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Data Access Statement: The coordinates of the CysF X-ray crystal structures were deposited to PDB 8RA0. The AlphaFold structure of BhCysFE can be accessed at <https://www.alphafold.ebi.ac.uk/entry/A0A562R406> (AF-A0A562R406-F1-model_v4). Structures used for modeling and docking studies can be accessed from PDB 5BSM, 5BSR, 5WM3, 5IE3, 4FUT, 4GXR and 4GXQ. All proteins characterized in this study can be accessed from UniProt using the accession codes presented in Supplementary Tables 1–3 and their synthetic gene sequences are provided in Supplementary Data 1. The remaining data are available in the main text or the Supplementary Information. Correspondence and requests for materials should be addressed to J.M.

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Supplementary Information

Cryptic Enzymatic Assembly of Peptides Armed with β-Lactone Warheads

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Supplementary Fig. 1. Synthesis of standards **1a/b**, **3a/b**, **4a/b**, **9**, and **S7** for the validation of βlactone warhead assembly pathway. **1a** is also commercially available. For detailed synthesis procedure see method section 5 (synthesis of substrates and standards).

Supplementary Fig. 2. SDS-PAGE gel image of all purified enzymes in this study. (a) All purified enzyme in the Cys pathway. **(b)** All purified enzyme in the Bel pathway. **(c)** Comparison of fused-CysFE and CysF. La = protein ladder, $G = CysG$ (26.5 kDa), $F = CysF$ (54.3 kDa) , $E = \text{CysE}$ (30.5 kDa), $C = \text{CysC}$ (43.0 kDa), $D = \text{CysD}$ (37.9 kDa), $I = \text{Bell}$ (25.3 kDa), H = BelH (54.3 kDa), R = BelR (29.3 kDa), V = BelV (43.1 kDa), U = BelU (47.4 kDa), FE* = *Bh*CysFE fusion (84.4 kDa).

Name $AA^{[2]}$		Function ^[4]	Expression	Uniprot ID	His-tag	MW
			vector		terminal	$(kDa)^{[3]}$
C _{ys} G	228	Methyltransferase	$pET-28a(+)$	A0A1W6R556	$\mathbf C$	26.53
C _{VS} F	491	Lactone synthetase	$pET-21a(+)$	A0A1W6R555	$\mathbf C$	54.28
C _{VS} E	271	Hydrolase	$pET-28a(+)$	A0A1W6R564	\mathcal{C}	30.48
C _{YS} C	392	Amide bond synthetase	$pET-28a(+)$	A0A1W6R559	\mathcal{C}	43.04
C _{ysD}	333	ATP-grasp ligase	$pET-21a(+)$	A0A1W6R558	\mathcal{C}	37.87

Supplementary Table 1. Cys pathway^[1] proteins

[1] Organism: *Kitasatospora cystarginea* NRRL B16505. [2] Amino acid length of the original protein without His-tag. [3] Molecular weight of the protein with His-tag. [4] Functions determined in this study.

Supplementary Table 2. Bel pathway^[1] proteins

[1] Organism: *Streptomyces* sp. UCK 14. [2] Amino acid length of the original protein without His-tag. [3] Molecular weight of the protein with His-tag. [4] Functions determined in this study.

Supplementary Fig. 3. Testing the proposed lactonisation activity of CysC. For reaction conditions see experimental method (enzyme assays).

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Supplementary Fig. 12. *In silico* docking of **2a**-AMP in the crystal structural of CysF and sequence alignment of CysF with other adenylate-forming enzymes. Pairwise levels of sequence identities between CysF and the related adenylate-forming enzymes (5IE3, 4GXR, 5WM3, $4GXQ \& 4FUT$ ^{39–43} are between 18 – 30% and the key residues involved in the binding of AMP are highly conserved (T290, D363, R378). The docked conformation of **2a**-AMP suggests H192

may perform the role of a general base during β -lactone formation. The close proximity of the C1-methyl ester to the phosphoryl group, of the docked **2a**-AMP, further underscores the potential for electrostatic repulsion if the C1-carboxylate group was not methylated. Polyethylene glycol (PEG4) is observed to occupy a region of the putative active site in the crystal structure of CysF, which is likely to be an artifact of the crystallisation process. Additional electron density is present in the crystal structure which is consistent with carboxylation resulting in an N-terminal carbamate stabilised by interactions to R131. Carboxylation is suggested to be a common, spontaneous and reversible post translation modification.^{S1} Given the CysF N-terminus is not located near the active site, it is unlikely that this modification has any effect on the catalytic mechanism of the enzyme.

Supplementary Fig. 13. Examples of BGCs that contain fused-CysFE in nature. [1] bifunctional lactone synthetase-hydrolase. [2]: Amino acid length of the original protein without His-tag. [3] Molecular weight of the protein with His-tag.

Supplementary Fig. 14. AlphaFold2 model of bifunctional enzyme *Bh*CysFE. (a) Structural prediction revealed two domains similar to CysF (aa. 1-487) and CysE (aa. 495-768), connected by a short linker (sequence ATPVNMR) colour coded showing regions with lower (orange) to higher accuracy (blue). (b) The position of the predicted active site residues of the F domain are highlighted in magenta based on sequence alignment and docking as described in supplementary fig. 12. The predicted catalytic triad present in the E domain Glu607, His739 and Ser582, which is highly conserved in hydrolase enzymes is also highlighted in magenta.

Supplementary Fig. 15. Assay of the bifunctional fusion *Bh*CysFE with **2a** results in direct formation of **4a**.

Supplementary Fig. 16. Stability comparison of **3a** and **4a** in KPi buffer. 0.02 mmol of **3a**/**4a** was dissolved in 90 µL of DMSO-*d6* and mixed with 540 µL of 100 mM deuterated KPi buffer. The mixture was transferred to NMR tube immediately and ¹H-NMR was recorded at different time points (T = 18 °C). Hydrolysis product formation is indicated by the red arrows.

Supplementary Fig. 17. Reconstitution of the Cys and Bel pathway *in vitro*. LC-MS data. For detailed experimental procedure, see method section 3 (enzyme assay).

Accepted Accepted
(Product confirmed by LCMS) L-amino acids: Val, Ile, Leu, Met, Ala, Ser, Thr, Asn, Arg, His, Lys

Not accepted (No product detected) L-amino acids: Phe, Tyr, Trp, Cys, Gly, Pro, Gln, Asp, Glu D-amino acids: Val

Accepted Accepted
(Product confirmed by LCMS) L-amino acids: Val, Ile, Leu, Met, Ala, Gly, Thr

Not accepted (No product detected)

L-amino acids: Phe, Tyr, Trp, Cys, Pro, Ser, Asn, Gln, Arg, His, Lys, Asp, Glu D-amino acids: Val

Supplementary Fig. 18. Ligation of natural donor carboxylic acid **4a** or **5** with acceptor proteinogenic amino acids catalysed by CysC or CysD. Reactions were carried out on analytical scale (see method section 3 enzyme assays). Tandem mass (MS/MS) data of products are shown in section 9.

Supplementary Fig. 19. Amino acid substrates tested for BelV and BelU. The reaction was analysed by LC-MS. Black colour compounds have anticipated product mass detected, while the red colour indicated no product mass was detected. For assay conditions see methods section 3 (enzyme assays). Tandem mass (MS/MS) data of products are shown in section 9.

Supplementary Fig. 20. BelVU enzyme cascade for the synthesis of belactosin analogues. The reaction was analysed by LC-MS. Black colour compounds have anticipated product mass detected, while the red colour product mass was not detected. Detailed experimental conditions see 'enzyme assay' section. Tandem mass (MS/MS) data of products are shown in section 9.

Supplementary Table 3. Crystallographic data collection and refinement statistics. Statistics for the highest-resolution shell are shown in parentheses.

2. Materials and general methods

General information

Chemicals were purchased from Sigma-Aldrich, Fluorochem, Acros Organics, Fisher Scientific UK, Bachem, Alfa Aesar or Apollo Scientific and used without further purification unless otherwise stated. Molecular biology enzymes were purchased from New England Biolabs unless otherwise stated. Codon optimised genes were synthesised by Twist Bioscience. Proteins were analysed by SDS-PAGE on precast gels (Invitrogen NovexTM WedgeWellTM 8-16% Tris-Glycine Gel). Low resolution LC-MS was performed on Agilent 1260 LC system fitted with Agilent 6130 Quadruple MS. High resolution Mass spectrometry (LC-HRMS) and tandem mass spectrometry (LC-MS/MS) was recorded on Agilent 6560 Q-TOF + Agilent 1290 Infinity LC system. GC-MS was performed on Agilent GC 7890B coupled with 5975 Series MSD. NMR spectra were recorded on Bruker machines.

Cloning

Synthetic genes for CysF, BelH, CysD and BelU were initially cloned into the pET28-a(+) plasmid (using *NdeI* and *XhoI* sites) with an N-terminal histidine tag sequence. However, N-terminal histidine tagged CysF produced insoluble protein. N-terminal histidine tagged CysD and BelU produced soluble expression but with no activity. CysF, CysD and BelU were therefore cloned into the pET21-a(+) plasmid (using *NdeI* and *XhoI* site) to insert a C-terminal histidine tag (Supplementary table 1-3). Synthetic genes for CysG, CysE, CysC, BelI, BelR, BelV and *Bh*CysFE were inserted into the pET28-a(+) plasmid (using *NcoI* and *XhoI* site) carrying C-terminal histidine tag sequences (Supplementary table 1-2).

Protein expression general method

LB media (10 mL) with 50 μ g/mL of kanamycin (pET28-a(+)) or 100 μ g/ml ampicillin (pET21a(+)) was inoculated with *E. coli* BL21(DE3) containing a plasmid and incubated for 18 hrs at 37 °C, 180 rpm. The resulting seed culture (8 mL) was then used to inoculate 800 mL of autoinduction 2YT broth (with trace elements from Formedium) containing 50 μg/mL of kanamycin (pET28a- (+)) or 100 μ g/mL of ampicillin (pET21-a(+)). After incubation for 4 hrs at 37 °C, with shaking (180 rpm), the temperature was reduced to 20 ºC and incubation was continued for a further 18 hrs (180 rpm). The cultures were then harvested by centrifugation (3000 $\times g$, 4 °C, 10 min), cells were resuspended in 80 mL PBS, transferred into 2×50 mL falcon tubes, pelleted by centrifugation $(3000 \times g, 4 \degree C, 15 \text{ min})$ and then frozen until further usage. CysE (with C-terminal His-tag) produced mainly insoluble protein. A small amount of soluble CysE was, however, obtained (ca. 5 mg of protein from 1 L of cell culture) after the standard protein purification method described below. For the three fused bifunctional CysFE enzymes tested, only *Bh*CysFE was produced in soluble form. *Ms*CysFE afforded a very low level of expression, whilst *Mp*CysFE showed good expression, but formed inclusion bodies.

Protein purification general method

Frozen cell pellets were thawed and resuspended in 40 mL lysis buffer (50 mM NaH_2PO_4 , 300 mM NaCl, 10 mM imidazole, 10% glycerol, pH 7.8) and lysed by sonication (10 min, 50% pulse, 60% amplitude). The lysate was then cleared *via* centrifugation (23224 \times *g*, 40 min, 4 °C), 1 mL of pre-equilibrated Ni-NTA resin was added and the tube incubated at 4 °C for 30 min. The lysate with resin was loaded onto a gravity-flow column (Bio-Rad) and flowthrough was collected. The resin was washed with 10 mL of lysis buffer, followed by 2×10 mL of wash buffer (50 mM NaH2PO4, 300 mM NaCl, 40 mM imidazole, 10% glycerol, pH 7.8), and eluted with 10 mL of elution buffer (50 mM NaH2PO4, 300 mM NaCl, 100 mM imidazole, 10% glycerol, pH 7.8). The eluent from the column was monitored by Bio-Rad protein assay and elution continued until no further protein could be seen eluting. Sample of wash and elution fractions were analysed by SDS-PAGE. The wash and elution fractions that contained the protein of interested (with good purity) were combined and concentrated down to 2.5 mL using a centrifugal concentrator (Sartorius, Vivaspin 20 MWCO 30 kDa or 10 kDa depending on the size of the protein of interest). The 2.5 mL solution was applied to an equilibrated PD-10 desalting column (GE Healthcare, performed according to manufacturer's instructions). The column was eluted with 3.5 mL of protein storage buffer (20 mM NaH₂PO₄, 300 mM NaCl, 10% glycerol, pH 7.8). If necessary, the resulting eluent was further concentrated to approximately 10 mg/mL or more. Protein was aliquoted into single use tubes, flash frozen using liquid nitrogen and stored at -80 °C.

Further purification for protein crystallisation

For the protein crystallisation, the plasmid encoding CysF gene was transformed with NiCo21(DE3) competent *E. coli* cells. Following transformation, glycerol stocks were prepared from the overnight cultures of a single colony (sequencing confirmed). The enzyme was expressed and first purified using Ni-NTA column according to the general procedure described above. The wash/eluted protein fraction with good purity (judged by SDS-PAGE) were combined and concentrated using a Vivaspin centrifugal concentrator (MWCO 30 kDa) up to 20 mg/mL. For further purification, approximately 0.6 mL of this concentrated protein solution was injected into a 2 mL loop attached to the $\ddot{A}KTA$ pureTM protein purification system. The protein was passed down a Superdex® 200 Increase 10/300 GL gel filtration column which was preequilibrated with gel filtration buffer (50 mM Tris-HCl, 300 mM NaCl, 10 mM MgCl2, 10% glycerol, pH 7.5). CysF was eluted with gel filtration buffer and buffer exchanged to crystallisation buffer (50 mM Tris-HCl, 100 mM NaCl, 10 mM $MgCl₂$, 5% glycerol, pH 7.5) using a PD-10 desalting column (preequilibrated with crystallisation buffer). The resulting fraction was concentrated to 8-10 mg/mL using an Amicon Ultra 0.5 mL (30 kDa MWCO) concentrator.

Crystallogenesis

Single crystals of CysF were prepared by mixing 200 nL of 8 mg/mL protein in crystallisation buffer with equal volumes of precipitant. All trials were conducted by sitting drop vapour diffusion and incubated at 4°C. Crystals of the apo protein were formed in 0.1 M sodium citrate pH 5.5, 20% w/v PEG 3000 (JCSG + Eco A2, Molecular Dimensions). Individual crystals were cryoprotected in mother liquor supplemented with 25% PEG 200 prior to flash cooling in liquid nitrogen. Data were collected from single crystals at Diamond Light Source (MX31850-i04) and

subsequently scaled and reduced with Xia2. Preliminary phasing was performed by molecular replacement in Phaser using a search model generated in AlphaFold. Iterative cycles of rebuilding and refinement were performed in COOT and Phenix.refine, respectively. Structure validation with MolProbity and PDBREDO were integrated into the iterative rebuild and refinement process. The resolution cut of the data was determined by paired refinement as implemented in PDBREDO. Complete data collection and refinement statistics can be found in the Supplementary Table 3. Coordinates and structure factors have been deposited in the Protein Data Bank under accession code 8RA0.

Bioinformatic analysis of CysF and the discovery of fused CysFE

Bioinformatic analysis was conducted on the Cys and Bel pathway enzymes using the Enzyme Function Initiative tools.^{S2} The analyses utilised databases UniProt 2022-04, InterPro 91, and corresponding ENA information. The identification of the fused CysFE configuration began with a BLAST query using Uniprot ID A0A1W6R555 for CysF to generate a Sequence Similarity Network (SSN) with default settings. An alignment score threshold of 106 was chosen to identify a sub-network containing both CysF and BelH as they are isofunctional in their enzymatic capabilities. The obtained SSN was further analysed with the Genome Neighbourhoods Tool, leading to the obtention of genome neighbourhood diagrams (Supplementary Fig. 13). Manual inspection of these diagrams revealed three genomes exhibiting a CysF and CysE fusion, indicating a bifunctional enzyme.

CysF closed conformation modelling

The crystal structure of CysF was used to search for homologues via Foldseek and Dali. Identified homologues were observed that displayed structures in both open and closed conformations. Crystal structures of 4-Coumarate CoA Ligase in both open and closed conformations (PDB-ID 5BSM open and PDB-ID 5BSR closed) were utilised as templates upon which to model a closed state of CysF. 4-Coumarate CoA Ligase structure revealed that domain closure is achieved through a hinge like rigid body reorganisation of the two domains. A closed model of CysF was therefore modelled by superposition of the N-terminal domain of CysF with the corresponding N-terminal domain of the template (RMSD of 1.86 Å after secondary structure alignment). Subsequently, the C-terminal domain of CysF was superimposed with the C-terminal domain of the template in the closed conformation (RMSD of 3.03 Å after secondary structure alignment) followed by an energy minimisation (Yasara).

CysF docking studies.

A model of **2a**-AMP was constructed and docked into the crystal structure of CysF. The pocket for docking was identified using ICM Pocket Finder as implemented in ICM-Pro.^{S3} The top hit from the docking as ranked by RTCNN score (-29.78) is presented in Supplementary fig. 12. The docked pose was compared to structures of similar enzymes (5WM3, 5IE3, 4FUT, 4GXR, & 4GXQ). A multiple sequence alignment of these enzymes is presented in Supplementary fig. 13.

Chromatography

LC-MS analysis was performed using a Kinetex XB-C18 Core Shell column (100 mm x 4.6 mm, 5 µm, Phenomenex), flow = 1.0 mL/min, column oven temperature = 40 °C, mobile phase A = water with 0.1% (v/v) formic acid, mobile phase $B = MeCN$ with 0.1% (v/v) formic acid, mobile phase gradient see table below.

Method 1:

Method 2:

GC-MS analysis was performed using a VF-5ht column (30 m x 0.25 mm x 0.1 µm, J&W), inlet temperature = 240 °C, split ratio = 100:1, inlet pressure = 7.6 psi, flow = 1 mL/min, carrier gas = helium, oven temperature programme see below.

3. Enzyme assays

Enzyme assays for testing proposed pathway.³²

CysC was initially assayed for the lactonisation of **1a** to **4a** (Fig. 2a) in a reaction mixture (100 μ L) containing 2 mM **1a**, 5 mM ATP, with or without 5 mM CoASH, 10 mM MgCl₂, and 20 μ M CysC in 100 mM KPi buffer (pH 7.8) incubated at 25 °C for 12 h. The reaction was quenched by addition of 100 µL MeCN and the precipitated protein was removed by centrifugation. The supernatant was subjected to LC-MS analysis (method 1).

CysGE and BelIR were tested for methylation-lactonisation activity (**1a** to 4a, Fig, 2a) in reactions (100 μ L) containing 2 mM **1a**, 5 mM SAM, 10 mM MgCl₂, 20 μ M CysG/BelI and 20 μ M CysE/BelR in 100 mM KPi buffer (pH 7.8) incubated at 25 \degree C for 12 h. The reactions were quenched and analysed by LC-MS analysis (as above).

The proposed amide-bond forming activities of CysF and BelH (Fig 4a and 4d) were tested in reactions (100 µL) containing 2 mM **4a** (CysF) or **4b** (BelH), 5 mM H-Val-Val-OH (CysF) or Ala-Orn (12, BelH), 5 mM ATP, 10 mM MgCl₂ and 20 µM CysF or BelH in 100 mM KPi buffer (pH 7.8, with 300 mM NaCl and 10% v/v glycerol) incubated at 25 °C for 12 h. The reactions were quenched and subjected to LC-MS analysis (as above).

The proposed amide-bond forming activities of CysD and BelU (Fig 4a and 4d) were also tested in reactions (100 µL) with 2 mM L-Val (for CysD) or 2 mM L-Orn and 2 mM L-Ala (for BelU), 5 mM ATP, 10 mM $MgCl₂$ and 20 μ M CysD or BelU in 100 mM KPi buffer (pH 7.8) incubated at 25 °C for 12 h. The reactions were quenched and analysed (as above).

Enzyme assays for new pathways (Fig. 2 and 4)

CysG and BelI assay mixtures (100 µL) containing 2 mM **1a** or **1b**, 5 mM SAM, 10 mM MgCl2, and 20 µM CysG or BelI in 100 mM KPi buffer (pH 7.8) were incubated at 25 °C for 12 h. The reactions were quenched by addition of 100 µL MeCN and the precipitated protein was removed by centrifugation. The supernatant was subjected to LC-MS analysis (method 1).

CysGF and BelIH cascade reactions (100 µL) containing 2 mM **1a** or **1b**, 5 mM SAM, 5 mM ATP, 10 mM MgCl2, 20 µM CysG/BelI and 20 µM CysF/BelH in 100 mM HEPES or KPi buffer (pH 7.8) were incubated at 25 °C for 12 h. The reaction was quenched by addition of 100 μ L MeCN and the precipitated protein was removed by centrifugation. The supernatant was subjected to LC-MS analysis (method 1). For GC-MS analysis, the reaction was scaled up to 200 µL, and reaction time was 5 h. The reaction was quenched by extracting with EtOAc $(200 \mu L)$. The organic layer was dried over MgSO₄ and analysed by GC-MS.

CysFE and BelHR cascade reactions (100 µL) containing 2 mM **2a** or **2b**, 5 mM ATP, 10 mM MgCl₂, 20 μ M CysF or BelH and 20 μ M CysE or BelR in 100 mM KPi buffer (pH 7.8) were incubated at 25 \degree C for 12 h. The reaction was quenched by addition of 100 μ L MeCN and the precipitated protein was removed by centrifugation. The supernatant was subjected to LC-MS analysis (method 1).

CysGFE and BelIHR cascade reactions (100 µL) containing 2 mM **1a** or **1b**, 5 mM SAM, 5 mM ATP, 10 mM $MgCl₂$, 20 µM CysG or Bell, 20 µM CysF or BelH and 20 µM CysE or BelR in 100 mM KPi buffer (pH 7.8) were incubated at 25 \degree C for 12 h. The reaction was quenched by addition of 100 µL MeCN and the precipitated protein was removed by centrifugation. The supernatant was subjected to LC-MS analysis (method 1).

CysC and BelV assays (100 µL) containing 2 mM **4a** or **4b**, 4 mM L-Val or L-Orn, 5 mM ATP, 10 mM MgCl₂, and 20 μ M CysC or BelV in 100 mM KPi buffer (pH 7.8) were incubated at 25 °C for 2 h. The reaction was quenched and analysed (see directly above).

CysD and BelU assays (100 µL) containing 2 mM **5** or **7**, 4 mM L-Val or L-Ala, 5 mM ATP, 10 mM MgCl₂, and 20 μ M CysD or BelU in 100 mM KPi buffer (pH 7.8) were incubated at 25 °C for 2 h. The reaction was quenched (as above) subjected to LC-MS analysis (method 1 for CysD and method 2 for BelU reactions). We noted that potassium ions serve as an activator for CysD catalysis and are essential for the activity of BelU.

CysCD and BelVU cascade reactions (100 µL) containing 2 mM **4a** or **4b**, 6 mM L-Val (CysC) or 4 mM L-Orn with 4 mM L-Ala (BelG), 10 mM ATP, 10 mM MgCl₂, 20 µM CysC or BelV, and 20 µM CysD or BelU in 100 mM KPi buffer (pH 7.8) at 25 °C for 12 h. The reaction was quenched (as above) and subjected to LC-MS analysis (method 1 for CysCD; method 2 for BelVU reactions).

Substrate scope analysis (Fig. 5)

CysGFECD enzyme cascades reactions (100 µL) containing 2 mM **1a**, 3 mM SAM, 9 mM ATP, 6 mM L-Val (or other amino acids), 10 mM MgCl2, 20 µM CysG, 20 µM *Bh*CysFE, 20 µM CysC, and 20 μ M CysD in 100 mM KPi buffer (pH 7.8) were incubated at 25 °C for 6 h. The reaction was quenched by addition of 100 μ L MeCN and the precipitated protein was removed by centrifugation. The supernatant was subjected to LC-MS analysis (method 1). Reaction yields (average of three replicates) were determined from calibration curves using synthetic product standards.

BelIHRVU enzyme cascade reactions (100 µL) containing 2 mM **1b**, 3 mM SAM, 9 mM ATP, 5 mM L-Orn (or other amino acids), 5 mM L-Ala (or other amino acids), 10 mM $MgCl₂$, 15 μ M Bell, 15 μ M BelH, 15 μ M BelR, 15 μ M BelV, and 15 μ M BelU in 100 mM KPi buffer (pH 7.8) were incubated at 25 °C for 6 h. The reactions were the quenched and analysed (as above).

CysC and BelV reactions mixture (100 µL) containing 2 mM **4a** or **4b**, 3 mM amino acid, 3 mM ATP, 10 mM $MgCl₂$, and 20 µM CysC or BelV in 100 mM KPi buffer (pH 7.8) were incubated at 25 °C for 5 h. The reaction was quenched by addition of 100 μ L MeCN and the precipitated protein was removed by centrifugation. The supernatant was diluted 10 times with MeCN/H₂O (50:50) and subjected to LC-MS analysis (method 1). Product yields for CysC reactions (average of three replicates) were determined from calibration curves using synthetic product standards. The yield of **25** was determined by ¹⁹F-NMR.

CysD and BelU reaction mixture (100 µL) containing 2 mM **5** or **7**, 3 mM amino acid, 3 mM ATP, 10 mM MgCl₂, and 20 μ M CysD or BelU in 100 mM KPi buffer (pH 7.8) were incubated at 25 °C for 5 h. The reaction was quenched as described above. The supernatant was diluted 10 times with MeCN/H2O (50:50) and subjected to LC-MS analysis (method 1). Product yields for CysD reactions (average of three replicates) were determined using calibration curves. The yield of **36** was determined by ¹⁹F-NMR.

4. Preparative scale enzymatic reactions

Preparative scale CysG catalysed methylation of **1a**

A reaction mixture (20 mL) consisting of **1a** (35.2 mg, 10 mM), SAM (Sigma, \geq 75% purity, 12 mM), $MgCl₂ (10 mM)$, purified CysG (5 μ M) in 100 mM KPi buffer (pH 7.5) was incubated at 30 °C with 200 rpm shaking for 18 h. A sample (50 µL) was taken for LC-MS analysis and indicated reaction completion before acidifying the reaction with 2 mL 1 M HCl to pH 2-3. The reaction was then extracted three times with EtOAc (20 mL, 10 mL, 10 mL). The organic layers were combined, washed with brine, dried over MgSO4, and concentrated *in vacuo* to obtain 30.7 mg of **2a** as colourless oil in 81% yield.

¹H NMR (400 MHz, CDCl3) δ 4.42 (d, *J* = 3.4 Hz, 1H), 3.79 (s, 3H), 2.62 (dd, *J* = 8.6, 3.4 Hz, 1H), 2.30 – 2.16 (m, 1H), 1.07 (dd, *J* = 11.1, 6.7 Hz, 6H).

¹³C NMR (101 MHz, CDCl₃) δ 177.8, 174.3, 69.9, 55.0, 52.9, 27.4, 21.0, 20.3.

HR-MS, m/z (ESI+) calcd for C₈H₁₄O₅: 213.0739 [M+Na]⁺, found 213.0732.

The NMR spectra agree with literature.^{S4}

Preparative scale BelI catalysed methylation of **1b**

A reaction mixture (10 mL) consisting of **1b** (19 mg, 10 mM), SAM (\geq 75% purity, treated as 75%, 12 mM), $MgCl_2$ (10 mM), purified BelI (5 µM) in 100 mM KPi buffer (pH 7.5) was incubated at 30 °C with 200 rpm shaking for 18 h. A sample ($10 \mu L$) was taken for LC-MS analysis and indicated reaction completion before acidifying the reaction with 2 mL 1 M HCl to pH 2-3. The reaction was then extracted with EtOAc three times (20 mL, 10 mL, 10 mL). The organic layers were combined, washed with brine, dried over MgSO⁴ and concentrated *in vacuo* to obtain 15.6 mg **2b** as colourless oil in 76% yield.

¹H NMR (400 MHz, CDCl3) δ 4.42 (d, *J* = 3.1 Hz, 1H), 3.80 (s, 3H), 2.77 (dd, *J* = 8.3, 3.0 Hz, 1H), 2.13 – 1.98 (m, 1H), 1.59 – 1.46 (m, 1H), 1.33 – 1.23 (m, 1H), 1.06 (d, *J* = 6.7 Hz, 3H), 0.94 (t, $J = 7.4$ Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 178.3, 174.4, 69.5, 53.2, 53.0, 33.7, 27.6, 16.4, 11.4. HR-MS, m/z (ESI+) calcd for C₉H₁₆O₅: 227.0890 [M+Na]⁺, found 227.0889.

Preparative scale CysF catalysed lactonisation of **2a**

A reaction mixture (15 mL) consisting of $2a$ (28.5 mg, 10 mM), ATP (50 mM), MgCl₂ (10 mM), purified CysF (10 µM) in 100 mM KPi buffer (pH 7.5) was incubated at 30 °C with 200 rpm shaking for 18 h before extracting three times with Et₂O (3 x 15 mL). The organic layers were combined, washed with brine, dried over MgSO4, and concentrated *in vacuo* to obtain 5 mg crude product. The crude product was subjected to 1 H-NMR analysis (see supplementary Fig. 8).

Preparative scale CysGFE enzymatic cascade for the synthesis of **4a**

A reaction mixture (25 mL) consisting of **1a** (22.0 mg, 5 mM), SAM (\geq 75% purity, 6 mM), ATP (10 mM), MgCl₂ (10 mM), purified CysG (20 μ M) and purified *BhCysFE* (20 μ M) in 100 mM KPi buffer (containing 10% glycerol v/v, pH 7.5) was incubated at 25 °C with 200 rpm shaking for 24 h. A sample (50 µL) was taken for LC-MS analysis and indicated reaction completion before acidifying the reaction with 5 mL 1 M HCl to pH 2-3. The reaction was then extracted with EtOAc $(3 \times 15 \text{ mL})$. The organic layers were combined, washed with brine (15 mL), dried over MgSO₄. and concentrated *in vacuo* to obtain 18.5 mg **4a** as light-yellow oil in 94% yield.

¹H NMR (400 MHz, CDCl3) δ 4.69 (d, *J* = 4.4 Hz, 1H), 3.62 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.29 –

2.17 (m, 1H), 1.14 (d, *J* = 6.7 Hz, 3H), 1.10 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 173.4, 168.2, 69.3, 64.8, 28.0, 20.1, 19.7.

The NMR spectra agree with chemically synthesised **4a**.

HR-MS, m/z (ESI-) calcd for C₇H₁₀O₄: 157.0506 [M-H]⁻, found 157.0508.

Preparative scale BelIHR enzymatic cascade for the synthesis of **4b**

A reaction mixture (25 mL) consisting of **1b** (23.7 mg, 5 mM), SAM (\geq 75% purity, 6 mM), ATP (10 mM), $MgCl_2$ (10 mM), purified BelI (20 μ M), BelH (20 μ M), and BelR (20 μ M) in 100 mM KPi buffer (pH 7.5) was incubated at 25 °C with 200 rpm shaking for 24 h. A sample (50 μ L) was taken for LC-MS analysis and indicated reaction completion before acidifying the reaction with 5 mL 1 M HCl to pH 2-3. The reaction was then extracted with EtOAc (3 x 15 mL). The organic layers were combined, washed with brine (15 mL), dried over MgSO4, and concentrated *in vacuo* to obtain 18.7 mg **4b** as light-yellow oil in 87% yield.

¹H NMR (400 MHz, CDCl3) δ 4.71 (d, *J* = 4.5 Hz, 1H), 3.76 (dd, *J* = 7.9, 4.5 Hz, 1H), 2.08 – 1.98 (m, 1H), 1.72 – 1.59 (m, 1H), 1.39 – 1.29 (m, 1H), 1.07 (d, *J* = 6.7 Hz, 3H), 0.95 (t, *J* = 7.5 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 173.75, 168.51, 68.79, 63.33, 33.83, 26.85, 16.37, 11.10. The NMR spectra agree with chemically synthesised **4b**.

HR-MS, m/z (ESI-) calcd for C₈H₁₂O₄: 171.0663 [M-H]⁻, found 171.0667.

Preparative scale CysCD enzymatic cascade (stepwise)

General method: A reaction mixture (20 mL) consisting of **4a-c** (4 mM, 1.0 equiv, 0.08 mmol), $AA1$ (4 mM, 1.0 equiv), ATP (4.4 mM, 1.1 equiv), MgCl₂ (10 mM), 100 mM NaCl, and purified CysC (20 μ M) in 100 mM KPi buffer (pH 7.8) was incubated at 25 °C with 200 rpm shaking. After 12 h of incubation, additional ATP (1.1 equiv, 0.88 mL of 100 mM stock solution in KPi buffer), **AA2** (1.25 equiv, 1.0 mL of 100 mM stock solution in KPi buffer), and purified CysD (20 μ M) were then added. The reaction mixture was incubated at 25 °C with 200 rpm shaking for another 12 h. The reaction mixture was then cooled to 0° C on ice before acidifying with 1.0 M HCl (1.8 mL) to pH 5-6. The resulting mixture was extracted with ice-cold EtOAc (3 x 40 mL). During extraction, the mixture was kept ice-cold to minimise acid catalysed β-lactone ring opening in water. The organic layers were combined, washed with brine (20 mL), dried over MgSO4, and concentrated *in vacuo* to obtain crude product. The crude product was purified by silica gel column (DCM/MeOH with 0.1% AcOH, 1-4% MeOH) to obtain purified warheadpeptides.

6a was obtained as white solid, 16 mg, 54% yield over two steps.

¹H NMR (500 MHz, MeOD) δ 4.81 (d, *J* = 4.3 Hz, 1H), 4.37 (d, *J* = 5.8 Hz, 1H), 4.30 (d, *J* = 7.9 Hz, 1H), 3.56 (dd, *J* = 8.5, 4.4 Hz, 1H), 2.23 – 2.15 (m, 1H), 2.14 – 2.07 (m, 1H), 1.95 – 1.86 (m, 1H), 1.58 – 1.48 (m, 1H), 1.29 – 1.21 (m, 1H), 1.10 (d, *J* = 6.8 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), $1.00 - 0.91$ (m, 12H).

¹³C NMR (126 MHz, MeOD) δ 174.5, 173.3, 170.6, 170.4, 72.2, 65.2, 60.2, 58.22, 38.3, 32.0, 28.8, 26.2, 20.4, 19.8, 19.7, 18.8, 16.0, 11.8.

HR-MS, m/z (ESI-) calcd for C₁₈H₃₀N₂O₆: 369.2031 [M-H]⁻, found 369.2054.

39 was obtained as white solid, 8 mg, 27% yield over two steps.

¹H NMR (500 MHz, MeOD) δ 4.81 (d, *J* = 4.4 Hz, 1H), 4.45 (t, *J* = 7.5 Hz, 1H), 4.26 (d, *J* = 7.8 Hz, 1H), 3.55 (dd, *J* = 8.5, 4.4 Hz, 1H), 2.22 – 2.08 (m, 2H), 1.72 (d, *J* = 6.7 Hz, 1H), 1.65 (t, *J* = 7.3 Hz, 2H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), 1.00 (d, *J* = 6.7 Hz, 3H), 0.97 (d, *J* = 1.4 Hz, 3H), 0.95 (d, *J* = 1.6 Hz, 3H), 0.91 (d, *J* = 6.4 Hz, 3H).

¹³C NMR (126 MHz, MeOD) δ 175.7, 173.2, 170.6, 170.4, 72.2, 65.3, 60.2, 52.0, 41.6, 32.0, 28.8, 25.9, 23.4, 21.8, 20.4, 19.8, 19.7, 18.8.

HR-MS, m/z (ESI-) calcd for C₁₈H₃₀N₂O₆: 369.2031 [M-H]⁻, found 369.2096.

40 was obtained as a light yellow solid, 24 mg, 63% yield over two steps. Unlike other examples, the racemic amino acid (**AA2**, 2.5 equiv) was used in this case. We observed the formation of only one diastereomer, indicating a complete kinetic resolution by the enzyme.

¹H NMR (500 MHz, MeOD) δ 5.41 (s, 1H), 4.82 (d, *J* = 4.4 Hz, 1H), 4.38 (d, *J* = 8.3 Hz, 1H), 4.36 – 4.27 (m, 1H), 3.66 (dd, *J* = 8.0, 4.4 Hz, 1H), 2.20 – 2.12 (m, 1H), 2.02 – 1.93 (m, 1H), 1.68 – 1.59 (m, 1H), 1.36 – 1.30 (m, 1H), 1.04 (d, *J* = 6.7 Hz, 3H), 0.99 (d, *J* = 6.7 Hz, 3H), 0.97

 -0.91 (m, 6H).

¹³C NMR (126 MHz, MeOD) δ 173.5, 170.8, 170.5, 71.6, 63.8, 60.2, 34.8, 31.6, 27.7, 19.6, 18.6, 16.6, 11.3.

¹⁹F NMR (471 MHz, MeOD) δ -63.6 (q, *J* = 9.3 Hz), -67.1 (q, *J* = 8.9 Hz).

HR-MS, m/z (ESI-) calcd for C₁₈H₂₄F₆N₂O₆: 477.1460 [M-H]⁻, found 477.1453.

41 was obtained as a light yellow solid, 10 mg, 32% yield over two steps.

¹H NMR (500 MHz, MeOD) δ 4.76 (d, *J* = 4.3 Hz, 1H), 4.37 (d, *J* = 5.8 Hz, 1H), 4.29 (d, *J* = 7.9 Hz, 1H), 3.70 (dd, *J* = 8.8, 4.3 Hz, 1H), 2.42 – 2.33 (m, 1H), 2.15 – 2.06 (m, 1H), 1.97 – 1.83 (m, 3H), 1.75 – 1.59 (m, 4H), 1.57 – 1.50 (m, 1H), 1.46 – 1.36 (m, 2H), 1.27 – 1.23 (m, 1H), 1.01 – 0.91 (m, 12H).

¹³C NMR (126 MHz, MeOD) δ 174.6, 173.2, 170.9, 170.5, 72.9, 62.9, 60.2, 58.3, 39.5, 38.3, 31.9, 31.2, 30.8, 26.2, 26.0, 25.7, 19.7, 18.9, 16.0, 11.8.

HR-MS, m/z (ESI-) calcd for C₂₀H₃₂N₂O₆: 395.2182 [M-H]⁻, found 395.2147.

42 was obtained as a white solid, 10 mg, 34% yield over two steps.

¹H NMR (500 MHz, MeOD) δ 4.79 (d, *J* = 4.4 Hz, 1H), 4.48 – 4.43 (m, 2H), 3.62 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.79 – 2.67 (m, 3H), 2.32 (t, *J* = 2.7 Hz, 1H), 2.22 – 2.13 (m, 1H), 2.08 – 1.97 (m, 3H), 1.93 – 1.81 (m, 3H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (126 MHz, MeOD) δ 172.4, 170.7, 170.6, 80.3, 72.2, 72.1, 65.4, 59.0, 53.0, 38.6, 28.9, 26.2, 26.2, 22.5, 20.4, 19.8, 18.8.

HR-MS, m/z (ESI-) calcd for C₁₈H₂₄N₂O₆: 363.1556 [M-H]⁻, found 363.1570.

43 was obtained as a white solid, 4 mg, 14% yield over two steps.

¹H NMR (500 MHz, MeOD) δ 4.79 (d, *J* = 4.3 Hz, 1H), 4.64 (dd, *J* = 8.7, 5.2 Hz, 1H), 4.34 (d, *J* = 8.4 Hz, 1H), 3.61 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.80 – 2.63 (m, 3H), 2.39 (t, *J* = 2.7 Hz, 1H), 2.22 – 2.14 (m, 1H), 2.07 – 1.95 (m, 3H), 1.93 – 1.79 (m, 3H), 1.11 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (126 MHz, MeOD) δ 172.0, 170.7, 170.6, 80.1, 72.4, 72.2, 65.4, 57.9, 53.4, 38.5, 28.9, 26.3, 25.9, 22.6, 20.5, 19.8, 18.7.

HR-MS, m/z (ESI-) calcd for C₁₈H₂₄N₂O₆: 363.1556 [M-H]⁻, found 363.1508.

5. Synthesis of substrates and standards

Synthesis of β-lactones 4a-c (adapted from literature with modifications)^{37, S5}

General procedure synthesis of S3 (Step 1): To a solution of Evans' chiral auxiliary **S2** (751 mg, 4.2 mmol, 1.0 equiv) in 10 mL DCM, at room temperature, was added EDC hydrochloride (1.6 g, 8.4 mmol, 2.0 equiv), carboxylic acid **S1** (5.0 mmol, 1.2 equiv), and DMAP (513 mg, 4.2 mmol, 1.0 equiv). The mixture was stirred at RT for 16-20 h. The reaction was diluted with DCM and washed with 1 M HCl, followed by sat. NaHCO₃, sat. NH₄Cl, and finally brine. The organic layer was dried over MgSO⁴ and concentrated *in vacuo*. The crude product was purified by silica gel column (EtOAc/Hexane, 20-30% EtOAc) to obtain **S3b** and **S3c**. A sample of **S3a** was also purchased from Fluorochem (UK) and used for the next step directly.

S3b was obtained as a white solid, 4.36 g, 89% yield.

¹H NMR (400 MHz, CDCl₃) δ 7.41 – 7.21 (m, 5H), 4.79 – 4.65 (m, 1H), 4.28 – 4.15 (m, 2H), 3.35 (dd, *J* = 13.3, 3.4 Hz, 1H), 2.99 – 2.71 (m, 3H), 2.12 – 1.96 (m, 1H), 1.55 – 1.41 (m, 1H), 1.38 – 1.22 (m, 1H), 1.03 (d, *J* = 6.7 Hz, 3H), 0.96 (t, *J* = 7.4 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 173.1, 153.6, 135.5, 129.6, 129.1, 127.5, 66.2, 55.4, 42.3, 38.1, 31.4, 29.5, 19.4, 11.5.

The NMR spectra is in agreement with published data.^{S6}

HR-MS, m/z (ESI+) calcd for C₁₆H₂₁NO₃: 298.1414 [M+Na]⁺, found 298.1410.

S3c was obtained as a white solid, 960 mg, 79% yield,

¹H NMR (400 MHz, CDCl₃) δ 7.42 – 7.20 (m, 5H), 4.76 – 4.63 (m, 1H), 4.28 – 4.12 (m, 2H), 3.33 (dd, *J* = 13.4, 3.3 Hz, 1H), 3.05 (dd, *J* = 16.6, 6.9 Hz, 1H), 2.93 (dd, *J* = 16.6, 7.4 Hz, 1H), 2.78 (dd, *J* = 13.4, 9.6 Hz, 1H), 2.44 – 2.28 (m, 1H), 1.99 – 1.84 (m, 2H), 1.74 – 1.53 (m, 4H), $1.33 - 1.15$ (m, 2H).

¹³C NMR (101 MHz, CDCl₃) δ 173.2, 153.6, 135.5, 129.6, 129.1, 127.4, 66.2, 55.3, 41.5, 38.1, 35.9, 32.7, 32.6, 25.1, 25.1.

The NMR spectra is in agreement with published data.²⁹

HR-MS, m/z (ESI+) calcd for C₁₇H₂₁NO₃: 310.1419 [M+Na]⁺, found 310.1422.

General procedure for the synthesis of S4: To a solution of **S3** (10.0 mmol, 1.0 equiv) in 50 mL of dry THF (cooled to -78 °C under N_2 atmosphere) was added NaHMDS (7.5 mL of 2 M solution in THF, 30 mmol, 1.5 equiv) dropwise and the solution was kept at -78 °C for 1 h before *tert*-butyl bromoacetate (3.9 g, 20 mmol, 2.0 equiv) was added dropwise. The resulting solution was stirred for 16 h and gradually reached room temperature before quenching with 1.3 mL of acetic acid. The mixture was concentrated *in vacuo* and the residue was added to 100 mL ethyl acetate, followed by washing with 100 mL water and 50 mL brine. The organic layer was dried
over MgSO⁴ and concentrated *in vacuo* to give crude product, which was either recrystallised in EtOAc/hexane (1/20) or purified by silica gel column to give **S4**.

S4a was obtained as light-yellow needle shape crystal, 3.0 g, 80% yield.

¹H NMR (400 MHz, CDCl₃) δ 7.37 – 7.26 (m, 5H), 4.72 – 4.60 (m, 1H), 4.20 – 4.08 (m, 3H),

3.35 (dd, *J* = 13.5, 3.3 Hz, 1H), 2.88 – 2.67 (m, 2H), 2.45 (dd, *J* = 16.9, 3.6 Hz, 1H), 2.06 – 1.92 (m, 1H), 1.42 (s, 9H), 1.01 (d, *J* = 6.8 Hz, 3H), 0.91 (d, *J* = 6.9 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 175.7, 172.0, 136.1, 129.7, 129.1, 127.3, 80.8, 65.9, 55.9, 44.6, 37.6, 33.7, 29.9, 28.2, 20.9, 18.5.

The NMR spectra is in agreement with published data.^{S7}

HR-MS, m/z (ESI+) calcd for C₂₁H₂₉NO₅: 398.1943 [M+Na]⁺, found 398.1962.

S4b was obtained as light-yellow needle shape crystal, 4.0 g, 64% yield.

¹H NMR (400 MHz, CDCl₃) δ 7.36 – 7.19 (m, 5H), 4.68 – 4.54 (m, 1H), 4.24 – 4.15 (m, 1H), 4.15 – 4.09 (m, 2H), 3.32 (dd, *J* = 13.5, 3.3 Hz, 1H), 2.88 – 2.65 (m, 2H), 2.34 (dd, *J* = 16.9, 3.5 Hz, 1H), 1.82 – 1.68 (m, 1H), 1.50 – 1.31 (m, 10H), 1.31 – 1.17 (m, 1H), 0.91 (t, *J* = 7.4 Hz, 3H), 0.83 (d, *J* = 6.8 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 175.7, 172.1, 153.1, 136.0, 129.7, 129.0, 127.3, 80.8, 65.9, 55.9, 43.6, 37.6, 35.8, 32.4, 28.2, 28.0, 14.9, 12.0.

HR-MS, m/z (ESI+) calcd for C₂₂H₃₁NO₅: 412.2100 [M+Na]⁺, found 412.2110.

S4c was obtained as white needle shape crystal, 1.0 g, 79% yield.

¹H NMR (400 MHz, CDCl₃) δ 7.35 – 7.21 (m, 5H), 4.73 – 4.54 (m, 1H), 4.27 – 4.17 (m, 1H), 4.14 – 4.08 (m, 2H), 3.36 (dd, *J* = 13.5, 3.3 Hz, 1H), 2.82 (dd, *J* = 16.8, 11.3 Hz, 1H), 2.69 (dd, *J* $= 13.5, 10.3$ Hz, 1H), 2.50 (dd, $J = 16.8, 3.7$ Hz, 1H), 2.06 – 1.89 (m, 1H), 1.80 – 1.45 (m, 6H), 1.39 (s, 9H), 1.31 – 1.16 (m, 2H).

¹³C NMR (101 MHz, CDCl₃) δ 176.4, 171.6, 153.3, 136.2, 129.6, 129.0, 127.3, 80.8, 65.9, 56.0, 42.9, 42.7, 37.5, 37.0, 30.2, 30.0, 28.2, 25.0, 24.9.

HR-MS, m/z (ESI+) calcd for C₂₃H₃₁NO₅: 424.2100 [M+Na]⁺, found 424.2102.

The NMR spectra is in agreement with published data.²⁹

General Procedure for the synthesis of S5: A solution of **S4a** (3.0 g, 8.0 mmol, 1.0 equiv) in 40 mL of THF and 7 mL of water was cooled to 0 $^{\circ}$ C and treated with 5.6 mL of a 30% wt. H₂O₂ solution. The mixture was stirred for 5 min, followed by addition of LiOH (monohydrate, 0.85 g, 20 mmol, 2.5 equiv, freshly prepared in 13 mL of water) dropwise. The reaction mixture was stirred and allowed to gradually reach room temperature for 16 h before cooling back to 0 °C and quenching with 9 mL of a 2 M Na₂S₂O₃ solution. The reaction mixture was concentrated *in vacuo* to remove THF and the resulting solution was diluted with 20 mL water. The pH was adjusted to 8-9 using 2 M NaOH solution (if necessary). The aqueous solution was washed with EtOAc to remove the Evans' chiral auxiliary. The aqueous layer was then acidified with 2 M HCl solution (to pH 1-2) and extracted with EtOAc three times. The organic layers were combined, washed with brine, dried over MgSO4, and concentrated *in vacuo*. The crude product was purified by silica gel column (EtOAc/Hexane, 20% EtOAc) to give 1.5 g of **S5a** in 87% yield.

S5a was obtained as a colourless oil, 1.5 g, 87% yield. ¹H NMR (400 MHz, CDCl₃) δ 2.75 – 2.57 (m, 2H), 2.36 (dd, *J* = 16.2, 3.7 Hz, 1H), 2.10 – 1.96 (m, 1H), 1.43 (s, 8H), 0.97 (dd, *J* = 11.5, 6.8 Hz, 6H). ¹³C NMR (101 MHz, CDCl₃) δ 171.7, 81.1, 47.6, 34.2, 30.0, 28.1, 20.3, 19.6. HR-MS, m/z (ESI+) calcd for C₁₁H₂₀O₄: 239.1259 [M+Na]⁺, found 239.1266.

The NMR spectra is in agreement with published data.³⁷

S5b was obtained as a colourless oil, 1.2 g, 62% yield.

¹H NMR (400 MHz, CDCl₃) δ 2.92 – 2.80 (m, 1H), 2.58 (dd, *J* = 16.6, 11.0 Hz, 1H), 2.26 (dd, *J* $= 16.6, 3.8$ Hz, 1H), $1.92 - 1.75$ (m, 1H), $1.50 - 1.32$ (m, 10H), $1.30 - 1.16$ (m, 1H), $0.96 - 0.81$ (m, 6H).

¹³C NMR (101 MHz, CDCl₃) δ 181.3, 171.8, 81.0, 45.8, 36.3, 32.8, 28.1, 27.3, 15.9, 11.9. HR-MS, m/z (ESI+) calcd for C₁₂H₂₂O₄: 253.1416 [M+Na]⁺, found 253.1410.

The NMR spectra is in agreement with published data.^{S8}

S5c was obtained as colourless oil, 480 mg, 80% yield.

¹H NMR (400 MHz, CDCl₃) δ 2.69 – 2.57 (m, 2H), 2.49 – 2.37 (m, 1H), 2.02 – 1.90 (m, 1H), 1.84 – 1.70 (m, 2H), 1.68 – 1.59 (m, 2H), 1.58 – 1.49 (m, 2H), 1.42 (s, 9H), 1.38 – 1.29 (m, 1H), $1.27 - 1.14$ (m, 1H). ¹³C NMR (101 MHz, CDCl₃) δ 181.1, 181.1, 171.4, 81.2, 46.5, 42.2, 36.8, 30.6, 30.6, 28.1, 25.1, 25.0.

HR-MS, m/z (ESI-) calcd for C₁₃H₂₂O₄: 241.1445 [M-H]⁻, found 241.1448.

The NMR spectra is in agreement with published data.²⁹

General Procedure for synthesis of S6: A solution of **S5a** (1.5 g, 6.9 mmol, 1 equiv) in 20 mL of dry THF was cooled to -78 °C and treated with 14 mL of 1 M LiHMDS (14 mmol, 2 equiv) dropwise. The solution was kept at -78 °C for 1 h before dry CCl₄ (1.3 g, 8.3 mmol, 1.2 equiv) was added dropwise. The reaction mixture was stirred and allowed to gradually reach room temperature for 12 h before concentrating *in vacuo*. The resulting gummy solid residue was suspended in 100 mL of Et_2O and 50 mL of 5% (w/v) NaHCO₃ solution. The mixture was vigorously stirred at room temperature for 24 h and then diluted with Et₂O, washed with sat. NaHCO³ solution and brine, dried over MgSO⁴ and concentrated *in vacuo*. The crude product was purified by silica gel column (EtOAc/Hexane, 2%-10% EtOAc) to give **S6a**.

S6a was obtained as a white solid, 1.0 g, 67% yield. ¹H NMR (400 MHz, CDCl3) δ 4.52 (d, *J* = 4.4 Hz, 1H), 3.45 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.27 – 2.08 (m, 1H), 1.51 (s, 9H), 1.12 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.7 Hz, 3H). ¹³C NMR (101 MHz, CDCl₃) δ 168.9, 167.6, 83.7, 70.3, 64.2, 28.1, 27.8, 20.1, 19.8. HR-MS, m/z (ESI+) calcd for C₁₁H₁₈O₄: 237.1103 [M+Na]⁺, found 237.1105. The NMR spectra is in agreement with published data.³⁷

S6b was obtained as a white solid, 760 mg, 64% yield.

¹H NMR (400 MHz, CDCl3) δ 4.53 (d, *J* = 4.4 Hz, 1H), 3.60 (dd, *J* = 7.7, 4.5 Hz, 1H), 2.05 – 1.90 (m, 1H), 1.68 – 1.56 (m, 1H), 1.50 (s, 9H), 1.39 – 1.26 (m, 1H), 1.03 (d, *J* = 6.7 Hz, 3H), 0.93 (t, $J = 7.5$ Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 169.2, 167.6, 83.6, 69.6, 62.5, 33.6, 28.0, 26.9, 16.4, 11.2. The NMR spectra is in agreement with published data.^{S5}

HR-MS, m/z (ESI+) calcd for C₁₂H₂₀O₄: 251.1259 [M+Na]⁺, found 251.1254.

S6c was obtained as a light-yellow solid, 172 mg, 36% yield. ¹H NMR (400 MHz, CDCl3) δ 4.49 (d, *J* = 4.3 Hz, 1H), 3.60 (dd, *J* = 8.6, 4.3 Hz, 1H), 2.41 – 2.27 (m, 1H), 1.99 – 1.80 (m, 2H), 1.74 – 1.58 (m, 4H), 1.50 (s, 9H), 1.45 – 1.32 (m, 2H). ¹³C NMR (101 MHz, CDCl₃) δ 169.2, 167.6, 83.6, 71.0, 61.7, 38.3, 30.2, 29.9, 28.1, 25.1, 24.9. The NMR spectra is in agreement with published data.²⁹ HR-MS, m/z (ESI+) calcd for C₁₃H₂₀O₄: 263.1259 [M+Na]⁺, found 263.1260.

General Procedure for the synthesis of 4: A solution of **S6a** (262 mg, 1.2 mmol) in 1 mL of DCM was cooled to 0 $^{\circ}$ C and treated with 1 mL of TFA dropwise. The mixture was stirred at -5 °C to 0 °C for 12 h before removal of the DCM and TFA at 0 °C under high vacuum to give **4a**. (Note that removal of DCM and TFA at higher temperature can lead to partial epimerisation of product). The crude product was purified (in the case of **4c**) by silica gel column (DCM/MeOH with 0.1% acetic acid, 0-5% MeOH).

4a was obtained as a viscous oil, 190 mg, in quantitative yield. ¹H NMR (400 MHz, CDCl3) δ 4.69 (d, *J* = 4.4 Hz, 1H), 3.63 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.30 – 2.17 (m, 1H), 1.14 (d, *J* = 6.7 Hz, 3H), 1.10 (d, *J* = 6.7 Hz, 3H). ¹³C NMR (101 MHz, CDCl₃) δ 173.7, 168.1, 69.2, 64.8, 28.0, 20.1, 19.7. HR-MS, m/z (ESI-) calcd for C₇H₁₀O₄: 157.0506 [M-H]⁻, found 157.0507. The NMR spectra is in agreement with published data. 37

4b was obtained as a viscous oil, 264 mg, in quantitative yield.

¹H NMR (400 MHz, CDCl3) δ 4.71 (d, *J* = 4.5 Hz, 1H), 3.76 (dd, *J* = 7.9, 4.5 Hz, 1H), 2.11 – 1.95 (m, 1H), 1.71 – 1.59 (m, 1H), 1.40 – 1.25 (m, 1H), 1.07 (d, *J* = 6.7 Hz, 3H), 0.95 (t, *J* = 7.5 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 173.9, 168.4, 68.8, 63.4, 33.8, 26.9, 16.4, 11.1.

The NMR data is in agreement with published data.^{S9}

HR-MS, m/z (ESI-) calcd for C₈H₁₂O₄: 171.0663 [M-H]⁻, found 171.0668.

4c was obtained as a viscous light-yellow oil, 45 mg, 60% yield.

¹H NMR (400 MHz, CDCl3) δ 4.67 (d, *J* = 4.3 Hz, 1H), 3.78 (dd, *J* = 8.5, 4.2 Hz, 1H), 2.46 – 2.34 (m, 1H), 2.02 – 1.83 (m, 2H), 1.77 – 1.55 (m, 4H), 1.47 – 1.33 (m, 2H). ¹³C NMR (101 MHz, CDCl₃) δ 173.6, 168.5, 70.1, 62.4, 38.3, 30.2, 30.0, 25.2, 25.0. HR-MS, m/z (ESI-) calcd for C₉H₁₂O₄: 183.0657 [M-H]⁻, found 183.0651.

Synthesis of standards for validation of β-lactone assembly pathway

Synthesis of 1: To a solution of **S6** (1.4 mmol, 1.0 equiv) in 14 mL THF was added LiOH solution dropwise (2.0 mmol, 1.4 equiv, dissolved in 7 mL of water). The mixture was stirred at room temperature for 4-6 h until reaction complete (judged by TLC). The reaction was diluted with water (40 mL) and concentrated *in vacuo* to remove THF. The resulting aqueous solution was washed with 40 mL EtOAc (this organic layer was discarded), and then adjusted to pH 2 using 1M HCl. The acidified aqueous solution was extracted with EtOAc three times. The organic layers were combined, dried over MgSO4, and concentrated *in vacuo*. The residue was dissolved in 1 mL DCM and cooled to 0 °C. To this solution was added 1 mL of TFA dropwise. The reaction was kept at 0° C for 16 h before solvent and excess reagent was removed by a stream of nitrogen gas at 0 °C. The residue was dissolved in water and lyophilised to obtain **1**.

(2*R*,3*S*)-2-hydroxy-3-isopropylsuccinic acid (**1a**) was obtained as a white powder, 201 mg, 82%. ¹H NMR (400 MHz, D2O) δ 4.55 (d, *J* = 4.4 Hz, 1H), 2.64 (dd, *J* = 9.0, 4.4 Hz, 1H), 2.17 – 1.99 (m, 1H), 1.02 (d, *J* = 6.7 Hz, 3H), 0.99 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (101 MHz, D₂O) δ 176.8, 176.6, 69.3, 55.4, 26.4, 19.9, 19.3.

HR-MS, m/z (ESI+) calcd for C₇H₁₂O₅: 199.0582 [M+Na]⁺, found 199.0578.

The NMR spectra is in agreement with published data.^{S10}

(2*S*,3*R*)-2-((*S*)-*sec*-butyl)-3-hydroxysuccinic acid (**1b**) was a white powder, 72 mg, 89% yield. ¹H NMR (400 MHz, D₂O) δ 4.57 (d, J = 4.2 Hz, 1H), 2.76 (dd, J = 8.9, 4.1 Hz, 1H), 1.98 – 1.86 (m, 1H), 1.55 – 1.43 (m, 1H), 1.29 – 1.16 (m, 1H), 1.01 (d, *J* = 6.8 Hz, 3H), 0.91 (t, *J* = 7.1 Hz, 3H).

¹³C NMR (101 MHz, D₂O) δ 177.1, 176.8, 69.1, 53.8, 32.7, 26.8, 15.4, 10.4. The NMR spectra is in agreement with published data.²⁷

HR-MS, m/z (ESI+) calcd for C₈H₁₄O₅: 191.0914 [M+H]⁺, found 191.0915.

Synthesis of S7: This procedure adapted from literature.^{S11} To a solution of **S6a** (43 mg, 0.2) mmol, 1.0 equiv) in 2 mL MeOH was added triethyl amine (81 mg, 0.8 mmol, 4.0 equiv). The reaction mixture was stirred at room temperature for 16 h before concentrating *in vacuo*. The residue was dissolved in 0.5 mL DCM and cooled to 0 °C. To this solution was added 0.5 mL of TFA dropwise. The reaction mixture was kept at 0° C for 16 h. The DCM and TFA was removed by a stream of nitrogen gas at 0 °C and the residue was further dried under high vacuum to obtain 39 mg of **S7** in quantitative yield.

¹H NMR (400 MHz, CDCl₃) δ 4.44 (d, *J* = 3.1 Hz, 1H), 3.72 (s, 3H), 2.72 (dd, *J* = 8.6, 2.0 Hz, 1H), 2.30 – 2.15 (m, 1H), 1.08 (d, *J* = 6.8 Hz, 3H), 1.00 (d, *J* = 6.8 Hz, 3H). ¹³C NMR (101 MHz, CDCl₃) δ 177.4, 174.9, 69.9, 54.2, 52.3, 28.0, 20.9, 20.5. HR-MS, m/z (ESI-) calcd for C₈H₁₄O₅: 189.0763 [M-H]⁻, found 189.0719.

Synthesis of 3: To a solution of **4a** (as an example, 0.21 mmol, 1.0 equiv) in 1.25 mL MeOH and 5 mL Toluene (MeOH/Toluene = 1:4, v/v) was added TMS-diazomethane solution (2 M in Hexane, 300 μ L, 3.3 equiv) dropwise at RT. The mixture was stirred at RT for 5-10 min until N₂ bubbling ceased and the yellow colour of the solution persists. The reaction was quenched by adding 50 µL acetic acid and the yellow colour of the solution disappear. The solvent was removed *in vacuo* and the crude product was purified by silica gel column (EtOAc/Hexane, 5-10% EtOAc) to obtain **3** as colourless oil.

3a was obtained as a colourless oil, 21 mg, 58% yield. ¹H NMR (400 MHz, CDCl3) δ 4.64 (d, *J* = 4.4 Hz, 1H), 3.84 (s, 3H), 3.55 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.26 – 2.13 (m, 1H), 1.11 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.8 Hz, 3H). ¹³C NMR (101 MHz, CDCl₃) δ 168.9, 168.4, 69.8, 64.3, 53.1, 27.8, 20.1, 19.6. HR-MS by ESI was not successful.

3b was obtained as a colourless oil, 19 mg, 88% yield.

¹H NMR (400 MHz, CDCl3) δ 4.66 (d, *J* = 4.4 Hz, 1H), 3.85 (s, 3H), 3.68 (dd, *J* = 7.8, 4.4 Hz, 1H), 2.07 – 1.93 (m, 1H), 1.71 – 1.56 (m, 1H), 1.39 – 1.25 (m, 1H), 1.05 (d, *J* = 6.7 Hz, 3H), 0.94 (t, $J = 7.5$ Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 169.0, 168.8, 69.3, 62.9, 53.1, 33.7, 26.9, 16.4, 11.1. HR-MS by ESI was not successful.

Synthesis of 9 (buffer adduct): A 100 µL solution of **3a** (200 mM, 3.4 mg, 0.02 mmol) in MeCN was mixed with 900 µL HEPES buffer (200 mM, pH 7.0). The mixture was incubated at room temperature for 3 h and then concentrated in vacuo. The residue was purified by preparative HPLC on a C18 column (mobile phase $A = H₂O$ with 0.1% formic acid, mobile phase $B =$ MeCN with 0.1% formic acid, gradient B: 2-50%) to obtain 1.5 mg of **9** as white solid in 37% isolated yield.

¹H NMR (400 MHz, D₂O with 0.3% DCl) δ 4.64 (d, *J* = 4.2 Hz, 1H), 4.60 – 4.44 (m, 2H), 3.80 (brs, 8H), 3.77 (s, 3H), 3.73 – 3.63 (m, 4H), 3.39 (dd, *J* = 8.4, 6.3 Hz, 2H), 2.81 (dd, *J* = 8.3, 4.2 Hz, 1H), 2.14 – 2.04 (m, 1H), 0.98 (d, *J* = 6.8 Hz, 3H), 0.95 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (201 MHz, D₂O with 0.3% DCl) δ 175.7, 173.1, 69.1, 58.3, 55.2, 55.2, 53.0, 52.3, 49.0, 48.9, 44.7, 26.4, 19.8, 19.1.

HR-MS, m/z (ESI-) calcd for C₁₆H₃₀N₂O₈S: 409.1645 [M-H]⁻, found 409.1602.

Synthesis of CysC product 5: At 0 °C, to a solution of lactone acid **4a** (80 mg, 0.5 mmol, 1.0 equiv) and N-methyl morpholine (NMM, 152 mg, 1.5 mmol, 3.0 equiv) in 10 mL THF was added H-Val-OBn hydrochloride **S9** (122 mg, 0.5 mmol, 1.0 equiv). The solution was stirred at 0 °C for 5 min before EDC·HCl (105 mg, 0.55 mmol, 1.1 equiv), and HOBt·H₂O (74 mg, 0.55) mmol, 1.1 equiv) were quickly added in one portion. The reaction was flushed with nitrogen and the mixture stirred and allowed to gradually reach room temperature for 16 h. The reaction mixture was concentrated *in vacuo*. The residue was taken up with EtOAc (50 mL), washed with 5% (wt) citric acid solution, sat. NaHCO3, brine, dried over MgSO⁴ and concentrated *in vacuo*. The crude product was purified by silica gel column (EtOAc/Hexane, 5-20% EtOAc) to obtain 95 mg **S10** as colourless oil in 55% yield.

¹H NMR (400 MHz, CDCl₃) δ 7.42 – 7.29 (m, 5H), 6.73 (d, *J* = 9.0 Hz, 1H), 5.24 (d, *J* = 12.2 Hz, 1H), 5.12 (d, *J* = 12.1 Hz, 1H), 4.62 (d, *J* = 4.5 Hz, 1H), 4.58 (dd, *J* = 8.9, 4.8 Hz, 1H), 3.42 (dd, *J* = 8.2, 4.6 Hz, 1H), 2.35 – 2.10 (m, 2H), 1.09 (dd, *J* = 9.3, 6.7 Hz, 6H), 0.95 (d, *J* = 6.8 Hz, 3H), 0.89 (d, *J* = 7.0 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 170.9, 168.6, 168.1, 135.2, 128.8, 128.8, 128.6, 71.2, 67.4, 64.6, 57.1, 31.0, 28.0, 20.1, 19.5, 19.2, 17.7. HR-MS, m/z (ESI+) calcd for C₁₉H₂₅NO₅: 370.1630 [M+Na]⁺, found 370.1625.

A solution of **S10** (95 mg, 0.27 mmol) in 5 mL of dry THF was treated with Pd/C (45 mg, 10% wt.). The reaction flask was flushed with hydrogen gas and the mixture stirred under hydrogen atmosphere at room temperature for 16 h. The mixture was diluted with THF and filtered through a celite plug, rinsing with THF. The filtrate was concentrated *in vacuo* to give 60 mg of **5** as white solid (yield 87%).

¹H NMR (400 MHz, CDCl₃) δ 6.77 (d, *J* = 8.8 Hz, 1H), 4.67 (d, *J* = 4.6 Hz, 1H), 4.57 (dd, *J* = 8.9, 4.8 Hz, 1H), 3.55 (dd, *J* = 8.2, 4.5 Hz, 1H), 2.42 – 2.11 (m, 2H), 1.12 (dd, *J* = 10.3, 6.6 Hz, 6H), 1.01 (d, *J* = 6.8 Hz, 3H), 0.98 (d, *J* = 6.8 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 175.5, 168.8, 168.7, 71.1, 64.6, 57.1, 30.8, 28.0, 20.1, 19.5, 19.2, 17.7.

HR-MS, m/z (ESI) calcd for C₁₂H₁₉NO₅: 280.1161 [M+Na]⁺, found 280.1150.

Synthesis of Cystargolide A (**6a**) and B (**6b**)

The procedure used for the synthesis of **6a/b** Cystargolide A and B were the same as the synthesis of **5a** mentioned above. Briefly, **5a** was coupled with either H-Val-OBn or H-Ile-OBn to obtain **S11a/b**, which underwent deprotection to obtain **6a/b**.

6b was obtained as white solid, 30 mg, 54% yield over two steps. ¹H NMR (400 MHz, DMSO-d6) δ 12.56 (brs, 1H), 8.55 (d, *J* = 9.0 Hz, 1H), 8.14 (d, *J* = 8.2 Hz, 1H), 5.02 (d, *J* = 4.4 Hz, 1H), 4.42 – 4.35 (m, 1H), 4.16 – 4.07 (m, 1H), 3.51 (dd, *J* = 8.3, 4.2 Hz, 1H), 2.19 – 1.99 (m, 3H), 1.00 (d, *J* = 6.7 Hz, 3H), 0.97 (d, *J* = 6.7 Hz, 3H), 0.92 – 0.80 (m, 12H).

¹³C NMR (101 MHz, DMSO-d6) δ 172.8, 170.8, 170.1, 167.3, 70.1, 62.7, 57.33, 57.26, 30.90, 29.60, 26.68, 19.42, 19.29, 19.09, 18.09, 17.88.

HR-MS, m/z (ESI-) calcd for C₁₇H₂₈N₂O₆: 355.1875 [M-H]⁻, found 355.1879.

The NMR spectra is in agreement with published data.³⁷

6a was obtained as white solid, 20 mg, 40% yield over two steps.

¹H NMR (400 MHz, MeOD) δ 4.81 (d, *J* = 4.3 Hz, 1H), 4.41 – 4.35 (m, 1H), 4.30 (d, *J* = 7.9 Hz, 1H), 3.56 (dd, *J* = 8.5, 4.4 Hz, 1H), 2.23 – 2.05 (m, 2H), 1.96 – 1.86 (m, 1H), 1.59 – 1.47 (m, 1H), 1.28 (d, *J* = 16.6 Hz, 1H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), 1.01 – 0.88 (m, 12H).

¹³C NMR (126 MHz, MeOD) δ 174.6, 173.2, 170.6, 170.4, 72.2, 65.3, 60.2, 58.3, 38.3, 32.0, 28.8, 26.2, 20.4, 19.8, 19.7, 18.8, 16.0, 11.8.

HR-MS, m/z (ESI-) calcd for C₁₈H₃₀N₂O₆: 369.2031 [M-H]⁻, found 369.2036.

Synthesis of **7**

Synthesis of S13: Cbz-Orn-(N-Boc) **S12** (672.8 mg, 2.0 mmol, 1.0 equiv) was dissolved in MeCN (17.5 mL). To this solution was added DIPEA (271.4 mg, 1.05 equiv, 2.1 mmol) and benzyl bromide (359.2 mg, 1.05 equiv, 2.1 mmol). The reaction was stirred at room temperature for 14 h, before solvent was removed *in vacuo*, and the residue was re-dissolved in ethyl acetate (25 mL) and washed with water and brine. The organic layer was dried over MgSO⁴ and concentrated *in vacuo*. The crude product was purified by silica gel column to obtain 680 mg of **S13** in 75% yield.

¹H NMR (400 MHz, CDCl3) δ 7.41 – 7.28 (m, 10H), 5.37 (d, *J* = 7.1 Hz, 1H), 5.20 – 5.03 (m, 4H), 4.58 – 4.34 (m, 2H), 3.15 – 2.99 (m, 2H), 1.94 – 1.78 (m, 1H), 1.74 – 1.63 (m, 1H), 1.43 (s, 11H).

¹³C NMR (101 MHz, CDCl₃) δ 172.2, 156.0, 136.3, 135.3, 128.8, 128.7, 128.5, 128.3, 128.2, 79.4, 67.4, 67.2, 53.8, 40.1, 30.1, 28.5, 26.1.

The NMR spectra is in agreement with published data.^{S12} HR-MS, m/z (ESI+) calcd for C₂₅H₃₂N₂O₆: 479.2158 [M+Na]⁺, found 479.2150.

Synthesis of S15: A solution of **S13** (137 mg, 0.3 mmol, 1.0 equiv) in 3 mL 4 M HCl in dioxane was stirred at room temperature for over 3 h. Afterwards, TLC indicated complete removal of Boc protecting group and the reaction was concentrated *in vacuo*. The residue (**S14**) was taken up in 1 mL THF and added to a solution of lactone acid **4b** (52 mg, 0.3 mmol, 1.0 equiv) and N-methyl morpholine (NMM, 91 mg, 0.9 mmol, 3.0 equiv) in 4 mL THF at 0 °C. The solution was stirred at 0 °C for 5 min before EDC·HCl (69 mg, 0.36 mmol, 1.2 equiv), and HOBt·H2O (49 mg, 0.36 mmol, 1.2 equiv) were quickly added in one portion. The reaction was flushed with nitrogen and the mixture stirred and allowed to gradually reach room temperature for 16 h. The reaction mixture was concentrated *in vacuo* and the residue was taken up with EtOAc (50 mL), washed with 5% (wt) citric acid solution, sat. NaHCO3, brine, dried over MgSO⁴ and concentrated *in vacuo*. The crude product was purified by silica gel column (EtOAc/Hexane, 20-50% EtOAc) to give 80 mg **S15** as white solid in 52% yield over two steps.

¹H NMR (400 MHz, CDCl₃) δ 7.45 – 7.28 (m, 10H), 6.38 (s, 1H), 5.38 (d, *J* = 8.9 Hz, 1H), 5.23 – 5.07 (m, 4H), 4.56 (d, *J* = 4.5 Hz, 1H), 4.49 – 4.36 (m, 1H), 3.57 (dd, *J* = 7.6, 4.6 Hz, 1H), 3.37 $- 3.21$ (m, 2H), $2.03 - 1.83$ (m, 2H), $1.76 - 1.62$ (m, 2H), $1.57 - 1.42$ (m, 2H), 1.33 (d, $J = 21.2$ Hz, 1H), 1.07 (d, *J* = 6.7 Hz, 3H), 0.95 (t, *J* = 7.5 Hz, 3H). ¹³C NMR (101 MHz, CDCl₃) δ 172.0, 169.3, 168.2, 156.0, 136.2, 135.2, 128.8, 128.7, 128.7, 128.5, 128.4, 128.3, 70.8, 67.5, 67.2, 63.0, 53.5, 38.6, 33.9, 30.1, 26.8, 25.3, 16.4, 11.1.

HR-MS, m/z (ESI+) calcd for C₂₈H₃₄N₂O₇: 533.2264 [M+Na]⁺, found 533.2261.

Synthesis of 7: A solution of **S15** (79 mg, 0.15 mmol) in acetic acid (10 mL) was treated with Pd/C (45 mg, 10% wt.). The reaction was flushed with hydrogen gas and the mixture stirred under a hydrogen atmosphere (balloon) at room temperature for 16 h. The mixture was filtered through a short celite plug, rinsing with acetic acid. The collected filtrate was concentrated *in vacuo* and the residual was purified by Bond ElutTM C18 column (Agilent, eluent H₂O/MeCN, 0-30% MeCN). The fractions containing pure product were combined, concentrated *in vacuo* to remove MeCN and then lyophilised to obtain 28 mg **7** as white powder in 63% yield.

¹H NMR (400 MHz, D₂O) δ 4.93 (d, *J* = 4.3 Hz, 1H), 3.86 (dd, *J* = 7.5, 4.4 Hz, 1H), 3.76 (t, *J* = 6.1 Hz, 1H), 3.34 (t, *J* = 6.8 Hz, 2H), 2.13 – 1.99 (m, 1H), 1.98 – 1.80 (m, 2H), 1.77 – 1.49 (m, 3H), 1.41 – 1.26 (m, 1H), 1.04 (d, *J* = 6.7 Hz, 3H), 0.92 (t, *J* = 7.5 Hz, 3H).

¹³C NMR (101 MHz, D₂O) δ 174.3, 172.6, 170.4, 71.0, 62.0, 54.4, 38.6, 32.8, 27.7, 26.2, 24.2, 15.4, 10.3.

HR-MS, m/z (ESI+) calcd for C₁₃H₂₂N₂O₅: 287.1607 [M+H]⁺, found 287.1609.

Synthesis of **Ala-Orn** and belactosin C (**8c**)

Synthesis of S17: Fmoc-Orn-(N-Boc) **S16** (909 mg, 2.0 mmol, 1.0 equiv) was added to MeCN (17.5 mL). To the mixture was added DIPEA (271.4 mg, 1.05 equiv, 2.1 mmol) and benzyl bromide (359.2 mg, 1.05 equiv, 2.1 mmol). The reaction was stirred at room temperature for 14 h before solvent was removed *in vacuo*, and the residue was taken up by ethyl acetate (25 mL) and washed with 5% wt. citric acid and brine. The organic layer was dried over MgSO₄ and concentrated *in vacuo*. The crude product was purified by silica gel column (EtOAc/Hexane, 20- 50% EtOAc) to obtain 710 mg of **S17** in 65% yield.

¹H NMR (400 MHz, CDCl3) δ 7.77 (d, *J* = 7.5 Hz, 2H), 7.60 (d, *J* = 7.6 Hz, 2H), 7.48 – 7.27 (m, 9H), 5.48 (d, *J* = 7.7 Hz, 1H), 5.26 – 5.10 (m, 2H), 4.60 – 4.32 (m, 4H), 4.21 (t, *J* = 7.1 Hz, 1H), 3.18 – 2.96 (m, 2H), 1.97 – 1.82 (m, 1H), 1.77 – 1.66 (m, 1H), 1.58 – 1.45 (m, 2H), 1.44 (s, 9H). ¹³C NMR (101 MHz, CDCl₃) δ 172.3, 156.1, 144.0, 143.8, 141.4, 135.3, 128.8, 128.7, 128.5, 127.8, 127.2, 125.2, 120.1, 79.4, 67.4, 67.1, 53.8, 47.3, 40.0, 30.0, 28.5, 26.2. HR-MS, m/z (ESI+) calcd for C₃₂H₃₆N₂O₆: 567.2471 [M+Na]⁺, found 567.2465.

Synthesis of S19: A solution of **S17** (700 mg, 1.3 mmol, 1.0 equiv) in 2.5 mL THF was treated with 2.5 mL diethylamine. The reaction was stirred at room temperature for 1 h before another 1 mL diethylamine was added. The mixture was stirred at room temperature for additional 2 h before concentrating *in vacuo*. The residue was azeotroped with toluene $(2 \times 2 \text{ mL})$ under reduced pressure, and the crude product was taken up in DMF (2 mL). To this solution was added Cbz-Alanine (290 mg, 1.3 mmol, 1.0 equiv), HBTU (606 mg, 1.6 mmol, 1.2 equiv) and DIPEA (504 mg, 3.9 mmol, 3.0 equiv). The reaction mixture was stirred at room temperature for 16 h before diluting with DCM (50 mL). The resulting solution was washed with 5% wt. citric acid, brine,

dried over MgSO⁴ and concentrated *in vacuo*. The crude product was purified by silica gel column (EtOAc/Hexane, 20-50% EtOAc) to give 531 mg **S19** as white solid in 78% yield over two steps.

¹H NMR (400 MHz, CDCl₃) δ 7.39 – 7.27 (m, 10H), 6.90 (s, 1H), 5.50 (s, 1H), 5.23 – 5.02 (m, 4H), 4.70 – 4.53 (m, 2H), 4.34 – 4.22 (m, 1H), 3.14 – 2.96 (m, 2H), 1.96 – 1.74 (m, 2H), 1.73 – 1.60 (m, 1H), 1.55 – 1.42 (m, 2H), 1.41 (s, 9H), 1.37 (d, *J* = 7.0 Hz, 3H). ¹³C NMR (101 MHz, CDCl₃) δ 172.4, 171.9, 156.3, 156.1, 136.4, 135.3, 128.8, 128.6, 128.5, 128.3, 128.2, 79.5, 67.4, 67.1, 52.3, 50.6, 39.9, 29.0, 28.5, 26.2, 18.6. HR-MS, m/z (ESI+) calcd for C₂₈H₃₇N₃O₇: 550.2529 [M+Na]⁺, found 550.2523.

Synthesis of Ala-Orn: A solution of **S19** (200 mg, 0.38 mmol, 1.0 equiv) in 5 mL 4 M HCl (in dioxane) was stirred at room temperature for over 3 h. After TLC indicated complete removal of Boc protecting group the reaction was concentrated *in vacuo*. The residue was taken up in acetic acid (5 mL). To this solution was treated with Pd/C (60 mg, 10% wt.). The reaction was flushed with hydrogen gas and the mixture stirred under a hydrogen atmosphere (balloon) at room temperature for 16 h. The mixture was filtered through a short celite plug, rinsing with acetic acid. The collected filtrate was concentrated *in vacuo* and the residual was purified by Bond $E[10^{TM} C18$ column (Agilent, eluent H₂O/MeCN with 0.1% HCl, 0-30% MeCN). The fractions containing pure product were combined, concentrated to remove MeCN and then lyophilised to obtain 80 mg **Ala-Orn** di-hydrochloride salt as yellow solid in 76% yield.

$$
H_2N \underbrace{\qquad \qquad}_{O} \underbrace{\qquad \qquad}_{COOH} \underbrace{\qquad \qquad}_{NH_2}
$$

¹H NMR (400 MHz, D₂O) δ 4.45 (dd, *J* = 8.4, 5.3 Hz, 1H), 4.15 (q, *J* = 7.0 Hz, 1H), 3.05 (t, *J* = 7.5 Hz, 2H), 2.07 – 1.95 (m, 1H), 1.91 – 1.71 (m, 3H), 1.57 (d, *J* = 7.2 Hz, 3H). ¹³C NMR (101 MHz, D₂O) δ 174.7, 170.9, 52.4, 48.9, 38.8, 27.3, 23.2, 16.4. HR-MS, m/z (ESI+) calcd for C₈H₁₇N₃O₃: 202.1197 [M-H]⁻, found 202.1204.

Synthesis of S21: A solution of **S19** (158 mg, 0.3 mmol, 1.0 equiv) in 3 mL 4M HCl (in dioxane) was stirred at room temperature for over 3 h. After TLC indicated complete removal of Boc protecting group the reaction was concentrated *in vacuo*. The residue (**S20**) was taken up in 1 mL THF and added to a solution of lactone acid **4b** (52 mg, 0.3 mmol, 1.0 equiv) and N-methyl morpholine (NMM, 91 mg, 0.9 mmol, 3.0 equiv) in 4 mL THF at 0 °C. The solution was stirred at 0 °C for 5 min before EDC·HCl (69 mg, 0.36 mmol, 1.2 equiv), and HOBt·H2O (50 mg, 0.36 mmol, 1.2 equiv) were quickly added in one portion. The reaction was flushed with nitrogen and the mixture stirred and allowed to gradually reach room temperature for 16 h. The reaction mixture was concentrated *in vacuo* and the residue was taken up with EtOAc (50 mL), washed with 5% (wt) citric acid solution, sat. NaHCO3, brine, dried over MgSO⁴ and concentrated *in vacuo*. The crude product was purified by silica gel column (EtOAc/Hexane, 50-60% EtOAc) to give 85 mg **S21** as white solid in 49% yield over two steps.

¹H NMR (400 MHz, CDCl₃) δ 7.45 – 7.25 (m, 10H), 6.76 (d, $J = 8.2$ Hz, 1H), 6.58 (s, 1H), 5.41 $(d, J = 6.8 \text{ Hz}, 1\text{ H}), 5.25 - 5.03 \text{ (m, 4H)}, 4.67 - 4.57 \text{ (m, 1H)}, 4.54 \text{ (d, } J = 4.5 \text{ Hz}, 1\text{ H}), 4.32 -$ 4.18 (m, 1H), 3.56 (dd, *J* = 7.7, 4.5 Hz, 1H), 3.34 – 3.13 (m, 2H), 2.03 – 1.81 (m, 2H), 1.78 – 1.58 (m, 4H), 1.57 – 1.41 (m, 2H), 1.37 (d, *J* = 7.1 Hz, 3H), 1.34 – 1.25 (m, 1H), 1.05 (d, *J* = 6.7 Hz, 3H), 0.93 (t, *J* = 7.4 Hz, 3H).

¹³C NMR (101 MHz, CDCl₃) δ 172.7, 171.7, 169.4, 168.3, 156.2, 136.2, 135.2, 128.8, 128.7, 128.6, 128.4, 128.3, 128.1, 70.9, 67.4, 67.2, 62.9, 51.9, 50.5, 38.5, 33.8, 29.3, 26.7, 25.4, 18.7, 16.4, 11.1.

HR-MS, m/z (ESI) calcd for $C_{31}H_{39}N_3O_8$: 604.2635 [M+Na]⁺, found 604.2610. The NMR spectra is in agreement with published data^{S9}.

Synthesis of 8c: A solution of **S21** (80 mg, 0.14 mmol) in acetic acid (10 mL) was treated with Pd/C (45 mg, 10% wt.). The reaction was flushed with hydrogen gas and the mixture stirred under a hydrogen atmosphere (balloon) at room temperature for 16 h. The mixture was filtered through a short celite plug, rinsing with acetic acid. The collected filtrate was concentrated *in vacuo* and the residual was purified by Bond ElutTM C18 column (Agilent, eluent H₂O/MeCN, 0-30% MeCN). The fractions containing pure product were combined, concentrated to remove MeCN and then lyophilised to obtain 26 mg Belactosin C **(8c)** as white powder in 53% yield.

(Belactosin C)

¹H NMR (400 MHz, D2O) δ 4.92 (d, *J* = 4.4 Hz, 1H), 4.17 (dd, *J* = 8.1, 5.2 Hz, 1H), 4.11 (q, *J* = 7.1 Hz, 1H), 3.85 (dd, *J* = 7.5, 4.4 Hz, 1H), 3.31 (t, *J* = 6.9 Hz, 2H), 2.13 – 1.98 (m, 1H), 1.89 – 1.78 (m, 1H), 1.78 – 1.67 (m, 1H), 1.66 – 1.49 (m, 6H), 1.40 – 1.28 (m, 1H), 1.03 (d, *J* = 6.7 Hz, 3H), 0.91 (t, *J* = 7.5 Hz, 3H).

¹³C NMR (101 MHz, D₂O) δ 178.1, 172.7, 170.2, 170.0, 71.0, 62.0, 55.1, 49.0, 38.8, 32.8, 28.6, 26.2, 24.9, 16.4, 15.4, 10.3.

HR-MS, m/z (ESI) calcd for $C_{16}H_{27}N_3O_6$: 358.1978 [M+H]⁺, found 358.1985.

The NMR spectra is in agreement with published data S13 .

Synthesis of Cystargolide analogues

General procedure A: Bn Protection of amino acids. To a solution of amino acid (**AA**) (2.1 mmol, 1.0 equiv) in 5 mL Toluene was added TsOH monohydrate (590 mg, 3.1 mmol, 1.5 equiv) and BnOH (2.2 mL, 21 mmol, 10.0 equiv). The mixture was stirred and heated under reflux for 18 h before diluting with 50 mL water and washed with $Et₂O$. The aqueous layer was basified with saturated aqueous NaHCO₃ and extracted with EtOAc (3 times) . The organic layers were combined, dried over MgSO⁴ and concentrated *in vacuo* to afford the crude **H-AA-OBn**, which was used in the coupling step without further purification.

General procedure B: tBu Protection of amino acids. To a solution of amino acid (**AA**) (0.88 mmol) in AcO*t*Bu (2.2 mL), 70% aqueous HClO⁴ (2.64 mmol, 3.0 equiv) was added dropwise at 0 °C. After completion of the addition of HClO₄, the reaction mixture was stirred for 12 h at room temperature, and then quenched with 1 M aqueous HCl. The aqueous layer was diluted with H_2O and washed with Et_2O . Then the aqueous layer was basified with saturated aqueous NaHCO₃ (pH 9) and extracted with DCM (3 times). The organic layer was dried over $MgSO₄$ and concentrated to afford the crude **H-AA-O***t***Bu**, which was used in the next reaction without further purification.

General procedure C: N-Boc protection of amino acids. At 0 °C, to a solution of amino acid $(AA, 4.0 \text{ mmol})$ and NaOH (6.0 mmol, 1.5 equiv) in H₂O/1,4-dioxane (H₂O/dioxane = 1:1, 30 mL) was added Boc2O (6.0 mmol dissolved in 8 mL 1,4-dioxane). The reaction was then allowed to reach room temperature and kept stirring for 12 h. The mixture was diluted with water and washed with EtOAc. The aqueous layer was adjusted to pH 2-3 with 5% citric acid, extracted with EtOAc, dried and concentrated *in vacuo* to give **Boc-AA-OH**.

General procedure D: coupling of protected amino acids. To a solution of **Boc-AA-OH** (1.0 mmol) and C-protected amino acid (**H-AA-OBn/O***t***Bu**, 1.0 mmol) in 2.5 mL DMF was added HBTU (1.0 mmol) and DIPEA (2.0 mmol). After stirring at RT for 12 h, the reaction was diluted with EtOAc, washed with sat. NaHCO₃, 1 M HCl, brine, dried over MgSO₄, and concentrated *in vacuo* to give protected dipeptide.

The coupling of β-lactone containing acid with C-protected amino acids or dipeptides followed the same procedure as the synthesis of CysC product **5** (using EDC, HOBt, NMM, THF). The crude product was deprotected using either H_2 , Pd/C (in the case of OBn protection, following the same procedure as described in the synthesis of **5**), or TFA/DCM (in the case of O*t*Bu protection, following the same procedure as described in the synthesis of **4**).

18 was prepared as a white solid, 22.3 mg, 29% yield over two steps.

¹H NMR (400 MHz, MeOD) δ 4.78 (d, *J* = 4.3 Hz, 1H), 4.42 – 4.32 (m, 1H), 3.58 (dd, *J* = 8.4, 4.3 Hz, 1H), 2.24 – 2.11 (m, 1H), 2.03 – 1.89 (m, 1H), 1.85 – 1.70 (m, 1H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.7 Hz, 3H), 0.98 (t, *J* = 7.4 Hz, 3H).

¹³C NMR (101 MHz, MeOD) δ 174.7, 170.7, 170.7, 72.2, 65.2, 55.0, 28.8, 25.5, 20.4, 19.8, 10.6. HR-MS, m/z (ESI-) calcd for C₁₁H₁₇NO₅: 242.1034 [M-H]⁻, found 242.1082.

21 was prepared as a white solid, 18.2 mg, 32% yield over two steps.

¹H NMR (400 MHz, MeOD) δ 4.85 (d, *J* = 4.4 Hz, 1H), 4.66 (d, *J* = 4.6 Hz, 1H), 3.55 (dd, *J* = 8.5, 4.3 Hz, 1H), 2.24 – 2.12 (m, 1H), 1.88 – 1.78 (m, 1H), 1.52 – 1.40 (m, 2H), 1.34 – 1.24 (m, 2H), 1.08 (dd, *J* = 16.5, 6.7 Hz, 6H), 1.01 – 0.87 (m, 6H).

¹³C NMR (101 MHz, MeOD) δ 169.3, 169.2, 70.6, 63.9, 53.7, 43.6, 27.4, 22.8, 22.4, 22.1, 19.0, 18.5, 10.6, 10.5.

HR-MS, m/z (ESI-) calcd for C₁₄H₂₃NO₅: 284.1503 [M-H]⁻, found 284.1569.

19 was prepared as a white solid, 30 mg, 35% yield.

¹H NMR (400 MHz, MeOD) δ 4.79 (d, $J = 4.3$ Hz, 1H), 4.40 (d, $J = 9.1$ Hz, 1H), 3.57 (dd, $J =$ 8.4, 4.4 Hz, 1H), 2.90 – 2.58 (m, 1H), 2.24 – 2.13 (m, 1H), 2.12 – 1.78 (m, 6H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (101 MHz, MeOD) δ 174.0, 170.8, 170.7, 72.1, 65.3, 57.9, 38.1, 28.8, 26.7, 26.2, 20.4, 19.8, 18.7.

HR-MS, m/z (ESI-) calcd for C₁₃H₁₉NO₅: 268.1190 [M-H]⁻, found 268.1187.

22 was prepared as a white solid, 32 mg, 38% yield.

¹H NMR (400 MHz, MeOD) δ 4.80 (d, $J = 4.3$ Hz, 1H), 4.39 – 4.32 (m, 1H), 3.56 (dd, $J = 8.5$, 4.3 Hz, 1H), 2.41 – 2.29 (m, 1H), 2.24 – 2.12 (m, 1H), 1.84 – 1.73 (m, 2H), 1.71 – 1.53 (m, 4H), 1.47 – 1.31 (m, 2H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (101 MHz, MeOD) δ 174.6, 170.6, 170.5, 72.1, 65.2, 57.3, 42.9, 30.4, 30.0, 28.8, 26.3, 25.9, 20.4, 19.8.

HR-MS, m/z (ESI-) calcd for C₁₄H₂₁NO₅: 282.1347 [M-H]⁻, found 282.1393.

20 was prepared as a white solid, 10 mg, 13% yield.

¹H NMR (400 MHz, MeOD) δ 4.79 (d, *J* = 4.4 Hz, 1H), 4.53 (dd, *J* = 8.1, 5.5 Hz, 1H), 3.59 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.28 – 2.08 (m, 1H), 1.89 – 1.63 (m, 2H), 1.11 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.7 Hz, 3H), 0.89 – 0.68 (m, 1H), 0.59 – 0.35 (m, 2H), 0.26 – 0.02 (m, 2H).

¹³C NMR (101 MHz, MeOD) δ 174.7, 170.7, 170.6, 72.3, 65.2, 54.2, 37.2, 28.9, 20.4, 19.8, 8.6, 5.2, 4.5.

HR-MS, m/z (ESI-) calcd for C₁₃H₁₉NO₅: 268.1185 [M-H]⁻, found 268.1166.

23 was prepared as a white solid, 3 mg, 5% yield.

¹H NMR (400 MHz, MeOD) δ 4.82 (d, *J* = 4.4 Hz, 1H), 4.65 (dd, *J* = 5.2, 3.6 Hz, 1H), 3.83 (dd, *J* = 9.8, 5.2 Hz, 1H), 3.70 (dd, *J* = 9.8, 3.6 Hz, 1H), 3.60 (dd, *J* = 8.3, 4.4 Hz, 1H), 3.36 (s, 3H), 2.25 – 2.10 (m, 1H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.8 Hz, 3H).

¹³C NMR (126 MHz, MeOD) δ 172.6, 170.6, 170.6, 72.6, 72.2, 65.3, 59.3, 53.9, 28.9, 20.4, 19.8. HR-MS, m/z (ESI-) calcd for C₁₁H₁₇NO₆: 258.0978 [M-H]⁻, found 258.0959.

24 was prepared as a white solid, 35 mg, 42% yield.

¹H NMR (400 MHz, MeOD) δ 4.82 (d, *J* = 4.4 Hz, 1H), 4.62 (dd, *J* = 7.6, 5.0 Hz, 1H), 3.59 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.88 – 2.67 (m, 2H), 2.39 (t, *J* = 2.6 Hz, 1H), 2.26 – 2.12 (m, 1H), 1.11 (d, *J* = 6.7 Hz, 3H), 1.08 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (101 MHz, MeOD) δ 172.7, 170.6, 79.9, 72.3, 72.1, 65.4, 52.3, 28.9, 22.0, 20.4, 19.8. HR-MS, m/z (ESI-) calcd for C₁₂H₁₅NO₅: 252.0877 [M-H]⁻, found 252.0889.

28 was prepared as a light-yellow oil, 15.8 mg, 24% yield over two steps.

¹H NMR (400 MHz, MeOD) δ 4.81 (d, *J* = 4.3 Hz, 1H), 4.36 – 4.26 (m, 2H), 3.57 (dd, *J* = 8.5, 4.3 Hz, 1H), 2.22 – 2.07 (m, 2H), 1.93 – 1.86 (m, 1H), 1.78 – 1.69 (m, 1H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), 1.03 – 0.93 (m, 9H).

¹³C NMR (101 MHz, MeOD) δ 173.6, 171.8, 169.2, 169.0, 70.8, 63.8, 58.7, 53.7, 30.7, 27.4, 24.5, 19.0, 18.4, 18.3, 17.4, 9.2.

HR-MS, m/z (ESI-) calcd for C₁₆H₂₆N₂O₆: 341.1718 [M-H]⁻, found 341.1788.

31 was prepared as a white solid, 20 mg, 35% yield.

¹H NMR (400 MHz, MeOD) δ 4.80 (d, *J* = 4.4 Hz, 1H), 4.61 (d, *J* = 4.8 Hz, 1H), 4.30 (d, *J* = 8.0 Hz, 1H), 3.54 (dd, *J* = 8.5, 4.3 Hz, 1H), 2.23 – 2.03 (m, 2H), 1.81 – 1.68 (m, 1H), 1.50 – 1.26 (m, 4H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), 1.03 – 0.86 (m, 12H).

¹³C NMR (101 MHz, MeOD) δ 175.1, 173.6, 170.6, 170.4, 72.2, 65.3, 60.2, 55.2, 45.0, 31.8,

28.8, 23.6, 23.4, 20.4, 19.9, 19.7, 18.8, 12.0, 12.0.

HR-MS, m/z (ESI-) calcd for C₁₉H₃₂N₂O₆: 383.2182 [M-H]⁻, found 383.2167.

29 was prepared as a white solid, 30 mg, 53% yield.

¹H NMR (400 MHz, MeOD) δ 4.81 (d, *J* = 4.4 Hz, 1H), 4.34 (d, *J* = 8.6 Hz, 1H), 4.30 (d, *J* = 7.7 Hz, 1H), 3.56 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.82 – 2.63 (m, 1H), 2.23 – 1.78 (m, 8H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), 1.00 (d, *J* = 6.8 Hz, 3H), 0.96 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (101 MHz, MeOD) δ 174.4, 173.3, 170.6, 170.4, 72.2, 65.2, 60.1, 58.0, 38.4, 32.0, 28.8, 26.3, 26.1, 20.4, 19.8, 19.7, 18.7, 18.7.

HR-MS, m/z (ESI-) calcd for C₁₈H₂₈N₂O₆: 367.1875 [M-H]⁻, found 367.1869.

32 was prepared as a white solid, 30 mg, 44% yield.

¹H NMR (400 MHz, MeOD) δ 4.80 (d, *J* = 4.4 Hz, 1H), 4.30 (dd, *J* = 9.7, 7.9 Hz, 2H), 3.55 (dd, *J* = 8.5, 4.3 Hz, 1H), 2.35 – 2.24 (m, 1H), 2.21 – 2.04 (m, 2H), 1.82 – 1.71 (m, 2H), 1.70 – 1.62 (m, 2H), 1.61 – 1.52 (m, 2H), 1.46 – 1.31 (m, 2H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), 0.99 (d, *J* = 6.7 Hz, 3H), 0.95 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (101 MHz, MeOD) δ 174.9, 173.2, 170.6, 170.4, 72.2, 65.3, 60.1, 57.2, 43.0, 32.0, 30.2, 29.9, 28.8, 26.3, 26.0, 20.4, 19.8, 19.7, 18.8. HR-MS, m/z (ESI-) calcd for C₁₉H₃₀N₂O₆: 381.2026 [M-H]⁻, found 381.2081.

30 was prepared as a white solid, 30 mg, 42% yield over two steps.

¹H NMR (400 MHz, MeOD) δ 4.81 (d, *J* = 4.3 Hz, 1H), 4.51 – 4.44 (m, 1H), 4.30 (d, *J* = 7.7 Hz, 1H), 3.56 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.24 – 2.06 (m, 2H), 1.78 – 1.61 (m, 2H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), 1.01 (d, *J* = 6.7 Hz, 3H), 0.96 (d, *J* = 6.8 Hz, 3H), 0.88 – 0.77 (m, 1H), 0.53 – 0.40 (m, 2H), 0.21 – 0.05 (m, 2H).

¹³C NMR (101 MHz, MeOD) δ 175.0, 173.0, 170.6, 170.4, 72.2, 65.2, 60.1, 54.2, 37.7, 32.1, 28.8, 20.4, 19.8, 19.7, 18.8, 8.6, 5.2, 4.7.

HR-MS, m/z (ESI-) calcd for C₁₈H₂₈N₂O₆: 367.1869 [M-H]⁻, found 367.1845.

33 was prepared as a white solid, 5 mg, 9% yield.

¹H NMR (400 MHz, MeOD) δ 4.82 (d, *J* = 4.4 Hz, 1H), 4.52 (s, 1H), 4.35 (d, *J* = 7.2 Hz, 1H), 3.79 (dd, *J* = 9.7, 4.5 Hz, 1H), 3.65 (dd, *J* = 9.7, 3.0 Hz, 1H), 3.60 (dd, *J* = 8.5, 4.3 Hz, 1H), 3.34 (s, 3H), 2.23 – 2.09 (m, 2H), 1.11 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.7 Hz, 3H), 1.00 (d, *J* = 6.8 Hz, 3H), 0.96 (d, *J* = 6.8 Hz, 3H).

¹³C NMR (126 MHz, MeOD) δ 172.8, 170.6, 170.5, 73.3, 72.2, 65.2, 60.0, 59.3, 32.1, 28.9, 20.4, 19.8, 19.7, 18.6.

HR-MS, m/z (ESI-) calcd for C₁₆H₂₆N₂O₇: 357.1662 [M-H]⁻, found 357.1506.

35 was prepared as a white solid, 25 mg, 32% yield.

¹H NMR (400 MHz, MeOD) δ 8.47 (d, *J* = 7.8 Hz, 1H), 8.19 (d, *J* = 8.7 Hz, 1H), 4.82 (d, *J* = 4.4 Hz, 1H), 4.59 – 4.49 (m, 1H), 4.39 – 4.30 (m, 1H), 3.59 (dd, *J* = 8.5, 4.3 Hz, 1H), 2.80 – 2.65 (m, 2H), 2.34 (s, 1H), 2.24 – 2.09 (m, 2H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.8 Hz, 3H), 1.00 (d, *J* = 6.7 Hz, 3H), 0.96 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (101 MHz, MeOD) δ 173.0, 170.6, 170.5, 80.1, 72.2, 72.2, 65.3, 60.0, 52.6, 32.2, 28.9, 22.3, 20.4, 19.8, 19.7, 18.6.

HR-MS, m/z (ESI-) calcd for C₁₇H₂₄N₂O₆: 351.1562 [M-H]⁻, found 351.1553.

34 was prepared as a white solid, 20 mg, 23% yield.

¹H NMR (400 MHz, MeOD) δ 7.39 – 7.21 (m, 5H), 4.81 (d, *J* = 4.4 Hz, 1H), 4.67 (t, *J* = 4.4 Hz, 1H), 4.59 – 4.49 (m, 2H), 4.42 – 4.31 (m, 1H), 3.89 (dd, *J* = 9.9, 5.0 Hz, 1H), 3.75 (dd, *J* = 9.9, 3.6 Hz, 1H), 3.57 (dd, *J* = 8.6, 4.4 Hz, 1H), 2.25 – 2.05 (m, 2H), 1.09 (d, *J* = 6.6 Hz, 3H), 1.06 (d, *J* = 6.8 Hz, 3H), 1.00 (d, *J* = 6.8 Hz, 3H), 0.96 (d, *J* = 6.8 Hz, 3H).

¹³C NMR (101 MHz, MeOD) δ 171.6, 171.4, 169.2, 169.0, 137.8, 128.0, 127.4, 127.3, 72.8, 70.8, 69.2, 63.8, 58.5, 52.7, 48.2, 48.0, 47.8, 47.6, 47.4, 47.2, 47.0, 30.8, 27.4, 19.0, 18.4, 18.3, 17.2.

HR-MS, m/z (ESI-) calcd for C₂₂H₃₀N₂O₇: 433.1975 [M-H]⁻, found 433.1964.

11 was prepared as an oil, 39.3 mg, 43% yield over three steps.

¹H NMR (400 MHz, MeOD) δ 4.77 (d, *J* = 4.4 Hz, 1H), 4.41 – 4.25 (m, 2H), 3.61 (dd, *J* = 8.4, 4.3 Hz, 1H), 2.24 – 2.09 (m, 1H), 1.93 – 1.85 (m, 2H), 1.81 – 1.66 (m, 2H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), 0.98 (t, *J* = 7.5 Hz, 6H).

¹³C NMR (101 MHz, MeOD) δ 175.0, 173.8, 170.6, 170.5, 72.2, 65.2, 56.0, 55.0, 28.8, 26.4, 25.9, 24.0, 20.4, 19.8, 10.6.

HR-MS, m/z (ESI-) calcd for C₁₅H₂₄N₂O₆: 327.1562 [M-H]⁻, found 327.1583.

12 was prepared as a white solid, 18.2 mg, 32% yield over three steps.

¹H NMR (400 MHz, MeOD) δ 4.78 (d, *J* = 4.4 Hz, 1H), 4.44 (d, *J* = 9.3 Hz, 1H), 4.34 (d, *J* = 8.4 Hz, 1H), 3.58 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.78 – 2.64 (m, 2H), 2.24 – 2.10 (m, 1H), 2.09 – 1.76 (m, 12H), 1.07 (dd, *J* = 16.3, 6.7 Hz, 6H).

¹³C NMR (101 MHz, MeOD) δ 172.8, 171.4, 169.2, 169.2, 70.8, 63.9, 57.6, 56.3, 37.2, 37.1, 27.4, 25.0, 24.8, 24.5, 24.5, 19.0, 18.4, 17.3, 17.3.

HR-MS, m/z (ESI-) calcd for C₁₉H₂₈N₂O₆: 379.1875 [M-H]⁻, found 379.1908.

15 was prepared as a white solid, 5 mg, 8% yield over three steps.

¹H NMR (400 MHz, MeOD) δ 4.77 (d, *J* = 4.4 Hz, 1H), 4.31 (d, *J* = 7.6 Hz, 1H), 4.28 (d, *J* = 9.6 Hz, 1H), 3.56 (dd, *J* = 8.5, 4.4 Hz, 1H), 2.35 – 2.23 (m, 2H), 2.22 – 2.11 (m, 1H), 1.84 – 1.50 (m, 13H), 1.47 – 1.33 (m, 4H), 1.10 (d, *J* = 6.7 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (126 MHz, MeOD) δ 173.4, 170.6, 170.3, 72.2, 65.3, 59.0, 57.4, 43.4, 43.2, 30.4, 30.2, 29.7, 28.8, 26.3, 26.2, 26.0, 25.9, 20.4, 19.8.

HR-MS, m/z (ESI-) calcd for C₂₁H₃₂N₂O₆: 407.2182 [M-H]⁻, found 407.2104.

16 was prepared as a white solid, 30 mg, 53% yield.

¹H NMR (400 MHz, MeOD) δ 4.80 (d, *J* = 4.4 Hz, 1H), 4.69 (t, *J* = 5.6 Hz, 1H), 4.60 (t, *J* = 4.0 Hz, 1H), 3.82 (dd, *J* = 9.8, 4.4 Hz, 1H), 3.71 (d, *J* = 5.6 Hz, 2H), 3.68 – 3.60 (m, 2H), 3.37 (s, 3H), 3.36 (s, 3H), 2.24 – 2.11 (m, 1H), 1.11 (d, *J* = 6.7 Hz, 3H), 1.07 (d, *J* = 6.7 Hz, 3H). ¹³C NMR (101 MHz, MeOD) δ 172.7, 171.4, 170.7, 170.6, 72.9, 72.7, 72.3, 65.3, 59.4, 59.3, 54.3, 54.1, 28.9, 20.4, 19.8.

HR-MS, m/z (ESI-) calcd for C₁₅H₂₄N₂O₈: 359.1454 [M-H]⁻, found 359.1436.

13 was prepared as a white solid, 29 mg, 24% yield.

¹H NMR (400 MHz, MeOD) δ 4.77 (d, *J* = 4.4 Hz, 1H), 4.60 – 4.45 (m, 2H), 3.61 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.24 – 2.11 (m, 1H), 1.74 – 1.65 (m, 4H), 1.10 (d, *J* = 6.6 Hz, 3H), 1.06 (d, *J* = 6.7 Hz, 3H), $0.88 - 0.73$ (m, 2H), $0.55 - 0.41$ (m, 4H), $0.21 - 0.07$ (m, 4H).

¹³C NMR (101 MHz, MeOD) δ 173.6, 173.5, 170.6, 170.4, 72.3, 65.2, 55.2, 54.2, 37.9, 37.8, 28.9, 20.4, 19.8, 8.5, 8.5, 5.2, 5.1, 4.7, 4.6.

HR-MS, m/z (ESI-) calcd for C₁₉H₂₈N₂O₆: 379.1875 [M-H]⁻, found 379.1912.

17 was prepared as a white solid, 20 mg, 30% yield.

¹H NMR (400 MHz, MeOD) δ 8.59 (d, *J* = 8.0 Hz, 1H), 8.37 (d, *J* = 7.8 Hz, 1H), 4.81 (d, *J* = 4.4 Hz, 1H), 4.74 – 4.62 (m, 1H), 4.60 – 4.49 (m, 1H), 3.63 (dd, *J* = 8.4, 4.4 Hz, 1H), 2.85 – 2.54 (m, 4H), 2.39 (t, *J* = 2.7 Hz, 1H), 2.35 (t, *J* = 2.6 Hz, 1H), 2.27 – 2.06 (m, 1H), 1.11 (d, *J* = 6.7 Hz, 3H), 1.08 (d, *J* = 6.7 Hz, 3H).

¹³C NMR (126 MHz, MeOD) δ 172.9, 171.7, 170.7, 170.6, 80.0, 79.9, 72.5, 72.4, 72.2, 65.5, 53.2, 52.6, 28.9, 22.5, 22.4, 20.5, 19.8.

HR-MS, m/z (ESI-) calcd for C₁₇H₂₀N₂O₆: 347.1243 [M-H]⁻, found 347.1263.

6. DNA and protein sequences

(DNA sequence codon optimised for E. coli, His-tag shown in bold)

cys pathway

>CysG DNA sequence

ATGGGCCAGACCGCCTCACCGAGAATTGAACTCTGGAATCCCGAGACGTATGACGC GCTTCGTCGCCAACTGATTCCCAGCTTTGACTTACTGTACGGCTCAGCAGTGAGCGT TGTGGCCATGTCAGTACCAGCTACAGCCAGAATTCTTGACTTAGGTGCCGGAACTGG TCTTCTGGGTGCTGCGCTGCGTGAGCGCCTTCCCGATGCGGAACTGCTGCTTCAGGA TCGATCCCAAGCAATGCTGGAGCAGGCGCGCCAACGTTTTGCCGACGACGACCAAG TGGCAATTCGCGTAGCTGACCACCTTGATGAGTTACCTGCAGGTCCGTTCGACGCTG TAGTGTCCGCCTTGTCCATTCATCATTTGGAGCATCAGGACAAGCAGGATTTATTCA CACGCATTCGTAAGATCCTGCGCCCAGGCGGTATTTTCGTCAACGTTGAGCAAGTGC TGGCGCCTACTTCAGAACTTGAGAAAATGTATGACCGCCAACACGAGGCTCATGTAC TGGCTTCTGACACTCCGGCAGAAGAGTGGGCGGCAGGCCGCGAAAGAATGAAGCAC GACATCCCAATCGATGTGGAGACTCAAATTCAATGGCTGAGAGACGCAGGGTTCAC TACCGCTGACTGTCTGGCTAAGGACTGGCGGTTTGCAACCTACGCGGGCTGGAATGG CAGT**CTCGAGCACCACCACCACCACCAC**TGA

>CysG protein sequence

MGQTASPRIELWNPETYDALRRQLIPSFDLLYGSAVSVVAMSVPATARILDLGAGTGLL GAALRERLPDAELLLQDRSQAMLEQARQRFADDDQVAIRVADHLDELPAGPFDAVVSA LSIHHLEHQDKQDLFTRIRKILRPGGIFVNVEQVLAPTSELEKMYDRQHEAHVLASDTPA EEWAAGRERMKHDIPIDVETQIQWLRDAGFTTADCLAKDWRFATYAGWNGS**LEHHH HHH**

>CysF DNA sequence

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>CysE protein sequence MAELLLEDGQSIHYQETGKGSPVLLVHGLGAPSAFLAATAEGLARDHRVVTFDLRGHG RTPLGTGPVGIDRCAADLHAVAGKLDLRAVTLVGWSLGATVAYRYLERYGAQRVARL VSVEQSPYLLYEDGWEHAAFGRLTAADAETVRQNLAGTDRAVAADQVAGYFAEGTVP DPDLLARLADAVATCSPAARQQLWQDVVRQDWRERLAALPVPVLFVHGARSRIYPSA VGSRLADTVPGARLEVFENSGHLPFLEEPERFQRTIRSWVAR**LEHHHHHH**

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MLYEALRDIAARRPDARAVTTADGASASYAELLDLIDRTAAGLRGHGVGAGDVIACSL RNSIRYVALILAAARIGARYVPLMSNFDRADIATALRLTGPRMIVTDHQREFPDQAPPRV RLETLEAATASPREAGERYDGLFRSLWTSGSTGFPKQMVWRQDRFLRERRRWLADTGI TADDVFFCRHTLDVAHATDLHVFAALLSGAELVLADPDAAPDVLLRQIAERRATAMSA LPRHYEEYVRAAAGRPAPDLSRLRRPLCGGAYVSAAQLTDAAEVLGIHIRQIYGSTEFGL AMGNMSDVLQAGVGMVPVEGVGVRLEPLAADRPDLGELVLISDCTSEGYVGSDEANA RTFRGEEFWTGDVAQRGPDGTLRVLGRVTETLAAAGGPLLAPVLDEEIAAGCPVLETAA LPAHPDRYSDEVLLVLHPDPDRPEQELRKAVAEVLDRHGLRASIRLTDDIPHTPVGKPD KPALRRRWESGALGPVGEWHHG**LEHHHHHH**

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>CysF protein sequence

>CysE DNA sequence

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58

>CysD DNA sequence ATGACAACCGCCCCAGCCGCACCGACCCGCCGTTTATGTTGGATCTACCCTGATCGA GGAACCGACCGCATGAGAGACAAGGAGTGGAAGCATGTTTGGGGCATTTATCGTGA AGTAGCCAGAGAAGGCGGTTGGGCTCTGTCTCTGCATAAACCAGAAGAAGTTGCAG TAGATGTATGCGGCCCTGGCGGGCCTAAAGTTTACCTCGACGGAGAACGCGTTACAC CTGAGGACACCGTTTTCGTGACGAGTTTGTGGTCCCTTCCTCATCACACTGTGGATGT ATGTAATCAACTCTATCTCTATACAATATTAGAGCAGGCCGGCTTTTACCTTCCAATT CCCCCGCATCTCAGCTTCATTGCAAATGATAAAGCAGCGACAATGCTTCACTTGGCG GATAGCCCACTCCCGCAAGTCCCTACGGTTCGGATTGGAACTGGCCGCGACACTGCC CAACGGTCATACGAGGCAGCACTGGCTTCGTTATCCTATCCTGCAATCGTGAAGCCA GCGTATTGGGGTATGGGAATGGGTGTATGCTTGGTGAGAAACGCTGAGGAACTTAA GGGCGTTGCCGGCATTGCCTCAGGCGCCGATACCGCTCTTGTGTGTCAACCATACCT CGGCGAAGGAATTAATGACTTTCGGGTTTGGGTAGTTGGTGGAAAGCCACATACGG

>CysC protein sequence MIGQIPTERLLTHARTLAEAGGAPVPPAARQLADLAVTGPAEIYALTGAAARSAGSVLM SSGGTTGRPKLTYVPHGMGLTRLLEHWRPLRPGNVLLNLFNAGRMWGSHYYMQTLAE RSGCTVIPSGPYSPAEVAGWLPMLAEVGVDALAGTPTGLADFAQGVIDAGGTLPVRTVI WMAEPWTGNKRELVRQAFPEAGLWGNYGSVETWVMCTNQPGCDETTLHLLPDQVME PDEDGALLSRVGEGWTVPVVRYRLGDRVAPVECRCGRPDALRVLGRADDSVTLRSALF KVSELVDLVRGEPGVLEAQLRLTRSADSPKAASALTLEFTGTADAEAVRGRLIGGFYHL AAVARQYPDALRARRVERLTRIERTNKVPAMVWQQAETDGAGVA**LEHHHHHH**

>CysC DNA sequence ATGATCGGACAAATCCCCACCGAGAGATTACTCACTCATGCTCGCACCTTAGCCGAA GCGGGTGGGGCTCCCGTACCCCCGGCAGCACGACAACTCGCCGACCTTGCTGTTACT GGTCCTGCAGAGATCTACGCATTAACCGGTGCAGCTGCTCGTAGCGCTGGAAGCGTT TTAATGTCGTCCGGCGGAACTACGGGCCGTCCGAAGTTAACATACGTCCCGCATGGA ATGGGATTGACTCGGCTGTTGGAACACTGGCGTCCGCTCCGCCCTGGTAACGTACTT CTGAACTTATTCAATGCGGGTAGAATGTGGGGCTCTCACTACTATATGCAAACATTG GCCGAGCGTAGTGGTTGCACAGTTATACCGTCAGGTCCTTATTCACCTGCGGAAGTA GCCGGTTGGCTGCCTATGTTAGCCGAGGTTGGAGTGGACGCCTTGGCGGGCACGCCT ACGGGCTTGGCCGACTTCGCACAGGGTGTTATAGACGCAGGTGGCACTCTGCCAGTG CGAACAGTTATTTGGATGGCCGAGCCTTGGACAGGTAACAAGCGTGAGCTCGTGCG TCAGGCGTTCCCCGAGGCTGGTTTATGGGGTAACTACGGATCAGTAGAGACGTGGGT GATGTGCACTAACCAACCCGGATGCGACGAGACTACCCTGCACTTGTTACCGGACC AGGTTATGGAGCCCGACGAGGATGGGGCTTTGTTAAGTCGCGTTGGCGAGGGCTGG ACTGTTCCTGTGGTTCGGTACCGTCTGGGCGATCGAGTCGCGCCTGTAGAGTGTCGA TGTGGTCGCCCTGATGCGCTGCGTGTCTTAGGGCGCGCCGACGACTCAGTCACACTC AGATCCGCCTTGTTTAAGGTCTCTGAACTGGTGGATCTGGTAAGAGGGGAGCCAGG GGTCTTAGAGGCTCAATTGCGGCTTACACGTAGCGCCGACTCCCCGAAGGCTGCAA GTGCCTTGACCTTAGAGTTCACGGGGACAGCAGACGCAGAGGCGGTTCGGGGCCGC CTTATAGGCGGGTTCTATCACCTCGCCGCAGTTGCCCGTCAATATCCAGACGCACTT CGAGCCCGCAGAGTTGAGCGTCTGACACGCATTGAACGCACAAATAAGGTGCCGGC TATGGTATGGCAACAAGCAGAGACAGACGGCGCGGGCGTTGCC**CTCGAGCACCAC CACCACCACCAC**TGA

59

>BelH DNA sequence **ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGG CAGCCAT**ATGACGGCTCTTCATGCTGCTGTTCACGAAATCGCACGCCGTCGTCCAGA TGCGATAGCCGTTGAGACTACTGCGGGAGAGAGAACAACGTATGCTGAACTTTTAG CTCGCGCTGATAGAATTGCCGCGGGTTTGAGAGCACGCGGGGTTACAGAAGGACGA

>BelI protein sequence MAQTFEIKGNDLWDPTTFDALRRQLIPSFDLIYEAAVRTVAATVPTAPRVLDLGAGTGL LSAAILRELPDSEVVLVDRSELMLTQARGRFASQDGVTVQTGDLTDPLPEGGFDAVVSG LAIHHLSHTGKRDLFRRIREALRPGGVFVNVEQVQGPLPHLESLYDSQHELHVIREQAPA HEWAAGRERMKFDVCIDLETQLQWLRDAGFRSVDCLAKDFRFATYAGWVS**LEHHHH HH**

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>CysD protein sequence MTTAPAAPTRRLCWIYPDRGTDRMRDKEWKHVWGIYREVAREGGWALSLHKPEEVAV DVCGPGGPKVYLDGERVTPEDTVFVTSLWSLPHHTVDVCNQLYLYTILEQAGFYLPIPP HLSFIANDKAATMLHLADSPLPQVPTVRIGTGRDTAQRSYEAALASLSYPAIVKPAYWG MGMGVCLVRNAEELKGVAGIASGADTALVCQPYLGEGINDFRVWVVGGKPHTVLRRIP KGASLTANLSSGGGMEHVPLPPELAETVDYVAARMPMPYIAVDFLWDGERFWLSEVEP DGAVGFADSEQTEREQRKVIADRFAAYADAHRQFLNRKDAIR**LEHHHHHH**

bel pathway

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GTTGTCGTTTGCTCAGGGCTGGCCAACGATGCTAGTTACTTGGCTTTTCTCTTAGGGC TGTGTGCCAACGGGGCCGCTTATGTCCCACTTCTGGCAGACTTCGACGCTACCGCTG TCGACAGAGCATTACGGATGACTCGCCCTGTCTTGTGGGTCGGCCCAGATAATCATC ACCGAGCAGGGGTTACATTGCCTCGCGTTGAATTAGCCGATCTGGAAACTCCCGCGC CAGCAACGGCTCCTGCCGCTGGTGGTCGAGCACTCGCCCCCGGAACATTTCGTATGC TCTGGACGTCGGGGAGTACAAAAGCTCCCAAATTGGTGACGTGGCGCCAGGAGCCC TTCGTTCGGGAGCGTCGTAGATGGATCGCACATATAGAGGCGACTGAACGGGACGC ATTCTTCTGTAGACATACATTAGACGTCGCCCATGCTACTGATTTACACGCCTTTGCA GCCCTTCTTGCAGGAGCCCGGCTTATTTTGGCCGACCCAGCGGCAGACCCTGCCACG CTGTTGGCCCAATTGGCCGCGACAGGTGCTACTTATACAAGTATGCTTCCTAACCAT TACGAGGACTTAATTGCCGCCGCGAGACAGCGCCCTGGGACGGATTTGTCTCGCTTA CGGCGGCCAATGTGTGGTGGAGCGTATGCTAGTCCAGCTCTCATAGCAGACGCTGCT GATGTTTTAGGAATCCACATTCGCCATATATATGGGTCTACTGAATTTGGTCTGGCG CTCGGTAATATGGCGGATGAAGTGCAAACTGTCGGTGGTATGCACGAGGTTGCTGG GGTACGGGCACGTCTGGAGCCCCTTGCTGGCTACGACGGGGATGATTTAGGCCACCT GGTTTTAACGTCGGATTGCACGTCTGACGGTTACTTGGACGACGACGAAGCGAATGC CGCCACGTTCCGGGGCCCCGATTTCTGGACGGGAGACGTCGCAAGACGTCTTGATG ATGGTTCCCTTCGCCTGTTGGGACGGGTCACAGATCTGGTTCTTACAACGGATGGAC CCCTGGCTGCACCCCATGTAGACGAGCTCGTGGCGCGTCATTGTCCTGTCGCGGAAA GTGTAACACTGGCAGCCGATCCCGACACACTTGGCAATCGGGTGTTGGTTGTATTAC GCGCCGCTCCGGGGACTAGTGATGCCGATGCGGTCGGAGCTGTCGACAAGCTTTTAG ATGCACACGGGTTGACAGGAGTTGTACTGGCATTTGACCGAATCCCTCGCACCGTGG TTGGAAAGGCTGATCGTGCTTTGCTGCGTCGTCGGCATCTTCCTGCTCCTAGCAGCTC ATGA

>BelH protein sequence

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>BelR DNA sequence

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GCGGCCTTTGTTGACCGAGTCCCTTAAAACTAGCAGACTTGCCCTTCTCGCGCTGTG GTCAGGCGTGCTGACGCAGGACTGGCGAGAACGCATTGGGGCTTTAACATTGCCCA CTCTGTTGGTACACGGTGCGCGGAGTCGCATCTTTCCTACTGAGGTGGGCAAATGGC TCTTAGGCGCGCTGCCCGATGCCCGCTTGGAGATGTTTGCCCATTCAGGACACGCCC CTTTCTTAGAGGAGACGGACCGTTTCGTGCGGGTTCTGCGTGACTTCGTTGGTGGCA CCGCCCGCCCA**CTCGAGCACCACCACCACCACCAC**TGA

>BelR protein sequence

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>BelV DNA sequence

ATGGTAGGAAAGATCGATAGAGACATCTTATTAGCTCATGCCCGTACCATCGCGTCA AGCGGCGGTAAGGCCGTCCCGGAAGGTGCGACGGAGCTCAGTGACTTGGAAGTCTG TGGTGCAGCAGAGATCACGGCGATGACACGAGCTGCAGCGGAGCGTGATGGCGGGG TCCTGGTTTCATCAGGCGGAACTACGGGCACACCTAAACTTACATACTTACCTCACC ACATGGCTTTTGATCGCCTGCTTCCTGTTTGGCGACCCCTGGGTGTGGGCGACGTTGT CTTAAATTTGTACGACGCCGGTCGCATGTGGGGTACCCACTATTTTGTGCAGAAGCT TGCAGAGCGTACAGAGTCTACAGTTATTCCCAGCGGGCCAATGACCGCAGAGGAAT TAGAGTTACGTTTACCAATGCTGCGGGAAGTCGGAGTTACTGCTCTGGCCTCGGTAC CGTCAGTTTTAGCAGACTTCGCGGAGATGGTTCTTAAGACGGGTGTTAAGCCGCCTG TTAAGACGATTATCTGGATGGGCGAGGCATGGACCGAATCCAAGCGGGAACTCGTG AGACAAGCATTTCCAGACGTCCAATTATGGGGAATTTATGGCTCTGTTGAAACGTGG GCTATGGGCTCCAATCGCCCGGGTTGCGACGAAACTACATTACATCTCCTGGCAGAC GAAATTTTCGAGTTGGAAGATGCAGGAGCTCTGCTGACACGTGCGGGAGAGGGTTG GACCGTGCCGGTAGTTCGTTACCGATTGGGAGATCGAATCGAAGCGGCTAGATGCC GTTGCGGAAGAGGTGACGCGTTCAGAGTGCTGGGAAGAGCCGATGATGGGTTCGGG TTATTGGGGAACTACGTTAACATCGCTGATATAGTTGACTCTGCCCGCCAATGCCCA GATGTGGTGGATGCACAACTGGTCCTGGTGAGAGATACGGATCTCGCGGACTCGGC TAGAAGTATGACCGTGGAGTACACGGGTACCGCTGCCCCCGAGGCTGTTAGAACGT GGTTAACGGGAAGCAATGTGCGACTTGGGACGGTCGATTCACAGCATCCCGAGGCA ATCTCTGCACGGCGTGTAGACCGCCTGCGTAGAATCGCGCGTACAAACAAAACTCC CGGAGCAGTTTGGCAAGATGCATTAGGCTCTGGCAGT**CTCGAGCACCACCACCAC CACCAC**TGA

>BelV protein sequence

MVGKIDRDILLAHARTIASSGGKAVPEGATELSDLEVCGAAEITAMTRAAAERDGGVLV SSGGTTGTPKLTYLPHHMAFDRLLPVWRPLGVGDVVLNLYDAGRMWGTHYFVQKLAE RTESTVIPSGPMTAEELELRLPMLREVGVTALASVPSVLADFAEMVLKTGVKPPVKTIIW MGEAWTESKRELVRQAFPDVQLWGIYGSVETWAMGSNRPGCDETTLHLLADEIFELED AGALLTRAGEGWTVPVVRYRLGDRIEAARCRCGRGDAFRVLGRADDGFGLLGNYVNI ADIVDSARQCPDVVDAQLVLVRDTDLADSARSMTVEYTGTAAPEAVRTWLTGSNVRL GTVDSQHPEAISARRVDRLRRIARTNKTPGAVWQDALGSGS**LEHHHHHH**

>BelU DNA sequence

ATGAACACGAAGACGGTGGTTCTGGTTGGTGTCCCCTGGAGTGTTCACGAGTTAGAT GATGCAATACGAGATGCCGCAACTCTTGGTGCTTCCCTTCTGGTTGTAGACACGCCA GAATCGCTCGCCCAGATCGGAGAGCAAACAGCCGTACGGACCCGCACTGTAAAGGC CCTTGACCCCTTATTAATCGCGGACTGTGTGCGTGACGATGAGCCAGCCACGGTATT AGCTATTACGGAGTTCTCAATGGAGCTTGCAGCAGCCGTTCGAGAACTGCTCGGTAT TCCCGGAACCCCTAGTGCCGTTGAGGCTCGGGTCTTGGATAAAGCCCAGACACGCG AAGTCCTTCGAGAACATGGGCTTACACGGGTTGGCTTTCATCGCTCAAGTCTTCTGG CACCTGAAGACTTGTTAGGTGGGCTGGAGCCGCCCGTAGTAGTGAAACCTCGCTCTT TCTCAGGGTCTCACGGGGTGACTTTCGTCGCAGACCGATCCGAGTTAGAGAGAGTCT TTGAACCTTATGACCTCGCAGAAACAGACCTGGATGACCGTGATGGACGCGTCGCTC ATCTCGATGGTGACCACCGAACACACGAAGTCATCGTAGAGGAATACGTACCCGGA CCTGAAATTAGCGCTGAGGGTTTAGTTGTAGATGGACGCCTTACATTGTTTAGTTTA ACAGATAAGGTGAACACAGGGATGCCCCATTTCGAAGAGGTTGGTCATCTTGTCCCC AGTAAGTATACCCGAGAACGCTCCGCGCAGGTCGAAGAATATTTACAGGCCGTTGT GTCTGCGTTAGGCTTTGTTACATCACCTATGCATGCTGAAATAAAATTGCTCGATGA TCGTATCGAGTTGGTTGAAATTCATACGCGGTATCCTGGCGACAGAGTTGTGGAGCT GCTGCAAAGTGCATACGATATTCGTCCATACGAGGCATATTTTGACGCCATGTTGAA CGGACGGGTGCCCCAAAGACCCAGACCAACAGGGGAGCACTACGGCGTTGGTTTCT TTAATGGGCCCACAGATGCCCCCTTCGCATGGCCGTCTTATGCATTCCCACACCCTG AAGCCGTCGTGTCCATTGACGTAGATCGACGCCGTGCACCGAAGGTCTTCGCATACG AGGGTCTCCGGATTCGCTACTGGAGAGCTGGCCATGCATTATTTGCCCACGAAGACC ATGCCCGCGTCCAAGAAAATATCGCCTTCTTATTAGATAATACACCTGGGCAAGGCG GAAGTGGAAGC**CTCGAGCACCACCACCACCACCAC**TGA

>BelU protein sequence

MNTKTVVLVGVPWSVHELDDAIRDAATLGASLLVVDTPESLAQIGEQTAVRTRTVKAL DPLLIADCVRDDEPATVLAITEFSMELAAAVRELLGIPGTPSAVEARVLDKAQTREVLRE HGLTRVGFHRSSLLAPEDLLGGLEPPVVVKPRSFSGSHGVTFVADRSELERVFEPYDLAE TDLDDRDGRVAHLDGDHRTHEVIVEEYVPGPEISAEGLVVDGRLTLFSLTDKVNTGMPH FEEVGHLVPSKYTRERSAQVEEYLQAVVSALGFVTSPMHAEIKLLDDRIELVEIHTRYPG DRVVELLQSAYDIRPYEAYFDAMLNGRVPQRPRPTGEHYGVGFFNGPTDAPFAWPSYA FPHPEAVVSIDVDRRRAPKVFAYEGLRIRYWRAGHALFAHEDHARVQENIAFLLDNTPG QGGSGS**LEHHHHHH**

Naturally occurring Fused-CysFE

>*Bh*CysFE DNA sequence

ATGGACAAAACGCGCCAGTCTATAGCTTCATCTATTCCTATCTTCGACGCTATCTCCC AAATAGCACGTGAGAATGCAAACGGAGTTGCCATCGAGGCTTTAAGTGGAGAAACA TGTACTTTTGGATCTTTGATCGAGCGTGCAGAAATGCAAGCACGTGGTCTCCACGCT CTGGGAGTTGGGGCTGGACACTGCGTAGCAGTTTATTGTAAGACTAGCATCTCCTAT GCTAGTTTGATATTAGCGGTTTGCCGTTTGGGCGCTTCCTACGTACCTATTCTGAATA ACTTCGATTTAGAAGCACGGCGCCGGGCCTTCCAAATGGCGCAACCTGTATTGGTTG TCCACGACGGTGTCCGTTCCTATTCTTCTTTCGGACGCCCGGCCGTAGAGATTCGTGC CCTGATAGAGCCCACCAGCGACCGGGGCTCCCCACCACGTCCTGACGCGGAGCACG TATTTCGCAAGTTATGGAGCTCGGGTTCCACAGGCGGCAGCAAATTGATAGGTTGGA CTCAGGGTAAGTTGCTTAAAGAACGGCTGCGCTGGCAAAACCACGTCGGCCTTCGTG GGTCTGACCGTTACTTCTGCAAGCACACACTGGATGTGGCGCACGCAACCGACTTGC ACCTGTTTAGCGCGCTGCTCTCAGGCGCCACATGTATTCTGGACGACGTCCACGCTG GAGACGCAGCATTATGGGAAACTATCGCAGACTGGCGTCCGACGGTGATGTCTGCG CTCCCAGAGCATTACCGTGACTGGTTACGGCATTACAGAGCGAATGGTACCCGACTG CCGGGCACTCTCCGTCTTGCAATGTGTGGTGGTACATACGTCTCACCAGAAACGGCG GCAGATGTGGCCGATGGTCTGGGCTTTCGGCTGAGACAAATCTACGGGTCGACCGA GTTTGGACTCGCAATGATTAGTGAGGAGAGCGCGGGAGACTTAGTGCTTGTTAACG GAGTCGGCGCTCGTCTTGAGCCGCTCCCCCAGGGTACGGCTGGTAATCTGGGCCATC TCATCCTCATCTCAGACTGTACATCCGAAGGGTATCTGGGAGACGCGGACGAGCAC GCAGCCGCTTTTCGCGGTGAAGAGTATGGCACTGGAGACGTAGCAGAGATGGTTTCT CCCAAGACTTATCGAATAGTTGGACGTACTAAGGAATTGCTTAATGTAGGTGGGCGC ATCACCACAACAAGTATGGTTGACCGCAGAATACAAGCGGAACTTCGTCTTCAAAA CTTCGCCACTGTTGTGGATCCCCGTTCGAGCGAATCAGTAACCGTCTTTGTTGATCAA CCGCCGGGCACTCCTGTTGAGGAAGAGCGCCTTCAACGAAGAATTACGGCGGCCAC CGAGCCATTAGGCTTAAAACCAAGTATCGTGTTCTTGCATCCCTTCCCCTACACTGA GGTTGGAAAGCCGGATAAAGCAGTATTGCGACAGAAACTGGCGACTCCTGTGAATA TGCGACTTAATTGCCGTGAGCTTGGACGAGGGTTCCCGCTGGTGATTCTGCCAGGTC TGTGCCTGACTGACGCGATATTTGAGCCGCTTATTGACTTAATACAGGATGAGTACC GCTTGTTACTTATCGACCTTCCAGGGCATGGTCAGAACCAGAGTCTGCCGCCGGAAG TTACTGCACGTCCAGGCATCATTGACCGTTTCTGTGAGGGCATCTACTCCTTGTTAGC GGAACGCGGGATCGAGAAATTTGCCGTAATGGGTGTTTCATTAGGAGCGACAGTAG CGTATGCGTTAGCCACCGGAAGACATGCAAATCAAATTAGCGCGCTGGTCTCTATCG AACAGACACCGTTCCTGTTAGCGGACGATGGTTGGGGTCACGCCGCGTTCGGCACTT TGACGCGTGAAGGGGCGCAGCAGATTTTGGCCGGATTAGCAACTGATTCCGGAGAA TTCTCCCGGCAAATCATAGCGGCTAGTCTGTTAGAGGCTACCCGTATAGACAAAGCA CTCAAGGGGCGCATAGTTAGAAGCTCTGCCGCATGCGATCCTAGAGCTATGGCCGC GCTGCTGGCAGATGCGCTCTCGCAGGACTGGCGTCCGGGCCTTCAAGGGGCAACTC GGAATGTTATGCTTGTGCACGGTTCCCAATCTGCGGTGTACCCGACCAACGTCGGGT CCTGGCTTAACGAGAACTGGGATGTGAAAGCACTTCTGCAGCTTAAGACGGGTGGT CACCTTCCCTTCATCGATGAACCTGTTATGTTCAGTAACACCGTTAAGGCCTTTCTGA AGTCTACATGTGGAGACCAGAATGACGAGCAT**CTCGAGCACCACCACCACCACCA C**TGA

>*Bh*CysFE protein sequence

MDKTRQSIASSIPIFDAISQIARENANGVAIEALSGETCTFGSLIERAEMQARGLHALGVG AGHCVAVYCKTSISYASLILAVCRLGASYVPILNNFDLEARRRAFQMAQPVLVVHDGVR SYSSFGRPAVEIRALIEPTSDRGSPPRPDAEHVFRKLWSSGSTGGSKLIGWTQGKLLKERL RWQNHVGLRGSDRYFCKHTLDVAHATDLHLFSALLSGATCILDDVHAGDAALWETIAD WRPTVMSALPEHYRDWLRHYRANGTRLPGTLRLAMCGGTYVSPETAADVADGLGFRL RQIYGSTEFGLAMISEESAGDLVLVNGVGARLEPLPQGTAGNLGHLILISDCTSEGYLGD ADEHAAAFRGEEYGTGDVAEMVSPKTYRIVGRTKELLNVGGRITTTSMVDRRIQAELRL QNFATVVDPRSSESVTVFVDQPPGTPVEEERLQRRITAATEPLGLKPSIVFLHPFPYTEVG KPDKAVLRQKLATPVNMRLNCRELGRGFPLVILPGLCLTDAIFEPLIDLIQDEYRLLLIDL PGHGQNQSLPPEVTARPGIIDRFCEGIYSLLAERGIEKFAVMGVSLGATVAYALATGRHA NQISALVSIEQTPFLLADDGWGHAAFGTLTREGAQQILAGLATDSGEFSRQIIAASLLEAT RIDKALKGRIVRSSAACDPRAMAALLADALSQDWRPGLQGATRNVMLVHGSQSAVYP TNVGSWLNENWDVKALLQLKTGGHLPFIDEPVMFSNTVKAFLKSTCGDQNDEH**LEHH HHHH**

7. NMR spectra of compounds synthesised enzymatically

F19-NMR

8. NMR spectra of chemically synthesised standards

9. LC-MS/MS data for assays described in supplementary figure 18-20.

Observed mass (m/z) of precursor ion $[M+H]^+$ is indicated in blue.

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10. Supplementary references

- S1. Blake, L. I. & Cann, M. J. Carbon Dioxide and the Carbamate Post-Translational Modification. *Front. Mol. Biosci.* **9**, 825706 (2022).
- S2. Zallot, R., Oberg, N. & Gerlt, J. A. The EFI Web Resource for Genomic Enzymology Tools: Leveraging Protein, Genome, and Metagenome Databases to Discover Novel Enzymes and Metabolic Pathways. *Biochemistry* **58**, 4169–4182 (2019).
- S3. An, J., Totrov, M. & Abagyan, R. Pocketome via Comprehensive Identification and Classification of Ligand Binding Envelopes. *Molecular & Cellular Proteomics*, **4**, 752- 761 (2005).
- S4. Wen, X., Leisinger, F., Leopold, V. & Seebeck, F. P. Synthetic Reagents for Enzyme-Catalyzed Methylation. *Angew. Chem. Int. Ed.* **61**, e202208746 (2022).
- S5. Armstrong, A. & Scutt, J. N. Total synthesis of (+)-belactosin A. *Chem. Commun.* **4**, 510–511 (2004).
- S6. Roeder, M., Spiegelstein, O., Schurig, V., Bialer, M. & Yagen, B. Absolute configuration of the four stereoisomers of valnoctamide (2- ethyl-3-methyl valeramide), a potentially new stereospecific antiepileptic and CNS drug. *Tetrahedron Asymmetry* **10**, 841–853 (1999).
- S7. Jiang, B., Shi, H. ping, Xu, M., Wang, W. jun & Zhou, W. shan. Stereoselective synthesis of Certonardolsterol D3. *Tetrahedron* **64**, 9738–9744 (2008).
- S8. Kawamura, S., Unno, Y., Asai, A., Arisawa, M. & Shuto, S. Design and synthesis of the stabilized analogs of belactosin A with the unnatural cis-cyclopropane structure. *Org. Biomol. Chem.* **11**, 6615–6622 (2013).
- S9. Kumaraswamy, G. *et al.* Oppolzer sultam directed aldol as a key step for the stereoselective syntheses of antitumor antibiotic belactosin C and its synthetic congeners. *J. Org. Chem.* **71**, 337–340 (2006).
- S10. Pirrung, M. C., Han, H. & Nunn, D. S. Kinetic Mechanism and Reaction Pathway of Thermus thermophilus Isopropylmalate Dehydrogenase. *J. Org. Chem.* **59**, 2423–2429 (1994).
- S11. Kawamura, S. *et al.* Investigation of the noncovalent binding mode of covalent proteasome inhibitors around the transition state by combined use of cyclopropylic strainbased conformational restriction and computational modeling. *J. Med. Chem.* **56**, 5829– 5842 (2013).
- S12. Martin, N. I., Beeson, W. T., Woodward, J. J. & Marletta, M. A. NG-aminoguanidines from primary amines and the preparation of nitric oxide synthase inhibitors. *J. Med. Chem.* **51**, 924–931 (2008).
- S13. Larionov, O. V. & De Meijere, A. Enantioselective total syntheses of belactosin A, belactosin C, and its homoanalogue. *Org. Lett.* **6**, 2153–2156 (2004).