

Molecular profiling of *Mycobacterium tuberculosis* identifies tuberculosis-specific nucleoside products of the virulence-associated enzyme Rv3378c

Emilie Layre^{a,1}, Ho Jun Lee^{b,1}, David C. Young^a, Amanda Jezek Martinot^c, Jeffrey Buter^d, Adriaan J. Minnaard^d, John W. Annand^a, Sarah M. Fortune^e, Barry B. Snider^f, Isamu Matsunaga^{g,2}, Eric J. Rubin^c, Tom Alber^{b,3}, and D. Branch Moody^{a,3,4}

^aDivision of Rheumatology, Immunology and Allergy, Brigham and Women's Hospital, Harvard Medical School, Boston, MA 02115; ^bDepartment of Molecular and Cell Biology and California Institute for Quantitative Biosciences, University of California, Berkeley, CA 94720; ^cDepartment of Immunology and Infectious Diseases, Harvard School of Public Health, Boston, MA 02115; ^dStratingh Institute for Chemistry, University of Groningen, 9747 AG, Groningen, The Netherlands; ^eDepartment of Immunology and Infectious Diseases, Harvard School of Public Health, Boston, MA 02115; ^fDepartment of Chemistry MS 015, Brandeis University, Waltham, MA 02453-2728; and ^gLaboratory of Cell Regulation, Department of Viral Oncology, Institute for Virus Research, Kyoto University, Sakyo-ku, Kyoto 606-8507, Japan

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To identify lipids with roles in tuberculosis disease, we systematically compared the lipid content of virulent *Mycobacterium tuberculosis* with the attenuated vaccine strain *Mycobacterium bovis* bacillus Calmette–Guérin. Comparative lipidomics analysis identified more than 1,000 molecular differences, including a previously unknown, *Mycobacterium tuberculosis*-specific lipid that is composed of a diterpene unit linked to adenosine. We established the complete structure of the natural product as 1-tuberculosinyladenosine (1-TbAd) using mass spectrometry and NMR spectroscopy. A screen for 1-TbAd mutants, complementation studies, and gene transfer identified Rv3378c as necessary for 1-TbAd biosynthesis. Whereas Rv3378c was previously thought to function as a phosphatase, these studies establish its role as a tuberculosinyl transferase and suggest a revised biosynthetic pathway for the sequential action of Rv3377c–Rv3378c. In agreement with this model, recombinant Rv3378c protein produced 1-TbAd, and its crystal structure revealed a *cis*-prenyl transferase fold with hydrophobic residues for isoprenoid binding and a second binding pocket suitable for the nucleoside substrate. The dual-substrate pocket distinguishes Rv3378c from classical *cis*-prenyl transferases, providing a unique model for the prenylation of diverse metabolites. Terpene nucleosides are rare in nature, and 1-TbAd is known only in *Mycobacterium tuberculosis*. Thus, this intersection of nucleoside and terpene pathways likely arose late in the evolution of the *Mycobacterium tuberculosis* complex; 1-TbAd serves as an abundant chemical marker of *Mycobacterium tuberculosis*, and the extracellular export of this amphipathic molecule likely accounts for the known virulence-promoting effects of the Rv3378c enzyme.

TbAd | terpenyl transferase

With a mortality rate exceeding 1.5 million deaths annually, *Mycobacterium tuberculosis* remains one of the world's most important pathogens (1). *M. tuberculosis* succeeds as a pathogen because of productive infection of the endosomal network of phagocytes. Its residence within the phagosome protects it from immune responses during its decades long infection cycle. However, intracellular survival depends on active inhibition of pH-dependent killing mechanisms, which occurs for *M. tuberculosis* but not species with low disease-causing potential (2). Intracellular survival is also enhanced by an unusually hydrophobic and multilayered protective cell envelope. Despite study of this pathogen for more than a century, the spectrum of natural lipids within *M. tuberculosis* membranes is not yet fully defined. For example, the products of many genes annotated as lipid synthases remain unknown (3), and mass spectrometry detects hundreds of ions that do not correspond to known lipids in the MycoMass and LipidDB databases (4, 5).

To broadly compare the lipid profiles of virulent and avirulent mycobacteria, we took advantage of a recently validated metabolomics platform (4). This high performance liquid chromatography–mass spectrometry (HPLC-MS) system uses methods of extraction, chromatography, and databases that are specialized for mycobacteria. After extraction of total bacterial lipids into organic solvents, HPLC-MS enables massively parallel detection of thousands of ions corresponding to diverse lipids that range from apolar polyketides to polar phosphoglycolipids. Software-based (XCMS) ion finding algorithms report reproducibly detected ions as molecular features. Each feature is a 3D data point with linked mass, retention time, and intensity values from one detected molecule or isotope. All features with equivalent mass and retention time from two bacterial lipid extracts are aligned, allowing pairwise comparisons of MS signal intensity to enumerate molecules that are overproduced in one strain with a false-positive rate below 1% (4).

Significance

Whereas most mycobacteria do not cause disease, *Mycobacterium tuberculosis* kills more than one million people each year. To better understand why *Mycobacterium tuberculosis* is virulent and to discover chemical markers of this pathogen, we compare its lipid profile with that of the attenuated but related mycobacterium, *Mycobacterium bovis* Bacillus Calmette–Guérin. This strategy identified a previously unknown *Mycobacterium tuberculosis*-specific lipid, 1-tuberculosinyladenosine, which is produced by the Rv3378c enzyme. The crystal structure of Rv3378c provides information supporting drug design to inhibit prenyl transfer. Discovery of 1-tuberculosinyladenosine provides insight into how *Mycobacterium tuberculosis* resists killing in macrophages and a new target for diagnosing tuberculosis disease.

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¹E.L. and H.J.L. contributed equally to this work.

²Present address: Okatani Hospital, 1-25-1 Kyobate-cho, Nara 630-8141, Japan.

³T.A. and D.B.M. contributed equally to this work.

⁴To whom correspondence should be addressed. E-mail: bmoody@rics.bwh.harvard.edu.

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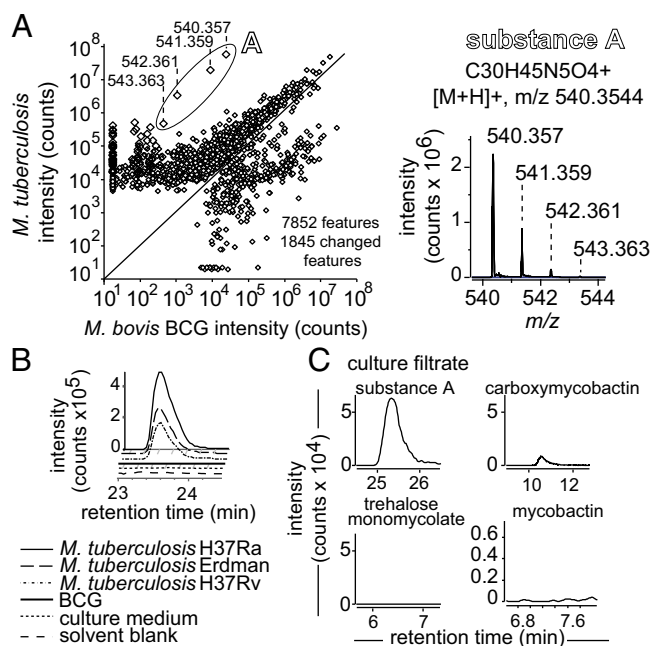


Fig. 1. Comparative lipidomic analysis of *M. tuberculosis* and BCG reveals a natural product constitutively produced and exported by *M. tuberculosis*. (A) Detected molecular features are shown as a scatterplot of intensity derived from *M. tuberculosis* H37Rv and BCG lipid extracts. Each feature corresponds to a detected ion and contains retention time and *m/z* values, which are detailed in *SI Appendix, Dataset S1*; 1,845 features out of 7,852 total features showed intensity ratios that deviate significantly from 1 (corrected *P* value, <0.05). The mass spectrum corresponds to the four *M. tuberculosis*-specific features of substance A. (B) Ion chromatograms extracted at *m/z* (540.3545) and retention time of substance A were used for the analysis of lipid extracts of reference strains. (C) Ion chromatograms from lipidomic analysis of filtered conditioned medium were extracted at the *m/z* of substance A or control compounds that are secreted (carboxymycobactin) and cell wall-associated lipids (trehalose monomycolate, mycobactin).

This comparative lipidomics system allowed an unbiased, organism-wide analysis of lipids from *M. tuberculosis* and the attenuated vaccine strain, *Mycobacterium bovis* Bacillus Calmette–Guérin (BCG). BCG was chosen because of its worldwide use as a vaccine and its genetic similarity to *M. tuberculosis* (6). We reasoned that any features that are specifically detected in *M. tuberculosis* might be clinically useful as markers to distinguish tuberculosis-causing bacteria from vaccines. Furthermore, given the differing potential for productive infection by the two strains, any *M. tuberculosis*-specific compounds would be candidate virulence factors. Comparative genomics of *M. tuberculosis* and BCG successfully identified “regions of deletion” (RD) that encode genes that were subsequently proven to promote productive *M. tuberculosis* infection (7), including the 6-kDa early secreted antigenic target (ESAT-6) secretion system-1 (ESX-1) (8, 9). We reasoned that a metabolite-based screen might identify new virulence factors because not all functions of RD genes are known. Also, biologically important metabolites could emerge from complex biosynthetic pathways that cannot be predicted from single-gene analysis.

Comparison of *M. tuberculosis* and BCG lipid profiles revealed more than 1,000 differences, among which we identified a previously unknown *M. tuberculosis*-specific diterpene-linked adenosine and showed that it is produced by the enzyme Rv3378c. Previously, Rv3378c was thought to generate free tuberculosin and isotuberculosin (10–12). This discovery revises the enzymatic function of Rv3378c, which acts as a virulence factor to inhibit phagolysosome fusion (13). Whereas current models of prenyl transferase function emphasize iterative lengthening of prenyl pyrophosphates using one binding pocket, the crystal

structure of Rv3378c identifies two pockets in the catalytic site, establishing a mechanism for heterologous prenyl transfer to nonprenyl metabolites.

Results

Comparative Lipidomics of *M. tuberculosis* and *M. bovis* Bacillus Calmette–Guérin. Using HPLC-MS for comparative analysis of lipid extracts of *M. tuberculosis* H37Rv and BCG (Pasteur strain), we detected 7,852 molecular features (Fig. 1 and *SI Appendix, Dataset S1*). By aligning datasets and seeking features that significantly differed in intensity (corrected *P* value <0.05), we identified 1,845 features that were overdetected in one bacterium or the other (Fig. 1A). Among these features, we focused on molecules selectively detected in *M. tuberculosis* that showed the highest fold-change ratios and intensity. We identified four molecular features corresponding to a singly charged molecular ion at *m/z* 540.357 ($C_{30}H_{45}N_5O_4$) and its isotopes (Fig. 1A), but this chemical formula did not match entries in the MycoMass (4) or other public databases. We named the unknown molecule substance A.

Substance A Is an Abundant Natural Product of *M. tuberculosis*. The molecular ion of substance A was one of the most intense ions in the *M. tuberculosis* lipidome (Fig. 1A), suggesting that it was produced in abundance. Identification of an apparently abundant molecule in a widely studied pathogen was unexpected, leading to questions about whether substance A was truly a natural product. However, this compound was absent in media, solvent blanks, and BCG lipid extracts but was reproducibly detected in three reference strains of *M. tuberculosis* (Fig. 1B). As observed with cell-associated compounds (Fig. 1A), culture filtrate (Fig. 1C) yielded bright ion at *m/z* 540.357 whose intensity was higher than that of the abundantly secreted siderophore, carboxymycobactin. Its release into the extracellular space likely results from transmembrane transport, rather than budding of intact cell wall fragments, because cell wall-embedded lipids, trehalose monomycolate and mycobactin, were not detected in filtered supernatants (Fig. 1C). We detected substance A in *M. tuberculosis* during exponential or stationary phase and several types of media or when subject to acid stress (*SI Appendix, Fig. S1 A and B*). Thus, substance A is a natural product that is constitutively produced in many conditions and accumulates within and outside *M. tuberculosis*.

M. tuberculosis often compartmentalizes lipid biosynthesis so that lipids are assembled after transport across the plasma membrane. Sulfoglycolipids and phthiocerol dimycocerosates become undetectable when MmpL transporters are interrupted, even when biosynthetic genes are intact (14–16). Because ESX-1 is a transport system lacking in BCG, lack of export of an ESX-1-dependent lipid synthase might account for the loss of substance A. However, ESX-1-deficient *M. tuberculosis* lacking either the *espA* gene (Rv3616c) or the entire RD1 locus (17), which are both necessary for ESX-1 function, produces substance A at normal

1-tuberculosinyladenosine (1-TbAd)

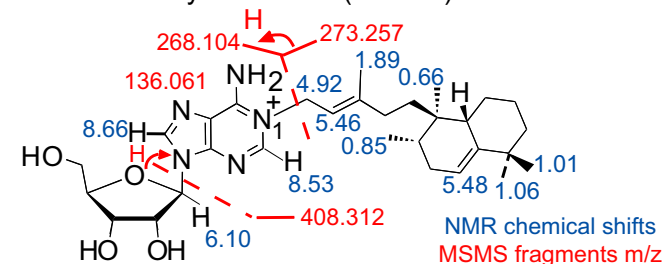


Fig. 2. Identification of 1-TbAd. The structure of substance A purified from *M. tuberculosis* lipid extract was characterized using CID-MS and NMR (800 MHz) analyses yielding key collision products and resonances detailed in *SI Appendix, Figs. S2–S9*.

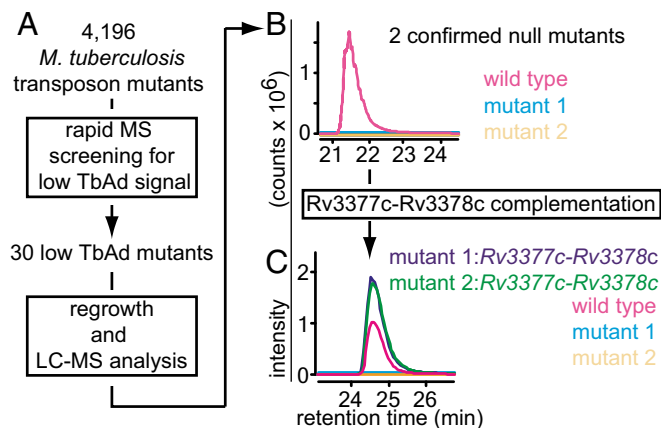


Fig. 3. *M. tuberculosis* biosynthesis of substance A requires Rv3378c. (A) The screening of 4,196 transposon mutants of *M. tuberculosis* H37Rv using a rapid 3-min HPLC-MS method yielded 30 strains with reduced 1-TbAd signal. (B) Rescreening with the 40-min HPLC-MS method confirmed absence of 1-TbAd signal in two mutants. (C) Both mutants were found to have spontaneous, non-transposon-induced mutations in Rv3378c and were subject to complementation of Rv3377c-Rv3378c and reanalysis for 1-TbAd production.

levels (SI Appendix, Fig. S1C). After ruling out a major known species-specific difference in transport, we devised a screen to detect genes responsible for substance A biosynthesis.

Substance A Is a 1-Tuberculosinyladenosine. Collision-induced mass spectrometry (CID-MS) identified the structural components of substance A as adenine ($[M+H]^+$, $C_5H_6N_5$, m/z 136.0618), adenosine ($[M+H]^+$, $C_{10}H_{14}N_5O_4$, m/z 268.1040), and a polyunsaturated C20 hydrocarbon ($[M+H]^+$, $C_{20}H_{33}$, m/z 273.2576) (Fig. 2 and SI Appendix, Figs. S2–S4). A common C20 diterpene is geranylgeraniol, and *M. tuberculosis* produces two C20 lipids containing bicyclic halimane skeletons: tuberculosinol and isotuberculosinol (18–20). Initially, CID-MS spectra could not distinguish among these three candidate diterpenes (SI Appendix, Figs. S3 and S4), but multistage CID-MS studies isolated the diterpene unit of substance A (m/z 273.3) and yielded collision patterns that matched tuberculosinol more closely than geranylgeraniol (SI Appendix, Fig. S4).

After purification of the natural product, we carried out NMR spectroscopy analyses using 1H 1D, 2D COSY, HMQC, and NOESY spectra (SI Appendix, Figs. S5–S9), which unequivocally established the structure of substance A as 1-tuberculosinyladenosine (1-TbAd) (Fig. 2). The NMR signals of the diterpene moiety matched those of tuberculosinol (10, 19–21) except for the expected difference in the side-chain protons and carbons. The spectral data of the adenosine and adjacent atoms correspond closely to those of 1-prenyladenosine analogs (22–24). The allylic methylene group absorbs downfield as a doublet at δ 4.92 ($J = 6.6$ Hz). A NOESY cross peak between the adenine H-2 at δ 8.53 and the alkene hydrogen and allylic methylene and methyl groups at δ 5.46, 4.92, and 1.89, respectively, confirm that the tuberculosinyl group is attached to the adenine at position 1. Thus, *M. tuberculosis* produces a previously unknown type of diterpene nucleoside.

Rv3378c Produces 1-TbAd. To identify the genes necessary for 1-TbAd production, an existing library of random transposon insertional mutants (25) was screened in high throughput (4,196 mutants) for 1-TbAd production using a simplified 3-min HPLC-MS method (Fig. 3A). Thirty mutants showing low or absent signals were rescreened using the original, high-resolution lipidomic separation method (Fig. 1). Reporting only mutants with complete signal loss of 1-TbAd signal in both assays, we identified two 1-TbAd-null mutants carrying transposons in Rv1796 (mutant 1) and Rv2867c (mutant 2) (Fig. 3B). The concurrently performed biochemical studies described above identified the highly

characteristic tuberculosinyl moiety as a component of 1-TbAd, and the Rv3377c-Rv3378c locus was known to encode enzymes needed for tuberculosinol and isotuberculosinol production (10, 11, 18–21). Sequencing identified spontaneous mutations in Rv3378c in both mutants (10, 18–21). Mutant 1 encoded a predicted Asp→Gly substitution at residue 34, and mutant 2 encoded a Pro→Ser substitution at residue 231. We generated complementation constructs to separately test whether the point mutations in Rv3378c or the transposon insertions were responsible for 1-TbAd loss. Transfer of Rv1796 and Rv2867c failed to restore 1-TbAd production (SI Appendix, Fig. S10), but transfer of Rv3377c-Rv3378c reconstituted 1-TbAd production in both mutants (Fig. 3C). Thus, Rv3377c-Rv3378c genes are necessary for 1-TbAd biosynthesis in *M. tuberculosis*.

The Biosynthetic Pathway of 1-TbAd. Furthermore, the known role of Rv3377c and Rv3378c enzymes in tuberculosinol production potentially provided a mechanism to connect Rv3377c and Rv3378c genes with the production of a nucleoside-modified tuberculosinol. Rv3377c is a terpene cyclase, which acts on geranylgeranyl pyrophosphate (GGPP) to generate tuberculosinyl pyrophosphate (TbPP). Rv3378c was thought to be a phosphatase, which converts TbPP to free tuberculosinol (10, 21). Extending current models (Fig. 4A), 1-TbAd might result from downstream action of an unknown enzyme on free tuberculosinol to transfer it to adenosine. Polyprenol synthase genes and the Rv3377c-Rv3378c locus are coordinately regulated and encoded at adjacent sites on the chromosome (26). Therefore, we searched *M. tuberculosis* databases for genes located near this locus that might plausibly function as adenosine transferases. We failed to find candidates and

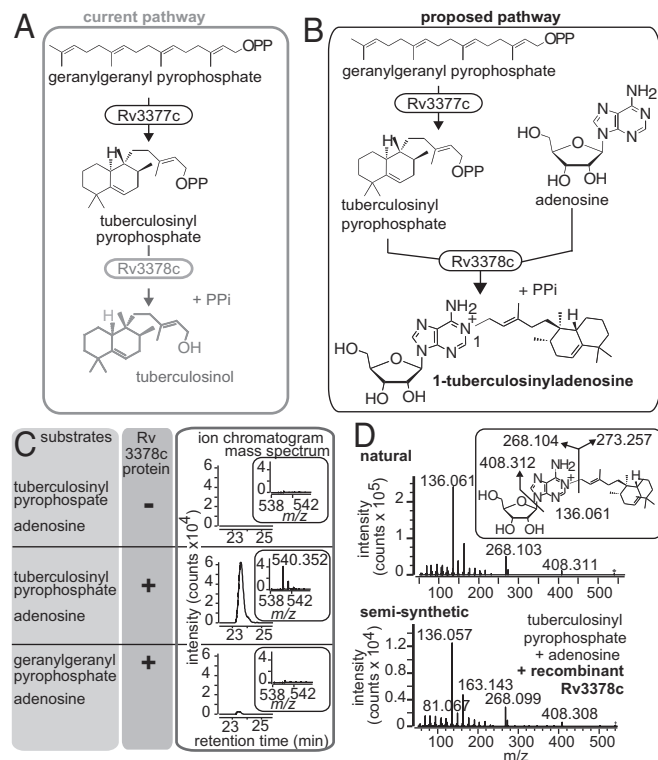


Fig. 4. Rv3378c acts as a tuberculosinyl transferase. (A) Rv3377c and Rv3378c are currently thought to produce tuberculosinol and isotuberculosinol. (B) The existence of 1-TbAd might be explained by a revised function of the Rv3378c enzyme, which acts as a tuberculosinyl transferase. (C and D) Ion chromatograms and mass spectra (insets) (C) and CID-MS (D) of the 1-TbAd standard and reaction products of enzymatic assays performed using recombinant Rv3378c protein.

noted that no transposon insertion that blocked 1-TbAd production mapped to genes adjacent to this locus.

Therefore, we considered a revised biosynthetic model in which Rv3378c protein is not a simple phosphatase, as currently believed, but instead acts with combined phosphatase and tuberculosinyl transferase functions, using adenosine as the nucleophilic substrate (Fig. 4B). This model is mechanistically simple and might explain the lack of an apparent stand-alone transferase gene. Also, whereas current models predict that tuberculosinol is the end product of this pathway, we did not detect tuberculosinol in lipidomics experiments (Fig. 1A and *SI Appendix, Dataset S1*). The revised model posits that 1-TbAd is the end product of Rv3378c pathway, explaining why it accumulates to high levels as one of the brightest ions in the lipidome (Fig. 1A). After chemical synthesis of TbPP (*SI Appendix, Fig. S11*), we tested TbPP and GGPP as substrates for the recombinant Rv3378c protein (18). Rv3378c catalyzed the condensation of adenosine and TbPP to generate 1-TbAd but produced little or no product from GGPP. Free tuberculosinol was not detected in these assays (Fig. 4C and D). Thus, Rv3378c shows tuberculosinyl transferase activity, which rules in the revised biosynthetic pathway (Fig. 4B).

Rv3377c-Rv3378c Is Sufficient for 1-TbAd Biosynthesis in Cells. To test the sufficiency of this locus for 1-TbAd production in cells, we transferred the *Rv3377c-Rv3378c* locus to *Mycobacterium smegmatis*. In all three clones tested, expression of *Rv3377c-Rv3378c* transferred production of a molecule with the mass, retention time, and CID-MS spectrum of 1-TbAd (Fig. 5 and *SI Appendix, Fig. S12*). Thus, no other *M. tuberculosis*-specific cofactor or transporter is needed for 1-TbAd production. *Rv3377c-Rv3378c* is sufficient to synthesize 1-TbAd from ubiquitous cellular precursors present in most bacteria, likely GGPP and adenosine.

Crystal Structure of Rv3378c. To understand whether the active site of Rv3378c is compatible with the revised function as a tuberculosinyl transferase, we determined its crystal structure. Lacking structures with high sequence similarity, single-wavelength anomalous dispersion phasing was used to calculate the initial electron-density map. The model was refined against native data to 2.2-Å resolution (*SI Appendix, Table S1*). As expected from gel-filtration studies, Rv3378c formed a homodimer (Fig. 6A). Although structural similarity was not predicted by sequence comparisons, Rv3378c adopts the fold seen in (Z)-prenyl or cis-prenyl transferases (27), including *M. tuberculosis* (Z)-farnesyl diphosphate synthase (Rv1086) and decaprenyl pyrophosphate synthase (Rv2361c), as well as *Escherichia coli* undecaprenyl pyrophosphate synthase (UPP) (28, 29) (Fig. 6B). These enzymes condense an allyl pyrophosphate and the five-carbon isopentyl pyrophosphate building block to produce linear isoprenoids (28, 29).

Structural Insight into Prenyl Unit Binding. In considering competing models that Rv3378c might simply hydrolyze the TbPP or

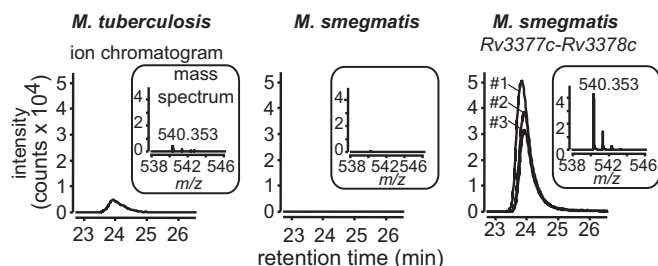


Fig. 5. The expression of *Rv3377c-Rv3378c* is sufficient for production of 1-TbAd in *M. smegmatis*. Extracted ion chromatograms and mass spectra (insets) of 1-TbAd (m/z 540.3545) for the HPLC-MS analysis of lipid extracts from *M. tuberculosis* (Left), *M. smegmatis* parental (Center), or each of three *M. smegmatis* *Rv3377c-Rv3378c* knock-in (Right) strains.

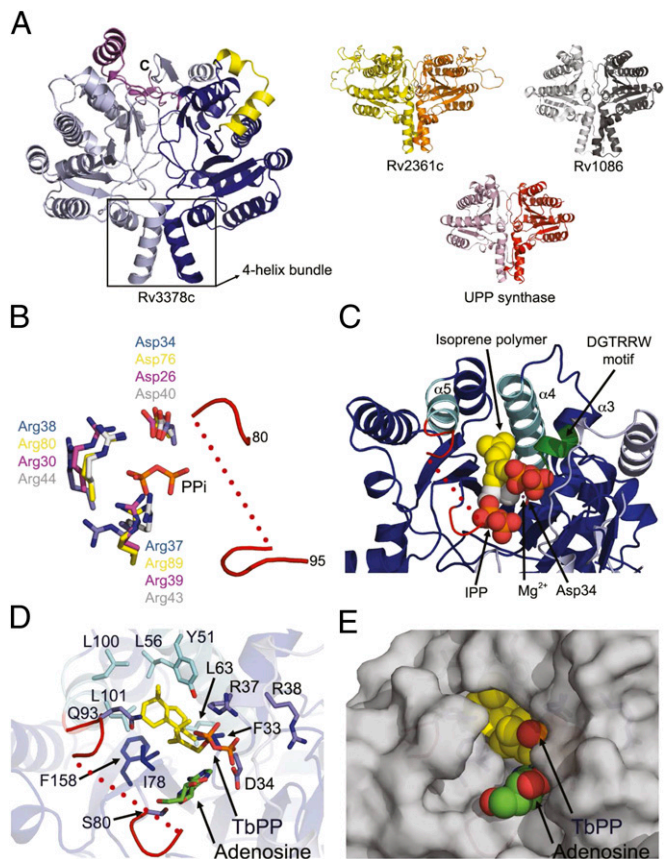


Fig. 6. Rv3378c adopts a (Z)-prenyl transferase fold. (A) Structure of the Rv3378c dimer is compared with conventional (Z)-prenyl transferases. (B) Superposition of the active site of Rv3378c and other (Z)-prenyl transferases with the pyrophosphate bound to Rv2361c (stick) shows conserved key residues for substrate binding and catalysis (Rv3378c, blue; Rv2361c, yellow; Rv1086, gray; *E. coli* UPP synthase, magenta for carbon atoms). (C) The monomeric subunits of Rv3378c and Rv2361c were superimposed and Rv2361c substrates (sphere) (carbon, yellow/gray; oxygen, red; phosphate, orange) are modeled in the active site of Rv3378c. The conserved residue, Asp34, is shown as a stick model, and the magnesium ion is shown as a magenta sphere. (D) Proposed model of Rv3378c shows two substrate pockets with hydrophobic residues lining the predicted prenyl binding pocket and D34 positioned adjacent to the predicted adenosine binding pocket. (B–D) The flexible P-loop of Rv3378c (residues 80–95) is colored in red, with the dotted line for disordered region (residues 84–90). (E) The translucent surface of Rv3378c was modeled with substrates (spheres) using the same view as D.

carry out the newly proposed role in adenosine transfer (Fig. 5A and B), we superimposed Rv3378c with the pseudosubstrate and product complexes of Rv2361c (29) to model an enzyme–substrate (ES) complex. In contrast to other (Z)-prenyl transferases, Rv3378c has a unique C-terminal helical segment (from residue 251 to end), which contributes to domain swapping. An extra N-terminal helical segment (residues 6–24) packs via hydrophobic interactions with adjacent helices (Fig. 6A and *SI Appendix, Fig. S13*).

Rv3378c shares functional motifs with the (Z)-prenyl transferases, including residues for substrate binding and catalysis: Asp34, Arg37, and Arg38 (Fig. 6B). (Z)-prenyl transferases bind the allyl pyrophosphate substrate through a characteristic DGNG/RRW amino acid sequence motif starting two residues before the N terminus of an α -helix (α 3). The aspartate chelates a magnesium ion, whereas the glycine, the helix terminus, and the arginine(s) engage the pyrophosphate (Fig. 6B and C) (27, 28, 30). In Rv3378c, Asp34 sits in the expected position to carry out its essential catalytic function providing a specific mechanism that likely explains why mutant 1, which contains an Asp34→Gly alteration, does not

produce 1-TbAd. As predicted by prior studies showing the role of aspartate in prenyl transfer (27, 28, 30) and the conserved location of Asp34 vis-à-vis the prenyl binding site (Fig. 6 *A* and *B*), mutation to asparagine or alanine abolished the prenyl transferase function of Rv3378c (*SI Appendix*, Fig. S14). In Rv2361c, the isoprenoid binding site is a hydrophobic pocket located between the β -sheet and the α 2 (residues 89–110) and α 3 (residues 129–152) helices (29). Rv3378c contains all of these features (Fig. 6*C*), including the 34-DGTRRW-39 motif and a deep pocket adjacent to helices α 4 (residues 51–68) and α 5 (residues 96–103). Hydrophobic residues (L56, L63, L100, and L101) line the pocket created by helices α 4 and α 5, and other hydrophobic residues (F33, I78, F158) further contribute to the hydrophobic character of the pocket. This binding pocket is predicted to position the pyrophosphate group of TbPP, which can interact with Arg37 and Arg38 from the DGTRRW motif and Tyr51 from the N terminus of helix α 4 (Fig. 6*D*).

A Second Pocket at the Catalytic Site. The binding mode of the nucleophilic adenosine substrate is harder to model, because the binding site is likely to be completed by the closure of the P-loop over the active site when native substrate is present. The P-loop is disordered in the unliganded structure, but it becomes ordered in a nonphysiological complex with mellitic acid (*SI Appendix*, Fig. S13). This structure suggests a specific mechanism by which substrate binding provides polar interactions with the P-loop to exclude water from the active site. Other considerations provide pertinent clues about the adenosine binding mode. As contrasted with Rv2361c, Rv1086, and UPP synthase, Rv3378c has a second pocket that can accommodate adenosine (Fig. 6 *D* and *E*). Superimposing N1 of the adenine on the isopentenyl pyrophosphate (IPP) nucleophile in complex with Rv2361c (29) guides the positioning of the adenosine substrate in the active site of Rv3378c. In Rv2361c, the pyrophosphate of IPP interacts with Arg244 and Arg250 (29). Corresponding to the fact that adenosine lacks the pyrophosphate, Rv3378c lacks this conserved pair of arginines, which are replaced with glycine and serine. These features distinguish Rv3378c from known (*Z*)-prenyl transferases and are consistent with adenosine binding and transfer.

Discussion

Overall, structural, genetic, and biochemical data strongly suggest a revised function of Rv3378c as a tuberculosinyl transferase that produces 1-TbAd, an abundant amphiphile that is exported outside *M. tuberculosis*. This result establishes the efficacy of unbiased lipidomic screens to identify previously unknown compounds. A C35 terpene cyclase activity is found in nonpathogenic mycobacteria (31, 32), but Rv3377c orthologs are only known within *M. tuberculosis* complex. Higher-order terpene-nucleosides are rare in nature, and we have not identified a precedent for 1-linked prenyl adenosines. Plant and marine sponges produce terpene-purine derivatives, such as cytokinins and agelasins, which regulate growth or show antimicrobial effects (33). However, these natural products contain adenine rather than adenosine, and the terpene moiety is carried at the N6 position of the adenine in the cytokinins and N7 or N9 in the agelasins. Furthermore, among microbes studied to date, we have only detected 1-TbAd in members of the *M. tuberculosis* complex, suggesting that 1-TbAd production is limited to pathogenic mycobacteria. Orthologs of Rv3377c or Rv3378c are limited to the *M. tuberculosis* complex. Although *M. bovis* and BCG strains encode orthologous genes, strains examined to date encodes a frameshift mutation in Rv3377c (11), and the Pasteur strain used here encodes a second coding point mutation in Rv3378c. Thus, both genetic and biochemical evidence suggest that 1-TbAd is a specific marker of *M. tuberculosis*, supporting the development of 1-TbAd or 1-TbAd-specific immune responses as candidate targets for diagnostic tests for tuberculosis.

The lack of 1-TbAd in BCG might represent evidence that changes in Rv3377c-Rv3378c might contribute to the vaccine strain's attenuation. More direct evidence for a role of this

locus in virulence comes from transposon studies showing that Rv3377c and Rv3378c play nonredundant roles in phagosome-lysosome fusion and survival in macrophages (13). This key finding initiated an intensive search for the actual functions of these virulence-associated genes. Rv3377c is a terpene cyclase (18–20). Rv3378c has few orthologs in nature, and its biochemical function was not apparent from predictive folding algorithms. Based on in vitro studies, Rv3378c is currently thought to function as a TbPP pyrophosphatase that yields free tuberculosinol (10). Tuberculosinol coupled to beads blocks phagosomal acidification (21). However, end products of biosynthetic pathways typically accumulate, and to our knowledge, the extent of accumulation of free tuberculosinol as a natural product in intact *M. tuberculosis* remains unknown. We did not detect free tuberculosinol or isotuberculosinol in lipidomics analysis of *M. tuberculosis* or among in vitro products of Rv3378c. This result does not rule out biosynthesis of free tuberculosinol, but it is notable that 1-TbAd is not only detected but substantially accumulates within and outside *M. tuberculosis*. Furthermore, we prove that the action of Rv3378c is a combined phosphatase and tuberculosinol transferase through in vitro study of purified proteins, gene transfer to *M. tuberculosis* and *M. smegmatis*, and a structural analysis of Rv3378c. Based on parallel lines of genetic, biochemical, and structural evidence, we propose that Rv3378c should be known as “tuberculosinyl adenosine transferase.”

The structures of enzymes that transfer prenyl pyrophosphates to substrates other than linear isoprenoids have not been determined previously. Like other (*Z*)-prenyl transferases, Rv3378c contains a characteristic allyl pyrophosphate-binding site, catalytic aspartate, and flexible P-loop in position to close over the active site. The canonical TbPP binding pocket structure is sufficiently conserved that it may be sensitive to available drugs or analogs that target other (*Z*)-prenyl transferases. However, the nucleophile binding site lacks conserved features that mediate recognition of pyrophosphate moiety of isoprene building blocks seen in previously characterized (*Z*)-prenyl transferases. Instead, Rv3378c active site contains a second pocket in which the adenosine can be positioned for nucleophilic attack on C1 of TbPP. We observed this reaction in vitro and found that Rv3378c does not act on GGPP and specifically produces the 1-linked form of 1-TbAd, defining two aspects of the substrate specificity. Whereas most prenyl transferases have one identifiable pocket, this revised two-pocket model suggests a broader paradigm for the prenylation of metabolites catalyzed by members of the (*Z*)-prenyl transferase family. Whereas current models emphasize iterative elongation through the repeated use of one pocket, the dual-substrate pocket of Rv3378c provides a general model for prenylation of nonprenyl substrates. Product specificity is determined by a conventional allyl pyrophosphate binding site and a second pocket tailored to bind and activate each target nucleophile.

The larger 1-TbAd biosynthetic pathway starts with two evolutionarily conserved systems, which produce geranylgeranyl pyrophosphate and adenosine. These pathways operate separately in most organisms, but *M. tuberculosis* joins these two pathways to generate a terpene nucleoside. The appearance of TbAd after transfer of Rv3377c and Rv3378c genes to *M. smegmatis* proves that additional *M. tuberculosis*-specific genes, such as transporters, are not required for 1-TbAd biosynthesis. More generally, these data represent an experimental demonstration that transfer of two genes is sufficient to reconstitute a complex metabolite, which likely requires more than 20 genes for its complete biosynthesis. Combining this observation with data suggesting that the ancestral Rv3377c and Rv3378c genes were acquired by horizontally ancient terpene and nucleotide biosynthetic pathways were joined together by transfer of two genes late in the evolution of the *M. tuberculosis* complex (26).

Rv3378c gene likely carries out its known effects in promoting *M. tuberculosis* infectivity via the production of 1-TbAd. Within minutes of phagocytosis, *M. tuberculosis* inhibits host defenses, including phagosome acidification and phagolysosome fusion

(34, 35). The *Rv3377c-Rv3378c* locus is required for optimal phagosome maturation arrest (13). The discovery of extracellular 1-TbAd provides specific insight into mechanisms by which an enzyme that is thought to be localized in the cytosol affects events outside the bacterium (13). To our knowledge, neither *Rv3378c* nor free tuberculosinol has been detected in culture filtrates (18). In contrast, 1-TbAd is an amphiphile that is released into the extracellular space using an export mechanism that is independent of ESX-1.

Future studies will be needed to understand the particular mechanisms by which 1-TbAd contributes to the effects of *Rv3377c-Rv3378c* on phagosome maturation. Adenosine is almost exclusively found inside cells, and terpene chains catalyze the transfer of pyrophosphate across the mycobacterial envelope for the biosynthesis of arabinogalactan (36). By analogy, prenylation might promote the transit of the nucleoside to the phagosomal space, where the adenosine could engage host receptors. Alternatively, tuberculosinol or isotuberculosinol might be the active moiety (12, 21), whose solubility or transport is influenced by adenosine. The cellular mechanism leading to altered mycobacterial survival might include changed integrity of the phagosomal membrane, intraphagosomal proton capture, or escape of 1-TbAd across the phagosomal membrane and into the host, where it might signal global changes in macrophage function.

Methods

Bacteria were cultured and extracted by chloroform/methanol mixtures or ethyl acetate, respectively, as described (4, 37). Lipid extracts were analyzed

using an Agilent 6520 Accurate-Mass Q-ToF and a 1200 series HPLC system with a Varian MonoChrom Diol column (4, 37) with data output from XCMS and MultiplotPreprocess and Multiplot modules of GenePattern (Broad Institute) (38). *Rv3378c* and GroES/GroEL chaperones were coexpressed in BL21-CodonPlus (Stratagene) cells and purified on a precharged Ni Sepharose Fast Flow column (Ni-NTA HisTrap FF, GE Healthcare). Purified *Rv3378c* (10 mg/mL) was crystallized by vapor diffusion, and 2.20-Å-resolution data were collected on the Advanced Light Source. The structure of *Rv3378c* was solved by single-wavelength anomalous diffraction phasing of a mercury derivative using Phenix AutoSol. Enzymatic assays were performed by incubating 56 μg of diterpene in presence of 33 μg of adenosine (Sigma) and 80 μg of purified *Rv3378c* in 1 mL of pH 7.4 Tris-HCl buffer 4 h at 37 °C under magnetic agitation. *M. tuberculosis* transposon mutants from a random library (25) were grown in 96-well format and heat-killed, followed by lipid extraction by 70:30 methanol:isopropanol. Lipids were analyzed by HPLC-MS to monitor 1-TbAd production; 1-TbAd-null strains were confirmed regrowing the bacteria and using a full lipidomic analysis method. 1-TbAd was purified from mycobacterial cell-associated lipid extract using normal and reversed-phase chromatography. Structures were solved using CID-MS and NMR spectroscopy using a Bruker Avance 800.

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Supporting Information Appendix

Molecular profiling of *M. tuberculosis* identifies tuberculosinyl nucleoside products of the virulence-associated enzyme Rv3378c

Emilie Layre, Ho Jun Lee, David C. Young, Amanda Jezek Martinot, Jeffrey Buter, Adriaan J. Minnaard, John W. Annand, Sarah M. Fortune, Barry B. Snider, Isamu Matsunaga, Eric J. Rubin, Tom Alber, D. Branch Moody

correspondence to: bmoody@rics.bwh.harvard.edu

Supporting Materials and Methods

Bacterial culture. Mycobacteria were cultured in triplicate in Tween-free Middlebrook 7H9 broth supplemented with 10% Oleic acid Albumin Dextrose Catalase (Becton Dickinson) in 50 mL polystyrene tubes (Corning) shaking at 100 rpm at 37 °C, and a fourth culture was treated with TWEEN to disperse bacteria just before taking the OD₆₀₀ measurement. Cultures were harvested when the TWEEN culture replicate reached a 0.6 OD (+/-0.1). Stationary phase cultures of mycobacteria were cultured similarly but harvested at an OD of 2. Acid stressed cultures were grown in 4.5 pH citrate buffer.

Mycobacterial lipid extraction. HPLC-MS grade solvents (Fisher) and clean borosilicate glassware (Fisher), amber vials (Supelco) and Teflon-lined caps (Fisher) were used. Bacterial cultures were centrifuged (4,000 rpm, 10 min) to clarify culture supernatants, which were passed twice through a 0.22 µm filter to remove intact membrane fragments (1). Cell pellets were washed twice in 10 mL Optima water, resuspended in 1 mL of CH₃OH, transferred to a 50 mL amber glass bottle and contacted with 25 mL CHCl₃/CH₃OH (2:1, v:v) overnight to sterilize bacteria. CHCl₃/CH₃OH suspensions were transferred in 50 mL conical glass tubes and rotated at 20 °C for at least 1 hr. After centrifugation, lipid extracts were decanted, and bacteria pellets subjected to 2 additional extractions using CHCl₃:CH₃OH (1:1, v:v) and CHCl₃:CH₃OH (1:2, v:v) with pooling of extracts and evaporation with GeneVac EZ-2 (SP Scientific) using the low boiling point mixture setting. Dried lipids were resuspended in CHCl₃:CH₃OH (1:1, v:v) and dried under nitrogen in preweighed vials and then reweighed in triplicate on microbalance (Mettler Toledo, XP205). Then extracts were redissolved in CHCl₃:CH₃OH (1:1, v:v) at 1 mg/mL.

HPLC-ESI-QToF based Lipidomics. Using an Agilent Technologies 6520 Accurate-Mass Q-ToF and a 1200 series HPLC system with a Varian Monochrom diol column (3

$\mu\text{m} \times 150 \text{ mm} \times 2 \text{ mm}$) and a Varian Monochrom diol guard column ($3 \mu\text{m} \times 4.6 \text{ mm}$), normal phase lipidomics was carried out as described (2). Total lipid extracts were resuspended at 0.5 mg/mL in solvent A (hexanes:isopropanol, 70:30 [v: v], 0.02% [m/v] formic acid, 0.01% [m/v] ammonium hydroxide), filtered or centrifuged at 1,500 rpm for 5 min to remove trace non-lipidic materials prior to transfer to a glass autosampler vial (Agilent). Ten μg of lipid was injected, and the column (20°C) was eluted at 0.15 mL/min with a binary gradient from 0% to 100% solvent B (isopropanol:methanol, 70:30 [v/v], 0.02% [m/v] formic acid, 0.01% [m/v] ammonium hydroxide): 0–10 min, 0% B; 17–22 min, 50% B; 30–35 min, 100% B; 40–44 min, 0% B, followed by additional 6 min 0% B post-run. Raw data files were converted to mzData using MassHunter and processed in R using the XCMS (version 1.24)(3) centWave peak finder (4). XCMS (<http://metlin.scripps.edu/xcms/index.php>) deconvoluted and aligned across samples using s/n threshold of 5, a maximum tolerated m/z deviation of 10 ppm, a frame width of $mzdiff=0.001$, a peak width of 20–120 s and a band width of 5.

Comparative lipidomics. XCMS data matrices listing detected features, median m/z and median RT of triplicate lipidic extracts was imported into GenePattern (Broad Institute) using MultiplotPreprocess and Multiplot modules (5).

Protein expression and purification. Rv3378c and GroES/GroEL chaperones were coexpressed in BL21-CodonPlusTM (Stratagene) cells. Cell cultures were grown at 37°C until OD_{600} reached ~ 0.6 and induced with 0.2 mM isopropyl β -D-thiogalactopyranoside (IPTG) and 0.2% (w/v) L-arabinose at 22°C overnight. Cells were lysed by sonication and lysate was purified on a Ni-NTA HisTrapTM FF column (GE Healthcare). Partially purified Rv3378c was cleaved with thrombin at 4°C overnight, loaded onto the Ni-NTA column, and flow-through fractions were concentrated and purified by gel filtration on a SuperdexTM 75 (GE Healthcare).

Rv3378c enzymatic assays. Fifty-six micrograms of dried TbPP or GGPP were resuspended in 1 mL of pH 7.4 Tris-HCl buffer (1 mM MgCl_2 , 0.1% Triton X-100 (w/v)) by sonication. Thirty-three μg of adenosine (Sigma) prepared at 1 mg/mL in pH 7.4 Tris-HCl buffer ($33 \mu\text{L}$) and $5 \mu\text{L}$ of recombinant Rv3378c at 16 mg/mL were added to the lipid solution and incubated 4 hr at 37°C under magnetic agitation. Lipid products were extracted three times from the reaction mixture using chloroform ($3 \times 0.5 \text{ mL}$), pooled, dried and analyzed by HPLC-MS as described above. The detection of 1-TbAd was confirmed based on m/z mass accuracy, retention time and MS/MS experiments (30 eV).

Cloning Rv3378c gene from *M. tuberculosis*. The Rv3378c gene (GenBankTM accession number: CAA15763.1) was amplified by PCR from *M. tuberculosis* H37Rv genomic DNA using PfuTurbo DNA polymerase (Stratagene), introducing flanking NdeI and XhoI restriction sites. Amplified and digested PCR products were ligated in predigested pET-28b vector (Novagen), resulting an N-terminal cleavable hexahistidine tag followed by the protein coding sequence. Clones were verified by DNA sequencing (Elim Biopharm).

Transposon mutant library screening. Transposon mutants from a random library (50) were grown in 96 well format in Middlebrook 7H9 media to confluence and heat killed, followed by extraction with 100 μ L of 70:30 methanol:isopropanol and shaking for 5 minutes. 100 μ L aliquot was transferred to a Millipore 96 well filter plate and centrifuged at 4500 rpm for 10 minutes. The collected filtrate was used for rapid HPLC-MS analysis using an isocratic gradient of 70:30 methanol:isopropanol for three minutes.. 1-TbAd production was monitored in MS positive mode spectra at 540.35 m/z and in MS/MS positive mode spectra by the detection of the adenine fragment at 136.06 m/z . Mutants negative for these ions were recorded as potential 1-TbAd null strains, which were confirmed using a full lipidomic analysis..

Rv3377c-Rv3378c knock-in *M. smegmatis* strain or complementation of *M. tuberculosis*. Wild-type *M. smegmatis* or TbAd deficient *M. tuberculosis* strains were transformed with a plasmid that episomally expresses *Rv3377c-Rv3378c* genes under the control of a tetracycline inducible promoter (pTETGW) (6).

Rv3378c and GroES/GroEL proteins expression and purification.

The Rv3378c gene (GenBankTM accession number: CAA15763.1) was amplified by PCR from *M. tuberculosis* H37Rv genomic DNA using PfuTurbo DNA polymerase (Stratagene) and cloned into pET-28b vector (Novagen). Rv3378c mutants were generated using the QuikChange method (Stratagene). All clones were verified by DNA sequencing (Elim Biopharm).

Rv3378c and GroES/GroEL chaperones were coexpressed in BL21-CodonPlusTM (Stratagene) cells to improve the solubility of Rv3378c. Cell cultures were grown at 37°C until OD600 reached ~0.6 and induced with 0.2 mM isopropyl β -D thiogalactopyranoside (IPTG) and 0.2% (w/v) L-arabinose at 22°C overnight. Cells were harvested by centrifugation (4,500 rpm, 20 min), resuspended in 20 mM Hepes, pH 7.5, 500 mM NaCl, 0.5 mM TCEP, and 25 mM imidazole with EDTA free protease inhibitor cocktail (Roche). Resuspended cells were lysed by sonication and centrifuged (16,000 rpm, 90 min). Cleared lysate was purified on a Ni-NTA HisTrapTM FF column (GE Healthcare) with gradient elution using buffer containing 300 mM imidazole. Partially purified Rv3378c fractions were cleaved with thrombin at 4°C overnight, loaded onto the Ni-NTA column, and flow-through fractions were concentrated and purified by gel filtration on a SuperdexTM 75 (GE Healthcare) column equilibrated in 20 mM Hepes, pH 7.5, 50 mM NaCl, 0.5 mM TCEP, 10% glycerol.

Crystallographic structure determination of Rv3378c. Purified Rv3378c (10 mg/mL) was crystallized by vapor diffusion from 100 mM citrate, pH 3.5, 10-15% (w/v) polyethylene glycol 3350. A cluster of crystals was separated by gentle mechanical prodding with a cat whisker. The resulting single crystals were transferred to mother liquor containing 25% ethylene glycol and directly plunged into liquid nitrogen prior to data collection. X-ray diffraction data were collected at 100 K on the Advanced Light Source (ALS) beamline 8.3.1 and processed using HKL2000 (7). The 2.20-Å resolution native data set and 2.30-Å resolution ethylmercury phosphate derivative data set were collected at wavelengths of 1.1111 and 1.0083 Å, respectively. Different crystal forms

were observed by additional screening with Silver Bullets HT kit (Hampton Research), and a 2.36 Å resolution data set was collected at 1.1111 Å at 100 K on ALS beamline 8.3.1. The structure of Rv3378c was solved by SAD phasing of a mercury derivative using Phenix AutoSol (8). Initial models built by Phenix AutoBuild (8) were improved using ARP/warp (9), followed by manual building in Coot (10). The native structures were solved by molecular replacement using the mercury-derivatized structure as a search model in Phaser (11). Structures were refined using Phenix Refine (8), with exclusion of 10 % of the reflections to calculate R_{free} . Models were validated using Molprobit (12). Secondary structures were assigned using DSSP (Dictionary of Protein Secondary Structure) (13) and structural figures were generated using PyMOL (<http://www.pymol.org/>) (14).

Purification of 1-tuberculosinyladenosine (Substance A). Gram quantities of *M. tuberculosis* H37Rv and H37Ra were extracted three times with chloroform and methanol solution as described above. 500 mg of lipid extract was concentrated under nitrogen, and the lipid slurry was loaded on an open silica gel column (2 cm × 1.6 cm) using chloroform. Fractions were eluted with the following sequence of solvents: chloroform, 95:5 chloroform/isopropanol, 95:5, 90:10 and 50:50 chloroform/methanol (v/v) with ion monitoring (m/z 540.5) to track substance A, which eluted in the 95:5 (v/v) chloroform/methanol and the 50:50 chloroform/methanol fractions. After drying, reversed phase HPLC (Waters Corporation) purification of pooled fractions enriched for the target ion was carried out using octadecyl-modified silica (5 micron) semi-preparative column (Higgins Analytical HAISIL C18, 250 × 10 mm). Using an isocratic 450:50:1 methanol/water/trifluoroacetic acid (v/v/v) gradient with a flow rate of 3.0 mL/min substance A appeared at 8 min. After drying with nitrogen and a 5-fold excess of acetonitrile HPLC chromatography was repeated giving pure 1-TbAd as assessed by MS and NMR spectroscopy.

Supporting figures legends

Fig. S1. Substance A constitutively accumulates independently of the ESX-1 apparatus.

Extracted ion chromatograms were detected at the m/z corresponding to substance A's molecular ion (540.3545) for the analysis of the extracted cell-associated lipids from (A) *M. tuberculosis* H37Rv harvested at exponential or stationary phase or (B) grown in acid media (C) *M. tuberculosis* parental strain and two strains lacking functioning ESX-1 secretion apparatus due to selective deletion of the EspA component of the secretion apparatus (Δ Rv3616c) or the entire region of deletion 1 (RD1).

Fig. S2. CID-MS spectra of substance A. The ion detected at m/z 136 (adenine) that arises from collision induced dissociation of either m/z 408 or m/z 268 indicates that both the C₂₀H₃₂ diterpene fragment, lost from m/z 408, and the C₅H₈O₄ fragment, lost from m/z 268, are connected to adenine. The fragmentations leading to m/z 136, 268, and 408 involve hydrogen transfer to the adenine group. The m/z 136 ion arises through sequential

losses of 272 Da and 132 Da. These spectra are consistent with a central adenine core structure separately connected to ribose and diterpene units.

Fig. S3. Low mass ion series of substance A. Enlargement of low-mass ion series detected in the MS2 (QTOF) spectrum of substance A from *M. tuberculosis* that shown in Figure S1. The ion at m/z 136 is removed to simplify the graphical display. Four overlapping low-mass ion series were observed having from 1 to 4 unsaturations as expected for a $C_{20}H_{33}$ hydrocarbon cation undergoing a complex multi-step fragmentation. The ion series with 1, 2, 3 or 4 unsaturation(s) are connected by dashed lines.

Fig. S4. Collisional Mass Spectrometry generates a low mass ion series of geranylgeraniol, tuberculosinol and substance A. The low-mass ion series of geranylgeraniol and tuberculosinol are compared with the the MS3 spectrum of substance A from *M. tuberculosis*. Under nanoelectrospray conditions using methanol at 700 V, the diterpene alcohols yielded ions arising from loss of water from the protonated parent alcohol that are analogous to the m/z 273 ion found in the spectrum of substance A. All three samples produce similar CID spectra, but the relative peak intensities of fragment ions of substance A more closely match those of tuberculosinol than geranylgeraniol, particularly for ions corresponding to m/z 191.2, 189.2 and 163.2.

Fig. S5. Summary of NMR data, with assignments for natural 1-tuberculosinyladenosine from *M. tuberculosis*. Purified substance A was analyzed in CD_3OD at 800 MHz using a Bruker Avance 800 with this summary supported by spectra shown in Figs. S5-S8.

Fig. S6. 1H NMR spectra of *M. tuberculosis* 1-tuberculosinyl adenosine dissolved in CD_3OD .

Fig. S7. COSY NMR spectra of *M. tuberculosis* 1-tuberculosinyl adenosine dissolved in CD_3OD .

Fig. S8. HMQC NMR spectra of *M. tuberculosis* 1-TbAd showing ^{13}C resonances of carbon atoms bonded to at least one hydrogen(s) and the corresponding 1H resonance(s).

Fig. S9. NOESY NMR spectra of *M. tuberculosis* 1-TbAd. Expanded views show correlation of two olefinic protons with nearby terpenoid and adenine protons or ribose resonances. Proton resonances and positions shown in red are based on numbering system in Fig. S4.

Fig. S10. Complementation of Rv1796 and Rv2867c failed to restore TbAd production. Ions chromatograms extracted at m/z 540.3545 within 10ppm mass accuracy corresponding to 1-TbAd. In contrary to Rv3377c-Rv337c, the complementation of tnRv1796 or tnRv2867c mutant strains by Rv1796 or Rv2867c, respectively, does not restore the production of TbAd.

Fig. S11. Synthesis of tuberculosinyl pyrophosphate (TbPP). To a solution of TTBAHPP (58 mg, 64.3 μmol , 2 eq.) in CH_3CN (1 mL), in an oven-dried Schlenk flask under nitrogen atmosphere was added a solution of tuberculosinyl chloride (15) (10 mg, 32.2 μmol) in dry CH_3CN (0.5 mL). The solution was stirred for 3 h after which TLC analysis, using *n*-pentane as an eluent, indicated complete conversion of the starting material. The solvent was removed under reduced pressure after which the residue was dissolved in dry methanol and passed through a pre-washed column DOWEX[®] 50WX2 Na^+ -form (50-100 mesh). This process was repeated twice after which the methanol was evaporated. High Resolution Mass Spectrometry (APCI) analysis detected tuberculosinol PP $[\text{M-OPP}]^+$ at 273.2581 m/z ($\text{C}_{20}\text{H}_{33}$, calculated m/z 273.2577). The compound was used without further purification. For a more detailed procedure see Davisson, V. J. *et al* (16).

Fig. S12. Expression of Rv3377c-Rv3378c in *M. smegmatis* is sufficient for the biosynthesis of 1-TbAd. Collisional experiment performed on the molecule detected, at the same m/z and retention time as *M. tuberculosis* 1-Tbad, in the lipid extract of *M. smegmatis* transformed by Rv3377c-Rv3378c, which also shows the characteristic fragmentation pattern of 1-TbAd.

Fig. S13. Structure of *M. tuberculosis* Rv3378c.

(a) Initial electron density map of Rv3378c. Density modified map (2.0 σ , 2.30-Å resolution) from single-wavelength anomalous dispersion (SAD) phasing of a mercury derivative (Ethylmercury phosphate) dataset is shown superimposed on the model of Rv3378c (yellow). (b) The figures illustrates superposition of Rv3378c (blue/light blue) and Rv2361c (yellow/orange) (rmsd = 2.65 for 406 $\text{C}\alpha$ atoms). (c) The figures illustrate an ordered P-loop in a nonphysiological complex with mellitic acid. Ribbon diagrams of Rv3378c apo (blue) and Rv3378c:mellitic acid complex (yellow) are shown. The P-loop (residues 80-95) of apo and mellitic acid complex are colored in red and green, respectively. Bound mellitic acid is shown in stick representation. Superimposition of the Rv3378c apo and mellitic acid complex is shown in the lower panel.

Fig. S14: Aspartate 34 is required for the terpenyl transferase activity of Rv3378c in vitro. Ion chromatograms of the 1-TbAd in reaction products of enzymatic assays performed using wild type or aspartate 34 mutant Rv3378c protein.

Table S1. Summary of crystallographic data for Rv3378c enzyme.

Dataset S1

XCMS software is used in R environment to list detected features from the HPLC-MS dataset obtained for *M. tuberculosis* and *M. bovis* BCG lipid extracts. Among all detected features, this list shows those features that pass the filters of a minimum fold change intensity of 2 and a corrected t-test p-value < 0.05.

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Fig. S1

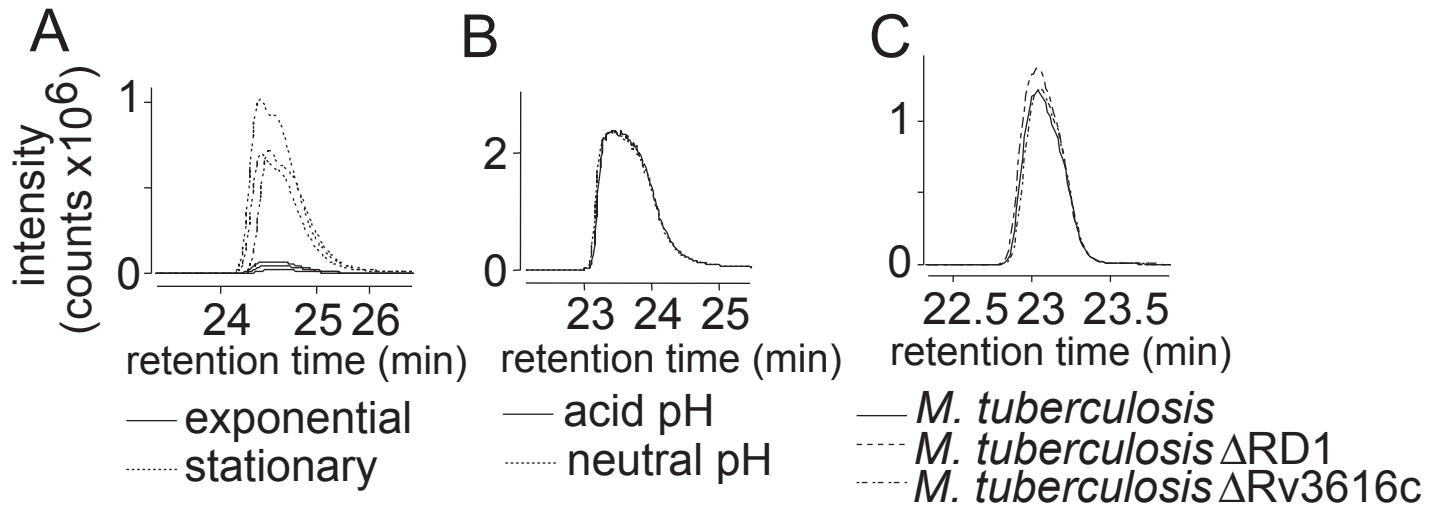
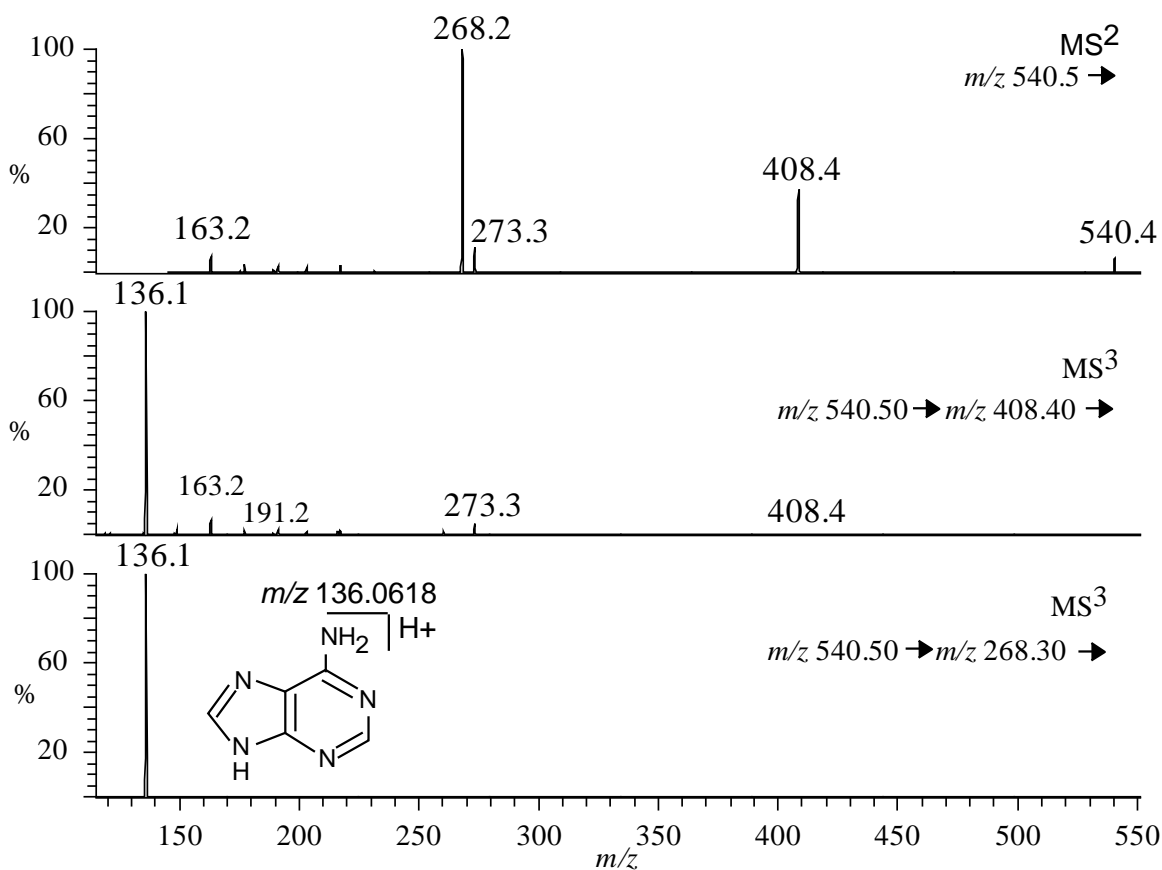


Fig. S2



Fragment ions at m/z 268 and m/z 408 in **1-TbAd** both on pathway to m/z 136.

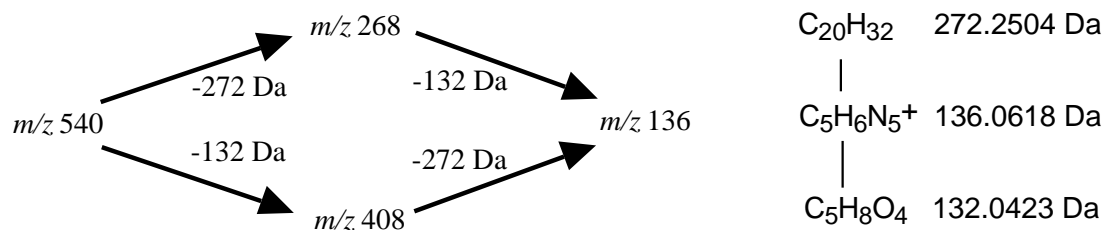


Fig. S3

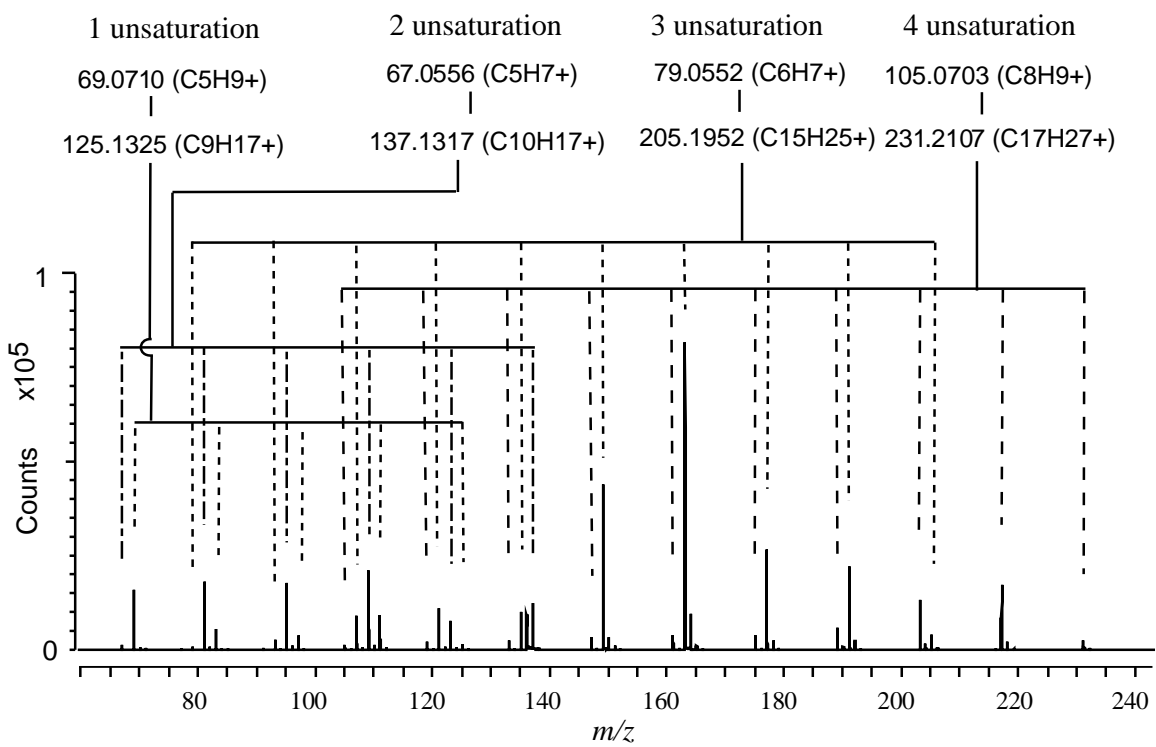


Fig. S4

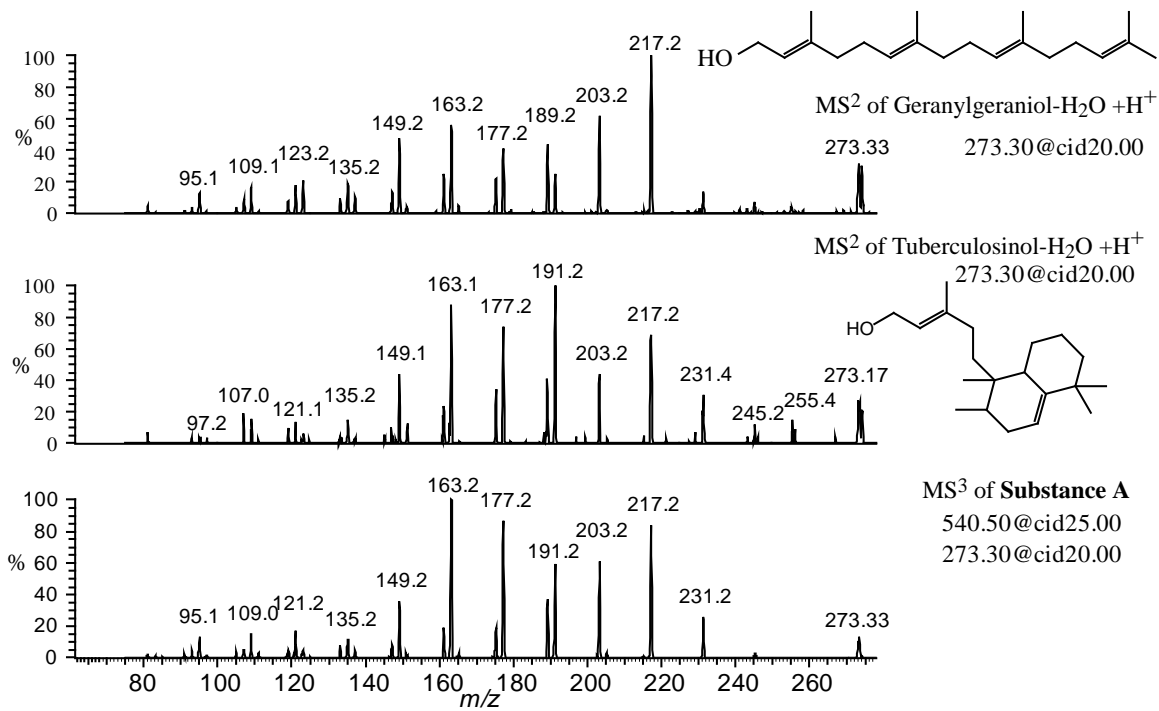
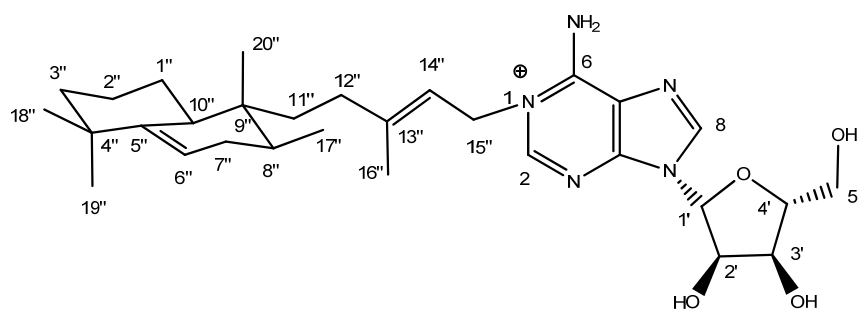


Fig. S5



Atom	Carbon	Hydrogen	COSY	NOESY
2	147.2	8.53		1'', ^a 15'', ^a 16'' ^a
8	144.2	8.66		1'', ^a 2'', ^a 3'' ^a
1'	90.2	6.10 (d, 5.2)	2'	8, ^a 2'
2'	76.4	4.61 (dd, 5.2, 5.1)	1', 3'	8, ^a 1', 3'
3'	71.8	4.34 (dd, 5.1, 4.1)	2', 4'	8, ^a 2', 5'
4'	87.3	4.14 (ddd, 4.1, 3.4, 3.1)	3', 5', 5'	5', 5'
5'	62.4	3.87 (dd, 12.6, 3.1)	4', 5'	4'
		3.78 (dd, 12.6, 3.4)	4', 5'	3', 4'
1α''	28.4	1.77	1'', 2'', 2''	1'', 2'', 10''
1β''		1.04	1'', 2'', 2''	1'', 2β'', 20''
2α''	23.0	1.62	1'', 1'', 3'', 3''	1'', 3'', 19''
2β''		1.62	1'', 1'', 3'', 3''	1'', 3''
3α''	41.9	1.41	3'', 2'', 2''	2'', 18'', 19''
3β''		1.21 (ddd, 13.1, 13.1, 4.8)	3'', 2'', 2''	2'', 18''
4''	--	--		
5''	--	--		
6''	117.2	5.48	7'', 7'', 10''	7'', 7'', 18''
7α''	32.5	1.87	6'', 7'', 8''	6'', 7'', 8'', 17''
7β''		1.77	6'', 7'', 8''	6'', 7'', 16'', 17'', 20''
8''	34.5	1.54	7'', 7'', 17''	7'', 7'', 10'', 17''
9''	--	--		
10''	41.1	2.22 (br d, 12.9)	1'', 1'', 6''	2'', 7'', 10'', 12'', 19''
11''	35.5	1.58	11'', 12'', 12''	8'', 10'', 12'', 16'', 17'', 20''
		1.42	11'', 12'', 12''	8'', 10'', 12'', 16'', 17'', 20''
12''	33.7	2.05	11'', 11'', 12''	10'', 11'', 11'', 14'', 16''
		2.05	11'', 11'', 12''	10'', 11'', 11'', 14'', 16''
13''	--	--		
14''	115.2	5.46	12'', 15'', 16''	2, ^a 12'', 12''
15''	49.5	4.92 ^b	14''	2, ^a 14'', 16''
		4.92 ^b	14''	2, ^a 14'', 16''
16''	16.9	1.89		2, ^a 12'', 15''
17''	15.3	0.85 (d, 6.7)	8''	7'', 7'', 8'', 11'', 11'', 20''
18''	30.1	1.06		3'', 3'', 6'', 19''
19''	29.3	1.01		2'', 3'', 10'', 18''
20''	16.5	0.66		1'', 7'', 11'', 17''

^a) The expected COSY and NOESY cross peaks are seen within the terpene, base and sugar fragments. NOESY cross peaks between the three fragments are seen between H₈ and the three sugar protons H_{1'}, H_{2'} and H_{3'} and between H₂ and the terpene protons H_{14''}, H_{15''}, and H_{16''}. ^b) The allylic methylene peak is the expected doublet.

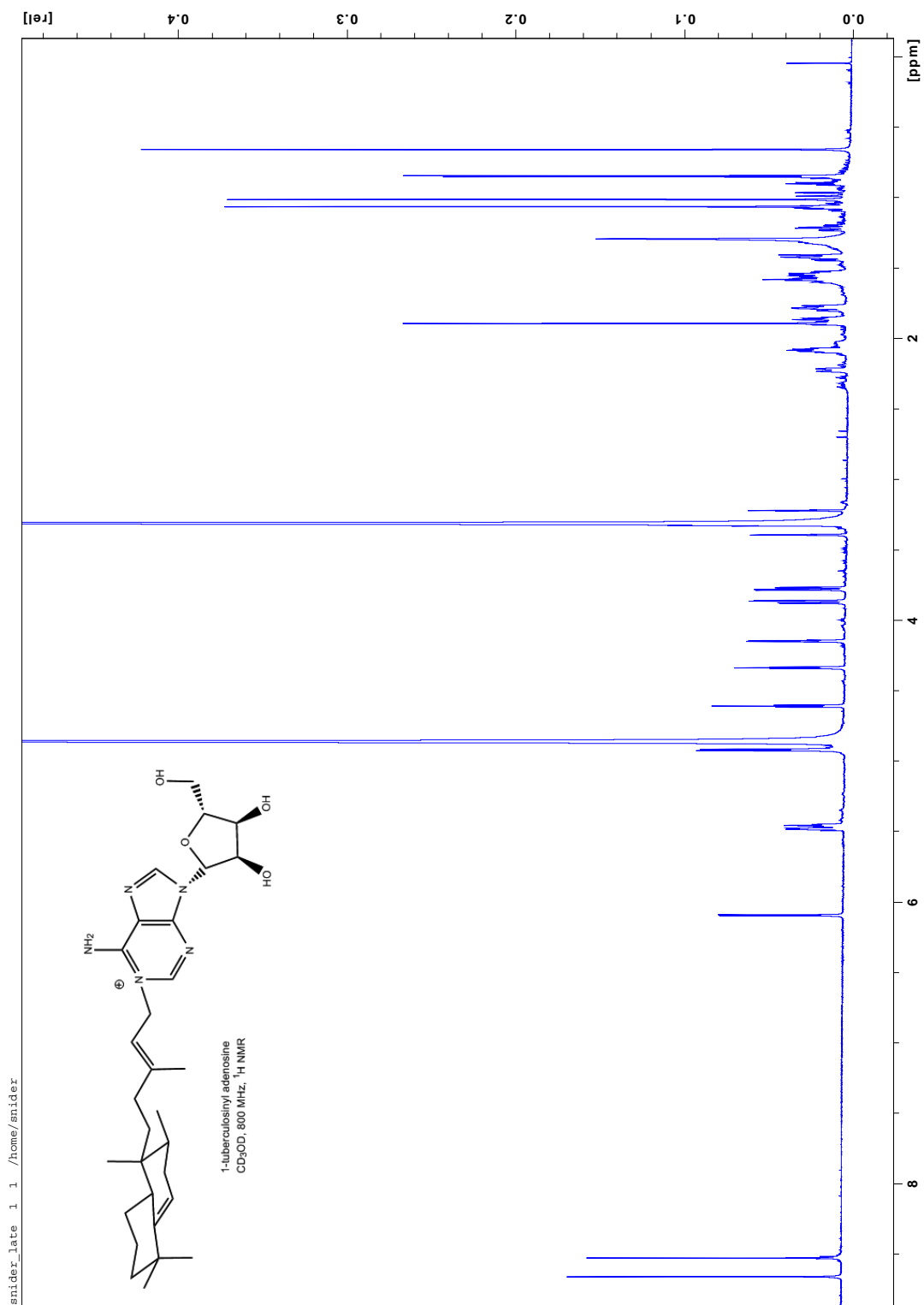


Fig. S6

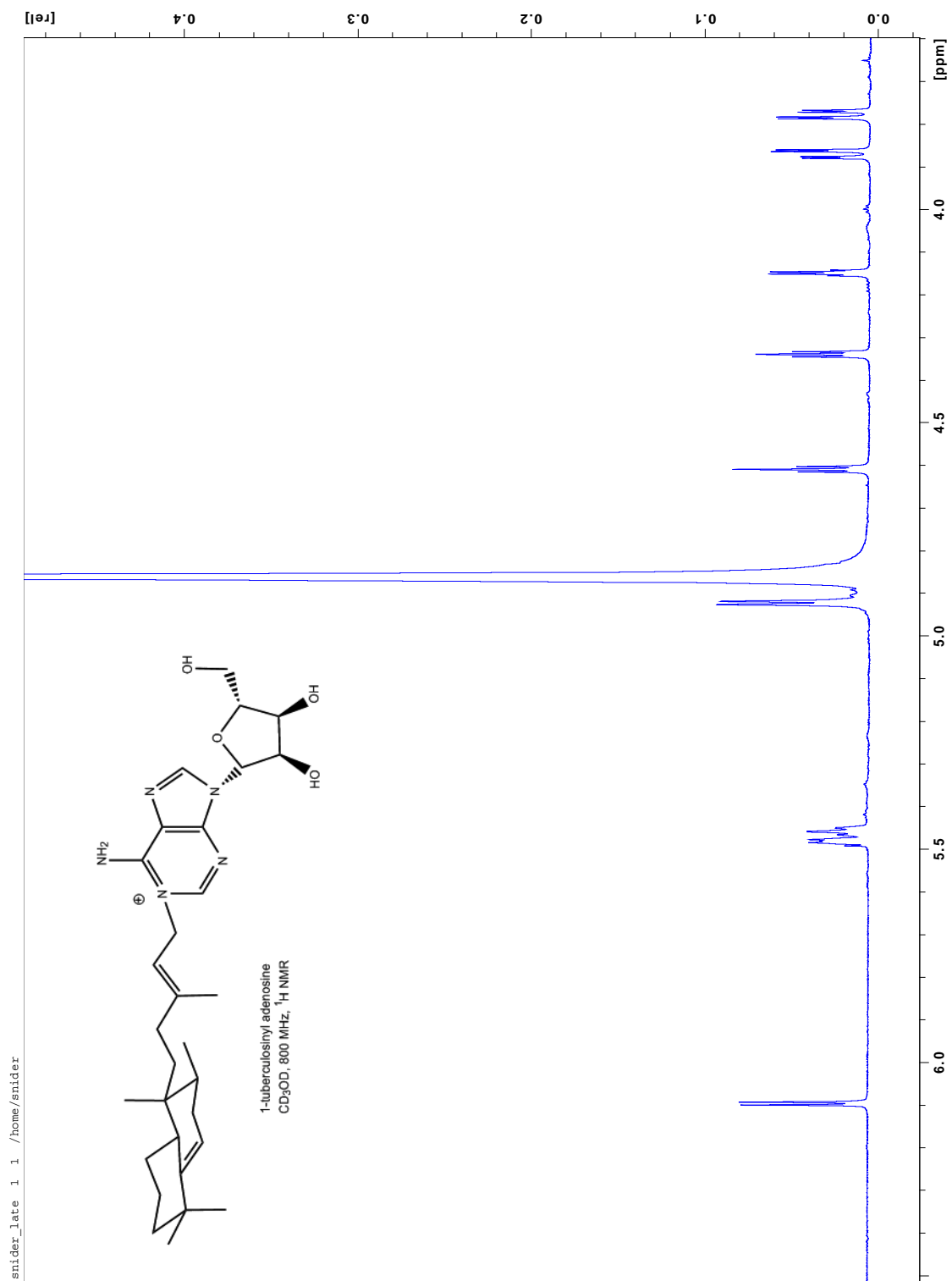


Fig. S6

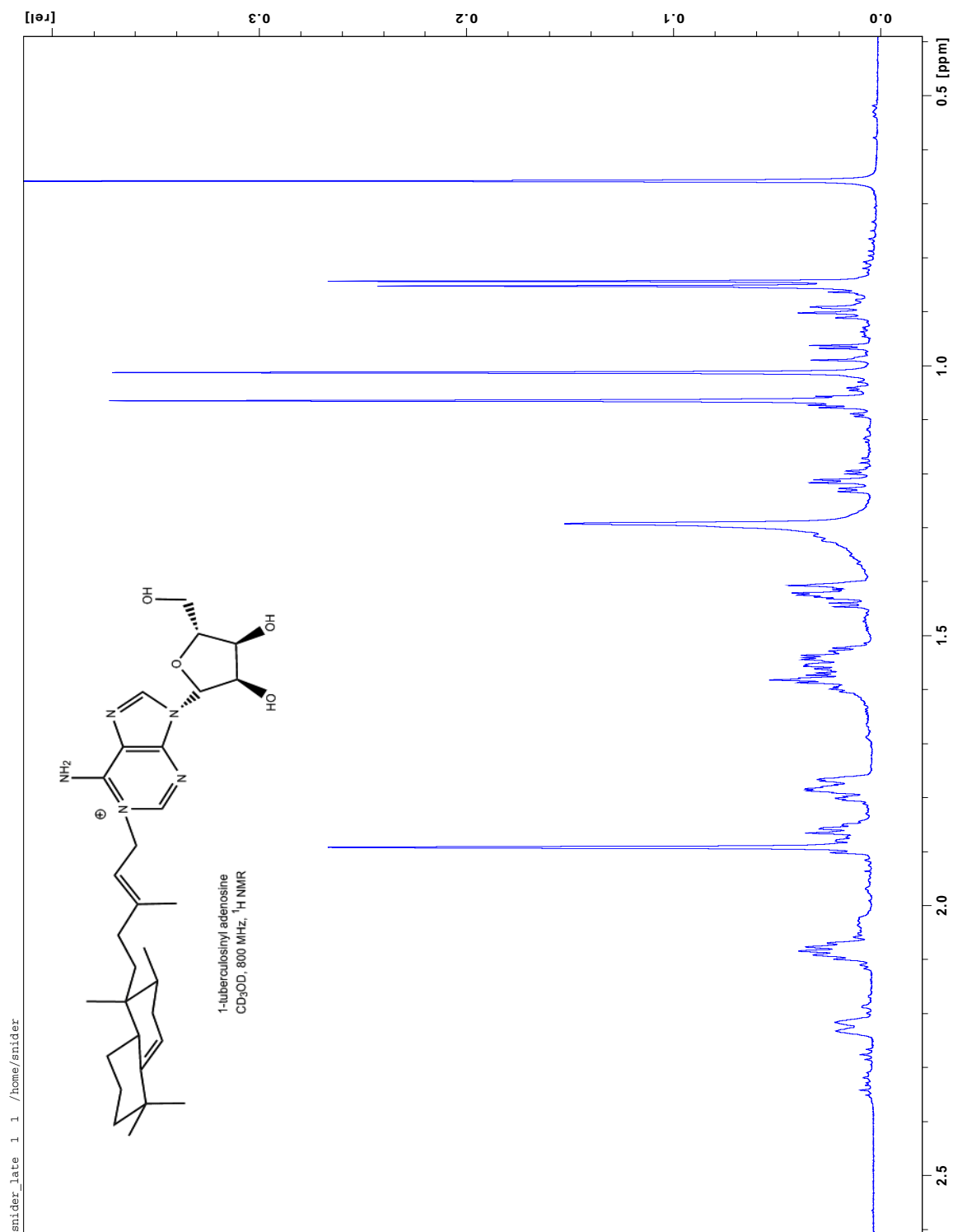


Fig. S7

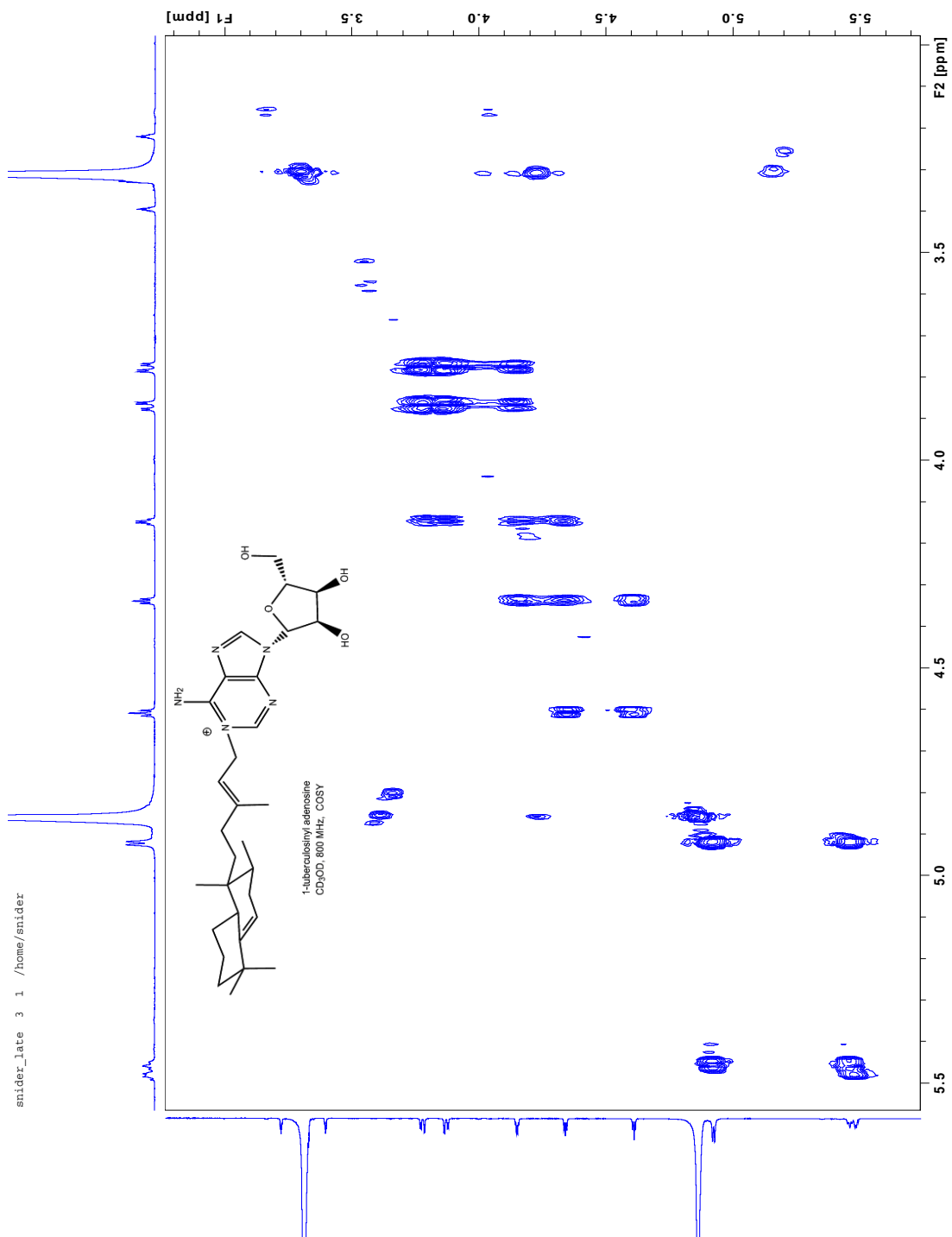


Fig. S7

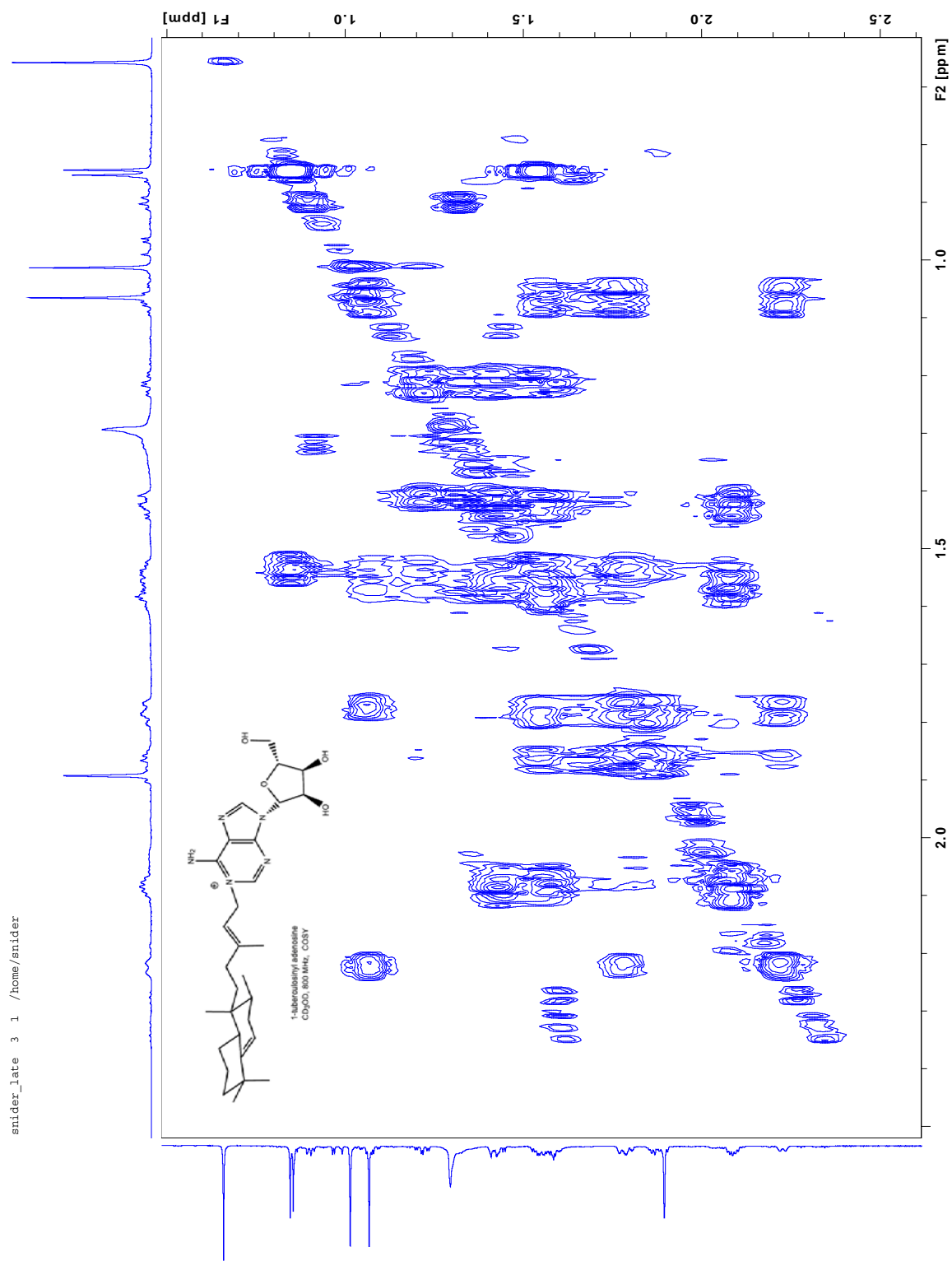
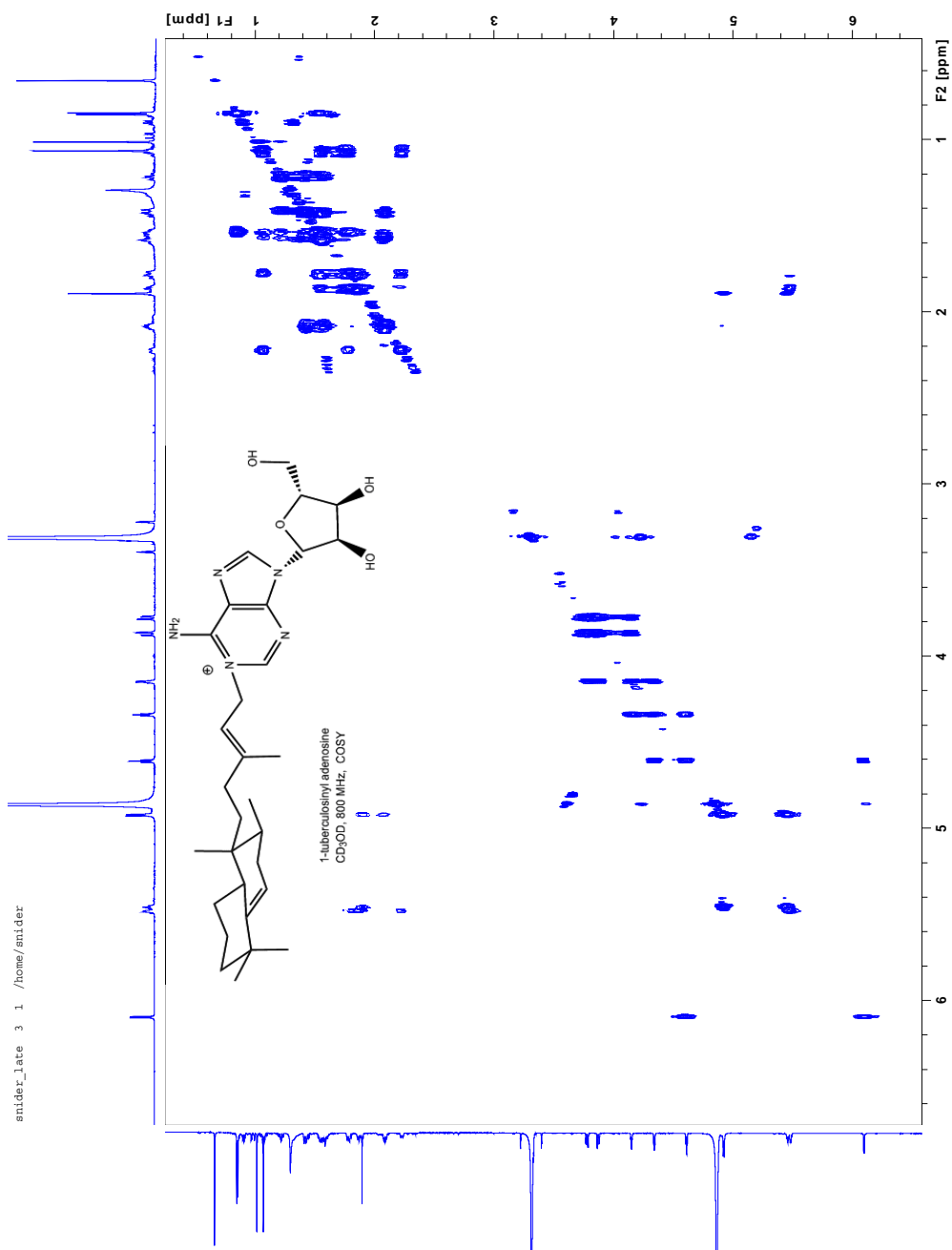
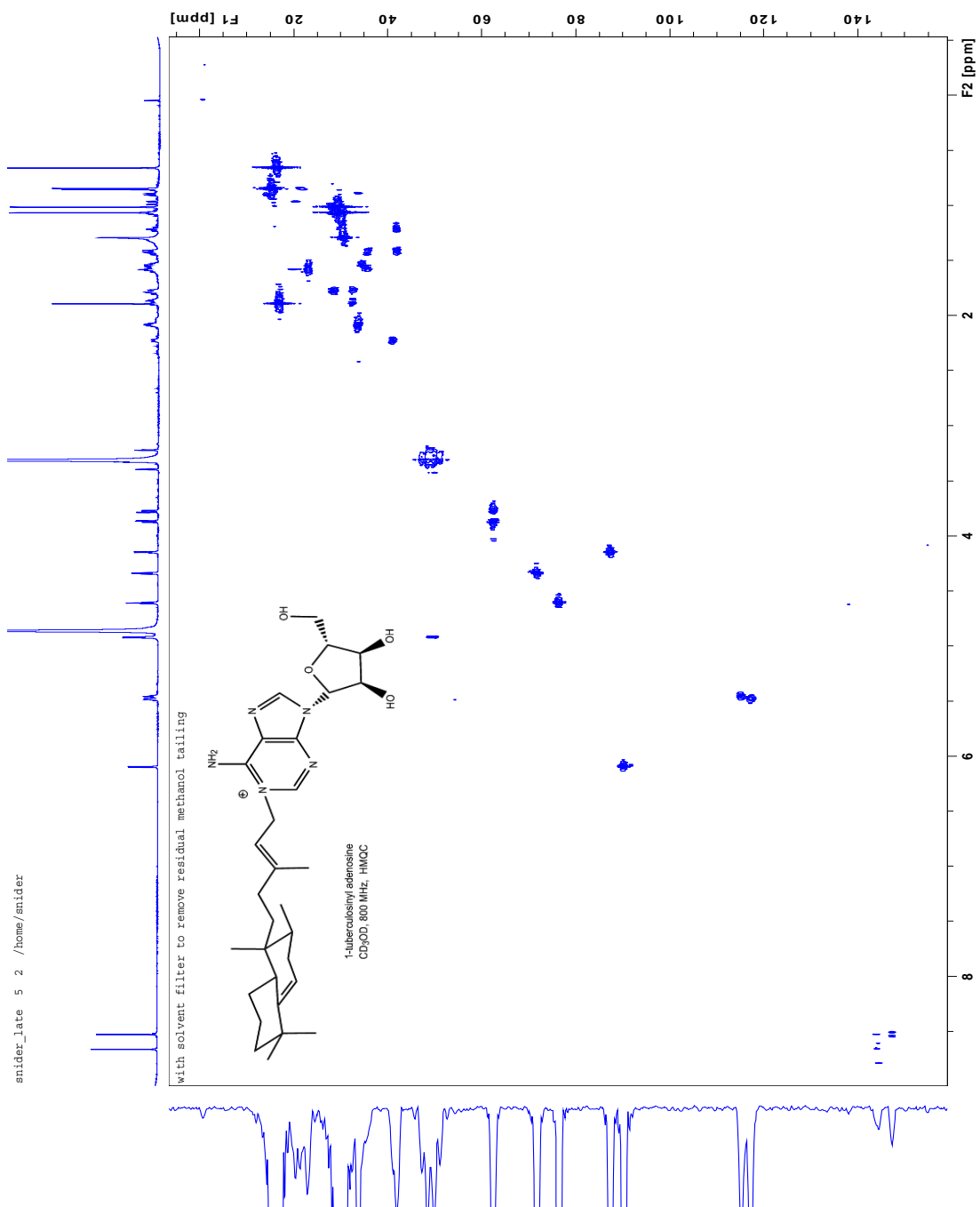


Fig. S7





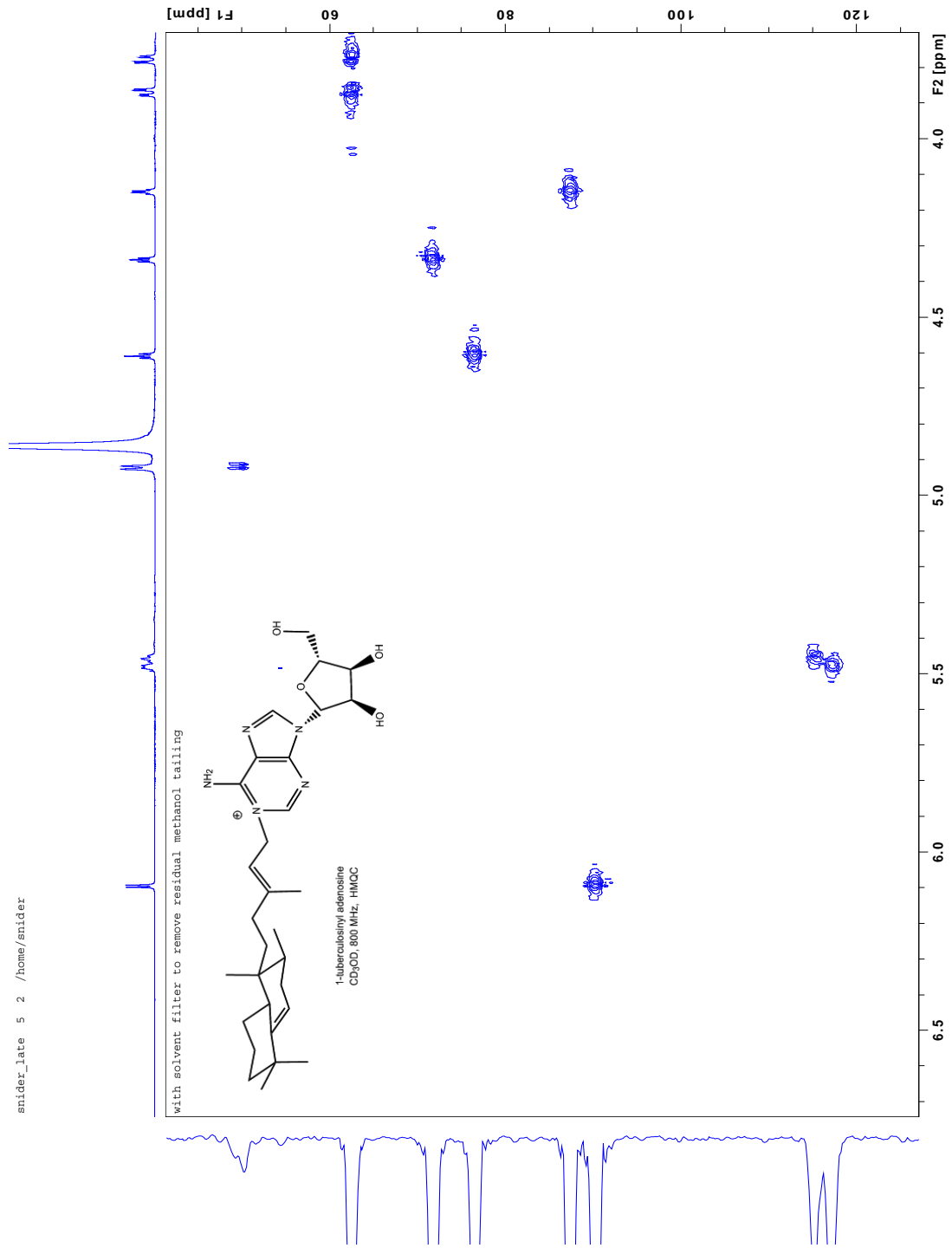


Fig. S8

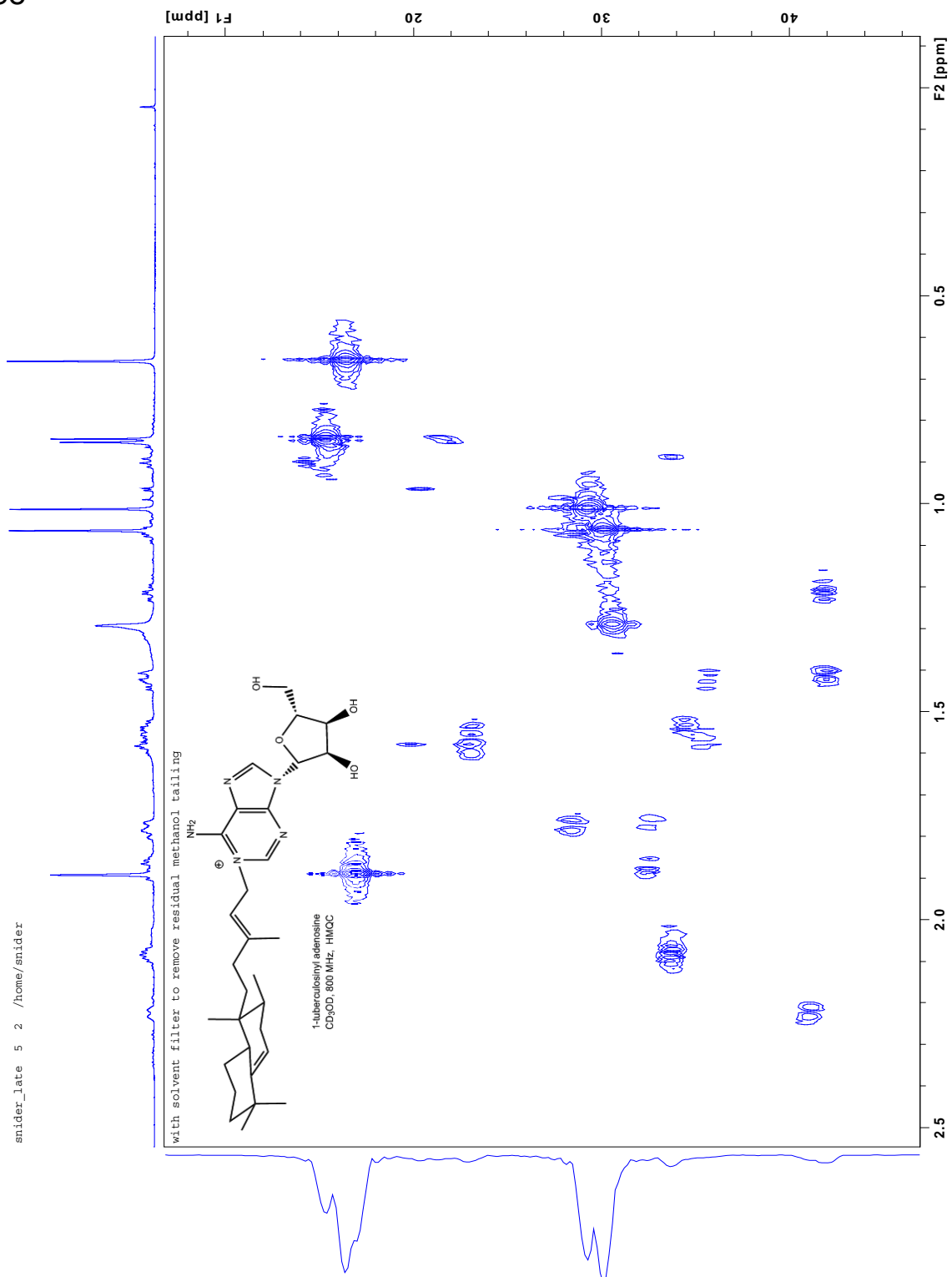


Fig. S9

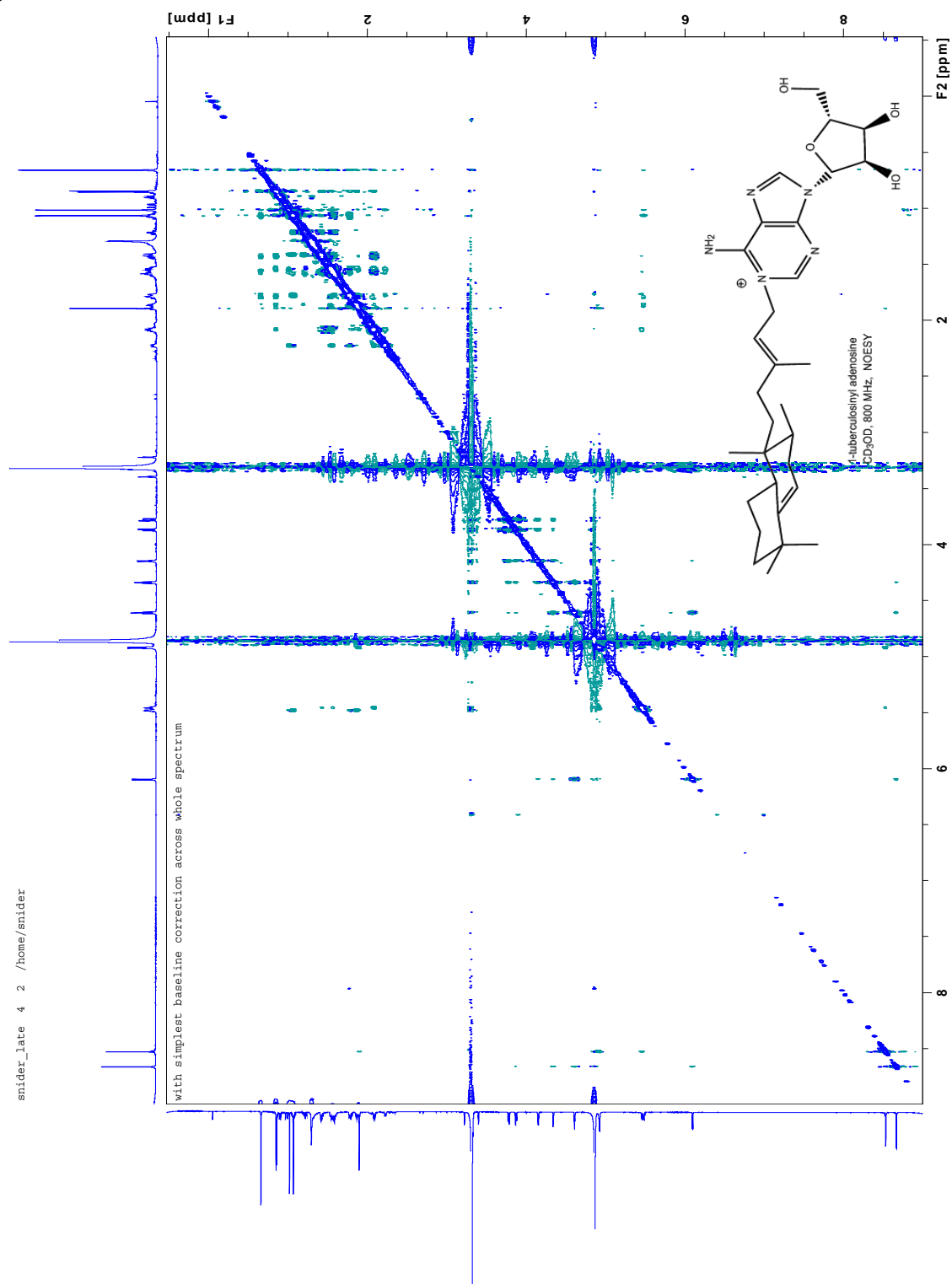


Fig. S9

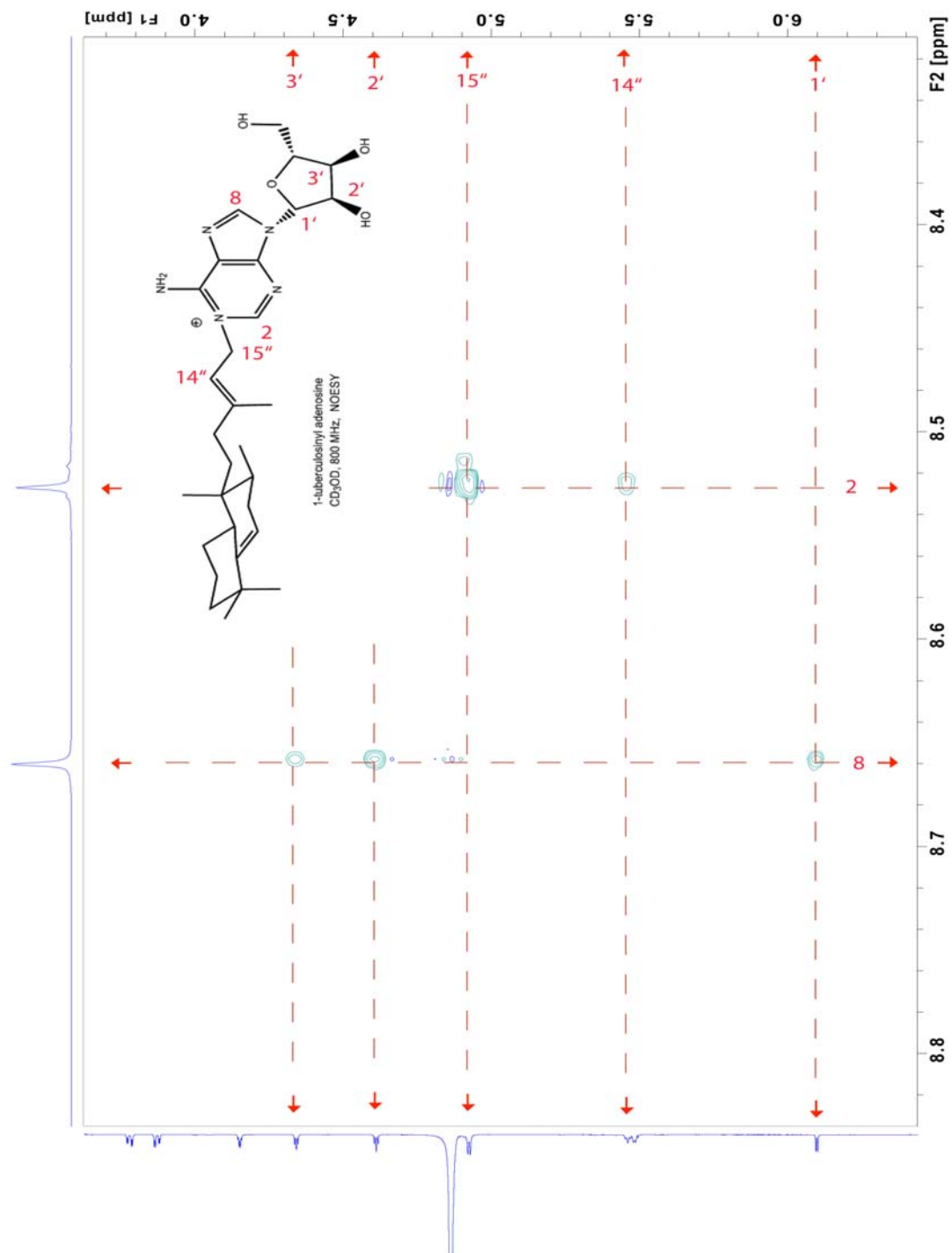


Fig. S9

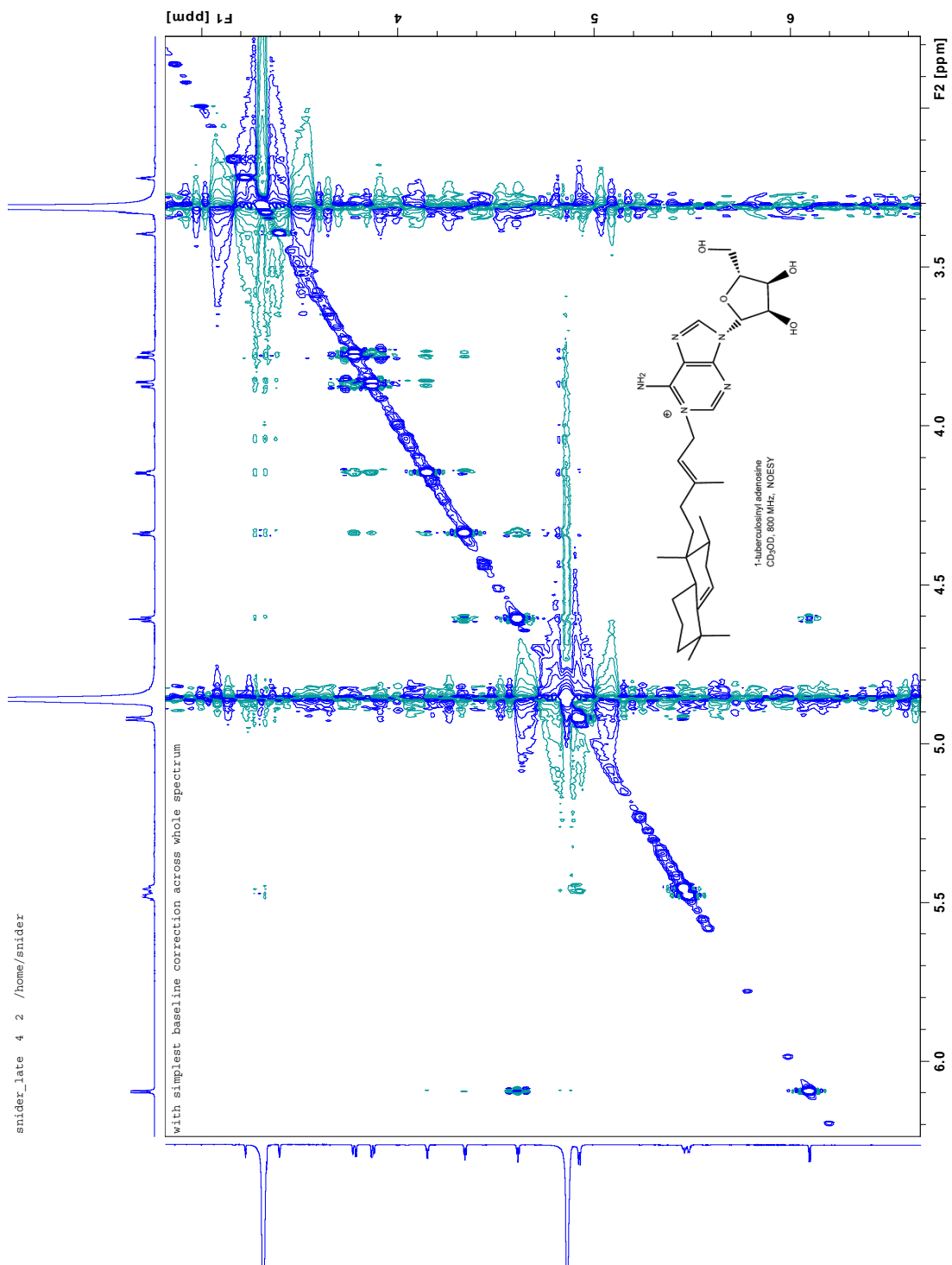


Fig. S9

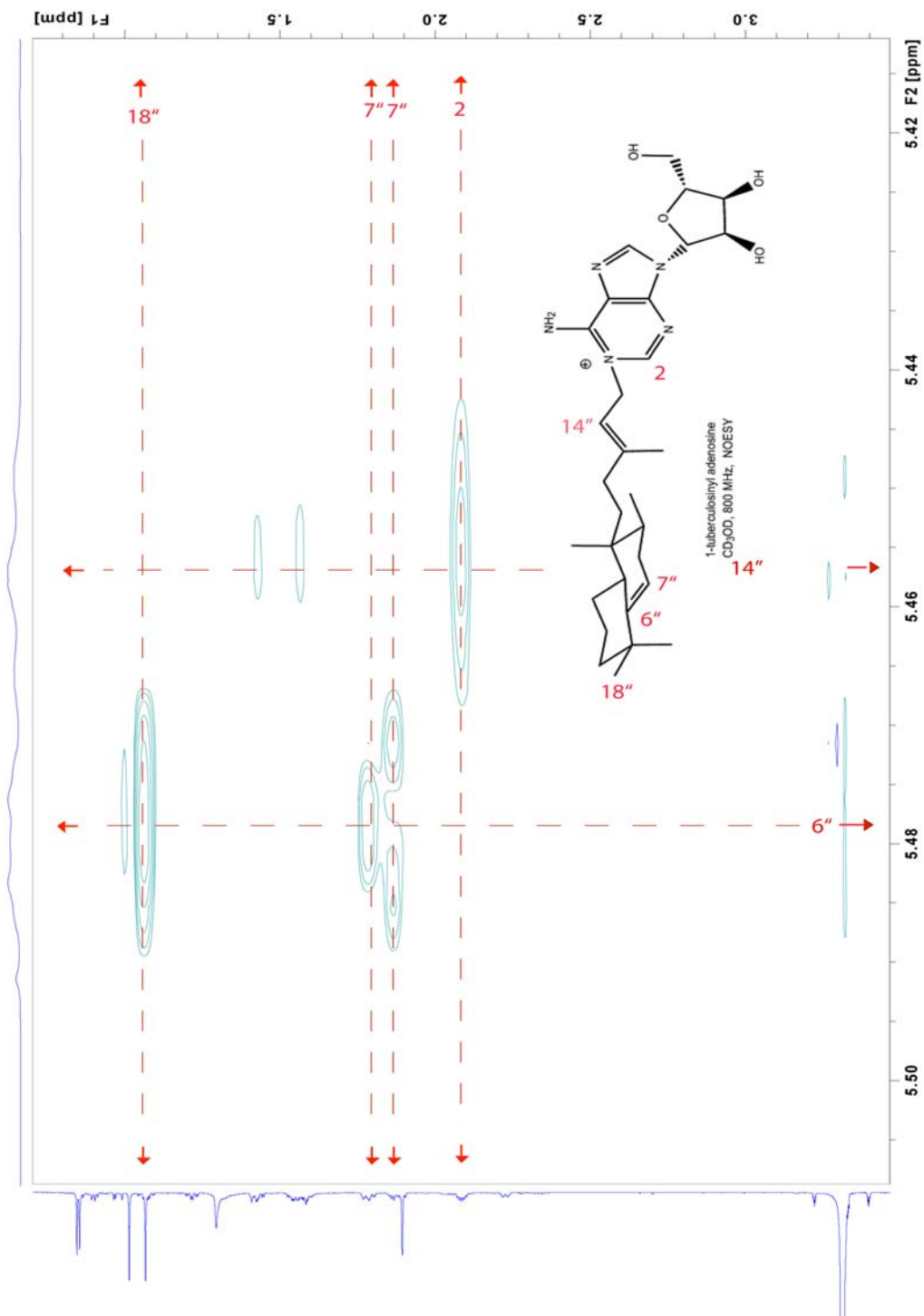


Fig. S9

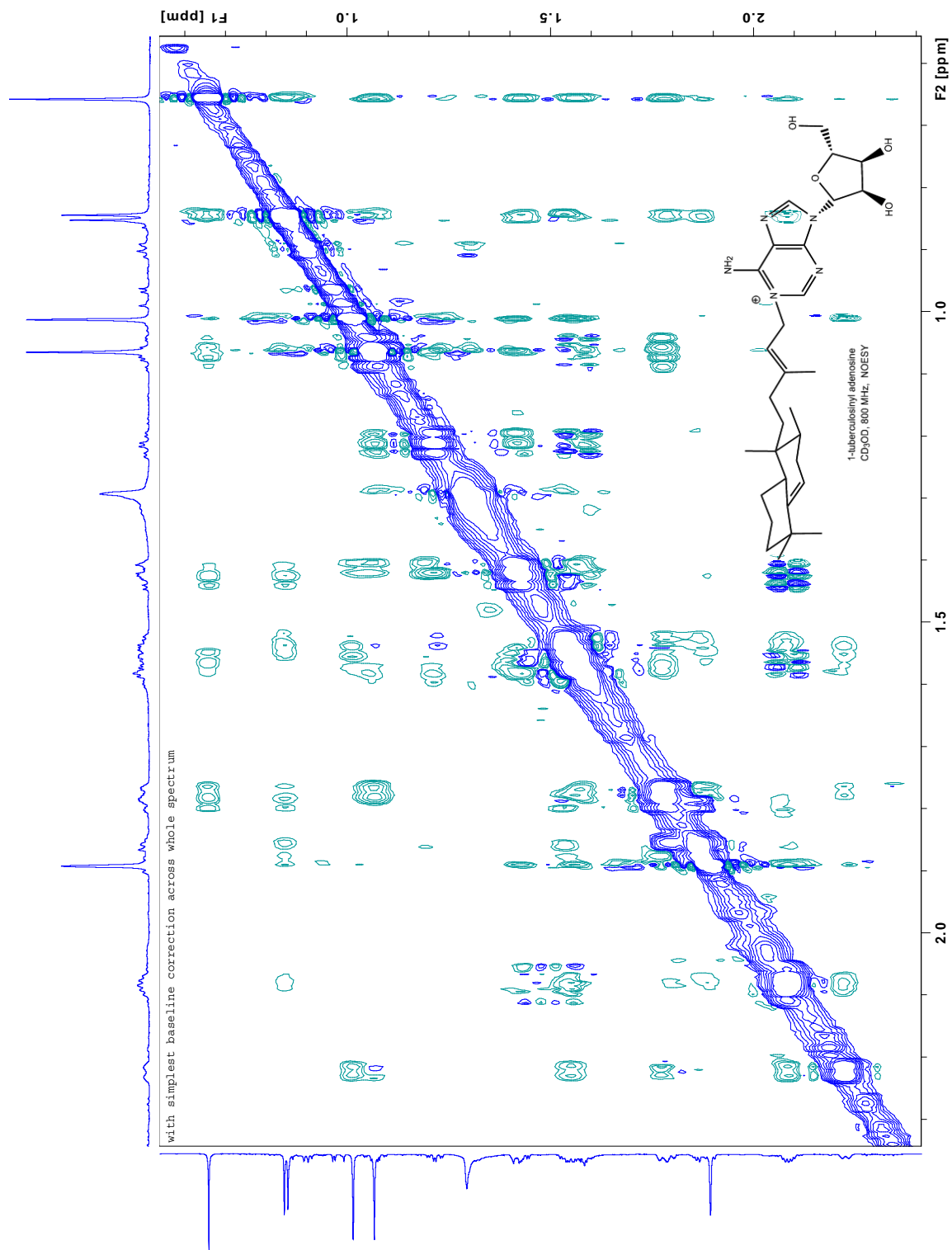


Fig. S10

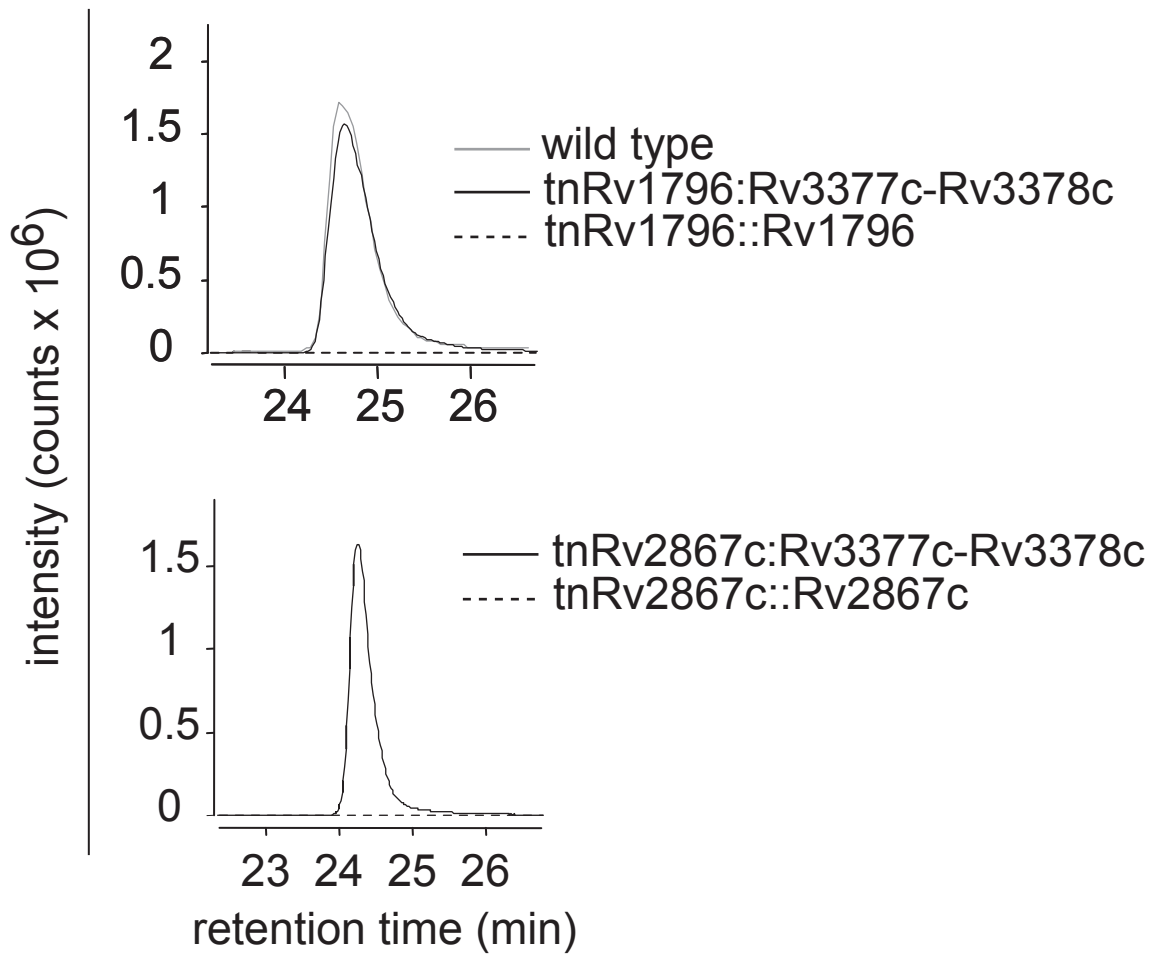


Fig. S11

Sodium (E)-3-methyl-5-((1R*,2S*,8aS*)-1,2,5,5-tetramethyl-1,2,3,5,6,7,8,8a-octahydronaphthalen-1-yl)pent-2-en-1-yl diphosphate

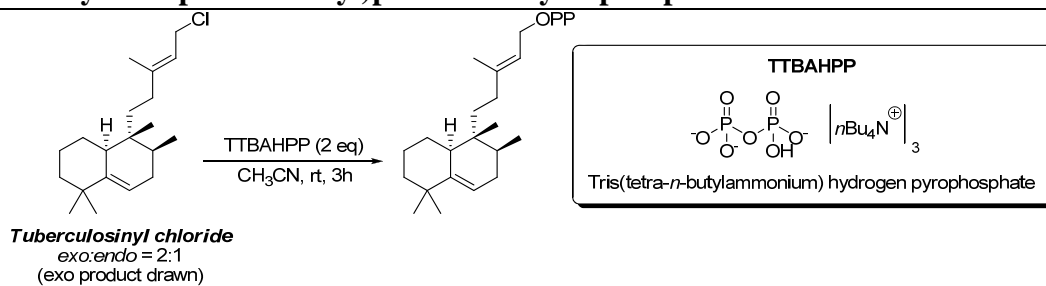


Fig. S12

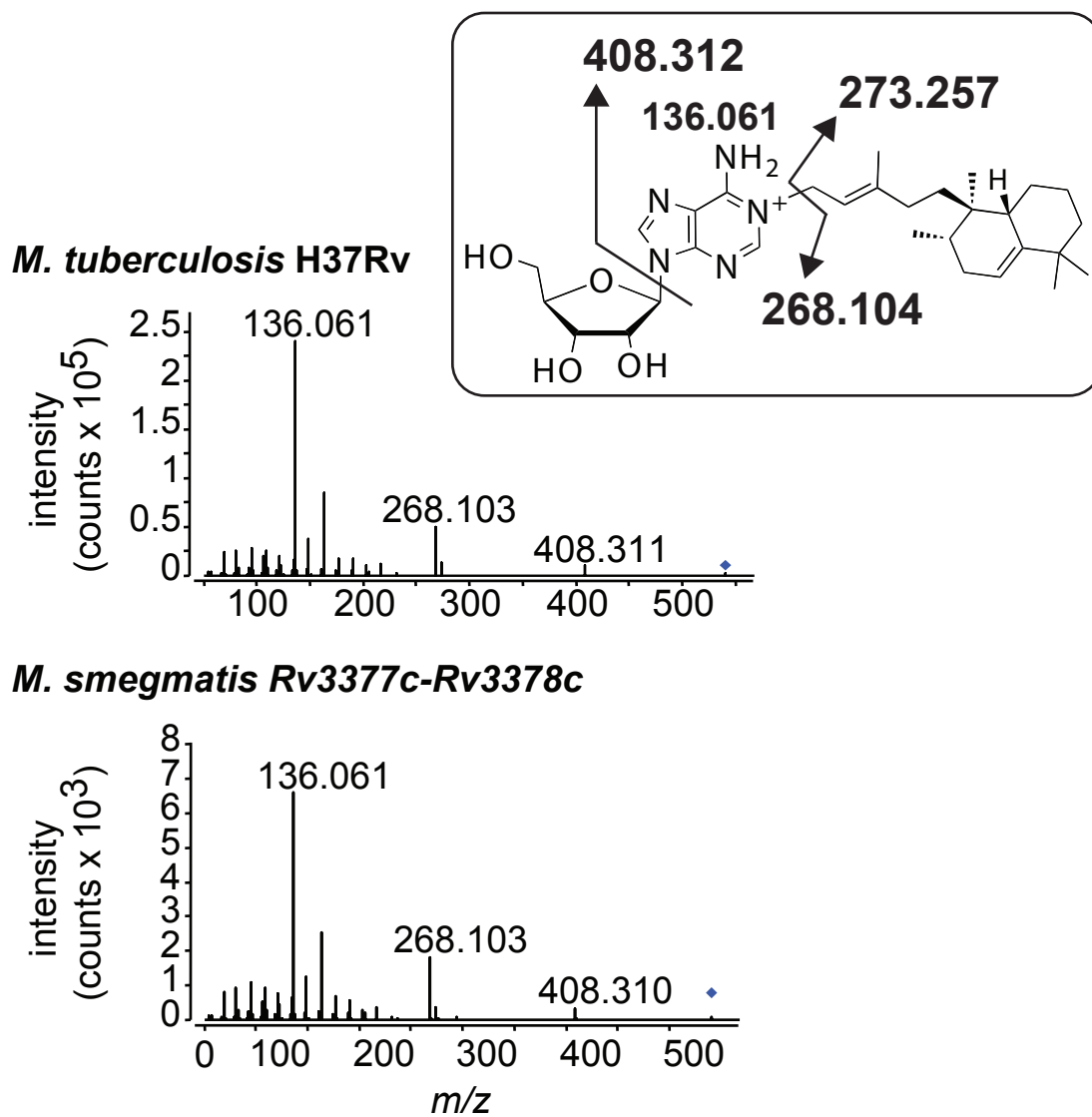


Fig. S13

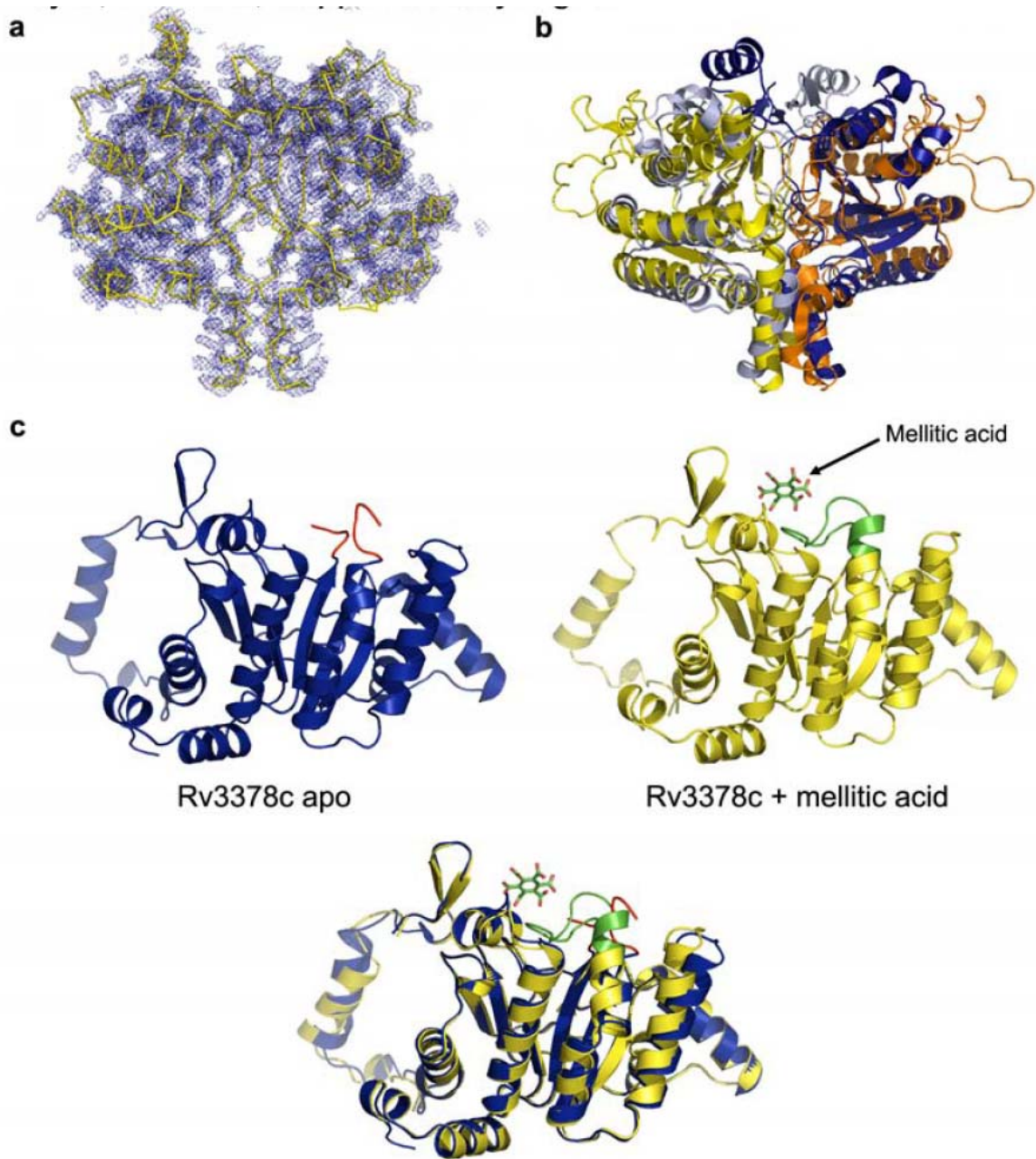


Fig. S14

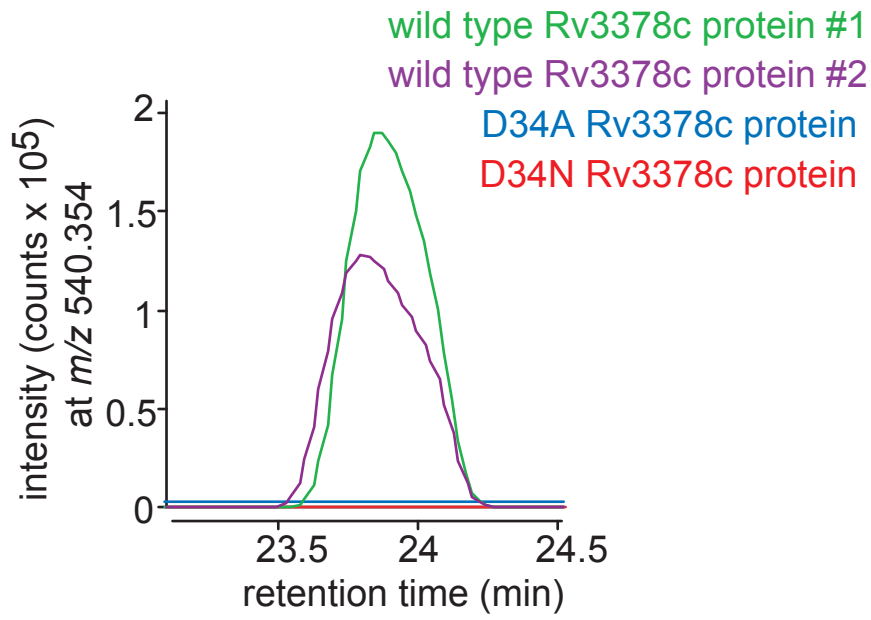


Table S1

Data collection, phasing and refinement statistics			
	Rv3378c Native	Rv3378c Hg-derivative	Rv3378c Mellitic acid
Data collection			
Space group	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁	P2 ₁ 2 ₁ 2 ₁
Cell dimensions			
<i>a</i> , <i>b</i> , <i>c</i> (Å)	77.17, 93.28, 101.26,	57.71, 94.98, 111.16	69.46, 94.23, 94.76
<i>a</i> , <i>b</i> , <i>g</i> (°)	90, 90, 90	90, 90, 90	90, 90, 90
		<i>Peak</i>	
Wavelength (Å)	1.1111	1.0083	1.1111
Resolution (Å)	50-2.20 (2.24-2.20)*	50-2.30 (2.34-2.30)	50-2.36 (2.40-2.36)
<i>R</i> _{sym} or <i>R</i> _{merge}	0.087(0.631)	0.123 (0.566)	0.133 (0.573)
<i>I</i> / <i>σ</i> <i>I</i>	18.4 (2.3)	15.1 (2.1)	15.2 (2.1)
Completeness (%)	100 (100)	100 (100)	100 (100)
Redundancy	4.2 (4.2)	4.1 (4.2)	4.2 (4.1)
Refinement			
Resolution (Å)	37.13-2.21	49.32-2.31	48.15-2.36
No. reflections	37,194	27,535	26,204
<i>R</i> _{work} / <i>R</i> _{free}	0.1767/0.2294	0.1885/0.2287	0.1638/0.2388
No. atoms			
Protein	4,757	4,648	4,754
Ligand/ion	39	51	91
Water	311	251	256
<i>B</i> -factors			
Protein	40.63	26.47	33.99
Ligand/ion	55.29	40.45	49.37
Water	39.39	29.10	36.10
R.m.s deviations			
Bond lengths (Å)	0.009	0.009	0.008
Bond angles (°)	1.171	1.171	1.116

*Values in parentheses are for highest-resolution shell.

p-value < 0.05 and fold change > 2

m/z	retention time (min)	intensity BCG	intensity H37Rv	intensity fold change BCG versus H37Rv	intensity fold change H37Rv versus BCG	p-value	color code
540.357157	25.2	27404.33	5.03E+07	5.45E-04	1834.388293	1.47E-04	substance A
541.395194	25.2	9850.37	1.74E+07	5.65E-04	1768.559902	4.94E-04	
542.361054	25.2	1215.75	2978237.88	4.08E-04	2449.712424	3.91E-04	
543.363113	25.2	489.41	423389.12	0.001155934	865.1010809	2.93E-04	
1631.48613	7.7	307.57	89122.52	0.003451096	289.7633709	0.00254282	
1632.4911	7.7	162.28	87395.26	0.001856852	538.5460932	0.00266305	
1633.49317	7.7	291.71	60765.74	0.004800561	208.3087313	0.00210582	
1634.49034	7.7	226.46	20851.99	0.010860358	92.07802702	0.0033099	
1645.50058	7.6	104.88	12911.24	0.008123147	123.1048818	3.21E-04	
1646.50221	7.7	92.38	14424	0.006404591	156.1376921	0.03389927	
1647.51153	7.7	91.25	18801.28	0.004853403	206.0414247	2.90E-05	
1659.5203	7.6	19.36	369466.72	5.24E-05	19084.02479	0.00265906	
1660.52403	7.6	79.82	450194.87	1.77E-04	5640.126159	0.00337204	
1661.52653	7.6	85.69	287250.59	2.98E-04	3352.206675	0.00245058	
1662.52936	7.6	177.15	131602.69	0.001346098	742.8884561	0.00433405	
1663.52795	7.6	459.02	41504.14	0.011059622	90.41902314	0.00466772	
1673.53152	7.5	19.36	15053.09	0.001286114	777.5356405	0.00122697	
1674.53303	7.6	19.36	24588.21	7.87E-04	1270.052169	0.00362322	
1675.53911	7.6	19.36	14099.56	0.001373093	728.2830579	0.00194387	
1687.55122	7.4	19.36	260826.16	7.42E-05	13472.42562	0.00118941	
1688.55476	7.4	219.92	325231.79	6.76E-04	1478.864087	0.00134432	
1689.55844	7.4	19.36	212177.95	9.12E-05	10959.60486	0.00138349	
1690.55887	7.4	19.36	96244.52	2.01E-04	4971.307851	0.00432984	
1691.55662	7.5	19.36	33876.18	5.71E-04	1749.802686	0.00498608	
1715.5818	7.4	19.36	88214.96	2.19E-04	4556.557851	5.96E-04	
1716.58528	7.4	19.36	115673.72	1.67E-04	5974.882231	0.00100637	
1717.58828	7.4	19.36	80389.41	2.41E-04	4152.345558	8.03E-04	
1718.58893	7.4	19.36	34413.59	5.63E-04	1777.561467	0.00186871	
1719.57881	7.4	193.04	42473.35	0.004544959	220.0235702	0.00120501	
1720.57887	7.4	67.99	35181.04	0.001932576	517.44433	0.0021668	
1731.58113	7.5	19.36	15093.45	0.001282676	779.6203512	0.00506366	
1732.57785	7.5	19.36	25934.34	7.47E-04	1339.583678	8.75E-04	
1733.58264	7.4	19.36	28521.4	6.79E-04	1473.21281	0.00397178	
1734.58544	7.4	149.99	17301.21	0.008669343	115.3490899	0.01424495	
1743.61073	7.3	19.36	22366.01	8.66E-04	1155.269112	0.0012017	
1744.61484	7.3	19.36	31450.83	6.16E-04	1624.526343	2.55E-04	
1745.61445	7.3	19.36	27999.17	6.91E-04	1446.23812	0.0019074	
1746.6103	7.4	19.36	16758.79	0.001155215	865.6399793	3.57E-05	
1747.60901	7.4	106.81	107737.98	9.91E-04	1008.688138	0.00212805	
1748.61335	7.4	251.55	133093.23	0.001890027	529.0925462	0.00162734	
1749.61507	7.4	19.36	87894.67	2.20E-04	4540.013946	0.00225653	
1750.6156	7.4	19.36	37837.19	5.12E-04	1954.40031	0.00443463	
1759.60875	7.4	19.36	48537.32	3.99E-04	2507.092975	8.60E-04	
1760.61091	7.4	19.36	57128.51	3.39E-04	2950.852789	5.17E-04	
1761.61878	7.4	98.92	59586.59	0.001660104	602.3715123	0.0026361	
1762.6222	7.4	96.29	42550.49	0.002262961	441.8993665	0.00159745	
1763.62711	7.4	110.62	24309.35	0.004550522	219.7554692	1.59E-04	
1775.63966	7.3	19.36	202861.42	9.54E-05	10478.37913	1.92E-04	
1776.64336	7.3	19.36	272369.13	7.11E-05	14068.65341	5.62E-04	
1777.6468	7.3	118.7	176830.97	6.71E-04	1489.73016	4.56E-04	
1778.65026	7.3	109.42	85719.11	0.001276495	783.3952659	5.14E-05	
1779.65418	7.3	196.68	27093.16	0.007259423	137.7524914	0.00895295	
1787.63995	7.3	95.77	68552.85	0.001397025	715.8071421	0.0027939	
1788.6454	7.4	19.36	91780.02	2.11E-04	4740.703512	0.00228083	
1789.64916	7.3	19.36	80663.3	2.40E-04	4166.492769	0.00191959	
1790.65176	7.3	19.36	49018.7	3.95E-04	2531.957645	0.00420651	
1791.65777	7.3	213.44	24750.07	0.008623812	115.9579741	4.68E-04	
1801.6556	7.3	234.78	36272.72	0.006472618	154.4966351	3.89E-04	
1802.6593	7.3	140.02	44552.98	0.003142776	318.1901157	0.00165269	
1803.67026	7.3	177.33	208510.61	8.50E-04	1175.833813	7.76E-04	
1804.67474	7.3	77.81	248364.99	3.13E-04	3191.941781	6.16E-04	
1805.67802	7.3	19.36	182402.77	1.06E-04	9421.630682	0.00128753	
1806.68008	7.3	19.36	85444.47	2.27E-04	4413.454029	0.0018874	

1807.67985	7.3	19.36	31681.66	6.11E-04	1636.44938	1.95E-04
1815.67102	7.3	19.36	15381.71	0.001258637	794.509814	2.83E-04
1816.67418	7.4	105.81	15728.63	0.006727212	148.6497496	0.01272156
1817.68256	7.3	100.14	34264.88	0.002922524	342.1697623	7.86E-04
1818.68893	7.3	19.36	35826.12	5.40E-04	1850.522727	0.00189254
1819.68706	7.3	73.87	21613.11	0.003417834	292.5830513	1.05E-04
1831.6997	7.3	19.36	46801.93	4.14E-04	2417.455062	0.0012416
1832.70318	7.3	19.36	59704.23	3.24E-04	3083.896178	3.78E-04
1833.70844	7.3	19.36	43861.45	4.41E-04	2265.570764	6.20E-04
1834.70961	7.3	19.36	21545.36	8.99E-04	1112.880165	3.16E-05
107.050398	6.2	50238.18	124446.89	0.40371417	2.477137707	0.04784898
109.011852	7.1	59003	141338.84	0.417536534	2.395451757	0.04906664
110.991868	7.2	28845.81	58321.96	0.494559842	2.021852047	0.04723357
114.091817	22.6	1241631.69	3695969.24	0.335908633	2.976703373	0.01609087
117.091342	5.0	156621.76	529432.06	0.295857988	3.380322504	0.04784182
121.050796	2.1	1162542.69	307752.64	3.773584906	0.264723732	0.02818439
135.043558	7.3	704530.47	1877525.86	0.375234522	2.664932093	0.02578206
136.047122	7.3	57005.41	150872.77	0.377786173	2.646639503	0.04550516
136.061762	25.2	13206.91	266419.14	0.049571209	20.17270807	3.34E-04
148.060575	13.2	488728.71	1072874.45	0.455580866	2.195235164	0.00395907
148.078371	7.8	302662.28	2975000.95	0.10173975	9.829440755	0.00214421
148.096935	29.1	1.00E+07	362176.36	27.77777778	0.036120859	0.00293852
152.070657	7.2	3285803.92	7461073.16	0.440334654	2.270699452	0.017268
152.217805	7.3	28209.07	87830.74	0.321130379	3.113563829	0.02236847
153.073927	7.3	260042.81	597476.85	0.43516101	2.297609574	0.01820844
167.107483	6.1	232105.69	526486.75	0.440917108	2.268306089	0.00231574
168.122945	7.3	87638.66	178330.01	0.491400491	2.034832687	0.01899361
173.078374	7.3	407360.76	902199.36	0.451467269	2.214742922	0.02680803
189.073414	8.8	209006.09	1018950.25	0.205128205	4.87521799	0.02693747
197.12373	6.2	66762.78	169963.11	0.392772977	2.545776404	6.60E-04
206.138858	6.6	80969.95	215953.16	0.374953131	2.667077848	8.94E-04
208.165322	5.1	49731.14	158599.46	0.313577924	3.189137832	0.038892
209.154074	5.0	135183.08	385362.08	0.350754121	2.850667998	0.02556275
212.053053	13.3	48603.02	121375.9	0.400480577	2.497291321	0.02813928
217.194885	25.1	8187.12	23246.44	0.352236703	2.83939163	0.01540274
229.143721	6.0	53592.38	153863.42	0.348310693	2.870994347	0.01084144
241.159902	5.1	35214.67	149562.26	0.235460325	4.24715779	0.03860428
247.150771	23.3	1154403.63	228305.44	5.050505051	0.197769163	9.23E-04
252.074668	7.7	677100.26	1713263.45	0.395256917	2.53029507	0.0066647
259.068097	6.1	261226.92	538751.34	0.484966052	2.062388287	0.03962621
263.093246	23.0	3.13E+07	320674.1	100	0.010237616	0.01537947
267.209338	4.9	40638.38	196805.67	0.206483585	4.84285225	0.00321367
273.256787	5.0	15958.92	73597.19	0.216825672	4.611664824	0.00576222
273.257888	25.1	6421.48	234263.63	0.027411529	36.48125199	6.18E-04
274.261824	25.2	13058.89	54864.95	0.238038562	4.20134866	0.00184422
276.261926	4.5	17943.4	39203.61	0.457665904	2.184848468	0.01865901
294.212976	5.3	248261.74	691781.77	0.358808755	2.786501738	0.04624054
295.126764	13.1	72936.66	164216.49	0.444247001	2.251494516	0.04076379
299.211404	4.7	24268.42	99583.06	0.243724104	4.103401045	0.04966019
307.12078	8.0	153218.13	325270.25	0.471031559	2.122922725	0.02207135
308.279819	4.8	106482.04	254574.85	0.418235048	2.390777356	0.04794608
312.253488	4.9	152519.25	379182.09	0.402252615	2.486126112	0.04379145
316.25702	4.0	29351.03	122162.96	0.240269101	4.162135366	0.00199808
320.316074	4.4	68083.93	158893	0.428449015	2.333781261	0.00743827
326.267891	4.8	55004.34	148979.04	0.369276219	2.708496093	0.02677235
327.133594	13.7	24629.34	116941.56	0.210614996	4.748059022	0.04669249
328.13689	13.8	4851.14	19091.79	0.254065041	3.935526495	0.04670077
333.282558	4.0	23220.9	67415.2	0.344471237	2.903212192	0.00391706
334.112375	6.7	446.03	36619.72	0.01218012	82.101473	6.25E-04
336.483138	4.8	23438.86	67054.43	0.349528137	2.860823009	0.01702235
342.137313	7.3	34916.32	84240.52	0.414421881	2.412640278	0.01515983
354.2858	4.4	33497.46	75829.67	0.441696113	2.263743878	0.01737567
354.334655	5.2	54263.65	233634.17	0.232234092	4.305537316	0.04630386
364.34215	4.6	369224.63	874529.48	0.422119038	2.368556724	0.01834679
365.345217	4.6	87101.02	215263.66	0.404694456	2.471425249	0.01059624
369.297261	4.5	45367.43	120367.31	0.376931775	2.653165718	0.02136384
374.234959	6.2	28843.26	72334.6	0.398724083	2.507851054	0.00752957

375.347524	4.5	12484.29	25228.45	0.494804552	2.020815761	0.00914344
376.247355	5.7	28992.64	189187.41	0.153256705	6.525359884	0.0366965
379.331496	24.1	20795.91	8187.49	2.538071066	0.393706743	0.00518149
388.251439	5.2	32647.26	102523.75	0.318471338	3.140347766	0.02368271
390.262624	5.1	45761.15	210163.68	0.217722621	4.592622344	0.00834873
392.373678	4.5	76040.61	153291.83	0.496031746	2.015920572	0.03240109
397.343475	24.1	94843.52	7258.58	12.98701299	0.076532166	0.04549232
398.362253	35.4	7211.16	16967.77	0.424989375	2.352987591	0.04562011
404.269541	4.9	51188.7	175946.01	0.290951411	3.43720411	0.01723218
406.296028	5.0	59645.15	404562.39	0.147427392	6.782821235	0.00136682
406.329257	1.8	759781.32	181679.25	4.184100418	0.239120448	0.03639546
408.312564	22.4	23352.55	185338.72	0.125992188	7.936551683	2.94E-04
408.312671	25.2	9469.24	67425.98	0.140429715	7.120527096	7.91E-04
409.315108	22.4	8938.39	52421.75	0.170502984	5.864786611	0.00416391
415.353282	24.1	22931.87	3029.63	7.575757576	0.132114389	0.0187194
415.35353	28.9	68172.81	23806.7	2.865329513	0.349211071	0.02868341
432.310875	5.0	32482.97	537922.04	0.060386473	16.56012489	4.81E-04
433.315855	5.0	55126.98	202198.82	0.272628135	3.667874061	0.0110292
434.167517	7.3	21974.31	47843.12	0.459347726	2.177229683	0.00135628
434.326708	4.9	46346.31	749774.7	0.061812338	16.17765686	7.55E-04
441.479456	8.4	7847.17	17192.19	0.456412597	2.19087773	0.02751989
443.295536	4.6	89569.11	808672.85	0.110766504	9.028479238	0.00611047
444.299177	4.7	99600.99	360045.83	0.276625173	3.614882041	0.00916435
457.35038	13.3	42936	106408.98	0.403551251	2.478316098	0.0255613
463.390213	23.1	4722.95	22545.9	0.209467951	4.773690172	0.00262452
466.299538	5.8	1314.16	95245.2	0.013797671	72.47610641	0.00258258
477.210143	19.1	700089.22	94002.47	7.462686567	0.134272129	0.00642714
480.309027	29.3	324483.75	67747.38	4.784688995	0.208785124	0.01137034
481.313063	29.2	65737.22	16238.53	4.048582996	0.247021855	0.04748079
488.336813	4.9	35892.48	94974.58	0.377928949	2.646085754	0.01018188
493.27994	13.4	44662.65	128504.74	0.347584289	2.877230527	0.00607139
493.307104	4.9	37271.82	155622.65	0.239520958	4.175343463	0.00243681
494.326122	4.7	28441.15	143203.42	0.198609732	5.035078399	6.51E-04
496.340412	28.8	499609.74	90270.9	5.524861878	0.180682827	0.00248956
497.344013	28.8	148390.5	24920.4	5.952380952	0.167937974	0.00180493
499.191823	19.3	420980.28	109996.44	3.831417625	0.261286443	0.0040644
504.324371	5.0	27684.58	75720.04	0.365630713	2.735098022	0.02863759
511.357169	4.8	24267.86	143892.31	0.168662506	5.929336579	0.00118806
511.358334	4.4	47803.96	294266.72	0.162443145	6.155697561	0.01316769
512.362752	4.4	17828.84	146721.01	0.121521449	8.229419861	0.00479049
524.345603	22.8	102749.27	19306.38	5.319148936	0.187897977	0.00889248
524.360079	25.1	17898.32	208839.26	0.085704491	11.66809287	0.00100316
525.363027	25.1	1855.09	70999.03	0.02612808	38.27255281	0.00113856
530.370985	22.4	12003.28	297083.16	0.04040404	24.75016495	0.00443873
531.374262	22.4	5853.76	91302.51	0.064114894	15.59724177	0.01248906
535.30359	7.1	15740.04	55861.15	0.281769513	3.548983992	0.04645801
535.474672	4.4	3349.72	18834.03	0.17784101	5.622568453	0.00174954
539.465756	6.1	76506.78	250726.49	0.305157156	3.277180009	0.00611163
540.466318	6.1	30433.19	86537.52	0.35161744	2.843524455	0.01835648
541.340103	8.2	14386.74	73472.99	0.195809673	5.106993662	0.01148179
543.346641	5.1	30717.07	113090.35	0.271591526	3.681677647	0.00178516
543.356693	9.7	22614.01	56153.47	0.402738623	2.483127495	0.02809252
544.36604	25.2	668.24	59311.3	0.011266717	88.75748234	1.72E-05
547.470156	22.0	17592.83	53315.5	0.329924117	3.030524367	8.50E-04
547.484056	23.3	10035.98	31350.04	0.320102433	3.123764695	0.00595323
549.487981	21.9	46854.91	220763.58	0.212224109	4.711642387	0.00179137
550.490482	21.9	21280.64	85091.85	0.250062516	3.998556904	6.35E-04
551.361802	5.4	30732.64	80819.66	0.380228137	2.629766268	0.0411237
551.550332	4.9	5778.59	33120.92	0.174459177	5.731661184	0.02775049
552.51228	3.8	4062.26	43015.42	0.094437624	10.58903664	0.01338677
554.525683	3.8	5301.3	47203.6	0.112309075	8.904155584	0.01215211
558.364837	26.7	2771.21	49244	0.05627462	17.76985505	0.0038207
558.508248	4.0	5546.5	26597.89	0.208550574	4.795436762	0.00795043
559.368513	26.7	2005.08	17027.2	0.11775789	8.492030243	0.0015545
562.336438	25.2	1285.03	70299.41	0.018279531	54.70643487	8.26E-05
562.389647	4.5	15157.8	66868.46	0.226705962	4.411488475	2.48E-04
563.339335	25.2	416.8	20640.01	0.020193861	49.52017754	6.56E-05

563.389647	4.5	8572.85	25530.89	0.335795836	2.978109963	0.01443893
563.503668	21.8	18535.9	70039.68	0.26462027	3.77859613	0.00166029
563.506766	3.9	5299.8	27933.68	0.189717321	5.270704555	9.84E-05
564.506188	21.8	11305.68	25844.41	0.437445319	2.285966877	0.01592115
566.527766	3.8	2455.26	26019.82	0.094357426	10.59758233	0.00848491
569.363278	4.7	22089.11	66669.75	0.331345262	3.018218027	0.02096235
573.488104	22.0	39715.84	170049.22	0.233535731	4.281647323	0.00284254
574.489971	22.0	17758.03	56247.7	0.315756236	3.16745157	0.02546501
575.504089	21.8	254945.27	810305.2	0.31466331	3.178349612	0.00277684
576.458915	5.0	13435.5	176581.51	0.076086129	13.14290573	0.03378304
576.506906	21.8	102043.92	329446.84	0.309789343	3.228480835	0.00382708
577.468536	5.0	16558.67	83246.96	0.198925801	5.027394108	0.00184372
577.520332	21.7	1181695.05	4101150.19	0.288101412	3.4705656	0.00317717
577.739243	21.7	11189.85	33109.74	0.337952011	2.958908296	0.02991831
578.52354	21.7	471538.18	1601216.15	0.294464075	3.395729589	0.0029136
579.528541	21.7	142029.21	443556.72	0.320204931	3.12299646	0.00550177
579.534366	24.6	613557.09	1327978.99	0.462107209	2.16439352	0.00948149
579.534502	19.4	87125.4	283507.91	0.307314075	3.25402133	0.01448683
580.529826	3.9	7762.9	39173.64	0.198176774	5.046263639	0.00444769
580.532741	21.7	39375.95	102321.64	0.384763371	2.598582129	0.00691976
580.53811	24.6	220975.04	514439.22	0.429553265	2.328042208	0.00825203
581.541526	24.6	42845.92	111546.97	0.384172109	2.603444389	0.0036687
582.365531	23.3	3085.13	42547.93	0.072511058	13.79129243	0.01997887
582.540337	3.8	860.42	22744.69	0.037830067	26.43440413	0.00760596
582.542921	24.6	7485.48	15226.43	0.491642085	2.03412874	0.02843356
583.525006	4.0	6726.29	17955.01	0.374672162	2.669377919	0.01166848
583.544942	3.8	466.18	10429.73	0.044696733	22.37275301	0.0276693
584.526158	4.0	28555.07	193037.99	0.147928994	6.760200203	0.01622322
585.528695	4.0	14104.68	69287.15	0.203583062	4.912351787	0.02944653
586.452452	7.8	61400.54	125113.55	0.490677134	2.037662047	0.03721632
586.540808	4.0	24011.65	159015.35	0.151011779	6.622424948	0.01531159
590.299394	6.1	71183.58	264684.18	0.268961807	3.718331952	0.01038038
591.535191	21.6	59942.26	188076.29	0.318674315	3.137624274	0.006667
592.538292	21.6	28618.34	76176.28	0.3756574	2.661799392	0.00442902
595.532152	4.0	6390.51	31568.62	0.20242915	4.939921853	0.04223423
601.518946	21.8	16101.12	39963.58	0.402900886	2.482037274	0.00385263
602.521215	3.9	10915.85	24695.42	0.442086649	2.262345122	0.04509095
603.535184	21.6	31935.32	128683.64	0.248138958	4.029508394	0.00237407
604.537854	21.6	19273.68	48773.13	0.395100751	2.530556178	0.00726191
605.550914	21.5	62807.13	237681.7	0.264270613	3.784310794	0.00401743
606.554115	21.5	25487	101242.42	0.251762336	3.972316083	0.00718687
606.554166	24.5	22886.31	47068.46	0.486144871	2.056620748	0.0203139
608.527797	4.0	16728.43	65479.24	0.255493102	3.914248976	0.00837645
610.185152	3.8	1886.86	40944.46	0.046082949	21.69978695	0.03385631
610.540268	4.0	68861.9	418575.42	0.164527805	6.078476197	0.03159604
611.186737	3.7	1234.8	22732.29	0.054318305	18.40969388	0.0263495
611.532333	4.9	19224.59	54598.69	0.352112676	2.840044443	0.04567976
611.544222	4.0	22081.71	170390.72	0.129600829	7.716373415	0.01788104
613.561203	4.0	133050.19	697189.08	0.190839695	5.24004573	0.03978859
614.56992	4.0	28985.74	286128.02	0.101306858	9.871337423	0.01635949
615.575409	3.9	9060.09	90900.55	0.099671085	10.03307362	0.01041859
618.628892	25.5	7056.55	19477.11	0.362318841	2.760146247	0.03865412
622.400345	7.6	27303.97	12506.61	2.183406114	0.458050972	0.02284852
623.373514	5.9	2778.32	32320.95	0.085962348	11.63327119	3.38E-06
625.541121	5.7	145075.09	441872.62	0.328299409	3.045820065	0.01596361
625.552228	24.3	1574617.91	27215.88	58.82352941	0.017284117	0.03469304
625.560372	4.0	1829.36	8010.87	0.22836264	4.379056063	0.00951982
626.554901	24.3	640874.75	12559.36	50	0.019597215	0.03169275
626.572562	3.9	8419.32	71111.35	0.118399242	8.44621062	0.04430154
627.557932	24.3	147325.52	4294.43	34.48275862	0.029149261	0.0334761
627.574395	4.0	3941.03	26256.25	0.150105074	6.66228118	0.04720757
628.561114	24.3	25376.73	6635.06	3.831417625	0.261462371	0.01000925
628.588107	3.9	16097.26	105603.43	0.152439024	6.560335734	0.02936371
629.58837	3.9	8544.81	41757.94	0.204624514	4.886936047	0.0331409
636.558316	4.0	14622.31	102685.12	0.14240957	7.022496446	0.04345123
637.552379	24.4	60277.83	6289.29	9.615384615	0.104338361	0.03311381
637.561247	4.0	8843.69	43854.39	0.201653559	4.958833926	0.03171687

638.55643	24.4	24243.65	3251.27	7.462686567	0.134108107	0.02723226
638.571952	4.0	32553.56	214628.54	0.15167602	6.593089665	0.02638768
639.566502	24.3	430036.3	10671.24	40	0.024814742	0.03823159
639.578037	4.0	24179.48	92059.73	0.262674022	3.807349455	0.03489999
640.370955	27.7	9503.54	27846.32	0.341296928	2.930099731	0.0351207
640.386986	25.2	1463.51	14077.59	0.103960911	9.619059658	0.02853652
640.577204	24.4	188598.75	11237.09	16.66666667	0.059581996	0.04166126
640.588655	3.9	15812.01	84504.66	0.187125749	5.344333832	3.42E-04
641.590615	4.0	7214.41	47705.7	0.151217299	6.612557368	0.0209651
649.552134	24.4	869504.25	14574.91	58.82352941	0.016762322	0.04999309
650.555293	24.4	379809.11	4002.03	90.90909091	0.010536951	0.04638059
651.389038	5.0	11017.2	40166.93	0.274273176	3.645838326	0.0176925
651.567546	24.2	3125993.23	79417.95	40	0.025405669	0.03315452
652.499057	6.8	151493.99	54667.08	2.770083102	0.360853127	0.03854039
652.570422	24.2	1317567.24	33726.8	38.46153846	0.025597783	0.03092266
654.386144	25.5	12785.44	309222.2	0.041347943	24.18549538	9.19E-04
654.586186	24.1	4171364.84	75423.42	55.55555556	0.018081233	0.03209675
654.895005	24.1	66680.79	1288.2	52.63157895	0.019318907	0.02339724
655.387642	25.5	19542.25	131313.04	0.148831671	6.719443258	0.00274603
655.496705	6.4	30571.27	66401.49	0.460405157	2.172022621	0.04956493
655.589354	24.1	951030.52	20323.94	47.61904762	0.021370439	0.02875739
656.3915	25.5	8485.73	29665.89	0.28604119	3.495973829	0.00741188
656.591695	24.1	177270.53	8757.03	20.40816327	0.049399243	0.0283272
657.593748	24.1	25600.03	1573.51	16.39344262	0.061465162	0.02951771
663.405693	5.0	15043.49	62760.02	0.239693193	4.171905588	0.03208047
665.308246	7.9	6559.34	17050.48	0.384763371	2.599420064	0.00229602
665.58243	24.2	972994.02	16994.49	58.82352941	0.017466181	0.03428772
666.586228	24.2	440863.45	11443.73	38.46153846	0.025957539	0.03310076
667.598416	24.1	5131137.2	29710.52	166.6666667	0.005790241	0.03533949
667.832658	24.1	69076.02	460.68	142.8571429	0.006669174	0.0313733
668.603001	24.1	2229725.4	30101.65	71.42857143	0.01350016	0.03367877
669.579955	24.1	484303.07	24486.11	19.60784314	0.050559477	0.02977701
669.604745	24.1	543143.6	25564.49	21.27659574	0.047067645	0.03491764
674.356396	6.1	2729.07	74271.98	0.036744442	27.21512457	8.23E-06
675.567408	24.3	875960.11	8347.85	100	0.009529943	0.04839548
676.570763	24.3	396835.62	3961.64	100	0.009983076	0.04718007
677.582519	24.2	1449523.58	42847.62	33.33333333	0.029559795	0.03234514
678.585658	24.2	644946.24	18919.11	34.48275862	0.029334398	0.03076578
679.510243	25.0	11692.28	100266.85	0.116618076	8.575474587	0.00463718
679.55115	6.2	39480.77	141421.68	0.279173646	3.58203956	0.01288685
679.599075	24.1	1.15E+07	152330.76	76.92307692	0.013283323	0.03437038
680.505134	25.0	3667.23	27600.1	0.132872708	7.526143711	5.16E-04
680.601982	24.1	5068136.59	61049.4	83.33333333	0.012045729	0.02916048
681.615615	24.1	5292309.9	206170.72	25.64102564	0.03895666	0.04316054
682.617597	24.1	2698588.62	128650.34	20.83333333	0.047673194	0.03557577
682.635261	23.2	1038696	252179.71	4.115226337	0.242784905	0.03438959
684.205154	3.7	3279.54	66971.23	0.048969198	20.42092184	0.03166271
685.206188	3.7	2238.69	46866.4	0.047766898	20.93474309	0.04118118
686.20349	3.7	1755.71	34615.84	0.050720227	19.71614902	0.03846608
687.204272	3.7	970.24	15213.93	0.063771443	15.68058419	0.03727742
690.350875	5.9	32121.21	244059.95	0.131613583	7.598093285	3.48E-04
691.597791	24.2	1212202.74	24630.32	50	0.020318647	0.03373169
692.60087	24.2	547750.59	14578.28	37.03703704	0.026614814	0.03569884
693.613884	24.1	4030851.15	42725.97	90.90909091	0.010599739	0.03783425
694.537074	22.6	136905.99	286438.53	0.478011472	2.092227886	1.44E-04
694.596498	24.1	1821550.02	25376.1	71.42857143	0.013931048	0.03586276
695.599017	24.3	4724614.56	242402.31	19.60784314	0.051306261	0.01790214
696.607931	24.2	2132936.17	84644.19	25	0.039684352	0.01658455
696.633806	23.5	5513614.77	44043.14	125	0.00798807	0.04793119
697.636679	23.5	1346996.42	22316.94	58.82352941	0.016567928	0.04793171
699.540619	6.0	26180.76	100336.79	0.260960334	3.832462847	0.0497682
699.597077	4.0	7341.56	31569.17	0.23255814	4.300062929	5.00E-04
699.639892	23.5	30928.49	7745.16	4	0.250421537	0.01292585
702.583097	24.2	28990.2	1966.54	14.70588235	0.067834648	0.04750756
705.613521	24.1	739431.8	16422.86	45.45454545	0.022210108	0.03749898
706.616517	24.1	327017.17	15281.41	21.27659574	0.046729687	0.03702989
707.630175	24.1	3294108.29	85572.17	38.46153846	0.02597734	0.03979244

707.630402	23.5	5329982.12	73844.63	71.42857143	0.013854574	0.03048138
707.868449	23.5	58239.08	679.33	83.33333333	0.011664504	0.00580563
708.562925	4.4	56657.4	121423.52	0.466635558	2.143118463	0.00434896
708.633754	23.5	2366723.44	52132.01	45.45454545	0.022027081	0.027346
709.618982	24.2	1308839.04	38653.42	33.33333333	0.0295326	0.04317564
709.643135	23.4	6453694.31	88998.32	71.42857143	0.013790291	0.03083366
709.967186	23.5	51336.51	3550.74	14.49275362	0.06916598	0.00373612
710.648866	23.5	2790578.81	101719.46	27.77777778	0.036451026	0.03178869
711.651699	23.5	715006.87	76289.59	9.345794393	0.106697702	0.03823402
712.573105	7.7	30224.38	114054.15	0.264970853	3.773581129	7.09E-05
713.521579	4.4	15053.7	42622.88	0.353232073	2.831388961	0.02128219
716.549521	6.1	67262.74	169097.41	0.397772474	2.513983373	0.02625014
717.560765	4.9	97452.15	500740.06	0.19462826	5.138317215	0.00255272
717.562372	3.8	3219.53	151238.91	0.021287919	46.97546226	4.11E-04
717.611671	23.4	255327.48	11113.52	22.72727273	0.043526533	0.03710013
718.596299	4.9	83671.76	328766.81	0.254517689	3.929244586	0.01576829
718.61079	23.5	112122.17	9783.12	11.49425287	0.087254109	0.01448071
719.559134	26.5	7761.74	57019.18	0.136128505	7.346185263	0.01609399
720.555196	24.6	2.01E+07	4.29E+07	0.467726848	2.137529438	0.01670169
721.502085	21.9	30552.9	143182.48	0.213401622	4.686379362	7.81E-04
721.558264	24.6	6941637.94	1.63E+07	0.427167877	2.341248672	0.01076488
721.645576	23.5	2717392.76	173576.05	15.625	0.063875952	0.04783681
721.795007	24.6	296020.01	674608.63	0.438788943	2.278929151	0.01874053
721.886112	24.6	254294.54	529969.2	0.479846449	2.084076205	0.01649548
722.560934	24.6	1594059.26	3698548.89	0.431034483	2.320207901	0.01053193
723.657135	23.3	1.38E+07	179812.85	76.92307692	0.012997584	0.03266711
723.660017	24.2	2426714.88	2706.62	1000	0.001115343	0.04760256
724.62788	25.7	27981.76	984048.3	0.028435749	35.16749125	1.54E-04
724.661249	23.3	6367972.11	85800.83	76.92307692	0.013473807	0.02926284
724.99091	23.2	150557.38	19710.28	7.633587786	0.130915402	0.04553404
725.63402	25.7	18197.86	405489.12	0.044879275	22.28224198	5.39E-06
725.63442	24.3	196159.43	727035.8	0.269832704	3.706351512	0.03115252
725.66814	23.2	1617781.01	21206.61	76.92307692	0.013108455	0.02776193
726.501226	5.1	14418.06	58435.01	0.246730817	4.052903789	0.02557555
726.57057	7.8	20512.69	42697.54	0.480307397	2.081518319	0.0014055
726.669815	23.3	309309.02	33040.66	9.345794393	0.106820874	0.03275679
729.611674	23.4	136014.05	12019.8	11.36363636	0.088371753	0.02952023
730.534574	24.8	329168.48	783357.18	0.420168067	2.379806171	0.02357408
730.614217	23.4	60228.67	9846.01	6.134969325	0.163477128	0.04508338
731.534637	24.8	164051.82	367701.43	0.446229362	2.241373671	0.02322802
732.543795	4.7	41967.52	104286.81	0.402414487	2.484940973	0.03999581
734.585014	4.0	25325.28	64853.87	0.390472472	2.56083526	0.04503994
735.544077	22.7	25878.42	56388.7	0.458926113	2.178985425	0.02562187
735.5723	6.0	53573.25	128493.31	0.417014178	2.398460239	0.04415961
735.660994	23.3	1989091.46	40519.25	50	0.020370732	0.02359082
736.607664	4.0	14147.28	182163.26	0.077663871	12.87620376	0.00231485
736.664105	23.3	1001620.04	17839.14	55.55555556	0.017810287	0.02120939
737.608224	4.0	15412.15	100603.21	0.153186275	6.52752601	2.26E-04
737.675894	23.3	3649899.89	44706.17	83.33333333	0.012248602	0.02223293
738.528895	21.9	169011.9	692420.4	0.244081035	4.096873652	0.00543958
738.679945	23.2	1736908.33	34077.39	50	0.019619567	0.02255593
739.682456	23.3	460547.31	17440.94	26.31578947	0.037870029	0.02148962
740.599055	7.3	24342.78	136631.18	0.178157848	5.612801003	2.61E-04
740.604016	7.6	67363.08	229518.15	0.293513355	3.407180165	0.04022174
741.604574	7.6	31290.79	128316.43	0.243842965	4.100773103	0.01322015
743.481726	22.0	57076.5	154896.12	0.368459838	2.713833539	0.03055363
745.500663	21.9	62385.14	197667.91	0.315556958	3.16850952	0.01277216
745.601211	25.6	19129.55	44486.88	0.429922614	2.325558103	0.00972754
747.518647	21.9	242760.77	622490.63	0.390015601	2.564214267	0.01210153
747.57078	5.2	10798.15	60524.82	0.178412132	5.605110135	0.00476035
747.573756	24.5	793600.65	1587921.58	0.499750125	2.00090761	0.02130049
747.60223	25.8	18602.64	50256.68	0.370096225	2.701588592	0.0049729
747.623349	24.1	5711.34	50797.26	0.11243535	8.894105411	0.03250654
747.660044	23.6	77597.21	22805.16	3.401360544	0.293891494	0.03896574
748.522747	21.9	91739.55	277740.41	0.330360093	3.027488253	7.76E-04
749.534147	21.7	759136.4	2602054.07	0.291715286	3.427650248	0.00349623
749.534394	22.4	176505.2	925901.79	0.190621426	5.245747944	0.00207664

749.555985	4.5	8004.3	57506.35	0.139198218	7.184432118	3.38E-04
749.597146	5.1	37106.97	256132.35	0.144864552	6.902540143	0.04883723
750.53766	21.7	361393.89	1199169.51	0.301386377	3.318178705	0.00343769
750.56369	4.6	11930.58	61540.6	0.193873594	5.158223657	0.00399165
750.587665	5.0	38999.02	179163.88	0.217675229	4.594061082	0.03193278
751.545071	21.7	96178.01	362355.34	0.265392781	3.767548736	0.0019557
751.565851	6.1	42918.69	146032.82	0.29385836	3.40254607	0.0187135
751.692073	23.1	3484454.49	111904.88	31.25	0.032115466	0.04458004
752.542073	21.8	55295.11	247365.48	0.223513634	4.473550735	0.00553277
752.695736	23.0	1708976.59	44413.44	38.46153846	0.025988326	0.04349137
753.698311	23.0	477622.52	16904.73	28.57142857	0.035393494	0.03942299
754.537251	4.9	1358.91	203431.65	0.006679937	149.7020774	2.86E-04
755.534572	4.9	4064.01	126411.08	0.032149172	31.10501204	2.41E-05
757.545202	4.6	17319.23	37383.08	0.46339203	2.158472403	0.03367608
757.642375	23.3	75591.41	11402.09	6.622516556	0.150838435	0.03213784
759.654103	23.2	57274	13169.32	4.347826087	0.229935398	0.04411168
762.528856	22.0	146655.39	764042.77	0.19193858	5.209783084	0.0020886
762.551962	22.6	124970.05	297604.02	0.4199916	2.381402744	0.0159728
764.539287	5.9	11253.14	40290.76	0.279329609	3.580401559	0.03545147
764.544466	22.5	342368.15	1262269.2	0.271223217	3.686876831	0.00913579
764.544982	21.8	1017759.2	3545590.86	0.287026406	3.483722731	0.0035767
765.704395	24.1	138882.84	16939.52	8.196721311	0.121969856	0.04729069
766.49128	7.7	410909.04	13049.31	31.25	0.031757174	0.0112214
766.559781	22.4	1261797.13	5692265.26	0.221680337	4.511236493	0.00666518
766.561292	21.7	4657184.79	1.74E+07	0.267737617	3.735245247	0.00360784
766.574262	4.3	13053.85	110368.74	0.118273211	8.454880361	7.57E-05
766.897177	21.7	73516.05	286804.93	0.256344527	3.901255984	0.00664703
767.494868	7.7	130837.09	1164.93	111.1111111	0.008903668	0.03646659
767.563051	22.4	568828.9	2480755.2	0.229305205	4.361162381	0.00618494
767.564475	21.7	1892571.56	7242435.18	0.26130128	3.82676953	0.00376003
767.576114	4.3	5527.43	36783.9	0.15026296	6.654792553	0.01211223
767.855649	21.7	51988.41	177715.01	0.292568754	3.418358246	0.0123181
768.491864	7.7	190820.31	2822.78	66.66666667	0.01479287	0.01193844
768.566951	22.5	215529.09	760633.75	0.283366393	3.529146576	0.00526353
768.568155	21.7	573109.13	2085195.57	0.274876306	3.638391819	0.00415121
768.583689	5.1	58958.17	164803.86	0.357781753	2.79526756	0.0402324
768.591319	4.3	18920.2	217931.43	0.086820629	11.51845276	2.07E-04
769.493743	7.8	70394.7	13466.16	5.235602094	0.191295083	0.02121087
769.571173	21.6	56981.75	229533.58	0.248262165	4.028194641	0.00447372
769.596141	4.3	11094.07	118817.24	0.093370682	10.70997749	0.00218219
770.523292	22.9	19961.34	50526.21	0.395100751	2.531203316	0.00922449
770.598503	4.4	7079.89	35632.81	0.198688655	5.032960964	0.02069402
771.51509	22.2	498599.58	1576712.05	0.316255534	3.162281144	0.01143191
771.570213	24.4	12790.9	28158.27	0.454338937	2.201429923	0.0049069
771.585468	23.0	45052.91	385689.32	0.116808784	8.56080817	0.00962436
771.592546	6.0	86800.16	237777.01	0.365096751	2.739361425	0.03786853
772.510596	19.8	118485.87	323437.45	0.366300366	2.729755455	0.01221599
772.518808	22.2	197812.99	674788.35	0.293169159	3.411243872	0.01023722
773.513377	19.8	49445.71	146963.56	0.336473755	2.972220644	0.00825119
774.523304	19.8	23490.18	67013.45	0.350508237	2.852828288	0.04924863
774.542367	21.7	51505.79	112231.13	0.458926113	2.179000264	0.04269126
774.561504	22.7	33022.28	82300.75	0.401284109	2.492279455	0.02027781
775.552352	21.6	66060.49	133582.84	0.494559842	2.022129112	0.00366774
775.560511	22.7	29106.44	67099.16	0.433839479	2.305302881	0.00404727
776.545148	19.6	129333.75	324390.06	0.398724083	2.508162487	0.03682313
776.559338	21.6	22252.64	47695.95	0.466635558	2.143383886	0.01706952
776.579294	22.6	194867.32	469452.34	0.415110004	2.409087065	0.04053476
778.559894	19.3	108774.38	597587.33	0.182016746	5.493824281	0.00353658
778.564164	21.8	65607.25	146490.82	0.447828034	2.232844998	0.00816633
778.580679	22.7	105953.11	430364.65	0.246184146	4.061840658	0.00570719
778.584184	22.4	137000.89	475279.62	0.288267512	3.46917177	0.0089467
778.706751	23.1	77687.77	20329.67	3.816793893	0.261684304	0.04656341
779.5649	19.3	46248.35	266150.86	0.173761946	5.754818496	0.00906936
779.589174	22.6	177025.11	496727.58	0.356379187	2.805972441	0.00893107
780.568038	19.3	16688.16	65747.9	0.253807107	3.939793243	0.03230493
780.577708	21.6	205750.64	729882.93	0.28192839	3.547415114	0.00237264
780.624747	4.5	16149.11	44000.06	0.366972477	2.724612068	2.65E-04

781.589694	22.6	33457.66	102248.2	0.327225131	3.056047554	0.01022368
782.562329	4.8	27071.56	361626.3	0.074861506	13.35816259	6.34E-05
782.5732	22.7	24772.88	61273.4	0.404367165	2.473406402	7.54E-04
782.574546	4.4	7909.81	40402.42	0.195771339	5.107887547	6.27E-04
782.723308	3.7	4136.59	48486.49	0.085316952	11.72136712	0.02508585
783.568706	4.8	36551.33	191278.77	0.191094974	5.233154854	4.80E-04
783.598649	21.5	223586.33	486643.05	0.459347726	2.176533109	0.02621153
784.578531	4.8	31470.07	96136.32	0.327332242	3.054849258	0.01151878
784.599764	21.5	54077.61	115921.6	0.46641791	2.143615445	0.02524433
784.602342	4.4	18234.18	37725.58	0.483325278	2.068948535	0.02409062
785.591213	5.9	32392.18	88093.47	0.367647059	2.719590654	0.0086805
785.625153	4.0	251891.04	909378.24	0.27700831	3.610204793	0.01373412
786.591073	5.9	20578.5	63865.07	0.322268772	3.103485191	0.00509099
786.629444	4.0	133455.33	511334.91	0.260960334	3.831506093	0.00275073
787.588752	5.8	523435.28	1636088.46	0.319897633	3.125674792	0.01007203
787.598046	4.9	105283.66	474363.44	0.22192632	4.505575129	0.00179551
787.63049	4.3	40551.61	117738.61	0.344471237	2.903426276	0.00483541
787.634379	4.0	44886.46	165754.6	0.270782562	3.692752781	0.00587558
788.592822	5.8	370431.17	1097887.43	0.337381916	2.963809525	0.0119231
788.633056	5.0	42586.84	231343.37	0.184094256	5.432273679	4.43E-04
789.602332	5.6	379456.83	1195339.78	0.317460317	3.150133785	0.03118798
789.604149	6.0	388822.37	1118630.09	0.347584289	2.876969476	0.02359078
790.561604	21.8	82762.21	304764.27	0.271591526	3.682408553	0.00147462
790.596774	8.0	2445245.71	74530.69	33.33333333	0.030479837	0.0222745
790.606485	5.6	190840.04	587406.96	0.32488629	3.0780069	0.03318088
790.607839	6.0	92142.26	606134.24	0.152021891	6.578243685	0.00608891
791.610851	6.0	67389.42	221429.46	0.304321363	3.285819347	0.01972124
791.610935	4.9	67138.88	181320.59	0.370233247	2.700679398	0.02942731
791.664737	24.2	12887.89	6102.06	2.114164905	0.473472384	9.44E-04
792.576258	19.0	306056.17	1111765.79	0.275254611	3.632554737	0.02242702
792.576596	21.6	156453.5	586059.38	0.266951415	3.74590137	0.00864972
793.604126	21.7	66192.69	136162.5	0.486144871	2.057062494	0.00222312
794.545893	8.2	3221484.2	119852.35	27.02702703	0.037204078	0.01663162
794.574984	19.6	167951.58	373163.46	0.450045005	2.221851441	0.04631967
794.591149	21.5	203561.62	963664.95	0.211237854	4.734020834	0.00710675
794.603058	22.6	66466.23	219974.52	0.302114804	3.309568182	0.02531147
795.595882	21.5	122069.88	382615.4	0.319081047	3.134396462	0.01018174
795.726951	3.7	12519.92	26112.45	0.479386385	2.085672273	0.00974593
796.522427	7.4	207585.52	19.36	10722.39256	9.32628E-05	0.001
797.522992	7.4	69537.31	962.44	71.42857143	0.996094641	2.26E-04
798.531465	19.6	195509.34	629820.89	0.310462589	2.835100629	0.03764782
799.557598	21.5	100065.26	218576.38	0.457875458	3.783398036	0.02748773
800.542419	19.4	167929.4	956364.51	0.175592625	2.382026467	0.00334886
801.570288	6.0	33352.49	89897.9	0.371057514	2.966829908	0.00527127
802.604831	8.0	683056.16	73502.57	9.259259259	1.013291951	0.01904606
802.630852	24.3	29849.87	48264.38	0.61842919	3.00283546	0.04953254
804.587006	6.1	102559.45	310785.83	0.330033003	2.69741107	0.00378563
804.59998	22.3	82747.43	364526.93	0.227014756	3.030299304	0.00273098
804.605922	5.2	18926.08	54026.94	0.350262697	4.405296092	0.02575129
804.620635	7.7	9876464.67	107715.78	90.90909091	0.930417817	0.02178747
804.654861	8.6	3500375.32	106088.81	33.33333333	1.083081312	0.0354227
805.603784	22.3	31415.99	229151.98	0.137098985	3.256362842	0.00323035
805.623188	7.7	4838889.12	110781.35	43.47826087	7.294119332	0.02440437
806.612468	22.3	7414.48	118805.82	0.062410285	3.978202808	0.01791038
806.625902	7.7	1345410.78	56676.57	23.80952381	16.02348648	0.02819806
806.675197	4.0	10538.72	64331.69	0.163826999	2.37443411	0.00276711
807.616811	22.3	9046.29	83540.3	0.108283703	2.726488303	0.02812887
807.751999	22.8	209632.97	53850.15	3.891050584	2.682401341	0.04079824
808.589779	19.4	42382.53	97771.79	0.433463372	2.199765105	0.02433766
808.736907	3.7	5203.76	25729.22	0.202265372	3.508993819	9.03E-05
808.867892	6.0	40158.14	134687.33	0.298151461	4.944351776	0.01304479
808.996103	23.1	10715.81	5189.69	2.066115702	1.576344178	0.04728202
809.564094	7.9	1917609.74	13398.55	142.8571429	0.752664495	0.00356231
809.622057	6.0	446286.96	2315471.77	0.192752506	2.61600729	0.00269748
810.495574	7.2	122391.45	255985.78	0.478011472	3.02628749	0.01780363
810.575948	7.7	850487.63	11172.14	76.92307692	0.890956085	0.02454085
810.625561	6.0	108081.09	451521.79	0.239348971	2.848610742	0.03113301

810.653419	9.5	512248	153370.06	3.344481605	4.177620618	0.04912093
810.749317	3.7	4505.85	22865.1	0.197044335	2.381541631	0.00153643
811.561416	7.8	134626.11	5082.44	26.31578947	0.873731074	0.00678903
812.64762	6.1	25455.03	45844.87	0.555247085	2.169599421	0.017033
814.557531	19.1	422027.18	1515921.51	0.278396437	52.05876651	0.00456598
814.603689	7.9	1690813.85	45876.8	37.03703704	0.107693896	0.04231717
815.574558	5.0	27256.03	66771.03	0.408163265	3.430791771	0.00660719
815.606376	7.9	871352.3	47736.93	18.18181818	2.449770931	0.0390672
816.618893	7.7	1396120.52	50286.11	27.77777778	1.181078956	0.01530361
816.710038	3.8	58804.78	15444.81	3.802281369	0.889955989	0.02217751
819.577739	8.0	195562.54	40054.74	4.87804878	0.759812416	7.03E-05
821.576844	7.9	384473.08	13636.71	28.57142857	0.696269912	4.42E-04
821.594565	6.0	646393.29	1958987.84	0.329924117	2.126471455	0.00798133
821.739743	3.7	19109.31	40594.84	0.470809793	2.563473796	0.04706091
822.609765	5.3	8323.1	46862.16	0.177619893	2.813410063	0.00899174
823.585345	7.8	53921.05	2074.58	26.31578947	5.704391148	0.02984729
823.757863	3.7	10870.61	45155.18	0.240731825	2.279357437	0.00365445
830.322056	8.2	38244.27	13633.81	2.808988764	1.130194329	0.04694105
832.242707	3.7	1763.89	63885.72	0.027609818	2.551267233	0.02927856
834.241178	3.7	1209.31	44944.36	0.026907036	2.281966161	0.02888643
835.241009	3.7	821.19	24739.86	0.033192817	3.326396308	0.02124943
837.661391	4.3	65301.96	269757.4	0.242072137	4.800908715	0.00199366
838.665712	4.3	29219	101736.68	0.287191269	2.014019228	5.04E-04
839.840501	39.8	132823.95	100182.19	1.326259947	2.027899516	0.03109136
849.77569	3.7	59588.22	155877.12	0.382262997	2.158915059	0.02043496
851.454807	22.4	3123.38	14388.29	0.217060994	3.444295649	0.00689781
851.588867	6.0	14600.7	38874.39	0.375516335	3.735905359	0.03926508
851.790428	3.7	38006.18	134187.99	0.283205891	2.233995421	0.0064606
852.661412	4.4	16938.18	72697.86	0.232991612	15.89252114	0.00140491
852.668277	4.8	25137.47	56667.87	0.443655723	4.291952264	0.04453052
852.796701	3.7	16173.56	69785.97	0.23174971	2.201310623	0.00930901
853.585624	6.3	80516.39	230927.92	0.348675035	3.142335263	0.01670559
853.598819	21.2	16791	110028.37	0.152601862	2.065332122	0.00763558
854.697267	3.8	5640.64	32578.71	0.173130194	2.620784309	0.04257466
871.59986	6.2	87400.1	241986.57	0.361141206	2.772282652	0.01023038
874.633925	6.4	9826.67	28864.17	0.340483487	2.15736914	0.01362512
877.806413	3.7	122269.82	293398.2	0.416666667	2.055854842	0.01759699
878.71711	9.1	6986.54	128176.48	0.054507795	2.200193288	0.01739528
878.815597	3.7	91759.95	235357.04	0.389863548	18.34620284	0.01843508
879.720519	9.1	10158.49	84346.77	0.120438396	9.169369193	0.01992168
881.425429	6.7	319694.42	47612.1	6.711409396	0.036602063	0.00560616
883.440979	6.7	328550.19	29898.57	10.98901099	1.44597415	0.0025993
884.444266	6.7	164727.73	5895.5	27.77777778	5.625210225	5.38E-04
885.446348	6.7	41175.34	1967	20.83333333	1.05168691	0.00331012
885.590037	6.7	30172.09	66855.92	0.451263538	5.912075818	0.02392454
885.591404	21.7	23691.13	120348.67	0.196850394	2.215819985	0.01887585
886.591964	6.7	43320.02	292522.63	0.148082334	3.927059163	1.25E-04
887.647864	6.1	15189.26	36884.06	0.411861614	4.042397253	3.49E-04
896.589587	21.7	163143.98	450488.36	0.362187613	6.278536489	0.00982043
898.615212	21.7	44517.65	114032.22	0.390320062	2.582003779	0.01740728
900.351554	39.8	42133.84	20374.42	2.066115702	2.255499677	0.02960595
903.822445	3.7	35574.57	114950.43	0.309501702	2.113080216	0.02427814
904.832751	3.7	34597.99	100492.73	0.344234079	2.854137499	0.01121592
906.261867	3.7	2069.29	21111.46	0.098019996	2.328481195	0.00441686
907.458765	6.7	53891.96	25932.44	2.079002079	0.627851119	0.00982001
908.260283	3.7	1921.78	16777.52	0.114547537	2.22493831	0.00640192
908.860795	3.7	13551.13	40029.03	0.338524035	2.288002051	0.00350822
910.257574	3.7	823.98	6258.14	0.131665569	2.422659958	0.02854852
910.608896	21.6	14074.69	47248.59	0.297885016	34.78085782	0.01077999
912.62376	21.5	32149.89	106958.59	0.300571085	13.28660758	0.01778232
913.624443	23.4	13785.4	70812.85	0.194666148	2.420463262	0.00321263
915.63801	23.3	10802.9	52836.89	0.204457166	2.221989422	0.00156071
918.846167	3.7	8560.97	30399.52	0.281610814	2.522872228	0.00728432
924.619171	21.5	18129.46	67937.34	0.266880171	2.768399057	0.00617447
926.639022	21.4	13332.26	22210.29	0.600240096	2.804576935	0.02437054
927.555687	8.6	48264.91	102579.25	0.470588235	4.278458857	0.04612078
934.647389	7.7	273553.5	22703.04	12.04819277	0.783236777	0.01141925

935.651013	7.7	176759.15	21889.84	8.064516129	0.966349678	0.01892451
936.651321	7.7	47730.78	17629.76	2.7100271	1.359325564	0.00519162
943.652964	24.5	8473.27	11887.8	0.712758375	4.198784302	0.01495917
944.539708	6.2	3642.62	55522.08	0.065608188	2.48388173	4.37E-04
944.620779	21.7	20533.66	64043.87	0.320615582	15.24234754	0.04197324
946.641889	7.7	40906.2	8129.04	5.025125628	2.163322256	0.0111385
956.668669	8.5	49355.82	13469.78	3.663003663	1.958482173	0.044652
957.7125	23.4	30116.9	3647.04	8.26446281	2.275140209	0.03510401
958.689451	23.2	162032.38	442582.1	0.366166239	2.056609044	0.00662698
960.6952	23.3	33053.72	104954.27	0.31496063	8.118747474	0.00426737
960.73158	6.4	20629.41	34821.61	0.592417062	3.17526348	0.02132448
965.650901	23.2	23993.55	71835.97	0.334001336	2.340637301	0.01650878
965.930686	3.7	9982.23	20472.53	0.48756704	2.702454397	0.02189252
969.712593	23.5	12692.29	4080.47	3.115264798	1.132848229	0.00871207
971.729628	23.4	37178.24	5000.61	7.407407407	0.391550968	0.02521812
974.641869	21.7	12728.71	29295.21	0.434404865	9.603770984	0.00274316
976.528806	6.2	6358.97	28372.49	0.224114747	3.136700015	0.02853431
976.764892	6.2	17181.25	36987.97	0.464468184	3.817549866	0.02554058
976.91879	3.7	8760.11	20916.8	0.418760469	2.152810186	0.01812048
977.956948	25.8	11069.66	432.66	25.64102564	2.354753298	1.77E-04
980.404353	4.9	24681.65	58436.29	0.422297297	11.52481857	0.04791864
980.592473	22.3	8408.43	24558.38	0.342348511	2.367600626	0.01114513
981.281357	3.7	756.89	12926.49	0.058554866	4.034783495	0.00223421
981.613145	5.9	42107.18	73122.33	0.575705239	2.316665366	0.01793695
982.686832	23.2	13132.89	35642.76	0.368459838	2.822353566	0.02556013
985.629081	23.3	36607.85	67182.21	0.544959128	13.06108105	0.03918776
986.750239	6.4	41668.09	91327.17	0.45620438	2.075761077	0.01965708
991.947068	3.7	41693.75	71123.59	0.586166471	6.28403277	0.04807884
993.705043	23.3	11826.27	3855.74	3.067484663	2.10085033	0.00430647
1000.75325	4.9	13977.9	29995.53	0.465983225	2.145925354	0.04593654
1000.76557	6.3	9729.31	30077.32	0.323519896	3.091413471	0.03004211
1000.91628	3.7	2473.07	15830.61	0.15622559	6.401197702	4.29E-05
1001.9182	3.7	2051.79	13711.42	0.149633398	6.682662456	0.00157618
1002.93354	3.7	3770.97	28447.1	0.132555673	7.543708913	7.09E-05
1003.94004	3.7	4745.82	16027.8	0.296120817	3.37724566	0.00708929
1004.67054	23.2	20532.59	66886.33	0.306936771	3.257569065	0.04023507
1004.94598	3.7	6838.6	23690.34	0.288683603	3.464209049	0.00719984
1007.69007	21.6	4181.54	12796.01	0.326797386	3.060118999	0.02722479
1007.75402	4.9	74631.97	23001.28	3.246753247	0.308196072	0.0456842
1009.72225	23.2	23179.33	47708.05	0.485908649	2.058215229	0.01616448
1012.76558	6.4	23566.96	70605.99	0.333778371	2.9959736	3.01E-04
1013.69776	26.1	11962.5	27645.59	0.432713111	2.311021108	0.01379937
1013.77017	6.4	16615.86	40117.33	0.414250207	2.414399857	0.01279973
1014.77968	6.3	29414.52	82843.39	0.355113636	2.816411419	0.0016727
1015.78454	6.3	15937.22	42182.97	0.377786173	2.646821089	0.03315969
1016.79508	6.2	21789.79	88945.26	0.244977952	4.081969583	0.00136119
1018.95944	3.7	11069.98	28874.17	0.383435583	2.608330819	0.00654809
1022.63315	19.3	23001.89	66261.81	0.347101701	2.880711542	0.02246055
1026.7525	22.9	258147.38	755071.42	0.341880342	2.924962554	0.01747646
1027.75584	23.0	183215.46	519620.54	0.352609309	2.836117323	0.01991096
1028.75921	23.0	70077.48	195486.73	0.358422939	2.789579905	0.0227082
1031.70786	23.0	132352.77	495124.31	0.267308206	3.740944069	0.01305594
1031.76233	4.8	119441.54	6698.96	17.85714286	0.05608568	0.03850289
1032.71095	23.0	97990.08	340713.77	0.287604257	3.477023082	0.01205594
1032.76612	4.8	78728.16	7848.44	10	0.099690378	0.04159643
1032.965	3.7	2415.44	9812.08	0.246184146	4.062232968	0.00235644
1033.71412	23.0	43395.43	130670.64	0.332115576	3.011161314	0.01095138
1033.771	4.9	42451.4	9359.17	4.545454545	0.220467876	0.04285591
1034.60635	22.2	40241.41	19902.48	2.02020202	0.494577104	0.04714544
1034.77107	4.9	16086.32	4610.8	3.484320557	0.286628638	0.00846478
1035.75979	8.0	23474.97	100892.29	0.232666356	4.297866621	0.01409017
1036.76314	8.0	14363.82	62194.81	0.230946882	4.32996306	0.01106837
1038.63604	11.0	28432.89	1700.74	16.66666667	0.059815939	0.00389414
1038.77816	8.0	8140.68	23765.78	0.342583076	2.919385113	0.00536656
1047.51394	8.6	3315.84	13772.38	0.240731825	4.153511629	0.00717281
1047.72237	5.8	194258.83	12719.81	15.38461538	0.065478671	0.03944991
1048.9086	4.5	12460.69	3181.3	3.921568627	0.255306889	0.03159044

1051.78597	7.8	11300.62	46872.65	0.241080039	4.147794546	0.01573505
1052.63385	8.6	3590.49	24754.65	0.145032632	6.89450465	0.00538649
1053.637	8.6	7062.58	14872.04	0.474833808	2.105751722	0.02762458
1053.691	23.0	32403.16	83637.88	0.387446726	2.581164306	0.01642693
1054.29836	3.7	647.79	9495.85	0.068217477	14.65884006	0.00674919
1054.65766	19.3	11510.2	32953.4	0.349283968	2.86297371	0.04575357
1054.69205	23.1	18628.65	49819.62	0.373971578	2.674354824	0.03915926
1055.30198	3.7	747.24	13113.33	0.056983304	17.5490204	2.81E-04
1056.29885	3.7	621.45	11673.83	0.053233963	18.78482581	2.76E-04
1057.29931	3.7	513.51	7443.96	0.068984547	14.49623182	0.01108313
1059.57887	6.2	11159.38	33428.36	0.333778371	2.995539179	0.00807041
1062.88126	23.0	17363.92	50710.73	0.342465753	2.92046554	0.01769448
1063.81078	24.2	1153.71	18036.43	0.063967249	15.63341741	0.01582688
1063.88439	23.0	10499.88	37827.27	0.277546489	3.602638316	0.01882519
1063.92876	4.3	11651.94	2563.84	4.545454545	0.220035462	0.03334186
1064.3121	24.1	238.92	24122.25	0.00990452	100.9637117	0.01870179
1064.81726	24.2	2013.69	37291.44	0.053998596	18.51895773	0.0328855
1064.89396	23.0	19599.02	47112.48	0.415973378	2.40381815	0.03477592
1065.32056	24.2	340.59	44323.13	0.007684269	130.1363223	0.00593384
1065.82209	24.2	1327.95	31694.88	0.041897101	23.86752513	1.11E-04
1066.32527	24.1	245.2	19535.92	0.012551303	79.67340946	7.25E-04
1066.60695	19.0	11004.68	28993.93	0.379506641	2.634690877	0.02935865
1068.67305	19.2	30058.35	70932.22	0.423728814	2.359817488	0.01226408
1072.3118	3.8	1002.99	8212.83	0.122129946	8.188346843	0.007145
1072.32508	24.2	176.43	6840.64	0.025791143	38.77254435	0.0017377
1073.73885	5.8	86406.65	13776.47	6.289308176	0.159437613	0.02806773
1077.3196	24.1	68.38	5189.45	0.013176793	75.8913425	0.00413026
1082.68548	19.1	22433.06	69372.03	0.323415265	3.092401572	0.00246371
1083.69367	19.1	12463.87	25715.72	0.484730974	2.063221134	0.03301206
1088.89592	23.0	6031.95	18019.26	0.334784064	2.987302614	0.01093282
1090.91405	22.9	25544.46	90576.58	0.282007896	3.545840468	0.02046567
1091.91606	22.9	21817.79	62513.46	0.34904014	2.865251705	0.04159293
1092.92414	22.8	17757.63	54991.11	0.322893122	3.096759534	0.00815974
1105.98003	4.2	12634.42	1879.34	6.711409396	0.148747628	0.01869335
1106.99651	23.3	14974.54	1751.13	8.547008547	0.116940487	0.00567011
1128.3196	3.7	728.59	11084.27	0.065733254	15.21331613	0.0010734
1130.31825	3.7	670.73	14259.5	0.047036689	21.2596723	0.00101077
1132.87267	21.7	6519.31	22651.13	0.287852619	3.47446739	0.02234977
1146.3323	3.7	445.1	7661.58	0.058095625	17.21316558	0.02356278
1147.32933	3.7	459.09	8378.89	0.054791518	18.25108367	0.01642045
1150.87592	20.6	50969.55	18391.93	2.770083102	0.360841522	0.02340536
1151.66598	23.2	3994.39	15325.5	0.260620276	3.83675605	0.04117143
1154.92634	7.0	4010.42	13262.39	0.302388872	3.30698281	0.04762114
1165.79711	6.0	95731.94	19770.33	4.830917874	0.206517595	0.04985278
1193.81194	5.5	167315.48	12976.94	12.82051282	0.077559709	0.02733684
1203.33904	3.7	721.08	13112.01	0.054993401	18.18384923	0.0023166
1204.33976	3.7	884.29	13771.71	0.06420958	15.57374843	4.49E-04
1205.33577	3.7	395.65	10147.65	0.038989395	25.64804752	0.00279782
1207.79942	5.3	1628401.72	23485.58	71.42857143	0.014422473	0.02489888
1208.80307	5.3	1239648.88	22484.05	55.55555556	0.018137434	0.02545856
1214.78784	6.0	19609.63	8923.34	2.197802198	0.455048871	0.01058795
1216.76883	5.9	155057.17	10212.74	15.15151515	0.065864352	0.04821873
1217.77581	5.9	101569.42	10983.2	9.259259259	0.108134909	0.02793169
1220.82628	5.4	39030.8	6328.91	6.172839506	0.162151685	0.01115072
1221.34954	3.7	416.34	7246.78	0.057451454	17.40591824	0.02025916
1221.81447	5.0	548108.16	12237.62	45.45454545	0.022327017	0.02639129
1223.16094	3.6	1963.77	9097.35	0.215842866	4.632594448	0.00534147
1224.82108	5.8	981859.56	13556.83	71.42857143	0.013807301	0.04273823
1225.82347	5.8	278222.46	10065.42	27.77777778	0.036177597	0.04375219
1226.26532	3.5	1238.06	34209.85	0.036189925	27.63181914	0.00183444
1227.26599	3.5	1574.99	28282.93	0.055685488	17.95752989	0.00416075
1228.79717	6.2	33193.73	14021.35	2.369668246	0.422409594	0.00407077
1233.81528	5.2	1237788	16963.99	71.42857143	0.013705085	0.02614681
1234.81829	5.2	851853.43	10578.81	83.33333333	0.01241858	0.04979949
1235.82815	5.1	1.01E+07	36028.12	250	0.003551564	0.03891996
1236.25892	5.1	143299.42	116.9	1000	0.000815774	0.02999133
1236.83274	5.1	7538445.04	32159.2	250	0.004266026	0.04011652

1237.83657	5.1	3202597.48	14022.61	250	0.004378512	0.02842668
1238.83401	5.8	1558907.21	14883.49	100	0.009547387	0.03691058
1239.83722	5.8	923231.47	16629.33	55.55555556	0.018012092	0.03975171
1242.78423	5.9	178986.36	9502.29	18.86792453	0.053089464	0.03034258
1245.79989	5.8	341060.07	9701.05	35.71428571	0.028443816	0.03560842
1246.8045	5.9	133238.01	8906.67	14.92537313	0.066847816	0.00691986
1247.82489	5.8	3611431.64	9960.66	333.3333333	0.002758092	0.04381392
1248.8283	5.8	2755363.62	10738.78	250	0.003897409	0.04608219
1250.84296	5.8	868753.13	14178.18	62.5	0.016320148	0.02333547
1251.9077	21.4	2562.6	16959.33	0.151103052	6.618016858	3.43E-04
1252.03241	5.5	33206.94	5802.64	5.714285714	0.174741786	0.0172806
1252.85147	5.1	1391458.35	27905.06	50	0.020054542	0.03349142
1252.91236	21.5	3561.41	17090.94	0.208376745	4.798925145	0.00985866
1253.85528	5.1	942988.79	27470.7	34.48275862	0.029131523	0.03128027
1254.30291	3.4	1871.94	81446.53	0.02298375	43.50915628	6.11E-04
1254.85794	5.1	402949.63	23600.69	16.94915254	0.058569827	0.03415562
1255.30558	3.4	1994.21	78715.78	0.025334414	39.47216191	3.84E-04
1255.81889	5.1	267971.29	8395.97	32.25806452	0.031331603	0.03687683
1256.3043	3.4	1631.3	35793.21	0.045574697	21.94152516	2.50E-04
1257.78674	5.9	77928.51	5295.06	14.70588235	0.067947661	0.0162055
1257.88349	25.2	3511.73	11332.91	0.309885342	3.227158694	0.04725552
1258.89019	25.2	987.51	10542.63	0.09366804	10.6759729	3.68E-04
1259.9027	25.2	196.09	15984.91	0.012267229	81.51823142	8.81E-04
1260.94154	25.2	151.85	14763.97	0.010285209	97.2273296	0.00200589
1261.84206	5.1	3257940.56	20561.09	166.6666667	0.00631107	0.02688009
1261.9245	21.3	1685.38	10196.19	0.165289256	6.049786992	0.04012062
1262.93093	21.3	2469.38	9813.69	0.251635632	3.974151406	0.00755099
1262.97119	25.2	174.96	73668.26	0.00237497	421.0577275	0.002466
1263.85442	5.1	2247231.21	25141.08	90.90909091	0.01118758	0.03141421
1263.97485	25.2	258.91	62278.33	0.004157313	240.5404581	7.35E-05
1264.85921	5.1	1505134.6	34911.22	43.47826087	0.023194749	0.02780486
1264.97977	25.2	180.48	29357.5	0.00614768	162.663453	0.01136855
1267.86103	5.8	125592.26	7710.53	16.39344262	0.061393353	0.04348406
1268.93643	21.4	2198.5	27216.07	0.080781969	12.3793814	2.79E-04
1269.94028	21.4	2631.69	20670.79	0.127307447	7.854568737	8.48E-04
1270.21854	3.6	6352.27	14517.58	0.437636761	2.28541608	0.04252542
1270.93649	21.4	2008.15	11514.43	0.174398326	5.733849563	2.26E-04
1273.82409	5.8	55462.63	4936.84	11.23595506	0.089012007	0.04184325
1273.89172	21.4	2409.46	17550.19	0.137287205	7.283868585	0.00263507
1274.82161	5.8	41585.13	7170.66	5.813953488	0.172433271	0.00381351
1274.89557	21.4	1975.35	10729.56	0.184094256	5.431726023	0.03054657
1275.8553	5.8	957405.32	11381.31	83.33333333	0.011887661	0.02698
1276.35808	3.7	2280.69	11288.29	0.202020202	4.949506509	0.01566619
1276.85864	5.8	960645.76	29495.64	32.25806452	0.030703971	0.03004166
1277.86221	5.7	494147.78	17520.44	28.57142857	0.035455871	0.04354861
1278.35518	3.7	902.18	13827.92	0.06524434	15.3272296	0.00540491
1278.87382	5.1	663683.01	18752.47	35.71428571	0.028255161	0.04378331
1279.35172	3.7	860.87	9896.85	0.086986778	11.4963351	0.004325
1279.87299	5.1	386880.24	9063.62	43.47826087	0.023427457	0.04756699
1279.94175	21.3	5199.93	44865.95	0.115901715	8.628183456	1.19E-04
1280.88056	5.1	305751.75	11424.35	27.02702703	0.03736479	0.04144604
1280.94525	21.3	10343.06	43901.76	0.23557126	4.244562054	0.00241954
1281.88468	5.0	184758.03	11143.44	16.66666667	0.060313698	0.03195742
1282.33323	3.4	1608.05	88200.02	0.018231873	54.8490532	0.00125061
1282.88682	5.0	80367.15	10992.23	7.299270073	0.136775162	0.02527493
1282.95146	21.3	4149.07	16780.89	0.247279921	4.044494308	0.0015955
1283.33725	3.4	2551.68	84542.78	0.030182301	33.1322031	4.10E-04
1284.33816	3.4	2571.99	37413.26	0.068747422	14.54642514	0.00505873
1289.87486	4.9	1786479.55	11936.35	142.8571429	0.006681493	0.03835431
1290.87792	5.0	1441900.44	15661.73	90.90909091	0.010861866	0.03251382
1291.88047	5.0	680480.2	17366.69	38.46153846	0.025521228	0.03497573
1292.88416	5.8	201100.54	9452.19	21.27659574	0.04700231	0.02088715
1293.95076	21.3	4853.41	24875.71	0.195121951	5.125408733	0.00316562
1294.95807	21.3	4779.47	30086.79	0.158856235	6.295005513	0.0037769
1296.96747	21.3	5231.28	70467.97	0.074233539	13.47050244	5.88E-04
1297.9707	21.3	3631.71	55795.4	0.065091453	15.36339631	7.87E-04
1298.84508	5.7	182339.93	26270.09	6.944444444	0.144072064	0.03776256

1298.97165	21.3	3052.2	27028.09	0.112930548	8.855281436	0.00506016
1299.95353	21.3	2004.67	8782.54	0.228258388	4.381040271	0.03147473
1301.92488	21.3	4759.34	48301.94	0.098531875	10.14887358	9.22E-04
1302.92743	21.3	3881.09	36740.03	0.105641242	9.466420516	0.00112695
1303.88813	4.8	104398.73	8769.71	11.9047619	0.084002076	0.03832991
1303.93321	21.3	2758.16	16253.16	0.169692856	5.89275459	2.19E-05
1304.94252	21.3	1440.52	8121.64	0.177367861	5.637991836	0.01556899
1307.90412	5.0	205378.64	9240.33	22.22222222	0.04499168	0.04292627
1307.97255	21.2	917.04	16521.43	0.055506217	18.01604074	0.00206726
1308.97637	21.2	888.78	16335.58	0.054406964	18.37977902	0.01216543
1309.90722	5.0	45420.09	8780.64	5.18134715	0.193320621	0.01780809
1310.98239	21.3	1837.18	32741.07	0.056113574	17.82137297	8.47E-04
1311.36135	3.3	941.03	17646.89	0.053324801	18.75273902	5.59E-05
1311.98512	21.3	1812.43	23834.95	0.076039845	13.15082514	5.05E-04
1312.36946	3.3	761.39	8146.87	0.093457944	10.69999606	2.53E-04
1312.98354	21.3	1430.4	13442.39	0.106405618	9.397644016	0.0040881
1315.7883	5.9	39918.05	3534.48	11.23595506	0.088543403	0.03199771
1315.9391	21.3	1791.15	18163.73	0.098609605	10.14082014	0.00109647
1316.7883	5.9	28988	4041.12	7.194244604	0.139406651	0.02006367
1316.9423	21.3	2426.68	16161.53	0.15015015	6.659934561	0.02179329
1317.25968	4.2	17203.5	39027.18	0.440722785	2.268560467	0.0187647
1318.26602	4.2	13119.17	37588.46	0.34904014	2.865155341	0.00109591
1318.90755	4.9	50112.95	12531.42	4	0.250063507	0.01503314
1319.90966	5.0	19549.44	6786.87	2.88184438	0.34716442	0.01619164
1319.97443	21.3	994.58	9631.43	0.103263114	9.683916829	0.00450486
1321.82612	5.8	460334.5	7554.52	62.5	0.016410936	0.03256681
1321.98625	21.2	2704.13	32573.69	0.083015109	12.04590386	0.00404244
1322.98663	21.3	1471.45	19441.8	0.075683039	13.21268137	0.0037934
1323.01623	20.7	1202.03	14813.45	0.081142486	12.32369408	0.00331651
1323.8355	5.8	153976.11	6477.22	23.80952381	0.042066396	0.01883615
1323.99302	21.1	685.93	9328.08	0.073534819	13.59917193	2.55E-05
1324.99693	21.2	1546.97	20801.59	0.074366603	13.44666671	0.01274014
1325.9988	21.2	870.91	12091.41	0.072025353	13.88365043	0.03210796
1326.04258	21.7	2660.32	16000.88	0.166251039	6.014644855	0.0166689
1327.04606	21.7	1912.86	15446.88	0.123839009	8.075279947	0.00330654
1329.95583	21.2	3264.57	20326.02	0.160616768	6.226247255	0.00144821
1333.97857	21.3	813.82	8603.3	0.094589482	10.5715023	7.83E-04
1336.0027	21.2	1543.43	42743.89	0.036108904	27.69409043	1.30E-04
1337.00522	21.2	2087.91	51593.64	0.040467808	24.71066282	0.00101866
1338.00271	21.2	1073.91	24730.05	0.043425395	23.02804704	0.00622738
1338.8517	5.8	247720.75	11057.13	22.22222222	0.044635462	0.04960907
1339.01244	21.2	1508.77	49857.37	0.030261764	33.04504331	0.00137052
1339.85437	5.8	190504.86	10676.06	17.85714286	0.05604088	0.04334067
1340.01444	21.2	1711.59	26001.06	0.065828451	15.19117312	0.02239528
1340.86254	5.8	81938.68	9912.25	8.26446281	0.120971561	0.03238845
1341.01099	21.2	1021.72	14822.03	0.06893224	14.50693928	0.00291495
1343.97105	21.2	1486.24	32252.97	0.046080826	21.70105097	5.46E-04
1344.97701	21.2	1444.44	26267.89	0.054987353	18.18551826	4.20E-04
1345.09732	24.8	14618.07	194.06	76.92307692	0.01327535	0.01761935
1345.98303	21.3	716.32	14673.52	0.048816207	20.48458789	0.00404024
1346.29933	4.2	7997.5	23964.71	0.333667	2.996525164	0.01973967
1347.01233	21.0	610.05	8413.35	0.072511058	13.79124662	0.0238034
1347.84395	5.8	136239.34	9637.34	14.08450704	0.070738305	0.01650821
1348.84565	5.8	133665	9990.73	13.33333333	0.074744548	0.03681728
1349.85008	5.8	100980.61	10076.97	10	0.099791138	0.04931437
1350.01528	21.1	956.53	12767.57	0.074917591	13.34779881	0.00501492
1350.86116	5.7	35849.58	5653.98	6.329113924	0.157713982	0.03802482
1351.01561	21.2	1257.17	25397.92	0.04950005	20.20245472	9.38E-05
1351.3739	3.7	921.07	13255.78	0.069483046	14.39171833	0.01103898
1352.00185	21.3	1069.48	17137.71	0.06240639	16.02433893	0.02772812
1352.37496	3.7	833.5	13247.65	0.062916824	15.8940012	0.00681711
1353.02895	21.2	994.02	61695.19	0.016111881	62.06634675	2.81E-04
1354.03105	21.2	944.29	45364.6	0.020815553	48.04096199	2.44E-05
1354.37101	3.7	645.29	9745.84	0.066212011	15.10303894	0.01419133
1355.02948	21.2	446.02	19113.03	0.023336134	42.85240572	1.08E-04
1356.98278	21.3	962.92	7316.63	0.131613583	7.598377851	0.00273717
1357.81652	6.1	29776.75	4171.6	7.142857143	0.14009588	0.04467423

1357.98417	21.2	948.83	40254.8	0.023570452	42.42572431	0.00115335
1358.40337	3.3	6996.17	16029.3	0.436490615	2.291153588	0.03269773
1358.98677	21.2	655.91	27229.45	0.024088259	41.51400345	2.49E-04
1359.11805	24.4	14054.42	19.36	1000	0.001377503	0.00853518
1359.99365	21.2	1022.79	25625.95	0.039912193	25.05494774	1.11E-04
1362.01679	21.2	756.81	24900.32	0.030393289	32.90167942	0.00159726
1363.02291	21.2	1274.89	24340.66	0.052377959	19.09236091	2.32E-04
1364.03314	21.0	1983.03	63162.92	0.031395203	31.85172186	0.00209497
1364.87194	5.8	89013.11	6846.61	12.98701299	0.076916872	0.02400992
1365.03761	21.0	969.5	56340.36	0.017207854	58.11280041	3.59E-04
1365.87256	5.8	69839.67	6449.69	10.86956522	0.09234995	0.02083818
1366.03134	21.0	1246.88	27387.03	0.045529048	21.96444726	6.71E-07
1367.03643	21.1	812.14	20545.69	0.039528817	25.29821213	0.00649792
1368.04522	21.0	1163.16	11016.13	0.105585471	9.470863854	0.01024555
1369.20667	6.7	24931.4	1362.98	18.18181818	0.054669212	0.01716672
1369.39716	3.7	6024.7	23820.9	0.252908447	3.953873222	0.03983368
1371.02896	24.9	50480.55	16608.38	3.039513678	0.329005528	0.03528696
1371.40837	3.6	5581.16	18011.82	0.309885342	3.227253833	0.03890462
1371.99977	21.1	940.2	13526.41	0.069507194	14.38673686	0.01072302
1372.07509	24.8	29733.7	2957.06	10.1010101	0.099451464	0.02650906
1372.40522	3.7	2024.32	11298.27	0.179179359	5.581266796	8.49E-04
1372.99939	21.1	927.56	10291.7	0.090130689	11.09545474	8.16E-04
1375.87553	5.7	52277.66	9011.45	5.813953488	0.17237669	0.01582736
1376.88084	5.7	36014.82	6840.92	5.263157895	0.189947361	0.03645337
1377.02799	21.2	427.62	10790.71	0.039629072	25.23434358	0.00611729
1377.24051	23.5	22960.48	1661.65	13.88888889	0.072370003	0.04818996
1378.04566	21.1	1117.95	20827.91	0.053676865	18.63044859	0.00425715
1379.04705	21.1	2131.4	53077.55	0.040155805	24.90266961	9.86E-04
1380.04212	21.1	1883.93	33945.86	0.055496975	18.01864188	9.47E-04
1381.05984	21.1	2218.4	72105.45	0.030766391	32.50335828	3.02E-05
1382.06305	21.0	1038.06	54103.08	0.019186861	52.11941506	0.00239855
1383.06152	21.0	1341.14	24993.35	0.053659584	18.63589931	7.51E-05
1385.1223	24.5	22268.08	1870.29	11.9047619	0.083989729	0.04566974
1385.43206	3.3	4592.44	19302.5	0.237925291	4.203103361	0.02278919
1386.01735	21.0	1780.17	65925.42	0.027002943	37.03321593	0.00106136
1387.02178	21.0	883.48	49986.54	0.017674402	56.57914158	6.80E-04
1387.14354	24.5	39062.51	2779.41	14.08450704	0.071152878	0.01977048
1388.02514	21.0	1587.08	24238.66	0.065479309	15.27248784	1.17E-05
1389.02651	21.0	977.44	14086.54	0.069386622	14.41166721	0.00938081
1389.14862	24.5	15220.88	4977.36	3.058103976	0.327008688	0.03971333
1392.05912	20.9	823.1	7948.94	0.103551828	9.657319888	0.00899866
1392.90328	5.7	26013.33	6048.94	4.291845494	0.232532321	0.00763148
1394.04235	21.1	1649.41	11538.5	0.142938822	6.995531736	0.0411164
1395.06955	21.1	1401.78	27138.67	0.051652893	19.36014924	8.16E-05
1398.23606	6.7	22129.08	2633.82	8.403361345	0.119020764	0.02611413
1398.43016	3.3	2978.37	10777.07	0.276395799	3.61844566	0.0398674
1399.32853	6.0	15240.72	499.39	30.3030303	0.032766825	0.01780659
1400.02894	21.0	1005.28	18212.23	0.055196777	18.11657449	0.01674778
1401.15105	24.5	32764.25	15708.48	2.087682672	0.479439633	0.0098819
1402.03192	21.0	558.42	9124.78	0.06119951	16.34035314	0.02472616
1403.25584	23.5	64306.62	7915.34	8.130081301	0.123087483	0.04364017
1404.26479	23.5	76627.98	10775.65	7.092198582	0.140622916	0.04819306
1405.06141	21.0	2092.98	12959.08	0.161498708	6.191688406	5.51E-04
1405.26969	23.5	55822.36	18528.69	3.012048193	0.331922369	0.04183772
1406.01195	24.0	4192084.58	9278578.71	0.451875282	2.213356752	0.00972795
1407.01575	24.0	2503522.19	6501207.71	0.385059684	2.59682448	0.02298492
1407.07384	20.9	351.98	13617.37	0.025847808	38.6879084	9.84E-06
1410.02514	24.0	475535.22	1172931.47	0.405350628	2.466550154	5.29E-04
1411.03203	24.0	353831.36	790507.65	0.447627574	2.234136765	1.02E-04
1411.44675	3.3	2710.63	9264.77	0.292568754	3.417939741	0.01261112
1413.03295	24.0	83858.38	211557.31	0.396353547	2.522792713	0.00237175
1413.46202	3.3	1577.03	23017.68	0.068511921	14.59558791	0.00521587
1415.08319	24.8	103174.71	222027.68	0.464684015	2.151958363	0.01137908
1415.24839	23.5	20369.76	3827.26	5.319148936	0.187889303	0.04918441
1416.08415	24.9	21923.86	61663.21	0.355492357	2.81260736	0.01764982
1416.35138	4.0	3555.14	9062.32	0.39231071	2.549075423	0.01538597
1418.28299	23.5	123639.98	48121.16	2.570694087	0.38920388	0.03121821

1419.2862	23.5	150754.66	66240.33	2.277904328	0.439391592	0.04390604
1420.28751	23.4	50334.86	8654.98	5.813953488	0.17194803	0.01657307
1421.08745	21.0	963.96	10544.03	0.091424392	10.93824433	0.03403706
1422.06736	21.0	1242.57	10297.53	0.12067093	8.287283614	0.01941861
1423.09925	20.9	1550.85	18851.88	0.082263903	12.15583712	0.0337766
1424.04305	24.0	1.29E+07	2.87E+07	0.450856628	2.218452789	0.01094039
1424.25162	6.7	45650.58	9521.22	4.784688995	0.208567339	0.03116606
1424.50689	23.9	470330.3	1110530.99	0.423549343	2.361172542	0.0058173
1425.40074	3.7	2134.18	11998.45	0.177872643	5.62204219	0.01995753
1426.04087	24.0	2355695.08	5101511.27	0.461680517	2.165607643	0.00363005
1426.39584	3.7	1445.34	13011.04	0.111086425	9.002061799	0.02851197
1427.30395	4.0	11715.84	2628.63	4.464285714	0.224365474	0.03869229
1427.39834	3.7	796.51	8716.8	0.091374269	10.94374207	0.02424912
1428.05955	20.9	2780.16	16528.76	0.168208579	5.945254949	1.70E-04
1428.99841	24.0	1054736.06	2176142.36	0.484730974	2.063210354	0.00140214
1430.00316	24.0	651296.81	1377073.78	0.473036897	2.114356709	4.25E-04
1431.00709	24.0	311875.82	729681.77	0.427350427	2.339654834	0.00135014
1433.38426	4.1	4129.74	22194.77	0.186081131	5.374374658	0.00132479
1434.03447	24.0	351299.83	1104256.39	0.318167356	3.143344504	0.00215156
1434.03622	23.7	222115.13	451249.37	0.492125984	2.031601224	8.53E-04
1434.3866	4.1	2308.12	16247.47	0.142065634	7.039265723	0.03053366
1437.05142	8.0	15678.49	34827.86	0.450247636	2.221378462	0.01161709
1437.05224	24.1	1055426.52	2414262.29	0.437254045	2.287475484	0.0379117
1439.06783	24.1	1221540.91	3177704.59	0.384467512	2.601390231	0.01471678
1439.06816	23.6	939493.76	1967762.89	0.477554919	2.094492772	3.97E-04
1440.07178	24.1	1084968.61	2883176.05	0.376364321	2.657381996	0.00606607
1440.09784	24.7	1416124.77	3443425.58	0.411184211	2.431583468	0.01069178
1441.07313	24.0	433627.2	1532834.48	0.282885431	3.534913124	9.81E-04
1441.10347	24.6	773430.79	2287968.06	0.338066261	2.95820659	0.004026
1441.31309	4.0	18561.47	927.97	20	0.049994424	0.04124983
1442.0656	23.6	49795.96	214650.58	0.231964741	4.310602306	0.01888497
1442.06965	25.1	80122.44	299876.43	0.267165375	3.742727131	0.0093773
1442.10712	24.6	321912.14	1007757.56	0.319386777	3.130536052	0.00282447
1442.3159	3.9	16687.91	1690.84	9.900990099	0.101321256	0.04145761
1442.4909	3.3	654.78	4870.31	0.134444743	7.438086075	0.00185465
1443.11188	24.6	102086.12	372951.09	0.273747605	3.653298705	0.0011088
1444.11506	24.6	22597.08	88257.24	0.256016385	3.90569224	0.00199268
1444.40109	3.7	2867.94	9095.95	0.315258512	3.171597035	0.00970982
1446.23988	25.6	6532.57	32247.36	0.202593193	4.936397161	0.01645485
1447.03446	24.0	488718.6	1295524.18	0.377216145	2.650859165	0.02137752
1447.0351	23.7	274221.74	627922.5	0.436681223	2.289834861	3.18E-04
1448.03996	24.0	307157.94	1246100.95	0.246487552	4.05687364	1.42E-05
1448.04105	23.7	236440.3	554394.69	0.426439232	2.344755484	3.90E-04
1449.0527	24.1	750059.51	2644471.52	0.283607487	3.525682276	0.01001685
1449.05338	23.6	620811.39	1356149.69	0.457875458	2.184479396	0.00141792
1450.05568	24.1	615468.57	1421035.69	0.433087917	2.308868006	0.0061408
1450.05745	23.6	493862.8	1060588.76	0.465549348	2.147537251	0.00206499
1450.83763	4.6	78.96	10213.03	0.007731321	129.3443516	0.00203364
1451.06606	24.1	679018.22	1879919.22	0.361141206	2.768584354	0.00150712
1451.06688	23.6	459656.05	1358110.63	0.338409475	2.954623637	6.14E-04
1452.06919	24.1	421285.29	1290959.83	0.326370757	3.064336355	8.45E-04
1452.0702	23.6	319629.61	936221.23	0.341413452	2.929081664	2.77E-04
1453.0721	24.1	327105.26	891213.89	0.366972477	2.724547719	0.02423804
1454.05634	24.0	211590.15	438321.41	0.482625483	2.071558671	0.00134376
1454.06835	23.6	77105.61	247792.92	0.311138768	3.213682117	1.48E-04
1455.05046	24.0	118974.53	288965.24	0.411692054	2.428799172	0.00459166
1455.06425	23.7	53586.57	125099.64	0.428265525	2.334533447	6.49E-04
1455.12098	24.6	2100133.21	4532997.84	0.46339203	2.158433483	0.00391522
1455.50977	3.3	794.5	8390.89	0.094688003	10.56122089	0.00687695
1456.03542	24.0	80896.16	307486.15	0.263088661	3.800998094	1.85E-04
1456.12399	24.6	916168.94	2096186.82	0.437062937	2.287991579	0.00407021
1456.51523	3.3	743.86	7746.61	0.096024582	10.41406985	6.21E-04
1457.00994	24.1	63815.21	164372.57	0.388198758	2.575758506	9.16E-04
1457.12722	24.6	298871.37	726462.79	0.411353353	2.430687121	0.001657
1458.03165	23.6	32153.42	76944.94	0.417885499	2.393056166	0.0211754
1458.1313	24.5	66282.83	160071.77	0.414078675	2.414980923	0.00714601
1461.4098	4.0	5159.48	19000.63	0.271517784	3.682663757	0.02951108

1462.41829	4.1	2544.47	16647.63	0.152835091	6.542670969	8.75E-05
1463.97939	22.0	6926.45	20534.1	0.337268128	2.964592251	0.03931982
1464.06095	24.0	33270.96	129690.49	0.256541816	3.898008654	0.03456974
1464.98222	22.0	5137.17	13942.95	0.368459838	2.714130543	0.02862225
1465.08217	23.6	69196.17	163312.82	0.423728814	2.360142476	0.00144653
1465.99407	21.9	6372.73	35276.73	0.180635838	5.535575805	0.01366181
1466.08885	23.6	45302.35	123582.51	0.366568915	2.727949212	0.01411257
1467.00019	21.9	7237.87	27815.01	0.260213375	3.842982811	0.02376387
1468.01199	21.9	13248.34	89780.83	0.147557916	6.776760711	0.00973958
1468.098	23.6	28362.04	101005.85	0.280819994	3.561304123	6.97E-04
1469.01541	21.9	9086.09	74923.5	0.121270919	8.245956181	0.00655209
1469.09765	23.6	15756.77	33936.27	0.464252553	2.153758035	0.03107173
1469.52446	3.2	908.39	5830.37	0.155811779	6.418355552	0.00283144
1470.02617	21.9	19198.85	177109.83	0.108401084	9.225022853	0.00518816
1470.52617	3.2	1068.75	6571.35	0.16262807	6.148631579	0.01969476
1471.03154	21.9	15217.18	142391.24	0.106871861	9.357268561	0.00480505
1471.3538	4.0	10104.21	1394.18	7.246376812	0.137980109	0.03040991
1472.03759	21.8	14253.57	124262.1	0.114705208	8.717963289	0.00573636
1473.04689	21.8	11463.03	75942.15	0.150943396	6.624963033	0.00534547
1474.05665	21.8	8967.53	34792.13	0.257731959	3.879789641	0.01041448
1475.0492	24.1	28884.98	78609.82	0.367511944	2.721477391	0.01476746
1475.06243	23.6	26442.33	56749.19	0.465983225	2.146149375	0.02440431
1477.09858	24.6	100993.56	212365.17	0.475511175	2.102759522	0.00924429
1478.08356	23.6	35963.56	77877.36	0.461893764	2.165451919	0.00146584
1479.08369	24.0	61254.14	136580.14	0.448430493	2.229729125	0.01180889
1479.09151	23.6	38611.32	82718.47	0.466853408	2.142337273	0.00189298
1480.01703	21.9	4258.75	13929.61	0.305716906	3.27082125	0.01744523
1481.00834	6.9	7622.9	1611.51	4.739336493	0.211403796	0.02927374
1481.01368	21.9	2482.63	12249.63	0.202675314	4.934134366	0.02958713
1481.08254	24.0	26082.95	64545.72	0.404040404	2.474632662	0.03673839
1481.13563	24.5	383785.38	774038.81	0.495785821	2.0168533	0.00752646
1482.03254	21.9	7992.92	34345.63	0.232720503	4.297006601	0.01880747
1482.14596	24.5	496757.99	1037472.87	0.478927203	2.088487535	0.01475856
1483.03756	21.9	5885.59	31810.09	0.185013876	5.404741071	0.01166122
1483.15044	24.5	363810.84	749902.2	0.485201359	2.061242045	0.01653053
1484.0538	21.8	16022.37	73648.03	0.217533174	4.596575288	0.01739398
1484.1529	24.5	164571.89	341762.07	0.481463649	2.076673422	0.02283676
1484.27863	6.8	18915.75	75664.25	0.25	4.000066082	0.00435921
1485.05996	21.9	15334.53	64901.6	0.236294896	4.232382734	0.00626239
1485.15348	24.5	58191.74	123645.1	0.470588235	2.124787814	0.01819209
1485.27763	6.8	22560.85	80658.01	0.27972028	3.575131699	1.86E-04
1486.09669	21.8	8672.2	63398.97	0.136780194	7.310598233	0.01361141
1487.08374	21.8	11309.89	60284.78	0.187617261	5.330271117	0.00730723
1488.12919	21.8	7914.46	46571.41	0.169952413	5.884344605	0.04560207
1489.13197	21.8	6817.11	41848.69	0.162892979	6.138772882	0.02456714
1489.99721	22.0	11610.25	70789.02	0.164015089	6.097114188	0.00104471
1491.00033	21.9	10207.49	61163.19	0.166889186	5.991991175	0.00194732
1492.00903	21.9	24082.45	173307.68	0.138966092	7.196430596	0.00290097
1493.01279	21.9	18720.92	139826.32	0.133886732	7.468987635	0.00278379
1494.02578	21.9	43094.67	299794.6	0.143740118	6.956651484	0.0046504
1495.02978	21.9	32147.64	241110.5	0.133333333	7.500099541	0.00561067
1496.04336	21.8	108826.1	833886.22	0.130497194	7.662557236	0.00607604
1497.04747	21.8	90020.85	697492.74	0.129065565	7.748124351	0.00610333
1498.06025	21.7	290557.68	2391525.27	0.121491921	8.230810729	0.00646488
1498.56218	3.3	685.9	6558.18	0.10459157	9.561422948	0.00226016
1499.06436	21.7	242167.67	1992336.58	0.121550991	8.227095632	0.00659449
1500.06886	21.7	129670.54	1039725.04	0.124719381	8.018205523	0.00639928
1501.07251	21.7	51937.6	435060.51	0.119374478	8.376600189	0.00672709
1502.08242	21.7	22795.75	157106.19	0.145095763	6.891907044	0.00895784
1503.10284	21.7	15141.24	72570.02	0.208637596	4.792871654	0.00197063
1504.12449	21.6	8223.53	31134.17	0.264131009	3.785986067	0.00319358
1505.01308	22.0	3794.91	15623.28	0.242895312	4.116903958	2.80E-04
1506.0258	21.9	12542.68	46538.11	0.269541779	3.710380078	0.00447385
1507.03022	21.8	13589.06	46743.91	0.290697674	3.439819237	0.0119399
1507.34624	6.6	56475.83	158663.62	0.355998576	2.809407493	0.00242022
1508.03767	21.9	13635.65	48264.14	0.282485876	3.539555503	0.0040818
1508.34892	6.6	63657.68	184361.99	0.345303867	2.896146859	0.00859793

1509.04539	21.8	11717.08	51108.59	0.229252636	4.361887945	2.14E-04
1511.06994	21.8	16531.78	95654.55	0.172830971	5.786101073	0.02676882
1511.39239	4.0	37044.45	1795.27	20.83333333	0.04846259	0.04811253
1512.0854	21.8	30071.57	161288.72	0.186462801	5.363495155	0.01392116
1512.30958	6.7	17901.3	39101.05	0.457875458	2.184257568	0.03581937
1513.08476	21.8	42948.45	247771.55	0.173340267	5.769045216	0.02476975
1513.30927	6.8	8487.06	44854.78	0.189214759	5.285078696	0.01351577
1514.13074	21.7	53866.28	335573.01	0.160513644	6.229741686	0.02960507
1515.11353	21.7	80805.81	396790.36	0.203665988	4.910418694	0.02454429
1516.03322	22.0	19969.64	141995.83	0.140627197	7.110585369	0.00273449
1517.101	21.7	23517.57	148705.73	0.158152776	6.323175821	0.03066717
1518.02853	21.9	113558.84	429020.41	0.264690312	3.77795696	0.00471822
1519.03085	21.8	99121.03	394757.55	0.251067035	3.982581194	0.00172681
1520.04213	21.7	323774.61	1210040.35	0.267594327	3.737292279	0.00639569
1521.04631	21.7	270459.41	980127.49	0.27593819	3.623935621	0.00847371
1522.0503	21.7	152290.33	602813.11	0.252652855	3.958315081	0.00480116
1523.05586	21.7	66004.13	298282.84	0.221287896	4.51915418	0.00301396
1524.06891	21.7	38359.93	268301.04	0.142979697	6.994304734	0.00475506
1525.07698	21.7	24152.89	184172.3	0.131147541	7.625269688	0.00661822
1526.08917	21.7	28619.13	228925.42	0.125015627	7.999034911	0.0072458
1526.41177	3.9	13686.92	199.42	66.66666667	0.014570115	0.04833694
1527.09581	21.7	21831.97	179438.54	0.121669303	8.219072305	0.00685589
1528.11243	21.6	18327.49	95433.51	0.192049165	5.207123834	0.03847047
1529.11403	21.7	15856.95	70795.35	0.223964166	4.464625921	0.01527652
1532.03053	22.0	7768.74	27987.47	0.277546489	3.602575192	0.0221172
1532.14212	21.6	11224.1	48918.43	0.229463056	4.358338753	0.03095727
1533.14853	21.6	17647.73	39471.11	0.447027269	2.236611168	0.00278388
1534.03129	21.8	31079.92	99097.74	0.313676286	3.18848118	0.00395647
1535.03546	21.8	31763.23	98511.11	0.32247662	3.101419786	0.00527913
1536.0474	21.7	57512.72	181516.91	0.316856781	3.156117638	0.00108151
1537.04444	21.7	58887.63	156355.89	0.376647834	2.655156779	3.13E-04
1538.01917	22.1	5229.06	36737.28	0.142328494	7.025599247	0.00518738
1538.10773	24.1	6325.34	16784.44	0.376789751	2.653523763	0.02220359
1539.0269	22.1	6328.61	21877.71	0.289268152	3.456953423	0.01780834
1539.08576	21.6	17115.28	61078.38	0.28019053	3.568646262	0.02529118
1539.41739	3.9	9239.04	1586.14	5.813953488	0.17167801	0.03332346
1540.10588	21.5	12506.23	40220.68	0.310945274	3.21605152	0.00380685
1541.10914	21.6	7098.85	35816.08	0.198216056	5.045335512	0.00364362
1541.36558	6.6	5974.7	16259.42	0.367511944	2.721378479	0.03549786
1542.02727	22.1	23489.12	95884.94	0.244977952	4.082100138	0.00866008
1543.03192	22.0	18227.7	67313.68	0.270782562	3.692933283	0.0096032
1544.03879	22.0	26751.75	59430.48	0.450045005	2.221554852	0.02139443
1545.1461	21.6	9203.63	33284.85	0.276548673	3.616491536	0.04573847
1546.05985	21.8	27430.85	101059.02	0.271444083	3.684137385	0.0091567
1547.06703	21.7	19407.87	71872.95	0.27005131	3.703288924	0.00780924
1548.07398	21.7	27644.51	124848.36	0.221434898	4.516208101	0.00523065
1549.07808	21.6	23628.41	96975.81	0.243664717	4.104203795	0.00348624
1550.07842	21.6	19616.59	77374.43	0.253549696	3.944336401	0.00246269
1550.14659	8.2	8561.25	865.16	9.900990099	0.101055337	2.73E-04
1551.08076	21.6	15148.88	48368.49	0.313185092	3.192875645	0.006944
1554.11529	21.5	9941.08	42444.37	0.234192037	4.269593445	0.00394601
1557.14952	21.5	9879.62	20609.43	0.479386385	2.086054929	0.01290249
1561.17245	23.5	6039.25	20118.73	0.300210147	3.331329221	0.00403441
1562.07794	21.6	5818.28	24600.69	0.236518448	4.228172243	0.04639756
1562.12804	8.2	93124.91	704.27	125	0.007562638	0.04483978
1562.17819	23.5	5614.14	16534.55	0.339558574	2.945161681	0.00267748
1563.16473	24.1	16592.69	66551.68	0.249314385	4.010903597	0.00448886
1564.1913	23.5	5385.95	26828.89	0.200762899	4.981273499	1.65E-04
1565.10317	21.5	6192.26	34086.74	0.181653043	5.504733328	0.04315963
1567.40059	6.6	22035.2	66094.2	0.333444481	2.999482646	0.01044553
1568.13633	24.1	20664.43	60813	0.339789331	2.942883012	0.00566943
1568.40458	6.6	17861.66	80442.63	0.222024867	4.503648037	0.01654706
1569.40611	6.6	8881.8	45931.67	0.193386192	5.171437096	0.02210526
1574.08757	21.5	6389.06	19859.94	0.321750322	3.108429096	0.00109367
1576.1064	21.5	3980.59	25138.88	0.158353127	6.31536531	0.00568219
1576.16783	25.7	7172.75	27059.61	0.265041081	3.772557248	0.0310825
1576.43175	3.7	568.64	6768.5	0.084012434	11.90296145	0.02345252

1577.08517	19.5	2877.16	24777.87	0.116117046	8.611919393	0.0365572
1577.11204	21.5	4515.53	20958.16	0.215470804	4.641351071	0.00536816
1578.09409	19.5	2868.95	36260.7	0.079120184	12.63901427	0.03827827
1578.11879	21.4	4175.2	14461.6	0.288683603	3.463690362	0.00557282
1579.1068	19.4	1721.7	31651.02	0.054395126	18.38358599	0.01781571
1582.13359	8.0	314948.07	169.41	1000	0.000537898	0.04762931
1586.08855	21.5	3015.27	12045.35	0.250312891	3.99478322	0.00270664
1591.10223	19.4	2984.68	26291.8	0.113520263	8.808917539	0.03299353
1591.4452	3.7	1300.3	4331.44	0.300210147	3.331108206	0.01901129
1592.11026	19.3	5034.52	59601.26	0.084466593	11.83851887	0.02051504
1593.11881	19.3	4223.74	46937.38	0.089984703	11.11275315	0.02203476
1595.14723	7.9	90425.03	557.24	166.6666667	0.006162453	0.04731439
1595.43321	6.6	31808.89	142202.72	0.22366361	4.470533866	5.91E-04
1596.14565	7.9	341959.22	1036.7	333.3333333	0.003031648	0.03880477
1596.43785	6.6	21823	164531.75	0.132643587	7.539373597	0.00730589
1597.44126	6.6	8424.06	84774.96	0.099373944	10.0634326	1.93E-04
1598.08722	21.5	1938.37	7352	0.263643554	3.792877521	0.00102922
1598.15407	7.9	151400.65	828.03	200	0.005469131	0.0309611
1598.44142	6.6	13062.8	35873.05	0.36416606	2.74619913	0.03537594
1607.13371	19.1	4407.63	38990.11	0.113045444	8.846048784	0.02102796
1607.14798	8.0	75087.97	1307.91	58.82352941	0.017418369	0.01331464
1608.1337	19.1	2296.63	22096.17	0.103939299	9.621127478	0.01477375
1614.21351	6.0	3300.45	9327.55	0.353857042	2.82614492	0.02327591
1617.09266	21.9	3358.52	10875.32	0.308832613	3.2381287	0.03957695
1623.46226	6.6	44892.28	169778.86	0.264410365	3.781916624	0.01781226
1624.16041	7.8	30146.52	1018.36	29.41176471	0.03378035	0.04446795
1624.46955	6.6	26308.07	153377.17	0.171526587	5.830042645	0.02373348
1625.47253	6.6	8648.78	80283.46	0.107723796	9.282634082	4.80E-04
1626.46817	6.6	1464.17	26668.43	0.054902822	18.21402569	0.02084351
1639.4846	6.5	4392.56	11511.67	0.381533766	2.620720036	0.04516083
1643.09749	21.9	6533.58	26483.74	0.246730817	4.053480634	0.00756673
1644.10332	21.8	7284.81	20766.4	0.350754121	2.850644011	0.00633404
1645.11367	21.7	12268.84	51189.85	0.239693193	4.172346367	8.26E-04
1646.11586	21.7	12799.12	52164.25	0.245338567	4.07561223	0.00149895
1646.45425	3.7	1272.56	4103.99	0.310077519	3.224987427	0.0218268
1647.12115	21.7	8025.02	29077.51	0.276014353	3.623356702	0.0016722
1651.49554	6.6	9142.87	29981.59	0.304971028	3.279231795	0.01471659
1652.49845	6.5	7676.97	36387.01	0.210970464	4.739761911	0.00354603
1653.50093	6.5	1046.41	20502.71	0.051038636	19.59338118	5.68E-04
1654.50332	6.5	600.23	9155.8	0.065556575	15.25381937	7.12E-04
1671.1288	21.7	3198.04	8512.02	0.3756574	2.661636502	0.03207816
1673.17445	8.6	23883.31	309.85	76.92307692	0.012973495	0.04830294
1675.22615	24.4	1175.08	4140.8	0.283768445	3.523845185	0.0065609
1676.38712	6.5	597.85	21686.9	0.027567195	36.2748181	0.01691132
1677.38852	6.5	394.29	23929.28	0.016477179	60.68954323	0.01185496
1704.5332	7.6	70.22	9617.61	0.007301189	136.9639704	0.01088786
1705.42024	6.5	255.96	26031.38	0.009832745	101.7009689	0.02270999
1706.42612	6.5	143.7	13909.46	0.010331112	96.79512874	0.05365037
1714.12367	26.2	374.48	73680.2	0.005082515	196.7533647	1.10E-04
1715.12579	26.2	890.05	49001.93	0.018163655	55.05525532	6.73E-04
1740.62367	26.0	7412.73	16315.4	0.454338937	2.200997473	0.00935972
1750.12135	26.0	37172.49	97733.69	0.380372765	2.629194063	0.01560514
1753.8027	24.2	85.14	12670.31	0.006719662	148.8173596	2.43E-04
1760.31787	24.2	136.3	6188.91	0.022023036	45.40652971	0.01134316
1761.31153	24.1	19.36	7276.42	0.00266065	375.8481405	3.87E-04
1765.30414	24.1	59.63	10680.35	0.005583161	179.1103471	0.00334015
1765.80297	24.1	19.36	17322.31	0.001117634	894.7474174	0.00747933
1766.31052	24.1	334.68	22220.66	0.015061602	66.39374925	0.00401533
1766.81262	24.1	67.03	29053.09	0.002307156	433.434134	0.00148001
1767.31675	24.1	69.64	34721.9	0.002005652	498.5913268	0.00397262
1767.82032	24.1	268.04	35977.25	0.007450288	134.2234368	0.00513753
1768.32319	24.1	194.96	33632.96	0.005796698	172.512105	0.00292415
1768.82234	24.1	117.7	27514.59	0.004277727	233.768819	0.01299914
1769.32585	24.1	105.91	17879.64	0.005923504	168.8191861	0.00291415
1774.62741	7.4	19.36	12955.92	0.001494297	669.2107438	0.0018642
1774.82513	24.2	170.65	14205.94	0.012012589	83.24605919	0.00103698
1776.33206	24.1	125.83	12363.04	0.01017791	98.2519272	4.18E-05

1793.26062	19.5	3105.06	15394.9	0.201694232	4.958004032	0.01236546
1813.37692	24.6	17749.06	37647.54	0.471475719	2.121100498	0.02240124
1814.37018	24.6	13305.57	35114.78	0.378931413	2.639103774	0.00482329
1817.34066	24.9	9141.28	23817.8	0.383729854	2.605521327	0.01478631
1817.86348	24.7	13984.44	30405	0.459981601	2.174202185	0.00234038
1821.38824	24.6	15184.23	39975.6	0.379794911	2.632705116	0.00432947
1821.8954	24.6	11805.65	33760.26	0.34965035	2.859669734	0.02208756
1827.84225	24.9	42916.48	11972.35	3.584229391	0.278968592	0.00112267
1832.86305	24.6	12543.42	26199.66	0.478697942	2.088717431	0.01407708
1833.89246	24.5	12114.1	25248.9	0.479846449	2.084257188	0.00627191
1856.73375	5.0	765.73	12441.44	0.061546036	16.24781581	0.00536342
1858.71634	4.9	996.23	7538.96	0.132152769	7.567489435	0.02592293
1859.72742	5.0	378.49	8623.92	0.043888523	22.78506698	5.79E-05
1860.7031	4.9	98.07	4860.02	0.020178784	49.55664321	0.00515583
1869.69965	4.8	38.65	8637	0.004474934	223.4670116	5.00E-04
1870.53993	8.6	19.36	5347.23	0.003620565	276.1998967	8.63E-04
1870.70389	4.8	19.36	6482.98	0.002986278	334.8646694	3.93E-04
1871.71271	4.8	112.57	4699.2	0.023954965	41.74469219	4.36E-04
1885.72907	4.8	258.86	17853.97	0.014498637	68.97152901	5.70E-06
1886.73179	4.8	402.67	20879.07	0.019285659	51.8515658	0.00142408
1887.73026	4.8	472.76	15270.37	0.030959752	32.30046958	0.00355794
1897.72942	4.8	19.36	5954.38	0.003251388	307.5609504	7.43E-07
1898.7333	4.8	19.36	5121.95	0.003779804	264.5635331	0.00133285
1912.74102	4.8	36.69	5160.03	0.007110403	140.6385936	2.53E-04
1914.76322	4.8	1580.21	14094.62	0.112120193	8.919460072	0.00895269
1916.77795	4.9	1038.99	7205.17	0.144196107	6.934782818	0.04370568
1917.79445	4.9	190.22	8745.24	0.021751425	45.97434549	3.72E-06
1941.77572	4.8	19.36	6184.34	0.003130488	319.4390496	0.00275978
1944.8243	4.9	1793.67	17106.69	0.104854776	9.537256017	0.02906022
1945.82801	4.9	548.76	22866.31	0.023998656	41.66905387	0.01991246
1946.83157	4.9	19.36	14695.67	0.001317395	759.0738636	0.01220412
1958.79727	4.8	69.94	6780.36	0.010315127	96.94538176	5.99E-08
1967.80416	5.0	19.36	7512.24	0.002577127	388.0289256	3.95E-04
1968.80361	4.9	19.36	7535.27	0.002569254	389.2184917	7.16E-07
1970.62803	8.3	106.43	7457.69	0.014271239	70.07131448	0.02746131
1971.64743	8.2	85.83	12589.36	0.006817655	146.6778516	0.01190222
1972.6529	8.1	160.18	12110.63	0.013226464	75.60638032	0.02217691
1972.84953	4.9	1725.18	17879.92	0.096487843	10.36408954	0.02111376
1973.85629	4.9	849.69	25447.17	0.033390096	29.94876955	0.00493924
1974.8613	4.9	55.6	18132.75	0.003066271	326.1285971	0.01310375
1975.85912	4.9	19.36	8873.87	0.002181686	458.3610537	0.0010971
1982.79858	4.8	19.36	6218.42	0.003113335	321.1993802	5.05E-05
1983.8081	4.8	19.36	6235.95	0.003104578	322.1048554	4.90E-04
1984.81744	4.8	843.59	15804.48	0.053376034	18.73478823	5.03E-04
1985.64177	8.2	19.36	5676.08	0.003410804	293.1859504	0.01592778
1985.82118	4.8	855.58	21626.73	0.039561657	25.2772739	4.71E-04
1986.82467	4.8	780.21	16013.77	0.048721072	20.52494841	4.41E-04
1987.83099	4.8	250.14	9748.78	0.025658789	38.97329495	2.83E-05
1994.82484	4.9	19.36	5895.98	0.003283598	304.5444215	0.00612716
1996.82226	4.8	45.72	7667.42	0.005962887	167.7038495	0.0026006
1998.8306	4.8	253.36	6684.94	0.037900322	26.38514367	5.20E-04
1999.83243	4.8	19.36	5684.79	0.003405577	293.6358471	9.66E-04
2001.87708	4.9	19.36	8387.39	0.002308227	433.2329545	0.00902207
2002.84997	4.8	43.9	9872.65	0.004446618	224.8895216	0.02084031
2005.6432	8.0	19.36	4399.92	0.004400072	227.268595	0.00449369
2010.82656	4.8	19.36	6086.39	0.003180864	314.3796488	7.25E-06
2011.69105	8.0	19.36	8793.59	0.002201605	454.2143595	2.85E-04
2011.83681	4.8	19.36	8028.38	0.002411446	414.6890496	0.00184583
2012.84977	4.8	19.36	16253.1	0.001191157	839.5196281	3.90E-04
2013.68787	8.0	19.36	11062.47	0.00175006	571.4085744	6.46E-04
2013.84924	4.7	19.36	20190.32	9.59E-04	1042.88843	2.50E-04
2014.70033	7.9	19.36	7705.92	0.002512355	398.0330579	0.00173322
2014.85431	4.8	19.36	15745.5	0.001229557	813.3006198	1.76E-04
2015.85701	4.7	87.39	9123.16	0.009578911	104.3959263	0.00155415
2019.40059	6.0	12697.05	19.36	500	0.001524764	0.01476724
2020.40856	6.0	9800.16	19.36	500	0.001975478	0.03238582
2027.5188	24.2	6125.19	19.36	333.3333333	0.003160718	0.00453397

2028.40789	6.0	12309.29	19.36	500	0.001572796	0.01095543
2028.53473	24.2	18885.65	67.87	250	0.003593734	0.00637358
2029.41798	6.0	9628.88	19.36	500	0.002010618	0.04218841
2029.53938	24.2	18952.77	151.48	125	0.007992499	0.00764456
2030.41585	6.0	8168.59	19.36	500	0.002370054	0.03169255
2030.87409	4.8	19.36	6407.16	0.003021623	330.9483471	1.37E-04
2031.55558	24.2	25216.78	115.63	200	0.004585439	0.04192651
2033.5589	24.2	9394.74	19.36	500	0.002060728	0.00640929
2033.67393	7.9	19.36	6494.54	0.002980964	335.4617769	6.26E-04
2039.71998	7.8	19.36	7709.61	0.00251115	398.223657	0.00730928
2040.88316	4.7	19.36	4482.49	0.00431902	231.5335744	2.29E-04
2044.40926	5.9	21047.5	19.36	1000	0.000919824	0.04159512
2044.56378	24.2	11357.3	101.04	111.1111111	0.008896481	0.01099419
2045.57063	24.1	10961.43	122.49	90.90909091	0.011174637	0.00825404
2047.4266	5.9	41346.25	92.92	500	0.002247362	0.04898729
2048.4292	5.9	27239.76	19.36	1000	0.000710726	0.04524826
2049.43033	6.0	14155.65	19.36	1000	0.001367652	0.04521353
2052.53547	24.1	12843.25	198.6	66.66666667	0.015463376	3.07E-04
2054.5502	24.2	43831.5	1363.33	32.25806452	0.031103886	0.02104312
2055.41569	6.0	5365.28	19.36	250	0.003608386	0.02826321
2055.55495	24.1	49336.62	1789.56	27.77777778	0.036272448	0.02028244
2055.74841	7.8	88.25	8832.03	0.009992006	100.0796601	0.02651333
2056.5673	24.1	109411.62	835.65	125	0.007637671	0.02926766
2057.57131	24.1	113939.49	1460.96	76.92307692	0.012822245	0.03398647
2059.70474	7.9	19.36	5874.14	0.003295805	303.4163223	0.00302782
2060.42806	6.0	6196.43	19.36	333.3333333	0.00312438	0.04503209
2060.70588	7.9	19.36	8901.49	0.002174915	459.7877066	8.90E-04
2061.43328	6.0	9715.02	19.36	500	0.001992791	0.03424436
2062.60045	24.1	18632.68	78.57	250	0.004216785	0.0464424
2063.44182	5.9	9723.41	19.36	500	0.001991071	0.03052416
2068.56319	24.1	12496.71	991.98	12.65822785	0.079379293	0.04326347
2069.56404	24.2	15608.11	163.37	100	0.010466994	0.00280953
2070.58079	24.1	39789.01	1011.31	40	0.025416817	0.01821245
2071.42022	6.0	7913.82	19.36	500	0.002446353	0.0053208
2071.58611	24.1	41338.42	913.23	45.45454545	0.022091556	0.01828764
2072.59656	24.1	61412.8	2652.58	23.25581395	0.043192624	0.03813208
2074.44398	5.9	14231.49	19.36	1000	0.001360364	0.02799271
2074.72474	7.8	19.36	3934.16	0.004920993	203.2107438	8.72E-04
2078.55188	24.2	13435.95	1188.57	11.36363636	0.088461925	0.03631657
2079.55164	24.2	14582.21	2062.83	7.092198582	0.141462097	0.01358788
2080.56656	24.1	36154.95	5546.78	6.535947712	0.15341689	0.02997969
2082.58167	24.1	95125.72	1911.51	50	0.020094565	0.02395754
2083.58856	24.0	105763.1	1959.63	52.63157895	0.018528485	0.03379414
2090.62506	24.0	15438.04	303.62	50	0.019667004	0.04590045
2096.58137	24.1	39357.7	3204.85	12.34567901	0.081428793	0.04593512
2103.64476	23.7	32545.24	2567.18	12.65822785	0.078880352	0.04829646
2106.57775	24.1	9023.09	1449.43	6.211180124	0.160635658	0.03724195
2108.59018	24.0	20001.1	1724.24	11.62790698	0.086207259	0.01795816
2109.59634	24.0	19869.16	1319.72	15.15151515	0.066420523	0.03056804
2110.61632	24.0	42773.38	3082.5	13.88888889	0.07206585	0.0349077
2111.62049	23.9	50585.58	3626.5	13.88888889	0.071690391	0.03105281
2112.63174	23.7	57822.4	3211.71	17.85714286	0.055544391	0.02966265
2113.63811	23.7	52811.27	1947.63	27.02702703	0.03687906	0.03920776
2114.6427	23.7	50387.94	2155.16	23.25581395	0.042771346	0.03870117
2115.64994	23.7	39114.95	3598.59	10.86956522	0.092000373	0.04246612
2116.65735	23.7	25783.96	1033.07	25	0.040066382	0.03856199
2128.62114	24.2	15300.28	42444.31	0.360490267	2.774087141	0.02500419
2130.63422	24.1	5195.94	31434.19	0.165289256	6.049760005	0.01216898
2153.87486	3.2	352.88	3964.42	0.089015489	11.23447064	0.00586216
2165.62481	24.6	45812	103883.21	0.440917108	2.267598228	0.0180319
2166.13118	24.7	31491.45	75922.93	0.414765657	2.410906135	0.04086156
2167.12138	24.7	26226.2	53945.96	0.486144871	2.056949158	0.03717978
2173.65383	24.6	147702.2	306429.23	0.481927711	2.074642287	0.01748033
2174.65507	24.6	92167.61	247073.8	0.372995151	2.680700953	0.01017107
2175.64661	24.6	58063.61	136860.01	0.424268137	2.357070289	0.03365098
2180.15224	24.6	43114.66	88423.32	0.48756704	2.050887564	0.04269157
2188.6758	24.6	150497.07	313758.36	0.479616307	2.084813744	0.02451969

2189.15619	24.6	19182.23	63376.21	0.302663438	3.303902101	0.01470439
2189.67815	24.6	96139.23	205584.41	0.467726848	2.138402918	0.02315876
2190.6753	24.5	48173.7	104668.13	0.460193281	2.172723499	0.0098651
2191.64624	24.6	31048.19	63517.34	0.488758553	2.045766275	0.04250173
2215.52223	21.9	92.11	5847.14	0.015752993	63.4799696	0.00361964
2216.52997	21.9	283.92	11242.12	0.025255076	39.5960834	0.00596861
2217.53593	21.9	292.9	9215.82	0.031782354	31.46404916	0.00300503
2218.55188	21.9	794.98	14447.25	0.055026688	18.17309869	0.00159789
2219.55105	21.9	605.94	14076.4	0.04304593	23.23068291	0.00684165
2220.56094	21.8	432.75	13493.34	0.032071841	31.18045061	0.00705895
2221.56632	21.8	90.27	9720.02	0.009287034	107.6771907	0.00717473
2222.5679	21.8	19.36	5220	0.003708814	269.6280992	0.01356749
2232.56391	21.8	764.67	7993.99	0.095657165	10.45416977	5.22E-04
2236.5128	22.0	174.53	5878.37	0.02969033	33.68114364	0.00129837
2237.5181	21.9	249.32	6492.54	0.038400983	26.0409915	0.00124766
2238.51408	21.9	655.45	12068.24	0.054312405	18.41214433	0.00575031
2239.52196	21.9	731.39	13116.87	0.055760009	17.93416645	0.00250554
2240.53187	21.9	1493.35	22117.02	0.067521945	14.81033917	0.00317361
2241.53373	21.9	1716.29	21880.69	0.078437525	12.74883033	0.00479049
2242.54764	21.9	3417.06	33817.23	0.101040719	9.896586539	0.01213658
2243.55394	21.9	3584.78	35363.85	0.101368474	9.864998689	0.00906271
2244.56497	21.8	6796.78	67771.7	0.100290843	9.971148102	0.00517714
2245.57084	21.8	5954.67	73788.2	0.080697224	12.39165227	0.00452579
2246.58383	21.7	12415.52	139123.94	0.089237908	11.20564745	0.00529826
2247.58865	21.7	13456.41	151486.14	0.088825724	11.25754492	0.00582659
2248.59199	21.7	10547.13	108859.6	0.096889836	10.32125327	0.00513439
2249.59664	21.7	4844.31	59305.51	0.081685999	12.24230283	0.00424776
2250.59598	21.7	2868.23	28545.05	0.100482315	9.952148189	0.00804981
2251.59948	21.7	839.28	11090.17	0.075677312	13.21390954	0.00401157
2254.5469	21.8	980.24	6851.31	0.143081986	6.989420958	0.02692511
2255.54751	21.8	1421.52	7589.88	0.187300993	5.33927064	0.01686794
2256.55391	21.9	1797.75	8846.68	0.20321073	4.920973439	0.00336675
2258.56654	21.8	2059.87	11953.69	0.17232466	5.803128353	0.00317253
2259.57651	21.8	793.56	11952.34	0.066392245	15.06167146	0.00696515
2260.53242	22.0	441.14	8109.71	0.054395126	18.38352904	3.02E-04
2260.59742	21.7	2508.42	23164.78	0.108283703	9.234809163	0.01122124
2261.60128	21.7	2849.03	29270.44	0.097333074	10.27382653	0.01144223
2262.60823	21.7	3385.66	28609.1	0.118343195	8.450080634	0.01440143
2263.54624	22.0	1410.73	14187.42	0.099433231	10.05679329	1.74E-04
2263.61429	21.7	5060.19	38000.09	0.133155792	7.509617228	0.03368005
2264.54162	21.9	4215.48	22210.58	0.189789334	5.26881399	0.004908
2264.61835	21.7	2916.6	29635.89	0.09841551	10.16110883	0.00606546
2265.54838	21.9	4890.46	26086.87	0.187476565	5.334236452	0.02588451
2265.62247	21.6	1621.15	16353.19	0.099137504	10.08740092	0.00600274
2266.55166	21.9	10795.35	51793.99	0.208420175	4.797805537	0.00320822
2267.5529	21.8	10821.32	57934.61	0.186776242	5.353747047	0.00264374
2268.56505	21.7	20666.71	107338.94	0.192529842	5.193808787	0.00288938
2269.57019	21.7	21988.24	110948.89	0.198176774	5.045828588	0.00389619
2270.5731	21.7	15664.51	84967.63	0.184365782	5.424212439	0.00352093
2270.62666	25.0	4288.31	370.71	11.62790698	0.086446642	0.02172895
2271.57945	21.7	8894.4	54111.7	0.164365549	6.083794298	9.55E-04
2272.58874	21.7	5997.22	39135.88	0.153233221	6.525670227	0.00475156
2273.59483	21.7	3861.21	25728.8	0.150082545	6.663403441	0.01770877
2274.60828	21.7	3419.99	26315.48	0.129954516	7.694607294	0.00996396
2275.61575	21.7	1999.75	20248.36	0.098765432	10.12544568	0.00984282
2276.61555	21.7	2496.07	18783.07	0.132890365	7.52505739	0.01998149
2277.62243	21.7	2424.98	13294	0.182415177	5.482107069	0.03396571
2278.63285	21.6	1685.45	10867.8	0.155086849	6.448010917	0.00332559
2280.5379	21.9	1773.77	9419.35	0.188323917	5.310355909	2.43E-04
2281.53939	21.9	1233.11	7107.85	0.173490632	5.764165403	0.0016915
2282.58134	21.7	4243.84	12437.24	0.341180484	2.930657141	0.04269854
2283.57526	21.7	4613.08	16014.14	0.288101412	3.471463751	0.00355577
2284.57782	21.7	6011.38	23520.24	0.255558395	3.912619066	0.00120182
2285.56889	21.7	4690.99	18990.03	0.247035573	4.048192386	6.68E-04
2286.52314	22.0	2034.14	15240.09	0.133475707	7.492153932	0.00164481
2286.59358	21.6	4187.84	12430.2	0.336927224	2.968164973	0.00467378
2287.52464	22.0	2042.84	12954.88	0.157678966	6.341602867	0.00614411

Dataset S1

2287.60145	21.6	2018.91	11045.3	0.182781941	5.470922428	0.00264882
2294.58052	21.7	4538.35	18344.99	0.247402276	4.042215783	0.00326226
2296.58899	21.7	4105.41	18755.31	0.218914186	4.568437744	0.00722756
2297.59742	21.6	4107.22	14856.96	0.276472215	3.617278841	0.01926004
2298.60276	21.6	3114.52	13031.96	0.239005736	4.184259533	0.01916241
2299.59676	21.6	3228.55	12017.35	0.268672757	3.722212758	0.00710665
2399.14214	3.0	1867.82	4223.11	0.442282176	2.260983392	0.03724559
2505.18795	6.3	19.36	7137.61	0.002712394	368.6782025	0.00750858
2519.19926	6.4	19.36	10636.96	0.001820068	549.4297521	0.00463417
2521.20426	6.5	19.36	5325.39	0.003635412	275.0717975	0.0066179
2532.22374	6.2	254.59	7878.47	0.032314354	30.94571664	5.87E-07
2547.22917	6.3	19.36	13020.53	0.001486883	672.5480372	0.00404746
2548.23999	6.2	101.12	12617.44	0.008014298	124.7768987	0.00418088
2548.42583	24.6	16718.46	36697.36	0.455580866	2.195020355	0.01207199
2553.93851	24.6	12677.52	28083.02	0.451467269	2.215182465	0.02529375
2555.44307	24.5	16536.44	33791.25	0.48947626	2.043441636	0.03436741
2560.25662	6.2	248.87	12162	0.02046287	48.86888737	7.31E-04
2561.25454	6.2	258.02	13370.36	0.019297941	51.81908379	6.22E-04
2562.25585	6.2	230.3	12395.67	0.018579073	53.82401216	0.00175396
2562.45018	24.5	14560.11	31203.04	0.466635558	2.143049743	0.03893115
2564.2477	6.4	19.36	6247.88	0.003098652	322.7210744	0.00778008
2575.27019	6.1	125.16	12566.58	0.009959763	100.4041227	0.00524944
2577.26939	6.1	19.36	10383.93	0.001864419	536.3600207	0.0021608
2578.27344	6.2	19.36	6485.95	0.002984914	335.0180785	9.64E-06
2587.27845	6.1	186.86	16241.55	0.011505097	86.91828107	8.24E-06
2588.28656	6.1	193.63	21062.94	0.009192951	108.7793214	6.48E-04
2589.28654	6.1	190.88	20414.49	0.009350251	106.9493399	2.93E-06
2591.29225	6.1	80.57	9831.34	0.008195243	122.0223408	0.00337958
2601.29766	6.1	19.36	9217.13	0.002100439	476.0914256	0.01829507
2602.29873	6.1	64.76	21715.46	0.002982208	335.3221124	1.00E-04
2603.2899	6.3	19.36	17733.63	0.001091711	915.9932851	0.004089
2604.29929	6.1	30.91	20162.73	0.001533028	652.3044322	2.12E-05
2605.31197	6.1	19.36	15980.14	0.001211504	825.4204545	0.00615498
2615.2989	6.1	27.9	7315.3	0.003813926	262.1971326	0.04287791
2616.31217	6.1	137.83	15174.1	0.00908323	110.092868	0.00247372
2617.30983	6.2	42.59	8901.17	0.004784758	208.9967128	7.49E-04
2618.31081	6.1	69.01	12770.66	0.005403799	185.0552094	1.21E-04
2628.31037	6.1	43.57	10623.3	0.004101369	243.8214368	0.00614619
2629.31978	6.1	29.82	17103.39	0.001743515	573.554326	0.0055799
2630.33187	6.0	36.45	20560.06	0.001772855	564.0620027	0.00151821
2631.32491	6.1	44.13	18044.3	0.002445646	408.8896442	0.02010126
2634.32919	6.1	27.99	7648.77	0.003659411	273.2679528	0.01453647
2643.34936	6.0	47.16	12860.62	0.003667006	272.701866	0.00112129
2645.34458	6.0	44.54	22762.29	0.001956744	511.0527616	3.78E-05
2646.35263	6.0	102.92	13397.78	0.007681849	130.1766421	0.01509961
2648.35883	5.9	39.95	11492.7	0.003476121	287.6770964	0.00641542
2657.3349	6.0	43.09	7689.21	0.005603968	178.4453469	6.60E-04
2658.36802	6.0	24.62	9814.22	0.002508605	398.6279448	5.79E-04
2660.3698	6.0	19.36	7952.96	0.002434316	410.7933884	0.00566186
2662.36951	6.0	23.56	5746.66	0.004099772	243.9159593	0.00630128
2672.37331	5.9	19.36	11500.92	0.001683343	594.0557851	0.00201903
2673.37785	5.9	49.32	15439.65	0.003194378	313.0504866	9.33E-06
2674.37027	6.1	51.04	10379.1	0.004917581	203.3522727	9.89E-04
2675.38697	5.9	20.76	8055.8	0.002577027	388.044316	0.00242349
2676.38254	5.9	20.73	4694.2	0.004416083	226.444766	1.74E-04
2685.38697	5.9	19.36	9964.82	0.001942834	514.7117769	3.80E-05
2686.38876	5.9	24.69	16311.73	0.001513636	660.6614014	6.78E-07
2687.39239	5.9	30.08	15300.07	0.001966004	508.6459441	9.26E-04
2690.39093	6.0	19.36	8657.22	0.002236286	447.1704545	4.05E-04
2699.39939	5.8	19.36	4900.13	0.003950914	253.1058884	2.46E-06
2714.41674	5.8	25.33	8600.51	0.002945178	339.5384919	2.79E-04
2715.42048	5.8	19.36	8314.85	0.002328365	429.4860537	0.00321265
2716.41596	5.8	20.11	8273.27	0.002430718	411.4007956	5.31E-05
2727.43853	5.8	19.36	4596.93	0.004211502	237.4447314	0.00136037
2829.03537	23.9	108966.71	229595.49	0.474608448	2.107024154	0.01787658
2831.02547	24.0	61278.42	124203.35	0.493339911	2.026869329	0.00954231
2831.51482	23.8	30859.37	63421.87	0.486618005	2.055190044	0.00266297

2835.01937	24.0	45060.43	106984.36	0.421229992	2.374241879	0.00269472
2836.02734	24.0	35257.59	79561.07	0.443066017	2.256565749	0.03205593
2840.0291	24.0	49317.83	105092.54	0.469263257	2.130923846	0.01475419
2841.53614	23.9	31423.73	77159.86	0.407331976	2.455464708	0.00296197
2842.53271	24.0	19956.83	48000.06	0.415800416	2.405194613	0.02791758
2843.04699	23.8	36613.65	107548.94	0.340483487	2.937400123	0.00128655
2843.53801	24.0	18069.12	39729.29	0.45475216	2.198739618	0.02546949
2843.54533	23.6	13940.23	33000.9	0.422475708	2.367313882	5.70E-04
2846.04539	24.0	17156.23	60056.81	0.285632676	3.50058317	0.00757272
2848.02552	24.0	19812.74	44103.03	0.449236298	2.225993477	0.00832101
2849.01925	24.0	18778.13	40361.07	0.465332713	2.149365778	0.00298982
2849.55184	23.6	14107.58	28692.15	0.491642085	2.033810902	0.00970798
2851.03734	23.6	14856.19	34642.71	0.428816467	2.331870419	2.06E-04
2855.04348	24.0	27334.25	59017.6	0.463177397	2.159108079	0.02062916
2855.05148	23.6	12238.65	29546.71	0.414250207	2.414213169	2.06E-04
2855.54646	23.6	7392.01	14890.47	0.49652433	2.014400684	0.00309058
2856.04803	24.1	23054.52	51878.89	0.444444444	2.250269795	0.02960718
2856.05916	23.6	13477.4	30523.26	0.441501104	2.264773621	0.00100682
2856.55196	23.6	6661.2	16354.39	0.407331976	2.455171741	0.01407345
2857.05889	23.6	10598.72	25643.35	0.413393964	2.419476125	8.09E-04
2859.03484	24.1	13657.27	29587.66	0.461680517	2.166440292	0.04983478
2860.03813	24.1	10696.8	26002.63	0.411353353	2.430879328	0.04078981
2862.9839	24.0	6526.52	15990.14	0.408163265	2.450025435	4.38E-04
2869.06559	23.6	2639.42	9908.52	0.266382525	3.754052027	5.23E-05
2890.16298	24.6	13325.9	27707.83	0.481000481	2.07924643	0.0063462
2892.17365	24.6	7706.21	20729.22	0.371747212	2.689937077	0.01390234
2995.09647	21.8	89.96	5598.72	0.016067871	62.23566029	0.00486699
2996.10157	21.7	19.36	5578.97	0.003470174	288.169938	0.00137674
2997.11283	21.7	19.36	4837.86	0.004001777	249.8894628	0.01068697