

2-Amino adipic Acid–C(O)–Glutamate Based Prostate-Specific Membrane Antigen Ligands for Potential Use as Theranostics

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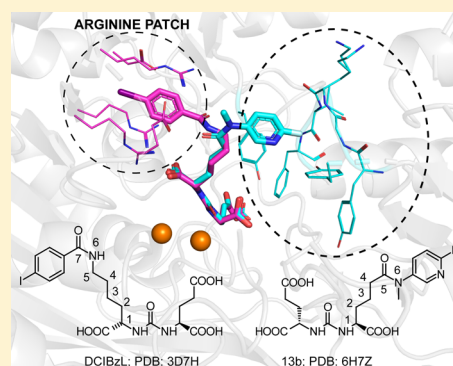
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Supporting Information

ABSTRACT: The design and synthesis of prostate specific membrane antigen (PSMA) ligands derived from 2-amino adipic acid, a building block that has not previously been used to construct PSMA ligands, are reported. The effects of both the linker length and of an N-substituent of our PSMA ligands were probed, and X-ray structures of five of these ligands bound to PSMA were obtained. Among the ligands disclosed herein, **13b** showed the highest inhibitory activity for PSMA. As ligand **13b** can readily be radiolabeled since its fluorine atom is adjacent to the nitrogen atom of its pyridine ring, the use of this and related compounds as theranostics can be pursued.



KEYWORDS: Theranostic, PSMA ligands, prostate cancer, PET imaging, X-ray structure, arginine patch

Prostate cancer (PCa) is the most frequently diagnosed cancer and the second leading cause of death in men in the US after lung cancer, with an estimated 180,890 new cases and 26,120 deaths in 2016. The aggregate cost of treating PCa patients has been estimated at \$8–10 billion/year in the US, thus making it a significant disease with a heavy societal cost-burden.^{1,2} The tissue-specific protein, prostate specific membrane antigen (PSMA), is an excellent target for imaging and therapy because it is a cell surface protein that presents a large extracellular target. Most PCa cells overexpress PSMA compared to the limited expression pattern observed in normal prostate cells, and the overexpression is significantly correlated to poor disease prognosis.^{3–7} Therefore, several PSMA ligands including antibodies,^{8,9} peptides,^{10,11} aptamers,¹² and small molecules^{13,14} have been developed to deliver imaging agents for the diagnosis of prostate cancer. Among them, small molecules exhibit favorable features: reproducible chemical synthesis, nonimmunogenicity, and, in general, fast clearance from normal tissues. In 2001, Kozikowski et al. first developed urea-based PSMA inhibitors as GCPII (glutamate carboxypeptidase II) inhibitors.¹⁵ Since then, many researchers have been using this urea-based scaffold for targeting PSMA due to the high affinity of these ureas for PSMA as well as their ease of synthesis. Recently, these urea-based PSMA ligands labeled with ¹⁸F or ⁶⁸Ga have been investigated as PET imaging agents in Phase III clinical trials.^{16,17} However, such studies have revealed that uptake of these radioligands also takes place in off-target tissues including the kidneys and salivary glands,

which might perhaps be avoided through proper design features. It is possible, for example, that such drawbacks can be overcome by enhancing the compounds' hydrophilicity, resulting in faster clearance from off-target tissues.^{18,19} Even though hundreds of PSMA ligands have been explored in the past decades, the influence on PSMA affinity of the length of the second amino acid moiety (in addition to the obligatory P1' glutamate) has not been elucidated yet since almost all of the PSMA ligands for PET imaging were synthesized starting from lysine or another molecule of glutamic acid.¹⁶

The internal substrate/inhibitor-binding cavity of PSMA can be divided into the prime (S1') and nonprime sections separated by the active site harboring two Zn²⁺ ions (Figure 1A). Within the nonprime section, one of the most prominent structural features is the so-called arginine patch comprising Arg463, Arg534, and Arg536. Ionic interactions between the positively charged patch and the P1 carboxylate of PSMA-selective inhibitors are critical for the design of high affinity urea inhibitors. Furthermore, the flexibility of the arginine side chains allows for the formation of an S1 accessory hydrophobic pocket upon inhibitor binding that can be in turn exploited for the design of high affinity inhibitors as reported herein.^{20–22} Our efforts focused on using 2-amino adipic acid as a novel building block and to investigate the best chain length for

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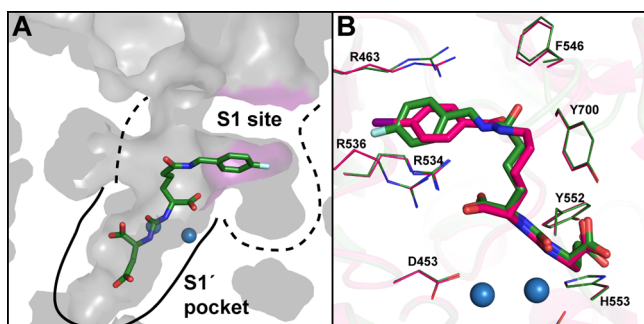
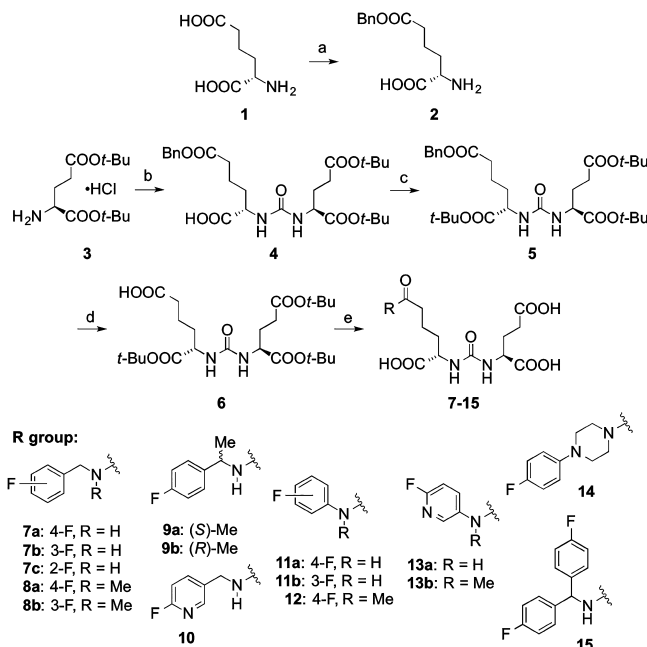


Figure 1. (A) Schematic representation of the internal cavity of PSMA (arginine patch, purple; zinc ions, light blue) in complex with 7a (green sticks). (B) Comparison of the binding modes of 7a (green) and 16 (DCIBzL, pink).

interaction with the S1 hydrophobic pocket to enhance the compounds' affinity for PSMA, with the goal of possibly reducing their dose of administration and achieving a higher image resolution.

We have chosen to concentrate on fluorinated PSMA ligands since it is well-known that the radionuclide ^{18}F has yielded improved imaging resolution compared to ^{68}Ga .²³ Fluorinated PSMA ligands incorporating 2-amino adipic acid were synthesized as shown in Scheme 1. First, the distal carboxyl group of L-2-amino adipic acid (enantiopurity: 98%) was protected by benzoylation, and the monobenzyl ester was directly coupled with the enantiopure requisite isocyanate.²⁴ The free carboxyl group of 4 was protected as *tert*-butyl ester, and then the

Scheme 1. Synthesis of Compounds 7–15^{4a}



^{4a}Reagents and conditions: (a) 12 M HCl, BnOH, 100 °C, 1 h, 84%; (b) i. triphosgene, DIPEA, DCM, -78 °C, 1 h, then rt, 15 min; ii. 2, DMF, -78 °C to r.t., overnight, 56%; (c) 2-*tert*-butyl-1,3-diisopropylisourea, DCM, reflux, overnight, 71%; (d) H₂, 10% Pd/C, MeOH, r.t., overnight, 80%; (e) i. amine, HATU, DIPEA, DMF, r.t., 16 h; ii. TFA, rt, 30 min. Yields: 7a, 76%; 7b, 89%; 7c, 76%; 8a, 89%; 8b, 85%; 9a, 72%; 9b, 83%; 10, 83%; 11a, 79%; 11b, 77%; 12, 72%; 13a, 62%; 13b, 24%; 14, 93%; 15, 68%.

benzyl ester was deprotected by hydrogenation to form the carboxylic acid 6. The desired amides 7–15 were obtained by amidation of 6, followed by deprotection of the tri-*tert*-butyl esters. All final compounds 7–15 were purified by preparative high-performance liquid chromatography (preparative HPLC), and their chemical structures were confirmed by NMR and LCMS-IT-TOF. The purities of all tested compounds were >95%, as determined by analytical HPLC. The inhibition constants (IC₅₀ values) of these compounds for the enzyme PSMA were determined using the radioenzymatic assay with [³H]NAAG as a substrate (Table 1). The IC₅₀ values of the

Table 1. PSMA Inhibitory Activity of Compounds 7a–c, 8a–b, 9a–b, 10, 9a–b, 12, 13a–b, 14, 15, 21a–b, and 22a–b^{4a}

compd	IC ₅₀ (nM)	compd	IC ₅₀ (nM)
7a	2.32 ± 0.55	12	0.20 ± 0.11
7b	2.91 ± 0.33	13a	0.99 ± 0.05
7c	2.11 ± 1.01	13b	0.075 ± 0.005
8a	0.64 ± 0.07	14	1.31 ± 0.18
8b	0.46 ± 0.10	15	1.19 ± 0.73
9a	5.24 ± 1.45	21a	0.94 ± 0.26
9b	5.44 ± 2.54	21b	0.15 ± 0.02
10	4.46 ± 1.03	22a	1.11 ± 0.22
11a	0.35 ± 0.01	22b	0.13 ± 0.01
11b	0.28 ± 0.09	16 (DCIBzL)	0.021 ± 0.004

^{4a}Inhibition constants of studied compounds were determined using the radioenzymatic assay with [³H]NAAG (radiolabeled at the terminal glutamate) as described previously.²²

benzylamide derivatives 7a–7c were almost identical, demonstrating that the position of the fluorine atom does not influence their potency. Introduction of a methyl group on the amide nitrogen of 7a and 7b, however, increased their potency for PSMA (compounds 8a and 8b). At the same time, however, compounds 9a and 9b that have a methyl group attached to the benzylic position showed approximately 2- and 10-fold lower inhibitory affinity for PSMA compared to 7a and 8a, respectively. The decrease in the inhibitory affinity of 9a and 9b is likely due to the steric hindrance of the methyl group clashing with the side chain of Arg463 and interfering thus with the full insertion of the inhibitor ring into the S1 hydrophobic accessory pocket. Additionally, it is plausible that the presence of the methyl group would also elicit a steric strain with the ring moiety within the inhibitor backbone at the rotation angle observed in the crystal structure of the PSMA/7a complex (see below). Compound 10, in which the benzene ring is replaced with a pyridine ring, showed marginally lower affinity compared to 7a.

To visualize the binding mode of one of our new PSMA ligands within the internal PSMA pocket, we first determined the crystal structure of the PSMA/7a complex to a final resolution of 1.48 Å (PDB code 5OF0). As expected, the position and interaction pattern of the urea-glutamate moiety in the S1' pocket is identical to PSMA/urea-based inhibitor complexes published previously.²⁰ Favorably, and in-line with our hypothesis, the aromatic ring of 7a is inserted into the S1 hydrophobic pocket, thereby increasing its inhibitor potency for PSMA through interactions contributed by the distal aromatic ring. It should be noted that the placement of the aromatic ring of 7a is virtually identical to that observed in the complex of PSMA with DCIBzL, a urea-based inhibitor bearing

lysine as the main moiety of the P1 linkers (Figure 1B). These findings suggest that when there are seven intervening atoms between the urea function and the P1 aromatic moiety, the distal aromatic ring is preferably inserted into the hydrophobic accessory pocket within the arginine patch.

We next evaluated a series of compounds 11–13 having the P1 linker shortened by one atom, i.e., having six intervening atoms between the urea function and the P1 aromatic moiety, as this linker length has not been explored before. All compounds from this series showed subnanomolar IC_{50} values (Table 1) revealing that amino adipic as the main moiety of the linker serves as an excellent substitute for the traditional lysine used in “canonical” urea-based compounds.

The affinities of the anilides 11–13 were on average higher than those of the corresponding benzylamides 7–10, which indicates that the distance between the aromatic ring and the urea moiety in the former is more suitable for strong interactions with residues in the internal pocket of PSMA, an aspect of these urea-based ligands that was not explored in detail in previous studies.^{24–27} Furthermore, the *N*-methylated anilides 12 and 13b exhibited enhanced affinity compared with the corresponding *N*-H derivatives 11a and 13a, respectively. Particularly, 13b showed the highest inhibitory activity (IC_{50} = 0.075 nM) for PSMA among all of the PSMA ligands synthesized from 2-amino adipic acid.

To provide a mechanistic explanation for these SAR findings, we determined the crystal structures of 11a (PDB code 6H7Y), 13a (PDB code 6HKJ), and 13b (PDB code 6H7Z) in complex with PSMA at a final resolution of 1.81, 2.09, and 2.00 Å, respectively (Supplementary Table S1). Compared to the structure of PSMA in complex with 7a, which has the P1 aromatic ring inserted into the S1 hydrophobic pocket of the arginine patch, the position of the P1 aromatic moiety of both 11a and 13a differs substantially (Figure 2). For 11a and 13a the distal ring is inserted into a

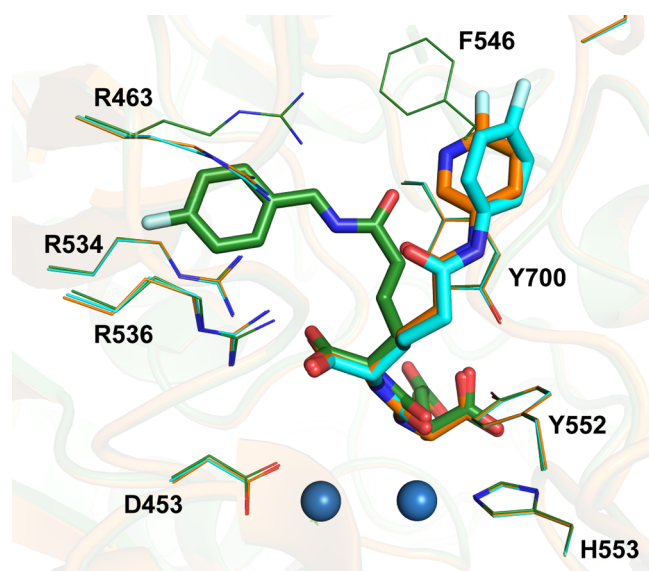


Figure 2. Comparison of binding modes of 7a (green), 11a (cyan), and 13a (orange); zinc ions are shown as blue spheres. Note that while the positioning of the glutamate-urea moiety in the PSMA internal cavity is indistinguishable for both complexes, the distal aromatic rings occupy different portions of the entrance funnel due to differences in the length of the linker connecting the urea nitrogen and the distal aromatic ring (6 vs 7 intervening atoms).

shallow pocket lined with the side chain of Y700 and the backbone of G206, K207, and V208. Also critical are F546, S547, G548, and W541, residues present within the flexible entrance lid²⁸ that form the opposite wall of the binding pocket (Figure S1).

Introduction of a *N*-methyl group into 13a, leading to 13b, is linked to a 10-fold increase in potency for PSMA and a slightly different interaction pattern. While the distal rings of 13b and 13a partially overlap, the former is inserted deeper into the pocket because of the *cis* conformation of the linking amide bond. Additionally, the increased potency of compounds with the pyridine ring in the *cis* conformation (e.g., 13b) vs ones with either the phenyl group (e.g., 22b) or pyridines in the *trans* conformation (e.g., 13a) can likely be attributed to the water-mediated contact between the ring nitrogen and the hydroxyl group of Y234 (Figure S2). It should be noted that the above-mentioned hydrophobic patch is one of the interaction hotspots in the PSMA internal pocket as it is exploited by other inhibitory scaffolds such as hydroxamates or phosphoramidates.²¹

The data presented here together with prior studies^{20,29} offer a comprehensive picture of relation between the P1 linker length and the position of the terminal aromatic moiety of urea-based compounds (Figure 3). For flexible linkers with

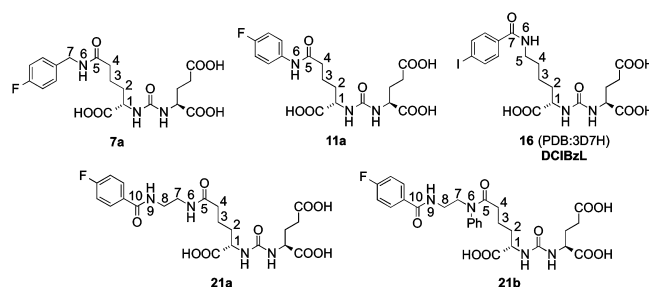


Figure 3. Chain length from the “left” nitrogen of the urea moiety to the aromatic ring in compounds 7a, 11a, 16, 21a, and 21b.

seven intervening atoms, the distal aromatic ring will most likely be located within the S1 accessory pocket of the arginine patch. In the case of shorter (6 intervening atoms) and longer (>8 atoms) linkers the distal aromatic groups will either interact with one of the defined hydrophobic patches lining the entrance funnel or adopt several diverse conformations inside the funnel. It should be noted that a key aspect of the linker chain is its extreme flexibility. When comparing the structures of 7a (reported here) and 16 (DCIBzL; PDB code 3D7H)²⁰ bound to PSMA, the position of their terminal halogenated rings inside the pocket is virtually identical, and this particular placement is facilitated by the linker’s flexibility, as it can adopt several (most favorable) conformations within the spacious internal cavity.

The crystal structure of the PSMA/13b complex shows that the fluorinated pyridine ring of 13b is constrained to adopt the *cis*-amide conformation with the *N*-methyl group pointing toward the unoccupied space of the entrance funnel (Figure 4A). This particular structural arrangement brings about the possibility of the addition of a second, larger substituent on the amide nitrogen. Such “branching” can be exploited for fine-tuning of both physicochemical and pharmacokinetic parameters to create the next generation of refined analogs.

To test this assumption, we synthesized compounds 21a,b and 22a,b as shown in Scheme 2. The starting material 18a

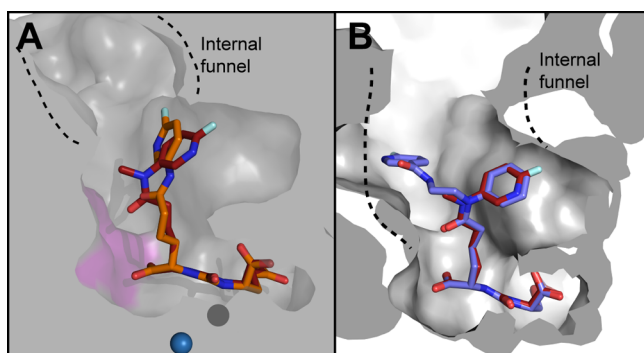
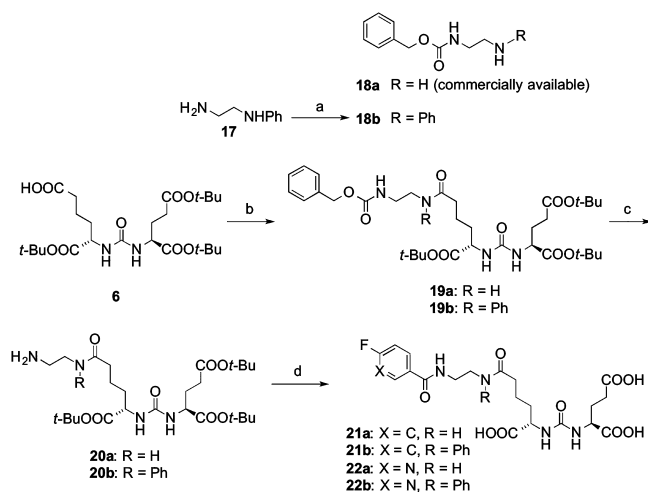


Figure 4. (A) Superposition of binding modes of **13a** (orange) and **13b** (red). (B) Detail of the amide methyl group (**13b**; red) and pyridine group (**22b**; blue; PDB code 6HKZ) pointing toward the unoccupied space of the internal funnel (dashed line).

Scheme 2. Synthesis of Compounds **21a–b** and **22a–b**^a



^aReagents and conditions: (a) Cbz-Cl, DIPEA, DCM, 0 °C to r.t., 1 h, 93%; (b) **18a** or **18b**, HATU, DIPEA, DMF, r.t., 16 h; (c) H₂, 10% Pd/C, MeOH, r.t., overnight. Yields: **20a**, 81%; **20b**, 59%; (d) i. carboxylic acid, HATU, DIPEA, DMF, r.t., 16 h; ii. TFA, r.t., 30 min. Yields: **21a**, 34%; **21b**, 52%; **22a**, 34%; **22b**, 57%.

was commercially available, while **18b** was obtained from *N*-phenyl-1,2-ethanediamine by monoprotection with a Cbz group. Both compounds underwent HATU-mediated amide formation with the building block **6** to give the *N*-H and *N*-Ph amide derivatives, respectively. The Cbz groups were removed by hydrogenation, and the obtained amines were reacted with 4-fluorobenzoic acid or 6-fluoronicotinic acid, followed by deprotection of the tri-*tert*-butyl esters to obtain the desired PSMA ligands **21a,b** and **22a,b**. As shown in Table 1, the derivatives **21b** and **22b** with an *N*-phenyl group exhibited 6- and 8-fold higher inhibitory activity for PSMA compared to the secondary amides **21a** and **22a**, respectively, suggesting that our strategy of using the phenyl ring as an anchor for these ligands is consistent with our working hypothesis (Figure 4B).

A similar strategy of using the distal P1 phenyl group as an anchor has been recently reported by Tykvart et al. However, exploiting the S1 accessory pocket of the arginine patch as an anchor point in their case led to mixed results as the insertion of the phenyl group into the pocket was unpredictable and strongly dependent on the physicochemical parameters of the branching functionality.²⁹ To the contrary, we believe that the

structure-assisted branching strategy outlined in this Letter will be mostly independent of the nature of the branching functionality as it exploits the unoccupied space of the entrance funnel free of obvious steric barriers.

In conclusion, we have designed and synthesized PSMA ligands derived from 2-aminoadipic acid, a building block that has not previously been used to construct PSMA ligands. The effects of both the linker length and an *N*-substituent on our PSMA ligands were probed. Among these ligands, **13b** showed the highest inhibitory activity for PSMA. Moreover, the labeling methods previously described for [¹⁸F]DCFPyL and [¹⁸F]PSMA-1007^{30,31} offer strong support that the preparation of [¹⁸F]**13b** could be possible. Finally, a branching moiety can be attached to the amide function of **13b**, thus allowing the facile modulation of physicochemical and pharmacokinetic properties of the next generation of compounds while preserving the high affinity of the original compound for PSMA.

■ ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/acsmmedchemlett.8b00318.

Synthetic methods, analytical characterization of compounds, methods of crystallization, diffraction data collection and structure determination, data collection and refinement statistics, and enzymatic assays (PDF)

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Notes

The authors declare no competing financial interest.

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■ ABBREVIATIONS

SAR, structure–activity relationship; ZBG, zinc-binding group; DIPEA, *N,N*-diisopropylethylamine; DCM, dichloromethane;

HATU, 1-[bis(dimethylamino)methylene]-1*H*-1,2,3-triazolo[4,5-*b*]pyridinium 3-oxide hexafluorophosphate; TFA, trifluoroacetic acid; PDB, Protein Data Bank

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