection volume and UV detector (UV/VIS) wavelength monitoring at 210, 254, 280 and 360 nm. Integrating Phenomenex Luna Omega polar C18 (3 µm, 150 x 3 mm) column enabled the separation with MS acquisition range of m/z 50-1800. A capillary voltage of 4500 V, nebulizer gas pressure (nitrogen) of 2 (1.6) bar, ion source temperature of 200 °C, the dry gas flow of 9 I/min source temperature, and spectral rates of 3 Hz for MS¹ and 10 Hz for MSMS were used. For MS/MS fragmentation, the 10 most intense ions per MS¹ were chosen for subsequent collision-induced dissociation (CID) with the stepped recommended CID energies.^[1] For the mass calibration, sodium formate was directly infused before each sample measurement.

Vacuum liquid chromatography (VLC) was accomplished using the reversed-phase (RP) C18 column (dimensions: 10×5 cm; material: Macherey-Nagel Polygoprep 50–60 C18 RP silica gel) whereas size exclusion chromatography was done using a Sephadex LH-20 (GE Healthcare) manually packed in a column (dimension: 3 × 32 cm) running under the atmospheric pressure.

HPLC profiling was carried out using a system consisting of Waters 1525 Binary Pump with a 7725i Rheodyne injection port, a Kromega Solvent Degasser, Waters 2998 Photodiode Array Detector, and a Luna Omega polar C18 (5 µm, 250 × 4.6 mm, Phenomenex). ACN (solvent A) and H₂O + 0.1% TFA (solvent B) were used for the gradient elution of the analytes with a steady flow rate of 0.5 ml/min with an injection volume of 7 μl. For the main separation and purification, the same previous RP-HPLC setup was recalled using a Phenomenex Kinetex EVO C18 column (5 µm, 4.6×250 mm); 1 ml/min flow rate, and UV monitoring at 211, 250 and 280 nm.

1.2 NMR spectroscopy

1D and 2D NMR spectra were measured on a Bruker Avance III HD spectrometer (400, 100 and 40.6 MHz for ¹H, ¹³C and ¹⁵N NMR, respectively) at 297 K using a 5 mm SMART probe head. The NMR spectra were recorded in (d₄-CH₃OH, d₃-CH₃OH, d₆-DMSO) processed with TopSpin 3.5 and MestReNova 12.0.4 and calibrated to the residual solvent signals (δ_{H/C} 3.31/49.15 => *d*₄-CH₃OH, *d*₃-CH₃OH & δ_{H/C} 2.50/39.51=> *d*₆-DMSO). Mixing times were 80 ms for TOCSY and 300 ms for NOESY spectra. Band-Selective constant time HMBC spectra were recorded to dissect the peptide carbonyl region better.

Further d₃-CH₃OH datasets were attained from Bruker Avance III HDX spectrometer (700, 176 and 71 MHz for ¹H, ¹³C and ¹⁵N NMR, respectively) equipped with a 5 mm Prodigy TCI CryoProbe head. Mixing times were 80 ms for TOCSY and 300, 500 ms for NOESY spectra. For both spectrometers, ¹⁵N unreferenced chemical shifts were reported in ppm (spectrometer default values). All NMR raw data have been deposited in an OA repository (http://doi.org/10.5281/zenodo.4661802).

1.3 Mass spectrometry data processing and molecular networking

Mass spectral data were analyzed using Compass Data Analysis 4.4 (Bruker Daltonik), while MetaboScape 3.0 (Bruker Daltonik) was consulted for molecular features selection. Raw data files were imported into MetaboScape 3.0 for the entire data treatment and pre-processing in which T-ReX 3D (Time aligned Region Complete eXtraction) algorithm is integrated for retention time alignment with an automatic detection to decompose fragments, isotopes, and adducts intrinsic to the same compound into one single feature. All the harvested ions were categorized as a bucket table with their corresponding retention times, measured m/z, molecular weights, detected ions, and their intensity within the sample. The Bucket table was prepared with an intensity threshold (1e⁴) for the positive measurement with a minimum peak length 3 for the retention time range of interest from 15 to 30 min possessing a mass range *m/z* 150 - 1600 Da.

Metaboscape bucketing parameters were as follow:

Intensity threshold [counts] 10000.0 Minimum peak length [spectra] 3 Minimum peak length (recursive) [spectra] 1 Minimum # Features for Extraction 1 Presence of features in minimum # of analyses 1 Lock mass calibration false Mass calibration true Primary Ion [M+H]⁺ Seed Ions $[M+Na]^+$, $[2M+H]^+$, $[2M+Na]^+$, $[M+2H]^2^+$, $[M+H+Na]^2^+$ Common Ions $[M-H_2O+H]^+$, $[M+H_2O+H]^+$, $[2M+H_2O+H]^+$, $[2M-H_2O+H]^+$ EIC correlation 0.8 Mass range: Start [m/z] 150.0 Mass range: End [m/z] 1600.0 Retention time range: Start [min] 15.0 Retention time range: End [min] 30.0 Perform MS/MS import true Group by collision energy true MS/MS import method average

The features list of the pre-processed retention time range was exported from MetaboScape as a single MGF file which was in turn uploaded to the GNPS online platform where Feature-Based Molecular Network (FBMN) was created. The precursor ion mass tolerance was set to 0.03 Da and a MS/MS fragment ion tolerance of 0.03 Da. A network was then created where edges were filtered to have a cosine score above 0.70 and more than 5 matched peaks. Further, edges between two nodes were kept in the network if and only if each of the nodes appeared in each other's respective top 10 most similar nodes. Finally, the maximum size of a molecular family was set to 100, and the lowest-scoring edges were removed from molecular families until the molecular family size was below this threshold. Cytoscape 3.5.1 was used for molecular network visualization.[2]

GNPS job URL: https://gnps.ucsd.edu/ProteoSAFe/status.jsp?task=450f6e9825bd4accb5fe353d4e4ebe42

1.4 Bacterial strains

Nocardia terpenica IFM 0406 was attained from the Medical Mycology Research Center (MMRC) culture collection, Chiba University, Chiba, Japan, while *N. terpenica* IFM 0706 (DSM 44935) was purchased from the DSMZ (German collection of microorganisms and cell cultures).^[3]

1.5 Isotopic labeling experiments

N. terpenica IFM 0406 was revived on Brain Heart Infusion (BHI) broth agar plates (2%) incubated at 37 °C for three successive days observed by the growth of colonies. Using fresh spores of IFM 0406, triplicates of seed cultures were prepared in BHI broth media (80 ml) in 250 ml baffled Erlenmeyer flasks at 37 °C with 150 rpm for four consecutive days.

0.4 ml of the grown preculture was used to inoculate 50 ml of the production medium consisting of glucose 0.5%, glycerol 2%, soluble starch 2.0%, Pharmamedia 1.5%, yeast extract 0.3%,^[4] in a 250 ml Erlenmeyer baffled flask at 37 °C with 150 rpm for five days to a final concentration of 2 mM of the corresponding labeled amino acid. After 5-6 days, the supernatant was freed from cells by centrifugation and extracted twice with 50 ml of n-BuOH. The organic phases were combined, dried *in vacuo*, dissolved in MeOH and submitted to LC/HRESI-MSMS.

1.6 Large scale fermentation, extraction scheme, and (sub)fractionation

Nocardia terpenica IFM 0406 was grown adopting both Ikeda's *et al.* nutrients recipe and Chen's *et al.* cultivation parameters up to twenty liters (22 L).[4,5]

Following large scale cultivation, cultures were centrifuged twice in a Thermo Scientific Heraeus Multifuge 4KR centrifuge at 4000 g at 4 °C for 30 min to discard the cells. Subsequently, using n-BuOH (1:1), the supernatant (SN) was extracted twice. Under reduced pressure, the n-BuOH extract was evaporated affording the crude extract (Bu SN extract), which was resuspended in methanol followed by centrifugation to get rid of debris prior to LC/MS analysis, HPLC profiling, and VLC. Fractionation of the Bu SN extract was accomplished through a VLC system by stepwise elution of H₂O mixed with methanol controlled by vacuum with a decreased polarity fashion, shifting from 100% H2O to pure methanol in ten fractions (750 ml per fraction).

The prioritized VLC fraction (70% MeOH VLC) was redissolved in a mixture of MeOH:H2O (40:60) to be further sub-fractionated over a Sephadex LH-20 open column with a gradual elution starting with 100% H2O and ending with 100% MeOH delivering eight subfractions.

1.7 Isolation of nocathioamides (A, B)

The subfractions A and B, arising from Sephadex LH-20, were further purified by RP-HPLC with a polar gradient for 23 min using the formerly described HPLC setup equipped with a Phenomenex Kinetex EVO C18 column (5µm, 4.6×250 mm); 1 ml/min flow rate, and UV monitoring at 211, 250 and 280 nm. An additional round of purification was completed with a shorter run time, which resulted in pure nocathioamide A (**1**) (25 mg) and nocathioamide B (**2**) (12 mg).

1.8 Biological assays

The antibacterial assays and the determination of the cytotoxicity were performed as previously described.[5] For MIC testing of *Mycobacterium smegmatis*, instead of cationadjusted Müller Hinton medium, Middlebrook 7H9 broth was used.

The minimal inhibitory concentration (MIC) of **1** and **2** against different *Candida* clinical isolates was determined by broth microdilution using the direct colony suspension method with an inoculum of 0.5-2.5 x 10⁵ CFU/ml, according to the recommendations of the European Committee on Antimicrobial Susceptibility Testing (EUCAST).^[6] Caspofungin was used as reference antifungal agent. MIC testing was performed in sterile 96-well microdilution plates using MOPS-buffered RPMI 1640 medium supplemented with glucose to a final concentration of 2%, pH 7.0. MICs were read after incubation of the microplates at 37°C for 24-48 h.

Results and Discussion

The gene cluster coding for nocathioamides has been deposited in the Minimum Information about a Biosynthetic Gene Cluster (MIBiG) repository^[7] under accession number BGC0002120.

Protein homology analysis found in the nocathioamide biosynthetic gene cluster (*nta* BGC) employing the web-based tool RODEO and a manual BlastP search.^[8] The manual BlastP search was limited to records that exclude the species ´*Nocardia terpenica* (taxid:455432)´; listed are the top 1-3 hits. The protein hits, which represent the products of the *nta* BGC in the bacterium *Longimycelium tulufanense* CGMCC 4.5737 are indicated in orange.

Table S1. Putative functions of proteins from the *nta* BGC based on the web-based tool RODEO and a manual BlastP search.

a The *nta* BGC of strain IFM 0706 is located on contig 5 of the genome (Accession: NZ_JABMCZ010000005.1).

b The *nta* BGC of strain IFM 0406 is located on contig 15 of the genome (Accession: LWGR01000007.1).

Figure S1. Overview of the adopted metabologenomic strategy for the discovery of nocathioamides

Figure S2. Extracted ion chromatograms (EICs) and MS¹ of nocathioamide A (1) (1315 Da [M+H]⁺) and B (2) (1331 Da [M+H]⁺)

Figure S2A. Comparative [M+2H]2+ MS2 of nocathioamide A, B, and C (**1**-**3**) (658, 666, and 674 Da)

Figure S3. Comparative MS¹ of nocathioamide A (1) (1315 Da [M+H]⁺, 658 Da [M+2H]²⁺) and its ¹⁵N-based version

Figure S3A. Enlarged doubly ([M+2H]²⁺, panel A) and singly ([M+H]⁺, panel B) charged ions of nocathioamide A (1) and its ¹⁵N-based version

Figure S4. Comparative MS¹ of nocathioamide B (2) (1331 Da [M+H]⁺, 666 Da [M+2H]²⁺) and its ¹⁵N-based version

Figure S4A. Enlarged doubly ([M+2H]²⁺, panel A) and singly ([M+H]⁺, panel B) charged ions of nocathioamide B (2) and its ¹⁵N-based version

Figure S5. Comparative MS¹ of nocathioamide A (1) and its ([²H₁₀] L-leucine)-based version

Figure S5A. Enlarged doubly ([M+2H]²⁺, panel A) and singly ([M+H]⁺, panel B) charged ions of nocathioamide A (1) and its ([²H₁₀] L-leucine)-based version

Figure S6. Comparative MS¹ of nocathioamide B (2) and its ([²H₁₀] L-leucine)-based version

Figure S6A. Enlarged doubly ([M+2H]²⁺, panel A) and singly ([M+H]⁺, panel B) charged ions of nocathioamide B (2) and its ([²H₁₀] L-leucine)-based version

Figure S7. Comparative MS¹ of nocathioamide A (1) and its ([²H₇] L-proline)-based version

Figure S7A. Enlarged doubly ([M+2H]²⁺, panel A) and singly ([M+H]⁺, panel B) charged ions of nocathioamide A (1) and its ([²H₇] L-proline)-based version

Figure S8. Comparative MS¹ of nocathioamide B (2) and its ($[^2H_7]$ L-proline)-based version

Figure S8A. Enlarged doubly ([M+2H]²⁺, panel A) and singly ([M+H]⁺, panel B) charged ions of nocathioamide B (2) and its ([²H₇] L-proline)-based version

Figure S9. MS¹ and molecular formula prediction of nocathioamide A (1)

Figure S10. MS1 and molecular formula prediction of nocathioamide B (**2**)

Figure S11. MS¹ and molecular formula prediction of nocathioamide C (3)

Figure S12. HPLC profile of the *n*-butanol extract of cell-free supernatant of IFM 0406

Figure S13. HPLC profiles of VLC fractions of the *n*-butanol extract (Upper) & HPLC profiles of Sephadex LH-20 subfractions of 70% MeOH VLC fraction (Bottom)

Figure S14. HPLC profile of fraction A-100% H2O LH-20 (Upper) & HPLC profile of prepurified nocathioamide B (**2**) (Bottom)

Figure S15. HPLC profile of fraction B-100% H2O LH-20 (Upper figure) & HPLC profile of prepurified nocathioamide A (**1**) (Bottom figure)

Structural elucidation: NMR spectroscopy

In combination with extensive NMR analyses, the suggested elemental compositions of nocathioamide A (1) possessing m/z 1315 [M+H]⁺ and 658 [M+2H]²⁺ was expected to be C₅₄H₇₄N₁₆O₁₅S₄ with 26 degrees of unsaturation (RDB) with no matched hits to any known naturally occurring compound from any natural resource.

Expectedly, ¹³C-NMR spectra in the differently used solvents (d_{4} -, d_{3} -CH₃OH) exhibited a greater number of signals due to the inseparable minor conformer(s), which were also observed in the LC/MS (Figure S2) and HPLC (Figure S15) profiles. Additionally, careful inspection of the 1D and 2D NMR data unveiled a pairing phenomenon of almost all signals emphasizing a mixture of conformers. The observation of multiple doubly charged species as 658 $[M+2H]^2$, 669 $[M+H+Na]^2$, 677 $[M+H+K]^2$ (Figure S2) with a large number of exchangeable amide NH protons (δ_H 6.5-10.5) and carbonyl carbons (δ_c 160-185) from 1D NMR (Figures S38-39) aligned with the postulated peptide nature.

Figure S16. Structural fragments **I**, and **II**

Analyzing various 2D (¹H-¹H, ¹H-¹³C and ¹H-¹⁵N) NMR experiments (COSY, TOCSY, NOESY, HSQC, HSQC-TOCSY, HMBC) instantly resulted in the assignment of four proteogenic amino acid residues encompassing leucine (**Leu**), proline (**Pro**), alanine (**Ala-12**), and asparagine/aspartic acid (**Asn**/**Asp** due to the initial inabilities to allocate the δ_H of either -CONH₂ or –COOH, respectively). Exploiting HMBC and NOESY correlations, the connectivity between these readily discovered spin systems were directly established, offering a pair of fragments (**I**, and **II**), each consisting of two-stitched residues (Figure S16).

The distinctive olefinic CH₂ [δ_{H/C} 5.35/111.63 ppm in *d*₃-CH₃OH (700/176 MHz)] and its characteristic downfield NH₂ signal [δ_{H/N} 10.05/127.35 ppm in *d*₃-CH₃OH (700/71 MHz)] in tandem with the correlations from HMBC and NOESY experiments could unequivocally outline extended fragment **II** with an extra unit in the form of 2,3-didehydroalanine (**Dha**) (Figure S17A).

The clearly found singlets and their conformers in the aliphatic and aromatic regions [δ_H (2.02–2.04 & 7.30–8.90) ppm in *d*₄-CH₃OH (400 MHz)] aided in constructing fragment III with the help of the derived data mostly from ¹H-¹³C and ¹H-¹⁵N HMBC experiments (Figures S39, and S48). It started with a terminal acetyl group (Ac) linked to an alanine residue (Ala-1) which was in turn found to be connected to the thiazole moiety (Thz). Guided by the unique Thz resonances of 3-CH (δ_{H/C} 8.16/126.66 ppm in *d*₄-CH₃OH), and –N= (δ_N 305.60 ppm in d₃-CH₃OH) in joint with the ¹H-¹³C and ¹H-¹⁵N HMBC couplings,^[9] Thz unit was completely assigned to be in in a direct fusion with **Ala-1** (Figure S17B).

Analogously, histidine (**His**) was deciphered from its characteristic imidazole signals (δ**5H/C** 7.48/119.05, *δ***6H/C** 8.86/135.23, δ**5N** 175.04, and δ**6N** 191.59 ppm in *d*4-CH3OH). The inter-residue NOESY proved its occurrence to be in a direct linkage with Thz unit. Moreover, the ¹H-¹³C HMBC exhibited several cross-peaks around δc 206 - 209 ppm corresponding to an intensely relaxed signal in the 1D ¹³C-NMR spectrum (Figures S29, 39, 53), which were identified as couplings between the 2-CH (αH), and 3-CH₂ (βH) of histidine with the genetically expected thioamide tailoring that typically resonates around (200–210 ppm).^[10] Thus, **His** was selectively posttranslationally modified into thiohistidine portraying fragment **III** (Figure S17B).

Figure S17. Structural fragments extended **II**, and **III**

The assembly of the highly morphed fragment **IV** was initiated by the guidance of ¹H-¹H TOCSY, ¹H-¹³C HSQC-TOCSY, and NOESY experiments, which enabled decoding of a common posttranslationally tailored motif as α-aminobutyrate (**Abu**), biosynthetically originating from threonine. Tracing up such spin system (**Abu**) with 1 H-13C HMBC, and NOESY correlations uncovered three additional transformed amino acid residues (**AlaS-6**, **AlaS-10**, and **AlaS-11**), comprising typical methyllanthionine (**MeLan = Abu** + **AlaS-10**) (Figures S108-108A), and lanthionine (**Lan = AlaS-6** + **AlaS-11**) bridges, [11] besides an exceptionally δ-oxidized leucine in the form of 4-methylglutamate (**4- Meglu**).[12] As a result of the highly similar (identical) chemical shifts of α- protons of **AlaS-6** and **AlaS-11** across the different datasets (Tables S2-4A), the NOESY analysis did not result in any convincing correlations using neither the β-, or α- protons of the **Lan** residues to validate the crosslink (Figures S108, and S108B-108C). [13] Mainly supervised by the homonuclear correlations arising from NOESY data, **MeLan** and **Lan** blocks were found to be directly bonded to each other on one side whilst being disjointed on the **Abu** flank by **4-Meglu** (Figure S18).

Figure S18. Structural fragment **IV**

Considering the deduced skeletons of fragments (**I**–**IV)**, it was clear that fragment **I** portrayed the C-terminus of the peptide while the amino-terminus was represented as fragment **III** N-capped with an acetyl group.

Besides the heteronuclear connections of αH and βH**-His** to 13C=S, an extra set of aligned couplings **(**δ**2H/C, major** 5.48/65.74, δ**2H/C, minor** 5.37/65.74 in *d*4-CH3OH) was identified signifying the αH of the Abu motif. The confirmatory observation of 1H-¹⁵N HMBC couplings between αH-His and NH of the Abu offered further unambiguous proof of fitting fragment **III** together with component **IV/A** (Figures S19, and S60). Notably, the uniquely deshielded NH signals of the **Abu** spin system [δ**H/N** 9.77/ 155.59 ppm in *d*3-CH3OH (700/71 MHz)] were also in alignment with its straight association with the thiocarbonyl group (Figure S19). The additional attachment of fragment **I** to **IV/D** was basically gleaned from both ¹H-¹³C HMBC along with ¹H-¹H NOESY data (Figure S19).

Figure S19. Structural fragments **III**+**IV/A**, and **I**+**IV/D**

Finally, the extended fragment **II** was found to be architecturally inserted within **IV** using solely NOE connections which placed the **Dha** structural brick in association with **AlaS-6** feature (**IV/B**), whereas **Pro** was attached to **AlaS-10** system (**IV/C**) (Figure S20).

Extended Fragment II (Pro) + IV/C

Figure S20. Structural fragments extended **II** (**Dha**) + **IV/B**, and extended **II** (**Pro**) + **IV/D**

Although fragment **IV** possessed five possible attachment sites (**A** – **E**), only four (**A** – **D**) could be structurally ruled out. Unfortunately, meticulous investigation of the different NMR datasets (*d*4-CH3OH, and *d*3-CH3OH) did not infer any valuable couplings that could sort out any structural connection with the last remaining decoration **E**.

However, bearing in mind the anticipated molecular formulae besides its RDB, one final macrocyclization has to be recruited. Driven by the inability to assign δ_H of neither the in-chain NH2 nor C-terminus CO2H of **Asn** of fragment **I**, two possible crosslinks have been suggested either as an imide or anhydride macrocyclization, respectively (Figure S21).

Figure S21. Possible crosslinks between fragment **I**-**Asn** and fragment **IV/E** (Upper) & Macrocylic imide PTM connected by NMR through NOESY and HMBC correlations (Bottom)
The possibility of having a macrocyclic anhydride makeup was apparently in strong contradiction with **1** in terms of the given chemical stability observed during the extraction, separation, purification and storage as well.

Luckily, the ¹H-¹⁵N HMBC spectrum of 1 in CD₃OH/700 MHz dataset, in an unintentional partial sweep width (partial SW) experiment, disclosed a so far non-interpreted pair of two unfamiliar cross-peaks (δ**3Ha/Asn** 2.64/ δ**^N** 172.80, δ**3Hb/Asn** 2.99/ δ**^N** 172.80 ppm) (Figures S60, and S114A) which were consistent with the reported 15N values of imides.[14] Additionally, ¹H-¹⁵N HSQC of NH glutarimide, an imide-containing standard, (δ_{H/N} 10.33/172.25 in *d*₃-CH₃OH) supported such a range of chemical shifts (Figure S100) and corroborated the imide linkage hypothesis.

Within the course of our preliminary NMR trials recording in various solvents, d_6 -DMSO was tested even though the data quality was not good enough to fully elucidate the structure of 1. Unexpectedly, the ¹H-¹⁵N HSQC spectrum (Figure S97) showed two characteristic downfield correlations (δ_{H/N} 10.55/161.63, and δ_{H/N} 11.19/174.72 ppm), which were tracked down by ¹H-¹H TOCSY, ¹H-¹H NOESY, and ¹H-¹³C HMBC correlations. The δ_{H/N} 10.55/161.63 ppm coupling was assigned to define the thioamide –NH- of **Abu** entity, whereas the sharp singlet δ**H/N** 11.19/174.72 ppm was found to be in an equivocal consistency with the presumed imide crosslink evidenced by a multitude of connectivities (Figures S21, S94, and S99-99A).

Regardless of the unsatisfactory NMR data quality in d_6 -DMSO compared to d_3 - and d_4 -CH₃OH, the dataset could still successfully and efficiently fill the remaining gap regarding the last unprecedented structural ornament and complete the 2D structure of nocathioamide A (**1**) (Figure S22).

Taking into account the suggested molecular formulae of the additional isolated feature, C54H74N16O16S4, it was envisioned that nocathioamide B (**2**) encode an extra oxygen atom within its architecture relative to **1**. Expectedly, **2** exhibited almost identical NMR spectra of **1** except with a lower degree of signals overlap besides a significant drift in the β-carbons chemical shifts of AlaSO-6 and AlaSO-11. The attained ¹H-¹³C HSQC spectra in *d*₃- and *d*₄-CH₃OH datasets all share that the Lan bridge forming residues (AlaSO-6, AlaSO-11) inherited an upfield shift with their α -carbons (δ c-Alase 55.49 => δ c-Alasos 51.50 & δ c-Alaso11 43.60 => δ c-Alaso11 49.46, d_3 -CH₃OH, 176 MHz) whilst the β carbons resonated strongly downfield (δ**C-AlaS6** 34.18 => δ**C-AlaSO6** 55.52 & δ**C-AlaS11** 35.43/35.52 => δ**C-AlaSO11** 59.73, *d*3-CH3OH, 176 MHz) (Figures S64, S73, S83, and S118). In addition, the **Lan** crosslink motifs in **2**, unlike **1**, were found to exhibit more resolved NOESY correlations proving the bridge formation between **AlaSO-6**, and **AlaSO-11** (Figures S103, and S121B-121C). Considering such changes in the chemical shifts that typically occurs upon diagnostic oxidation of the thioether functionality,[15] **2** was deduced to be the S-monooxidized congener of **1** (Figure S22).

Figure S22. Structures of nocathioamide A (**1**), and B (**2**)

Nocathioamide A (1): C₅₄H₇₄N₁₆O₁₅S4. White amorphous powder, [α]p²³= +2.1 (c 0.75, MeOH); ¹H-NMR (400 / 700 MHz, in *d*4-CH₃OH, and *d*₃-CH₃OH): see Tables (S2 – S4); 13C-NMR (100 / 176 MHz, in *d*4-CH3OH, and *d*3-CH3OH): see Tables (S2 – S4); 15N-NMR (40.6 / 71 MHz, in *d*4-CH3OH, and *d*3-CH3OH): see Tables (S2 – S4); FT-IR (ATR) n (cm-1): 3415, 3254, 2925, 2829, 1651, 1538, 1199, 1023 (see Figure S140); UV (MeOH): lmax (log ε) 272 nm (4.1): see Figure S140. HR-ESIMS *m/z* 658.2276 [M+2H]²⁺ (calcd for C₅₄H₇₆N₁₆O₁₅S₄, 658.2274); 1315.4461 [M+H]⁺ (calcd for C₅₄H₇₅N₁₆O₁₅S₄, 1315.4475). HRMSMS: see Figure S2A.

Nocathioamide B (2): C₅₄H₇₄N₁₆O₁₆S₄. White amorphous powder, $\left[\alpha\right]_{2}^{23}$ = -1.6 (c 0.75, MeOH); ¹H-NMR (400 / 700 MHz, in d₄-CH₃OH, and d₃-CH₃OH): see Tables (S5 – S7); **Nocathioamide B (2**): C₅₄H₇₄N₁₆O₁₆S4. White amorphous powder, [ɑ]p²³= -1.6 (c 0.75, MeOH); ¹H-NMR (400 / 700 MHz, in *d*4-CH₃OH, and *d*3-CH3OH): see Tables (S5 – S7);
¹³C-NMR (100 / 176 MHz, in *d*4-CH3OH Figure S140); UV/Vis (MeOH): λ_{max} (log ε) 271 nm (4.0): see Figure S140. HR-ESIMS *m/z* 666.2260 [M+2H]²⁺ (calcd for C₅₄H₇₆N₁₆O₁₆S₄, 666.2249); 1331.4433 [M+H]⁺ (calcd for C54H75N16O16S4, 1331.4424). HRMSMS: see Figure S2A.

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [n.d] not determined

Table S2. ${}^{1}H$, ${}^{13}C$, and ${}^{15}N$ -NMR data of nocathioamide A (1) (d₃-CH₃OH; 400/100/40.6 MHz; major conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [n.d] not determined

Table S2A. ¹H, ¹³C, and ¹⁵N-NMR data of nocathioamide A (1) (d₃-CH₃OH; 400/100/40.6 MHz; minor conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [n.d] not determined Table S3. ¹H, ¹³C, and ¹⁵N-NMR data of nocathioamide A (1) (d₃-CH₃OH; 700/176/71 MHz; major conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [n.d] not determined

Table S3A. ${}^{1}H$, ${}^{13}C$, and ${}^{15}N$ -NMR data of nocathioamide A (1) (d_3 -CH₃OH; 700/176/71 MHz; minor conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [n.d] not determined Table S4. ¹H, and ¹³C-NMR data of nocathioamide A (1) $(d_4$ -CH₃OH; 400/100 MHz; major conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [n.d] not determined Table S4A. ¹H, and ¹³C-NMR data of nocathioamide A (1) (d₄-CH₃OH; 400/100 MHz; minor conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [nd] not determined Table S5. $1H$, and $13C$ -NMR data of nocathioamide B (2) (d_3 -CH₃OH; 400/100 MHz; major conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [nd] not determined Table S5A. ¹H, and ¹³C-NMR data of nocathioamide B (2) (d₃-CH₃OH; 400/100 MHz; minor conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [nd] not determined Table S6. ¹H, and ¹³C-NMR data of nocathioamide B (2) $(d_3$ -CH₃OH; 700/176 MHz; major conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [nd] not determined Table S6A. ¹H, and ¹³C-NMR data of nocathioamide B (2) (d₃-CH₃OH; 700/176 MHz; minor conformer)

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [nd] not determined Table S7. ¹H, and ¹³C-NMR data of nocathioamide B (2) (d₄-CH₃OH; 400/100 MHz; major conformer)

 $\overline{}$

[*] AA with modified CO within the backbone, [a] Overlapped, [b] Masked by water/solvent ¹H/¹³C-NMR signals, [c] Interchangeable, [d] Weak, [nd] not determined Table S7A. ¹H, and ¹³C-NMR data of nocathioamide B (2) (d₄-CH₃OH; 400/100 MHz; minor conformer)

Figure S23. ¹H-¹³C HMBC spectra of fractions 70% (panel A), 80% (panel B), 90% (panel C), and B LH20_70% (panel D) MeOH (*d*₄-CH₃OH, 400/100 MHz), respectively exhibiting cross correlations typical for oxazole and/or thiazole entities (δ_{H/C}, 8.18/148.32 and δ_{H/C}, 8.18/174.91 ppm). Only fraction 70% and the LH20_70% fractions show the correlations of interest, while these resonances are absent in the 80% and 90% fractions.

Figure S24. ¹ H-NMR spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 400 MHz)

Figure S25. 13C-NMR spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 100 MHz)

Figure S26. DEPT-135 spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 100 MHz)

Figure S27. ¹H-¹³C HSQC spectrum of nocathioamide A (1) (d₄-CH₃OH, 400/100 MHz)

Figure S28. ¹ H-13C HSQC-TOCSY spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 400/100 MHz)

Figure S29. ¹ H-13C HMBC spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 400/100 MHz)

Figure S30. Band-Selective ¹H-¹³C-HMBC spectrum of nocathioamide A (1) (d₄-CH₃OH, 400/100 MHz)

Figure S31. ¹H-¹H COSY spectrum of nocathioamide A (1) (d₄-CH₃OH, 400/400 MHz)

Figure S32. ¹ H-1 H TOCSY spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 400/400 MHz)

Figure S33. ¹ H-1 H NOESY spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 400/400 MHz, d8 = 300 msec)

Figure S34. ¹ H-NMR spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400 MHz)

Figure S35. ¹³ C-NMR spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 100 MHz)

Figure S36. DEPT-135 spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 100 MHz)

Figure S37. ¹ H-13C HSQC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/100 MHz)

Figure S38. ¹ H-13C HSQC-TOCSY spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/100 MHz)

Figure S39. ¹ H-13C HMBC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/100 MHz)

Figure S40. ¹ H-13C Band-Selective HMBC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/100 MHz)

Figure S41. ¹ H-1 H COSY spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/400 MHz)

Figure S42. ¹H-¹H TOCSY spectrum of nocathioamide A (1) (d₃-CH₃OH, 400/400 MHz)

Figure S43. ¹H-¹H TOCSY WET spectrum of nocathioamide A (1) (d₃-CH₃OH, 400/400 MHz)

Figure S44. ¹ H-1 H NOESY spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/400 MHz, d8 = 300 msec)

Figure S45. ¹ H-1 H NOESY WET spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/400 MHz, d8 = 300 msec, PLW1 = 27)

Figure S46. ¹ H-15N HSQC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/40.6 MHz)

Figure S47. Enlarged ¹H-¹⁵N HSQC-TOCSY spectrum of nocathioamide A (1) (d₃-CH₃OH, 400/40.6 MHz)

Figure S48. ¹ H-15N HMBC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/40.6 MHz)

Figure S49. ¹ H-NMR spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700 MHz)

Figure S50. ¹³C-NMR spectrum of nocathioamide A (1) (d_3 -CH₃OH, 176 MHz)

Figure S51. ¹ H-13C HSQC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700/176 MHz)

Figure S52. ¹ H-13C HSQC-TOCSY spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700/176 MHz)

Figure S53. ¹ H-13C HMBC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700/176 MHz)

Figure S54. ¹H-¹H COSY spectrum of nocathioamide A (1) (d₃-CH₃OH, 700/700 MHz)

Figure S55. ¹ H-1 H TOCSY spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700/700 MHz)

Figure S56. ¹H-¹H NOESY spectrum of nocathioamide A (1) (d₃-CH₃OH, 700/700 MHz; d8 = 300 msec)

Figure S57. ¹H-¹H NOESY spectrum of nocathioamide A (1) (d₃-CH₃OH, 700/700 MHz; d8 = 500 msec)

Figure S58. ¹H-¹⁵N HSQC spectrum of nocathioamide A (1) (d_3 -CH₃OH, 700/71 MHz)

Figure S59. ¹ H-15N HMBC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700/71 MHz)

Figure S60. ¹H-¹⁵N HMBC partial SW spectrum of nocathioamide A (1) (d₃-CH₃OH, 700/71 MHz)

Figure S61. ¹ H-NMR spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 400 MHz)

Figure S62. ¹³ C-NMR spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 100 MHz)

Figure S63. DEPT-135 spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 100 MHz)

Figure S64. ¹ H-13C HSQC spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 400/100 MHz)

Figure S65. ¹ H-13C HSQC-TOCSY spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 400/100 MHz)

Figure S66. ¹ H-13C HMBC spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 400/100 MHz)

Figure S67. ¹ H-1 H COSY spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 400/400 MHz)

Figure S68. ¹ H-1 H TOCSY spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 400/400 MHz)

Figure S69. ¹ H-1 H NOESY spectrum of nocathioamide B (**2**) (*d*4-CH3OH, 400/400 MHz, d8 = 300 msec)

Figure S70. ¹ H-NMR spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 400 MHz)

Figure S71. ¹³ C-NMR spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 100 MHz)

Figure S72. DEPT-135 spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 100 MHz)

Figure S73. ¹ H-13C HSQC spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 400/100 MHz)

Figure S74. ¹ H-13C HSQC-TOCSY spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 400/100 MHz)

Figure S75. ¹ H-13C HMBC spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 400/100 MHz)

Figure S76. Band-Selective HMBC spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 400/100 MHz)

Figure S77. ¹ H-1 H COSY spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 400/400 MHz)

Figure S78. ¹H-¹H TOCSY spectrum of nocathioamide B (2) (d₃-CH₃OH, 400/400 MHz)

Figure S79. ¹ H-1 H TOCSY WET spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 400/400 MHz)

Figure S80. ¹ H-1 H NOESY WET spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 400/400 MHz, d8 = 300 msec, PLW1=15)

Figure S81. ¹ H-NMR spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 700 MHz)

Figure S82. ¹³ C-NMR spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 176 MHz)

Figure S83. ¹ H-13C HSQC spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 700/176 MHz)

Figure S84. ¹ H-13C HSQC-TOCSY spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 700/176 MHz)

Figure S85. ¹H-¹³C HMBC spectrum of nocathioamide B (2) (d₃-CH₃OH, 700/176 MHz)

Figure S86. ¹ H-1 H COSY spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 700/700 MHz)

Figure S87. ¹H-¹H TOCSY spectrum of nocathioamide B (2) (d₃-CH₃OH, 700/700 MHz)

Figure S88. ¹ H-1 H NOESY spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 700/700 MHz, d8 = 300 msec)

Figure S89. ¹ H-NMR spectrum of nocathioamide A (**1**) (*d*6-DMSO, 400 MHz)

Figure S90. ¹³C-NMR spectrum of nocathioamide A (1) (d_6 -DMSO, 100 MHz)

Figure S91. DEPT-135 spectrum of nocathioamide A (1) (d_6 -DMSO, 100 MHz)

Figure S92. ¹ H-13C HSQC spectrum of nocathioamide A (**1**) (*d*6-DMSO, 400/100 MHz)

Figure S93. ¹ H-13C HSQC-TOCSY spectrum of nocathioamide A (**1**) (*d*6-DMSO, 400/100 MHz)

Figure S94. ¹ H-13C HMBC spectrum of nocathioamide A (**1**) (*d*6-DMSO, 400/100 MHz)

Figure S95. ¹ H-1 H COSY spectrum of nocathioamide A (**1**) (*d*6-DMSO, 400/400 MHz)

Figure S96. ¹H-¹H TOCSY spectrum of nocathioamide A (1) (d₆-DMSO, 400/400 MHz)

Figure S97. ¹H-¹⁵N HSQC spectrum of nocathioamide A (1) (d_6 -DMSO, 400/40.6 MHz)

Figure S98. ¹H-¹⁵N HMBC spectrum of nocathioamide A (1) (d₆-DMSO, 400/40.6 MHz)

Figure S99. ¹ H-1 H NOESY spectrum of nocathioamide A (**1**) (*d*6-DMSO, 400/400 MHz, d8 = 300 msec)

Figure S99A. Enlarged ¹H-¹H NOESY spectrum of nocathioamide A (1) (d6-DMSO, 400/400 MHz, d8 = 300 msec)

Figure S100. ¹ H-15N HSQC spectrum of glutarimide (*d*3-CH3OH, 400/40.6 MHz)

Figure S101. Annotated 1 H-NMR spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700 MHz)

Figure S101A. Annotated ¹H-NMR spectrum of nocathioamide A (1) (d₃-CH₃OH, 700 MHz)

Figure S101B. Annotated ¹H-NMR spectrum of nocathioamide A (1) (d₃-CH₃OH, 400 MHz)

Figure S102. Annotated 13 C-NMR spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 176 MHz)

Figure S102A. Annotated ¹³C-NMR spectrum of nocathioamide A (1) (d₃-CH₃OH, 176 MHz)

Figure S102B. Annotated 13 C-NMR spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 176 MHz)

Figure S103. Annotated 1 H-13C HSQC spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 400/100 MHz)

Figure S104. Annotated 1 H-13C HSQC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/100 MHz)

Figure S105. Annotated 1 H-13C HSQC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700/176 MHz)

Figure S106. Annotated ¹H-¹H TOCSY spectrum of nocathioamide A (1) (d₃-CH₃OH, 400/400 MHz)

Figure S107. Annotated ¹H-¹H TOCSY spectrum of nocathioamide A (1) (d₃-CH₃OH, 700/700 MHz)

Figure S108. Annotated ¹H-¹H NOESY spectrum of nocathioamide A (1) (d₃-CH₃OH, 700/700 MHz). Cross correlations color code: a blue circle indicates resonances, observed within each amino acid residue; a green asterisk indicates through-space interactions with the adjacent amino acids of the peptidic backbone; a red diamond indicates through-space interactions with distant/unexpected residues.

Figure S108A. Annotated ¹H-¹H NOESY spectrum of the MeLan bridge of nocathioamide A (1) (d₃-CH₃OH, 700/700 MHz). Cross correlations color code: a blue circle indicates resonances, observed within each amino acid residue; a green asterisk indicates through-space interactions with expected components of **AlaS-10** and **Abu**; a red diamond indicates through-space interactions with distant components of **AlaS-10, AlaS-11**, and **4-Meglu**.

Figure S108B. Annotated ¹H-¹H NOESY spectrum of the Lan bridge of nocathioamide A (1) (d₃-CH₃OH, 700/700 MHz). Cross correlations marked with a blue circle indicate resonances, observed within each amino acid residue.

Figure S108C. Annotated ¹H-¹H NOESY spectrum of the NH- AlaS-6 of nocathioamide A (1) (d₃-CH₃OH, 700/700 MHz). Cross correlations color code: a blue circle indicates resonances, observed within each amino acid residue, while a red diamond indicates through-space interactions with **βHa- AlaS-11**.

Figure S109. Annotated 1 H-15N HSQC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 400/40.6 MHz)

Figure S110. Annotated 1 H-15N HSQC spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700/71 MHz)

Figure S111. Annotated ¹H-¹⁵N HSQC-TOCSY spectrum of nocathioamide A (1) (d₃-CH₃OH, 400/40.6 MHz)

Figure S112. Annotated 1 H-15N HMBC spectrum of nocathioamide A (**1**) (*d*4-CH3OH, 400/40.6 MHz)

Figure S113. Annotated ¹H-¹⁵N HMBC spectrum of nocathioamide A (1) (d₃-CH₃OH, 400/40.6 MHz)

Figure S114. Annotated ¹H-¹⁵N HMBC spectrum of nocathioamide A (1) (d₃-CH₃OH, 700/71 MHz)

Figure S114A. Annotated 1 H-15N HMBC partial SW spectrum of nocathioamide A (**1**) (*d*3-CH3OH, 700/71 MHz)

Figure S115. Annotated ¹H-NMR spectrum of nocathioamide B (2) (d₃-CH₃OH, 700 MHz)

Figure S115A. Annotated 1 H-NMR spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 700 MHz)

Figure S116. Annotated ¹H-NMR spectrum of nocathioamide B (2) (d₃-CH₃OH, 400 MHz)

Figure S117. Annotated 13 C-NMR spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 176 MHz)

Figure S117A. Annotated 13 C-NMR spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 176 MHz)

Figure S117B. Annotated 13 C-NMR spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 176 MHz)

Figure S118. Annotated 1 H-13 C HSQC spectrum of nocathioamide B (**2**) (*d*3-CH3OH, 700/176 MHz)

Figure S119. Annotated ¹H-¹H TOCSY spectrum of nocathioamide B (2) (d₃-CH₃OH, 400/400 MHz)

Figure S120. Annotated ¹H-¹H TOCSY spectrum of nocathioamide B (2) (d₃-CH₃OH, 700/700 MHz)

Figure S121. Annotated ¹H-¹H NOESY spectrum of nocathioamide B (2) (d₃-CH₃OH, 700/700 MHz). Cross correlations color code: a blue circle indicates resonances, observed within each amino acid residue; a green asterisk indicates through-space interactions with the adjacent amino acids of the peptidic backbone; a red diamond indicates through-space interactions with distant/unexpected residues.

Figure S121A. Annotated ¹H-¹H NOESY spectrum of the Melan bridge of nocathioamide B (2) (d₃-CH₃OH, 700/700 MHz). Cross correlations color code: a blue circle indicates resonances, observed within each amino acid residue; a green asterisk indicates through-space interactions with the expected components of **AlaS-10** and **Abu**; a red diamond indicates through-space interactions with unexpected components of **AlaSO-6**, and **AlaSO-11**.

Figure S121B. Annotated ¹H-¹H NOESY spectrum of the sulfoxideLan bridge of nocathioamide B (2) (d₃-CH₃OH, 700/700 MHz). A blue circle indicates resonances, observed within each amino acid residue.

Figure S121C. Annotated 1 H-1 H NOESY spectrum of the **αH- AlaSO-6** of nocathioamide B (**2**) (*d*3-CH3OH, 700/700 MHz). Cross correlations color code: a blue circle indicates resonances, observed within each amino acid residue; a green asterisk indicates through-space interactions with **Dha**; a red diamond indicates through-space interactions with **βHa- AlaSO-11**.

Figure S122. UV spectra of nocathioamide A (**1**) (panel I) and B (**2**) (panel II) & FT-IR spectra of nocathioamide A (**1**) (panel III) and B (**2**) (panel IV).

Figure S123. Different fates of oxidized δ-Methyl leucine (4-methylglutamate)

PEPMASS

1314.44184

1330.43915

1332.45412

1218.40976

1344.45326

1314.44522

1314.44339

1330.43875

1352.38846

1346.43423

665.21966

1346.46989

1316.06202

1352.40163

1331.44224

663.26733

687.19994

679.20313

1234.4057

684.22549

691.21533

Rt_min

23.2775

19.934

22.6835

21.7325

21.7325

Elucidated by NMR

Difficult to be anticipated

ADDUCT

 $ION=[M+2H]2+$

 $ION=[M+2H]2+$

 $ION=[M+2H]2+$

 $ION=[M+2H]2+$

 $ION=[M+H+H]2+$

 $ION=[M+H+H]2+$

 $ION=[M+2H]2+$

 $ION=[M+2H]2+$

 $ION=[M+2H]2+$

 $ION=[M+H]+$

 $ION=[M+H+H]2+$

 $ION=[M+H+H]2+$

 $ION=[M+H+H]2+$

 $ION=[M+H+H]2+$

 $ION=[M+H+H]2+$

 $ION=[M+2H]2+$

 $ION=[M+H]+$

 $ION=[M+H]+$

 $ION=[M+H]+$

 $ION=[M+H]+$

687.70141 ION=[M+H]+

Envisioned by MS¹, MF, RDB, and few MS² fragments

 $ION=[M+2H]2+$

Figure S124. Molecular network of nocathioamide molecular family

Table S8. Annotation of some selected features within the nocathioamides positive cluster

Table S9. Bioassay results. The letters indicated in red refer to the ESKAPE panel, an acronym comprising the scientific names of six highly virulent and resistant bacterial pathogens.

3. Supplemental References

- [1] N. Garg, C. A. Kapono, Y. W. Lim, N. Koyama, M. J. A Vermeij, D. Conrad, F. Rohwer, P. C. Dorrestein, *Int. J. Mass Spectrom.* **2015**, *377*, 719 -727.
- [2] M. Wang, J. J. Carver, V. V. Phelan, L. M. Sanchez, N. Garg, Y. Peng, D. D. Nguyen, J. Watrous, C. A. Kapono, T. Luzzatto-Knaan, C. Porto, A. Bouslimani, A. V. Melnik, M. J. Meehan, W.-T. Liu, M. Crüsemann, P. D. Boudreau, E. Esquenazi, M. Sandoval-Calderon, R. D. Kersten, L. A. Pace, R. A. Quinn, K. R. Duncan, C.-C. Hsu, D. J. Floros, R. G. Gavilan, K. Kleigrewe, T. Northen, R. J. Dutton, D. Parrot, E. E. Carlson, B. Aigle, C. F. Michelsen, L. Jelsbak, C. Sohlenkamp, P. Pevzner, A. Edlund, J. McLean, J. Piel, B. T. Murphy, L. Gerwick, C.-C. Liaw, Y.-L. Yang, H.-U. Humpf, M. Maansson, R. A. Keyzers, A. C. Sims, A. R. Johnson, A. M. Sidebottom, B. E. Sedio, A. Klitgaard, C. B. Larson, C. A. Boya P, D. Torres-Mendoza, D. J. Gonzalez, D. B. Silva, L. M. Marques, D. P. Demarque, E. Pociute, E. C. O'Neill, E. Briand, E. J. N. Helfrich, E. A. Granatosky, E. Glukhov, F. Ryffel, H. Houson, H. Mohimani, J. J. Kharbush, Y. Zeng, J. A. Vorholt, K. L. Kurita, P. Charusanti, K. L. McPhail, K. F. Nielsen, L. Vuong, M. Elfeki, M. F. Traxler, N. Engene, N. Koyama, O. B. Vining, R. Baric, R. R. Silva, S. J. Mascuch, S. Tomasi, S. Jenkins, V. Macherla, T. Hoffman, V. Agarwal, P. G. Williams, J. Dai, R. Neupane, J. Gurr, A. M. C. Rodriguez, A. Lamsa, C. Zhang, K. Dorrestein, B. M. Duggan, J. Almaliti, P.-M. Allard, P. Phapale, L.-F. Nothias, T. Alexandrov, M. Litaudon, J.-L. Wolfender, J. E. Kyle, T. O. Metz, T. Peryea, D.-T. Nguyen, D. VanLeer, P. Shinn, A. Jadhav, R. Müller, K. M. Waters, W. Shi, X. Liu, L. Zhang, R. Knight, P. R. Jensen, B. O. Palsson, K. Pogliano, R. G. Linington, M. Gutierrez, N. P. Lopes, W. H. Gerwick, B. S. Moore, P. C. Dorrestein, N. Bandeira, *Nat. Biotechnol.* **2016**, *34*, 828–837.
- [3] a) A. Buchmann, M. Eitel, P. Koch, P. N. Schwarz, E. Stegmann, W. Wohlleben, M. Wolański, M. Krawiec, J. Zakrzewska-Czerwinska, C. Méndez, A. Botas, L. E. Núñez, F. Morís, J. Cortés, H. Gross, *Genome Announc.* **2016**, *4*, e01391-01316; b) A. Buchmann, H. Gross, *Microbiol. Resour. Announc.* **2020**, *9*, e00689-20.
- [4] Y. Ikeda, H. Nonaka, T. Furumai, H. Onaka, Y. Igarashi, *J. Nat. Prod.* **2005**, *68*, 1061– 1065.
- [5] J. Chen, A. Frediansyah, D. Maennle, J. Straetener, H. Broetz-Oesterhelt, N. Ziemert, L. Kaysser, H. Gross, *ChemBioChem* **2020**, *21*, 2205-2213.
- [6] M. C. Arendrup, J. Meletiadis, J. W. Mouton, K. Lagrou, P. Hamal, J. Guinea and the Subcommittee on Antifungal Susceptibility Testing (AFST) of the ESCMID European Committee for Antimicrobial Susceptibility Testing (EUCAST). Method for the determination of broth dilution minimum inhibitory concentrations of antifungal agents for yeasts. EUCAST DEFINITIVE DOCUMENT E.DEF 7.3.2. April 2020. Accessed under https://www.eucast.org/astoffungi/methodsinantifungalsusceptibilitytesting/susceptibility_testing_of_yeasts/
- [7] S. A. Kautsar, K. Blin, S. Shaw, J. C. Navarro-Munoz, B. R. Terlouw, J. J. J. van der Hooft, J. A. van Santen, V. Tracanna, H. G. Suarez Duran, V. P. Andreu, N. Selem-Mojica, M. Alanjary, S. L. Robinson, G. Lund, S. C. Epstein, A. C. Sisto, L. K. Charkoudian, J. Collemare, R. G. Linington, T. Weber, M. H. Medema, *Nucl. Acids Res.* **2020**, *48*, D454-D458.
- [8] J. I. Tietz, C. J. Schwalen, P. S. Patel, T. Maxson, P. M. Blair, H.-C. Tai, U. I. Zakai, D. A. Mitchell, *Nat. Chem. Biol.* **2017**, *13*, 470–478.
- [9] a) J. E. Leet, W. Li, H. A. Ax, J. A. Matson, S. Huang, R. Huang, J. L. Cantone, D. Drexler, R. A. Dalterio, K. S. Lam, J. Antibiot. 2003, 56, 232-242; b) X. Bai, H. Guo, D. Chen, Q. Yang, J. Tao, W. Liu Org. *Chem. Front.* **2020**, *7*, 584-589.
- [10] a) B. J. Burkhart, C. J. Schwalen, G. Mann, J. H. Naismith, D. A. Mitchell, *Chem. Rev.* **2017**, *117*, 5389-5456; b) L. Kjaerulff, A. Sikandar, N. Zaburannyi, A. Sebastian; J. Herrmann, J. Koehnke, R. Mueller, ACS Chem. Biol. 2017, 12, 2837-2841; c) L. Frattaruolo, R. Lacret, A. R. Cappello, A. W. Truman, ACS Chem. Biol. 2017, 12, 2815-2822; d) T. Kawahara, M. Izumikawa, I. Kozone, J. Hashimoto, N. Kaqaya, H. Koiwai, M. Komatsu, M. Fujie, N. Sato, H. Ikeda, K. Shin-ya, J. Nat. Prod. 2018, 81, 264-269; e) C. J. Schwalen, G. A. Hudson, B. Kille, D. A. Mitchell, J. Am. Chem. Soc. 2018, *140*, 9494-9501; f) N. Mahanta, D. M. Szantai-Kis, E. J. Petersson, D. A. Mitchell *ACS Chem. Biol.* **2019**, *14*, 142-163.
- [11] a) M. Montalban-Lopez, T. A. Scott, S. Ramesh, I. R. Rahman, A. J.van Heel, J. H.Viel, V. Bandarian, E. Dittmann, O. Genilloud, Y. Goto, M. J. Grande Burgos, C. Hill, S. Kim, J. Koehnke, J. A. Latham, A. J. Link, B. Martinez, S. K. Nair, Y. Nicolet, S. Rebuffat, H-G. Sahl, D. Sareen, E. W. Schmidt, L. Schmitt, K. Severinov, R. D. Sussmuth, A. W. Truman, H. Wang, J-K. Weng, G. P. van Wezel, Q. Zhang, J. Zhong, J. Piel, D. A. Mitchell, O. P. Kuipers, W. A. van der Donk, Nat. Prod. Rep. 2021, 38, 130-239; b) L. M. Repka, J. R. Chekan, S. K. Nair, W. A. van der Donk, Chem. Rev. 2017, 117, 5457-5520.
- [12] a) J. Ma, H. Huang, Y. Xie, Z. Liu, J. Zhao, C. Zhang, Y. Jia, Y. Zhang, H. Zhang, T. Zhang, J. Ju, Nat. Commun. 2017, 8, 1-10; b) C. Sun, Z. Liu, X. Zhu, Z. Fan, X. Huang, Q. Wu, X. Zheng, X. Qin, T. Zhang, H. Zhang, J. Ju, J. Ma, *J. Nat. Prod.* **2020**, *83*, 1646-1657.
- [13] C. T. Lohans, J. C. Vederas, *J. Antibiot.* **2014**, *67*, 23-30.
- [14] a) G. C. Levy, R. L. Lichter in Nitrogen-15 Nuclear Magnetic Resonance Spectroscopy, J. Wiley & Sons, New York, 1979; b) https://wissen.science-and-fun.de/chemistry/spectroscopy/15n-chemicalshifts/; c) https://www.pascal-man.com/pulseprogram/BrukerAlmanac2012.pdf.
- [15] a) S. Somma, W. Merati, F. Parenti Antimicrob. Agents Chemother. 1977, 11, 396-401; b) L. Vertesy, W. Aretz, A. Bonnefoy, E. Ehlers, M. Kurz, A. Markus, M. Schiell, M. Vogel, J. Wink, H. Kogler J. *Antibiot.* **1999**, *52*, 730−741; c) M. Simone, P. Monciardini, E. Gaspari, S. Donadio, S. I. Maffioli, *J. Antibiot.* **2013**, *66*, 73–78.
- [16] L. Huo, W. A. van der Donk, *J. Am. Chem. Soc.* **2016**, *138*, 5254 -5257.
- [17] K. I. Mohr, C. Volz, R. Jansen, V. Wray, J. Hoffmann, S. Bernecker, J. Wink, K. Gerth, M. Stadler, R. Müller, *Angew. Chem. Int. Ed.* **2015**, *54*, 11254-11258.