




Metamorphosis of prostate specific membrane antigen (PSMA) inhibitors

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Abstract

Prostate-specific membrane antigen (PSMA), also called glutamate carboxypeptidase II (GCP(II)), is a Zn-dependent metalloprotease that is known as a well prostate cancer indication and a potential targeting towards anti-cancer medicines and drug delivery. Because of its centrality in the diagnostics and treatment of prostate cancer, several types of inhibitors are designed with particular scaffolds. In this study, important groups of related inhibitors as well as reported experimental and computational studies are being reviewed, in which we examined three functional groups on each group of structures. The importance of computational biochemistry and the necessity of extensive research in this area on PSMA and its effective ligands are recommended.

Keywords Prostate-specific membrane antigen (PSMA) · GCP(II) · Prostate cancer (PCa) · Inhibitor · Computational biochemistry

Introduction

Prostate-specific membrane antigen (PSMA), also known as glutamate carboxypeptidase II (GCPII), is a 750 amino acid transmembrane protein in the central nervous system, and as a surface membrane protein, it has a high degree of availability (Jones et al. 2020, Lutje et al. 2017). This type II transmembrane metallopeptidase catalyzes the configuration of N acetylaspartylglutamate (NAAG) to N acetylaspartate (NAA) and glutamate (Ferraris et al. 2012). It is really a Zn²⁺-dependent metalloprotease out from M28 peptidase group that is found on the cytoplasmic and apical surfaces of the prostate epithelium in benign prostatic cells.

PSMA is shifted from the cytoplasm to the luminal surface of the prostatic channels when it undergoes malignant transformation, where that displays substrates with such a huge extracellular domain (Wright et al. 1995). It is also an important proposition for molecular imaging and targeted treatment utilizing highly specific radiolabeled PSMA ligands, in other words, inhibitors, owing to their strong and constant expression in PCa (Jones et al. 2020, Lutje et al. 2017).

The related ligands may now be synthesized using a variety of scaffold structures. Similar to glutamate, pentanedioic acid contains a zinc-binding group that almost always interacts with the catalytic zinc atom throughout the PSMA binding site and a substituent that generally resides either inside the S1 binding pocket or even inside of the protein that really extends to the substrate (Yang et al. 2016). Scaffolds consisting of several groups: phosphonates/phosphinates (Jackson et al. 2001), phosphoramidates (Maung et al. 2004), and ureas (Kozikowski et al. 2001) are efficient zinc-binding groups for binding related to GCPII. Furthermore, thiol (Majer et al. 2003) and hydroxamate (Stoermer et al. 2003) are known to be beneficial zinc-binding groups (Lutje et al. 2017). All the details related to three important general groups as effective inhibitors of PSMA, and related research studies will be discussed in this study.

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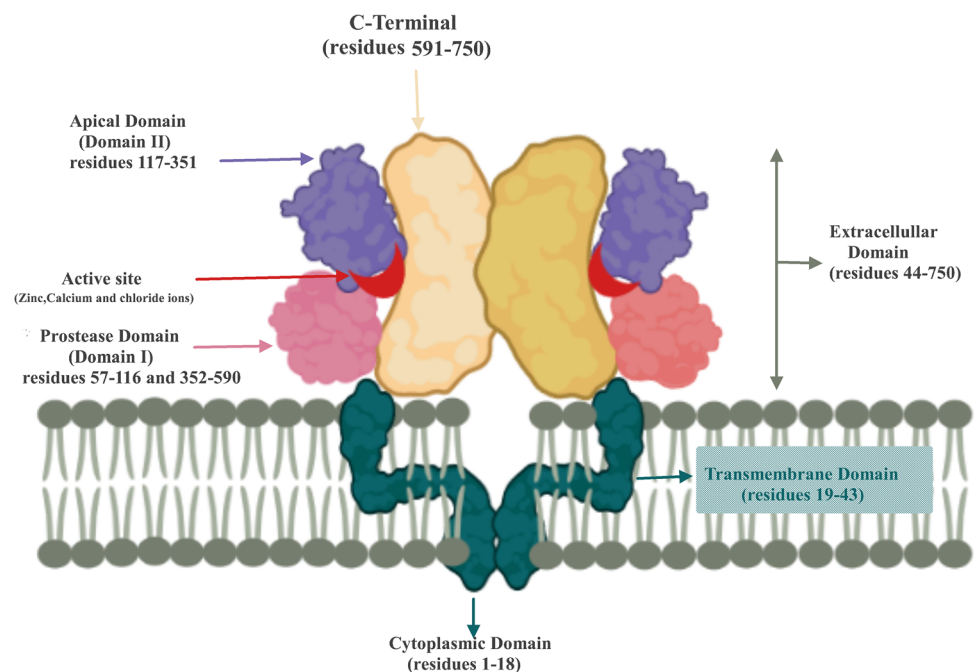
GCPII structure

The ectodomain of GCPII is based on three interwoven domains (Davis et al. 2005). The extracellular part of GCPII folding into 3 different domains and residues arising from each of the three domains participate to substrate recognition by shaping the GCPII identification pocket (Fig. 1). The protease domain spans amino acids 57 to 116 and 352 to 590, and the apical domain protects the active site and forms the wide substrate binding tube with the protease domain. The GCPII structure contains two other inorganic ions in addition to two zinc ions: Cl^- and Ca^{2+} (Hloučová et al. 2012).

As well as the zinc ions, the active site of PSMA is containing a water molecule that has already been activated and interacts with the carbonyl oxygen of the inhibitors' ureido motif (Pastorino et al. 2020). The binding site is required for PSMA's hydrolytic activity, whereas inhibitors block the hydrolysis of enzyme and operate as an amide-bio isostere. In addition, the active site of the protein consists of two pockets: the S1' pocket which is regarding the glutamate-sensing and the S1 pocket that is related to the non-pharmacophore site (Mesters et al. 2006; Bařinka et al. 2012) (Fig. 2). Furthermore, the "arginine patch," which may transition among two different conformations and moreover specify the diameter of the S1 derivative pocket, is a key component of the S1 pocket (Bařinka et al. 2002; Machulkin et al. 2016) (Fig. 2).

In addition, significant studies have been performed on mutated structures of GCPII. Mlochová et al. created and analyzed 12 GCPII mutants that targeted amino acids around substrate/inhibitor binding sites. The experimental findings, combined with molecular modeling, suggest that the amino acid residues delineating the S1' pocket of enzyme, specifically Arg210, contribute primarily to the high affinity binding of GCPII substrates/inhibitors. However, the residues forming the S1 pocket may be more important for GCPII substrate specificity "fine-tuning" (Mlochová et al. 2007). Klusák and colleagues also created a mutant of human GCPII (GCPII(E424A)) in which Glu424, a potential proton shuttle residue, is replaced with alanine to study peptide hydrolysis in greater detail. Considering N-Ac-Asp-Glu as a substrate, kinetic analysis of GCPII(E424A) demonstrated a complete loss of catalytic activity, implying that Glu424 is directly involved in peptide hydrolysis (Klusák et al. 2009). Furthermore, Bařinka et al. in their research found that N-glycosylation is required for correct folding and subsequent secretion of human GCPII (Bařinka et al. 2004). The predicted N-glycosylation sites are also critical for GCPII carboxypeptidase activity, according to the analysis. Researchers further reveal that an oligosaccharide moiety occupies all anticipated N-glycosylation sites and that glycosylation at sites other than the putative catalytic domain is crucial for GCPII's NAAG-hydrolyzing activity, and it casts doubt on the validity of previously characterized structural models of GCPII (Bařinka et al. 2004). Human glutamate

Fig. 1 Graphical representation of PSMA/GCPII transmembrane protein



et al. 2003). Compounds having a zinc-binding group of hydroxamate were also investigated; however, they were shown to be less effective GCPII inhibitors than those based on phosphonate or thiol (Stoermer et al. 2003). Aside from the inhibitors listed above, urea-based compounds have also been shown to effectively inhibit GCPII (Kozikowski et al. 2001, 2004). In this study, three different types of inhibitors were investigated. Researchers in the field of drug design will benefit from having a thorough understanding of the various classes of PSMA protein inhibitors. The goal of this study is to review current investigations of these three main categories of PSMA-related inhibitors, with the hope that the findings will provide new ideas to continue in the field of design and synthesis of effective multifunctional compounds in both imaging and therapy, and it was discovered that urea-based inhibitors are the most efficient, while phosphorus and thiol-based inhibitors are less effective.

The main ligand-binding cavity of PSMA is separated into three groups (related to the zinc-binding group called ZBG): phosphorus-based compounds, e.g., phosphonates and phosphinates, urea-based structures, and thiols (Fig. 2).

Phosphorus (and its related structures)-based GCPII inhibitors

Phosphorus-containing inhibitors were the first GCPII inhibitors to be discovered, and they were essential in gaining a better knowledge of GCPII's physiological activities (Haas et al. 2010). The tetrahedral phosphorus group resembles the cleaved peptide bond's (tetrahedral) transition state.

Phosphinate and phosphonates inhibitors

When in 1996, the phosphonate-based GCPII inhibitor 2-(phosphonomethyl)pentanedioic acid (2-PMPA) was developed, it quickly became a benchmark in terms of its performance and efficiency (Haas et al. 2010). With the exception of 2-PMPA and the other phosphonates, a variety of phosphinate PSMA inhibitors have been reported (Su et al. 1995). Nonetheless, due to a lack of oral bioavailability, they have never achieved their potential as therapeutic agents, and research has moved in a new path, particularly into urea-based inhibitors (Chang et al. 2005). As a result, the publication of orally accessible 2-PMPA prodrugs in 2016 came as a surprise (Kalariti et al. 2004). The early studies on phosphonate and phosphate inhibitors, including the effective PSMA inhibitor 2-PMPA with IC₅₀ 0.9 nM along with thiol-based PSMA inhibitors, were done at ZEN-ECA and afterward Guilford Pharmaceuticals (Jackson et al. 1996; Majer et al. 2003).

Phosphoramidate inhibitors as radiopharmaceutical compounds

Berkman's group then performed extensive studies with phosphoramidate inhibitors (IC₅₀s 0.5–20 nM). The effectiveness of inhibitors is often reported by criteria called IC₅₀ or Ki. IC₅₀ is the half-maximal inhibitory concentration. This criterion, in reality, assesses a substance's ability to impede a certain biological or metabolic activity. (Anderson et al. 2007; Liu et al. 2008b; Maung et al. 2004; Foss et al. 2012). Agents designed to target prostate-specific membrane antigen (PSMA) are a fast-developing category of radiopharmaceuticals for prostate cancer diagnostic imaging, according to Behr and co-workers (Behr et al. 2019).

CTT1057 is a potential new phosphoramidate PSMA-targeting ¹⁸F-labeled PET radiopharmaceutical with comparable biodistribution to urea-based PSMA-targeted therapies. Kopka and his colleagues claimed that the novel PSMA radioligands had quite a significant influence on the clinical management of the disease (Kopka et al. 2017). One of several problems as to inhibitors of PSMA in terms of providing therapeutic payloads, according to Choy et al., is their fast urine excretion. They used a ¹⁷⁷Lu-labeled phosphoramidate-based PSMA inhibitor (CTT1298) (Choy et al. 2017). Keeping this research going, Huang and Heston provided the list of PSMA inhibitors with an average to low molecular weight and addressed a critical question in the study mentioned by Choy et al. on the efficacy of Lutecium-177 labeled phosphoramidate-based PSMA inhibitors (Huang and Heston 2017). The issue was whether adding an albumin-binding entity to low-molecular-weight medicines would improve the efficacy of PSMA targeted treatment. Further, to obtain improvement in tumor absorption and to increase PSMA targeted anti-tumor action, Choy and his colleagues utilized a tiny molecule reversibly linked to a bigger protein, albumin (Huang and Heston 2017).

Dannoon and colleagues tested a variety of synthetic phosphoramidate-based PSMA inhibitors with varying lipophilicity, as well as their fluorine-18 analogs, as PET imaging agents for prostate cancer (Dannoon et al. 2016). A highly precise and accurate molecular imaging agent or technique for classifying the patient with PCa was a major therapeutic need, according to Mease et al. (Mease et al. 2013). Nedrow-Byers et al. showed that copper-free link chemistry can easily build a PSMA-targeted SPECT agent (Nedrow-Byers et al. 2013). An irreversible phosphoramidate inhibitor, CTT-54, was also improved in one of Nedrow-Byers et al.'s studies to transport ^{99m}Tc-(CO)3-DTPA as a SPECT imaging payload to PSMA+ cells in vivo and in vitro (Nedrow-Byers et al. 2012).

The chemical combination of Cy5.5 N-hydroxysuccinimide ester (Cy5.5-NHS) with a powerful PSMA inhibitor CTT-54.2 resulted in the development of a close fluorescent

imaging probe (Cy5.5-CTT-54.2) in the research by Liu et al. (Liu et al. 2010). The goal of the study by Lapi et al. was to investigate phosphoramidates as a novel classification of effective PSMA inhibitors with better selectivity and approval characteristics (Lapi et al. 2009). Several findings that discovered which phosphoramidate peptidomimetic inhibitors of PSMA can be divided into three categories by Liu et al.: pseudoirreversible, moderately reversible, and rapidly reversible inhibitors (Liu et al. 2008a). According to the outcomes of such tests, the development of pseudoirreversible PSMA inhibitors is likely to open up novel research and treatment possibilities for PCa and neurological diseases. Several examples of this type of inhibitor are shown in Fig. 3.

Urea-based GCPII inhibitors

The most utilized category of selective GCPII inhibitors is urea-based inhibitors, which were discovered throughout the twenty-first century (Kozikowski et al. 2001, 2004). The inhibitors typically require a glutamate residue that binds to the S1' pocket of the enzyme, while the ureido group replicates the planar peptide bond of cleaved substrate (Ferraris et al. 2012; Chen et al. 2008). As a result, several other urea-based inhibitors (radionuclides, fluorophores, and poisons are all linked in some way) have been synthesized and effectively employed in prostate cancer experimental imaging and treatment (Zhou et al. 2005; Eder et al. 2012; Foss et al. 2005). DCIBzL, which has a phenyl ring that binds to the hydrophobic pocket at the S1 site, is a great example of this kind of molecule and one of the most powerful GCPII inhibitors (Chen et al. 2008).

Kozikowski et al. studied some simple substances to serve as powerful urea-based GCPII inhibitors (Kozikowski et al. 2004). Chandran et al. employed a combination of methods to coat a nanoparticle's surface using a peptidomimetic

inhibitor of PSMA depending on urea (Chandran et al. 2008). The extremely effective acyclic Ga (III) chelator N,N'-bis [2-hydroxy-5-(carboxyethyl)benzyl] ethylenediamine N,N'- diacetic acid (HBED-CC) was added as a lipophilic side chain in the hydrophilic pharmacophore and was observed to interact positively with the PSMA "active binding site" by Eder and co-workers (Eder et al. 2012). To improve binding characteristics and pharmacokinetics, Schäfer et al. used the ^{68}Ga chelator N, N'-bis[2-hydroxy-5(carboxyethyl)benzyl] ethylenediamine-N, N'-diacetic acid (HBED-CC) to dimerize the pharmacophore Glu-ureido-Lys (Schäfer et al. 2012). Scientists indicated that using a specially designed linker, the pharmacokinetics of tracers with the Glu-urea-based binding motif might be even better. Wüstemann et al. looked examined how the chelator moiety may affect pharmacokinetics, including tumor cell internalization (Wustemann et al. 2016). The findings suggest that drugs containing the chelator CHX-A"-DTPA uses a Glu-urea-based binding site in combination with hydrophobic linkers might be useful in the treatment of PCa. Zha et al. presented a new [^{68}Ga]-Glu-NH-CO-NH-Lys (Ahx)-linker-HBED-CC conjugate using a unique O-(carboxymethyl)-L-tyrosine as like the collection of linkers in order to build innovative agents with improved characteristics for PET imaging (Zha et al. 2018). The first findings strongly imply that [^{68}Ga] might be a good choice to detect PSMA expression in PCa using PET imaging. PSMA I&T, a theranostic tracer improved by Wirtz et al., was improved by altering the peptidic structure in an attempt to optimize PSMA binding and internalization in PSMA-expressing tumor cells (Wirtz et al. 2018). Giesel et al. also provided an intraindividual study of tracer-specific features of ^{18}F -DCFPyL against ^{18}F -PSMA-1007 in their clinical research (Giesel et al. 2018).

The production of isocyanate intermediates and urea linkages are the first two stages in the synthesis of urea-based PSMA inhibitors. According to Mosayebnia and

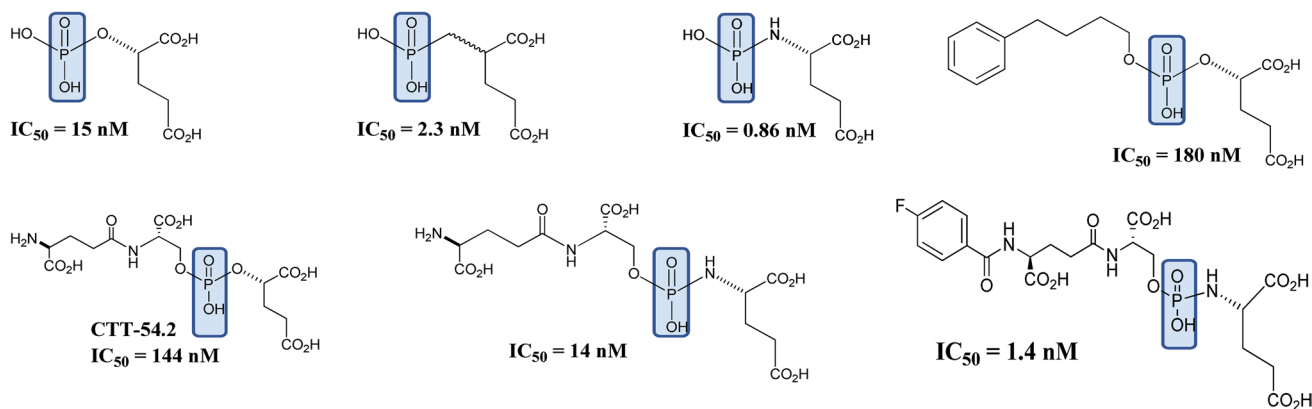


Fig. 3 Phosphorus-based GCPII inhibitors

colleagues, the isocyanate is produced in the liquid phase and subsequently interacts with the amine in the liquid phase or attached to the solid phase to establish the urea connection (Mosayebnia et al. 2018). Moreover, Mosayebnia et al. developed novel ^{99m}Tc -labeled peptides as a PSMA inhibitors for the finding of selective PCa inhibitors at a preliminary phase in another investigation (Mosayebnia et al. 2020). Glutamate-ureido inhibitors with labels seem to be a very often PSMA-targeting agents for nuclear medicine application fields, according to Pastorino et al. (Pastorino et al. 2020). Thus, recently, nuclear imaging tools and radiotherapeutics have been designed and tested, and more other most common PSMA-targeting drugs for nuclear medicine purposes are identified glutamate-ureido inhibitors.

In terms of clinical practice, PSMA is a possible candidate for both diagnostics and radioligand treatment (RLT) of prostate cancer, as Tateishi explains in a review study (Tateishi 2020). More research is needed to evaluate the diagnostic usefulness of PSMA-ligand PET for PCa (Felber et al. 2021). There are some examples of this kind of inhibitors in Fig. 4.

Thiol-based and other GCPII inhibitors

2-MPPA, a powerful thiol-based GCPII inhibitor

Thiol-based GCPII inhibitors are distinguished by their availability in the mouth (oral bioavailability). As a matter of fact, they were created in reaction to the phosphorus-based GCPII inhibitors' poor pharmacokinetic profile and high polarity. In 2003, 2-(3-mercaptopropyl) pentanedioic acid (2-MPPA), a powerful thiol-based GCPII inhibitor, was discovered. 2-MPPA has been found to be orally accessible in rats (Majer et al. 2003) and, more significantly, effective in a variety of illnesses in association with models of animals, including neuropathic pain (Majer et al. 2003), diabetic neuropathy (Zhang et al. 2006), and related muscular dystrophy (Ghadge et al. 2003). 2-MPPA was tested in phase I clinical research (van der Post et al. 2005), but progress was suspended due to the animal toxicity. In general, compounds based on thiols are not good medicines since this group of inhibitors could be easily oxidized.

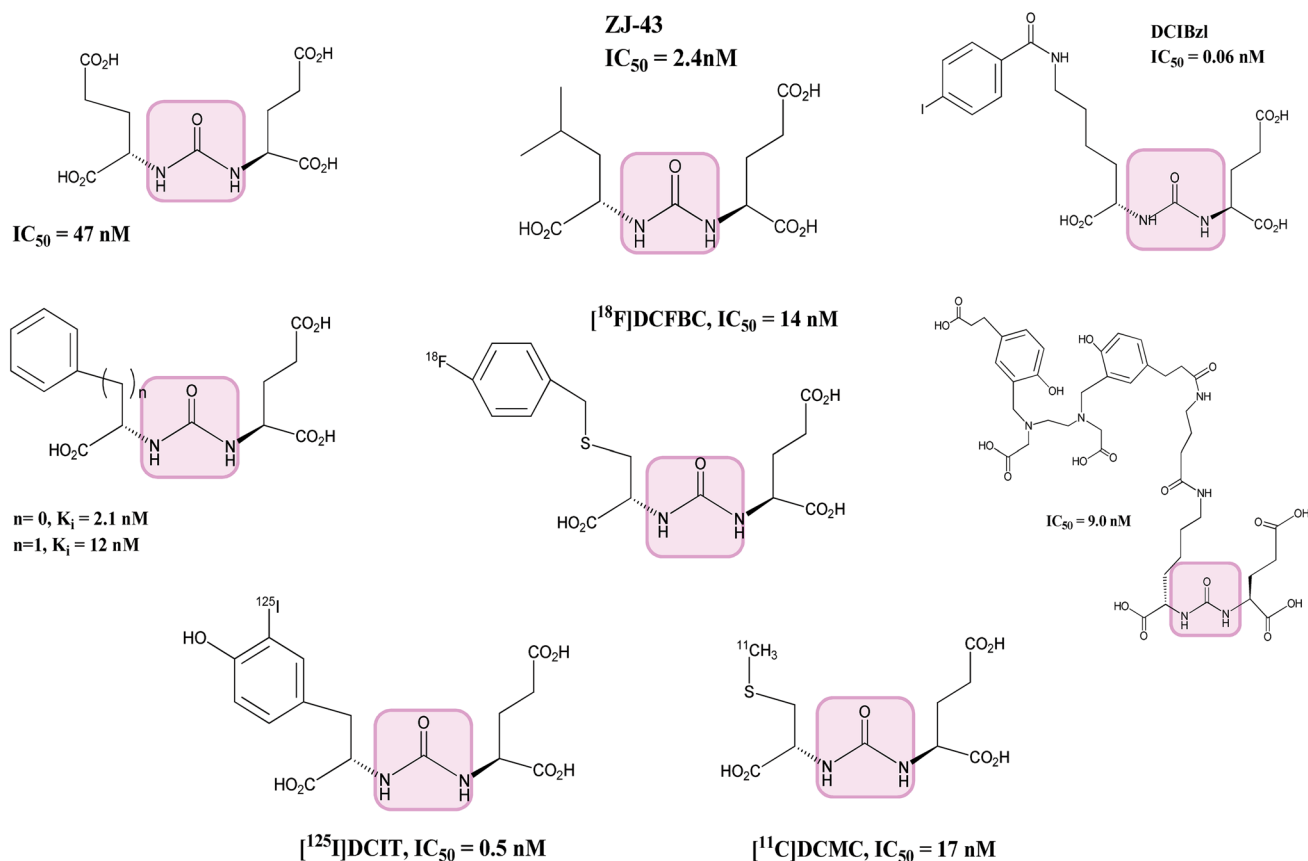


Fig. 4 Urea-based PSMA inhibitors

Hydroxamate compounds

Another potential zinc-binding group is hydroxamate compounds (Novakova et al. 2016b; Stoermer et al. 2003). Inhibitors based on hydroxamic acid with human GCPII nanomolar sensitivity have recently been found. They have a novel binding mechanism that contains a glutamates-like moiety which binds to the entering funnel rather than the S1' pocket (Novakova et al. 2016b).

Stoermer et al. developed hydroxamic acids in a sequence as possible inhibitors of PSMA in a research investigation (Stoermer et al. 2003). They expanded their structure–activity relationship (SAR) analyses to include other ZBG and discovered that phosphinate and thiol-based PSMA inhibitors were effective in animal studies of a variety of neurological diseases. Then, he and other colleagues also developed a variety of thiol-based PSMA inhibitors using a scaffold of 3-(mercaptomethyl) benzoic acid or 2-(2-mercaptoethyl) benzoic acid in additional investigations. Majer et al. prepared a variety of 2-(thioalkyl)pentanedioic acids along with PSMA inhibitors (Stoermer et al. 2003). The number of methylene units between the thiol group and pentanedioic acid was discovered to affect the inhibitory efficacy of these thiol-based drugs towards PSMA. In previous investigations, Majer and co-workers developed and evaluated a variety

of thiol-based inhibitors with a benzyl moiety for their ability to inhibit PSMA.

Takatsu et al. investigated the effects of 2-(3-mercaptopropyl) pentanedioic acid (2-MPPA), a novel PSMA inhibitor that may be taken orally, on impairments in pre-pulse inhibition (PPI) following injection of the N-methyl-D-aspartate (NMDA) receptor antagonist dizocilpine (Takatsu et al. 2011). GCP II inhibition may be a therapy option that works for schizophrenia, according to their findings. Ferraris and colleagues developed-thiolactones as prodrugs from thiol-based PSMA inhibitors (Ferraris et al. 2014). The pharmacological of several radiopharmaceuticals utilized for the theranostic therapy of PCa was highlighted in research by Vahidfar et al. (Vahidfar et al. 2019). Some examples of this type of inhibitor are shown in Fig. 5.

Studies in the field of computational biochemistry

Wu et al. developed a brief digital collection, which was displayed the inhibitory efficacy versus PSMA to find the best pharmacophores from a phosphoramidate peptidomimetic inhibitor of PSMA. Computational docking was utilized to suggest that PSMA active site

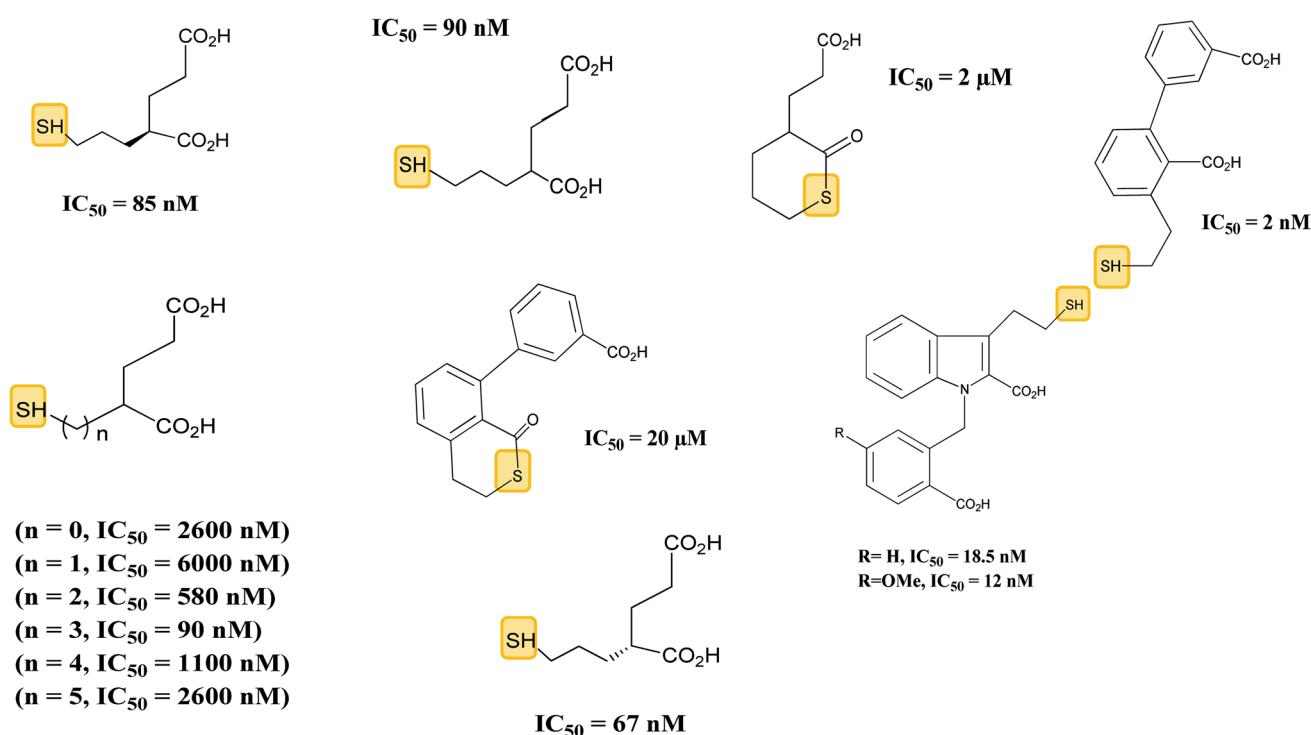


Fig. 5 Thiol-based inhibitors of PSMA

has a pharmacophore description, based on information on enzyme inhibition and the recombinant a new X-ray crystal structure of the protein (Wu et al. 2007). In the other case, Wu et al. developed and tested a small analog library for inhibitory efficacy towards PSMA in order to find the pharmacophore of a phosphoramidate peptidomimetic inhibitor of PSMA. The lead inhibitor's structure is based on N-acyl derivatives and includes a phosphoramidate group that has some important interactions with the active site of the PSMA, containing two zinc atoms. Docking studies were employed to suggest a pharmacophore model (Wu et al. 2007). Also, Wu et al. created six glutamate-containing phosphoramidate derivatives of different hydroxysteroids. Individual compounds in the collection had inhibitory potencies equivalent to a simple phenyl alkyl analog. Molecular docking was utilized in this research to get the binding energy (Wu et al. 2008).

Phosphoramidate peptidomimetic inhibitors of PSMA may be divided into three categories, according to Liu et al.'s findings: pseudoirreversible, moderately reversible, and quickly reversible inhibitors (Liu et al. 2008a). The development of pseudoirreversible PSMA inhibitors is likely to open up novel research and treatment possibilities for PCa patients. RNA aptamers, according to Rockey et al., are a new class of medicines with a huge future for prostate cancer diagnostics and therapy. They employed a “rational truncation” method guided by RNA structure determination and protein/RNA docking algorithms (Rockey et al. 2011). Novakova et al. conducted a detailed structural and computational analysis aiming at determining the role of the effector function in PSMA binding and affinity (Novakova et al. 2016a). They achieved this by determining the crystal structures of human GCPII in combination with a variety of phosphoramidate-based inhibitors. As a result, their findings indicate that phosphoramidates had better binding affinities than matching phosphonates.

Naushad et al. used molecular visualization software to develop models of different versions applying the crystal structure of PSMA as a pattern to establish a possible future inhibitor, that all eight prevalent genetic variations have been reported to be effective (Naushad et al. 2016). Pandit et al. used computational methods to discover active sites and interactions of urea-based PSMA inhibitors with the protein by altering the core structure of the ligand (Pandit et al. 2018). A novel PSMA inhibitor was also created to confirm the *in silico* study, and they were able to effectively test the three-dimensional quantitative SAR (3D-QSAR) and molecular docking-based development

of the PSMA inhibitors. Sharma and Baruah summarized the most frequently reported dysregulated miRNAs in PCa from the literature and reviewed the already available evidence in a review (Sharma and Baruah 2019). Differentially expressed genes (DEGs) in prostate cancer were discovered using a combined bioinformatics technique (Baruah and Sharma 2019).

Ivanenkov et al. developed and synthesized a PSMA-specific small-molecule carrier loaded with Doxorubicin for a preliminary biological assessment (Dox) (Ivanenkov et al. 2019). A 3D molecular docking research was also carried out to clarify the exact principle and mechanism of binding and to improve the target affinity by further optimizing the linker region. Glu-urea-Lys-based PSMA-targeting conjugates with paclitaxel were developed, according to the study by Machulkin et al. (Machulkin et al. 2019). A number of novel PSMA-targeting conjugates containing paclitaxel have been developed and produced. Finally, 3D-molecular docking research was carried out, too. Abdullahi et al. conducted *in silico* modeling investigations on some unique inhibitors of prostate cancer (PC3) cell lines employing C14-urea-tetrandrine components (Abdullahi et al. 2020). They used the DFT and QSAR models to optimize each structure. Their findings following computational studies might contribute to the development and production of novel C14-urea-tetrandrines with improved inhibitory properties against the PC3 prostate cell line. *In silico* docking studies were used to evaluate a collection of peptides holding such a well Glu-Urea-Lys pharmacophore and PSMA inhibitor using only new non-urea functional groups for accurate PCa identification at a preliminary phase by Mosayebnia and colleagues (Mosayebnia et al. 2020). LLE (Liquid–liquid extraction) in flow-based ^{45}Ti purification, using computer-aided design, and the manufacturing of a salan- $^{nat}\text{Ti}/^{45}\text{Ti}$ -chelidamic acid (CA)-PSMA ligand comprising the Glu-urea-Lys pharmacophore were presented by Pedersen et al. (Søborg Pedersen et al. 2020). In our recent study, new compounds as urea-based inhibitors were proposed by using the CADD method including molecular dynamic simulation and docking study (Nikfarjam et al. 2021).

Over the last few years, GCPII crystal structures have been explored in a variety of methods utilizing a range of ligands, including GCPII inhibitors based on phosphorus and urea. These discoveries give insight on the structural features of each of GCPII's key binding sites, as well as the potential for developing novel inhibitors. In Table 1, GCPII-related structures in RCSB database are provided.

Table 1 GCPII-related structures in the Protein Data Bank (RCSB database)

PDB	Important points related to the study	Resolution	Reference
1Z8L	The PSMA ectodomain's 3.5- Å crystal structure, which also displays a homodimer featuring structural similarities to transferrin receptor, an iron-loaded transferrin receptor which loses protease function	3.50 Å	(Davis et al. 2005)
2C6P	At different resolutions, crystal structures of the extracellular domain of GCPII in combination including both powerful and weaker inhibitors, as well as glutamate, are presented	2.39 Å	(Mesters et al. 2006)
2C6G		2.20 Å	
2C6C		2.20 Å	
2PVW	At various resolutions, crystal structures of human GCPII given in combination by 3 glutamate mimetics/derivatives, 2-(phosphonomethyl)pentanedioic acid (2-PMPA), quisqualic acid (QA), and L-serine O-sulfate (L-SOS), are provided	1.71 Å	(Bařinka et al. 2007)
2OR4		1.62 Å	
2PVV		2.11 Å	
2JBK	With resolutions of 2.99 and 2.19 Å, crystal structures of the extracellular domain of GCPII (including residues 44 to 750) in combination with two effective inhibitors, quisqualate and 2-PMPA, have been studied	2.99 Å	(Mesters et al. 2007)
2JBJ		2.19 Å	
3BI0	The crystal structures of adult GCPII in association with foyl-gamma-glutamate, aspartyl-glutamate, and gamma-glutamyl-glutamate phosphapeptide analogs at several resolutions are provided	1.67 Å	(Barinka et al. 2008b)
3BI1		1.50 Å	
3BHX		1.60 Å	
3D7H	Low molecular weight GCPII ligands based on urea have shown effectiveness in a variety of neurological diseases models and can be used as imaging agents for prostate cancer	1.55 Å	(Barinka et al. 2008a)
3D7D		1.69 Å	
3D7G		1.75 Å	
3D7F		1.54 Å	
3IWW	Several glutamate-free inhibitors with $K(i)$ values less than 20 nM were discovered through structure–activity relationship investigations of the P1' site of ZJ-43- and DCIBzL-based ligands	2.30 Å	(Wang et al. 2010)
3RBU	Offer only one selectivity filtration method appropriate for released protein purification. The system relies on biotin's interaction with mutant streptavidin	1.60 Å	(Tykvar et al. 2012)
3SIX	Discussion on discovery as well as characterization of increased lipophilicity GCPII inhibitors generated from such a collection of recently found dipeptidic GCPII ligands with nonpolar aliphatic side chains at just the C-terminus	1.66 Å	(Plechanovová et al. 2011)
3SJE		1.70 Å	
3SJF		1.65 Å	
3SJG		1.65 Å	
2XEJ	Reported that ARM-Ps (antibody-recruiting compounds targeting prostate cancer) are a new class of small compounds' means of achieving antibody-mediated immunity identification of prostate cancer cells	1.78 Å	(Zhang et al. 2010)
2XEF		1.59 Å	
2XEI		1.69 Å	
2XEG		1.59 Å	

Conclusion

PSMA is the most attractive proposition for researchers looking to use nuclear medicine techniques to detect and treat individuals with PCa. Reviewing the studies performed on each group of important PSMA inhibitors, it was observed that the research process is being carried out with considerable speed and accuracy by experts and researchers. Considering that the protein considered in these studies is a metalloprotein and due to the range of appropriate computational tools and packages for the study of metalloproteins, it is suggested that researchers in computational biochemistry further study each group of inhibitors that are introduced in this review. Researchers will also be able to improve the process of developing and conducting research to find suitable inhibitors by using drug design and drug delivery methods in

computational chemistry and computational biochemistry. In addition, the reported findings in the literature review reveal a variety of inhibitor binding mechanisms inside the non-prime site(s) of GCPII, which might be used to develop new GCPII-specific drugs. In addition, by using the integration of quantum mechanics and molecular dynamics techniques, the mechanism of action of each group of inhibitors is studied as much as possible. Then, using new programming methods in the field of drug design such as machine learning (ML), the need for biochemical calculations along with laboratory and clinical research can be addressed.

Author contribution ZN: literature search and data analysis, writing—original draft, visualization. FZ: literature search and data analysis. AN: supervision, editing. OB: conceptualization, supervision, writing—review and editing.

Declarations

Ethics approval This article does not contain any studies with human participants or animals performed by any of the authors.

Conflict of interest The authors declare no competing interests.

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