NMR-guided fragment-based approach for the design of tRNA(Lys3) ligands.

Florence Chung, Carine Tisné, Thomas Lecourt, Frédéric Dardel, Laurent Micouin

HAL Id: hal-00218344
https://hal.archives-ouvertes.fr/hal-00218344

Submitted on 27 Jan 2008

# NMR-guided fragment-based approach for the design of tRNA$^{Lys}_3$ ligands.[∗∗]

Florence Chung, Carine Tisné, Thomas Lecourt, Frédéric Dardel* and Laurent Micouin**

RNA is a key player in many cellular processes or in viral infection and is thus an attractive target in drug discovery.[1] The clinical utility of antibiotic drugs targeting the bacterial ribosome has demonstrated that RNA can indeed be a relevant target.[2] Among other druggable RNAs, functional sites within the genomic RNA of HIV-1, such as TAR, RRE or the dimerisation initiation site, have been selected as possible targets for new anti-viral strategies.[3]

Like all retroviruses, HIV-1 uses a cellular tRNA, tRNA$^{Lys}_3$ for priming reverse transcription.[4] In virions, the 18 3'-terminal nucleotides of tRNA$^{Lys}_3$ are base-paired to the genomic RNA. This complex in turn specifically recruits the reverse transcriptase.[5] The aim of this study was to find molecules that bind to tRNA$^{Lys}_3$ and serve as leads for inhibitors of the formation of the HIV-1 reverse transcription initiation complex. Indeed, destabilisation of this process by oligodeoxyribonucleotides has been reported to result in an efficient inhibition of reverse transcription, providing the proof of concept of a possible new antiviral strategy.[6]

Despite recent breakthroughs in the understanding of the interaction between aminoglycosides and ribosomal RNAs,[7] the *de novo* design of new compounds that specifically bind to structured RNAs is still a standing challenge. A recent promising approach for the synthesis of shape-specific 2-deoxystreptamine (2-DOS) dimers that can bind selectively to RNA loops has been reported.[8] Rational design of selective tRNA$^{Lys}_3$ binder is however difficult because of the lack of known ligands[9] and of its shape-similarity to other tRNAs. A combinatorial approach only led to low-affinity structure-specific peptidic ligands.[10] However, the availability of crystallographic[11] and NMR data[12,13] and of an efficient expression system made it possible to undertake a fragment-based

[∗]   Dr. C. Tisné, Prof. F. Dardel
        Cristallographie et RMN Biologiques, Université Paris
        Descartes, CNRS, 4 avenue de l'Observatoire, 75006 Paris
        (France)
        Fax: (+33) 1 53 73 99 25
        E-mail: carine.tisne@univ-paris5.fr

        F. Chung, Dr. T. Lecourt, Dr. L. Micouin
        Chimie Thérapeutique, Université Paris Descartes, CNRS, 4
        avenue de l'Observatoire, 75006 Paris (France)
        Fax: (+33) 1 43 29 14 03
        E-mail: laurent.micouin@univ-paris5.fr

approach.[14] We used NMR screening[15] to identify ligands from spectral changes induced by their binding on the target.[16] A primary screen was performed over a focussed collection of 50 in-house or commercial organic compounds using 1D NMR on the RNA imino proton window (10-15 ppm), which is devoid of ligand signals. As result, compounds **1** and **2** were detected to bind to tRNA$^{Lys}_3$ (Figure 1).
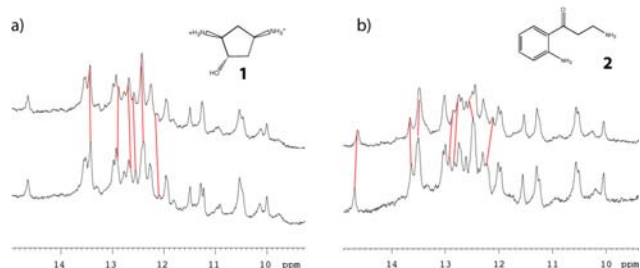
Figure 1. Binding of a) compound **1** (2.1 mM) and b) kynuramine **2** (0.6 mM) to tRNA$^{Lys}_3$ monitored by NMR chemical shift perturbation of the RNA imino protons (top spectra). Bottom: reference tRNA$^{Lys}_3$ spectrum (0.3 mM).

Their NMR footprints on the target were then determined on 2D HMQC spectra using ^{15}N-labeled tRNA. Kynuramine **2** interacts with the D-stem (Figure 2), and **1** exhibits binding to at least two specific sites located in the T and D-stems.[17] From NMR titrations, the apparent dissociation constants of **1** and **2** for tRNA$^{Lys}_3$ were estimated to be 2mM and 5mM, respectively.
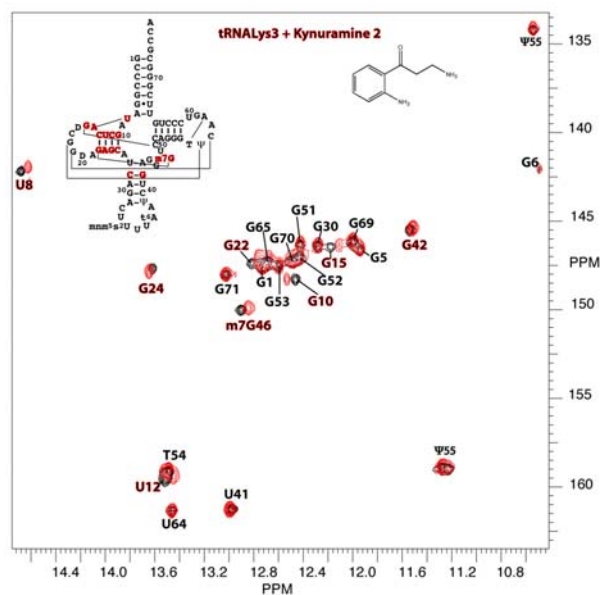
Figure 2. Superimposition of HMQC spectra of tRNA$^{Lys}_3$ alone (0.8 mM) in black and tRNA$^{Lys}_3$ mixed with compound **2** (1.6 mM) in red.

A qualitative specificity study was conducted with these two compounds by analysing their NMR footprints with two other tRNAs: *E. coli* tRNA$_f^{Met}$ and tRNA$_m^{Met}$. **1** binds to both tRNA which have very similar T-arms sequences. Interestingly, **2** only binds to the D-arm of tRNA$_m^{Met}$, showing that this compound, despite its moderate affinity, appears to interact in a sequence-specific manner with tRNA$_m^{Met}$ and tRNA$^{Lys}_3$ with identical D-stems (Figure 4). Structural elements required for the binding of kynuramine **2** were then investigated (Scheme 1). Qualitative comparison of chemical shift perturbations indicated that binding
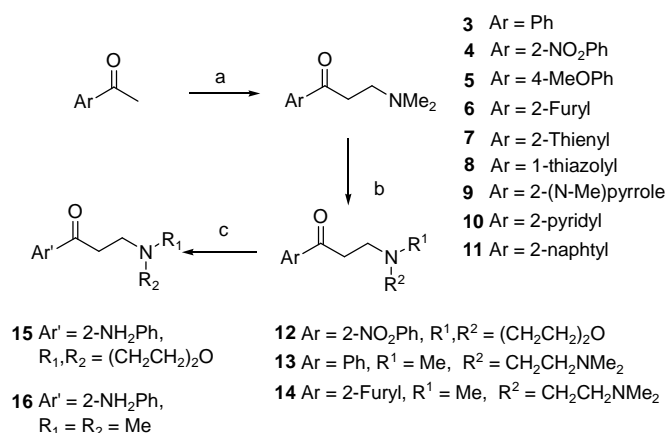
was improved when the aniline moiety was changed for other heterocycles, except for compounds **4**, **12** and **16**. Reduction of the carbonyl function to the corresponding alcohol led to the loss of interaction. Binding of **3** was not improved by introduction of an extra nitrogen atom on the side chain (compound **13**).

3 Ar = Ph
4 Ar = 2-NO$_2$Ph
5 Ar = 4-MeOPh
6 Ar = 2-Furyl
7 Ar = 2-Thienyl
8 Ar = 1-thiazolyl
9 Ar = 2-(N-Me)pyrrole
10 Ar = 2-pyridyl
11 Ar = 2-naphtyl

15 Ar' = 2-NH$_2$Ph, R$_1$,R$_2$ = (CH$_2$CH$_2$)$_2$O

16 Ar' = 2-NH$_2$Ph, R$_1$ = R$_2$ = Me

12 Ar = 2-NO$_2$Ph, R^1,R^2 = (CH$_2$CH$_2$)$_2$O
13 Ar = Ph, R^1 = Me, R^2 = CH$_2$CH$_2$NMe$_2$
14 Ar = 2-Furyl, R^1 = Me, R^2 = CH$_2$CH$_2$NMe$_2$

Scheme 1. a) (CH$_2$O)$_n$, Me$_2$NH.HCl, 35% aq. HCl, EtOH, Δ then K$_2$CO$_3$; b) CH$_3$I, CH$_2$Cl$_2$, r.t., then R^{1}R^{2}NH, CH$_3$Cl, 60 °C; c) H$_2$, Pd/C, MeOH.

The fluorescent properties (λ$_{exc}$ = 341 nm, λ$_{em}$ = 478 nm) of compound **11** were used to estimate its dissociation constant to tRNA$^{Lys}_3$ (Kd = 191 ± 86 μM), and its binding to tRNA$^{Lys}_3$ D-arm was confirmed by a 2D TROSY experiment.

The next step was to attempt to covalently link the two ligands in order to improve binding. **1** is a 2-DOS surrogate and hence an "RNA-friendly" compound, which probably binds to several sites on tRNA. As evidenced by the discrete NMR shifts, this multiple binding is nevertheless specific, resulting from the constrained amine geometry, a situation already described for 2-DOS with 16S ribosomal RNA.[18] This can be considered as an advantage for our strategy, as it should improve the chances to get a productive linkage.
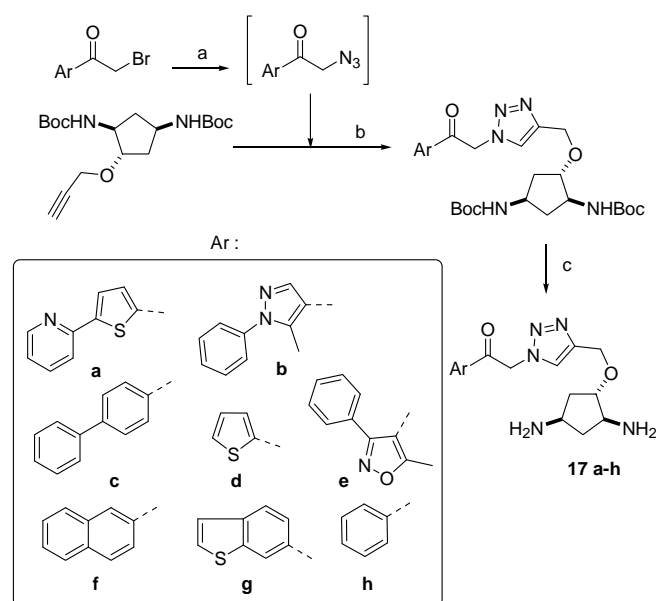

Scheme 2. a) NaN$_3$, H$_2$O/Acetone; b) CuSO$_4$, sodium ascorbate; c) HCl, MeOH then amberlyst resin, then NH$_3$, MeOH.

A library of connected fragments was prepared using a one-pot procedure leading to compounds **17a-h** in 6-66% overall yield after a catch-and-release purification on sulfonic acid resin (Scheme 2). Binding of these compounds to tRNA$^{Lys}_3$ was then monitored in a TROSY experiment, showing improved affinity and specificity with the D-arm region (Figure 3 for **17f**) under stoichiometric conditions.
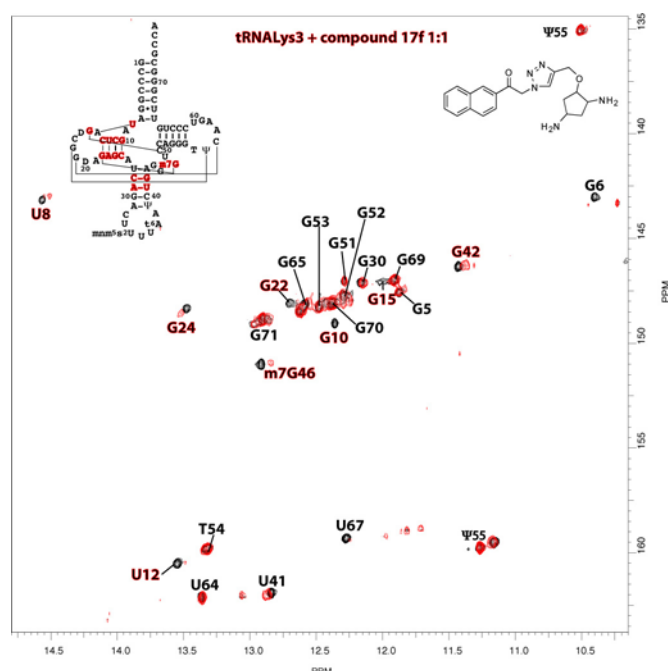
Figure 3. Superimposition of TROSY spectra of tRNA$^{Lys}_3$ alone (0.3 mM) in black and tRNA$^{Lys}_3$ mixed with compound **17f** (0.3 mM) in red.

Fluorescence binding assays were then conducted on tRNA$^{Lys}_3$, tRNA$_m^{Met}$ and tRNA$_f^{Met}$ leading to a Kd of 1.8 μM for compound **17f** with tRNA$^{Lys}_3$, at physiological ionic strength. Interestingly, compound **17f** exhibited a significant sequence selectivity for the D-arm of tRNA$^{Lys}_3$ and tRNA$_m^{Met}$ against that of tRNA$_f^{Met}$ (Table 1 and Figure 4). This specificity is correlated with a reduced ionic-strength dependence of the interaction with tRNA$^{Lys}_3$. The strong ionic-dependence of the affinity to tRNA$_f^{Met}$ reflects poorly selective binding, dominated by electrostatic effects.[19]
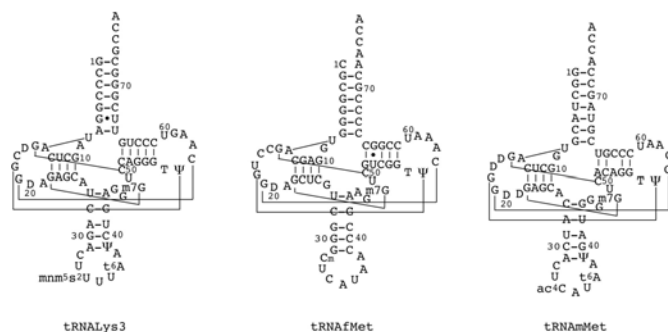
Figure 4. Sequence and secondary structure of the various tRNA used in this study.

Table 1. Dissociation constants of compound **17f** for three different tRNA at various ionic strengths.

	tRNA$^{Lys}_3$	tRNA$_f^{Met}$	tRNA$_m^{Met}$
	Kd (μM)	Kd (μM)	Kd (μM)
KCl (150 mM)	1.8 ± 0.9	13.2 ± 5.9	4.1 ± 0.9
KCl (50 mM)	1.1 ± 0.3	2.5 ± 0.8	1.1 ± 0.2
no KCl	0.3 ± 0.1	-	-

In conclusion, a selective ligand of tRNA$^{Lys}_3$ with micromolar dissociation constant has been synthesised for the first time. This study outlines the power of a fragment-based strategy in the field of RNA-ligand discovery, providing potential lead compounds for antiviral drug development. The use of compound **17f** as an inhibitor of reverse transcription in cell-free assays will be investigated. Beside this important application, this work provides new information on the design of small RNA interacting molecules. This step is crucial for achieving a challenging goal: the cellular regulation at RNA level by small molecular effectors.

[1]   G. J. R. Zaman, P. J. A. Michiels, C. A. A. Van Boeckel, *Drug. Discov. Today* **2003**, *8*, 297-206.
[2]   a) E. Westhof, *Biochimie* **2006**, *88*, 931-933; b) J. Poehlsgaard, S. Douthwaite, *Nat. Rev. Microbiol.* **2005**, *3*, 870-881.
[3]   N. W. Luedtke, Y. Tor in *Small Molecule DNA and RNA Binders: From Synthesis to Nucleic Acic Complexes* (Eds.: M. Demeunynck, C. Bailly, W. D. Wilson), Wiley-vch, Weinheim **2003**, vol. 1.
[4]   R. Marquet, C. Isel, B. Ehresmann, *Biochimie* **1995**, *77*, 113-124.
[5]   Z. Zhang, S. M. Kang, C. D. Morrow, *AIDS Res. Hum. Retroviruses* **1998**, *14*, 979-988.
[6]   X. Wei, M. Götte, M. A Wainberg, *Nucleic Acid Res.* **2000**, *28*, 3065-3074.
[7]   B. François, R. J. M. Russel, J. B. Murray, F. Aboul-ela, B. Masquida, Q. Vincens, E. Westhof, *Nucleic Acid Res.* **2005**, *33*, 5677-5690 and references therein.
[8]   a) X. Liu, J. R. Thomas, P. J. Hergenrother, *J. Am. Chem. Soc.* **2004**, *126*, 9196-9197; b) J. R. Thomas, X. Liu, P. J. Hergenrother, *J. Am. Chem. Soc.* **2005**, *127*, 12434-12435; c) J. R. Thomas, X. Liu, P. J. Hergenrother, *Biochemistry* **2006**, *45*, 10928-10938.
[9]   A few studies on the interaction between aminoglycoside derivatives and tRNA^{Phe} are available: a) S. R. Kirk, Y. Tor, *Bioorg. Med. Chem.* **1999**, *7*, 1979-1991; b) R. Szilaghi, S. Shahzad-Ul-Hussan, T. Weimar, *ChemBioChem* **2005**, *6*, 1270-1276; c) N. E. Mikkelsen, K. Johansson, A. Virtanen, L. A. Kirsebom, *Nat. Struc. Biol.* **2001**, *8*, 510-514.
[10]   C. Tisné, F. Guillière, F. Dardel, *Biochimie* **2005**, *87*, 885-888.
[11]   P. Benas, G. Bec, G. Keith, R. Marquet, C. Ehresmann, B. Ehresmann, P. Dumas, *RNA* **2000**, *6*, 1347-1355.
[12]   C. Tisné, B. P. Roques, F. Dardel, *J. Mol. Biol.* **2001**, 443-454
[13]   C. Tisné, B. P. Roques, F. Dardel., *J. Biol. Chem.* **2004**, *279* 3588-3595.
[14]   a) D. C. Ress, M. Congreve, C. W. Murray, R. Carr, *Nature Rev. Drug. Disc.* **2004**, *3*, 660-672; b) D. A. Erlanson, R. S. McDowell, T. O'Brien, *J. Med. Chem.* **2004**, *47*, 3463-3482.
[15]   For NMR-guided discovery of RNA binders, see: a) L. Yu, T. K. Oost, J. M. Schkeryantz, J. Yang, D. Janowick, S. W. Fesik, *J. Am. Chem. Soc.* **2003**, *125*, 4444-4450; b) M. Mayer, T. L. James, *J. Am. Chem. Soc.* **2004**, *126*, 4453-4460.
[16]   This "target-observe" strategy (as opposed to ligand-observe schemes such as saturation transfer) is essential to filter-out promiscuous binders which inevitably arise through non-specific electrostatic interactions with the highly charged nucleic acid. Promiscuous binders cause a general broadening of the NMR spectrum of the target, whereas specific binders induce only a peak shifts which further allow the identification of the binding site. For a general review, see: H. O. Villar, J. Yan, M. R. Hansen, *Curr. Opin. Chem. Biol.* **2004**, *8*, 387-391.
[17]   Not surprisingly, aminoglycosides (neomycin and kanamycin) were also detected as tRNA$^{Lys}_3$ ligands. They are however too complex for a fragment-based approach. On the contrary, compound **1** is an excellent 2-deoxystreptamine surrogate in the design of "RNA-friendly" compounds: L. Micouin, F. P. Dardel, C. Tisne-Vicrobeck, F. Maurice, M. Bonin, A. Perez Luna, C. J. Bournaud, G. Bégis, WO2006024784.
[18]   a) S. Yoshizawa, D. Fourmy, R.G. Eason, J.D. Puglisi, *Biochemistry* **2002**, *41*, 6263-6270 and ref. 7.
[19]   Both enantiomerically enriched (e.r. = 93/7) isomers of compound **17f** were prepared and individually studied, leading to Kd = 1.2 ± 0.6 μM for (*R*)-**17f** and Kd = 1.1 ± 0.7 μM for (*S*)-**17f** at 150 mM KCl. Interaction with tRNA$^{Lys}_3$ is thus not stereospecific and racemic ligands can be used in this approach. For the enantioselective preparation of **1**, see: a) A. Pérez Luna, M.-A. Ceschi, M. Bonin, L. Micouin, H.-P. Husson, S. Gougeon, G. Estenne Bouthou, B. Marabout, M. Sevrin, P. George, *J. Org. Chem.* **2002**, *67*, 3522-3524; b) A. Pérez Luna, M. Bonin, L. Micouin, H.-P. Husson, *J. Am. Chem. Soc.* **2002**, *124*, 12098-12099.
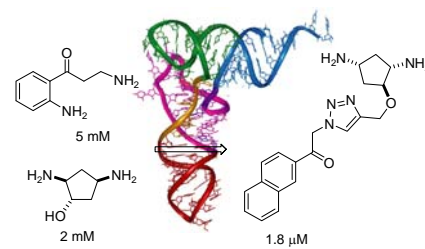
RNA recognition

Florence Chung, Carine Tisné,*
Thomas Lecourt, Frédéric Dardel* and
Laurent Micouin*

NMR-guided fragment-based
approach for the design of tRNA$^{Lys}_3$
ligands

An NMR-guided fragment-based
approach has been used for the
synthesis of a micromolar tRNA$^{Lys}_3$ D-
stem binder from two millimolar ligands
detected by flow-injection NMR
screening.

4

**NMR-guided fragment-based approach for the design of tRNA$^{Lys}_3$ ligands**

Florence Chung, Carine Tisné,* Thomas Lecourt, Frédéric Dardel* and Laurent Micouin*

Chemistry

Compound **1** and its N-Boc derivative were prepared according to reported procedures.[1] Kynuramine **2** was purchased from Sigma.

Typical procedure for the synthesis of Mannich Base:

Paraformaldehyde (1.43 g, 1 equiv.), dimethylamine hydrochloride (11.64 g, 3 equiv.) and acetophenone (13 mL, 2.3 equiv.) were dissolved in ethanol (10 mL). Hydrochloric acid 35% (0.2 mL) was added and the mixture refluxed for 5 hours. The yellowish solution was diluted with cold acetone (50 mL) and chilled for several hours at 0 °C. The crystals were filtrated, washed with acetone (2x20 mL), dissolved in water (20 mL) and then extracted in ethyl acetate (2x35 mL). The aqueous layer was treated with potassium carbonate (pH=10) and extracted in ethyl acetate (5x35 mL). The organic phases were dried over sulphate magnesium and concentrated under reduced pressure to give the Mannich base as an oil (77%).

3
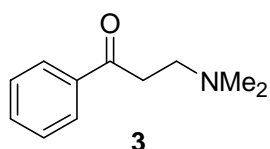
^{1}H NMR δ 2.19 (s, 6H), 2.66 (t, 2H, J = 7.3 Hz), 3.05 (t, 2H, J = 7.3 Hz), 7.35 (t, 2H, J = 7.4 Hz), 7.44 (t, 1H, J = 7.4 Hz), 7.86 (d, 2H, J = 7.1 Hz); ^{13}C NMR δ 36.9, 45.5, 54.4, 128.1, 128.6, 133.0, 137.0, 199.0, MS (ESI): 178 [M+H]$^+$.


4
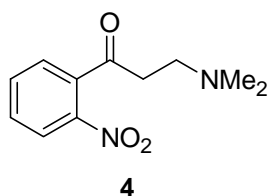
^{1}H NMR (CDCl$_3$) δ 2.21 (s, 6H), 2.70 (t, 2H, J = 7.2 Hz), 2.94 (t, 2H, J = 7.2 Hz), 7.42 (dd, 1H, J = 7.5, 1.3 Hz), 7.58 (td, 1H, J = 7.5, 1.3 Hz), 7.70 (td, 1H, J = 7.5, 1.0 Hz), 8,1 (dd, 1H, J = 7.5, 1.0 Hz); ^{13}C NMR (CDCl$_3$) δ 41.3, 45.3, 54.2, 124.4, 127.7, 130.5, 134.4, 138.0, 145.6, 201.8; MS (ESI): 223 [M+H]$^+$.

5
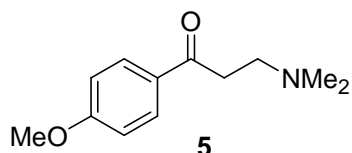
^{1}H NMR (CDCl$_3$) δ 2.25 (s, 6H), 2.73 (t, 2H, *J* = 7.4 Hz), 3.08 (t, 2H, *J* = 7.4 Hz), 3.13 (s, 3H), 6.89 (d, 2H, *J* = 8.9 Hz), 7.90 (d, 2H, *J* = 8.9 Hz); ^{13}C NMR (CDCl$_3$) δ 36.0, 45.0, 54.1, 55.0, 113.2-113.3, 129.6-129.9, 130.1, 163.0, 196.9; MS (ESI): 208 [M+H]$^{+}$.

6
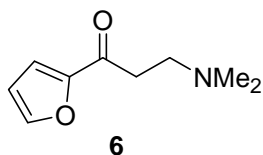
^{1}H NMR (CDCl$_3$) δ 2.17 (s, 6H), 2.64 (t, 2H, *J* = 7.3 Hz), 2.91 (t, 2H, *J* = 7.3 Hz), 6.45 (dd, 1H, *J* = 3.5, 1.6 Hz), 7.12 (d, 1H, *J* = 3.5 Hz), 7.51 (d, 1H, *J* = 1.6 Hz); ^{13}C NMR (CDCl$_3$) δ 36.7, 45.4, 54.2, 112.3, 117.1, 146.4, 152.7 188.2; MS (ESI): 168 [M+H]$^{+}$.

7
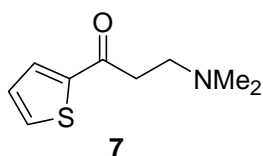
^{1}H NMR (CDCl$_3$) δ 2.10 (s, 6H), 2.61 (t, 2H, *J* = 7.3 Hz), 2.95 (t, 2H, *J* = 7.3 Hz), 6.99 (dd, 1H, *J* = 4.9, 3.8 Hz), 7.49 (dd, 1H, *J* = 4.9, 0.9 Hz), 7.60 (dd, 1H, *J* = 3.8, 0.9 Hz); ^{13}C NMR (CDCl$_3$) δ 37.6, 45.4, 54.5, 128.2, 131.9, 133.7, 144.3, 191.9; MS (ESI): 184 [M+H]$^{+}$.

8
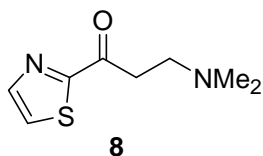
^{1}H NMR (CDCl$_3$) δ 2.25 (s, 6H), 2.77 (t, 2H, *J* = 7.1 Hz), 3.30 (t, 2H, *J* = 7.1 Hz), 7.65 (d, 1H, *J* = 3.1 Hz), 7.97 (d, 1H, *J* = 3.1 Hz); ^{13}C NMR (CDCl$_3$) δ 36.6, 45.3, 54.0, 126.3, 144.7, 167.0, 192.8; MS (ESI): 185 [M+H]$^{+}$.

9
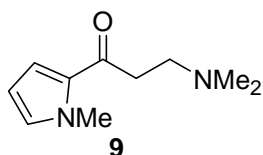
^{1}H NMR (CDCl$_3$) δ 2.26 (s, 6H), 2.69 (t, 2H, *J* = 7.4 Hz), 2.94 (t, 2H, *J* = 7.4 Hz), 3.9 (s, 3H), 6.11 (dd, 1H, *J* = 4.1, 2.4 Hz), 6.78 (dd, 1H, *J* = 2.4, 1.6 Hz), 6.97 (dd, 1H, *J* = 4.1, 1.6 Hz); ^{13}C NMR (CDCl$_3$) δ 37.2, 45.4, 55.1, 107.9, 119.2, 130.7, 131.1, 189.8; MS (ESI): 181 [M+H]$^{+}$.

10
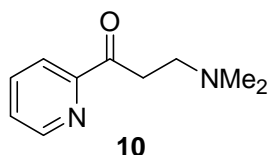
^{1}H NMR (CDCl$_3$) δ 2.29 (s, 6H), 2.78 (t, 2H, J = 7. 2 Hz), 3.40 (t, 2H, J = 7.2 Hz), 7.47 (td, 1H, J = 7.7, 1.1 Hz), 7.83 (td, 1H, J = 7.7, 1.7 Hz), 8.05 (dd, 1H, J = 7.7, 1.1 Hz), 8.68 (dd, 1H, J = 7.7, 1.7 Hz); ^{13}C NMR (CDCl$_3$) δ 35.8, 45.5, 54.5, 121.9, 127.2, 136.9, 149.0, 153.4, 200.7; MS (ESI): 179 [M+H]$^+$.

11
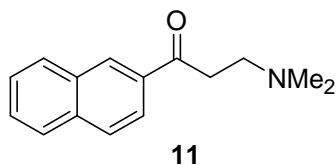
^{1}H NMR (CDCl$_3$) δ 2.47 (s, 6H), 3.02 (t, 2H, J = 7.3 Hz), 3.46 (t, 2H, J = 7.3 Hz), 7.59 (m, 2H), 7.89 (m, 2H), 8.01 (m, 2H), 8.52 (s, 1H); ^{13}C NMR (CDCl$_3$) δ 37.0, 45.6, 54.5, 123.8, 126.8, 127.8, 128.5, 129.6, 129.7, 132.5, 134.2, 135.6, 199.0; MS (ESI): 228 [M+H]$^+$.

**Typical procedure for transamination**

Compound **3** (213 mg, 1 equiv.) and methyl iodide (374 μL, 5 equiv.) were dissolved in dichloromethane (4 mL) and stirred at room temperature for 3 hours. The mixture was concentrated, dissolved in chloroform (4 mL) and stirred with *N,N,N'*-trimethylethyldiamine (305 μL, 2 equiv.) at 60 °C for 18 hours. The crude product was washed with AcOEt (10 mL), H$_2$O (2x 25 mL) and dried over MgSO$_4$. Purification by silica gel column chromatography (AcOEt/MeOH (98/2), AcOEt/MeOH (95/5), AcOEt/MeOH (90/10)) afforded the compound (24%).


13
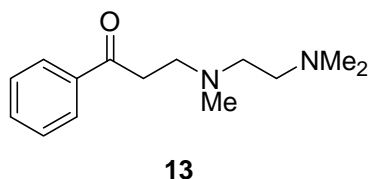
^{1}H NMR (CDCl$_3$) δ 2.23 (s, 6H), 2.31 (s, 3H), 2.42-2.54 (2t, 4H, J = 6.8 Hz), 2.87 (t, 2H, J = 7.4 Hz), 3.18 (t, 2H, J = 7.4 Hz), 7.47 (t, 2H, J = 7.4 Hz), 7.55 (t, 1H, J = 7.4 Hz), 7.97 (d, 2H, J = 7.4 Hz); ^{13}C NMR (CDCl$_3$) δ 36.3, 42.4, 45.6, 52.7, 55.3, 57.1, 127.9, 128.5, 133.0, 136.9, 199.3; MS (ESI): 235 [M+H]$^+$.

12
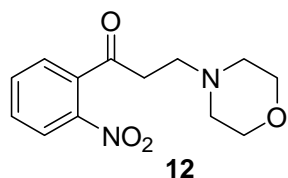
^{1}H NMR (CDCl$_3$) δ 2.44 (d, 4H, J = 4.5 Hz), 2.79 (t, 2H, J = 7.0 Hz), 2.98 (t, 2H, J = 7.0 Hz), 3.67 (d, 4H, J = 4.5 Hz), 7.46 (dd, 1H, J = 7.5, 1.3 Hz), 7.61 (td, 1H, J = 7.5, 1.3 Hz), 7.73 (td, 1H, J = 7.5, 1.0 Hz), 8.14 (dd, 1H, J = 7.5, 1.0 Hz); ^{13}C NMR (CDCl$_3$) δ 40.2, 53.4, 66.8, 124.2, 127.6, 130.4, 134.2, 138.0, 180.9, 201.6; MS (ESI): 265 [M+H]$^+$.

14
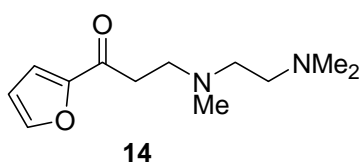
^{1}H NMR (CDCl$_3$) δ 2.21 (s, 3H), 2.25 (s, 6H), 2.46-2.48 (2 t, 4H, J = 9.7 Hz), 2.78 (t, 1H, J = 7.2 Hz), 2.95 (t, 1H, J = 7.2 Hz), 6.46 (dd, 1H, J = 3.6, 1.7 Hz), 7.15 (dd, 1H, J = 3.6, 0.6 Hz), 7.52 (dd, 1H, J = 1.7, 0.6 Hz); ^{13}C NMR (CDCl$_3$) δ 36.1, 42.4, 45.6, 52.5, 55.0, 56.9, 112.4, 117.6, 146.8, 152.7, 188.6; MS (ESI): 225 [M+H]$^+$.

Typical procedure for nitro reduction

Compound **4** hydrochloride (69 mg, 0.27 mmol) was dissolved in methanol (4 mL) and stirred with 10% palladium hydroxide (7 mg) under H$_2$ atmosphere for 2 hours. The mixture was filtrated through celite and concentrated under vacuum (92%).

15
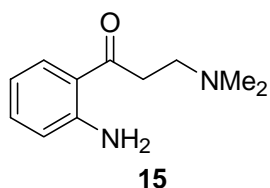
^{1}H NMR (CD$_3$OD) δ 2.94 (s, 6H), 3.53 (m, 4H), 6.61 (td, 1H, J = 7.1, 0.9 Hz), 6.79 (dd, 1H, J = 7.1, 0.9 Hz), 7.27 (td, 1H, J = 7.1, 1.4 Hz), 7.78 (dd, 1H, J = 7.1, 1.4 Hz); ^{13}C NMR (CD$_3$OD) δ 34.6, 42.8, 52.7, 124.7, 134.8, 198.8; MS (ESI): 193 [M+H]$^+$.

16
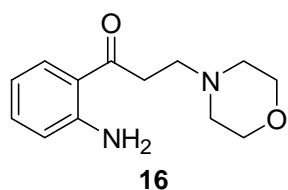
^{1}H NMR (CD$_3$OD) δ 2.54 (t, 4H, J = 4 Hz), 2.83 (t, 2H, J = 7.2 Hz), 3.17 (t, 2H, J = 7.2 Hz), 3.73 (t, 4H, J = 4 Hz), 6.65 (m, 2H), 7.27 (td, 1H, J = 7.0, 1.3 Hz), 7.74 (dd, 1H, J = 7.0, 1.3 Hz); ^{13}C NMR

(CD$_3$OD) δ 36.0, 53.1,54.0, 66.9, 115.8, 117.4, 131.0, 134.4, 150.4, 178.8, 201.1; MS (CI): 235 [M+H]$^+$.

Protected diaminocyclopentanol (100 mg, 0.32 mmol) and propargyl bromide (105 μL, 0.96 mmol) were dissolved in 2.5 mL of anhydrous THF under argon atmosphere at 0 °C. After the slow addition of KHMDS (0.5M in toluene, 640 μL, 0.32 mmol) the mixture was stirred at room temperature for 18 hours. H$_2$O (10 mL) was then added and the crude was extracted by EtOAc (2x 25 mL). The organic phases were washed with brine and dried with MgSO$_4$. After purification by silica gel column chromatography (EtOAc:Cyclohexane 20:80, 30:70) the product was obtained as an oil (60%).
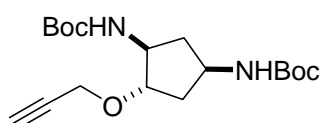
^{1}H NMR (CDCl$_3$) δ 1.47 (brs, 19H), 1.93 (m, 1H), 2.04 (m, 1H), 2.42 (t, 1H, *J* = 2.4 Hz), 2.52 (dt, 1H, *J* = 13.9 Hz, 8.2 Hz), 3.82 (m, 1H), 4.01 (m, 2H), 4.20 (m, 2H), 4.98 (m, 1H), 5.19 (m, 1H); ^{13}C NMR (CDCl$_3$) δ 28.5, 37.1, 49.3, 55.9, 56.7, 74.3, 79.5, 80.1, 83.5, 155.4; MS (ESI): 377 [M+Na]$^+$.

**Typical procedure for the synthesis of triazoles:**

α-bromo-2'-acetonaphtone (225 mg, 2 equiv.) and sodium azide (61 mg, 2.05 equiv.) were stirred at room temperature in a 1/2 water/acetone mixture (4.5 mL) for 1 hour. Alkyne (160 mg, 1 equiv.) in acetone (1.5 mL) was then added, followed by the addition of sodium ascorbate (0.5 equiv.) and copper sulfate (0.5 equiv.). The resultant mixture was then stirred at room temperature until complete consumption of the alkyne (2 days) monitored by TLC (AcOEt:Cyclohexane 1:1). The precipitate was filtrated, rinsed with water and dried under vacuum. The crude product was then stirred for 1 hour in a 2M solution of methanolic hydrochloride (6 mL). After evaporation of the solvent, Amberlyst 15 resin (380 mg, 4 equiv.) and MeOH (6 mL) were added and stirred overnight. The resin was filtrated, rinsed with MeOH (5x5 mL), and stirred for 3 hours in a 2M solution of methanolic ammonia (6 mL). The resin was filtrated and rinsed with MeOH. Evaporation of the organic phase led to compound **17f** as an oil (46%).


17f
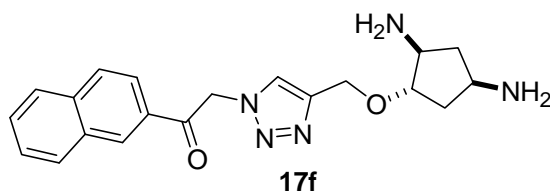
^{1}H NMR (CD$_3$OD) δ 1.23 (dt, 1H, *J* = 12.8, 8.5 Hz), 2.00 (m, 1H), 1.85 (m, 1H), 2.32 (dt, 1H, *J* = 12.8, 6.7 Hz), 3.19 (m, 1H), 3.43 (m, 1H), 3.79 (m, 1H), 4.65 (2d, 2H, *J* = 12.3 Hz), 7.62-7.71 (m, 2H), 7.95-8.11 (m, 5H), 8.73 (s, 1H); ^{13}C NMR (CD$_3$OD) δ 38.8, 40.9, 48.7, 57, 62.1, 86, 122.9, 125.6,

126.9, 127.6, 128.5, 128.9, 129.5, 130.2, 131.5, 132.5, 136.1, 144.9, 191.4; HRMS (ESI) m/z calcd for $C_{20}H_{24}N_5O_2$ [M+H]$^+$: 366.1930. Found: 366.1921.


17a
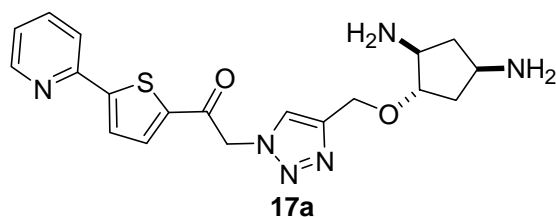
^{1}H NMR (CD$_3$OD) δ 1.95 (m, 1H), 2,35 (m, 2H), 2.78 (m, 1H), 3.73(m, 1H), 3.91 (m, 1H), 4.47 (m, 1H), 4.90 (2d, 2H, *J* = 12,6 Hz), 6.41 (m, 2H), 8.11 (m, 1H), 8.30 (m, 1H), 8.50-8.40 (m, 2H), 8.53 (m, 1H), 8.72 (m, 1H), 8.91 (m, 1H); ^{13}C NMR (CD$_3$OD) δ 32.7, 34, 48.5, 55.1, 57, 61.5, 80.5, 125.7, 126.4, 132.0, 134.8, 140.6, 142.4, 144.9, 147.3, 184; MS (ESI): 399 [M+H]$^+$.


17b
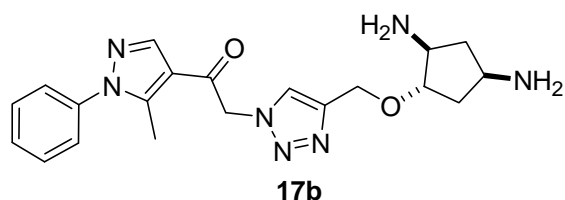
^{1}H NMR (400 MHz, CD$_3$OD, 50°C) δ 2.07 (m, 1H), 2.57 (m, 2H), 2.80 (s, 3H), 3.00 (dt, *J* = 13.6, 6.9 Hz), 3.94 (m, 1H), 4.13 (m, 1H), 4.69 (m, 1H), 5.11 (2d, 2H, *J* = 12.9 Hz), 6.32 (s, 2H), 7.74-7.83 (m, 5H), 8.62 (s, 2H); ^{13}C NMR (75 MHz, CD$_3$OD) δ 11.1, 32.6, 33.9, 47.2, 55.0, 57.0, 61.5, 80.3, 117.4, 125.5, 129.3, 134.0, 141.0, 144.6, 185.4; HRMS (ESI) m/z calcd for $C_{20}H_{26}N_7O_2$ [M+H]$^+$: 396.2148. Found: 396.2172.


17c
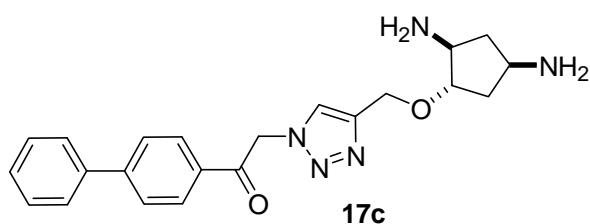
^{1}H NMR (CD$_3$OD) δ 1.21 (dt, 1H, *J* = 13 Hz, 8.5 Hz), 1.83 (m, 1H), 2.01 (m, 1H), 2.33 (dt, 1H, *J* = 13.0, 6.5 Hz), 3.20 (m, 1H), 3.43 (m, 1H), 3.80 (m, 1H), 4.66 (2d, 2H, *J* = 12.3 Hz), 7.47 (m, 3H), 7.71 (m, 2H), 7.83 (m, 2H), 8.03 (s, 1H), 8.15 (m, 2H); ^{13}C NMR (CD$_3$OD) δ 38.8, 41.0, 48.5, 57, 62.1, 86.0, 125.5, 127.1, 126.9, 128.3, 128.8, 128.6, 132.8, 139.3, 144.9, 146.8, 191.0; HRMS (ESI) m/z calcd for $C_{22}H_{26}N_5O_2$ [M+H]$^+$: 392.2087. Found: 392.2103.

**17d**
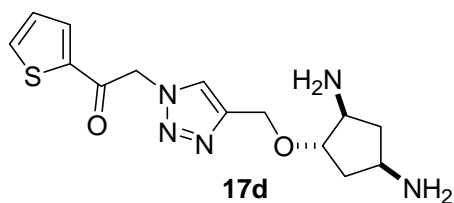
^{1}H NMR (CD$_3$OD) δ 1.17 (dt, 1H, *J* = 13.0, 8.7 Hz), 1.78 (m, 1H), 1.97 (m, 1H), 2.31 (dt, 1H, *J* = 13.0, 6.5 Hz), 3.15 (m, 1H), 3.38 (m, 1H), 3.76 (m, 1H), 4.65 (2d, 2H, *J* = 12.2 Hz), 7.29 (dd, 1H, *J* = 4.9, 3.7 Hz), 7.98 (d, 1H, *J* = 4.9 Hz), 8.06 (s, 1H), 8.09 (d, 1H, *J* = 3.7 Hz); ^{13}C NMR (75 MHz, CD$_3$OD) δ 39.1, 41.4, 49.1, 57.0, 62.0, 86.2, 125.5, 128.5, 133.7, 135.5, 140.3, 144.9, 184.5; HRMS (ESI) m/z calcd for C$_{14}$H$_{20}$N$_5$O$_2$S [M+H]$^+$: 322.1338. Found: 322.1307.

17e
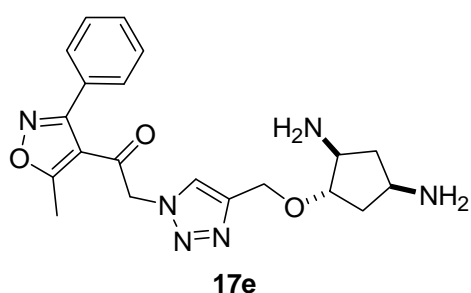
^{1}H NMR (CD$_3$OD, 50°C) δ 2.18 (m, 1H), 2.55 (m, 2H), 3.00 (m, 1H), 3.10 (s, 3H), 3.92 (m, 1H), 4.13 (m, 1H), 4.67 (m, 1H), 5.06 (d+m, 2H, *J* = 12.7 Hz), 5.75 (s, 2H), 7.98 (m, 3H), 8.41 (m, 2H), 8.64 (s, 1H); ^{13}C NMR (CD$_3$OD) δ 12.8, 29.3, 33.9, 49.5, 55.0, 58.3, 61.9, 80.0, 114.3, 126.8, 128.6, 129.1, 143, 130.2, 161.7, 176.7, 185.6; HRMS (ESI) m/z calcd for C$_{20}$H$_{25}$N$_6$O$_3$ [M+H]$^+$: 397.1988. Found: 397.1981.

17g
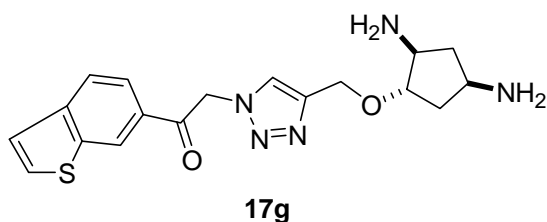
^{1}H NMR (CD$_3$OD) δ 1.30 (dt, 1H, *J* = 13.3, 7.9 Hz), 2.03 (m, 1H), 1.91 (m, 1H), 2.31 (dt, 1H, *J* = 13.3, 6.7 Hz), 3.24 (m, 1H), 3.49 (m, 1H), 3.83 (m, 1H), 4.68 (2d, 2H, *J* = 11.6 Hz), 7.57 (d, 1H, *J* = 5.4 Hz), 7.75 (d, 1H, *J* = 5.4 Hz), 8.04 (m, 3H), 8.63 (s, 1H); ^{13}C NMR (CD$_3$OD) δ 37.9, 39.9, 48.5, 22.6, 56.8, 62.1, 84.0, 122.7, 124.1, 124.4, 125.6, 128.5, 130.6, 139.7, 144.8, 145.4, 191.4; HRMS (ESI) m/z calcd for C$_{18}$H$_{22}$N$_5$O$_2$S [M+H]$^+$: 372.1494. Found: 372.1463.

17h
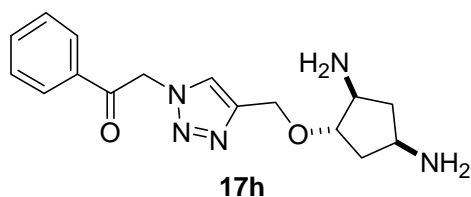
^{1}H NMR (300 MHz, CD$_3$OD) δ 1.87 (dt, 1H, J = 13.1, 8.9 Hz), 2.27 (m, 2H), 2.70 (dt, 1H, J = 13.1, 7.7 Hz), 3.66 (m, 1H), 3.86 (m, 1H), 4.37 (m, 1H), 4.81 (2d, 2H, J = 12.6 Hz), 6.25 (s, 2H), 7.62 (m, 2H), 7.75 (m, 1H), 8.11 (m, 2H), 8.26 (s, 1H); ^{13}C NMR (75 MHz, CD$_3$OD) 32.5, 33.9, 47.1, 55.0, 56.4, 61.9, 80.1, 126.7, 128, 128.8, 134.0, 134.2, 191.1; HRMS (ESI) m/z calcd for C$_{16}$H$_{22}$N$_5$O$_2$ [M+H]$^{+}$: 316.1774. Found: 316.1764.


Biologicals

Sample preparation

Human tRNALys3 was expressed *in vivo* in *E. coli* from a recombinant plasmid and purified as previously described.[2]


NMR experiments

Experiments were recorded on a Bruker Avance DRX 600 spectrometer equipped with a 3mm triple-resonance flow-injection probe. The probe was connected to a Gilson 215 liquid handler controlled by the NMR console (Bruker BEST system). For tRNA:ligand mixtures, solvent suppression was achieved by using the 'jump-and-return' sequence to avoid the saturation of imino protons.[3] All NMR experiments were conducted at 15°C. Samples for 1D NMR screening contained 0.3 mM of tRNA and 1.2 mM of ligand in 10mM phosphate buffer pH 6.5, in a total volume of 200 μl in 96-well plates. The injected sample volumes were 160 μl. For ligands identified in the primary screen, ^{1}H-^{15}N HMQC spectra[4] or TROSY spectra[5] were recorded using a sample containing 0.2 mM to 0.4 mM ^{15}N labelled tRNA for equivalent of ligand concentration (1, 2, 4 and 7) in 10mM phosphate buffer pH 6.5. For the measurement of the dissociation constant (Kd) between kynuramine or **1** and tRNALys3, a sample containing 0.55 mM of tRNALys3 in 10mM phosphate buffer pH 6.5 was titrated by increasing concentrations of ligand in the same buffer : 2, 4, 5, 7, 10, 15 and 20 mM. Kd values were extracted by non-linear least square fitting of the variation of imino proton chemical shifts to a single-site binding hyperbolic function. Confidence limits on the Kd were estimated by Monte-Carlo sampling using the MC-fit program.[6]
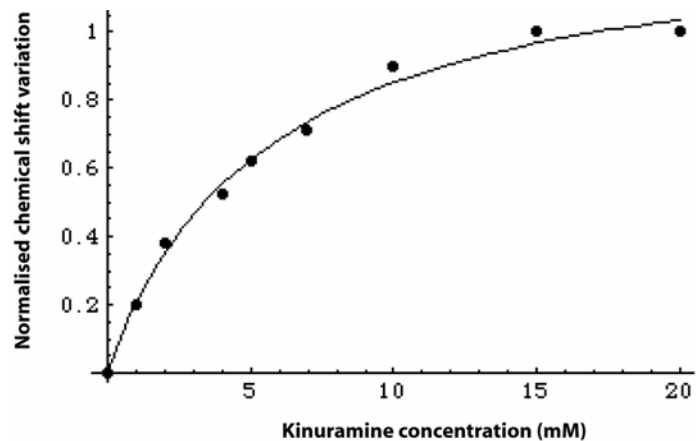
Figure 1: NMR titration of tRNALys3 (0.55 mM) by kynuramine **2**. The NMR signal of G24 imino proton is followed in 1D NMR experiment at 15°C.[3]
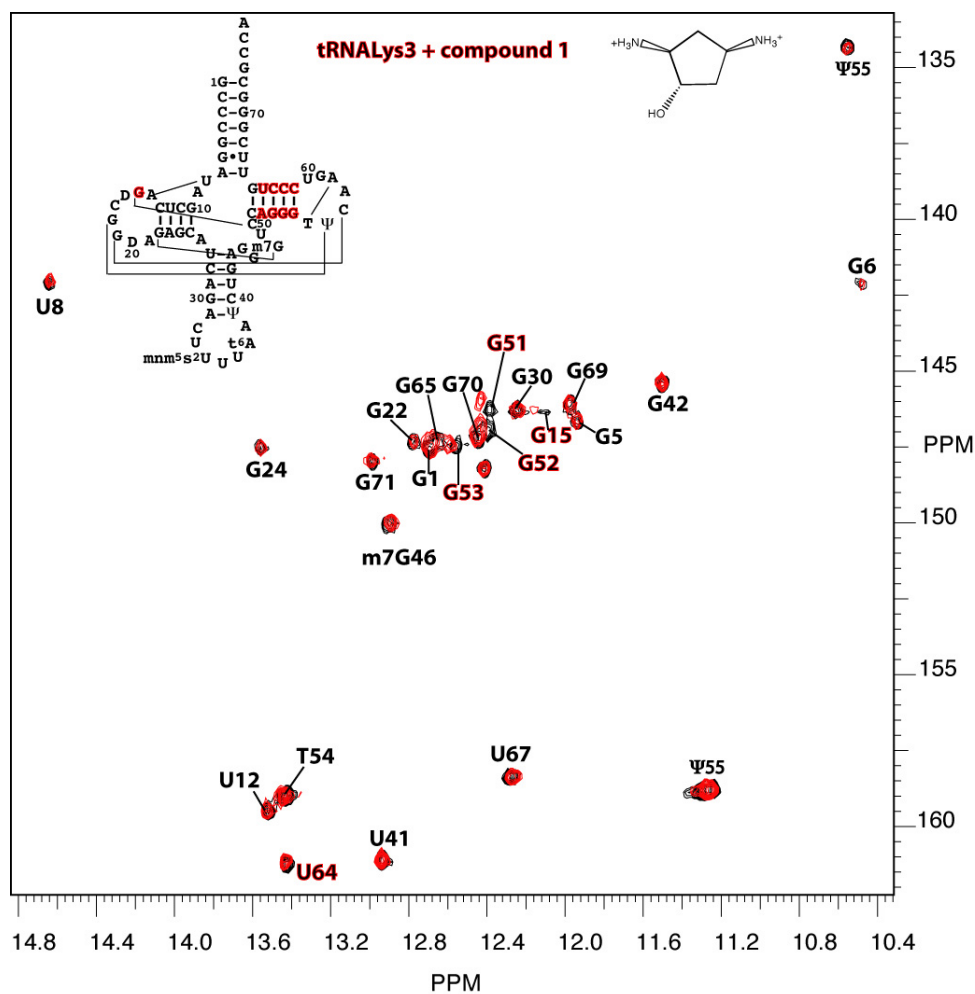
Figure 2: Superimposition of HMQC spectra of tRNA$^{Lys}_3$ alone (0.2 mM) in black and tRNA$^{Lys}_3$ mixed with compound **1** (1.4 mM) in red, no KCl. A preferential affinity for the T-arm can be observed at a 7/1 ligand/target ratio, but shift of G15 shows a possible secondary binding site on the D-arm.
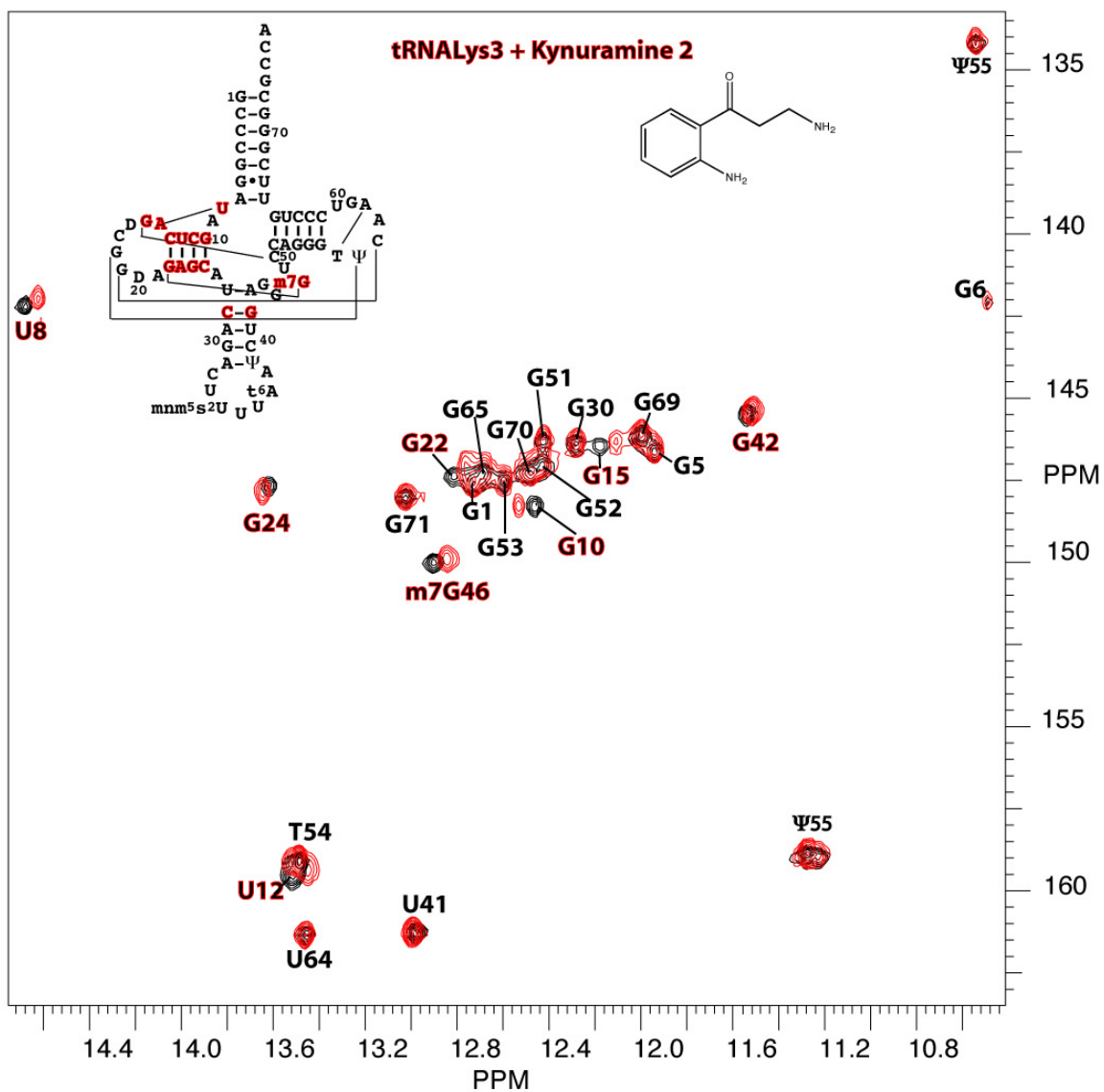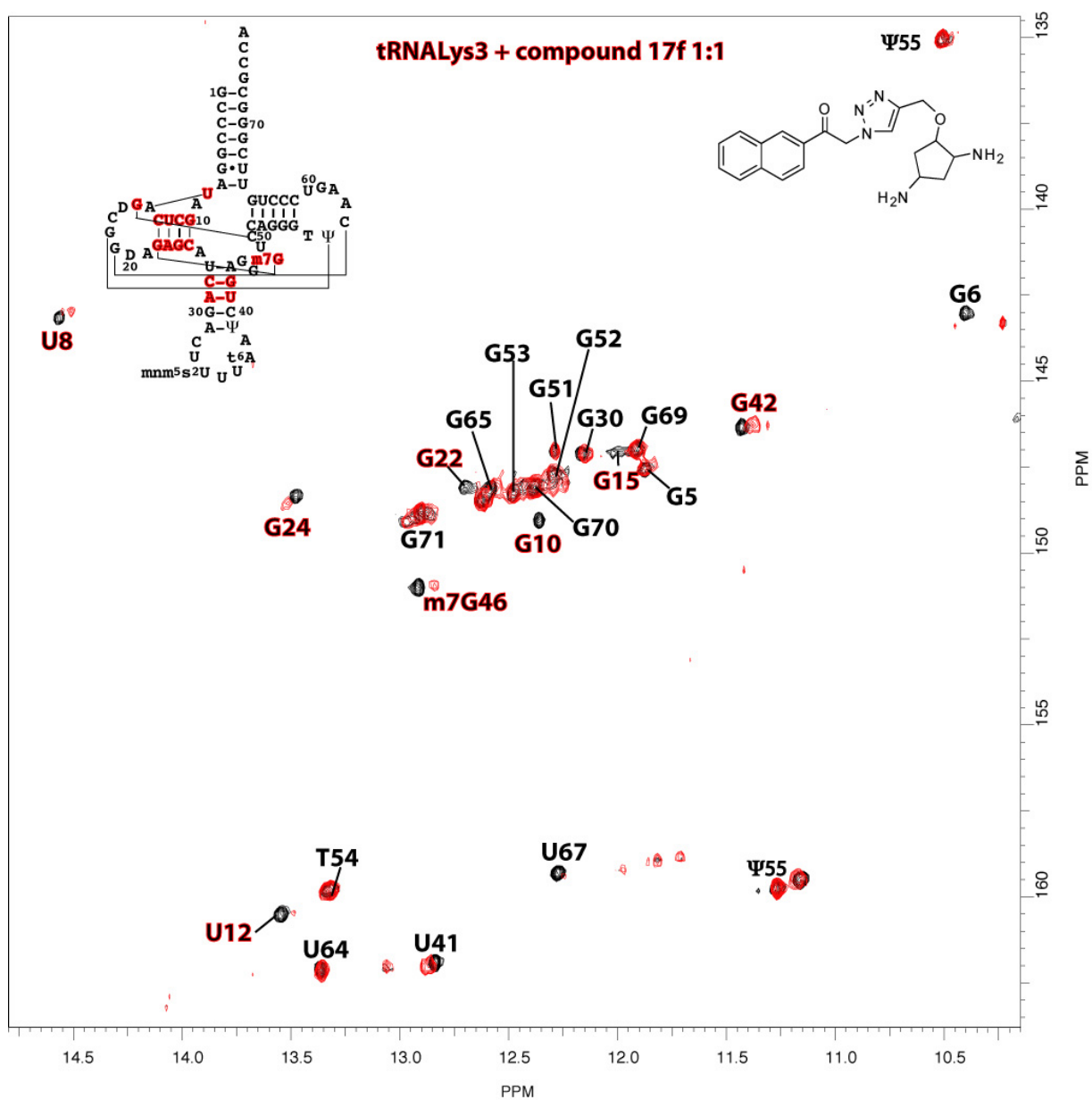
Figure 3: Superimposition of HMQC spectra of tRNA$^{Lys}_3$ alone (0.8 mM) in black and tRNA$^{Lys}_3$ mixed with compound **2** (1.6 mM) in red, no KCl .
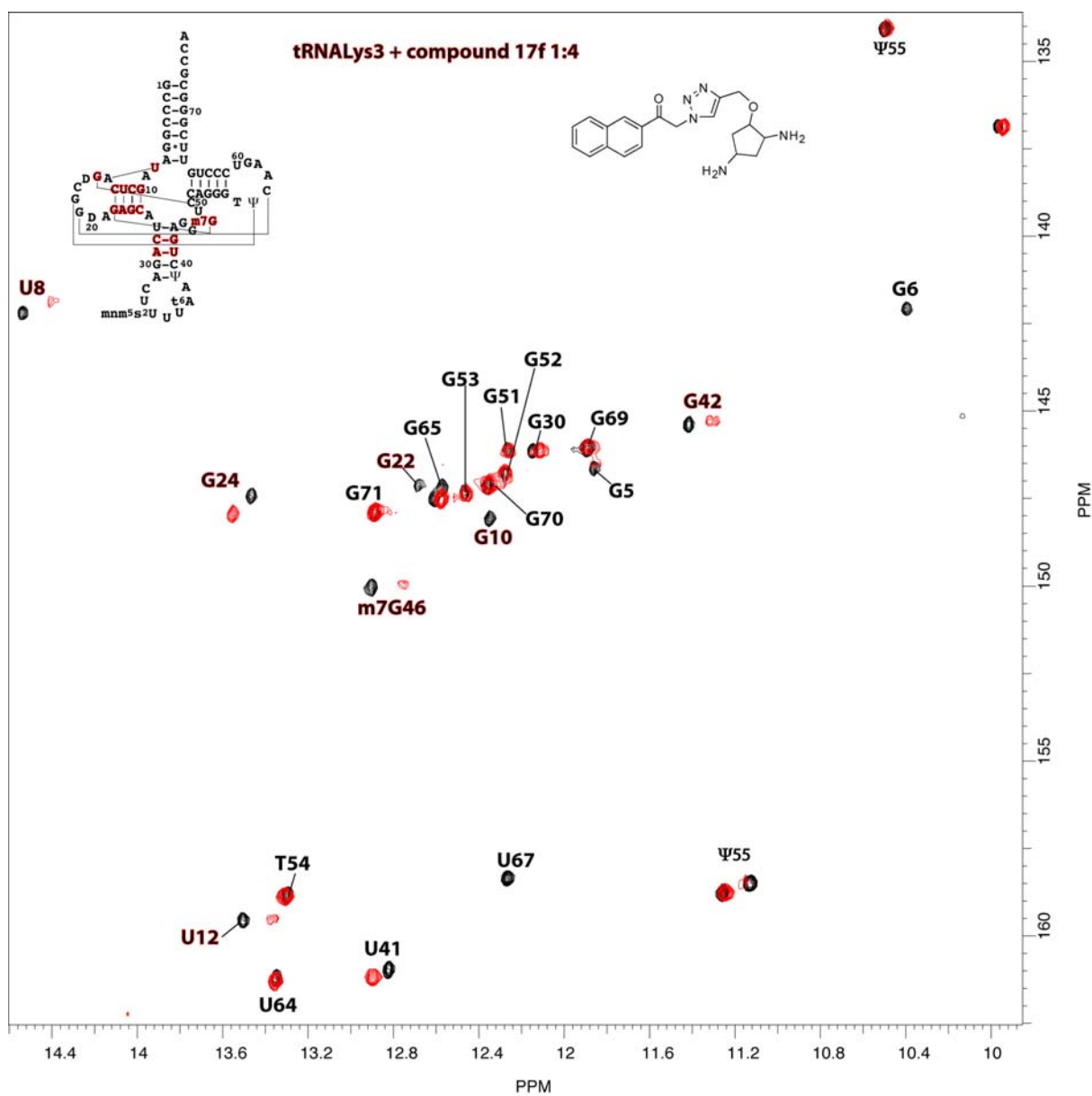
Figure 4: Superimposition of TROSY spectra of tRNA^Lys_3 alone (0.3 mM) in black and tRNA^Lys_3 mixed with compound **17f** (1.2 mM) in red, 150 mM KCl .

Figure 5: Superimposition of TROSY spectra of tRNA$^{Lys}_3$ alone (0.3 mM) in black and tRNA$^{Lys}_3$ mixed with compound **17f** (0.3 mM) in red, 150 mM KCl .
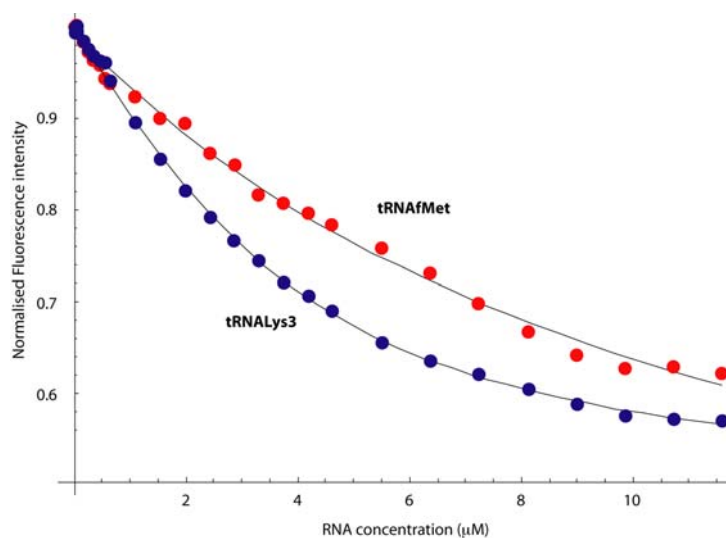
Fluorescence titrations

Fluorescence titrations were conducted at 25.0°C on a JASCO spectrofluorimeter. Excitation and emission wavelengths were 341 nm and 478 nm respectively. The excitation and emission bandwidths were 5 nm.

Fluorescence titrations experiments were performed by adding increasing concentrations of nucleic acid to a fixed amount of ligand (2 μM) in buffers with different ionic strength (10 mM KPO₄ pH 6.5, for three salt concentrations, 0 mM, 50 and 150 mM NaCl). Fluorescence intensities were corrected for dilution and were fitted using equation (1). Confidence limits on the Kd were estimated by Monte-Carlo sampling using the MC-Fit program.[6]

$$I = I_0 - \frac{I_0 - I_\infty}{2nN_t}\left(K_d + L_t + nN_t - \sqrt{(K_d + L_t + nN_t)^2 - 4L_t nN_t}\right) \tag{1}$$

where I_0: Fluorescence intensity without RNA, I: fluorescence intensity at a given concentration of RNA, I_∞: fluorescence intensity at the plateau, n: number of RNA binding sites on the ligand, L_t: total concentration of RNA, N_t: total concentration of ligand.

Figure 6: Comparison of fluorescence titration of compound **17f** with tRNALys3 (in blue) and tRNAfMet (in red) at 150 mM KCl.
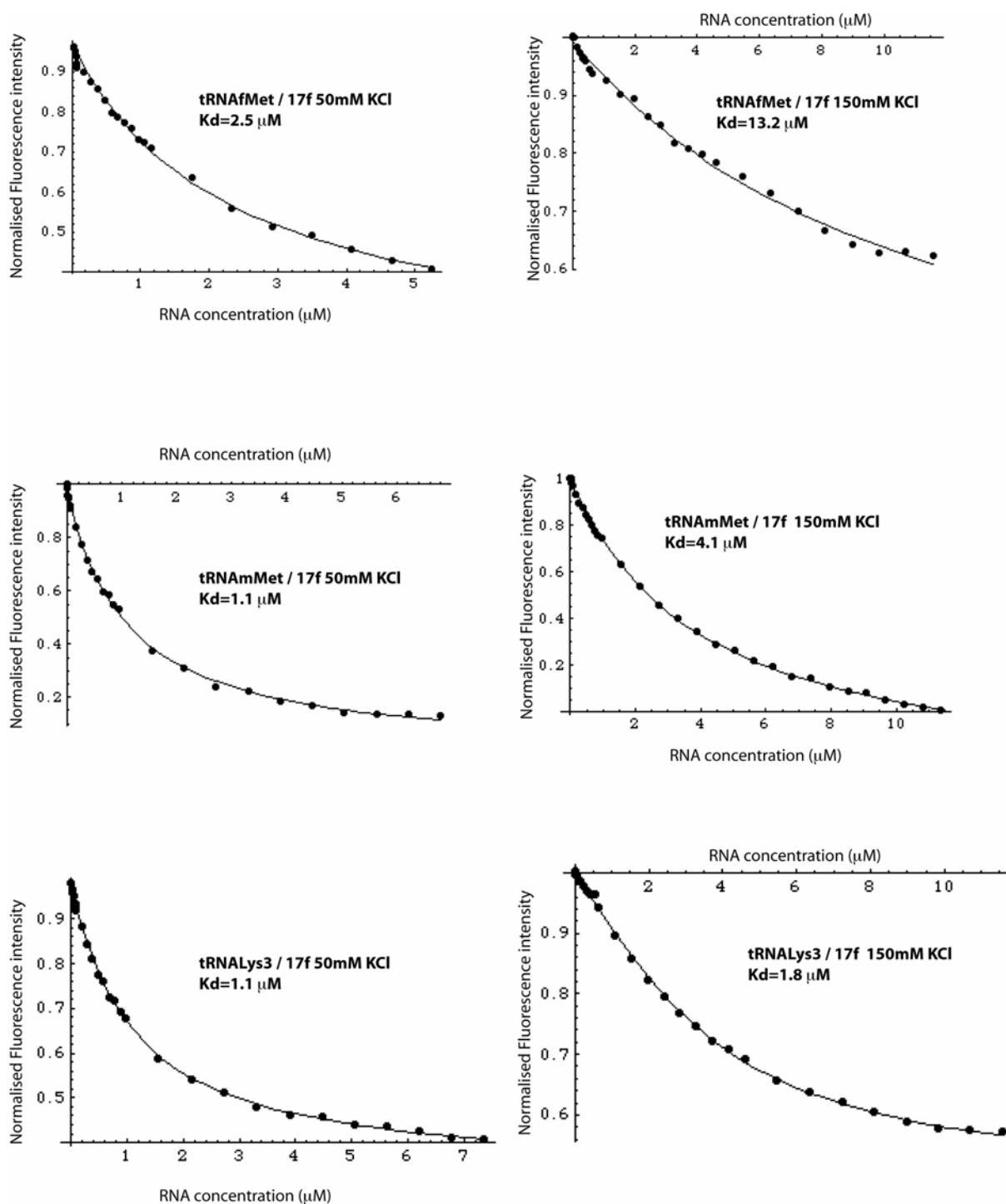
Figure 7: Fluorescence titration of compound **17f** with tRNA$^{Lys}_3$, tRNA$_f^{Met}$ and tRNA$_m^{Met}$ at various ionic strengths.

[1]   L. Micouin, F. P. Dardel, C. Tisne-Vicrobeck, F. Maurice, M. Bonin, A. Perez Luna, C. J. Bournaud, G. Bégis, WO2006024784.
[2]   C. Tisné, M. Rigourd, R. Marquet, C. Ehresmann, F. Dardel, *RNA* **2000**, *6*, 1403-1412.
[3]   P. Plateau, M. Guéron, *J. Am. Chem. Soc.* **1982**, *104*, 7310-7311.
[4]   A. A. Szewczak, G. W. Kellogg, P. B. Moore, FEBS Letters **1993**, *327*, 261-264.
[5]   J. Weigelt *J. Am. Chem. Soc.* **1998**, *120,* 10778-10779.
[6]   F. Dardel. *Comput. Appl. Biosci.* **1994**, *10,* 273-275.