

Identification of a fluorometabolite from *Streptomyces* sp. MA37: (2*R*,3*S*,4*S*)-5-Fluoro-2,3,4-trihydroxypentanoic acid

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1. Sequence alignment

Sequence alignment of FdrC (termed Frib/1 in the annotation) and SalM (a short-chain dehydrogenase/reductase enzyme from the marine actinomycete *Salinispora tropica*) was performed using JalView software. This alignment of FdrC showed a 69% similarity to SalM.

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      10      20      30      40      50
SalM/1-255 1 MTNG - - - - GRLSGK VSLI TGAAHG IGHATAVWFAREGARLVVSDVDGAAL EKC 49
FribC/1-261 1 VSPAPELRP GRLSGK SAVVTGAARG IGRATALRFAREGALLTLTDVDGKALGEL 54

      60      70      80      90     100
SalM/1-255 50 HAELAESGA EVTTV IADVSDATQAHRMVQTAVDVYNRLDVVANAGV I PLHEIT 103
FribC/1-261 55 AAELTAQGT EPATV AGDVSPADAERM IAAVEAYDRLDVLVANAGI LPLIRIT 108

     110     120     130     140     150     160
SalM/1-255 104 EA TEQDWDE VMAVDG KGMFLTCKYGI DAMLAT - GGSIVCLSSI SGVAGQRGQST 156
FribC/1-261 109 DASADDWDH VMAVDGR GMFLTCKFA IERMAAAGGGAIVCLSSI SGLAGQAGQST 162

     170     180     190     200     210
SalM/1-255 157 YGPAKFVASGLTKHLAVECARHCI RVNAVAPGT IRTNRVRRLE EEPGGPEYLED 210
FribC/1-261 163 YGPAKFVATGLTKHLAVEWADRGI RVNAVAPGT IRTDRVRRLP DEPGGAAYLAE 216

     220     230     240     250
SalM/1-255 211 I VRLHPAGRLGEPSEVAAAIGFLASDEASFITGVVLPVDGGYLAQ 255
FribC/1-261 217 IERRHPMGRIGEPDEVAAAIVFLASDEASFVTGAVLPVDGGYLAQ 261
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Figure S1. Primary sequence alignment of FdrC (termed FribC/1 in the annotation) with SalM (a short-chain dehydrogenase/reductase enzyme from the marine actinomycete *Salinispora tropica*).

2. MALDI-TOP MS analysis of purified FdrC protein

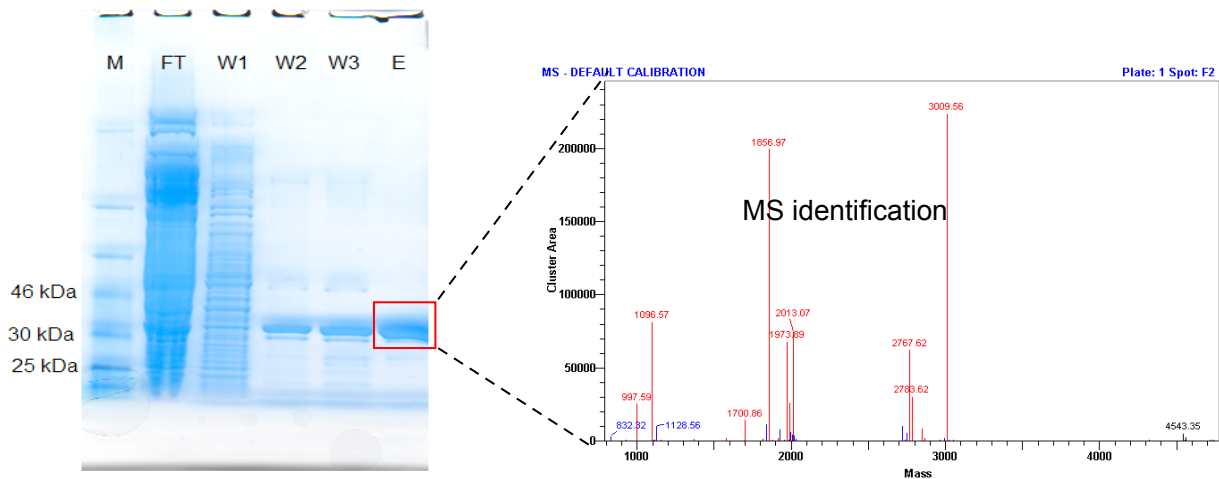


Figure S2. SDS-PAGE of overexpressed FdrC (left), and the ESI-MS identification of purified FdrC (right) (M = molecular marks; FT = flow through; W = wash fraction; E = elution fraction). The gel band was excised and cut into 1mm cubes. These were then subjected to in-gel digestion, using a ProGest Investigator in-gel digestion robot (Genomic Solutions, Ann Arbor, MI) using standard protocols¹. Briefly the gel cubes were destained by washing with acetonitrile and subjected to reduction and alkylation before digestion with trypsin at 37 °C. The peptides were extracted with 10 % formic acid. The digest solution (0.5 mL) was applied to the MALDI target along with alpha-cyano-4-hydroxycinnamic acid matrix (0.5 mL, 10 mg/mL in 50:50 acetonitrile: 0.1 % TFA) and allowed to dry.

MALDI MS was acquired using a 4800 MALDI TOF/TOF Analyser (ABSciex, Foster City, CA) equipped with a Nd:YAG 355 nm laser and calibrated using a mixture of peptides. The spot was initially analysed in positive MS mode between 800 and 4000 m/z, by averaging 1000 laser spots. The most intense peptides (up to 15) were selected for MSMS analysis and acquired to a maximum of 3000 laser shots or until the accumulated spectrum reached an S/N ratio of 35. All MS/MS data were acquired using 1 keV collision energy.

The MS data were analysed, using GPS Explorer (ABSciex) to interface with the Mascot 2.1 search engine (Matrix Science, London, UK), against the Swiss-Prot and internal databases. No species restriction was applied. The data was searched with tolerances of 100 ppm for the precursor ions, trypsin as the cleavage enzyme, assuming up to one missed cleavage, carbamidomethyl modification of cysteines as a fixed modification and methionine oxidation selected as a variable modification. The MSMS data was also analysed using the Mascot search engine using similar criteria.

3. GC-MS analysis for the identification of 5-fluoro-2,3,4-trihydroxypentanoic acid (5-FHPA 10) from the supernatant of the *Streptomyces* sp. MA 37 fermentation.

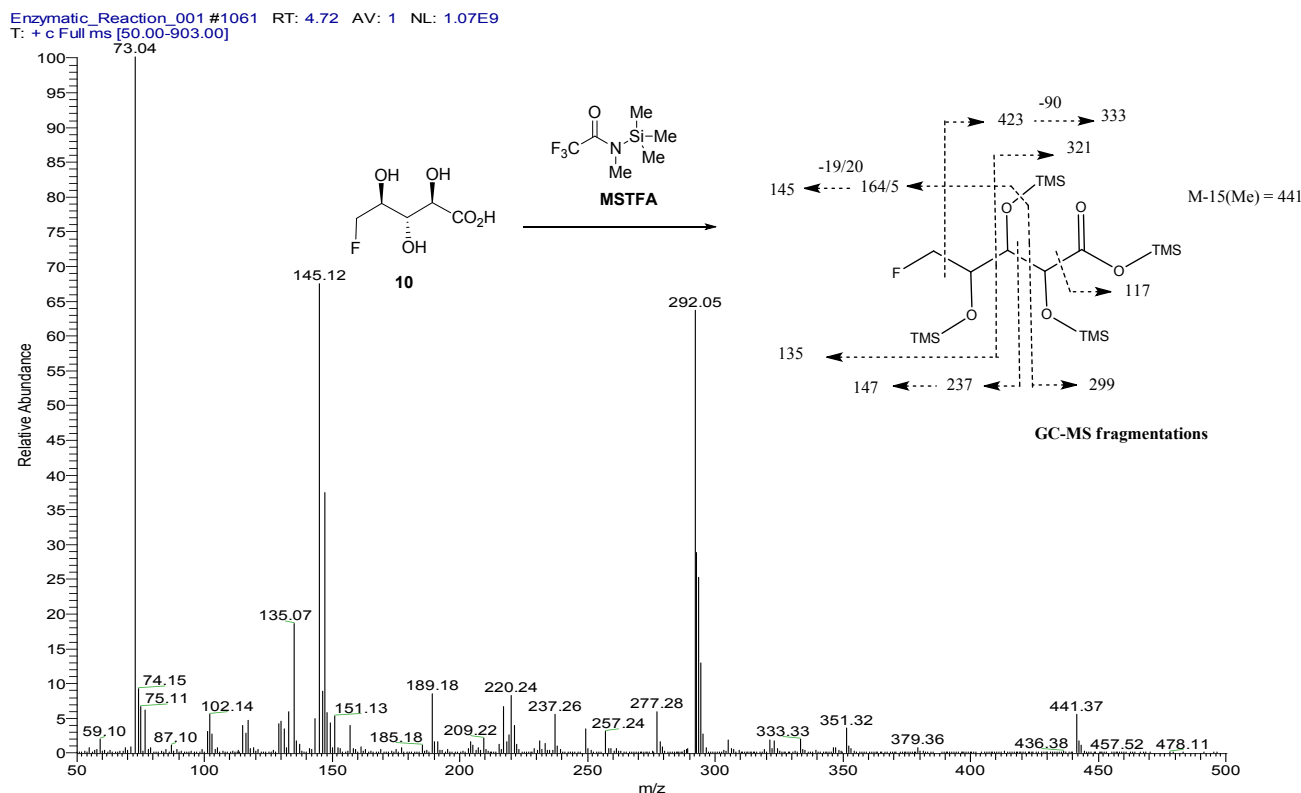


Figure S3. GC-MS fragmentation analysis of MSTFA treated extract shows the mass spectrum and fragmentation pattern of 5-fluoro-2,3,4-trihydroxypentanoic acid (TMS)₄.

Freeze dried samples of enzymatic reaction product (5.6 mg), and bacterial culture product (29.8 mg) were transferred to a glass culture tube fitted with a screw cap and PTFE seal. To this 100 μ L *N*-methyl-*N*-trimethylsilyltrifluoroacetamide (MSTFA, ThermoFisher, UK) and 100 μ L of anhydrous pyridine (Sigma-Aldrich, UK) was added. The tube was heated on a hot block at 80 $^{\circ}$ C for 1 h. The derivatised sample solution was filtered through tissue paper held in the constriction of a Pasteur pipette, which had been pre-washed with dichloromethane, directly into an autosampler vial for analysis by GC-MS. Samples were analysed using a Trace DSQII GC-MS system (Thermo Scientific, Hemel Hempstead, UK) fitted with a CombiPalautosampler (CTC Analytics, Switzerland). Samples (1 μ L) were injected into a programmable temperature vaporising (PTV) injector fitted with a Merlin MicrosealTM high pressure septum (Agilent Technologies, UK) and operating at a split of 40:1. The PTV conditions were injection temperature 132 $^{\circ}$ C for 1 min, transfer rate 14.5 $^{\circ}$ C s⁻¹, transfer temperature 320 $^{\circ}$ C for 1 min, clean rate 14.5 $^{\circ}$ C s⁻¹ and clean temperature 400 $^{\circ}$ C for 2 min. Chromatography was effected on a DB5-MSTM column (15 m \times 0.25 mm \times 0.25 μ m; Agilent Technologies, UK) using helium at 1.5 mL/min (constant flow). The GC temperatures were 100 $^{\circ}$ C for 2.1 min, 25 $^{\circ}$ C min⁻¹ to 320 $^{\circ}$ C then isothermal for 3.5 min. The GC-MS interface temperature was 250 $^{\circ}$ C. MS acquisition conditions were electron impact (EI) ionisation at 70 eV, solvent delay 1.25 min, source temperature 200 $^{\circ}$ C, mass range 50-900

a.m.u. at 6 scans s^{-1} . Data were acquired using the XcaliburTM software package V. 2.07 (Thermo Scientific, Hemel Hempstead, UK).

4. Kinetics profiles for FdrC

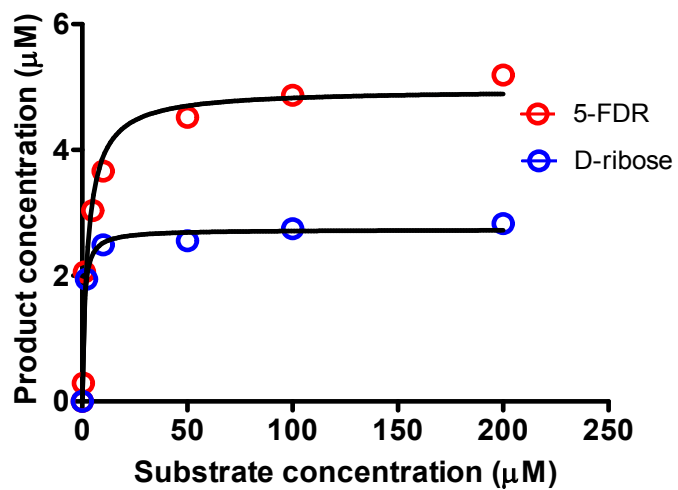


Figure S4. Michaelis-Menten curve of FdrC for 5-fluorodeoxyribose (5-FDR) and D-ribose.

5. Fermentation condition of screening fluorometabolites in *Streptomyces sp* MA37

For metabolite analysis, spores of *Streptomyces sp* MA37 were inoculated into ISP2 liquid medium (1% malt extract, 0.4% yeast extract, 0.4% D-glucose, pH 7.0, 50 mL) in an Erlenmeyer flask (250 mL) and cultivated in a rotary incubator (180 rpm, Barnstead Lab-line MaxQ 5000) at 28 °C. After 7-day cultivation, the seed culture was then transformed to a production culture in 6 different cultivation media supplemented with 2.5 mM KF. The fermentation media include International *Streptomyces* Protocol (ISP) 2-6² and a defined medium previously reported³ for the fluorometabolite production in *Streptomyces cattleya*. After a 12-day cultivation, the supernatants were then subjected to ¹⁹F {¹H} NMR analysis (Bruker Avance 500 MHz in D₂O).

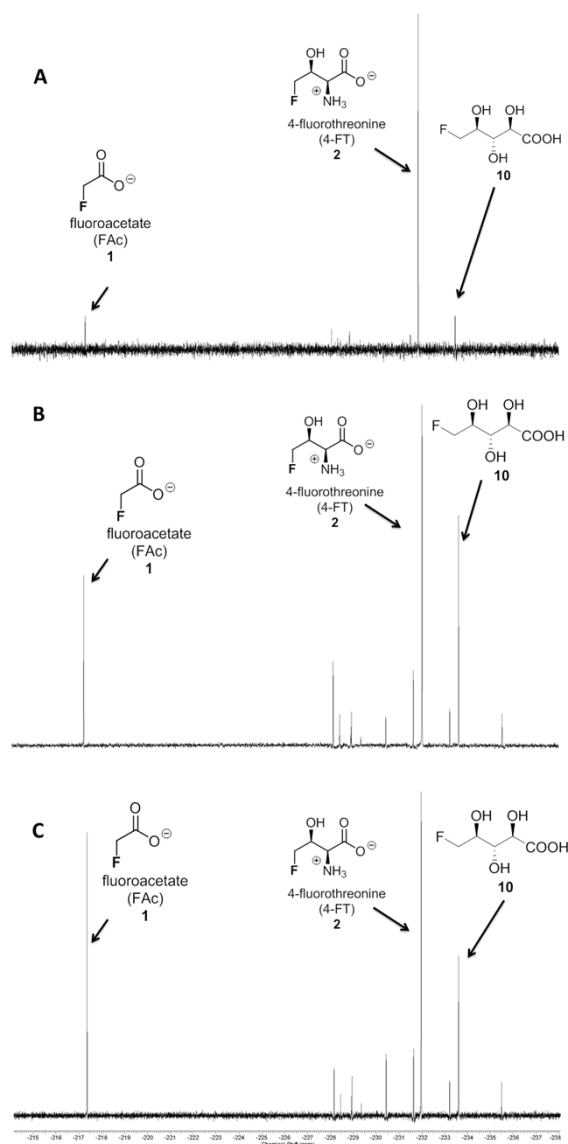


Figure S5 ¹⁹F NMR time course analysis of the supernatants of MA37 ISP2 medium supplemented with 2.5 mM KF, indicating that FAC 1, 4-FT 2 and 5-FHPA 10 are stable fluorometabolites over the cultivation period of up to 19 days. (A) 8-day culture; (B) 12 day culture; (C) 19-day culture.

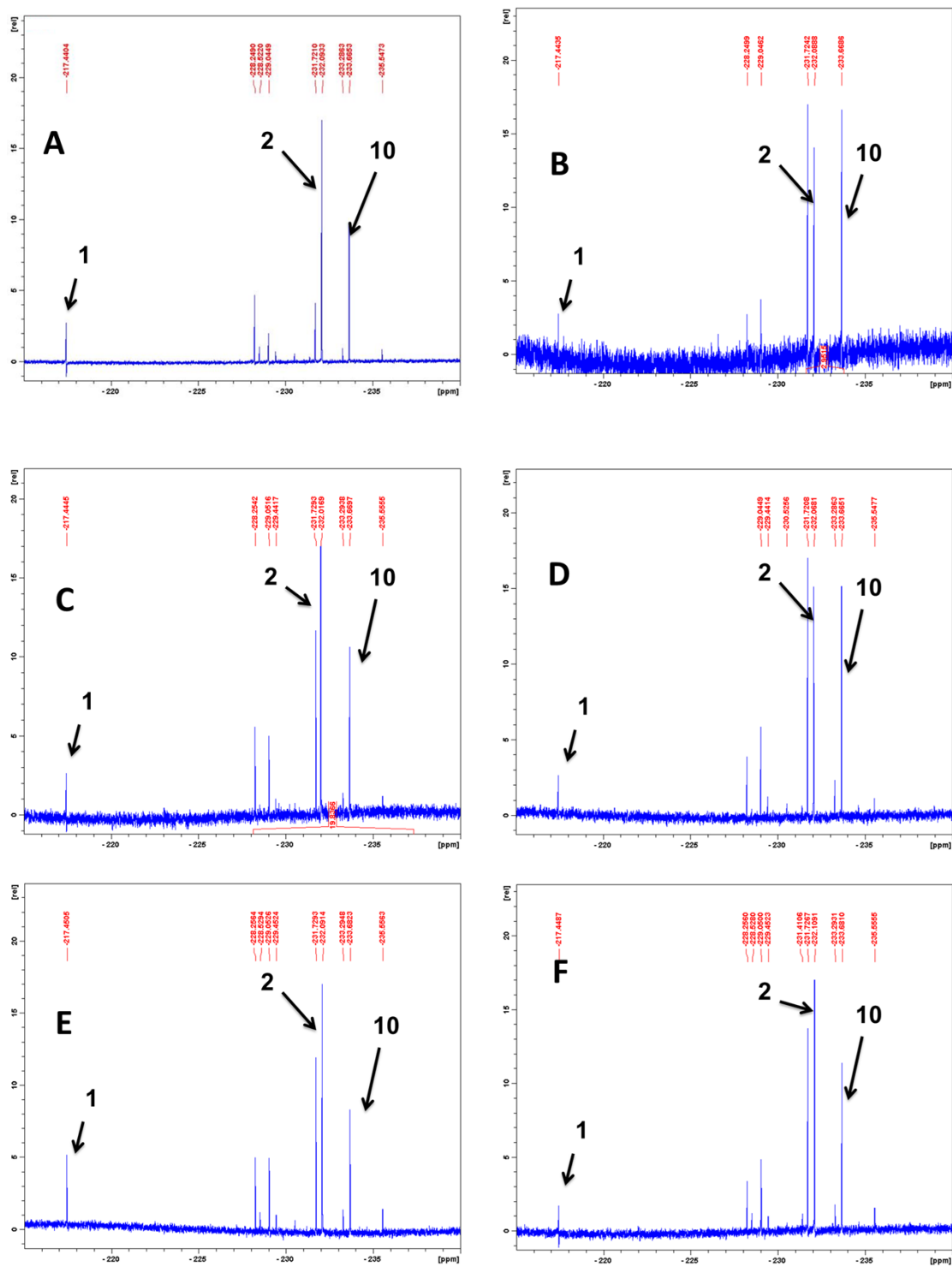


Figure S6 ^{19}F NMR analysis of the supernatants of MA37 culture, indicating that FAc **1**, 4-FT **2** and 5-FHPA **10** are stable fluorometabolites in six cultivation media: (A) ISP 2 media; (B) ISP 3 media; (C) ISP4 media; (D) ISP5 media; (E) ISP6 media; (F) a defined medium previously reported for the fluorometabolite production in *Streptomyces cattleya*.³

6. Synthesis of (2*R*,3*S*,4*S*)-5-fluoro-2,3,4-trihydroxypentanoic acid **10**

2,3-*O*-Isopropylidene-D-ribose **12**

A suspension of D-ribose **11** (3.0 g, 20.0 mmol, 1 eq.) in acetone (30 mL) was cooled to 0 °C before 2,2-dimethoxypropane (2.5 mL, 20.6 mmol, 1.03 eq.) and 4-toluene sulfonic acid (0.19 g, 1.0 mmol, 0.05 eq.) were added. After stirring at room temperature for 1 h, the clear mixture was neutralised with saturated aqueous sodium bicarbonate solution and filtered through pad of a celite. The filtrate was concentrated and the residue was dissolved in EtOAc (60 mL), and then washed with water (15 mL). The aqueous layer was extracted with EtOAc (2 × 30 mL). The combined organic layer was dried (MgSO₄), filtered and the filtrate was concentrated. The crude mixture was purified by column chromatography (EtOAc) to afford 2,3-*O*-isopropylidene-D-ribose **12** (0.91 g, 24 %) as a colorless oil: $R_f = 0.38$ (EtOAc); $[\alpha]_D^{20} : -29.8^\circ$ (c 0.5, CHCl₃); **¹H NMR** (CDCl₃, 300 MHz) δ_H 5.31 (1H, s, H-1), 4.73 (1H, d, $J = 5.9$ Hz, H-2), 4.47 (1H, d, $J = 5.9$ Hz, H-3), 4.30 (1H, t, $J = 3.1$ Hz, H-4), 3.68-3.55 (2H, m, CH₂), 1.38 (3H, s, CH₃), 1.21 (3H, s, CH₃); **¹³C NMR** (CDCl₃, 100 MHz) δ_C 112.22 (C(CH₃)₂), 103.12 (CH, C-1), 87.95 (CH, C-4), 87.03 (CH, C-3), 81.84 (CH, C-2), 63.79 (CH₂, C-5), 26.50 (CH₃), 24.85 (CH₃); **IR** ν_{max} (neat): 3419, 2987, 2942, 1458, 1377, 1212, 1067, 870; **HRMS** m/z (ES⁺) (calculated C₈H₁₄NaO₅⁺ = 213.0733) found 213.0728 [M+Na]⁺.

2,3-*O*-Isopropylidene-D-ribo-1,4-lactone **13**

An aliquot K₂CO₃ (1.99 g, 14.4 mmol, 3 eq.) and iodine (3.65 g, 14.4 mmol, 3 eq.) were added to a solution of 2,3-*O*-isopropylidene-D-ribose **12** (0.91 g, 4.8 mmol, 1 eq.) in CH₂Cl₂ (15 mL). The reaction mixture was stirred at room temperature for 4 h then quenched by addition of a saturated aqueous solution of Na₂SO₃ (10 mL) and the reaction was vigorously stirred for a further 30 min. The organic phase was collected and the aqueous phase extracted into EtOAc (3 × 20 mL). The combined organic extracts were dried (MgSO₄) and evaporated. The product was then purified by chromatography (EtOAc) to afford 2,3-*O*-isopropylidene-D-ribo-1,4-lactone **13** (0.88 g, 97 %) as a white solid: $R_f = 0.38$ (EtOAc); $[\alpha]_D^{20} : -62.8^\circ$ (c 0.25, CHCl₃); **m.p.** 129-133 °C; **¹H NMR** (CDCl₃, 300 MHz) δ_H 4.84 (1H, d, $J = 5.6$ Hz, H-2), 4.78 (1H, d, $J = 5.6$ Hz, H-3), 4.63 (1H, br s, H-4), 4.00 (1H, d, $J = 11.9$ Hz, H-5), 3.82 (1H, d, $J = 11.9$ Hz, H-5), 1.48 (3H, s, CH₃), 1.39 (3H, s, CH₃); **¹³C NMR** (CDCl₃, 100 MHz) δ_C 175.46 (C=O), 113.34 (C(CH₃)₂), 82.55 (CH, C-4), 78.36 (CH, C-3), 75.75 (CH, C-2), 62.24 (CH₂, C-5), 26.87 (CH₃), 25.63 (CH₃); **IR** ν_{max} (neat): 3460, 1763, 1377, 1221, 1196, 1153, 968, 854, 808, 773; **HRMS** m/z (ES⁺) (calculated C₈H₁₂NaO₅⁺ = 211.0577) found 211.0572 [M+Na]⁺.

5-Deoxy-5-fluoro-2,3-*O*-isopropylidene-D-ribo-1,4-lactone **14**

Deoxo-fluor® (50% in THF, 0.62 mL, 1.67 mmol, 3.04 eq.) was slowly added to a stirred solution of 2,3-*O*-isopropylidene-D-ribo-1,4-lactone **13** (0.104 g, 0.55 mmol, 1 eq.) in CH₂Cl₂ (1.5 mL) at room temperature. After stirring at 40 °C for 30 min, ice water was carefully added to quench the excess of Deoxo-fluor®. The aqueous phase was extracted into EtOAc (3 × 5 mL) and the organic phases combined and dried (MgSO₄). The product was then purified by column chromatography (Petrol/EtOAc 3:1) to afford 5-deoxy-5-fluoro-2,3-*O*-isopropylidene-D-ribo-1,4-lactone **14** (55 mg, 52 %) as pale white solid: R_f = 0.55 (EtOAc/PE 1:1); $[\alpha]_D^{20}$: -74.4° (*c* 0.25, CHCl₃); **m.p.** 65-68 °C; **¹H NMR** (CDCl₃, 300 MHz) δ_H 4.82 (1H, d, *J* = 5.4 Hz, H-2), 4.79 (1H, dd, *J* = 5.6 Hz, 3.3 Hz, H-3), 4.75-4.59 (3H, m, H-4 & CH₂), 1.41 (3H, s, CH₃), 1.41 (3H, s, CH₃); **¹³C NMR** (CDCl₃, 100 MHz) δ_C 169.90 (C=O), 115.40 (C(CH₃)₂), 82.58 (CH₂, d, *J* = 172.0 Hz, C-5), 80.42 (CH, d, *J* = 18.2 Hz, C-4), 77.37 (CH, d, *J* = 4.9 Hz, C-3), 75.28 (CH, d, *J* = 3.8 Hz, C-2), 26.90 (CH₃), 25.75 (CH₃); **¹⁹F NMR** (CDCl₃, 376 MHz) δ_F -235.50 (1F, dddd, *J* = 48.5 Hz, 45.3 Hz, 34.4 Hz, 3.3 Hz); **IR** ν_{max} (neat): 3545, 2995, 1788, 1383, 1269, 1055, 847; **HRMS** *m/z* (ES⁺) (calculated C₈H₁₁FNao₄⁺ = 213.0534) found 213.0526 [M+Na]⁺.

5-Deoxy-5-fluoro-D-ribo-1,4-lactone **9**

A solution of 5-deoxy-5-fluoro-2,3-*O*-isopropylidene-D-ribo-1,4-lactone **14** (120 mg, 0.63 mmol, 1 eq.) in a mixture of TFA/water (5 mL, 9:1) was stirred at room temperature for 5 h. The reaction mixture was co-evaporated five times with Et₂O (5 mL), affording 5-deoxy-5-fluoro-D-ribo-1,4-lactone **9** (90.5 mg, 96 %) as white amorphous solid: $[\alpha]_D^{20}$: +7.6° (*c* 0.25, H₂O); **m.p.** 81-85 °C; **¹H NMR** (CDCl₃, 300 MHz) δ_H 4.63-4.60 (1H, m), 4.58-4.48 (3H, m), 4.38 (1H, d, *J* = 5.5 Hz, H-2); **¹³C NMR** (CDCl₃, 100 MHz) δ_C 177.96 (C=O), 84.20 (CH, d, *J* = 17.8 Hz, C-4), 82.20 (CH₂, d, *J* = 168.5 Hz, C-5), 68.89 (CH, d, *J* = 2.1 Hz, C-2), 68.64 (CH, d, *J* = 5.1 Hz, C-3); **¹⁹F NMR** (CDCl₃, 376 MHz) δ_F -231.64 (1F, td, *J* = 46.7 Hz, 33.2 Hz); **IR** ν_{max} (neat): 3429, 3280, 1751, 1190, 1140, 966, 895, 781; **HRMS** *m/z* (ES⁺) (calculated C₅H₇FO₄ = 150.0328) found 173.0219 [M+Na]⁺.

(2*R*,3*S*,4*S*)-5-Fluoro-2,3,4-trihydroxypentanoic acid **10**

LiOH (27.8 mg, 0.66 mmol, 1.1 eq.) was added to a solution of 5-deoxy-5-fluoro-D-ribo-1,4-lactone **9** (90.5 mg, 0.6 mmol, 1 eq.) in water (3 mL). The resultant mixture was stirred at room temperature for 72 h. The pH was adjusted to pH=7 by careful addition of dil HCl. The reaction mixture was evaporated, affording (2*R*,3*S*,4*S*)-5-fluoro-2,3,4-trihydroxypentanoic acid **10** as white solid in quantitative yield: $[\alpha]_D^{20}$: -4.0° (*c* 0.25, H₂O); **m.p.** 165-168 °C; **¹H NMR** (CDCl₃, 300 MHz) δ_H 4.61-4.41 (2H, m, CH₂), 4.04 (1H, d, *J* = 3.1 Hz, H-2), 3.94-3.82 (2H, m, H-3 & H-4); **¹³C NMR** (CDCl₃, 100 MHz) δ_C 177.93 (C=O), 84.97 (CH₂, d, *J* = 164.6 Hz, C-5), 73.36 (CH, C-2), 72.15 (CH, d, *J* = 7.3 Hz, C-3), 69.80 (CH, d, *J* = 17.8 Hz, C-4); **¹⁹F NMR** (CDCl₃, 376 MHz) δ_F -233.46 (1F, td, *J* = 47.4 Hz, 24.5 Hz); **IR** ν_{max} (neat): 3209, 1604, 1408, 1336, 1096, 1036, 949, 910, 810; **HRMS** *m/z* (ES⁻) (calculated C₅H₇FO₅ = 168.0434) found 167.0358 [M-H]⁻.

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