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In silico, in vitro and in vivo evaluation of new candidates for alpha-synuclein PET imaging

Mathieu Verdurand, Elise Levigoureux, Wael Zeinyeh, Laurent Berthier, Meriem Mendjel-Herda, Florence Cadarossanesaib, Caroline Bouillot, Thibaut Lecker, Raphaël Terreux, Sophie Lancelot, Fabien Chauveau, Thierry Billard, and Luc Zimmer

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3 ***In silico, in vitro and in vivo* evaluation of new candidates for alpha-**
4 **synuclein PET imaging**
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51 **Short title:** Towards alpha-synuclein PET neuroimaging
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ABSTRACT

Accumulation of α -synuclein (α -syn) is a neuropathological hallmark of synucleinopathies. To date, no selective α -syn positron emission tomography (PET) radiotracer has been identified. Our objective was to develop the first original, selective and specific α -syn PET radiotracer.

Chemical design inspired from three structural families that demonstrated interesting α -syn binding characteristics was used as a starting point. Bioinformatics modelling of α -syn fibrils was then employed to select the best molecular candidates before their syntheses. An *in vitro* binding assay was performed to evaluate the affinity of the compounds. Radiotracer specificity and selectivity were assessed by *in vitro* autoradiography and *in vivo* PET studies in animal (rodents) models. Finally, gold standard *in vitro* autoradiography with patients' *post-mortem* tissues was performed to confirm/infirm the α -syn binding characteristics.

Two compounds exhibited a good brain availability and bound to α -syn and A β fibrils in a rat model. In contrast, no signal was observed in a mouse model of synucleinopathy. Experiments in human tissues confirmed these negative results.

KEYWORDS

Synucleinopathies; Parkinson's disease; multiple system atrophy; alpha-synuclein; radiotracer; positron emission tomography.

INTRODUCTION

Several neurodegenerative diseases share common pathological mechanisms whereby certain endogenous proteins (amyloid-beta or A β , alpha-synuclein or α -syn, Tau) form fibrillary aggregates composed of β -sheet structures that are linked with the pathological processes¹. Among neurodegenerative proteinopathies, those characterized by α -syn protein aggregates form a heterogeneous group of diseases called “synucleinopathies”. Alpha-synuclein aggregates are localized inside neurons in Parkinson’s disease (PD), PD with dementia (PDD) and dementia with Lewy bodies (DLB), while they form oligodendroglial cytoplasmic inclusions in multiple system atrophy (MSA)².

International guidelines have highlighted a crucial need to develop tools for brain imaging in the diagnosis and follow-up of these diseases³⁻⁵. Positron emission tomography (PET) enables non-invasive *in vivo* and *in situ* visualization, characterization and quantification of physiological processes at cellular or molecular level. In the absence of early clinically relevant biomarkers, PET imaging of α -syn would allow better understanding of pathophysiological processes involving α -syn, differential and possibly pre-symptomatic diagnosis of synucleinopathies and, finally, evaluation of disease-modifying drugs targeting α -syn⁶.

The development of a radiopharmaceutical specifically binding to α -syn aggregates raises numerous challenges: first in terms of sensitivity, as α -syn aggregates are present at lower density than A β aggregates *in vivo*; and second in terms of localization, as α -syn aggregates that are localized intracellularly and thus need a radiotracer able to cross the blood-brain barrier (BBB) and neuron or oligodendrocyte membranes. Last but not least, a successful radiotracer will have to be selective against the other proteins that also form β -sheets 3-dimensional (3D) structures: A β , Tau, TDP-43, and insulin. The most noticeable are amyloid A β aggregates, found in

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3 Alzheimer disease (AD) but also in other neurodegenerative diseases, including
4 synucleinopathies ^{7, 8}. Concurrently, the majority of DLB patients exhibit extensive cortical A β
5 deposition ⁹. This overlap complicates the quantification of PET images, pushing the PET
6 imaging community to investigate in depth the precise selectivity of the radiotracers already
7 developed and of those to come. In this regard, a particularly important and difficult point is to
8 find one or several models (cell lines overexpressing α -syn, *in vitro* α -syn fibrils, transgenic
9 animals overexpressing α -syn) that accurately reflect the aggregation process occurring in
10 humans ¹⁰, knowing that the gold-standard will always be evaluation performed on human tissue
11 and, ultimately, *in vivo* in patients.

12
13 All these challenges can explain that there is still no PET radiotracer available to measure α -syn
14 protein brain accumulation. If the amyloid radioligand 5-(E)-2-[6-(2-[¹⁸F]fluoroethoxy)-1,3-
15 benzoxazol-2-yl]ethenyl]-N,N-dimethyl-1,3-thiazol-2-amine (BF227), radiolabeled with carbon-
16 11 or fluorine-18, has demonstrated interesting binding properties to fibrils *in vitro* ¹¹ and α -syn
17 glial inclusions in MSA patients ¹², these results have not been extended to α -syn accumulation in
18 other synucleinopathies such as PD, PDD or DLB. Other lead compounds such as [¹²⁵I]SIL23,
19 that bind selectively to α -syn *in vitro* ¹³, or [¹⁸F]46a, with a higher selectivity for α -syn
20 recombinant fibrils than for A β fibrils ¹⁴, all failed *in vivo*.

21
22 The aim of this study was thus to develop a PET radiotracer of aggregated α -syn proteins. The
23 present study followed a rational and multidisciplinary approach to orient the design and the
24 evaluation of α -syn PET radiotracer-candidates. Several steps were undertaken with, firstly, the
25 chemical design of candidate molecules derived from three structural families that demonstrated
26 interesting α -syn binding characteristics in the literature^{11, 15-18}. The second step used
27 bioinformatics modeling tools to model an α -syn fibril, propose an interesting docking site along
28 the fibril, and evaluate the docking capabilities of our candidates toward this interaction site and

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3 also their ability to reach the identified binding pocket. As a final step, the “best” candidates were
4 synthesized, radiolabeled with fluorine-18, tested *in vitro*, evaluated by *in vitro/in vivo* imaging
5 studies in several animal models and, ultimately, *post-mortem* on AD, PD, MSA patients' brains.
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11 **MATERIALS AND METHODS**

13 **Computational studies**

14 ***Modelization of α -syn fibrils***

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17 The sequence of α -syn was obtained from the UniProt database. Using the Protein Data Bank
18 structure 2MPZ as scaffold¹⁹, mutations were made to replace the amino acids by the α -syn
19 sequence. The resulting layer model was duplicated on the fibril axes, following beta-pleated
20 conformation determined from a cryo-electron microscopy map (EMD-6482)²⁰, to obtain a final
21 model composed of 18 layers. After energy minimization, the structure was processed in a 20 ns
22 molecular dynamics simulation.
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34 ***Identification of a docking site***

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36 Simulations were performed with AMBER software version 16. All simulations were performed
37 in the conditions of a solution, using 5-site transferable interaction potential (TIP5P) as water
38 model, and the system was neutralized with chloride ions (Cl⁻). The periodic boundary condition
39 was chosen as a parallelepiped with about 12 Å extension in all directions. The molecular
40 simulation time step was set at 2 fs, with 300 K as final temperature and 1 atm as pressure,
41 leading to the discrimination of different conformations. The binding sites were identified for
42 these fibril structures, using the Site Finder program implemented in Molecular Operating
43 Environment (MOE).
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55 ***Evaluation of docking performance***

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3 All docking scores were performed with MOE 2014 in the interaction site determined using Site
4 Finder and the best conformations of the complex were transferred to umbrella sampling
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6 simulations.
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9 ***Ability to reach the identified docking site***

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12 Umbrella sampling simulations were performed with 220 windows, with distances between the
13 center of mass of the tracer and the atoms of the protein ranging from 27 Å to 5.1 Å at 0.1Å
14 intervals. In each window, a harmonic potential with 25 kcal/mol.Å² force constant was applied
15
16 to maintain these previous distances. Also, positional restraints were applied to backbone atoms
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18 of the two proteins which are at the edge of the fibril and the atoms of the protein concerned by
19
20 the reaction coordinate. For each window, we performed a simulation of 40 ps duration for
21
22 equilibration and 100 ps duration for production, with data collection every 50 fs at 300 K and 1
23
24 atm. Finally, the weighted histogram analysis method was employed to reconstruct the free
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26 energy profile along the reaction coordinate from the biased probability distribution of each
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28 window.
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37 **Chemical syntheses**

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39 These syntheses are showed in Figure 1.
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43 ***Synthesis of tert-butyl N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-N-methylcarbamate*** 44 **(3)**

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46 To a solution of **1** (0.435 mL, 3.70 mmol) and **2** (0.725 g, 3.08 mmol) in THF / tert-butanol (30
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48 mL / 1.8 mL), cooled at 0°C, was added potassium tert-butoxide (0.442 g, 4.01 mmol). After 1h
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50 at 0°C, the reacting mixture was stirred overnight at room temperature. Then, a saturated aqueous
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52 solution of NaHCO₃ was added, followed by extraction with ethyl acetate. Organic phase was
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54 then washed with brine and dried over MgSO₄. After evaporation, purification by flash
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3 chromatography (eluent: pentane/ethyl acetate, 90:10) was performed to obtain **3**, as a yellow
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5 solid (0.843 g, 78 %).

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7 ^1H NMR (CDCl_3 , 300MHz): δ 7.86 (d, 1H, $J=16.2\text{Hz}$), 7.80-7.70 (m, 1H), 7.62-7.51 (m, 3H),
8
9 7.40-7.28 (m, 4H), 7.08 (d, 1H, $J=16.2\text{H}$), 3.30 (s, 3H), 1.48 (s, 9H).

10 11 12 13 **Synthesis of 4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]-N-methylaniline hydrochloride (4)**

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15 To a solution of **3** (0.82g, 2.34 mmol) in CH_2Cl_2 (19 mL), cooled at 0°C , was added
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17 trifluoroacetic acid (1.9 mL). The solution was stirred at 0°C for 4h an, then, the solvents were
18
19 evaporated in vacuo and the resulting mixture was extract with ethyl acetate and saturated aqueous
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21 solution of NaHCO_3 . The organic phase is washed with brine and dried over Na_2SO_4 . After
22
23 evaporation, THF and HCl (37%) were added. The precipitated solid was filtered and washed
24
25 with THF. All the resulting organic phases were neutralized with a saturated aqueous solution of
26
27 NaHCO_3 . After evaporation, the resulting mixture was then extracted with ethyl acetate. The
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29 organic phase was then evaporated and HCl (37%) is added to form another precipitate. All the
30
31 obtained solids were combined to afford **4**, as a yellow solid (0.551 g, 82%).

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36 ^1H NMR (CD_3OD , 300MHz): δ 7.93-7.81 (m, 3H), 7.73-7.60 (m, 2H), 7.49-7.35 (m, 4H), 7.21
37
38 (d, 1H, $J=16.3\text{H}$), 3.07 (s, 3H).

39 40 41 **Synthesis of N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-4-fluoro-N-methylbenzene-1- 42 43 sulfonamide (4FBox)**

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45 To a solution of **4** (0.128 g, 0.45 mmol) and 4-fluorobenzenesulfonyl chloride (0.088 g, 0.45
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47 mmol) in anhydrous CH_2Cl_2 (7 mL), cooled at 0°C , was added trimethylamine (0.155 mL, 1.12
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49 mmol). The reacting mixture is then stirred at room temperature for 24h. After evaporation of
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51 solvents, the resulting mixture was dissolved with CH_2Cl_2 and washed with an aqueous solution
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of KHSO₄ (5%) and then with brine. After purification with flash chromatography (CH₂Cl₂ / diethyl ether), **4FBox** (0.1 g, 55%) was obtained as a yellow solid.

¹H NMR (DMSO-d₆, 400MHz): δ 7.84-7.77 (m, 3H), 7.76-7.69 (m, 2H), 7.63-7.57 (m, 2H), 7.47-7.35 (m, 4H), 7.33 (d, 1H, *J*=16.4Hz), 7.23-7.18 (m, 2H), 3.17 (s, 3H).

¹³C NMR (DMSO-d₆, 100MHz): δ 164.7 (d, *J*=252 Hz), 162.6, 149.8, 142.0, 141.7, 138.3, 133.6, 132.1 (d, *J*=2.7 Hz), 130.5 (d, *J*=9.8 Hz), 128.5, 126.2, 125.6, 124.8, 119.6, 116.6 (d, *J*=23.0 Hz), 114.4, 110.6, 37.6.

¹⁹F NMR (DMSO-d₆, 282MHz): δ -105.91.

Synthesis of N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-2-fluoro-N-methylbenzene-1-sulfonamide (2FBox)

Similar procedure to **4FBox** with 2-fluorobenzenesulfonyl chloride. **2FBox** is obtained as yellow solid (0.1 g, 64%).

¹H NMR (DMSO-d₆, 400MHz): δ 7.83-7.63 (m, 7H), 7.51-7.25 (m, 7H), 3.29 (d, *J*=1.3 Hz, 3H).

¹³C NMR (DMSO-d₆, 100MHz): δ 162.3, 158.1 (d, *J*=254.9 Hz), 149.8, 141.69, 141.65, 138.3, 136.3 (d, *J*= 8.6Hz), 133.5, 130.9, 128.5, 125.9, 125.6, 125.1 (d, *J*=3.6 Hz), 124.8, 124.6 (d, *J*=14.6 Hz), 119.6, 117.6 (d, *J*=21.5 Hz), 114.3, 110.6, 37.6 (d, *J*=2.8 Hz).

¹⁹F NMR (DMSO-d₆, 282MHz): δ -108.61.

Synthesis of N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-N-methyl-4-nitrobenzene-1-sulfonamide (4NBox)

Similar procedure to **4FBox** with 4-nitrobenzenesulfonyl chloride. **4NBox** is obtained as yellow solid (0.145 g, 87%).

¹H NMR (DMSO-d₆, 400MHz): δ 8.43-8.37 (m, 2H), 7.85-7.78 (m, 5H), 7.76-7.70 (m, 2H), 7.44-7.38 (m, 2H), 7.35 (d, 1H, *J*=16.4Hz), 7.25-7.21 (m, 2H), 3.23 (s, 3H).

¹³C NMR (DMSO-d₆, 100MHz): δ 162.2, 150.1, 149.8, 141.7, 141.5, 141.2, 138.3, 134.0, 129.0, 128.6, 126.6, 125.6, 124.8, 124.6, 119.7, 114.6, 110.6, 37.9.

Synthesis of *N*-{4-[(*E*)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-*N*-methyl-2-nitrobenzene-1-sulfonamide (2NBox)

Similar procedure to **4FBox** with 2-nitrobenzenesulfonyl chloride. **2NBox** is obtained as yellow solid (0.07 g, 42%).

¹H NMR (DMSO-d₆, 400MHz): δ 8.00 (dd, *J* = 8.0 Hz, 1.1 Hz, 1H), 7.92 (td, *J* = 7.7 Hz, 1.1Hz, 1H), 7.88-7.68 (m, 7H), 7.45-7.29 (m, 5H), 3.33 (s, 3H).

¹³C NMR (DMSO-d₆, 100MHz): δ 162.2, 149.8, 147.9, 141.7, 141.2, 138.3, 135.2, 134.0, 132.3, 130.4, 129.0, 128.7, 126.7, 125.6, 124.8, 124.3, 119.7, 114.6, 110.6, 38.4.

Radiolabeling of [¹⁸F]BF227, [¹⁸F]2FBox and [¹⁸F]4FBox

Fluorine-18 was obtained via the ¹⁸O (p,n)¹⁸F reaction (IBA Cyclone18/9 cyclotron). Fluoro substitution of the precursor was performed on a standard Neptis® synthesizer (ORA™): after initial fluoride preparation (collection, drying and Kryptofix activation), 1.0-2.0 mg radiolabeling precursor of [¹⁸F]BF227, [¹⁸F]2FBox or [¹⁸F]4FBox was introduced and the reaction mixture was heated at 150°C for 10 min in DMSO (**Figure 2**). The reaction mixture was passed through an activated C18 cartridge for pre-purification and the crude product was eluted from the cartridge with methanol. Pure [¹⁸F]BF227 was obtained after separation on a preparative high-performance liquid HPLC. For biological use, the product was diluted with sterile water, loaded onto a C18 cartridge (SEP-Pak Light, Waters), eluted with ethanol and diluted with isotonic saline to an ethanol concentration of 5%. Quality control of [¹⁸F]BF227, [¹⁸F]2FBox or [¹⁸F]4FBox consisted in determining radiochemical purity and specific activity, by analytic HPLC assay (UV and

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3 radioactive detections). The identity of [¹⁸F]BF227, [¹⁸F]2FBox or [¹⁸F]4FBox was confirmed by
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5 co-injection with an authentic non-radioactive sample.
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10 **Screening material**

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12 **Preparation of fibrils.** Lyophilized α -synuclein (α -syn) protein and amyloid- β 1-42 (A β 42)
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14 peptide (recombinant human proteins, rPeptide®) were dissolved in water for injection (WFI)
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16 with 0.02% azide to a final concentration of 200 μ M. The solutions were incubated at 37°C with
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18 constant agitation at 250 rpm using a thermomixer (Thermo-Shaker PHnT, Grant-bio®). Fibril
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20 aggregation was confirmed through thioflavin S (ThS) fluorescence staining.
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24 **Injected rats.** In order to evaluate both the ability of radiotracer candidates to cross the blood
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26 brain barrier and to detect α -syn and A β 1-42 fibrils, a model of rat was designed. These animals
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28 constitute robust and easy to implement and control animal model of proteinopathies. Adult male
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30 Sprague-Dawley rats (8-9 weeks old) weighing 250-400 g were used (Charles River Laboratories,
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32 L'Arbresle, France). All animal experiments were performed in accordance with the European
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34 guidelines (2010/63/UE) and were approved by the Animal Use Ethics Committee of the
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36 University of Lyon (C2EA-42; Comité d'Ethique en Expérimentation Animale Neurosciences
37
38 Lyon; celyne.lyon@inserm.fr). Rats were anesthetized with isoflurane inhalation in air (4%
39
40 isoflurane in 1 L/min air) and then transferred to a stereotaxic apparatus (Stoelting, USA)
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42 equipped with a mask delivering isoflurane at 1.25%-2.5% for the duration of the experiment.
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44 Body temperature was maintained by a heating pad set at 37°C and monitored rectally. A pulse
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46 oximeter was used to measure heart rate, respiratory rate and oxygen saturation. Pain was
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48 controlled by the potent opioid analgesic buprenorphine (Buprecare, Axience) injected
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50 subcutaneously at a dose of 0.05 mg/kg 20 minutes before any surgical act was performed.
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Animals (n=7) were stereotaxically injected (1 nmol in 5 μ L per injection site) with pre-

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3 aggregated A β 1-42 at the level of the caudate putamen (CPu) and α -syn in the contralateral CPu,
4 randomly (stereotaxic coordinates relative to bregma: AP = -3.2 mm; ML = \pm 1.2 mm; DV = -3.6
5 mm), according to the stereotaxic atlas of the rat brain ²¹. Fibrils were slowly infused at a
6 constant rate of 1 μ L/min with 30-gauge needles. The needles were left in place for 2 minutes and
7 then slowly withdrawn. After injections, the scalp was sutured, an antiseptic (povidone-iodine)
8 and local analgesic (lidocaine) were applied, and the rats were allowed to recover from
9 anesthesia. A 7-day post-injection interval was observed before euthanasia and subsequent
10 studies.
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21 ***Transgenic mice.*** The “accelerated” version of the transgenic (Tg) mouse model (M83)
22 expressing human A53T mutated α -syn was used ²². In this accelerated model, α -syn aggregates
23 appear \sim 100 days after inoculation, especially in the brainstem and midbrain ²². This period
24 corresponded to the age of animal used for *in vitro* autoradiography brain sections. C57Bl/6S
25 brain sections of a mouse presenting a deletion of the α -syn locus (α -syn KO) (Harlan, Gannat,
26 France) were used as control. The transgenic mouse model (PDAPP line J20), overexpressing 2
27 human mutations of APP genes ²³, was obtained from collaborators (Dr N. Rama, CRCL, UMR
28 INSERM 1052, CNRS 5286, Lyon). Animal brain sections were used when they expressed large
29 A β plaques in hippocampus and cortex.
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42 ***Human postmortem brains.*** Human brain tissue sections were obtained as frozen sections from
43 London Neurodegenerative Diseases Brain Bank and a local brain bank in Lyon (Cardiobiotec,
44 HCL). Consecutive medulla sections from patients with various synucleinopathies were used for
45 *in vitro* autoradiography. These included one PD patient (79 year-old male), one MSA patient (71
46 year-old male) and one control patient (63 year-old female). Consecutive brain sections, at the
47 level of cortex and hippocampus, from one AD patient (67 year-old male) were also included in
48 the *in vitro* autoradiography experiments.
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***In vitro* binding assay**

Synthetic α -syn and A β 42 fibrils (200 nM) were incubated with increasing concentrations of radiotracer (0.5-200 nM). In order to evaluate the non-specific binding of the compounds, the below-mentioned reactions were performed in the presence of 50 μ M unlabeled compound. Samples were incubated for 1 hour at room temperature in 200 μ L assay buffer (phosphate buffer saline: PBS, 0.1% bovine albumin serum: BSA). Bound radiolabeled tracer was separated from free tracer by filtration under reduced pressure (Multiscreen HTS Vacuum Manifold; Multiscreen HTS-FB 1.0/0.65 μ m, Millipore). Filters were washed three times with 200 μ L PBS. Washed filters were assayed for radioactivity by gamma counter (Gamma Wizard 2480-160715, Perkin Elmer). Binding data were analyzed with curve-fitting software that calculated K_d and B_{max} on non-linear regression (GraphPad Software, Prism 5). All experiments were conducted in triplicate.

***In vivo* small-animal PET imaging**

Fibril-injected (n=5) and non-injected control rats (n=5) were used for *in vivo* PET imaging experiments in isoflurane-anaesthetized animals (4% induction and 2% maintenance). Each experiment was performed in duplicate for each group (fibril-injected vs non-injected) and for each radiotracer ($[^{18}\text{F}]\text{BF227}$, $[^{18}\text{F}]\text{2FBox}$, and $[^{18}\text{F}]\text{4FBox}$). PET scans were acquired in list mode, using a Siemens INVEON PET/CT scanner, with a nominal in-plane resolution of \sim 1.4 mm full-width-at-half-maximum in the center of the FOV. A 60-minute list mode acquisition started immediately after caudal intravenous injection of $[^{18}\text{F}]\text{BF227}$, $[^{18}\text{F}]\text{2FBox}$ or $[^{18}\text{F}]\text{4FBox}$. The reconstructed images led to a volume of 159 slices of 128 x 128 voxels, with voxel size

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3 0.388 x 0.388 x 0.796 mm. The dynamic images obtained were analyzed on the INVEON
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5 Research Workplace (IRW, Siemens).

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7 PET was co-registered with CT, and both were co-registered with our in-house rat MRI atlas²⁴,
8
9 to extract radioactivity values in the whole brain (general brain uptake) but also in the region of
10
11 interest (ROI), the CPu, where the fibrils were injected. Time activity curves (TAC) were
12
13 expressed as percentage of injected dose per gram (%ID/g) and standardized uptake values
14
15 (SUV)²⁵ over time. SUV summed over the 40-60 min. period (where TAC plateaued) were also
16
17 calculated at the fibril-injected sites (CPu) and divided by the SUV measured in an area devoid of
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19 fibrils (cerebellum (Cb)) to give an index of radiotracer uptake (SUV ratio = $SUVR = [SUV_{CPu}] /$
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21 $[SUV_{Cb}]$).

22 23 24 25 26 27 28 ***In vitro* autoradiography**

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31 Animals (fibril-injected rats and transgenic mice) were deeply anesthetized with isoflurane in the
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33 inducing chamber (4% isoflurane in 1 L/min air flow) and rapidly euthanized by decapitation.
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35 Brains were dissected and frozen in 2-methylbutane with dry ice (-30°C). Thirty-micrometer
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37 sections were cut across the respective ROIs: coronal CPu sections for fibril-injected rats, sagittal
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39 sections encompassing midbrain and brainstem for M83 mice, and sagittal sections through
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41 hippocampus and cortex for PDAPP transgenic mice. Sections were then thaw-mounted on slides
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43 (Superfrost[®], Roth, France) and allowed to air-dry for 30 minutes before storage at -80°C until
44
45 use. On the day of tracer synthesis, the slides (animal and human postmortem) were allowed to
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47 thaw at RT for 30-60 minutes and sections were incubated at RT for 30 minutes in Tris-buffered
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49 saline (TBS) supplemented with HCl (TBS-HCl buffer) (138 mM NaCl, 2.7 mM KCl, pH
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51 adjusted to 7.5) containing 37 kBq/mL of either [¹⁸F]BF227, [¹⁸F]2FBox or [¹⁸F]4FBox. After
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53 incubation, slides were dipped twice in an 8:1 ethanol/water mixture at RT for 1 minute then
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3 dried under cool air, and exposed on a sensitive phosphor imaging plate BAS-IP MS 2025,
4 Fujifilm) overnight. The distribution of radioactivity was then qualitatively visualized on a Bio-
5 imaging analyser system (BAS-5000, Fujifilm).
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10 11 12 **Immunofluorescence**

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14 The frozen sections used for *in vitro* autoradiography or adjacent frozen brain sections were used
15 for immunofluorescence studies. Brain sections were post-fixed in 4% paraformaldehyde in PBS
16 for 20 minutes followed by 3 PBS washes of 5 min each, and transferred to a PBS solution
17 (0.02% azide) at 4°C until use. An antigen retrieval/unmasking step was conducted with 99%
18 formic acid solution for 10 min followed by 3 PBS washes of 5 min each. Slides were then
19 dipped in blocking and permeabilization buffer (PBST with 5% BSA and 0.5% Triton X-100) for
20 30 min followed by 3 PBS washes of 5 min each. Incubation in PBST containing primary
21 antibodies was then performed overnight at 4°C. The primary antibodies used were 4G8 clone for
22 A β (1/1000; anti- β -amyloid, 17-24 antibody, mouse IgG2b), or 5G4 clone for α -syn (1/1000;
23 anti-aggregated α -synuclein, monoclonal mouse IgG1 κ). Slides were then incubated in PBST
24 containing the secondary antibody Alexa Fluor 594 (1/1000; AF594 anti-mouse,
25 LifeTechnologies) for 1 hour at room temperature followed by 3 PBS washes of 5 min each.
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27 Alternatively to immunofluorescence, thioflavin-S staining was performed with 0.0025%.

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Fluorescence was first observed using an imaging microscope (Axioplan-2, Zeiss; Oberkochen, Germany). A Texas Red (ex 587 \pm 25 nm, em 647 \pm 70 nm) filter was used for AF594 secondary antibody and a GFP (ex 470 \pm 40 nm, em 525 \pm 50 nm) filter for ThS. Images were captured using a digital camera interfaced with image-analysis software (Axiovision 3.0 software, Zeiss). Fluorescence was then observed and captured with a digital slide scanner (Axio Scan.Z1, Zeiss) (CIQLE Imaging Platform, University of Lyon, France) equipped with similar

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3 filters, in order to have a full view and digital image of each brain section. For human
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5 postmortem immunofluorescence images, the green channel (non-specific auto-fluorescence
6
7 binding) was subtracted (Adobe Photoshop CS6 tool) from the red channel in order to obtain
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9 images with only red specific immunolabeling.
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14 RESULTS

15 Chemical Design

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17 The chemical design of ten candidate molecules derived from three structural families that
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19 demonstrated moderate to high affinity towards α -syn fibrils, and modified to be easily
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21 radiolabeled with fluorine-18, were explored.
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26 The first structural family consisted of tricyclic antidepressants that were mentioned in a patent
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28 that demonstrated an interesting binding of imipramine and nortryptilline towards α -syn fibrils¹⁵.
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30 Five fluorinated compounds (4FN, 2FN, 4FD, 2FD, F2CN) were drawn (**Figure 3A**).
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33 Inspired by the structure of the dyes used in histochemistry to reveal the α -syn aggregates in *post-*
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35 *mortem* studies, and from whom BF227 was derived¹¹, the second family consisted of
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37 benzoxazoles derivatives. The benzoxazole-vinyl cores were conserved with the aim to reproduce
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39 and improve these binding properties (**Figure 1**). The pharmaco-modulation focused on the
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41 amino-thiazole part which was substituted by an amino-benzene moiety. A benzene sulfonyl part
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43 was also added on the amino function to allow a subsequent facilitated radiolabeling with
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45 fluorine-18. These structures have a poly-conjugated planar structure interesting for interactions
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47 with β -sheet structures of α -syn fibrils. Two candidate molecules were developed: 2FBox and
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49 4FBox (**Figure 3B**).
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53 The last series of molecules were derived from benzimidazoles derivatives which demonstrated
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55 moderate α -syn binding affinity but 2-3 fold higher selectivity towards α -syn in comparison to
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3 amyloid- β aggregates¹⁶⁻¹⁸. Some of these compounds having demonstrated a E/Z double-bond
4 isomerization,¹³ the central double bonds were replaced by a triple bond to conserve the
5 conjugation of the structure without isomerization abilities. With their planar structure, these
6 benzimidazoles derivatives present promising conformation in order to bind (through π - π
7 interactions) to the channels formed along the β -sheets fibrils/filaments. Three candidate
8 molecules were developed and included F4SBIYB, F3CBIYB and F2PBIYB (**Figure 3C**).
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19 **Computational modeling, docking site identification and accessibility**

20 *Modelization of the α -syn fibrils*

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22 The sequence of α -syn was obtained from the UniProt database (www.uniprot.org) under the
23 reference P37840-1. Modeling of α -syn fibril structure was based on a cryo-electron microscopy
24 (cryo-EM) study²⁰ and consisted in a fragment of α -syn fibrils with two entwined,
25 asymmetrically associated protofibrils. A portion of α -syn fibril with 36 α -syn proteins (18 layers
26 of duplicated α -syn proteins) was reproduced in all-atoms resolution. After a molecular dynamic
27 of 20 ns in the isothermal-isobaric ensemble, 5 representative conformations of the fibril were
28 sampled by 2D-RMSD (root mean square deviation), in which a common interaction site was
29 identified by Site Finder. This site was oriented parallel to the fibril axis, located between amino-
30 acids 67 and 75 of the α -syn protein, and formed a loop in the fibril (**Supplementary Figure**
31 **S.A1**).
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46 *Docking scores*

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48 Computation of docking simulations gave a score evaluating the affinity of all our 10 candidate
49 molecules for the identified docking site (with the highest pseudo-affinities for the lowest
50 numerical values). The tricyclic antidepressant family was the one that showed, overall, the less
51 interesting docking scores (**Table 1**). The benzimidazoles derivatives' docking scores varied
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from -5.0 kcal/mol to -6.9 kcal/mol. The benzoxazoles derivatives were the ones with the highest docking scores towards the identified α -syn binding pocket with an improved docking score in comparison to BF227 (docking score for 4FBox = -9.0 kcal/mol, 2FBox = -8.7 kcal/mol and BF227 = -8.3 kcal/mol). The docking results showed that the chemical modifications brought to BF227 derivatives' 2FBox and 4FBox were not predicted to annihilate their binding to the α -syn fibril.

Structural Families	Candidate Molecules	α -syn fibril docking scores (kcal/mol)
Tricyclics	4FD	-4,3
	2FN	-3,9
	4FN	-3,5
	2FD	-3,4
	F2CN	-3,2
Benzoxazoles	4FBox	-9,0
	2FBox	-8,7
<i>additional info</i>	<i>BF227</i>	<i>-8,3</i>
Benzimidazoles	F3CBiYB	-6,5
	F2PBiYB	-6,4
	F4SBiYB	-5,0

Table 1. Docking scores of our candidate molecules towards the identified docking site on the α -syn fibril model. Values are expressed in kcal/mol and reflect pseudo-affinities (the highest pseudo-affinities for the lowest values). Scores presented are GBVI/WAS (Generalized-Born Volume Integral/Weighted Surface Area).

Ability to reach the docking site

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3 Umbrella sampling calculations (highly demanding in terms of computing power) were only
4 performed for the two candidate molecules that demonstrated the highest docking scores towards
5 the α -syn binding pocket, namely, 2FBox and 4FBox. The identified radiotracer interaction site
6 was deeply buried within the α -syn structure. Candidate molecules must thus penetrate the
7 structure between strand ladders to reach the interaction site. In order to simulate and calculate an
8 energy profile for the whole access process, umbrella sampling simulations were performed.
9
10 Calculation speed was enhanced by extracting a fragment of 13 α -syn proteins in which the
11 sequence was reduced to amino-acids 35-91. The potential of mean force results (PMF) graphical
12 illustration is the umbrella sampling method we chose to reflect the accessibility of our candidate
13 molecules to the interaction site (**Supplementary Figure S.1B**). The energetic barrier was the
14 highest for 2FBox (7.1 kcal/mol), intermediate for 4FBox (6.5 kcal/mol) and the lowest for
15 BF227 (6 kcal/mol). PMF for 4FBox and 2FBox showed similar profiles and penetration patterns.
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33 **Candidate molecules and radiolabeling**

35 **Synthesis of non-radioactive FBox compounds and their precursors for radiolabeling**

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37 The non-radioactive FBox compounds and their precursors for radiolabeling (NBox) were
38 synthesized following a divergent strategy (**Figure 1**). The common intermediate **4** was obtained
39 from the reaction between 2-methylbenzoxazole (**1**) and aldehyde **2**, followed by Boc
40 deprotection of the obtained compound **3**. The FBox molecules could be then obtained through
41 reaction with the corresponding fluorobenzenesulfonyl chloride (ortho-substituted for N-{4-[(E)-
42 2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-2-[¹⁸F]fluoro-N-methylbenzene-sulfonamide (2FBox)
43 and para-substituted for N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-4-[¹⁸F]fluoro-N-
44 methylbenzenesulfonamide (4FBox)). Similarly, NBox compounds were formed from the
45 corresponding nitrobenzenesulfonyl chloride (ortho-substituted for N-{4-[(E)-2-(1,3-benzoxazol-
46 2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-2-[¹⁸F]fluoro-N-methylbenzene-sulfonamide (2FBox)
47 and para-substituted for N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-4-[¹⁸F]fluoro-N-
48 methylbenzenesulfonamide (4FBox)). Similarly, NBox compounds were formed from the
49 corresponding nitrobenzenesulfonyl chloride (ortho-substituted for N-{4-[(E)-2-(1,3-benzoxazol-
50 2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-2-[¹⁸F]fluoro-N-methylbenzene-sulfonamide (2FBox)
51 and para-substituted for N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-4-[¹⁸F]fluoro-N-
52 methylbenzenesulfonamide (4FBox)). Similarly, NBox compounds were formed from the
53 corresponding nitrobenzenesulfonyl chloride (ortho-substituted for N-{4-[(E)-2-(1,3-benzoxazol-
54 2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-2-[¹⁸F]fluoro-N-methylbenzene-sulfonamide (2FBox)
55 and para-substituted for N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-4-[¹⁸F]fluoro-N-
56 methylbenzenesulfonamide (4FBox)). Similarly, NBox compounds were formed from the
57 corresponding nitrobenzenesulfonyl chloride (ortho-substituted for N-{4-[(E)-2-(1,3-benzoxazol-
58 2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-2-[¹⁸F]fluoro-N-methylbenzene-sulfonamide (2FBox)
59 and para-substituted for N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-4-[¹⁸F]fluoro-N-
60 methylbenzenesulfonamide (4FBox)). Similarly, NBox compounds were formed from the

2-yl)ethenyl]phenyl}-N-methyl-2-nitrobenzenesulfonamide (2NBox) and para-substituted for N-{4-[(E)-2-(1,3-benzoxazol-2-yl)ethenyl]phenyl}-N-methyl-4-nitrobenzenesulfonamide (4NBox).

The overall yields of these 3-step syntheses were generally satisfactory to good.

The radiolabeled compounds were obtained successfully through nucleophilic substitution of nitro group from 4NBox and 2NBox, with satisfactory radiochemical yields (10-19%) (**Figure 2**).

Specific activity (SA) was relatively high (range, 68-543 GBq.μmol⁻¹) for our 2 tracers. The logD values were in accordance with good permeation of brain blood barrier (Figure 2).

***In vitro* radioactive saturation assays**

[¹⁸F]BF227, [¹⁸F]4FBox and [¹⁸F]2FBox selectivity were tested against synthetic α-syn and Aβ42 fibrils. First, successful formation of fibrils from recombinant proteins²⁶ was determined by thioflavin S staining and direct observation of fibrils from recombinant proteins by transmission electronic microscopy (**Supplementary Figure S.2**). According to the literature¹¹, for [¹⁸F]BF227, K_d was equal to 14.03 ± 43.52 nM and B_{max} = 11.98 ± 9.49 pmol/nmol of fibrils for α-syn fibrils. For Aβ42 fibrils, K_{d1} was equal to 0.82 ± 1.08 nM and B_{max1} = 0.91 ± 0.41 pmol/nmol of fibrils while K_{d2} was equal to 125.2 ± 29.05 nM to Aβ 1-42 and B_{max2} = 14.43 ± 10.07 pmol/nmol of fibrils (**Supplementary Figure S.3**). [¹⁸F]4FBox bound with low affinity to α-syn fibrils (K_d = 155.4 ± 96.5 nM and B_{max} = 2.073 ± 0.821 pmol/nmol of fibrils) and with better affinity to Aβ42 fibrils (K_d = 7.7 ± 2.6 nM and B_{max} = 0.802 ± 0.070 pmol/nmol of fibrils, **Figure 4 C and D**). In contrast, [¹⁸F]2FBox bound α-syn fibrils with high affinity (K_d = 3.3 ± 2.8 nM and B_{max} = 0.128 ± 0.025 pmol/nmol of fibrils, and with lower affinity to Aβ42 fibrils (K_d = 145.3 ± 114.5 nM and B_{max} = 0.592 ± 0.251 pmol/nmol of fibrils).

***In vitro* autoradiography in rats and mice**

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3 In the striata of fibril-injected rats, all three radiotracers were able to non-selectively detect α -syn
4 and A β 42 synthetic fibrils in autoradiography experiments, as shown by intense radioactive
5 signal located on the site where immunofluorescence confirmed the presence of aggregated α -syn
6 and A β 42 fibrils (**Figure 5**).

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12 In the midbrain and brainstem of the Tg mouse model overexpressing a mutated form of α -syn
13 (M83) and in the cortex and hippocampus of the Tg mouse model overexpressing 2 mutated
14 forms of APP (PDAPP line 20), none of the three radiotracers were able to detect the α -syn or A β
15 aggregates stained with ThS (**Figure 5**). The Tg mouse model lacking α -syn expression, as
16 confirmed by absence of ThS staining, gave a similar negative radioactive signal (**Figure 5**).

26 ***In vivo* PET imaging in rats**

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28 PET imaging study was performed in our rat model, which exhibit α -syn on one side and A β 1-42
29 fibrils on the other side of the caudate putamen, compared to non-injected rat. The 60-minute
30 acquisition started immediately after caudal intra-venous injection of [18 F]BF227 (10.9 ± 5.5
31 MBq; range, 7.4-17.2 MBq), [18 F]2FBox (12.4 ± 1.8 MBq; range, 10.8-14.9 MBq), or
32 [18 F]4FBox (9.4 ± 6.6 MBq; range, 4.7-14.1 MBq). Biological evaluation of the three radiotracers
33 indicated crossing of the blood-brain barrier and entry to the brain (**Figure 6**). Initial whole-brain
34 uptake was higher and faster with [18 F]BF227 (0.65 %ID/g peak at 2 minutes post-injection) than
35 with [18 F]4Fbox (0.47 %ID/g peak at 10 minutes p.i.) or [18 F]2FBox (0.47 %ID/g peak at 12
36 minutes p.i.). Standardized uptake values (SUV) approximating 2 at peak are usually desirable
37 for PET brain radiotracers²⁷. Calculated SUV at peak was close to 2, with values of 2.7, 1.6 and
38 1.6 for [18 F]BF227, [18 F]4FBox and [18 F]2FBox, respectively. Washout kinetics was moderate,
39 with half of overall brain activity (calculations performed on the whole brain activity) still
40 present after 60 min (5min/60min ratio: 2.2 for [18 F]BF227, 1.7 for [18 F]2FBox, 1.5 for

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3 [¹⁸F]4FBox). Injected fibrils were not detected by any of the three radiotracers *in vivo* (**Figure 6**).
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5 Calculated SUVR (mean ± SD) with [¹⁸F]BF227 was 1.05 ± 0.03, 1.10 ± 0.12 and 1.05 ± 0.02 in
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7 control, Aβ42 and α-syn-injected striata, respectively. PET imaging with [¹⁸F]2FBox gave SUVR
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9 = 1.08 ± 0.02, 1.13 ± 0.04 and 1.10 ± 0.02 in control, Aβ42 and α-syn -injected striata,
10
11 respectively. Finally, [¹⁸F]4FBox did not perform better, with SUVR (mean ± SD) of 1.12 ± 0.03,
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13 1.05 ± 0.06 and 1.07 ± 0.05 in control, Aβ42 and α-syn -injected striata, respectively.
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19 ***In vitro* autoradiography in post-mortem patients' brain**

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21 In human *post-mortem* PD brain (medulla oblongata), none of the three radiotracers were able to
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23 image Lewy bodies or neurites, as seen from the absence of radioactive signal in these α-syn rich
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25 regions immunostained by 5G4 antibody, which preferentially labels aggregated synuclein²⁸
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27 (**Figure 7**). In human *post-mortem* MSA brain where glial cytoplasmic α-syn inclusions were
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29 immunostained by 5G4, no radioactive signal could be detected with any of the three radiotracers
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31 (**Figure 7**). Similarly, in control human *post-mortem* brain, no radioactive signal or
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33 immunostaining could be detected (**Figure 7**). In human *post-mortem* AD brain, large Aβ plaques
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35 were immunostained by 4G8 antibody in the cortex and hippocampus. The [¹⁸F]BF227 signal
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37 clearly co-localized with 4G8 staining and binding was displaced with non-radioactive BF227 in
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39 excess (data not shown). However, neither [¹⁸F]2FBox nor [¹⁸F]4FBox were able to detect Aβ
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41 plaques (**Figure 7**).
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49 **DISCUSSION**

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54 The development of an α-syn PET radiotracer is particularly challenging as indicated by the fact
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56 that all published attempts were failures. This general observation incited us to propose a slightly
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3 different screening paradigm to evaluate our PET candidates. Starting from a “classical” chemical
4 design of candidate molecules derived from three structural families that demonstrated interesting
5 α -syn binding characteristics, we then developed a bioinformatics modelization approach
6 (modelization of α -syn fibrils, identification of docking site, evaluation of candidate molecules
7 docking scores and ability to reach the binding pocket) to select the “best” candidates and
8 confirm the chemical choice before embarking in synthesis and radiolabeling, *in vitro* assays
9 performed with synthetic fibrils, *in vitro/in vivo* imaging studies with animal models and, finally,
10 *in vitro post-mortem* autoradiography studies.
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21 From the design of 10 candidate molecules derived from three structural families, our
22 objective was that this pharmaco-modulation could bring interesting selectivity and specificity
23 properties towards α -syn fibrils. The cryo-EM α -syn fibril model we used for subsequent
24 computational modeling was relevant because fibrils are known to be composed of multiple
25 protofibrils^{29,30}. Even if a recent α -syn fibril NMR structure has been characterized³¹, our model
26 remained relevant as the NMR structure does not consider associations of multiple protofibrils. A
27 recent study on A β styrylbenzoxazole candidate radiotracers showed that there was only a weak
28 correlation between docking scores and experimental binding affinities³². Therefore, our docking
29 results only gave indications (no definitive answers) on which structural families were more
30 interesting. The tricyclic antidepressants and benzimidazoles structural families were the less
31 interesting, with low docking scores. However, the chemical modifications brought to BF227’s
32 structure to produce our benzoxazoles derivatives 2FBox and 4FBox did not result in a drop/fall
33 in the docking scores. Overall, our computational modeling experiments suggested that these last
34 two candidate molecules retained a binding ability similar to BF227 (docking scores), though at
35 the price of greater energy required to reach the binding site (umbrella sampling). We thus
36 decided to attempt their radiolabeling with fluorine-18, and succeeded.
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3 Consecutive saturation filter binding assays with recombinant synthetic fibrils showed
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5 that [¹⁸F]2FBox was clearly the best of our two candidates. In our experimental conditions,
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7 [¹⁸F]2FBox detected ~16-fold less binding sites (B_{max}) on α-syn fibrils than [¹⁸F]4FBox but it
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9 did so with a ~47-fold better affinity (K_d) and a nearly 44-fold selectivity towards α-syn versus
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11 Aβ42 fibrils, when [¹⁸F]4FBox was more selective towards Aβ42 than α-syn fibrils (~20-fold).
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13 These results should nonetheless be interpreted with caution, as reproducibility issues were
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15 encountered. Though filter binding assay is a robust technique for “receptology”, it might be less
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17 well adapted to fibrils, a very different type of target, which consequently generated non-specific,
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19 non-saturable binding in our experiments. Indeed, cerebral aggregates and synthetic fibrils
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21 display a high propensity to coat to surfaces^{33, 34}. Another confounding feature of protein
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23 aggregates is their so-called structural polymorphism³⁵⁻³⁷, the formation of several types of fibril,
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25 distinguished by variable 3D structures (differences in folding in the formation of folded β-
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27 sheets) and variable quaternary structures. These conformational changes could lead to different
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29 binding sites on these fibrils for candidate radiotracers. An aggregation polymorphism was
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31 observed by electronic microscopy: a modification of pH or of aggregation time showed
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33 formation of fibrils with different structures (data not shown). This heterogeneity of structure
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35 may be the source of significant variability in binding experiments, but it is also an opportunity
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37 for exploration with molecular imaging and computational modeling.
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44 Evaluation in synthetic-fibril-injected rats demonstrated the ability of our radiotracers to
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46 non-selectively detect Aβ42 and α-syn recombinant human fibrils *in vitro* and *ex vivo* (data are
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48 presented in **Supplementary Figure S.4**). However, *in vivo* small-animal PET imaging in this
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50 same rat model showed that both radiotracers failed to detect either Aβ42 or α-syn fibrils despite
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52 good uptake in cerebral tissue. This discrepancy between *in vivo* and *in vitro* results is probably
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54 due in part to the low spatial resolution of small-animal PET imaging³⁸ in comparison to *in vitro*
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3 autoradiography³⁹. Low specific activity is another potential factor that has previously been
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5 implicated in the failure to detect A β plaques in animal models of AD⁴⁰⁻⁴². However, in the
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7 present study, specific activity was unlikely to be responsible for non- detection *in vivo*, as
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9 specific activity (SA) was relatively high (range, 68-543 GBq. μ mol⁻¹) for both tracers.

12 Similarly, [¹⁸F]2FBox and [¹⁸F]4FBox were unable to detect A β or α -syn in transgenic
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14 mouse models of Alzheimer's (PDAPP) and Parkinson's (M83) disease. [¹⁸F]BF227, a derivative
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16 of a well-known carbon-11 A β radiotracer^{43, 44}, was not able to image either α -syn, as previously
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18 demonstrated by our team⁴⁵ or, more surprisingly, A β plaques. Hypotheses for this lack of A β
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20 plaques binding include methodological issues. It is known in PET imaging that radiotracer
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22 binding with good imaging contrast is a function of target-site density (Bmax; higher is better)
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24 relative to radiotracer affinity to the binding site (Kd; lower is better)⁴⁶. It may be that the density
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26 of α -syn and A β plaque inclusions in these models were too low to achieve a good PET imaging
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28 contrast⁴⁵. Concerning our candidate α -syn radiotracers, in the "PD-like" accelerated Tg mouse
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30 model (M83) expressing the human A53T mutated α -syn²², neither [¹⁸F]2FBox nor [¹⁸F]4FBox
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32 were able to detect α -syn aggregates. Similarly, in the Tg mouse model (PDAPP line J20)
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34 overexpressing 2 human mutations of APP genes²³, [¹⁸F]2FBox and [¹⁸F]4FBox were not able to
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36 image the confirmed presence of A β plaques. These negative results obtained with transgenic
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38 mice models that overexpress human forms of the fibrils highlight the first "gap" between the
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40 feasibility of imaging synthetic recombinant human fibrils but the complexity of accessing to a
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42 binding site on human mutated fibrils produced in an animal model. In the search for an α -syn
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44 PET radiotracer, a very important and difficult point is to find one or several animal models that
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46 accurately reflect human pathology¹⁰. Negative results in the search for an α -syn PET imaging
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48 radiotracer highlight the challenges to overcome, particularly in terms of selectivity¹³ and
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3 predictivity of the models ¹⁰. The gold-standard will always be evaluation in human tissue and,
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5 ultimately, *in vivo* in patients.
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8 Gold-standard *in vitro* autoradiography experiments in *post-mortem* brain tissue of
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10 confirmed synucleinopathy cases, including PD and MSA, also failed to detect α -syn aggregates
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12 in Lewy bodies or glial cytoplasmic inclusions, respectively. Several hypotheses can be put
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14 forward to explain these negative results. Firstly, the size and density of the fibrils/aggregates: α -
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16 syn aggregates are much smaller in size and lower in density than A β plaques. In AD patient
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18 brain, A β plaques were 60-200 μ m in diameter, while in PD brain Lewy neurites were only 30-40
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20 μ m (~5-fold smaller) ^{47, 48}. Lewy neurites were even thinner (<10 μ m diameter), but rather long
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22 (~600 μ m long) ⁴⁹. Glial cytoplasmic inclusions were 20-60 μ m in diameter ⁵⁰. Density was
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24 clearly low in PD brain, with only 6 Lewy bodies that could be observed in one section (while
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26 there were more glial cytoplasmic inclusions in MSA brain), whereas more than a hundred A β
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28 plaques could be counted in one section of AD brain. Additionally, not all A β plaques were
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30 actually detected by [¹⁸F]BF227. So there seem to be some A β plaques that do not have all
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32 characteristics necessary for [¹⁸F]BF227 to access its binding site. Alternatively, the A β plaques
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34 in one AD patient had different structures, enabling [¹⁸F]BF227 to bind only to certain A β
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36 plaques. The same argument could be applied to α -syn radiotracers: that one good tracer is not
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38 able to bind to all α -syn Lewy bodies, making the discovery of an α -syn radiotracer even more
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40 challenging. It is, however, encouraging that some radiotracers do successfully target neuronal
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42 receptors present at even lower densities ^{6, 13}. The negative results obtained with human *post-*
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44 *mortem* brains highlight the second “gap” between the feasibility of imaging synthetic
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46 recombinant human fibrils and the complexity of accessing a binding site in human *post-mortem*
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48 brain.
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3 The discrepancy between results obtained with, on the one hand, computational modeling
4 and recombinant human fibrils *in vitro* in injected rats and, on the other hand, *in vivo* with *post-*
5 *mortem* human brain tissue, casts doubt on the predictivity of computational modeling, on
6 screening candidate molecules with recombinant human fibrils produced *in vitro*, and on
7 evaluating candidate radiotracers with animal models that do not perfectly reflect the full
8 pathology. To overcome this major issue, several strategies can be put forward. First, concerning
9 computational modeling, the failure of the experimental studies compared to the *in silico*
10 predictions may come from the use of an α -syn fibril model that did not reflect the *in vivo*
11 pathophysiology, as most information on α -syn fibril structure comes only from fibrils produced
12 *in vitro*. An interesting research axis would be to have access to fibril structures (NMR or cryo-
13 EM) derived from patients. There may be an important gap between fibrillary polymorphisms
14 obtained *in vitro* and those present in the brains of patients, because of both the maturation
15 environment and the speed of aggregation. The second strategy would be to perform filter
16 binding assays with human *post-mortem* brain homogenates, as this is the reference method for
17 quantification purposes ^{11, 51-53}. Another approach would be to produce fibrillary strains of A β
18 and α -syn by amplification of recombinant human peptides with patient material isolated from
19 human samples, in order to control structural polymorphism.
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44 CONCLUSION

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49 After the chemical design of 10 molecules derived from three structural families, bioinformatics
50 modelling tools enabled us to select two original benzoxazole candidate ligands that were
51 successfully labeled with fluorine-18. Evaluation in rats demonstrated the ability of both
52 radiolabeled molecules to non-selectively detect A β and α -syn recombinant human fibrils *in*
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3 *vitro*. However, small-animal PET imaging in this rat model showed that, although both
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5 candidate radioligands were able to cross the blood-brain barrier, they failed to detect either A β
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7 or α -syn fibrils *in vivo*. Similarly, [^{18}F]2FBox and [^{18}F]4FBox were unable to detect A β or α -syn
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9 in transgenic mouse models of Alzheimer's (PDAPP) and Parkinson's (M83) disease. Finally,
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11 gold-standard *in vitro* autoradiography experiments in *post-mortem* brain tissue of confirmed
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13 synucleinopathy cases, including PD and MSA, also failed to detect α -syn aggregates in Lewy
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15 bodies or glial cytoplasmic inclusions, respectively. [^{18}F]2FBox and [^{18}F]4FBox are not suitable
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17 α -syn PET radiotracers. This study presented an experimental paradigm, theoretically adapted to
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19 the research of PET tracers for aggregated proteins, but that needs to be improved in terms of the
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21 predictivity of computational modeling in order to be ready for application in subsequent
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23 radiotracer candidates.
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ABREVIATIONS

α -syn : alpha-synuclein; PET : positron emission tomography; PD : Parkinson disease; PDD : Parkinson disease with dementia; DLB : Dementia with Lewy bodies; MSA : Multiple system atrophy; BBB : Blood brain barrier; 3D : Three dimension; AD, Alzheimer's disease; TIP5P : 5-site transferable interaction potential; MOE : Molecular operating environment; A β 42: amyloid- β 1-42; WFI : water for injection; ThS: Thioflavin S; Cpu : Caudate putamen; Tg : Transgenic; PBS: Phosphate Buffer Saline; BSA : Bovine serum albumin; IRW: INVEON Research Workplace; ROI : region of interest, TAC : Time activity curves , SUV : standardized uptake values; SUVR : standardized uptake values ratio; PMF : potential of mean force.

Supplementary Data:

Supplementary Figure S.1. Localization of the interaction site on one of the two protofibrils constituted of 18 α -synucleins (A). Potential of mean force (PMF) along reaction coordinate (0.1Å) for the 3 molecules, BF227, 4FBox and 2FBox, to access the docking site (B).

Supplementary Figure S.2 Transmission Electron Microscopy (TEM) images of A β 1-42 fibrils (A) and α -syn fibrils. Scale bars as noted.

Supplementary Figure S.3. *In vitro* binding assays of [18 F]BF227. (A) Saturation binding curve for [18 F]BF227 specific binding to α -syn fibrils. (B) Saturation binding curve for [18 F]BF227 specific binding to A β 1-42 fibrils.

Supplementary Figure S.4. *Ex vivo* autoradiography performed with [18 F]BF227 and [18 F]2FBox showing the ability of the tracers to non-selectively detect A β 42 and α -syn.

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Conflict of Interest Statement

All authors declare that they have no conflict of interest.

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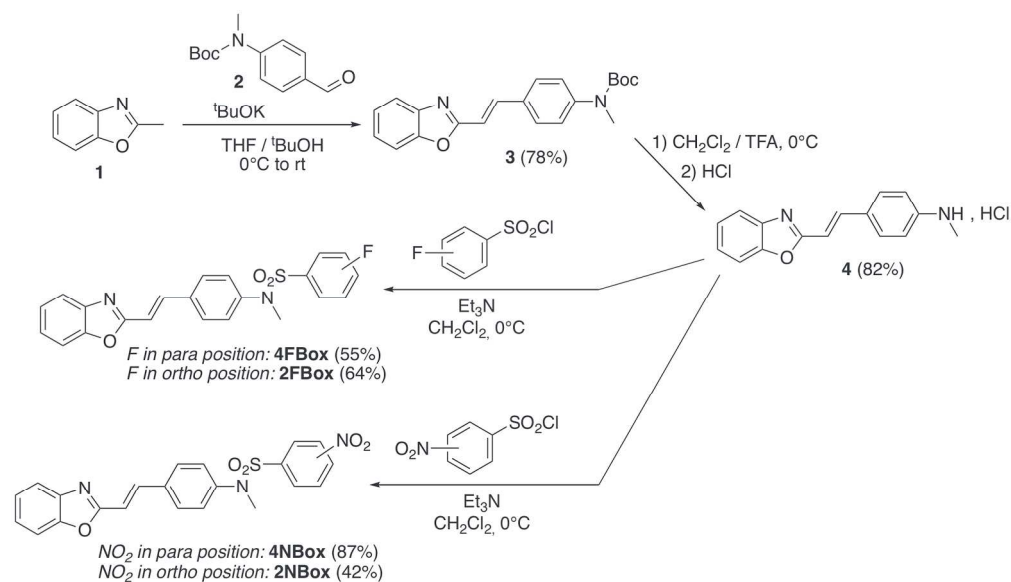
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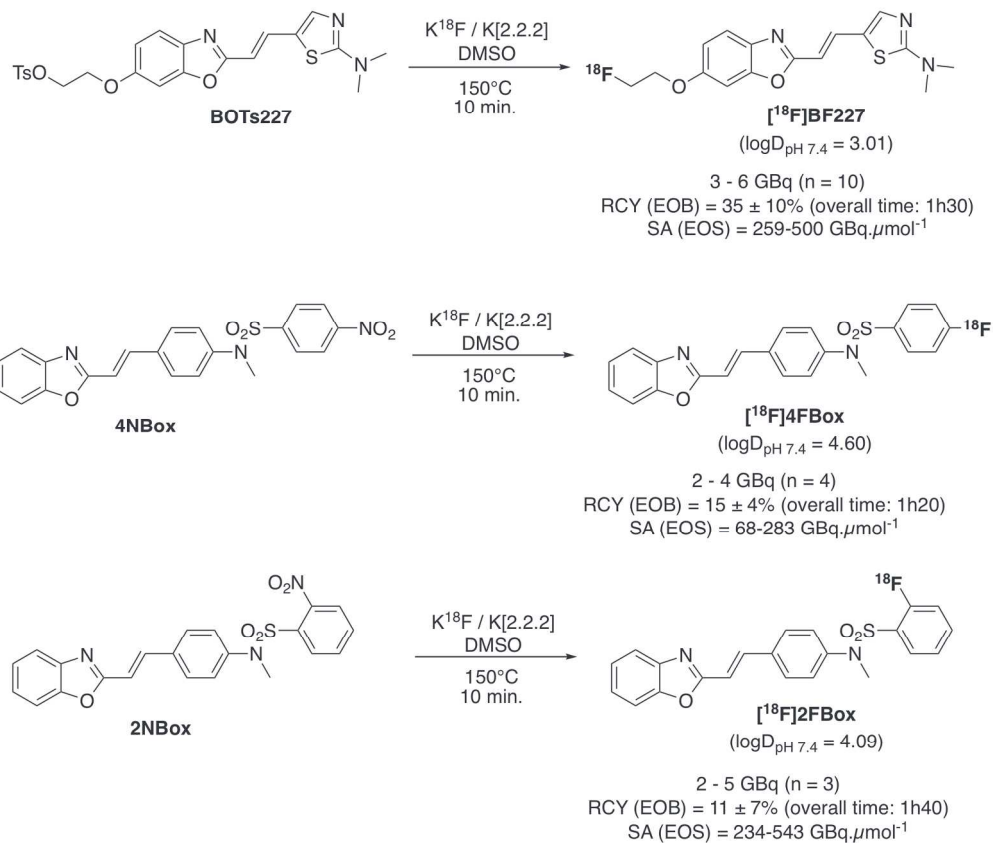
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26 Figure 1. Diagram of the chemical syntheses of the non-radioactive FBox compounds and their precursors
27 (Nbox) for radiosyntheses.

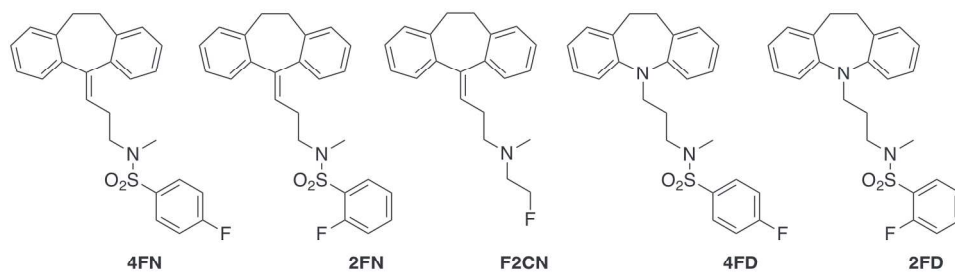
28 196x112mm (300 x 300 DPI)



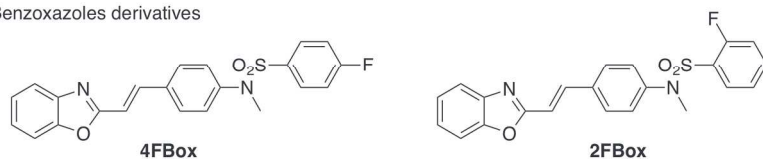
34 Figure 2. Diagram of the radiosynthesis of [¹⁸F]BF227 (A), [¹⁸F]4FBox (B) and [¹⁸F]2FBox (C). RCY data
 35 are mean±SD values.

36 182x153mm (300 x 300 DPI)

A: Tricyclic antidepressants derivatives



B: Benzoxazoles derivatives



C: Benzimidazoles derivatives

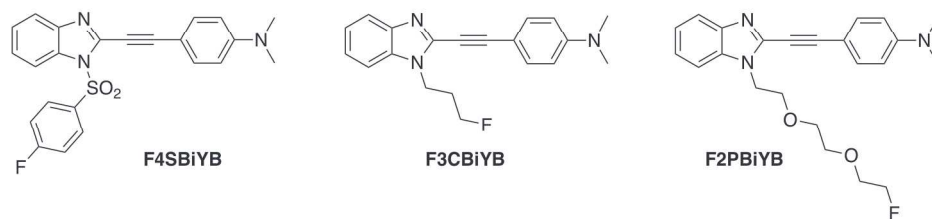


Figure 3. Diagram of the 10 molecules derived from three structural families with (1A) the antidepressant tricyclic derivatives, (1B) the benzoxazoles derivatives and (1C) the benzimidazoles derivatives.

189x145mm (300 x 300 DPI)

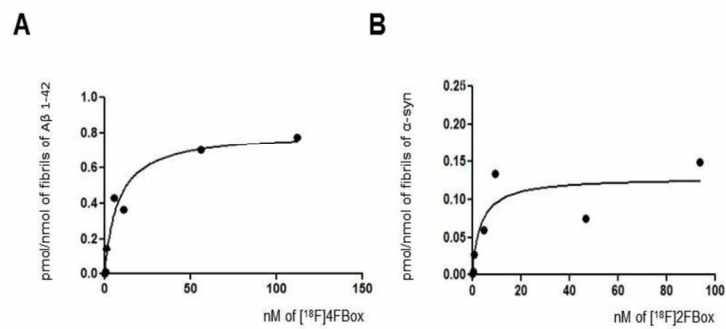


Figure 4. In vitro binding assays. (A) Saturation binding curve for [18F]4FBox specific binding to Aβ42 fibrils. (B) Saturation binding curve for [18F]2FBox specific binding to α-syn fibrils.

127x95mm (300 x 300 DPI)

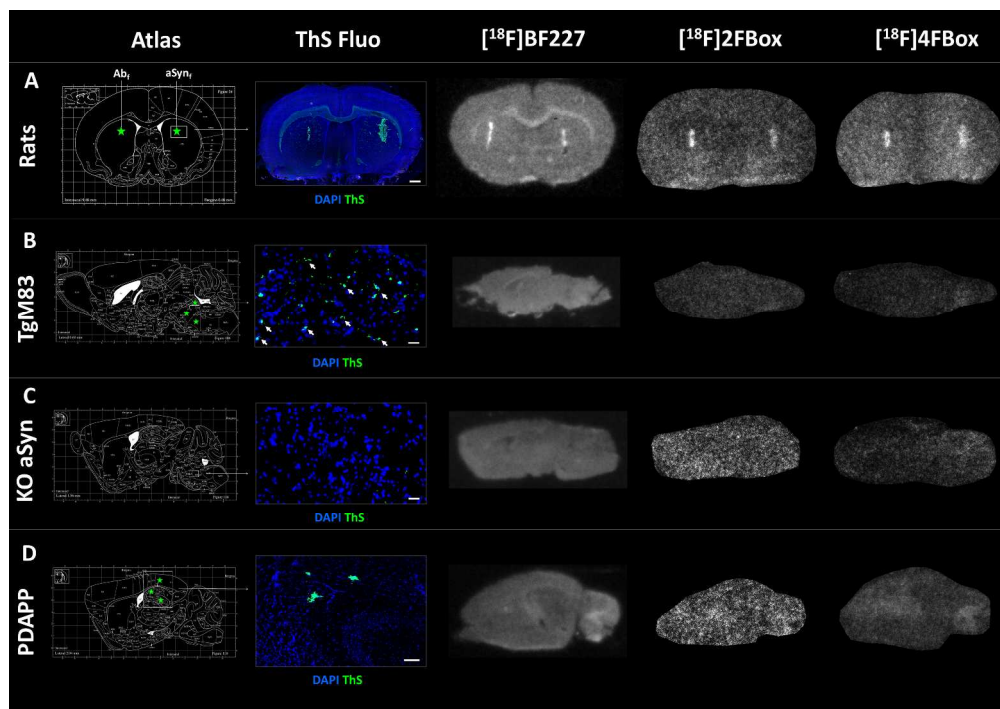
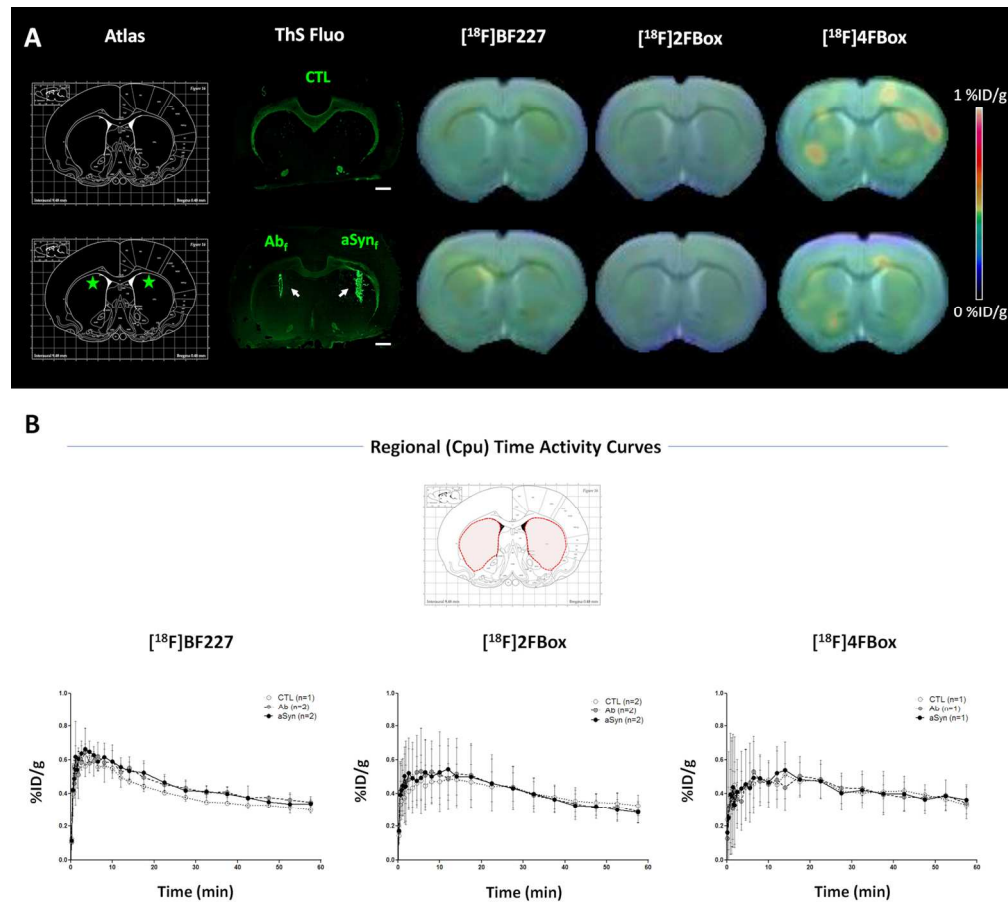


Figure 5. In vitro autoradiography with $[^{18}\text{F}]\text{BF227}$, $[^{18}\text{F}]\text{2FBox}$ and $[^{18}\text{F}]\text{4FBox}$ in animal models. (A) fibril-injected rats; (B) M83 transgenic mice expressing human mutated form of $\alpha\text{-syn}$; (C) $\alpha\text{-syn}$ knock-out transgenic mouse model; and (D) PDAPP transgenic mouse model overexpressing 2 mutated forms of human amyloid precursor protein. On the left, stereotaxic atlas figures of the anatomical level represented in the various animal models (green stars indicate fibril injection sites). Green ThS fluorescence images illustrate the localization (white arrows) and confirm the presence of $\alpha\text{-syn}$ and $\text{A}\beta$ aggregates in the various animal models (DAPI blue fluorescence indicates cell nuclei). Scale bars represent $200\ \mu\text{m}$ in rats and PDAPP mice, and $20\ \mu\text{m}$ in M83 and $\alpha\text{-syn}$ KO mice.

1418x997mm (55 x 55 DPI)



39 Figure 6. Small-animal PET imaging with $[^{18}\text{F}]\text{BF227}$, $[^{18}\text{F}]\text{2FBox}$ and $[^{18}\text{F}]\text{4FBox}$ in control and fibril-
40 injected rats. (A) Summed PET images were co-registered with CT images and radioactivity index was
41 reflected by a color scale representing %ID/g. Thioflavin S fluorescence staining of A β 42 and α -syn
42 fibrils injected in the striata is presented (white arrows), with the corresponding stereotaxic brain atlas region
43 (green stars representing injection sites). Scale bar represent 1 mm on ThS fluorescence staining. (B) Time
44 activity curves (expressed in %ID/g over time) for each radiotracer are presented. Values (mean \pm SD)
45 were extracted from the striata regions thanks to an in-house made MRI atlas that was co-registered to PET-
46 CT images.

47 169x169mm (300 x 300 DPI)

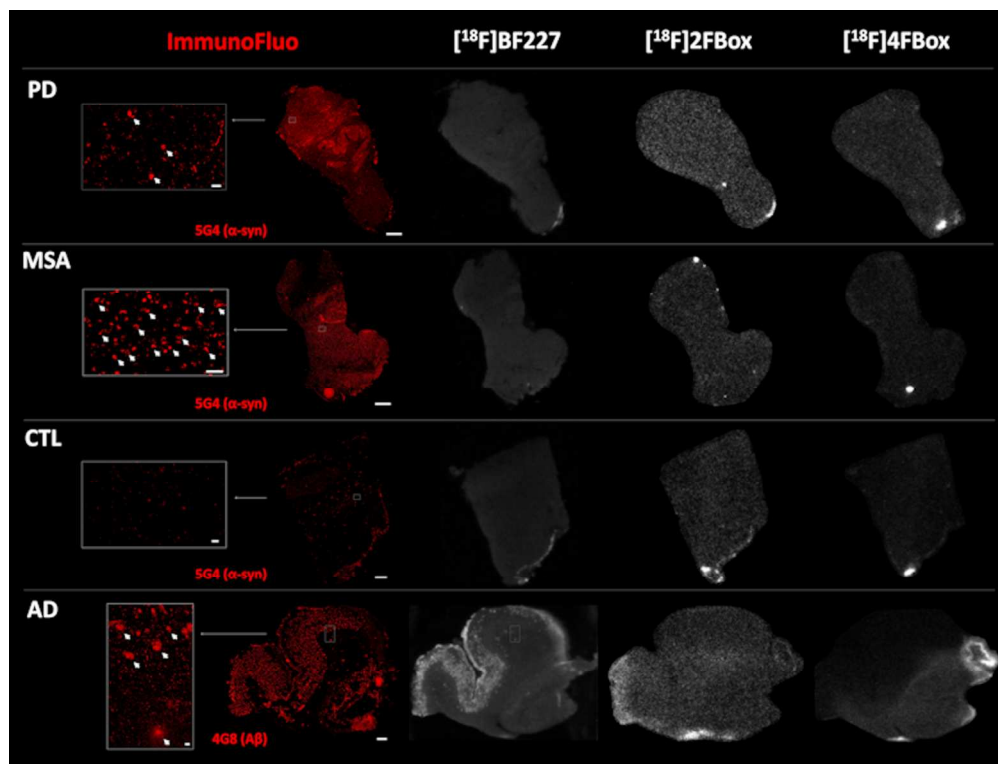


Figure 7. In vitro autoradiography with $[^{18}\text{F}]\text{BF227}$, $[^{18}\text{F}]\text{2FBox}$ and $[^{18}\text{F}]\text{4FBox}$ in postmortem human brain. (A) PD patient, (B) MSA patient and (C) control patient medulla oblongata, and (D) AD patient cortex and hippocampus region. Left: immunofluorescence staining with α -syn proteins labeled with 5G4 antibody, and $\text{A}\beta$ proteins with 4G8 antibody (white arrows). Scale bars in the zoom box represent $50\ \mu\text{m}$ in PD, MSA and CTL, and $100\ \mu\text{m}$ in AD brain. In the digitized whole-brain sections, scale bars represent 2 mm. Note that only $[^{18}\text{F}]\text{BF227}$ was able to label $\text{A}\beta$ plaques in the AD patient, as demonstrated by the co-localization of $[^{18}\text{F}]\text{BF227}$ radioactive signal (in white) and 4G8 immunostaining (in red).

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