

Topics in Medicinal Chemistry 17

Jacob Schwarz *Editor*

# Atypical Elements in Drug Design

 Springer

17

## Topics in Medicinal Chemistry

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Jacob Schwarz

Editor

# Atypical Elements in Drug Design

With contributions by

R. Abdur · S. Dörrich · A. Draganov · Z. Huang · S.W. May ·  
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# Preface

The chemistry of drug discovery revolves primarily around the use of carbon, hydrogen, nitrogen, oxygen, sulfur, and phosphorus. Over time, nontraditional elements have been incorporated into drug-like compounds for a number of purposes, for instance to slow metabolism or to impart novelty. As a demonstration of the validity of this approach, several examples of compounds containing nontraditional elements have advanced into human clinical trials. This volume will survey three nontraditional elements (B, Si, Se), providing perspective not only on the general properties they impart to organic molecules but also on their utility in specific drug classes.

South San Francisco, CA, USA

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# Contents

<b>The Future of Boron in Medicinal Chemistry: Therapeutic and Diagnostic Applications</b> . . . . .	1
Alexander Draganov, Danzhu Wang, and Binghe Wang	
<b>Drug Design Based on the Carbon/Silicon Switch Strategy</b> . . . . .	29
Reinhold Tacke and Steffen Dörrich	
<b>Silicon Mimics of Unstable Carbon</b> . . . . .	61
Scott McN. Sieburth	
<b>Selenium-Based Drug Design</b> . . . . .	87
Sheldon W. May	
<b>Selenium-Functionalized Molecules (SeFMs) as Potential Drugs and Nutritional Supplements</b> . . . . .	119
Rob Abdur and Zhen Huang	
<b>Index</b> . . . . .	155



# The Future of Boron in Medicinal Chemistry: Therapeutic and Diagnostic Applications

Alexander Draganov, Danzhu Wang, and Binghe Wang

**Abstract** Because of its unique electronic structure, boron has special properties useful in designing new diagnostic and therapeutic agents. Specifically, boron's strong Lewis acidity and ability to undergo fission under neutron bombardment form the foundation for boron-containing compounds to be developed as inhibitors of hydrolytic enzymes, chemosensors and artificial receptors for carbohydrates and other Lewis bases, and boron neutron capture agents. A number of boron-containing compounds have been evaluated in animal and human studies for diagnostics and therapeutic applications. One compound in particular, Velcade, has been approved as an anticancer agent. This chapter highlights some of the most significant contributions in the field.

**Keywords** Boronic acid, Bortezomib, Chemosensor, Diagnostics, Imaging mass spectrometry, MALDI-IMS, Velcade

## Contents

1	Introduction .....	2
2	Boronic Acid Compounds as Therapeutic Agents .....	3
2.1	Boronic Acid Compounds as Anticancer Agents .....	3
2.2	Boronic Acid Compounds as NS3 Protease Inhibitors Targeting Hepatitis C Virus .....	8
2.3	Boronic Acid Compounds as Antibacterial and Antifungal Agents .....	10
2.4	Boronic Acids Compounds as Anticoagulant Agents .....	12
2.5	Boronic Acid Compounds as Diabetes Therapeutic Agents .....	13
2.6	BNCT (Boron Neutron Capture Therapy) .....	14

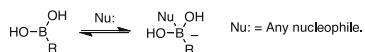
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3	Boronic Acids as Carbohydrate Binders/Receptors .....	14
3.1	BisBoronic Acid Sensors for $sLe^x$ as a Cancer Diagnostic Tool .....	15
3.2	Boronic Acids as a Tool for Bacterial Detection .....	18
3.3	Boronic Acids as a Tool for Viral Infection Detections .....	18
3.4	Fluorescent Boronic Acids as a Tool for Glucose Detection .....	19
4	Conclusions .....	20
	References .....	20

## 1 Introduction

Although boron is ubiquitous and is implicated in various biological processes, its potential in the development of pharmaceutically relevant therapeutic agents had not been widely explored until about two decades ago [1, 2]. Recent activities, however, have shown boron's exciting potential in developing both therapeutics and diagnostics [3–6]. Velcade, a US Food and Drug Administration (FDA)-approved anticancer drug by Millennium Pharmaceuticals, is the poster child of success in using a boron/boronic acid moiety in a pharmaceutical agent and there are several more in clinical trials [6, 7]. Much of the design in using boron/boronic acid for the development of pharmaceutical agents relies on at least one of the following chemical and radiochemical properties [1, 3–8]. First, boron is trivalent in its neutral form and has an open shell. Thus, boronic acid is a Lewis acid and can readily react with Lewis bases/nucleophiles (Scheme 1) such as alcohols [3, 9–25], amino alcohols [26–28], hydroxyl acids [29–32], amino acids [33], as well as cyanide [34, 35] and fluoride [35–39]. Second, because of its Lewis acidity, boronic acid can bind with diols [3, 4, 40–56], commonly found on carbohydrates, with high affinity and reversibility. Especially important is boronic acid's ability to bind diols or hydroxyl groups on carbohydrates because of their important roles in physiological and pathological processes such as in cancer development [57–64]. For example, different cell types carry a number of characteristic complex carbohydrates on the cellular surface that are part of signature structures [65]. Cell surface carbohydrates, such as sialyl Lewis X ( $sLe^x$ ), sialyl Lewis A ( $sLe^a$ ), Lewis X ( $Le^x$ ), and Lewis Y ( $Le^y$ ), are closely related with the development and progression of many types of cancers [66]. Furthermore, interactions between carbohydrates and other biomolecules are seen as “triggers” for different types of diseases [67–71]. Molecules such as boronic acid-containing compounds, capable of binding to carbohydrates have various biological and biomedical applications as diagnostics and/or therapeutics. Third, neutron bombardment of boron-10 leads to the formation of lithium nuclei with the concomitant emission of high-energy  $\alpha$ -particles, which cause localized ionization and thus damages. Thus, boron has been explored for the development of neutron capture therapy (NCT) agents. There are a number of reviews that discuss in detail the developments of boron-containing pharmaceutically relevant agents; thus, this chapter only highlights some of the most important developments in the field.



**Scheme 1** The reaction of a boronic acid with a Lewis base/nucleophile

## 2 Boronic Acid Compounds as Therapeutic Agents

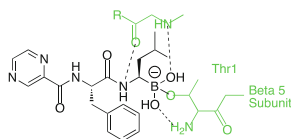
Significant effort has been made in the development of pharmaceutically relevant boronic acid compounds as therapeutic agents [1, 4–6]. This section briefly summarizes the most recent and significant developments in the field, introducing FDA approved-drugs as well as compounds in phase II and III clinical trials [1, 5]. However, before discussing the development of boronic acid-based therapeutic agents, it is important to understand some basic physicochemical properties. Most commonly used arylboronic acids have a  $\text{p}K_{\text{a}}$  in the range of 4.5–8.8 depending on the nature of the aromatic rings and substituents [32, 72, 73]. It is important for one to understand that the acidity of boronic acids is not related to its deprotonation, but rather to its ability to react with water (or other protic solvents) with a concomitant release of proton and formation of the tetrahedral anionic species (Scheme 1). The design of many inhibitors of hydrolytic enzymes takes advantage of such properties not only because of covalent bond formation between boronic acid and an active site nucleophile but also because the tetrahedral species mimics the transition state of such reactions [8].

### 2.1 Boronic Acid Compounds as Anticancer Agents

A few promising boronic acid-containing inhibitors have been summarized in the literature [1, 4, 5]. Before discussing in more detail, major recent developments in the boronic acid anticancer field can be grouped into five sections based on their mechanism of actions: (1) proteasome inhibitors [74–86], (2) FAP (fibroblast activation protein) inhibitors [87, 88], (3) HDAC (histone deacetylase) inhibitors [89, 90], (4) HIF-1 $\alpha$  (hypoxia-induced factor-1 $\alpha$ ) [91] and MDM2 (murine double minute 2 protein)/p53 inhibitors [92], and (5) ATX (autotaxin) inhibitors [93].

#### 2.1.1 Proteasome Inhibitors

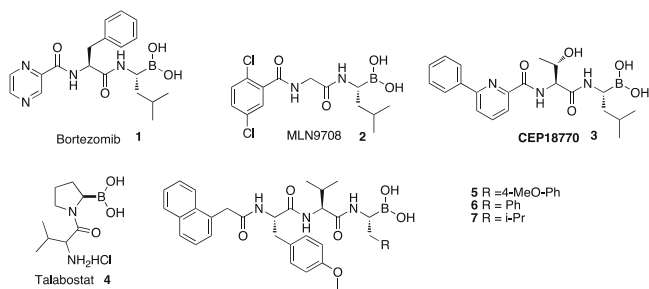
The proteasome is a eukaryotic enzymatic complex that is responsible for protein degradations in mammalian cells [94] and is a major regulator of enzymatic concentrations in the cytoplasm [95–97]. Proteins covalently tagged by ubiquitin are recognized by the protease complex and degraded to small peptides and amino acids. Thus, inhibition of this enzymatic machinery results in accumulation of proteins in the cell and consequently apoptosis. The importance of the proteasome function makes it a good target for the development of inhibitors, especially in



**Fig. 1** Binding interactions between bortezomib and the proteasomal  $\beta 5$  subunit

cancer therapy because of the rapid proliferation of cancer cells [8, 98]. A number of boronic acid compounds targeting the proteasome have been developed with the most significant achievement in the area being bortezomib (trade name Velcade) [4, 5, 8, 85]. Peptide boronates appeared to be some of the most potent reversible inhibitors of the proteasome [5, 8, 85, 99]. Some of these peptide boronates are excellent drug candidates, possessing the chemical characteristics of a peptide and a boronic acid giving rise to soluble, physiologically stable compounds, with good bioavailability [1, 5, 8]. In 2003, Velcade was approved by the FDA for clinical use against multiple myeloma, and a year later against mantle cell lymphoma [8]; (<http://bortezomib.org/>). Additional studies showed that Velcade has potent activities against a number of solid tumors such as that of the breast, lung, colon, pancreas, and prostate [76–78, 80, 82, 84].

The success of Velcade lies not only in its physicochemical properties but also on its mechanism of action. Bortezomib is selective for the chymotrypsin-like activity of the proteasome, which, for the most part, is provided through the  $\beta 5$  subunit [8, 85, 99]. After extensive cytotoxicity studies in 1999, Adams and co-workers in partnership with the National Cancer Institute reported bortezomib as a proteasomal inhibitor with inhibitory potency ( $K_i$ ) of  $\sim 0.6$  nM and average  $GI_{50}$  (across 60 cell lines) of  $\sim 7$  nM [85]. After screening 60 cell lines, it was established that the compound possesses activity against a number of solid cancer types. The presence of the boronic acid moiety allows for the formation of reversible covalent interactions of the available boron orbital and the nucleophilic threonine of the proteasome [85]. The crystal structure of the compound in complexation with the S20 yeast proteasome gave insights into the mechanism of actions of the drug and the specific interactions involved in the proteasome [19]. Threonine 1 from the  $\beta 5$  subunit covalently binds with the boron atom giving rise to the tetrahedral anionic form stabilized by a hydrogen donating glycine 47 and an additional hydrogen bonding interaction with the free amino group of threonine 1 (Fig. 1) [8]. Despite its utility, Velcade does have a number of side effects including cardiovascular disorders, nausea, and neurologic disorders (<http://bortezomib.org/>) [100]. It is important to note that mechanistic studies have shown that the toxicity of Velcade is not related to boron itself [1, 101]. Knowing the mechanistic details of the inhibition process has allowed for the development of other di- and tripeptide boronates as protease inhibitors, some of which are in advanced stages of clinical trials for various indications (compounds 2, 3, 5–7, Fig. 2) [4, 5, 8, 102, 103]. There is still more work to be done in the development of boronic acid-based drugs with



**Fig. 2** Examples of boronic acid agents as proteasome inhibitors

low toxicity. Nevertheless, the development of bortezomib and others opened the doors for developing boronic acid-containing therapeutics.

### 2.1.2 FAP (Fibroblast Activation Protein) Inhibitors

Another peptide boronate compound (Talabostat, Fig. 2) was initially designed as a DPP4 (dipeptidyl peptidase 4) inhibitor for treatment of diabetes but also showed potency as an anticancer agent. It was studied in clinical trials against non-small cell lung cancer based on its inhibitory properties towards fibroblast activation protein (FAP) [1, 49]. FAP is a membrane protein from the serine protease family that is widely expressed in epithelial cancers, soft tissue sarcomas, and some bone cancers [104, 105]. The importance of this protein is related to the structural formation and stability of the cancerous cell. The protein has some structural similarities to DPP4 and a common exopeptidase activity [104]. The compound reached phase III clinical trials, but did not meet the required efficacy standards [1, 106]. Although single-dose tolerance was 500  $\mu\text{g}$ , the plasma levels achieved top concentration within 2 h, and the compound was considered suitable for daily dosage; its lack of selectivity for FAP and efficacy forced termination of the studies [1, 106]. FAP is a transmembrane enzyme that possesses endo- and exopeptidase activity. The exopeptidase activity of that FAP is a dipeptidyl peptidase activity (DPP), common for enzymes such as DPP4 [49]. The specific endopeptidase activity that FAP has makes this enzyme a good therapeutic target. Despite the fact that Talabostat showed a lack of direct *in vitro* anticancer activity, phase I clinical trials showed reduction of tumor volume of up to 90% (WEHI 164 fibrosarcoma mouse model) at 5  $\mu\text{g}$  dose [107]. FAP inhibitory studies during phase II clinical trials of Talabostat showed about 90% enzymatic inhibition of the exopeptidase activity of FAP; however, there was only a 21% decrease of the endopeptidase activity [49]. Thus, the lack of inhibitory selectivity of the compound towards the specific function of the enzyme makes the anticancer drug candidate inapplicable.

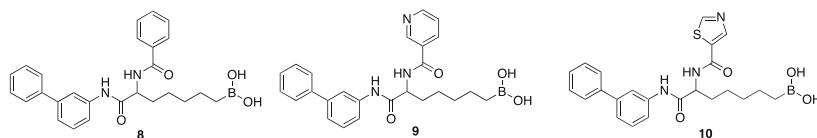


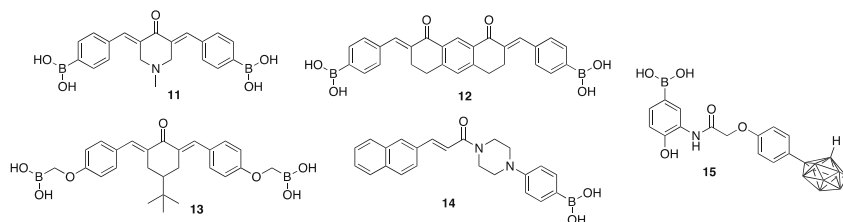
Fig. 3 Examples of boronic acids as HDAC inhibitors

### 2.1.3 HDAC (Histone Deacetylase) Inhibitors

The importance of histone deacetylases in the mammalian system has been extensively studied throughout the years, and the importance of HDACs as therapeutic targets has been well defined [89, 108]. Inhibition of HDAC results in histone overacetylation giving rise to activation of genes closely associated with growth arrest and apoptosis, such as p21 [108]. In 2009 Suzuki and co-workers reported the first boronic acid compounds bearing  $\alpha$ -amino acid moiety that showed inhibitory effects on HDAC (Fig. 3) [90]. The HDAC inhibitory concentrations of the compounds were studied in MKN45 cells (stomach cancer) and were reported to be 2.0, 2.0, and 1.4  $\mu\text{M}$  for compounds **8**, **9**, and **10**, respectively. Western blot studies confirmed that the anticancer activity ( $\text{GI}_{50}$  9.3, 5.5, and 3.5  $\mu\text{M}$ , respectively) of these compounds was in fact due to HDAC inhibition [90]. Interestingly enough, the S-isomers of the compounds showed low micromolar activity, while the R-isomers had no effect. The compounds showed selectivity towards HDAC2 and HDAC6 with  $\text{IC}_{50}$  as low as 0.1  $\mu\text{M}$  [90]. The most potent compound of the series (**10**) was tested against a number of cancer cell lines and retained low micromolar  $\text{IG}_{50}$ , some of which are as low as 1.3  $\mu\text{M}$  against LOX-IMVI (melanoma) cells [90]. Extensive computational studies showed that the boronic acid group of the active agents was indeed playing an important role in the HDAC binding pocket [90]. In fact the tetrahedral anionic form of the boronic acid is stabilized by a histidine and a tyrosine residue while interacting with the zinc ion in the active site [90]. The significance of this work is that never before had a boron-containing compound been recognized as an HDAC inhibitor. However, the designed compounds did not show desirable pharmacokinetic qualities for a drug candidate, and thus, there was no further development of these compounds.

### 2.1.4 HIF-1 $\alpha$ and MDM2 Expression Inhibitors

During the past decade, HIF-1 $\alpha$  and MDM2 have been identified as two important anticancer targets and a number of research groups and pharmaceutical companies have put substantial effort in the development of therapeutic agents targeting these two proteins [109–111]. Although extremely important and independent of each other, we are introducing them under one section because of the recent development of boronic acid compounds, which target these two proteins [91, 92]. Despite the lack of structural diversity and conclusive experimental data, the boronic acid



**Fig. 4** Boronic acids as MDM2 (**11–14**) and HIF-1 $\alpha$  (**15**) inhibitors

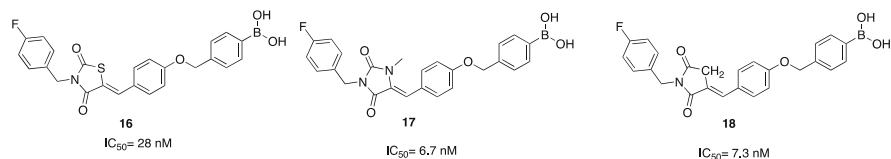
compounds targeting MDM2 and HIF-1 $\alpha$  are worth noting as they may carry an answer to the design of successful anticancer agents.

MDM2 is a negative regulator of p53, a tumor suppressor protein or so-called “genome guardian” [112]. There are a number of ways that the p53 protein suppresses tumor development: apoptosis, autophagy, senescence, and promoting growth arrest [113, 114]. MDM2 regulates p53 in two distinct ways. The first and most obvious way of p53 regulation by MDM2 is through its E3 ubiquitin ligase activity, meaning that p53 is ubiquitinated by MDM2 leading to proteasomal degradation [115, 116]. The second method of p53 inactivation by MDM2 is shown to be through binding to the transactivation domain of p53 and blocking the transcription activity of the protein on its substrates [117, 118]. In either case, the interaction between the two proteins is extremely important for the cells. Designing an inhibitor that prevents the two proteins from interacting is a commonly employed strategy [110]. However, to our best knowledge only Khan and co-workers have reported boronic acid compounds inhibiting the interactions between MDM2 and p53 (Fig. 4, compounds **11–14**) [92]. The reported IC<sub>50</sub> values are in the low micromolar range, which by itself does not mean that the reported compounds have true potential to be developed into drug candidates. However, these compounds are another example of boronic acid compounds used as potential therapeutic agents against cancer and a novel class of MDM2 inhibitors.

In 2010 Shimizu and co-workers reported boronic acid compound **15** that showed an IG<sub>50</sub> around 16  $\mu$ M in HeLa-based HRE reporter assays with an IC<sub>50</sub> of 750 nM in its inhibition of HIF-1 transcriptional activities (Fig. 4) [91]. In addition, immunoblotting assays showed inhibition of HIF-1 $\alpha$  expression, and RT-PCR showed that the expression of VEGF, induced under hypoxic conditions, decreased upon addition of compound **15** in a concentration-dependent manner [91]. Although no mechanistic data for the compound is present at this point, this new class of HIF-1 inhibitors seems to have good potential.

### 2.1.5 ATX (Autotaxin) Inhibitors

Autotaxin (ATX) is a nucleotide phosphodiesterase that produces lysophosphatidic acid (LPA) by hydrolysis of phospholipid lysophosphatidylcholine (LPC) [93, 119–123]. Many biological processes, such as chronic inflammation [124], fibrosis [125, 126], and tumor progression [127], are related to the ATX-LPA signaling



**Fig. 5** Boronic acid compounds as ATX inhibitors. \* $\text{IC}_{50}$  values obtained through choline release assay

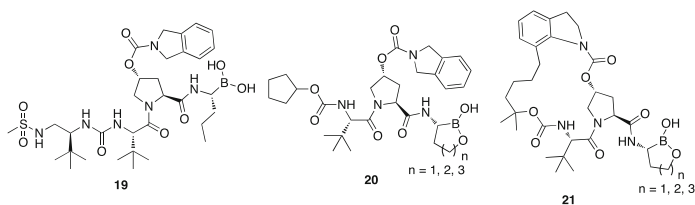
pathway. Since LPA acts on multiple receptors in the mammalian system [123, 128], direct targeting of LPA receptors is not a plausible strategy. Because of this drawback, targeting ATX has become an attractive method for addressing some of the related issues. In recent years, various synthetic boronic acids have been explored as ATX inhibitors [129–132]. Huib Ovaa and co-worker screened small-molecule libraries in 2009 to search for unique ATX inhibitors [93]. Thiazolidinedione analogues were found to selectively inhibit ATX activity. They optimized these compounds by using “active-site-targeted strategy,” which was successfully used for the development of bortezomib [99, 133]. The results show that their boronic acid-based inhibitors potently inhibit ATX both in vitro and in vivo. Albers and co-workers have developed boronic acid compounds that showed single-digit nM activities (Fig. 5, compounds 17 and 18) [134]. An almost fourfold decrease of the LPA levels in mouse blood plasma was achieved by compound 16 at serum concentration of 350 nM [93]. The reported in vivo data clearly indicates the relationship between ATX inhibition by the boron-containing compounds and a decrease of LPA in the blood plasma [93]. It can be safely concluded that boronic acid-based inhibitors hold promise as drug candidates to target the ATX-LPA axis in vivo [93]. In 2011, molecular docking and X-ray crystallographic studies were reported using a boronic acid-based inhibitor of ATX, compound 17 (Fig. 5) [134]. Crystal structural studies of the ATX complex with the inhibitor gave good insights explaining the compound’s activity [134]. The exploration of structure–activity relationships and the study of the lipophilic pocket near the ATX active site should allow for the future design of more potent inhibitors.

The examples summarized above clearly show that boronic acid compounds can serve as good structural scaffold for anticancer drug discovery. However, cancer is not the only condition against which boronic acid compounds have shown potency; recently advances have been made in the development of successful serine protease inhibitors for treatment against hepatitis C virus (HCV) [4, 5, 8].

## 2.2 Boronic Acid Compounds as NS3 Protease Inhibitors Targeting Hepatitis C Virus

Hepatitis C is a contagious liver disease caused by HCV. According to the World Health Organization (WHO), between three and four million people are infected with HCV every year and about 150 million have chronic infection and live with the





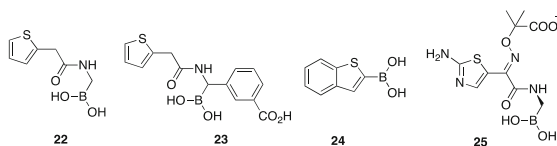
**Fig. 6** Examples of boronic acid-based NS3 protease inhibitors

risk of developing liver cirrhosis (<http://www.who.int/mediacentre/factsheets/fs164/en/>). The fact that over 350,000 people die from HCV-related diseases every year is alarming and has stimulated interest in developing new therapeutic agents to target this virus (<http://www.who.int/mediacentre/factsheets/fs164/en/>). The most widely used treatment against HCV is a combination of interferon and ribavirin, which can cause serious side effects and in some cases lacks positive responses (<http://www.who.int/mediacentre/factsheets/fs164/en/>). The field of boronic acid-based therapeutics has a significant contribution to the battle against HCV. Efforts in targeting HCV and more specifically its vital NS3 serine protease, by utilizing boronic acid analogues, have been ongoing since the mid-1990s [135]. However, only in the recent years, significant progress has been made in the development of boronic acid-containing compounds (**19**, **20**) as NS3 protease inhibitors. Some such compounds have gone into phase II and III clinical trials (Fig. 6) [136–139]. The main target, NS3 protease, is an important enzyme in the transcriptional process of the virus [140, 141]. The significance of the enzyme in the development of a mature HCV makes it an extremely important target [137]. The enzyme has been well studied, and its crystal structure revealed that the catalytic site possesses a classic catalytic triad aspartate–histidine–serine [137, 139]. The serine residue in the catalytic site has been shown to covalently bind to the boron of the peptide boronates, stabilize the tetrahedral anionic form of the boronic acid moiety, and thus inhibit the NS3 protease activity [139]. To understand the mechanistic details of action of the active boronic acid compounds, a number of boronopeptides were synthesized with enzymatic activity in the low to sub-nanomolar range [5, 139, 142]. The inhibitory effects of these compounds were evaluated and the cyclic boronopeptides were shown to have potential for further exploration as antiviral agents [67]. Structure–activity relationship analysis showed that the size of the boron-containing rings in compounds with the core structure resembling **20** and **21** (Fig. 6) significantly affects the activity. For example, the compound containing core **20**, where  $n=3$ , possesses potent NS3 inhibitory activity ( $IC_{50}$ , ~24 nM), while the activity drops to 320 nM (almost tenfold) when  $n=2$  [139]. Although significant advancement in the development of boronic acid-based NS3 inhibitors has been made, there has not been a single compound that has been fully developed and reached the end of the pharmaceutical pipeline yet. The promising results in the past 5 years, however, bring optimism to this area.

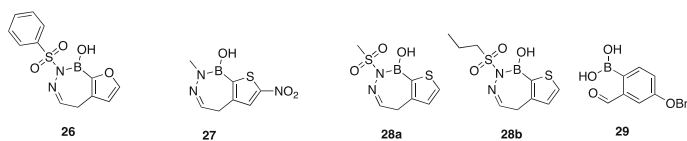
### 2.3 *Boronic Acid Compounds as Antibacterial and Antifungal Agents*

Another major challenge of modern-day medicinal chemistry is the development of efficient antibacterial agents to counter the constant emergence of drug-resistant strains of bacteria. One of the most widely used classes of antimicrobials is  $\beta$ -lactam antibiotics [5, 8]. However, the biggest challenge in using these  $\beta$ -lactam antibiotics has been the rapid development of drug resistance due to the overproduction of four different classes of  $\beta$ -lactamases that catalyze the hydrolysis and thus inactivation of  $\beta$ -lactams [143, 144]. The classes of  $\beta$ -lactamases are A, C, D (serine hydrolases), and B (metallohydrolase) [143]. Two of the clinically most relevant classes are A and C with representatives such as TEM penicillinase and AmpC cephalosporinase, respectively [8, 143]. The  $\beta$ -lactam antibiotics achieve their effect by acting on enzymes responsible for the cell wall synthesis; more specifically they inactivate transpeptidases such as the penicillin-binding proteins (PBP) [5]. PBPs are attractive targets for developing new antibiotic agents because they catalyze unique steps of the biosynthesis of peptidoglycans in bacteria [145, 146]. A common strategy in the prevention of  $\beta$ -lactam-related drug resistance is the synergistic use of  $\beta$ -lactam antibiotics and  $\beta$ -lactamase inhibitors such as clavulanic acid, tazobactam, and sulbactam [147]. In search for new  $\beta$ -lactamase inhibitors, Grundstrom and co-workers conducted detailed studies of class C  $\beta$ -lactamase and simple aryl boronic acids including ortho-, meta-, and para-substituted methyl-, hydroxymethyl-, formyl-, and phenylboronic acids [148, 149]. Crystallographic studies showed evidence that the hydroxyl group of a serine (Ser-221) residue of AmpC acts as a nucleophile and forms a covalent bond with the boronic acid in the active site [20, 150]. As mentioned earlier, most of the clinically relevant  $\beta$ -lactamases are serine-based hydrolases. Compounds containing a boronic acid moiety are excellent candidates for inhibitor development against these  $\beta$ -lactamases because the electrophilic boron can readily interact with the nucleophilic serine, resulting in covalent tetrahedral anionic intermediate and thus enzyme inactivation [151]. For example, Pechenov and co-worker developed a series of boronic acid analogues, and the peptide boronic acid Boc-L-Lys(Cbz)-D-boroAla showed an inhibitory effect with an  $IC_{50}$  value of 370 nM [152]. Their crystal structural studies demonstrated that the boron atom is covalently attached to the serine. The complex is a transition state analogue of the enzyme-catalyzed reaction [153]. Strynadka [154], Prati [155], Shoichet [151, 156], and White [157] also reported highly potent, nanomolar boronic acid  $\beta$ -lactamase inhibitors (compounds 22–25, Fig. 7). Despite the potent inhibition activities, no boronic acid-based inhibitors of  $\beta$ -lactamases have made to phase II or III clinical trials yet.

Diazaborines, first invented by Dewar and then further developed by Gronowitz, are another class of boron-containing compounds with antibacterial activities [158, 159]. However, due to toxicity problems in a number of analogues (26–28, Fig. 8), further development of this class of compounds was stopped [1].



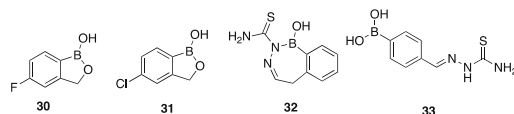
**Fig. 7** Boronic acid-based inhibitors of  $\beta$ -lactamases



**Fig. 8** Some boronic acid based compounds designed as antibacterial agents

In 2009 Wang and co-workers reported boronic acid-based antibacterial agents that interfere with bacterial quorum sensing and can be potentially used as antibacterial agents [160–163]. Briefly, bacterial quorum sensing is a term describing the bacterial ability to control gene expression and other biologically relevant processes through the detection of minimal concentrations of signal molecules called autoinducers [163]. There are a number of autoinducers in the bacterial quorum sensing process. Among them, autoinducer-2 (AI-2) is a signaling molecule that is universal for both Gram-positive and Gram-negative bacteria, thus an important therapeutic target. In *Vibrio harveyi*, AI-2 exists as a boric acid complex [163]. Wang and co-workers studied the idea of using phenyl boronic acid compounds that can mimic AI-2 in bacterial quorum sensing, thus inhibiting the signaling pathway. Compound **29** is one example from the library of quorum sensing inhibitors that carries sub-micromolar  $IC_{50}$  ( $0.7 \mu M$ , Fig. 8) [163]. To our best knowledge, this is the most potent boron-containing compound to inhibit the AI-2 signaling pathway.

In addition to the antibacterial boron-containing antibiotics, boronic acids with antifungal activity (dihydrobenzoxaboroles) were reported by Baker and co-workers in 2006 and were investigated in phase II and III clinical trials [164]. These compounds have been proven to target fungal leucyl tRNA synthetase [164, 165], which is an extremely important class of enzymes in protein synthesis. They are responsible for the attachment of specific amino acids to the corresponding tRNA. The importance of this class of enzymes makes them very attractive therapeutic targets. One major setback of this strategy is that these enzymes are present in all eukaryotic cells including the mammalian system; therefore, there is an issue for binding specificity. However, crystal structural analysis revealed that certain benzoxaborole compounds bind specifically to the fungal leucyl tRNA synthase and form a stable inhibitor–enzyme complex [164, 166]. The compounds (**30–33**) were tested against a number of fungal strains, and two of the most potent compounds **30** and **31** (Fig. 9) showed MIC as low as

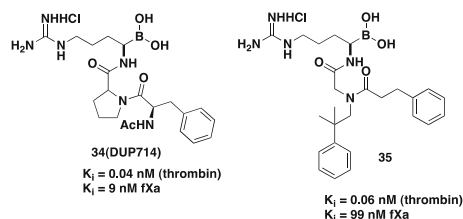


**Fig. 9** Boronic acid derivatives as potential antifungal agents

0.25  $\mu\text{g/mL}$  against *A. fumigatus* [164]. As of 2009 compounds **30** and **31** were being investigated in phase I and II clinical trials as topical agents for treatment of onychomycosis (fungal infection of the nail) [1].

## 2.4 Boronic Acids Compounds as Anticoagulant Agents

Cardiovascular diseases (CVD) are one of the major causes of mortality in the modern-day society. An estimate provided by the WHO states that over 17 million people per year die from cardiovascular diseases. Such a number makes CVDs the leading cause of death worldwide (<http://www.who.int/mediacentre/factsheets/fs317/en/>). Thromboembolic diseases are one of the top three causes of CVD-related deaths [167]. Thrombin is a serine protease involved in the final steps of the blood coagulation cascade. This protein is an important target for the development of anticoagulant agents [4]. A major concern with using thrombin inhibitors as anticoagulant agents is the nonspecific inhibition of other enzymes. For example, DuPont have identified a boronic acid thrombin inhibitor DUP 714 with  $K_i$  of 40  $\mu\text{M}$  (Fig. 10) [168, 169]. The compound appeared to be very potent in its inhibition of thrombin; however, it exhibited severe side effects in animal studies that were proven to be related to strong inhibition of complement factor I [169]. After careful analyses of the crystal structure of the inhibitor DUP 714 and its interactions with  $\alpha$ -thrombin and the complement factor I homologue factor Xa, it was observed that the binding pockets were significantly different between these two proteins. Such information allowed for structural optimization of DUP 714 to afford a more selective fit, the  $\alpha$ -thrombin pocket [170, 171]. The optimized compound **35** (Fig. 10) was more selective towards  $\alpha$ -thrombin compared to factor Xa; however, the  $K_i$  values for both enzymes were at or below nanomolar concentrations (0.06 and 99 nM, respectively), which is undesirable. When designing an enzyme inhibitor, it is important not only to have high potency but also have selectivity. Although compound **35** is more selective for thrombin, the inhibitory concentration is too close to the one against fXa. Thus, the “inhibitory margin” is too narrow and does not allow for the development of a pharmaceutical agent. Ideally when designing an inhibitor, the “inhibitory margin” should be a few orders of magnitude larger. The designed boronic acid compounds exhibited potent inhibitory activity towards  $\alpha$ -thrombin through covalent interaction of the boron with serine-195 in the P1 binding pocket and formation of a tetrahedral species,

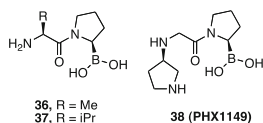


**Fig. 10** Boronic acid-based thrombin inhibitors

which is considered a transition state analogue inhibitor. However, in this case, the boronic acid compounds never advance further as anticoagulant agents.

## 2.5 Boronic Acid Compounds as Diabetes Therapeutic Agents

Earlier in the chapter Talabostat was introduced as a promising anti-cancer agent by inhibiting FAP and DPP4. This compound was initially designed as a DPP4 inhibitor for the development of treatment options for diabetes. There have been a number of DPP4-targeting boronic acid compounds reported, and a few of them were reported to have been studied in clinical trials [1]. DPP4 is a membrane-bound serine protease that specifically cleaves two N-terminal amino acids followed by either a proline or alanine residue [172]. DPP4 has become a key target towards the development of diabetes therapeutics, because it plays such a crucial role in the degradation of the glucagon-like peptide 1 (GLP-1) [173], which is a hormone responsible for the increases of insulin release from the pancreas upon elevation of blood glucose levels [173]. Inhibition of DPP4 results in an increase of GLP-1 levels and thus proper control of blood glucose concentrations. A number of non-boron-containing DPP4 inhibitors have been clinically used for treatment of diabetes; some examples of commercially available DPP4 inhibitors include saxagliptin (Onglyza, by BMS), vildagliptin (Galvus, by Novartis), and sitagliptin (Januvia, by Merck). Another interesting aspect about DPP4 as a drug target is that its catalytic triad is atypical for the serine proteases order: serine–aspartate–histidine. The presence of this catalytic triad suggests that boronic acid-containing compounds can have the potential to be developed as successful DPP4 inhibitors. A number of dipeptide boronates have been synthesized and have shown activity in the low nanomolar to picomolar range, which in principle makes them more potent than the clinically used DPP4 inhibitors [174]. However, a major downside of compounds such as **36** and **37** is that at physiological pH they can undergo intramolecular cyclization between the primary amine and the boronic acid moiety (Fig. 11). It is clear that the open-shell orbital of the boronic acid can easily accept electrons and interact with strong nucleophiles such as free amines or alcohols. The



**Fig. 11** Boronic acid-based DPP4 inhibitors

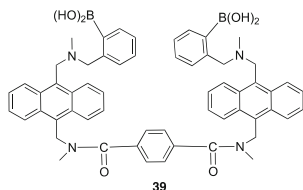
free amine (and a strong nucleophile at physiological pH) that is in proximity to the boron, as in compounds **36** and **37**, can easily undergo nucleophilic intramolecular cyclization to form a stable six-membered ring (Fig. 11). Later, analogues containing mono-alkyl-protected amino groups that carry nanomolar inhibition were developed. However, these small peptides carry low nano-molar activity against not only DPP4 but also DPP9 and FAP. Thus, the lack of selectivity made these small molecules unsuitable as drug candidates [175–177]. In 2008 after clinical trials, compound PHX1149 (**38**, Fig. 11) was reported to have not only just excellent activity (DPP4,  $IC_{50} = 25$  nM) but also high patient tolerance via oral administration in doses up to 400 mg/kg [106, 178, 179]. This orally bioavailable, water-soluble small molecule reached phase III clinical trials and may possibly be the next boron-containing marketed drug because of its DPP4 selectivity.

## 2.6 BNCT (Boron Neutron Capture Therapy)

In addition to being enzymatic inhibitors and carbohydrate binders, some boron-containing compounds have been used in BNC therapies. This type of therapy is based on the fact that neutron irradiation of boron-10 leads to high-energy  $\alpha$ -particles and lithium nuclei, which cause localized ionization and thus tissue damage. There is one critical aspect to consider when designing a BNCT agent [4]. Due to the highly damaging effect of high-energy  $\alpha$ -particles on tissue, cancer-selective compounds that can deliver boron-10 precisely to the cancer tissue and at high density need to be utilized. A number of BCN agents have been developed throughout the years, some of which are currently being clinically used for cancer therapy outside of the USA. Studies in this area have been summarized in a number of reviews and therefore are not to be discussed in detail [4, 5, 180].

## 3 Boronic Acids as Carbohydrate Binders/Receptors

Carbohydrates in the form of oligosaccharides and polysaccharides are a major class of biomolecules in the mammalian system. A well-known fact is that mammalian cells are decorated with complex carbohydrates such as glycolipids and glycoproteins, playing various functional roles in biological systems [3, 181–183]. Carbohydrates are involved in a number of major physiological events in

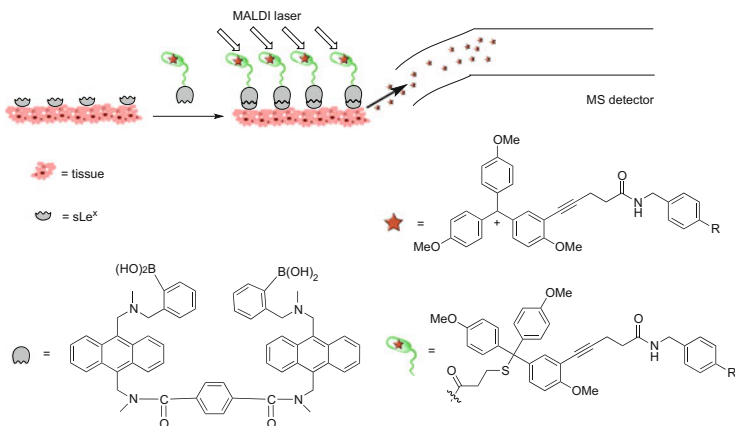


**Fig. 12**  $sLe^x$  selective bisboronic acid

the mammalian system [3]. In cellular adhesion and inflammation processes, it is the interactions between carbohydrates and carbohydrate-binding proteins (lectins) that trigger the leucocyte response [184]. Another example of the importance of carbohydrate functions in the mammalian system is HIV infection, which is mediated by the binding of a glycoprotein to the cellular surface receptor [185, 186]. Furthermore, the surface of cancer cells is coated with glycoproteins; interactions of lectins with these carbohydrates can trigger biological events such as metastasis, cell adhesion, apoptosis, etc [187–189]. Understanding the interactions between carbohydrates and other molecules has also inspired the development of a number of therapeutically relevant compounds [3, 4]. Therefore, the physiological importance of saccharides and polysaccharides brings the need for the development of molecular probes that can be used as tools and potential diagnostics and therapeutics. In this section, we focus on the progress made in the development of boronic acids as carbohydrate binders and sensors as well as their applications as diagnostic and potential therapeutic agents. Non-boronic acid-based sensors for carbohydrates have been discussed in various reviews [190–195] and thus are not discussed here in detail.

### 3.1 *BisBoronic Acid Sensors for $sLe^x$ as a Cancer Diagnostic Tool*

Lectin mimics capable of selective and high affinity recognitions of carbohydrate biomarkers can be very useful tools in the diagnostics field [3]. This is especially true in the field of cancer and diabetes. For example, the development of gastrointestinal, pancreatic, and breast cancer has been associated with overexpression of various  $sLe^x$ -containing glycoproteins [196]. Therefore, the development of  $sLe^x$ -selective sensors could aid in the diagnosis and early detection of these forms of cancer. In 2002, Wang and co-workers first reported a series of anthracene-based bisboronic acids, some of which possess selectivity for  $sLe^x$  (39, Fig. 12). Among the same series, there was also a sensor with selectivity for glucose over fructose. When compared to normal arylboronic acids, the bisboronic fluorescent sensor showed selectivity improvement of over 1,400-fold [197].  $sLe^x$ -selective sensor has been used in various applications.



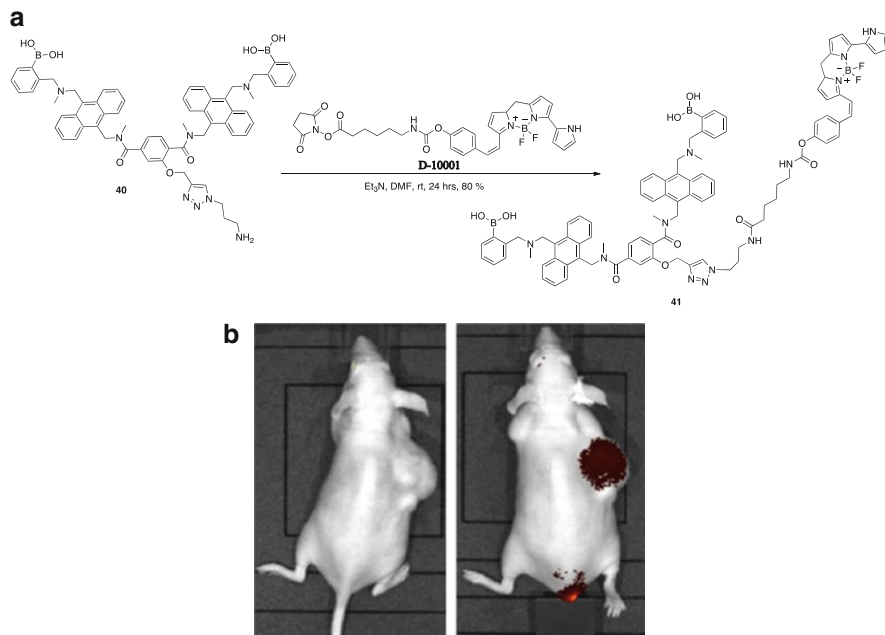
**Scheme 2** The general concept of Boronolectin–MS tag conjugation for imaging applications

### 3.1.1 MALDI-IMS Imaging for Histological Analysis of Cancer Tissues

In modern histological work, especially in cancer, there is a need for the development of methods for the simultaneous detection of multiple biomarkers, i.e., multiplexing. With the traditional histochemistry work, fluorescent and/or visible dyes are used in staining tissues. One drawback with this approach is the issue of spectral signal overlap. With the spectral window of 500–700 nm and the normal spectral bandwidth of more than 50 nm, possible signal overlap issues severely limit the ability to simultaneously detect multiple biomarkers [198]. In addition, the issue of dye stability, photobleaching, and difficulty in quantitation are all issues associated with the traditional histological work [198]. Recently, the development of matrix-assisted laser desorption/ionization imaging mass spectrometry (MALDI-IMS) allowed for the direct examination of tissue biopsies without the need for microdissection and biomarker solubilization prior to analysis (Scheme 2) [198]. MALDI-IMS can generate images correlating exact locations within a thin tissue section and exact molecular mass [199–202]. Very importantly, one can monitor a large number of ions simultaneously because of the extremely high resolution of mass spectrometry, allowing for multiplexing.

In the very first example of this field, Wang and co-workers conjugated sLe<sup>x</sup>-selective **39** with a trityl-based tag through a thioether linkage for matrix-free MALDI-IMS analysis of cancer tissues that contain detectable levels of sLe<sup>x</sup>. Because the trityl cation is very stable, MALDI laser can ionize the conjugate by cleaving the thiol linkage to give the trityl carbocation [203]. Using kidney cancer as an example, the conjugate was used to treat the tissue and then subjected to systematic analysis by a grid of MALDI laser shots. The mass tag peaks were observed in the cancer tissue region (expressing sLe<sup>x</sup>) and the MALDI-IMS results were consistent with that of tissue immunostaining [198]. Because of the





**Fig. 13** (a) Structures of conjugate **41**. (b) Optical (fluorescent) imaging of tumor by targeting cell surface carbohydrate biomarker (*left*: mouse before imaging agent injection; *right*: mouse 24 hours after tail vein injection of the contrast agent showing almost exclusive delivery to the tumor site)

widespread presence of carbohydrate biomarkers in cancer, it is hoped that the MALDI-IMS methods will find increasing utility in the diagnosis of cancer.

### 3.1.2 In Vivo Fluorescent Imaging Application

Multiple glycosyltransferase genes responsible for the further glycosylation of glycoconjugates were found to be upregulated in many forms of cancer, resulting in the high-level expression of various glycobiomarkers. Furthermore, high concentrations of sLe<sup>x</sup> have been found in the sera of patients with colon cancer, presumably due to the shedding of such carbohydrates by cancer cells [204]. In terms of the pathological relevance for the observed high levels of carbohydrate biomarkers, sLe<sup>x</sup> has also been implicated in mediating the metastasis and invasiveness of colon and other forms of cancer [205–208].

Wang and co-worker conjugated Le<sup>x</sup>-selective bisboronic acid **40** to a fluorophore (BODIPY) to examine the feasibility of using such a conjugate to image tumor in vivo [209]. Thus, conjugate **41** (Fig. 13) was synthesized and evaluated. Specifically, fluorescent agent **41** was injected into mice with implanted tumor, which overexpress sLe<sup>x</sup>. After a 24-h washout period, it was found that the

fluorescent agent was concentrated in the tumor area, allowing for ready detection of the tumor (Fig. 13; some injury probably occurred during tail vein injection, which led to diffusion and retention of the fluorescent agent in the tail area) [209]. This work represents the very first example that a small molecule capable of recognizing a carbohydrate biomarker was used for optical imaging applications and demonstrates the tremendous potential of this area of studies.

### **3.2 Boronic Acids as a Tool for Bacterial Detection**

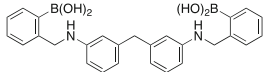
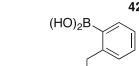
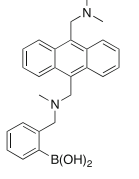
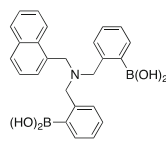
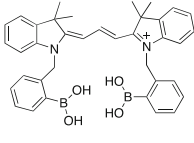
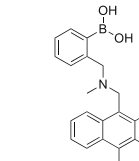
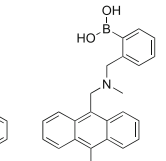
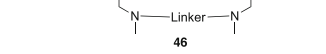


Carbohydrates are one of the major constituents of the bacterial cell wall and surface, which are important for the immunological properties of microorganisms, signal transduction, and cell–cell recognition. Boronic acids have been used for the recognition of bacterial surface carbohydrates and thus bacterial detection [210–215].

One example in bacterial detection is 3-aminophenylboronic acid (3-APBA). Thavarungkul and co-workers were the first group to detect bacteria in drinking water by using 3-APBA [212]. Briefly, 3-APBA was immobilized on a gold electrode via a self-assembled monolayer. The binding between 3-APBA and bacteria in a flow system resulted in the change in capacitance of the sensing surface. The results showed good performance with a wide linear range  $1.5 \times 10^2$ – $1.5 \times 10^6$  CFU mL<sup>-1</sup> and low detection limit 100 CFU mL<sup>-1</sup>. Compared with the normal detection limit, which is set at 500 CFU mL<sup>-1</sup>, the new method increased detection sensitivity of total bacteria in drinking water by fivefold. 3-APBA was shown to bind with several types of bacteria; however, it is only well suited for a rapid analysis of total bacteria in water samples without any selectivity for a particular type of bacteria. This work could serve as a model for the further development of rapid and accurate water contamination detection methods.

### **3.3 Boronic Acids as a Tool for Viral Infection Detections**

Boronic acids not only can be used for bacterial detection, it also studied for the rapid, accurate, sensitive, and low-cost detection of viruses [216, 217]. For example, Say and co-workers developed a detection method for influenza virus based on boronic acid–carbohydrate interactions and applied this method to quartz crystal microbalance (QCM) and surface plasmon resonance (SPR) sensing [218]. 4-Aminophenyl boronic acid (4-APBA) can bind to sialic acid (SA), which has an important role in viral binding to hemagglutinin (HA) and thus infection. In these studies, QCM and/or SPR chips were modified by immobilizing 4-APBA. Viral binding, through interactions between boronic acid and SA, would give a signal in the sensogram, and thus allow for viral detection. In using this method, the authors

**Table 1** Selected examples of potent boronic acid glucose binders

Compound	Binding affinity	Author and References	
	$K_a = 140 \text{ M}^{-1}$	James [243]	
 42	$K_a = 3.6 \text{ M}^{-1}$ (43)	Shinkai [43, 225]	
			
			
	$K_a = 178 \text{ M}^{-1}$ (46a) $K_a = 1,472 \text{ M}^{-1}$ (46b) $K_a = 638 \text{ M}^{-1}$ (46c)	Wang [197]	
			
			
			
Compound	46a	46b	46c
Linker			$-(\text{CH}_2)_4-$

were able to calculate the detection limit by QCM ( $4.7 \times 10^{-2} \mu\text{M}$ ) and affinity constant of SA immobilized sensor for HA ( $1.79 \times 10^6 \text{ M}^{-1}$ ) by SPR. Atomic force microscopy (AFM) was used to show that the HA molecule was homogeneously bound to 4-APBA-SA on the sensor surface [219–221]. This method has comparable detection limit to other reported HA detection methods. More importantly, the developed method could help overcome certain issues related to influenza detection, such as protein denaturation, requiring lengthy time, tedious labor work, and expensive agents such as antibodies [218].

### 3.4 Fluorescent Boronic Acids as a Tool for Glucose Detection

Diabetes is a disease that afflicts millions of people all over the world. One of the key issues in diabetes management is the monitoring of blood glucose concentrations. Commercially available glucose monitoring systems rely on redox chemistry and color reactions. These approaches work very well in blood sample analysis,

which gives a snap shot of glucose concentration at a given time point. One of the trends in diabetes management is the development of continuous glucose monitoring systems, which can be coupled with an insulin delivery device. In addition, in hospital settings and intensive care units (ICU), there are also needs for continuous glucose concentration monitoring. Thus, this has been an area of intense interest. For example, there have been interests in developing contact lens-type of glucose sensors for easy concentration determinations. Along these lines, chemosensing systems provide tremendous advantages over existing methods. In developing chemosensors for glucose, boronic acid-based compounds occupy a special place. The field of boronic acid-based glucose chemosensing development is a very active one. Along this line, the labs of Czarnik [33, 45], Shinkai [43, 222–226], Heagy [47, 227–230], Strongin [231–235], Singaram [29], Lakowicz [35, 236–239], James [54, 138, 240–246], and Wang [3, 53, 56, 67, 73, 197] have reported many such chemosensors. However, because this field has been heavily reviewed, readers are referred to these excellent review articles and selected examples are only listed in a table format (Table 1).

## 4 Conclusions

Because of its unique chemistry, boron has shown exciting potential in the development of both therapeutics and diagnostics. As we move into the future, there is an increasing emphasis on therapeutic approaches that are either guided by or coupled with biomarker detection. Boronic acid-based compounds are uniquely positioned for the development of theranostics because of their utilities as enzyme inhibitors, sensors, targeting molecules, and BNCT agents. We hope this chapter will stimulate more interest in boron chemistry and its application in biomedical sciences.

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# Drug Design Based on the Carbon/Silicon Switch Strategy

Reinhold Tacke and Steffen Dörrich

**Abstract** Silicon chemistry has been demonstrated to be a novel source of chemical diversity in drug design. The carbon/silicon switch strategy, i.e., the strategic replacement of a carbon atom with a silicon atom (sila-substitution) within a well-known drug, with the rest of the molecule being identical, is one of the methods that are currently used for the design and development of new silicon-based drugs. Some of the fundamental differences between carbon and silicon (e.g., differences in the covalent radii and electronegativities) can lead to marked alterations in the physicochemical and biological properties of the sila-drugs. In general, the sila-analogues share the same mode of action as the parent carbon compounds but may have altered biological properties. Incorporation of silicon into a drug can affect and, ideally, improve the pharmacological potency and selectivity, the pharmacodynamics, and the pharmacokinetics. Examples resulting from the carbon/silicon switch strategy are sila-venlafaxine, sila-haloperidol, and disila-bexarotene, the silicon analogues of the serotonin/noradrenaline reuptake inhibitor venlafaxine, the dopamine antagonist haloperidol, and the retinoid agonist bexarotene, respectively. Using these particular examples, the basic principles of the carbon/silicon strategy in drug design are illustrated in this review.

**Keywords** Bexarotene, Bioisosterism, Carbon/silicon switch, Drug design, Haloperidol, Sila-drugs, Silicon, Synthesis and SAR, Venlafaxine

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## Contents

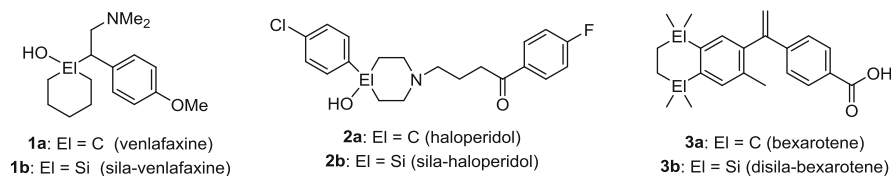
1	Introduction .....	30
2	Sila-Substitution of Drugs: The Concept .....	31
3	Sila-Substitution of Drugs: Selected Examples .....	32
3.1	Sila-Venlafaxine: A Silicon Analogue of the Serotonin/Noradrenaline Reuptake Inhibitor Venlafaxine .....	32
3.2	Sila-Haloperidol: A Silicon Analogue of the Dopamine Antagonist Haloperidol .....	37
3.3	Disila-Bexarotene: A Silicon Analogue of the Retinoid Agonist Bexarotene .....	45
3.4	Structures of Other Sila-Drugs .....	53
4	Appendix: Sila-Substitution of Odorants .....	55
5	Summary and Outlook .....	56
	References .....	57

## 1 Introduction

Over the past five decades, many biologically active organosilicon compounds have been synthesized, and silicon chemistry has been demonstrated to be a novel source of chemical diversity in drug design (for reviews, see [1–17]). There are two different approaches that can be used for the design of silicon-based drugs: (1) synthesizing a silicon analogue of a known drug in which at least one carbon atom has been replaced by a silicon atom, with the rest of the molecule being identical (carbon/silicon exchange, carbon/silicon switch, sila-substitution) and (2) synthesizing completely new silicon-based classes of compounds (the carbon analogues of which are unknown or do not exist for principal reasons) that exploit specific features of silicon chemistry to address a well-validated target. This contribution is focused exclusively on the first approach, the carbon/silicon switch strategy. The second approach is discussed in [18] of this book.

Almost 50 years ago, Fessenden et al. reported on the first silicon analogues of known organic drugs [19–22]. Following this pioneering work, many sila-drugs have been synthesized and pharmacologically characterized over the past five decades, and nowadays the carbon/silicon switch strategy is an established method in drug design, not only in academia but also in pharmaceutical industry.

As there are many reviews dealing with the carbon/silicon switch strategy, this contribution has not been written as another, updated overview. Instead, this article is focused on the discussion of a few selected examples of this approach to demonstrate the strategic background and to highlight the huge potential of the carbon/silicon switch strategy for drug design. The examples chosen are selected studies of our group and refer to sila-venlafaxine (**1b**), sila-haloperidol (**2b**), and disila-bexarotene (**3b**) and derivatives. These compounds are silicon analogues of the serotonin/noradrenaline reuptake inhibitor venlafaxine (**1a**), the dopamine antagonist haloperidol (**2a**), and the retinoid agonist bexarotene (**3a**), respectively. The chemical structures of the C/Si pairs **1a/1b**, **2a/2b**, and **3a/3b** are shown in Fig. 1.



**Fig. 1** Chemical structures of the C/Si pairs **1a/1b–3a/3b**

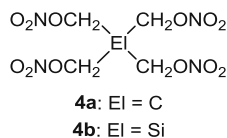
## 2 Sila-Substitution of Drugs: The Concept

Silicon is similar to carbon in that it forms four covalent bonds with many other elements. Like carbon, silicon is a Group 14 element, possessing many similarities to carbon but also presenting some crucial differences. The following are some of the fundamental differences that can be used to provide a benefit in drug design by using the carbon/silicon switch strategy [1, 4, 8–12, 14, 15, 17].

Silicon (1.17 Å) has a larger covalent radius than carbon (0.77 Å), resulting in the formation of longer silicon–element bonds compared with the analogous carbon–element bonds. For example, the average C–C bond length is 1.54 Å, whereas the Si–C bond length is 1.87 Å. This increase in bond lengths leads to an increase in the size and conformational flexibility of the sila-analogue and also affects its shape. These subtle changes in size, shape, and conformational flexibility can lead to changes in the way the sila-analogue interacts with specific proteins when compared with its parent carbon counterpart, with consequential effects on its pharmacodynamic and pharmacokinetic properties. In the case of lipophilic organic substituents attached to a central carbon atom of a given drug, the corresponding sila-analogue is more lipophilic due to the different covalent radii of carbon and silicon. This change in lipophilicity can modify in many ways the in vivo properties of a drug.

Silicon (1.74, Allred–Rochow) is less electronegative than carbon (2.50), leading to different polarizations of analogous carbon–element and silicon–element bonds. These differences can also affect the pharmacodynamics and pharmacokinetics. A special effect is an increase in acidity of a silanol ( $R_3Si-OH$ ) compared with that of an analogous alcohol ( $R_3C-OH$ ), particularly in those cases where electron-withdrawing substituents are bound to the silicon atom. As a result, the hydrogen bond strength of the silanol will be more favorable as a donor than that of the analogous alcohol. In pharmacophores, in which the COH group functions as a hydrogen bond donor, the carbon/silicon switch ( $\rightarrow SiOH$  group) can be beneficial in providing improved ligand–receptor binding.

However, there are also some striking differences between carbon and silicon that lead to stability-driven limitations of the carbon/silicon switch strategy. Unlike carbon, silicon can form thermodynamically stable five- or six-coordinate compounds that can be isolated. Conversely, coordination numbers two and three are disfavored over the coordination number four in the case of silicon. Generally,



**Fig. 2** Chemical structures of the C/Si analogues **4a** and **4b**

silicon–element double and triple bonds are thermodynamically unstable and can only be kinetically stabilized by very bulky substituents. Thus, replacement of an sp- or sp<sup>2</sup>-hybridized carbon atom in a drug by a silicon atom is not possible.

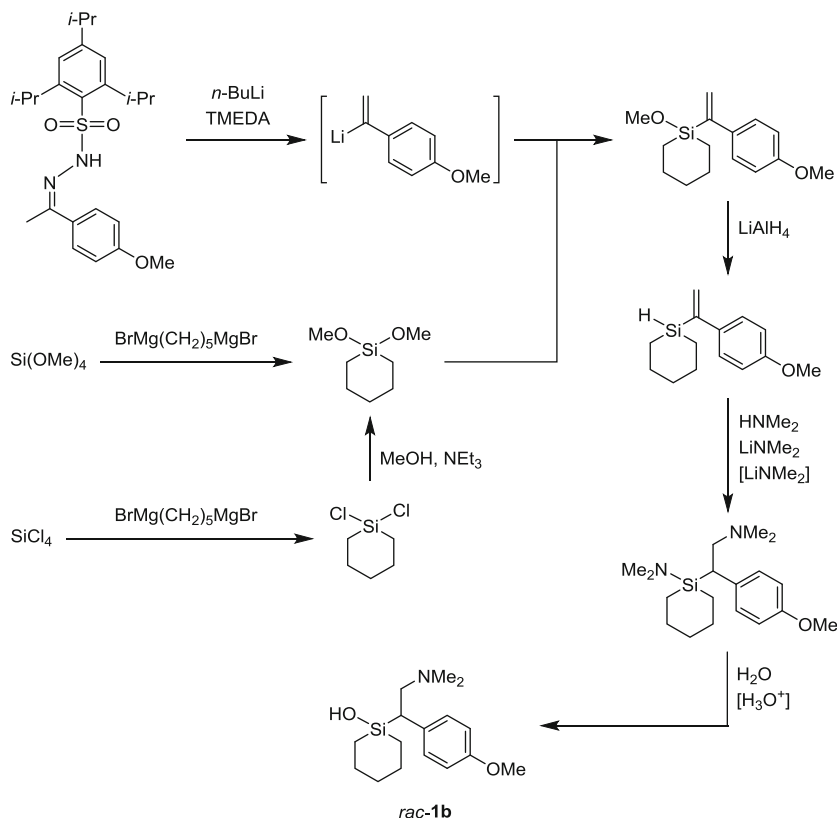
Another limitation concerns the hydrolytic instability of many silicon–element bonds, such as the Si–H, Si–O, Si–S, Si–N, and Si–P bond. Under physiological conditions, these bonds undergo hydrolysis ( $\text{R}_3\text{Si–H} + \text{H}_2\text{O} \rightarrow \text{R}_3\text{Si–OH} + \text{H}_2$ ;  $\text{R}_3\text{Si–XR} + \text{H}_2\text{O} \rightarrow \text{R}_3\text{Si–OH} + \text{HXR}$  (X=O, S);  $\text{R}_3\text{Si–XR}_2 + \text{H}_2\text{O} \rightarrow \text{R}_3\text{Si–OH} + \text{HXR}_2$  (X=N, P)). On the other hand, this hydrolytic instability offers possibilities for the development of short-acting drugs that undergo a controlled hydrolytic decomposition. Also, this hydrolytic lability could be useful for prodrug strategies.

In this context, another stability issue (although very special) should be briefly mentioned. Some years ago, the silicon analogue of the coronary vasodilator pentaerythritol tetranitrate (**4a**), sila-pentaerythritol tetranitrate (**4b**), was successfully synthesized but then turned out to be a very dangerous explosive that did not allow any biological characterization (Fig. 2) [23]. The carbon compound **4a** is also shock-sensitive and is a well-known commercial explosive (nitropenta, PENT), but it can be handled relatively easily. In contrast, the silicon analogue **4b** is an extremely shock-sensitive material that is very difficult to handle (for sila-analogues of other explosives, see [24, 25]). This different behavior of the C/Si analogues **4a** and **4b** once again demonstrates that, in spite of the many similarities of carbon and silicon, the carbon/silicon switch can significantly affect the chemical and physicochemical properties.

### 3 Sila-Substitution of Drugs: Selected Examples

#### 3.1 Sila-Venlafaxine: A Silicon Analogue of the Serotonin/ Noradrenaline Reuptake Inhibitor Venlafaxine

Racemic venlafaxine (*rac*-**1a**) is a serotonin/noradrenaline reuptake inhibitor that is in clinical use as an antidepressant. *rac*-Sila-venlafaxine (*rac*-**1b**), a silicon analogue of *rac*-**1a**, was synthesized in multistep syntheses, starting from SiCl<sub>4</sub> or Si(OMe)<sub>4</sub> (Scheme 1) [26, 27]. An alternative synthesis of *rac*-**1b**, starting from SiCl<sub>4</sub>, is shown in Scheme 2 [28, 29]. The single enantiomers of sila-venlafaxine, (*R*)-**1b** and (*S*)-**1b**, were obtained by resolution of *rac*-**1b**, using (+)- and (–)-10-camphorsulfonic acid as resolving agents [26]. The absolute configuration of (*R*)-**1b**



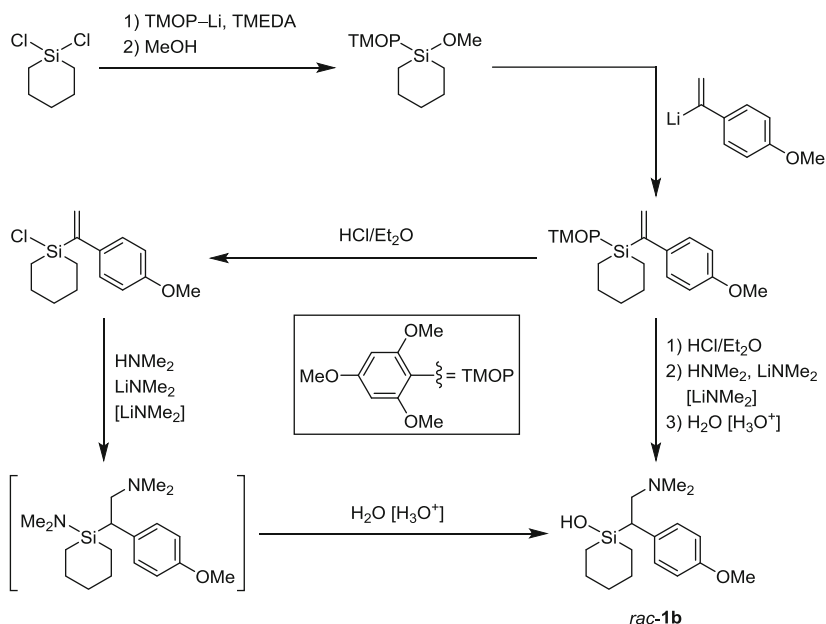
**Scheme 1** Synthesis of *rac*-**1b**

was determined by a crystal structure analysis of the corresponding hydrobromide (*R*)-**1b**·HBr [26]. The molecular structure of the cation of (*R*)-**1b**·HBr is depicted in Fig. 3 [26].

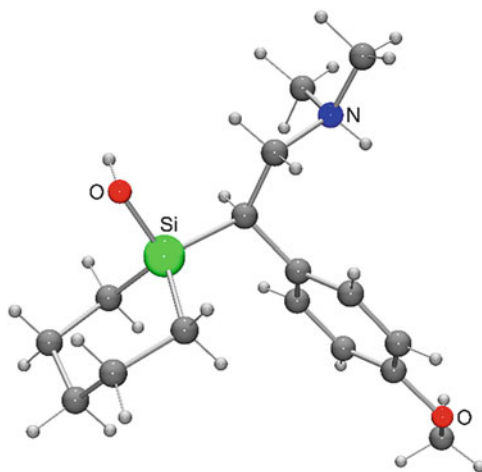
Figure 4 shows a superposition of the cyclohexane skeleton of (*S*)-**1a**·HBr and the 1-silacyclohexane skeleton of the (*S*)-enantiomer of *rac*-**1b**·HCl (structures determined by single-crystal X-ray diffraction) [26]. Due to the longer covalent radius of the silicon atom, the 1-silacyclohexane ring is more flat than the cyclohexane ring, leading to different relative orientations of the OH and NH groups of the two C/Si analogues. These different structures may affect the ligand–receptor interactions of venlafaxine (**1a**) and sila-venlafaxine (**1b**).

To get information about their physicochemical properties, compounds *rac*-**1a** and *rac*-**1b** were studied for their  $pK_a$ ,  $\log P$ , and  $\log D$  ( $\log P$  at pH 7.4) values [26]. As can be seen from Table 1, very similar physicochemical profiles were observed for the two C/Si analogues, suggesting similar brain penetration profiles of venlafaxine (**1a**) and sila-venlafaxine (**1b**). At pH 7.4 (physiological pH), both compounds exist predominantly in their protonated form (degree of protonation ca. 90%).



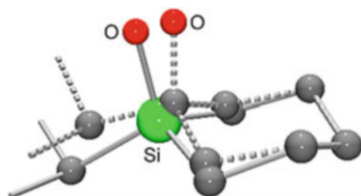


**Scheme 2** Synthesis of *rac-1b*



**Fig. 3** Molecular structure of the cation of (*R*)-**1b**-HBr in the crystal [26]

Compounds (*R*)-**1a**, (*S*)-**1a**, (*R*)-**1b**, and (*S*)-**1b** were studied for their efficacy in serotonin, noradrenaline, and dopamine reuptake inhibition assays [26]. Human HEK-293 (serotonin), MDCK (noradrenaline), and CHO-K1 (dopamine) cell lines and the radioligands [<sup>3</sup>H]serotonin, [<sup>3</sup>H]noradrenaline, and [<sup>3</sup>H]dopamine,



**Fig. 4** Superposition of the cyclohexane skeleton of (*S*)-**1a**·HBr (*dashed bonds*) and the 1-silacyclohexane skeleton of the (*S*)-enantiomer of *rac*-**1b**·HCl (*solid bonds*) (hydrogen atoms are omitted for clarity) [26]

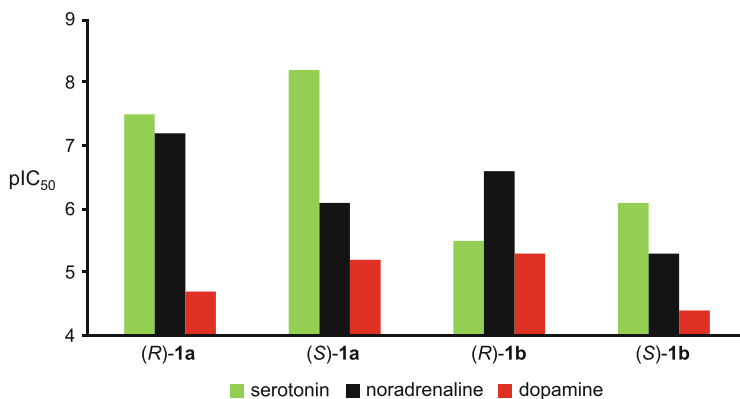
**Table 1**  $pK_a$ ,  $\log P$ , and  $\log D$  ( $\log P$  at pH 7.4) data for *rac*-**1a** and *rac*-**1b** [26]

Compound	$pK_a$	$\log P$	$\log D$
<i>rac</i> - <b>1a</b>	9.7	3.13	0.88
<i>rac</i> - <b>1b</b>	9.7	3.21	0.92

**Table 2** Serotonin, noradrenaline, and dopamine transporter inhibition profiles of (*R*)-**1a**, (*S*)-**1a**, (*R*)-**1b**, and (*S*)-**1b** ( $IC_{50}$ ,  $\mu M$ ) [26]

Compound	Serotonin	Noradrenaline	Dopamine
( <i>R</i> )- <b>1a</b>	0.030	0.061	19.600
( <i>S</i> )- <b>1a</b>	0.006	0.754	6.670
( <i>R</i> )- <b>1b</b>	3.168	0.251	5.270
( <i>S</i> )- <b>1b</b>	0.791	4.715	36.350

The data represent the mean of at least two determinations



**Fig. 5** In vitro efficacy of (*R*)-**1a**, (*S*)-**1a**, (*R*)-**1b**, and (*S*)-**1b** regarding serotonin, noradrenaline, and dopamine reuptake inhibition [26].  $pIC_{50}$  denotes the negative decadic logarithm of the half-maximum effect concentration (M). The data represent the mean of at least two determinations

respectively, were used in these studies. The results obtained are shown in Table 2 and Fig. 5.

As can be seen from Table 2 and Fig. 5, the sila-venlafaxine enantiomers (*R*)-**1b** and (*S*)-**1b** exhibit a substantially altered monoamine reuptake inhibition profile when compared with the respective venlafaxine enantiomers (*R*)-**1a** and (*S*)-**1a**.

While activity at the noradrenaline and dopamine transporters is only slightly affected by sila-substitution, the potency at the serotonin transporters is reduced by two orders of magnitude, resulting in totally altered selectivity profiles. (*S*)-Venlafaxine ((*S*)-**1a**) is a potent and selective serotonin reuptake inhibitor, being about 100- and 1,000-fold more potent at serotonin transporters than noradrenaline and dopamine transporters, respectively. Sila-substitution of (*S*)-**1a** ( $\rightarrow$  (*S*)-**1b**) makes this compound a rather weak mixed serotonin/noradrenaline reuptake inhibitor, with only about 50- and 6-fold, respectively, selectivity over dopamine and noradrenaline transporters. (*R*)-Venlafaxine ((*R*)-**1a**) is also a mixed serotonin/noradrenaline reuptake inhibitor, with about 500-fold selectivity over dopamine transporters and a significantly higher potency than that of (*S*)-**1b**. Sila-substitution of (*R*)-**1a** ( $\rightarrow$  (*R*)-**1b**) results in a substantially altered selectivity profile. (*R*)-Sila-venlafaxine ((*R*)-**1b**) is a selective noradrenaline reuptake inhibitor being about 10-fold more potent at noradrenaline transporters than at serotonin and dopamine transporters. This is one of the most impressive examples demonstrating that sila-substitution can affect both pharmacological potency and pharmacological selectivity.

To evaluate the potential of the noradrenaline selectivity of (*R*)-sila-venlafaxine ((*R*)-**1b**) for the treatment of various CNS disorders, the compound was profiled further and was tested *in vitro* across a panel of 68 common receptors/channels and 16 enzymes [30]. In the majority of assays, (*R*)-**1b** was found to be inactive (<50% inhibition at 10  $\mu$ M), including opioid receptors. Only weak affinity at  $\text{Ca}^{2+}$  and  $\text{Na}^{+}$  channels was observed. (*R*)-Sila-venlafaxine ((*R*)-**1b**) was also shown to display only low *in vitro* activity at the cytochrome P450 enzymes CYP2D6, CYP1A2, CYP2C19, and CYP3A4 (<50 % inhibition at 10  $\mu$ M). In conclusion, (*R*)-**1b** can be indeed regarded as a selective noradrenaline reuptake inhibitor.

Following the idea that this particular selectivity profile may have utility in the treatment of emesis, (*R*)-**1b** was evaluated in a ferret model of morphine-induced emesis [30]. As the C/Si analogues *rac*-**1a** and *rac*-**1b** have almost identical physicochemical properties (Table 1), and based on the evidence that *rac*-**1a** achieves high clinical efficacy in the treatment of depression, one would have high confidence that (*R*)-**1b** would also readily reach its site of action in the CNS. (*R*)-Sila-venlafaxine ((*R*)-**1b**) was dosed orally 2 h prior to the emetogen morphine (0.125 mg/kg, *s.c.*), and the animals were monitored for retching and vomiting events for up to 2 h following the administration of morphine. At 50 mg/kg, (*R*)-**1b** completely abolished emetic episodes, and almost complete inhibition (93 %) was achieved at 5 mg/kg. In male ferrets, dosed at 5 mg/kg orally, (*R*)-**1b** displayed a plasma half-life of 1.1 h, with a  $C_{\text{max}}$  of 225 ng/ml. In conclusion, the selective noradrenaline reuptake inhibitor (*R*)-sila-venlafaxine ((*R*)-**1b**) has been demonstrated to effectively inhibit emetic episodes caused by an emetogen in a well-characterized *in vivo* model.

Following this proof of principle, the antiemetic potential of (*R*)-sila-venlafaxine ((*R*)-**1b**) was further evaluated. For this purpose, the potential of (*R*)-**1b** to antagonize cisplatin (15 mg/kg, *i.p.*)-induced acute and delayed emesis in the ferret was studied [31]. At 5 and 15 mg/kg/4 h (*i.p.*), (*R*)-**1b** was highly effective in reducing

emetic episodes during the 0–24-h period (acute emesis), and at 15 mg/kg/4 h (i.p.), (*R*)-**1b** was also active to reduce emesis during the 24–72-h period (delayed emesis). These studies provided evidence for an antiemetic potential of the selective noradrenaline reuptake inhibitor (*R*)-sila-venlafaxine ((*R*)-**1b**) to reduce chemotherapy-induced acute and delayed emesis.

### 3.2 Sila-Haloperidol: A Silicon Analogue of the Dopamine Antagonist Haloperidol

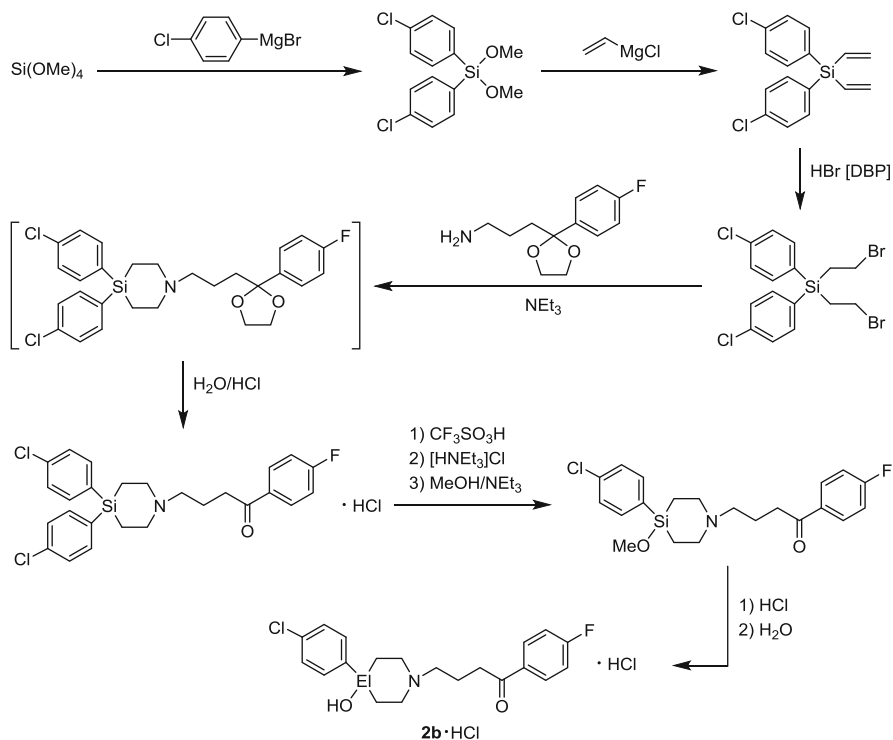
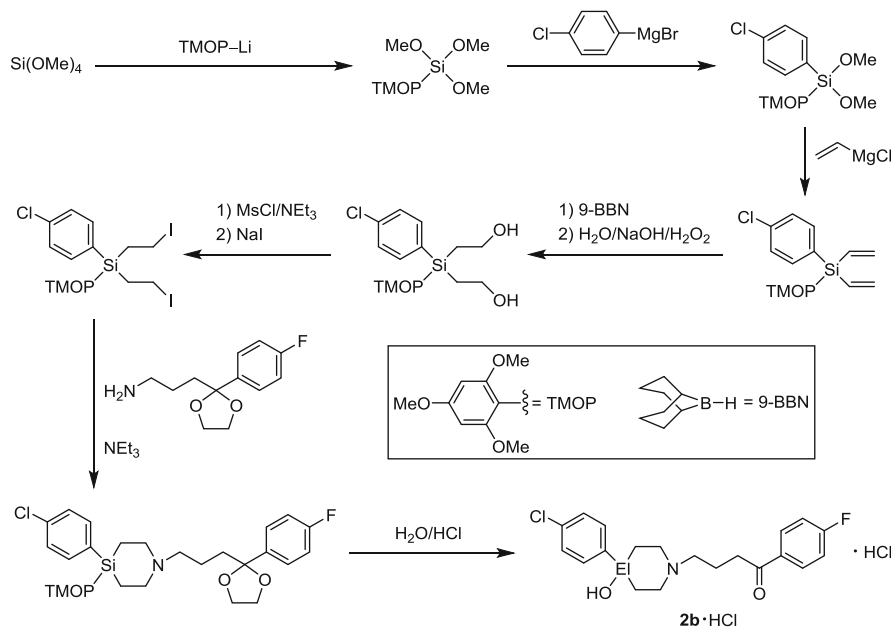
Haloperidol (**2a**) is a dopamine (D<sub>2</sub>) antagonist that is in clinical use as an antipsychotic agent for the treatment of schizophrenia. Sila-haloperidol (**2b**), a silicon analogue of **2a**, was synthesized in a multistep synthesis, starting from Si(OMe)<sub>4</sub> (Scheme 3) [32, 33]. An alternative synthesis, also starting from Si(OMe)<sub>4</sub>, is shown in Scheme 4 [34]. In both cases, sila-haloperidol (**2b**) was isolated as the hydrochloride **2b**·HCl.

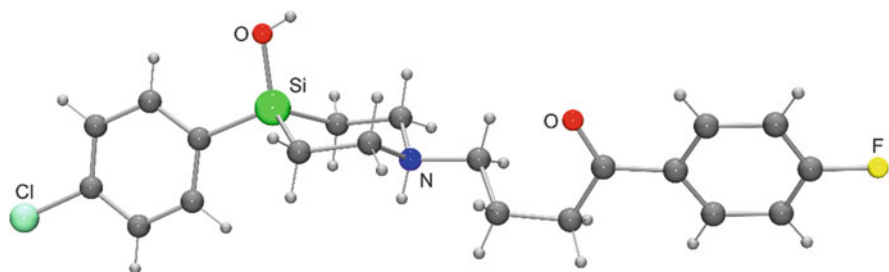
Compound **2b**·HCl was structurally characterized by single-crystal X-ray diffraction [32]. The molecular structure of the cation of **2b**·HCl is depicted in Fig. 6.

Figure 7 shows a superposition of the piperidinium skeleton of **2a**·HCl and the 4-silapiperidinium ring of **2b**·HCl (structures determined by single-crystal X-ray diffraction) [32]. Due to the longer covalent radius of the silicon atom, the 4-silapiperidinium ring is more flat than the piperidinium skeleton, leading to different relative orientations of the *N*-organyl side chain toward the hydroxy and 4-chlorophenyl groups. These different structural features may affect the ligand–receptor interactions of haloperidol (**2a**) and sila-haloperidol (**2b**).

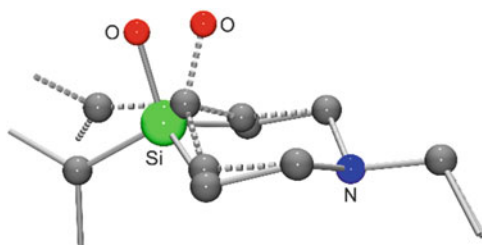
As shown by NMR spectroscopic studies in DMSO at room temperature, two conformers of the piperidinium cation of **2a**·HCl exist in solution (molar ratio ca. 1:13) [32]. This ratio differs significantly from that found for the 4-silapiperidinium cation of **2b**·HCl (molar ratio ca. 1:2), indicating considerable differences in the energies of the respective two conformers of the piperidinium and 4-silapiperidinium ring systems [32]. The structures of the two conformers  $\alpha$  and  $\beta$  are depicted in Fig. 8. The different populations of these two conformers may affect the pharmacological potency of haloperidol (**2a**) and sila-haloperidol (**2b**).

To get information about their physicochemical properties, compounds **2a** and **2b** were studied as hydrochlorides for their p*K*<sub>a</sub> and log*D* (log*P* at pH 7.4) values and for their solubility in HBSS buffer (pH 7.4) [34]. As can be seen from Table 3, similar physicochemical profiles were observed for the two C/Si analogues. The apparent permeability (*P*<sub>app</sub>) of **2a** and **2b** was also similar (studied in a human Caco-2 model) [34]. In both cases, the *P*<sub>app</sub> values were high (**2a**, *P*<sub>app</sub> = 18.9 × 10<sup>-6</sup> cm s<sup>-1</sup>; **2b**, *P*<sub>app</sub> = 19.8 × 10<sup>-6</sup> cm s<sup>-1</sup>), and the recovery rate was around 90%, indicating that both compounds passed the cellular barrier more or less unchanged. As haloperidol (**2a**) is known to possess good bioavailability in humans, these results suggest a high permeability for sila-haloperidol (**2b**) as well.

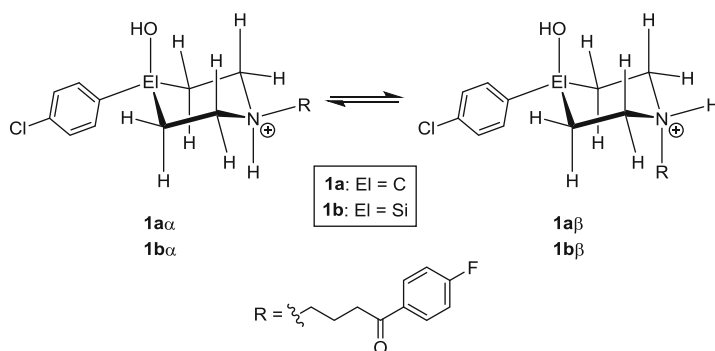
Scheme 3 Synthesis of **2b·HCl**Scheme 4 Synthesis of **2b·HCl**



**Fig. 6** Molecular structure of the cation of **2b**-HCl in the crystal [32]



**Fig. 7** Superposition of the piperidinium skeleton of **2a**-HCl (*dashed bonds*) and the 4-silapiperidinium skeleton of **2b**-HCl (*solid bonds*) (hydrogen atoms are omitted for clarity) [32]



**Fig. 8** Conformers  $\alpha$  and  $\beta$  of the piperidinium skeleton of **2a**-HCl and the 4-silapiperidinium skeleton of **2b**-HCl [32]

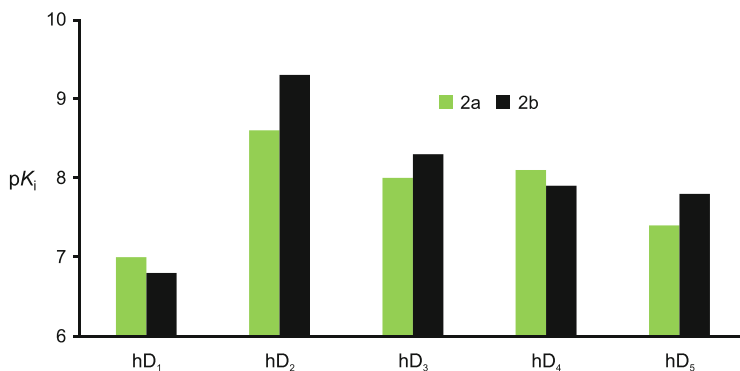
Haloperidol (**2a**) and sila-haloperidol (**2b**) were studied for their affinities at all five human dopamine receptors in competitive radioligand receptor binding assays [34]. The results obtained are shown in Table 4 and Fig. 9. All Hill slopes were not significantly different from unity, thus assuming a single binding site for **2a** and **2b** at all receptors.

**Table 3**  $pK_a$ ,  $\log D$  ( $\log P$  at pH 7.4), and solubility (in HBSS buffer at pH 7.4) data for **2a** and **2b** [34]

Compound	$pK_a$	$\log D$	Solubility ( $\mu\text{M}$ )
<b>2a</b>	$9.07 \pm 0.07$	$2.42 \pm 0.03$	$90 \pm 2$
<b>2b</b>	$9.27 \pm 0.10$	$2.77 \pm 0.13$	$78 \pm 7$

**Table 4** Affinities of **2a** and **2b** at human dopamine receptors [34]

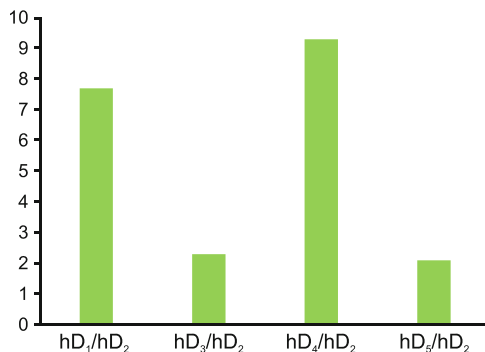
Receptor subtype	$K_i$ (nM) for <b>2a</b>	$K_i$ (nM) for <b>2b</b>
hD <sub>1</sub>	$107 \pm 22.0$	$162 \pm 34.5$
hD <sub>2</sub>	$2.84 \pm 0.26$	$0.55 \pm 0.06$
hD <sub>3</sub>	$10.4 \pm 1.47$	$4.73 \pm 0.51$
hD <sub>4</sub>	$7.94 \pm 0.69$	$14.1 \pm 1.09$
hD <sub>5</sub>	$38.0 \pm 4.72$	$16.6 \pm 3.20$

**Fig. 9** Affinities of **2a** and **2b** at human dopamine receptors [34]

As can be seen from Table 4 and Fig. 9, sila-haloperidol (**2b**) shows a significantly higher affinity for hD<sub>2</sub> receptors than haloperidol (5.1-fold), whereas the silicon compound **2b** is approximately equipotent to its carbon analogue **2a** at all the other dopamine receptors (differences are less than 2.3-fold). As a result, the subtype selectivity of **2b** for hD<sub>2</sub> over the other dopamine receptors is somewhat higher than that of **2a** (Fig. 10). Sila-haloperidol (**2b**) has an approximately 2-fold higher selectivity than haloperidol (**2a**) for D<sub>2</sub> over D<sub>3</sub> and D<sub>2</sub> over D<sub>5</sub> but an 8- to 9-fold higher selectivity for D<sub>2</sub> over D<sub>1</sub> and D<sub>2</sub> over D<sub>4</sub> relative to **2a**.

The C/Si analogues **2a** and **2b** were also characterized by functional studies at human dopamine D<sub>1</sub> and D<sub>2</sub> receptors using a calcium fluorimetric functional assay [35]. The functional data for **2a** (hD<sub>1</sub>,  $K_i = 398$  nM; hD<sub>2</sub>,  $K_i = 0.36$  nM) and **2b** (hD<sub>1</sub>,  $K_i = 194$  nM; hD<sub>2</sub>,  $K_i = 0.12$  nM) were similar to the binding data (Table 4). None of the compounds displayed any agonist activity at D<sub>1</sub> or D<sub>2</sub> receptors.

To further characterize the pharmacodynamic properties of **2a** and **2b**, the two C/Si analogues were also studied for their  $\sigma_1$  (guinea pig brain) and  $\sigma_2$  (rat liver) receptor affinities using competitive radioligand receptor binding assays (Table 5)



**Fig. 10** Ratios of the subtype selectivities hD<sub>1</sub>/hD<sub>2</sub>, hD<sub>3</sub>/hD<sub>2</sub>, hD<sub>4</sub>/hD<sub>2</sub>, and hD<sub>5</sub>/hD<sub>2</sub> of **2a** and **2b**, shown as **2a/2b** ratios [34]

**Table 5** Affinities of **2a** and **2b** at  $\sigma_1$  (guinea pig brain) and  $\sigma_2$  receptors (rat liver) [34]

Receptor subtype	$K_i$ (nM) for <b>2a</b>	$K_i$ (nM) for <b>2b</b>
$\sigma_1$	$1.9 \pm 0.4$	$3.4 \pm 0.4$
$\sigma_2$	$78.1 \pm 2.4$	$309 \pm 55$

[34]. At the  $\sigma_1$  receptor, **2a** and **2b** are approximately equipotent, whereas **2a** exhibits a 4-fold higher affinity for the  $\sigma_2$  receptor than the silicon analogue **2b**. As a result, the subtype selectivity of sila-haloperidol (**2b**) for the  $\sigma_1$  over the  $\sigma_2$  receptor is approximately 3-fold higher than that of haloperidol (**2a**).

In conclusion, in comparison with haloperidol (**2a**), sila-haloperidol (**2b**) shows a higher potency at dopamine D<sub>2</sub> receptors and a higher subtype selectivity at both dopamine and  $\sigma$  receptors.

To determine the rate of decomposition of haloperidol (**2a**) and sila-haloperidol (**2b**) in vitro, the intrinsic clearance and half-lives were measured in human and female rat liver microsomes [34]. As can be seen from Table 6, the C/Si analogues **2a** and **2b** showed a similar moderate stability in the presence of human liver microsomes. However, decomposition in the presence of rat liver microsomes was significantly increased by sila-substitution.

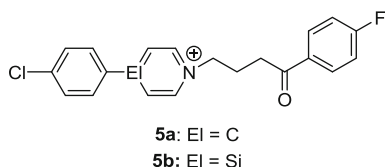
Haloperidol (**2a**) and sila-haloperidol (**2b**) were also studied for their CYP inhibition of the five major isoforms of cytochrome P450 [34]. No CYP inhibition of either **2a** or **2b** against CYP1A2, CYP2C9, and CYP2C19 could be detected ( $IC_{50} > 20 \mu M$ ). However, the silicon compound **2b** showed an almost 3-fold increased inhibitory potency against CYP3A4 ( $IC_{50} = 9.6 \pm 1.4 \mu M$ ) compared to the carbon analogue **2a** ( $IC_{50} = 26.2 \pm 7.9 \mu M$ ). CYP2D6 was also inhibited by **2a** and **2b**, with almost identical  $IC_{50}$  values (**2a**,  $2.1 \pm 0.6 \mu M$ ; **2b**,  $1.7 \pm 0.9 \mu M$ ).

Haloperidol (**2a**) and sila-haloperidol (**2b**) were also investigated for their in vitro metabolism [34, 36]. It is known that one of the major metabolites of **1a**, the pyridinium species HPP<sup>+</sup> (**5a**, Fig. 11), has neurotoxic properties and is suspected to cause severe extrapyramidal side effects, including Parkinsonism and tardive dyskinesia. As a matter of principle, an analogous metabolite of the



**Table 6** Intrinsic clearance  $Cl_{\text{int}}$  ( $\mu\text{L min}^{-1} \text{mg}^{-1}$ ) and half-life  $t_{1/2}$  (min) of **2a** and **2b** in human and rat liver microsomes [34]

Compound	$Cl_{\text{int hu}}$	$Cl_{\text{int rat}}$	$t_{1/2 \text{ hu}}$	$t_{1/2 \text{ rat}}$
<b>2a</b>	$20 \pm 2$	$21 \pm 5$	51	65
<b>2b</b>	$21 \pm 2$	$78 \pm 7$	65	18

**Fig. 11** Chemical structures of the C/Si analogues **5a** and **5b**

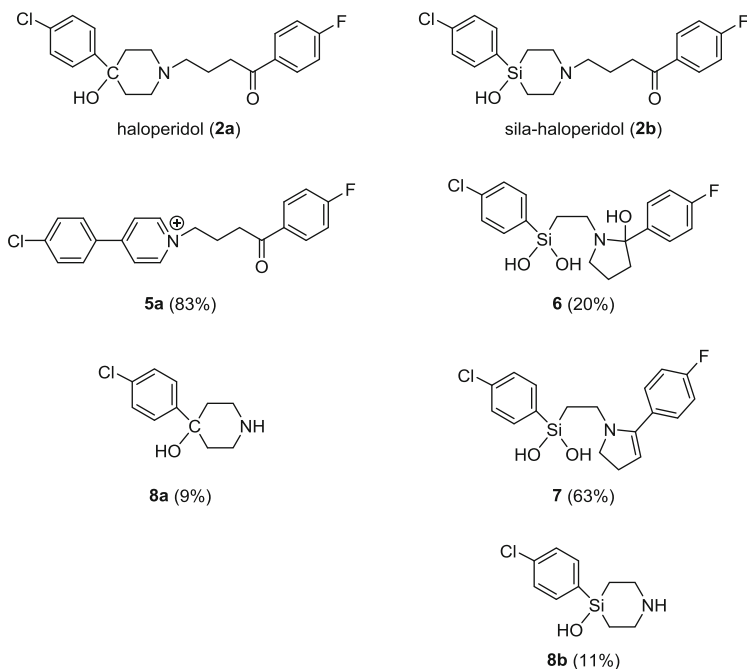
silicon analogue **2b**, the silapyridinium species sila-HPP<sup>+</sup> (**5b**, Fig. 11), cannot be formed, because the silicon–carbon double bond is unstable [32].

The phase I metabolism of haloperidol (**2a**) and sila-haloperidol (**2b**) was investigated in rat and human liver microsomes [34, 36]. The phase II metabolism of **2a** and **2b** was studied in rat, dog, and human hepatocytes and also in rat and human liver microsomes supplemented with UDP-glucuronic acid (UDPGA) [36]. These studies were performed using mass-spectrometric techniques. The structures of the proposed metabolites were assigned based on accurate mass measurements and interpretation of MS–MS spectra. The relative metabolite amounts were estimated by integration of extracted ion chromatograms and refer to the respective fractions metabolized.

The phase I and II metabolism of sila-haloperidol (**2b**) differs significantly from that of haloperidol (**2a**). This is demonstrated exemplarily in Figs. 12 and 13, where the major metabolites in human liver microsomes (incubation time 60 min) and human hepatocytes (incubation time 120 min) are shown.

For the carbon compound **2a**, the pyridinium metabolite **5a** was identified as a major metabolite in the microsomal incubations. The analogous silapyridinium metabolite **5b** was not formed. Instead, two ring-opened metabolites, the silanediols **6** and **7**, were observed. These two metabolites were the major metabolites of sila-haloperidol (**2b**) in human liver microsomes, followed by the *N*-dealkylated metabolite **8b**. The corresponding carbon analogue **8a** was also observed in microsomal incubations of haloperidol (**2a**).

Figure 14 shows the proposed pathway for the metabolic ring opening of sila-haloperidol (**2b**) to give the silanediols **6** and **7** [36]. By analogy to the pathway leading to the pyridinium metabolite of haloperidol (**2a**), the metabolism of the silapiperidine ring of the silicon analogue **2b** is most likely initiated by an enzymatic hydroxylation at the  $\beta$ -carbon atom ( $\beta$  to the silicon atom), followed by ring opening (C–N bond cleavage) to form an intermediate with an aldehyde and a secondary amine functionality. This intermediate, an  $\alpha$ -silylaldehyde, is very reactive and easily undergoes hydrolytic cleavage of the Si–C bond. The proposed

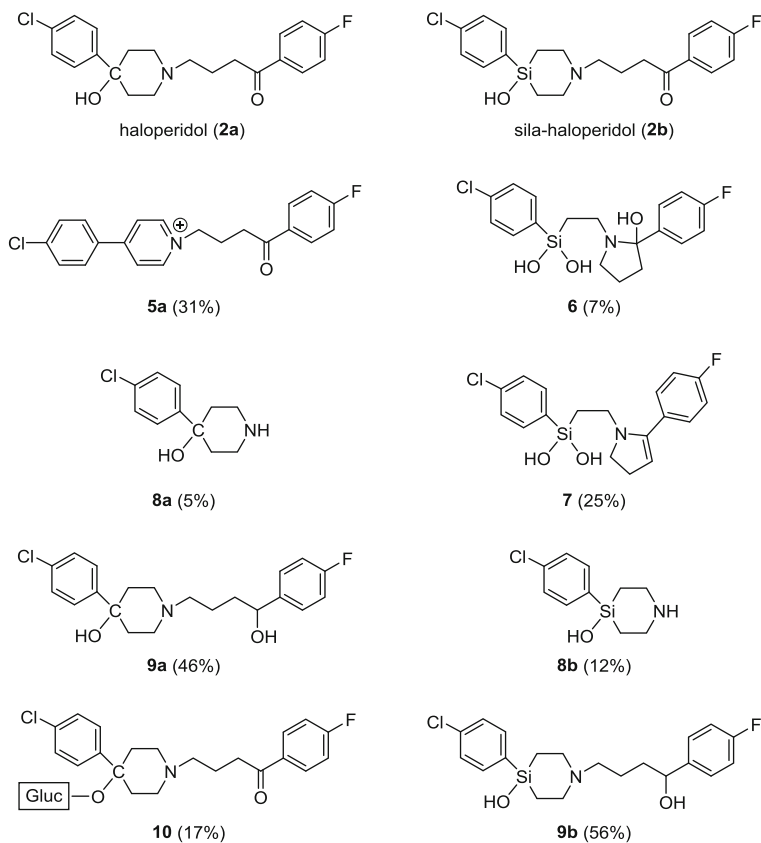


**Fig. 12** Major metabolites of the C/Si analogues **2a** and **2b** in human liver microsomes. Relative metabolite amounts of the respective fraction metabolized (**2a**, 41%; **2b**, 35%) are given in percent [36]

cyclization following the elimination of acetaldehyde then yields the metabolite **6**, which upon water elimination affords **7**.

The major metabolites of haloperidol (**2a**) in hepatocytes were the pyridinium metabolite **5a**, the *N*-dealkylated metabolite **8a**, reduced haloperidol (**2a**) (metabolite **9a**), and the glucuronidation metabolite **10** (not observed in dog hepatocytes). Reduced sila-haloperidol (**2b**) (metabolite **9b**) was the major metabolite in the dog and human hepatocytes, whereas the *N*-dealkylated metabolite **8b** and a metabolite originating from hydroxylation and glucuronidation were the major metabolites in rat hepatocytes. The metabolites **8b** and **9b** were found in all hepatocytes, and the ring-opened metabolites **6** and **7** were only formed in dog and human hepatocytes.

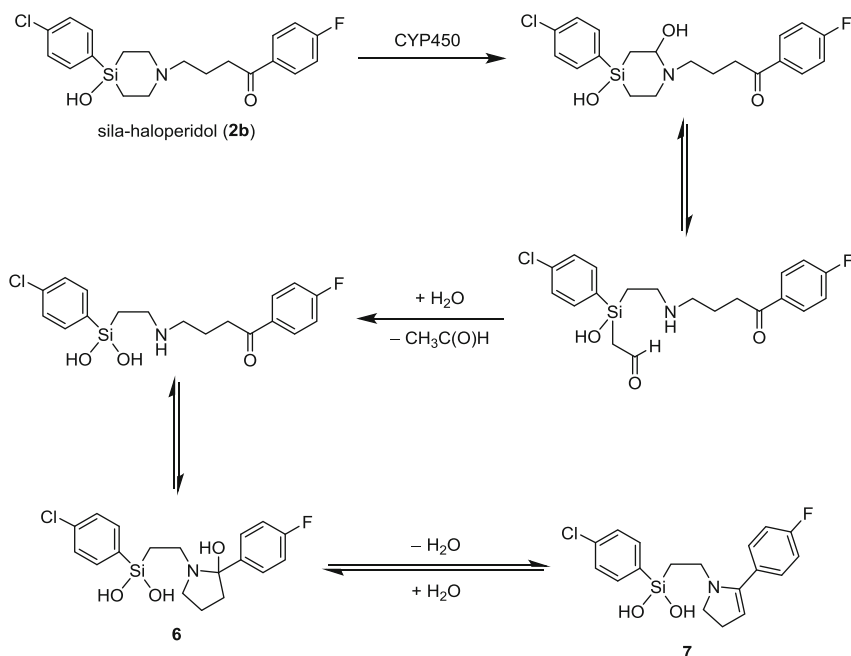
While haloperidol (**2a**) undergoes a direct glucuronidation of the OH group in rat and human hepatocytes and in rat and human liver microsomes supplemented with UDPGA, an analogous glucuronide conjugation was not observed for sila-haloperidol (**2b**). One could speculate that the direct glucuronidation of the SiOH group of **2b** occurs but that the resulting conjugate with its hydrolytically sensitive Si–OC bond then undergoes a spontaneous hydrolysis to give **2b** and free glucuronic acid. In this context, it is important to note that the chemical reactivity of the thermodynamically very stable (but against water kinetically labile) Si–OC bond of alkoxysilanes (alkyl silyl ethers) differs significantly from that of the C–OC bond of analogous dialkyl ethers. An alternative explanation for the absence of



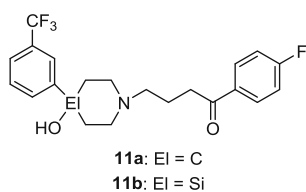
**Fig. 13** Major metabolites of the C/Si analogues **2a** and **2b** in human hepatocytes. Relative metabolite amounts of the respective fraction metabolized (**2a**, 14%; **2b**, 6%) are given in percent [36]

glucuronidation of the SiOH group of sila-haloperidol (**2b**) might be that **2b** is a poor substrate for the UDP-glucuronosyltransferases. Anyway, these results clearly demonstrate that sila-substitution of haloperidol (**2a**) strongly affects the phase II metabolism.

In conclusion, haloperidol (**2a**) and sila-haloperidol (**2b**) differ significantly in their phase I and II metabolism. These differences can be directly correlated with the silicon-specific reactivity profile of **2b**. Studies on the in vitro metabolism of the structurally related dopamine ( $D_2$ ) antagonists trifluoperidol (**11a**) and sila-trifluoperidol (**11b**) led to similar results (Fig. 15) [36].



**Fig. 14** Proposed mechanism for the metabolic ring opening of sila-haloperidol (**2b**) to give the silanediol metabolites **6** and **7** [36]

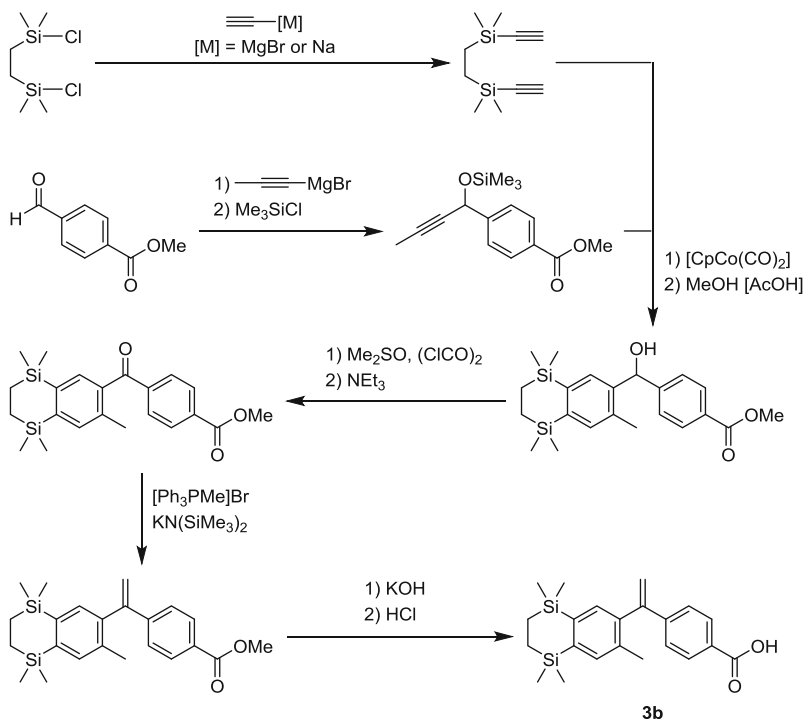


**Fig. 15** Chemical structures of the C/Si analogues **11a** and **11b**

### 3.3 Disila-Bexarotene: A Silicon Analogue of the Retinoid Agonist Bexarotene

Bexarotene (**3a**) is an RXR-selective retinoid agonist that is in clinical use for the treatment of cutaneous T-cell lymphoma. Disila-bexarotene (**3b**), a silicon analogue of **3a**, was synthesized in a multistep synthesis, starting from ClMe<sub>2</sub>Si(CH<sub>2</sub>)<sub>2</sub>SiMe<sub>2</sub>Cl (Scheme 5) [37, 38]. An alternative synthesis, also starting from ClMe<sub>2</sub>Si(CH<sub>2</sub>)<sub>2</sub>SiMe<sub>2</sub>Cl, is shown in Scheme 6 [39].

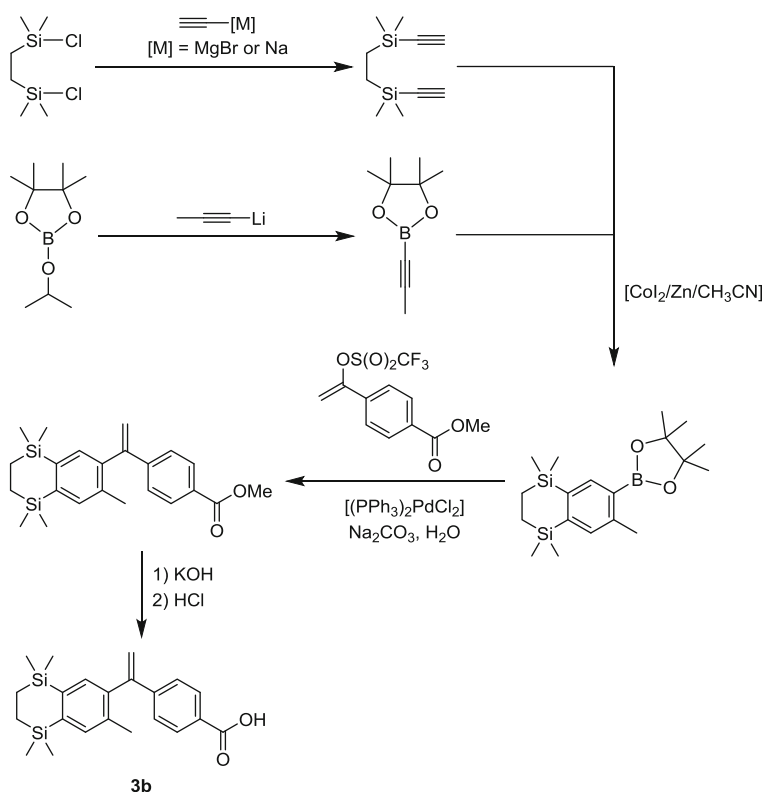
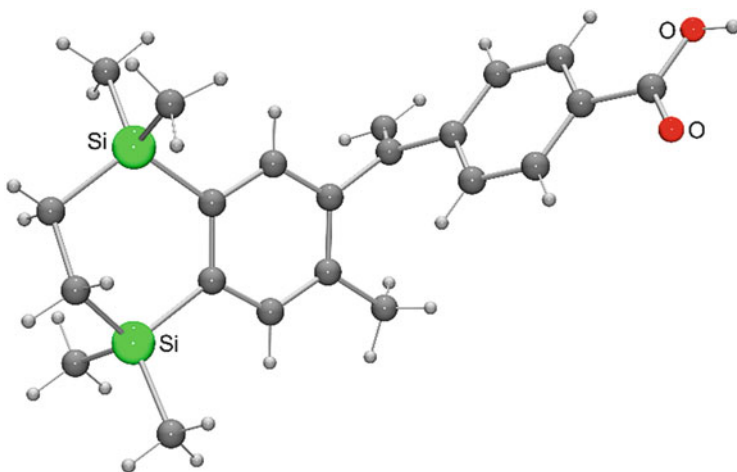
Compound **3b** was structurally characterized by single-crystal X-ray diffraction [37]. The molecular structure of **3b** is depicted in Fig. 16.

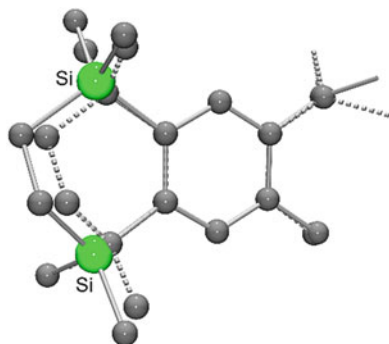


**Scheme 5** Synthesis of **3b**

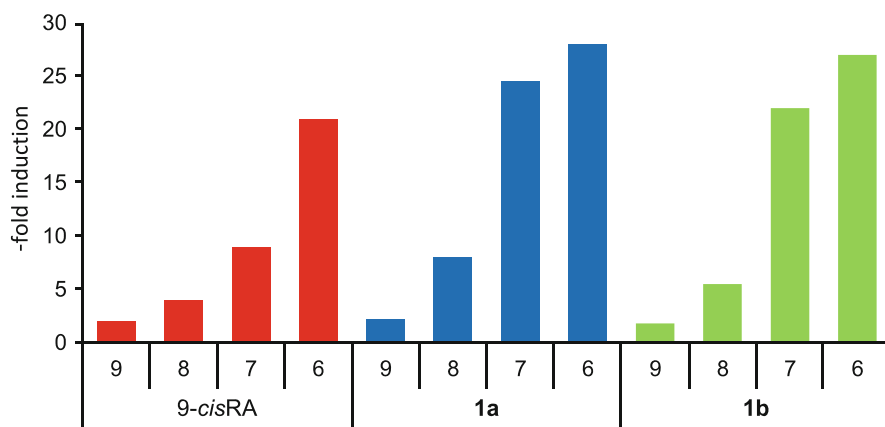
Figure 17 shows a superposition of the tetrahydronaphthalene skeleton of **3a** and the tetrahydrodisilanaphthalene skeleton of **3b** (structures determined by single-crystal X-ray diffraction) [37]. Due to the longer covalent radius of the silicon atom, the two molecular frameworks differ in their size and shape. As shown by experimental [40] and computational [41] studies, disila-substitution of bexarotene (**3a**) also affects the electronic structure (electrostatic potential) of the bicyclic skeleton. As the tetrahydronaphthalene ring of **3a** and structurally related retinoid agonists is known to play a crucial role in receptor binding, the structural and electronic differences between bexarotene (**3a**) and disila-bexarotene (**3b**) may affect the ligand–receptor interactions of these two C/Si analogues.

As a proof of principle, compounds **3a** and **3b** were studied for their RXR $\beta$  agonistic potency in a HeLa cell-based receptor assay [37]. The cell line was engineered to express a chimeric receptor composed of the DNA binding domain of the GALA4 yeast transcription factor and the ligand binding domain of human RXR $\beta$  (GALA4-hRXR $\beta$ ). In these studies, the natural ligand 9-*cis*-retinoic acid (9-*cis*RA) served as the positive control. As can be seen from Fig. 18, bexarotene (**3a**) is more potent than 9-*cis*-retinoic acid, and disila-bexarotene (**3b**) has a profile comparable to that of its carbon analogue **3a**. Thus, despite of the structural and electronic changes upon C/Si exchange, very similar RXR $\beta$  agonistic potencies of the C/Si analogues **3a** and **3b** were observed.

**Scheme 6** Synthesis of **3b****Fig. 16** Molecular structure of **3b** in the crystal [37]



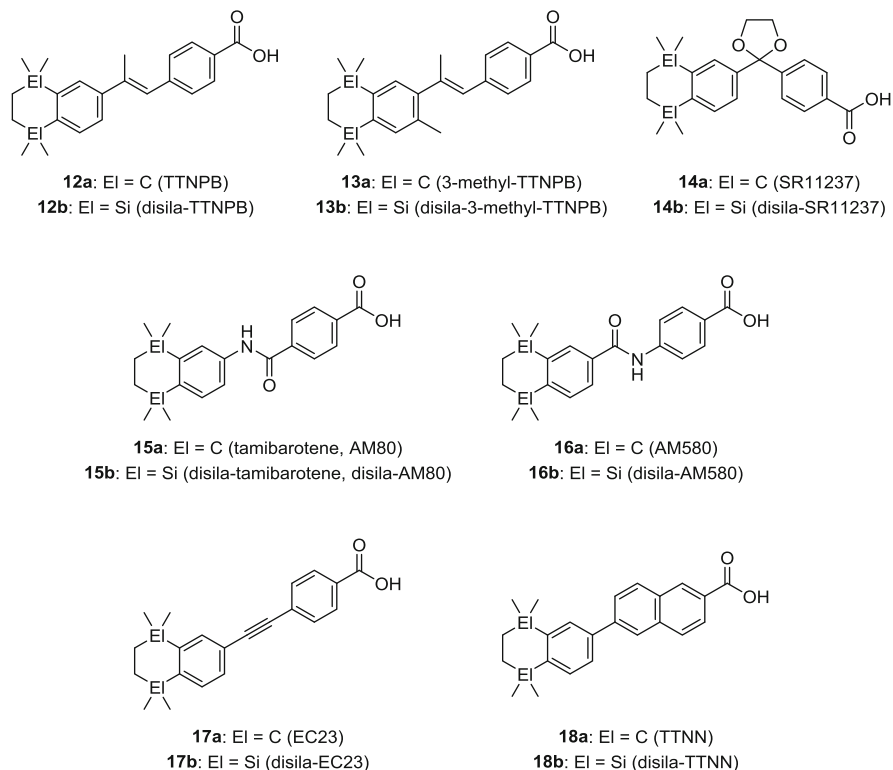
**Fig. 17** Superposition of the tetrahydro-naphthalene skeleton of **3a** (*dashed bonds*) and the tetrahydrodisilananaphthalene skeleton of **3b** (*solid bonds*) (hydrogen atoms are omitted for clarity) [37]



**Fig. 18** Concentration-dependent RXR $\beta$  agonistic potency of 9-cis-retinoic acid (9-cisRA), bexarotene (**3a**), and disila-bexarotene (**3b**). The data were obtained using a HeLa cell-based receptor assay [37]

As shown in a more recent study, bexarotene (**3a**) may partially act to induce cell differentiation and cell death pathways in pluripotent TERA2.cl.SP12 stem cells [42]. However, disila-bexarotene (**3b**) did not show the ability to induce stem cell differentiation in this study but may possess some enhanced functions over **3a**, such as cell death induction and regulation of cell numbers [42].

As disila-substitution of bexarotene (**3a**  $\rightarrow$  **3b**) did not lead to any detrimental effects on the biological activity in terms of its ability to activate target genes through the RXR receptor [37], these studies were extended, and a series of further disila-analogues of retinoid agonists (both RXR and RAR agonists) was synthesized and studied for their biological activity: disila-TTNPB (**12b**) [43], disila-3-methyl-TTNPB (**13b**) [43], disila-SR11237 (**14b**) [41], disila-tamibarotene (disila-AM80, **15b**) [44], disila-AM580 (**16b**) [44], disila-EC23 (**17b**) [45], and disila-TTNN (**18b**)

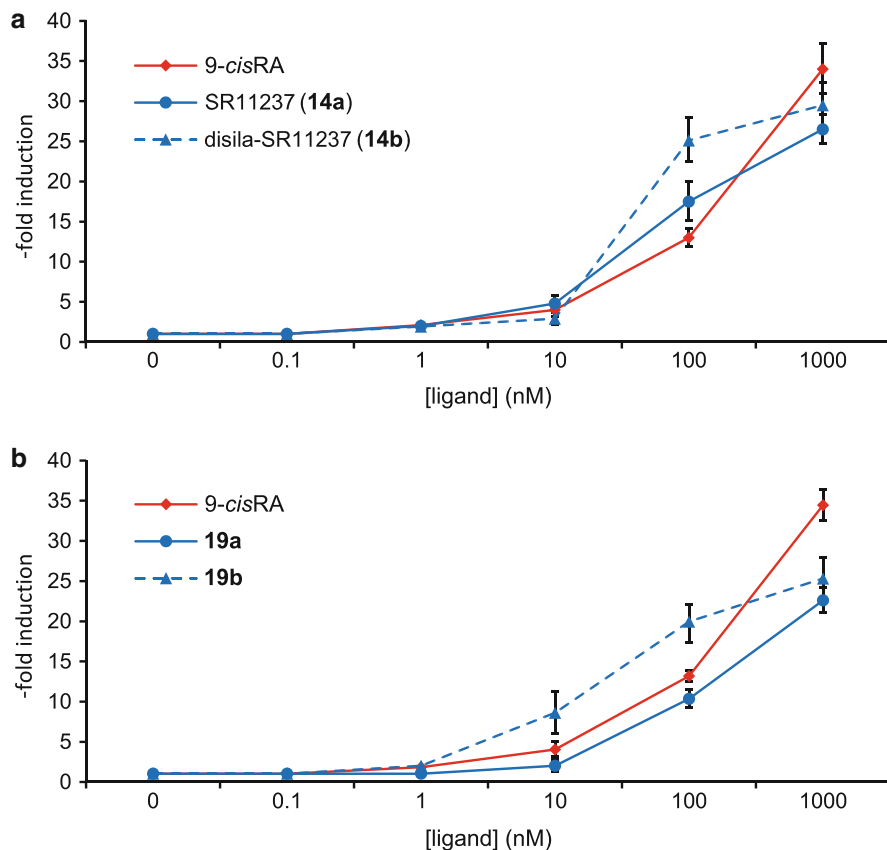


**Fig. 19** Chemical structures of the C/Si pairs **12a/12b–18a/18b**

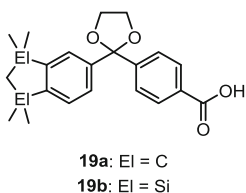
[45] – the silicon analogues of the retinoid agonists TTNPB (**12a**), 3-methyl-TTNPB (**13a**), SR11237 (**14a**), tamibarotene (AM80, **15a**), AM580 (**16a**), EC23 (**17a**), and TTNN (**18a**), respectively (Fig. 19).

In these studies, some of the tested silicon compounds showed an enhanced agonistic potency compared to the parent carbon compounds. For example, as can be seen from Fig. 20, 2-fold sila-substitution of the pan-RXR-selective retinoid agonist SR11237 (**14a** → **14b**) resulted in an increased RXR $\beta$  agonistic potency [41]. Whereas the dose–response curves of the C/Si analogues **14a** and **14b** are very similar up to 10 nM, there is a stronger activation by the silicon compound **14b** at higher concentrations. This difference in the activities is even more pronounced for the related C/Si analogues **19a** and **19b** (Fig. 21) [41]. As shown in Fig. 20, 2-fold sila-substitution of **19a** (→ **19b**) resulted in a 10-fold increased RXR $\beta$  agonistic potency. It is worth noting that at low concentrations **19b** is even more potent than the natural ligand 9-*cis*RA, which served as the positive control. The 10-fold higher activity of the silicon compound **19b** could be explained with an increased receptor affinity of **19b**, which is in line with the results of crystal structure analyses of the ternary complexes formed by **19a** and **19b**, respectively, with the ligand binding domain of hRXR $\alpha$  and a peptide of the co-activator TIF2/GRIP1 [41]. These



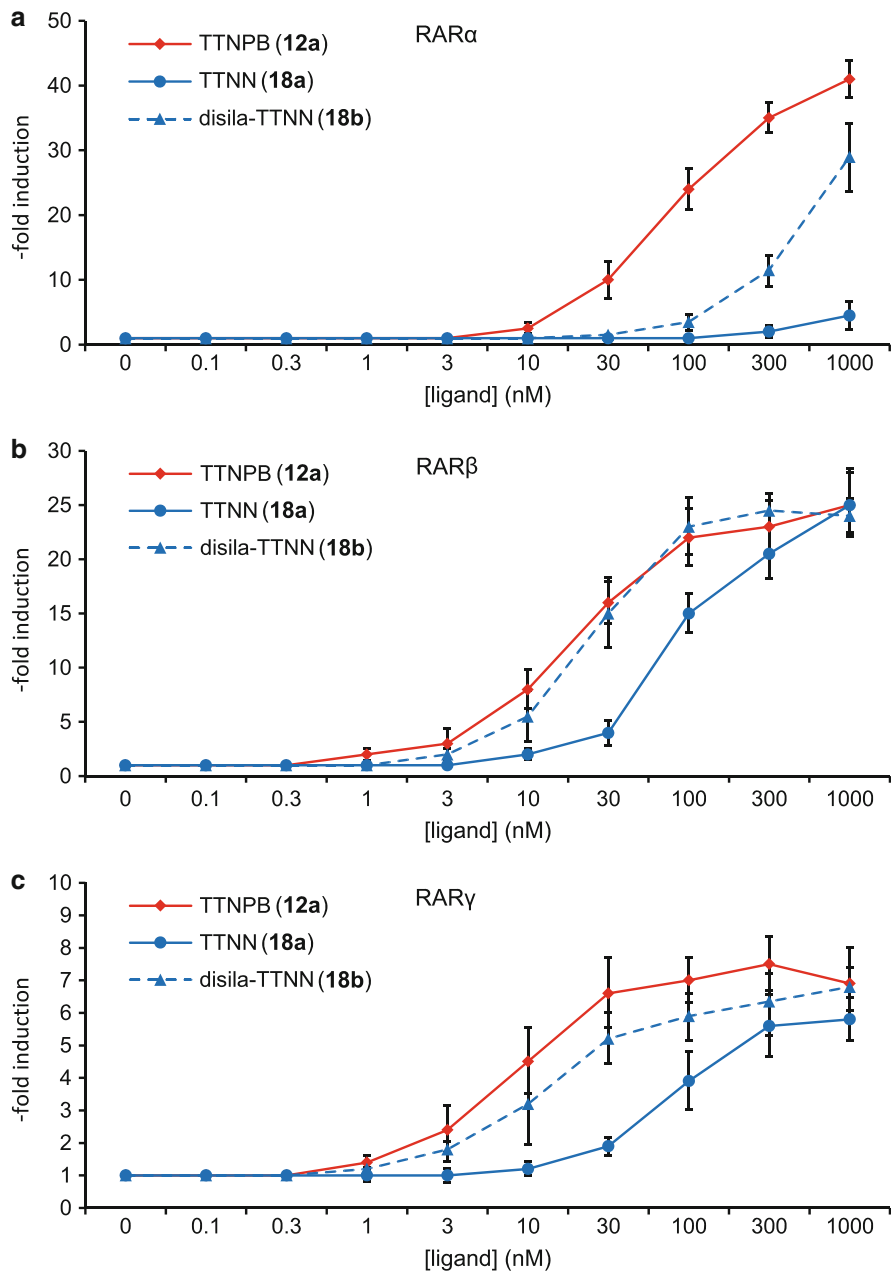


**Fig. 20** Dose–response curves for the transcription activation of RXR $\beta$  by (a) SR11237 (**14a**) and disila-SR11237 (**14b**) and by (b) **19a** and **19b** [38]. 9-*cis*-Retinoic acid (9-*cis*RA) served as the positive control. For the HeLa cell-based receptor assay, see [37]

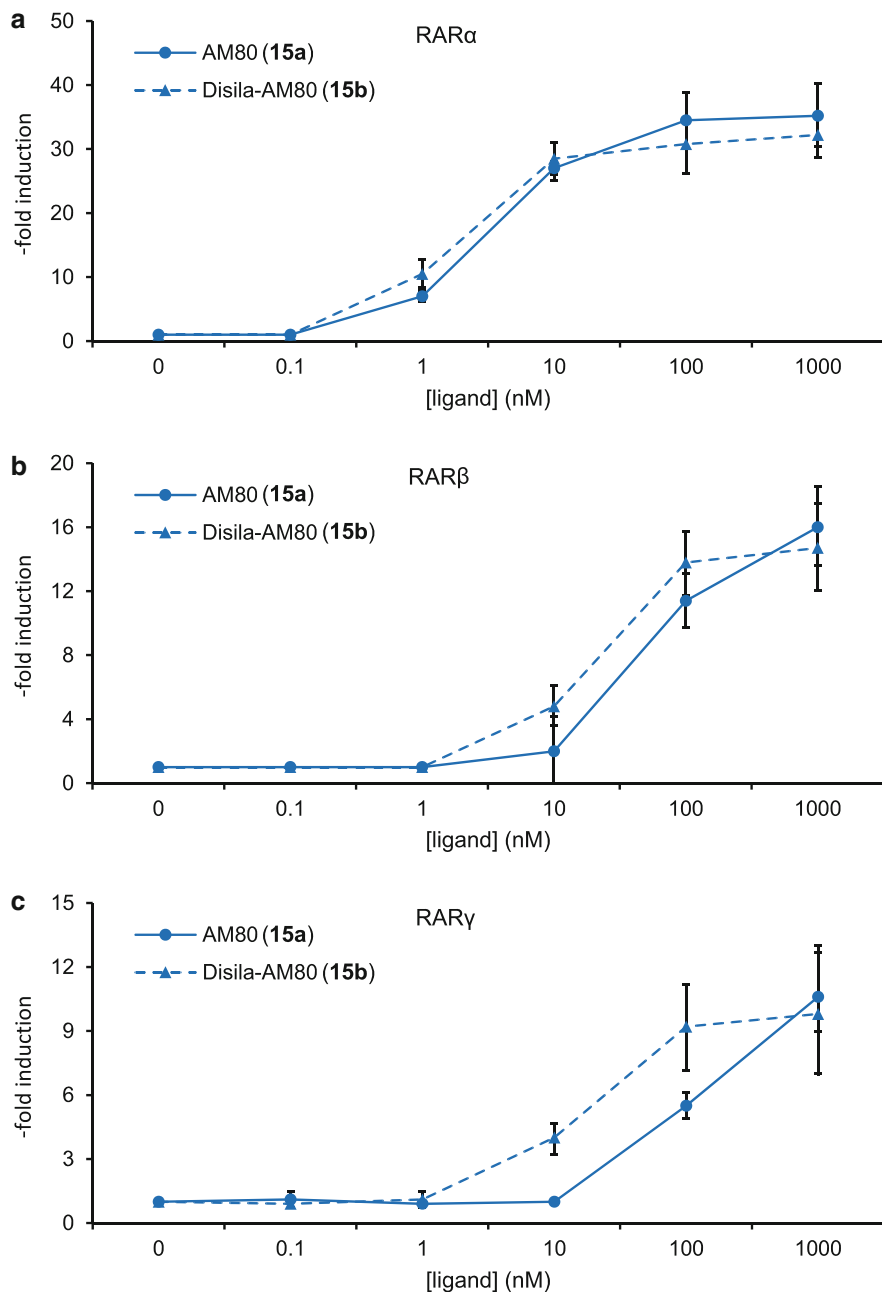


**Fig. 21** Chemical structures of the C/Si analogues **19a** and **19b**

structural investigations revealed additional interactions of **19b** with the H7 and H11 residues. In contrast, crystal structure analyses of the ternary complexes formed by TTNPB (**12a**) and disila-TTNPB (**12b**), respectively, with the ligand binding domain of hRAR $\beta$  and a peptide of the co-activator SRC-1 revealed nearly



**Fig. 22** Dose-response curves for the transcription activation of (a) hRAR $\alpha$ , (b) hRAR $\beta$ , and (c) hRAR $\gamma$  by TTNN (18a) and disila-TTNN (18b) [45]. TTNPB (12a) served as the positive control



**Fig. 23** Dose–response curves for the transcription activation of (a) hRAR $\alpha$ , (b) hRAR $\beta$ , and (c) hRAR $\gamma$  by tamibarotene (AM80, **15a**) and disila-tamibarotene (disila-AM80, **15b**) [44]

isomorphous structures [43]. This finding correlates with the very similar agonistic potencies of the C/Si analogues **12a** and **12b** at RAR $\alpha$ , RAR $\beta$ , and RAR $\gamma$ , respectively. Compounds **12a** and **12b** were also studied as differentiation- and apoptosis-inducing agents on the basis of their RAR $\alpha$  receptor-activation potential [43]. Upon exposure of NB4 acute promyelocytic leukemia cells to TTNPB (**12a**) and disila-TTNPB (**12b**), respectively, the same strong induction of differentiation and apoptosis of these cells was observed for **12a** and **12b**, which is again in line with the results of the abovementioned structural investigations.

As can be seen from Fig. 22, disila-substitution of the weak retinoid agonist TTNN (**18a**  $\rightarrow$  **18b**) resulted in a significant gain in transcription activation potential for hRAR $\alpha$ , hRAR $\beta$ , and hRAR $\gamma$  [45]. Disila-TTNN (**18b**) can be regarded as a powerful RAR $\beta,\gamma$ -selective retinoid agonist, displaying a similar potency as the powerful reference compound TTNPB (**12a**), which served as the positive control.

In the case of the RAR $\alpha$ -selective retinoid agonist tamibarotene (AM80, **15a**), disila-substitution ( $\rightarrow$  **15b**) did affect not only the agonistic potency but also the retinoid receptor selectivity [44]. Figure 23 shows the dose–response curves of **15a** and **15b** in RAR $\alpha$ , RAR $\beta$ , and RAR $\gamma$  reporter cells. In the case of RAR $\alpha$ , both compounds inhibited virtually identical profiles, with EC<sub>50</sub> values around 5 nM. However, in the case of RAR $\beta$  and even more pronounced for RAR $\gamma$ , there was a significant left shift of the dose–response curves of the silicon compound **15b**. In the case of RAR $\gamma$ , disila-tamibarotene (disila-AM80, **15b**) displayed an up to 10-fold higher activity. As a result, the RAR $\alpha$  selectivity of tamibarotene (AM80, **15a**) is reduced upon disila-substitution. Similar results were also observed for the C/Si analogues AM580 (**16a**) and disila-Am580 (**16b**) [44].

### 3.4 Structures of Other Sila-Drugs

To demonstrate the structural diversity of other sila-analogues of drugs that have been synthesized and biologically characterized in recent years, a series of selected C/Si pairs is compiled in Fig. 24: the muscarinic antagonists **20a/20b** [46], **21a/21b** [46], and **22a/22b** [47]; the  $\sigma$  receptor ligands **23a/23b–26a/26b** [48]; the calcium channel antagonists niguldipine (**27a**) and sila-niguldipine (**27b**) [49]; the histaminic H<sub>1</sub> antagonists terfenadine (**28a**), sila-terfenadine-A (**28b**), sila-terfenadine-B (**28c**), disila-terfenadine (**28d**), fexofenadine (**29a**), and sila-fexofenadine (**29b**) [50]; the  $\sigma$  receptor ligands panamesine (**30a**) and sila-panamesine (**30b**) [51]; the GnRH antagonists AG-045572 (**31a**) and disila-AG-045572 (**31b**) [52]; the antiviral agents **32a/32b–35a/35b** [53]; the antiallergic agents **36a/36b** [54]; the  $\sigma$  receptor ligands **37a/37b–40a/40b** [55]; the estrogenic agents **41a/41b** [56]; and the androgen receptor antagonists LG190178 (**42a**), sila-LG190178 (**42b**), LG190176 (**43a**), and sila-LG190176 (**43b**) [57].

The collection of these compounds shall emphasize the high synthetic potential of modern organosilicon chemistry. This field is rapidly developing, and a huge variety of new classes of organosilicon compounds have been synthesized in recent

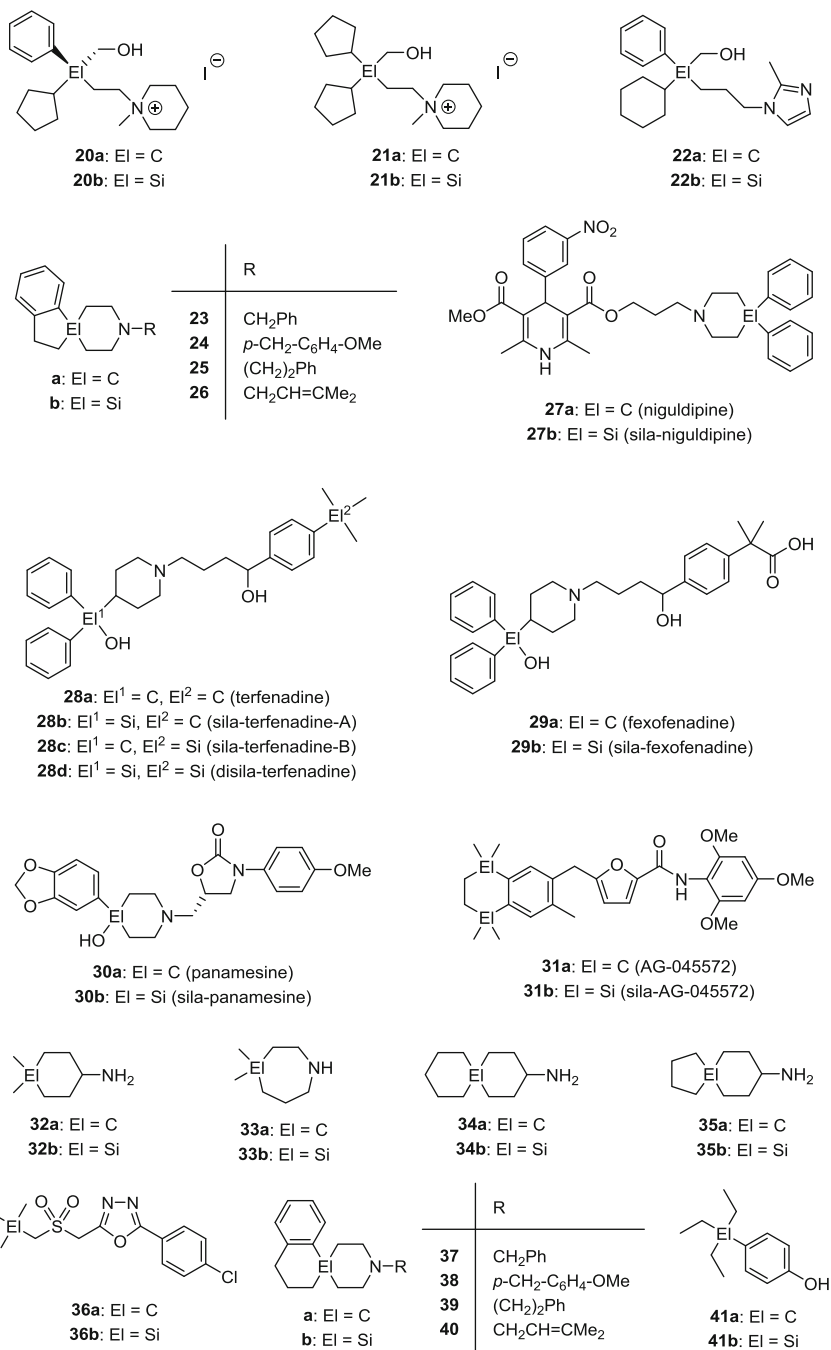
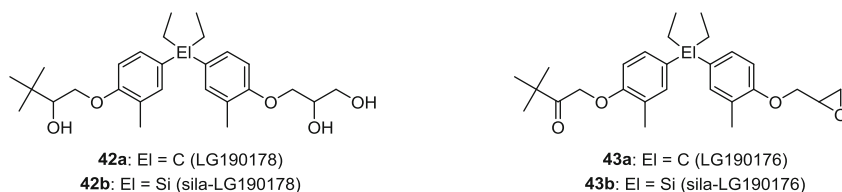


Fig. 24 (continued)



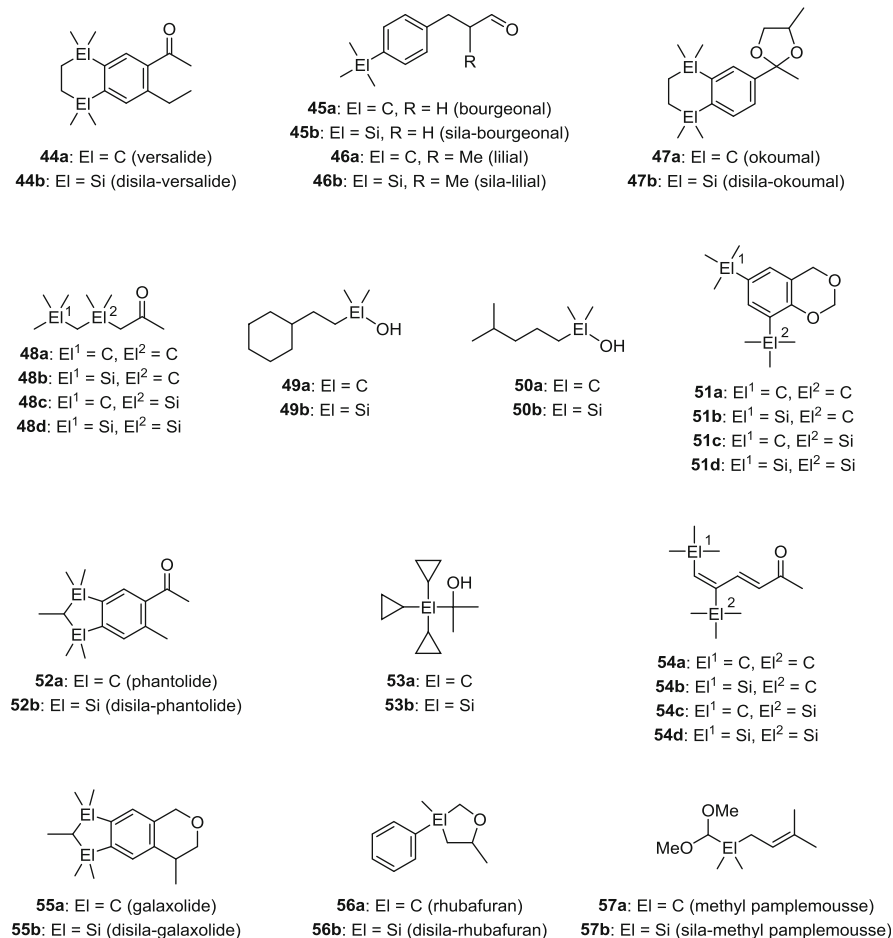
**Fig. 24** Chemical structures of the C/Si pairs **20a/20b–43a/43b**, **28a/28c**, and **28a/28d**

years, and many novel silicon-based molecular scaffolds for drug design will be seen in the near future. In this context, it should also be mentioned that there is an efficient chemical industry, with a special expertise in organosilicon chemistry, that supports this development and can supply pharmaceutical industry with the silicon-based fine chemicals needed.

## 4 Appendix: Sila-Substitution of Odorants

In context with the studies reported in this article, it should be mentioned that the carbon/silicon switch strategy has also successfully been used for the design of silicon-based odorants. As odorant recognition is also based on ligand–receptor interactions (in this case between odorants and olfactory receptors), this approach follows similar principles as described for the design of sila-drugs. To demonstrate the structural diversity of sila-analogues of odorants that have been synthesized and olfactorily characterized in recent years, a series of selected C/Si pairs is compiled in Fig. 25: the musk odorants versalide (**44a**) and disila-versalide (**44b**) [58]; the lily-of-the-valley odorants bourgeonal (**45a**), sila-bourgeonal (**45b**), lilial (**46a**), and sila-lilial (**46b**) [59]; the ambergris odorants okoumal (**47a**) and disila-okoumal (**47b**) [60]; the woody-ambery odorant **48a** and its sila-analogues **48b–48d** [61]; the floral odorants coranol (**49a**), sila-coranol (**49b**), dimetol (**50a**), and sila-dimetol (**50b**) [62]; the musk odorant **51a** and its sila-analogues **51b–51d** [62]; the musk odorants phantolide (**52a**) and disila-phantolide (**52b**) [63]; the patchouli odorants **53a** and **53b** [64]; the musk odorant **54a** and its sila-analogues **54b–54d** [65]; the musk odorants galaxolide (**55a**) and disila-galaxolide (**55b**) [66]; and the grapefruit odorants rhubafuran (**56a**), sila-rhubafuran (**56b**) [67], methyl pamplemousse (**57a**), and sila-methyl pamplemousse (**57b**) [68].

Sila-substitution of odorants can alter and, ideally, optimize the olfactory properties by affecting the binding affinity to the olfactory receptors, which can change both the olfactory profile and the odor threshold. These are quite promising perspectives for fragrance industry, which indeed has started to use the high potential of the carbon/silicon switch strategy for odorant design and development.



**Fig. 25** Chemical structures of the C/Si pairs **44a/44b–57a/57b**, **48a/48c**, **48a/48d**, **51a/51c**, **51a/51d**, **54a/54c**, and **54a/54d**

## 5 Summary and Outlook

Following the first pioneering studies on biologically active organosilicon compounds five decades ago, silicon chemistry is nowadays accepted to be a novel source of chemical diversity in drug design. The carbon/silicon switch strategy, i.e., the strategic replacement of a carbon atom with a silicon atom (sila-substitution) within a well-known drug, with the rest of the molecule being identical, is one of the methods that are currently used for the design and development of new silicon-based drugs. As members of Group 14 of the periodic table, the elements carbon and silicon show many similarities in their chemical properties, but there are also some fundamental differences that can lead to striking differences in the physicochemical

and biological properties of drugs and their corresponding sila-analogues. In general, the sila-analogues share the same mode of action as the parent carbon compounds (carbon/silicon bioisosterism) but may have altered biological properties. Generally, sila-substitution can affect and, ideally, improve the pharmacological potency and selectivity, the pharmacodynamics, and the pharmacokinetics. Thus, the strategic sila-substitution of existing drugs is a very promising approach for the search of new drug candidates that have beneficial properties. The carbon/silicon switch strategy is a very powerful tool for both (1) the evaluation of structure–activity relationships in basic research and (2) the development of new silicon-based drugs for clinical applications. In this context, it is important to note that up to now there are no indications for a silicon-specific toxicity associated with organosilicon compounds, in contrast to the element-associated toxicity of organogermanium, tin, and lead compounds. This lack of inherent toxicological issues with silicon and the increasing clinical experience with organosilicon compounds will stimulate the search for new silicon-based drugs for clinical applications.

When assessing the potential of the carbon/silicon switch strategy for the design and development of new silicon-based drugs, some fundamental limitations have also to be mentioned. There are chemistry-driven rules in terms of both synthetic accessibility and chemical stability that dictate whether or not and where a silicon atom can be introduced into a given drug scaffold. Synthetic organosilicon chemistry is a very rapidly developing field, and therefore, the issue “synthetic accessibility” will constantly change depending on the future developments in synthetic organosilicon chemistry, whereas the issue “chemical stability” is of course a constant factor.

The perspectives of the carbon/silicon switch strategy for pharmaceutical industry look quite promising. Generally, incorporation of silicon into a known drug can affect the pharmacological potency and selectivity, the pharmacodynamics, and the pharmacokinetics and therefore can lead to beneficial biological properties that can be used with a clear IP position. The carbon/silicon switch strategy allows to follow in the development footsteps of the already optimized parent carbon compound and thereby to speed up the development process of the sila-analogue. There is a very efficient chemical industry, with a special expertise in organosilicon chemistry, that can supply pharmaceutical industry with the silicon-based fine chemicals needed. Nowadays, the carbon/silicon switch strategy is already an established tool in drug design and development in pharmaceutical industry, and it is anticipated that this approach will play an increasingly important role in the future.

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# Silicon Mimics of Unstable Carbon

Scott McN. Sieburth

**Abstract** Silicon–carbon bonds are unknown in nature, yet the search for bioactive organosilanes has a rich and successful history. Substitution of silicon for a stable quaternary carbon in biologically active molecules often leads to bioactive organosilanes. An alternative approach is the substitution of silicon for an unstable carbon, such as a hydrated carbonyl. The proclivity of carbon to favor a carbonyl over a 1,1-diol is reversed for silicon. Tetrahedral, hydrated carbonyls are ubiquitous intermediates in the reactivity of carbonyl compounds including many enzymatic reactions, and hydrolase enzymes are critical mediators of a broad range of biological processes. Proteases, one group of hydrolase enzymes, can be potently inhibited by silanediol-based peptide mimics when the silanediol substitutes for the hydrated carbonyl of amide bond hydrolysis. This chapter outlines the key parameters for bioactive organosilanes, the evolution of the silanediols as protease inhibitors, the supporting chemistry, and the current status.

**Keywords** Angiotensin-converting enzyme, Chymotrypsin, Enzyme inhibitor, Factor XIa, HIV, Hydrolase inhibitor, Hydrosilylation, Protease inhibitor, Silanediol, Silyl anion, Sulfinimine, Thermolysin

## Contents

1	Introduction .....	62
1.1	Discovery of Bioactive Organosilanes .....	62
1.2	Silicon as a Substitute for Carbon .....	62
1.3	The Pyrethrin Pathway .....	63

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1.4 Silanols .....	64
1.5 Silanols, Silanones, and Siloxanes .....	65
1.6 Protease Enzymes and Their Inhibition .....	66
2 Silanediols in Drug Design .....	67
2.1 Synthesis of Silanediol Peptidomimetics .....	68
3 Summary and Future Prospects .....	77
3.1 Mechanistic Considerations and Future Challenges .....	77
References .....	81

## 1 Introduction

### 1.1 *Discovery of Bioactive Organosilanes*

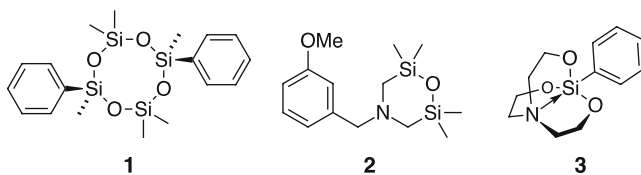
Among the elements most closely associated with bioactive molecules – carbon, hydrogen, nitrogen, and oxygen – only oxygen and hydrogen are present in the Earth’s crust at substantial levels. Oxygen is the most abundant element by weight at 47 % and hydrogen tenth most abundant at 0.14 %. Carbon is 16th (0.03 %) and nitrogen 21st (0.005 %). Silicon is the second most abundant element (28 % of the Earth’s crust), and while silicon is the element most similar to carbon, virtually all naturally occurring silicon is in the form of silicates, bonded only to oxygen atoms (silicon carbide, which has no Si–O bonds, is naturally occurring but rare substance, discovered in the 1950s [1]). Following the emergence of organosilicon chemistry more than a century ago [2], a search for biologically active organosilanes emerged, a search that continues today ([3]; for reviews, see [4–13]). The absence of naturally occurring substances with bonds between silicon and carbon makes bioactive organosilanes all the more interesting.

There are two fundamental approaches for discovery of novel bioactive molecules: design and random screening. Random screening is an extraordinarily useful approach for discovering breakthrough bioactive molecules and uses for otherwise arbitrary compounds, such as the laundry-additive-turned-billion-dollar-herbicide Roundup [14]. Random screening will discover bioactive structures that could not be derived through a design process, but for the most part, intellectual involvement by chemists comes only after identification of a lead molecule.

Random screening presumably was responsible for discovery of bioactive organosilanes for which there are no carbon analogs, such as cisobitan (**1**) [15], SAN 58–112 (**2**) [16], and phenyl silatrane (**3**) (Fig. 1) [17].

### 1.2 *Silicon as a Substitute for Carbon*

In contrast, the design process requires, by its very nature, involvement of chemists from the outset. One of the most reliable ways to prepare a biologically active organosilane is replacement of a carbon atom by a silicon atom (see reference

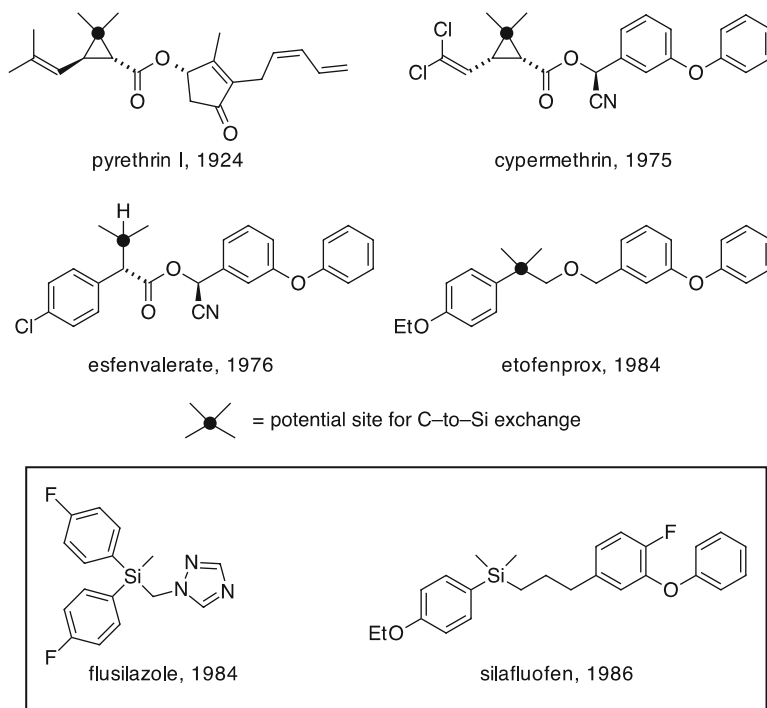


**Fig. 1** Bioactive organosilanes without carbon analogy, identified by random screening

[4–13], especially [7] and [12]). This is arguably the most subtle change one can make in terms of size and electronegativity (outside of hydrogen–deuterium exchange), but not all carbons are replaceable by silicon. Silicon does not form stable double bonds [18, 19]. The Si–O, Si–N, and Si–halogen bonds are strong, but they hydrolyze readily [20]. Silicon–hydrogen bonds are readily oxidized *in vivo* [21]. Replacement of a quaternary carbon by silicon is therefore the most readily realized approach to bioactive organosilane discovery, yet even swapping quaternary carbon with silicon has limitations. These parameters are nicely illustrated by the naturally occurring pyrethrin insecticides and the evolution of the synthetic, commercial analogs of these natural products (Fig. 2).

### 1.3 The Pyrethrin Pathway

Pyrethrin I is an insecticidal compound isolated from the common chrysanthemum flower (Fig. 2) [22]. The pyrethins, however, are not light stable and therefore unsuitable for field use. Cypermethrin is a potent, light-stable commercial analog that has been used in the field with great success [23]. In both of these molecules, the sole quaternary carbon (black dot) cannot be replaced by silicon because silicon in a three-membered ring is extremely unstable [24, 25]. In addition, this quaternary carbon is alpha to a carbonyl, and silicon alpha to a carbonyl is also unstable [26]. In the third pyrethroid, esfenvalerate [27], the dimethylcyclopropane has been replaced by an isopropyl group, but this structure remains unsuitable for a C to Si exchange (at the black dot) for two reasons: the resulting Si–H bond would be rapidly oxidized [21] and the silane remains adjacent to a carbonyl. In the fourth pyrethroid etofenprox, only the gem-dimethyl group and the central oxygen atom remain from the natural pyrethrin I [28]. Etofenprox does retain the quaternary carbon, not in a cyclopropane, and therefore was the first analog of the natural product in which silicon substitution was possible. Replacement of this quaternary carbon with silicon retained insecticidal properties, and the resulting silafluofen is a commercial insecticide [29, 30]. Silafluofen and the agricultural fungicide flusilazole [31] are currently the only organosilanes manufactured because of their biological activity.



**Fig. 2** Naturally occurring insecticide pyrethrin I and three carbon-based commercial analogs. Years of discovery are given. Only etofenprox is compatible with silicon substitution. Two organosilanes are produced commercially for their biological activity: fungicide flusilazole and insecticide silafluofen

## 1.4 Silanols

Silicon ethers, the Si–O–C linkage, have stability that is related to the nature of the component alcohol and the silane components [32]. Some silane-derivatized alcohols and amines have been found to enhance the bioactivity of the parent compounds, presumably by hydrolysis *in vivo* to the alcohol/amine and the corresponding silanol (see reference [4–13], especially [7] and [12]). Some silanols have been found to have very intriguing biological properties, most notably the hypnotic properties of diphenylsilanediol **4** [33] and sila-haloperidol **5** [34, 35] (Fig. 3). The hydroxyls of silanols exchange rapidly in the presence of water, but they remain silanols (see Fig. 12). The primary instability of silanols is dehydration and formation of siloxanes, structures containing the Si–O–Si bonding arrangement (see Fig. 4). Siloxanes are generally more stable than their Si–O–C counterparts (see Fig. 1). The many useful properties of siloxanes form the basis of the large organosilane industry [36].

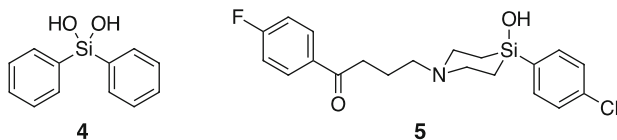


Fig. 3 Bioactive organosilanols

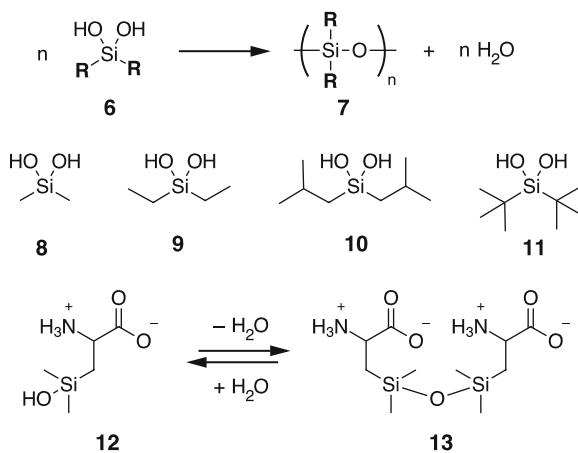
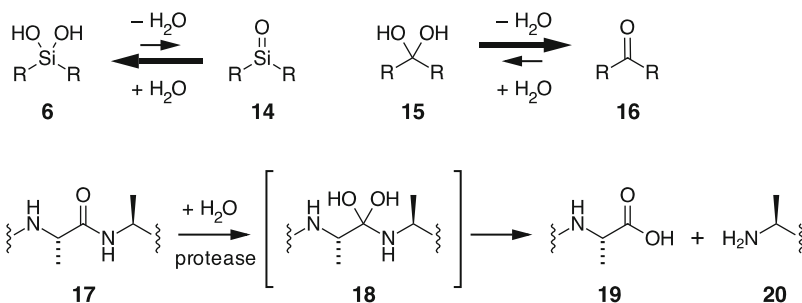


Fig. 4 Silanediols can readily dehydrate to form siloxanes (silicones), but steric hindrance can slow or prevent oligomerization

### 1.5 Silanols, Silanones, and Siloxanes

Silanediols (6) are best known as precursors of siloxanes 7 (aka silicones), the product of a condensation reaction that is catalyzed by both acid and base (Fig. 4). The polymerization of dimethylsilanediol 8 is reported to be spontaneous, with even very pure 8 being unstable [37]. Steric hindrance plays a significant role here; dimethylsilanediol 9 polymerizes at one tenth the rate of 8 [38, 39]. Diisobutylsilanediol 10 is a liquid crystal, illustrating both stability and the outstanding ability of silanols to be hydrogen bond donors and acceptors [40, 41]. With sufficient steric bulk, as in di-*tert*-butylsilanediol 11, even forcing conditions do not lead to polymerization. Solvation of silanols can also play a significant role as well. Tacke found that dimethylsilanol-substituted alanine 12 formed siloxane 13 when it was isolated, but dissolving 13 in water gave a spontaneous, quantitative hydrolysis to yield 12 [42, 43]. This finding suggests that the insolubility of most siloxanes in water adds to their hydrolytic stability.

The stability of simple silanediols like 10 provided encouragement for efforts to design biologically active analogs that would remain monomeric [44, 45]. An early example of a bioactive silanediol is 4 (Fig. 3) which has barbiturate-like properties [33].



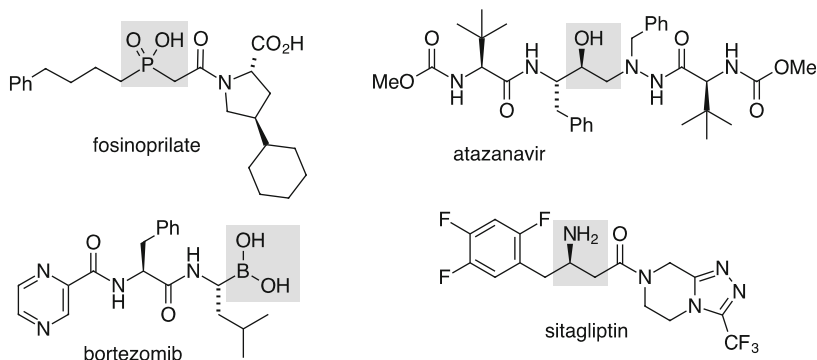
**Fig. 5** Silanones **14** are very unstable toward hydration, whereas ketones **16** are more stable than their hydrates. Amides such as **17**, much less prone toward hydration than ketones, are substrates for protease enzymes

Silicones (e.g., **7**) were first prepared more than 100 years ago in an attempt to make silicon analogs of ketones, inadvertently illustrating the instability of double bonds to silicon (**14**) [46]. This contrasts with the proclivity of 1,1-diols **15** to dehydrate and form carbon–oxygen double bonds **16**. The stability of carbonyls relative to their hydrates is particularly pronounced for carboxylic acid derivatives, especially amides such as **17**. Peptides **17** are polyamides that can be hydrolyzed by protease enzymes to their respective acid **19** and amine **20** under mild physiological conditions. Proteases catalyze the addition of water (or alcohol or thiol) to the amide carbonyl, in part by stabilizing the tetrahedral intermediate **18** [47]. Tight binding, nonhydrolyzable mimics of this tetrahedral group can be effective inhibitors of these enzymes and therefore pharmaceuticals [48–50].

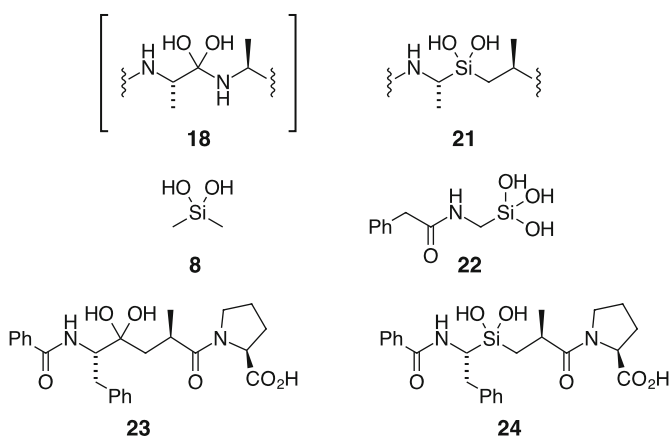
## 1.6 Protease Enzymes and Their Inhibition

Protease enzymes mediate many important biological processes and are pharmaceutical targets for a broad range of diseases [48–50]. Protease inhibitors as pharmaceuticals were first introduced to treat hypertension nearly 40 years ago [51]. Figure 6 shows four examples of commercial protease inhibitors, with gray boxes highlighting the functional group that replaces and mimics the tetrahedral intermediate of amide hydrolysis **18**. Fosinoprilate utilizes a phosphinic acid to replace the hydrated carbonyl and interact with the active site zinc ion of angiotensin-converting enzyme [52, 53]. Inhibiting this metalloprotease lowers blood pressure [54]. Atazanavir is an inhibitor of the HIV protease, an aspartic protease, and prevents reproduction of the HIV virus [55, 56]. In this case, a hydroxyethylene group replaces the hydrated amide and hydrogen bonds to the active site aspartic acids. The boronic acid bortezomib is a treatment for cancer; the electrophilic boron binds to the nucleophilic threonine hydroxyl group at the active site [57]. Sitagliptin binds to the active site of a serine protease (DPP-4) and is a treatment for diabetes [58].





**Fig. 6** Examples of commercial protease inhibitor drugs used for the treatment of hypertension (fosinoprilate), HIV infection (atazanavir), cancer (bortezomib), and diabetes (sitagliptin)



**Fig. 7** Silanediol **21** as an isostere of hydrated amide **18**. Compounds **8** and **22** had been found to be ineffective as hydrolase inhibitors. Redesigning protease inhibitor **23** (shown as the ketone hydrate) gave the silanediol inhibitor **24**

## 2 Silanediols in Drug Design

Silanediols **21** seemed nearly ideal isosteres of the hydrated amide carbonyl **18**, but at the beginning of our investigations, this idea had only been investigated sparingly (Fig. 7) [59]. The testing of silanediols as hydrated carbonyl mimics was largely suppressed by the general knowledge of the instability of silanediols toward polymerization (Fig. 5) and a dearth of methods for preparing silanediols with functionality and stereochemistry.

Prior to our studies, two silanols had been evaluated as inhibitors of hydrolase enzymes, **8** and **22**. An aqueous solution of dimethylsilanediol **8** was found to be ineffective as an inhibitor of the metalloprotease angiotensin-converting enzyme at

300 mM [60]. In addition, silanetriol **22** was prepared as a potential inhibitor of a beta-lactamase and was inactive at the highest concentration tested, 0.1 mM [61].

Our first vehicle for testing structure **21** as a nonhydrolyzable analog of **18** and the centerpiece of a protease inhibitor was silanediol **24**, by analogy with **23**. Structure **23** is shown as the hydrate of a ketone that was tested as a replacement for an Ala-Phe dipeptide and was found to be a 1 nM inhibitor of angiotensin-converting enzyme [62]. The hydrate **23** is presumably the form that binds at the ACE active site [63]. The silanediol in **23** was anticipated to have a steric environment that would inhibit oligomerization, shielded on each side by branched alkyl substituents, not unlike diisobutylsilanediol **10** (Fig. 4).

## 2.1 Synthesis of Silanediol Peptidomimetics

### 2.1.1 First-Generation Silanediol Syntheses

A synthesis of **24** was needed, including a strategy for carrying the silanediol through the synthetic manipulations that would be required. Diethers of silanes (silyl acetals) are rather unstable toward hydrolysis and were rejected as a viable form of protected silanediol [64]. Acid-catalyzed hydrolysis, “protodesilylation,” appeared to be an interesting alternative [65]. Acidic cleavage of Si–C bonds of aryl silanes is a classic electrophilic aromatic substitution reaction and therefore electronically tunable if simple phenyl groups proved to be less than perfect (see Fig. 9) [66]. The precursor of silanediol **24** therefore was diphenylsilane **25** (Fig. 8).

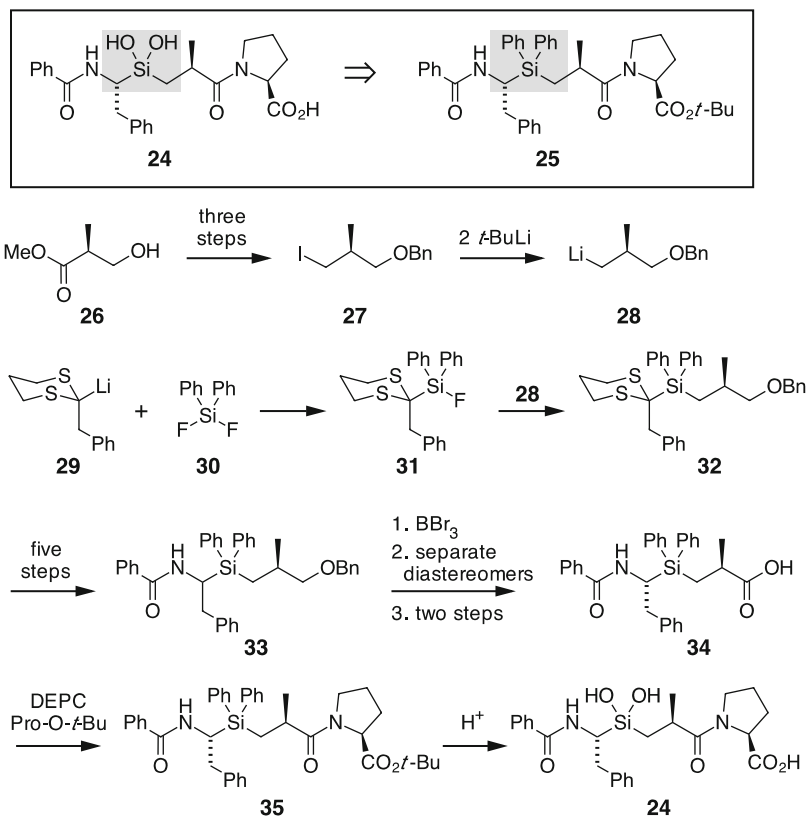
In this initial exploration of silanediol synthesis, difluorodiphenylsilane **30** was coupled with metalated dithiane **29** followed by the reaction with enantiomerically pure lithium reagent **28** [67]. The resulting silane **32** contains all the carbons of dipeptide mimic **24** but with functional group elaboration required. Lithium reagent (*R*)-**28** was prepared from commercially available (*S*)-ester **26**.

The dithiane in **32** was hydrolyzed to the corresponding ketone and then reduced to the corresponding alcohol. The nitrogen of **33** was introduced as a phthalimide using Mitsunobu chemistry, followed by hydrolysis and conversion of the amine to benzamide **33**.

Following cleavage of the benzyl ether of **33**, the diastereomers were separated and the alcohol of the (*S,R*) stereoisomer was oxidized to acid **34**. Condensation with the *tert*-butyl ester of (*S*)-proline gave silane **35** [67].

### 2.1.2 Silanediols from Diphenylsilanes

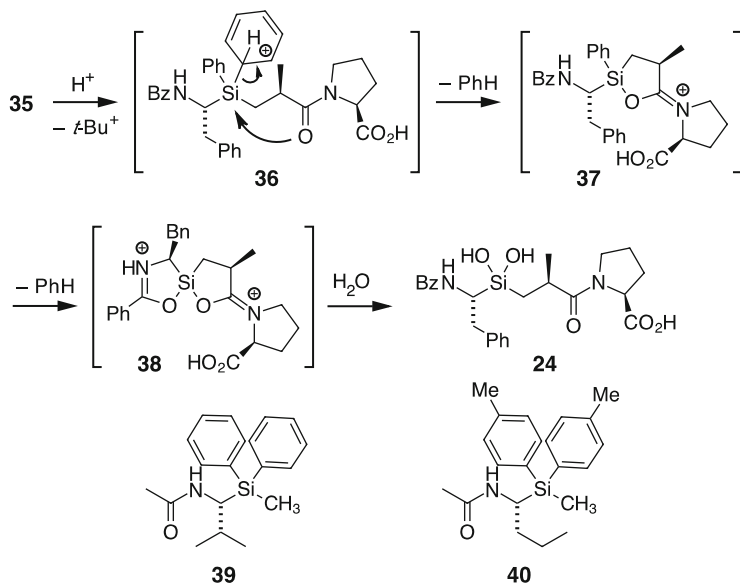
In the ultimate synthetic step, deprotection of **35** (Fig. 8) was accomplished by treatment with triflic acid, serving to remove the *tert*-butyl ester and both phenyl groups on silicon. The optimized sequence for isolation of silanediol **24** involved neutralization of the mixture with ammonium hydroxide and then conversion of the



**Fig. 8** ACE inhibitor **24** and its synthesis beginning with difluorodiphenylsilane **30**

silane to a crystalline difluorosilane with aqueous hydrofluoric acid [68]. Hydrolysis of the difluorosilane to the silanediol was readily accomplished by treatment with aqueous base.

Direct conversion of diarylsilanes to silane ditriflates using triflic acid is well known [69]; however, acidic hydrolysis of the diphenylsilane **35** and related compounds is believed to involve participation of the flanking amide carbonyls (Fig. 9). Beginning with *ipso*-protonation of the aromatic ring (**36**), loss of benzene requires a nucleophile to attack silicon, allowing departure of the benzene, a role readily fulfilled by either of the flanking amides. A second protonation–nucleophilic attack leads to **38**. Five-membered silyl ethers are strained, and therefore, these undergo a facile hydrolysis to the silanediol [70]. Participation of the amides is consistent with our observations of intermediates by <sup>1</sup>H NMR [71] and the work of Nielsen and Skrydstrup with monoamide **39** [72]. Whereas triflic acid hydrolysis of diamide **35** leads to **38** within minutes, and thus the silanediol **24**, treatment of monoamide **39** under similar conditions results in rapid loss of the first phenyl group and a very slow cleavage of the second [72]. Recent work by the Skrydstrup

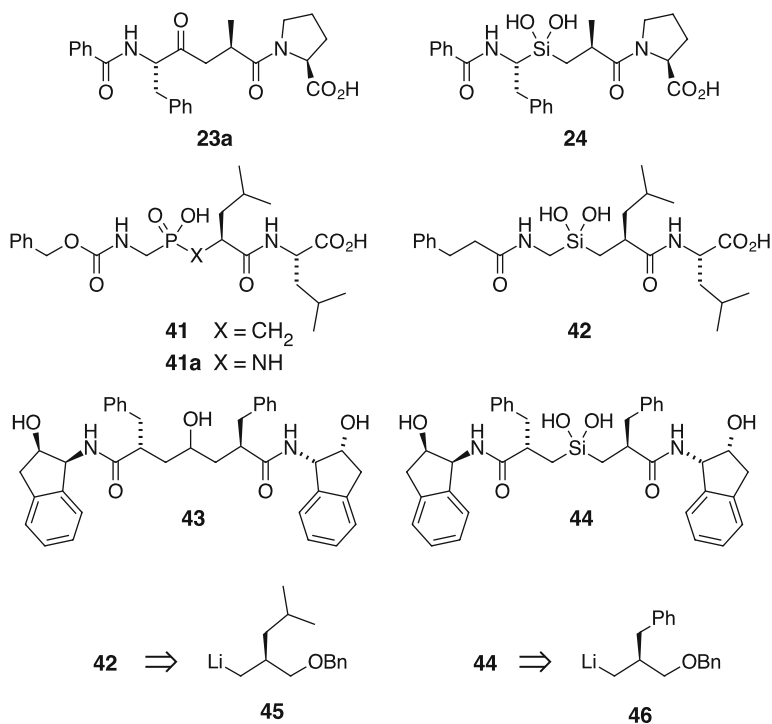


**Fig. 9** Acid-catalyzed hydrolysis of the diphenylsilane involves participation of the adjacent amides

group has shown that activation of the aromatic rings by alkyl substitution, as in **40**, allows for hydrolysis of both Si–aryl bonds with trifluoroacetic acid instead of triflic acid, presumably by lowering the activation energy for the *ipso*-protonation step (see also Fig. 20) [73].

### 2.1.3 Inhibition of Metallo- and Aspartic Proteases

Using chemistry related to the initial investigation (Fig. 8), a set of silanediols were prepared as analogs of other known protease inhibitors (Fig. 10). Silanediol **24**, an isostere of hydrated **23a** (see Fig. 7), was found to be an effective inhibitor of angiotensin-converting enzyme (ACE), a metalloprotease with a zinc ion at the active site [74]. Compound **23a** inhibits ACE with an  $\text{IC}_{50}$  of 1 nM, and silanediol **24** was found to inhibit this enzyme with a  $K_i$  of 3.8 nM [62]. Similarly, silanediol **42** was prepared as an analog of phosphinic acid **41**, an inhibitor of thermolysin [75, 76]. Silane **42** and phosphinic acid **41** are constructed around second row elements. As such, the silane and phosphorus units are closer in size than silicon is to carbon, but are also dramatically different in their acidities. Silanediols have  $\text{pK}_a$  values of approximately 12 [44, 77] and would be unionized at physiological pH, whereas phosphinic acids have a  $\text{pK}_a$  in the range of 3–4 and are anionic at physiological pH. Ionized phosphinic acid **41** would be expected to benefit from a Coulombic attraction to the active site zinc cation and silanediol would not. Nevertheless, phosphinic acid **41** inhibits thermolysin with an  $\text{IC}_{50}$  of 10 nM, and silane **42**



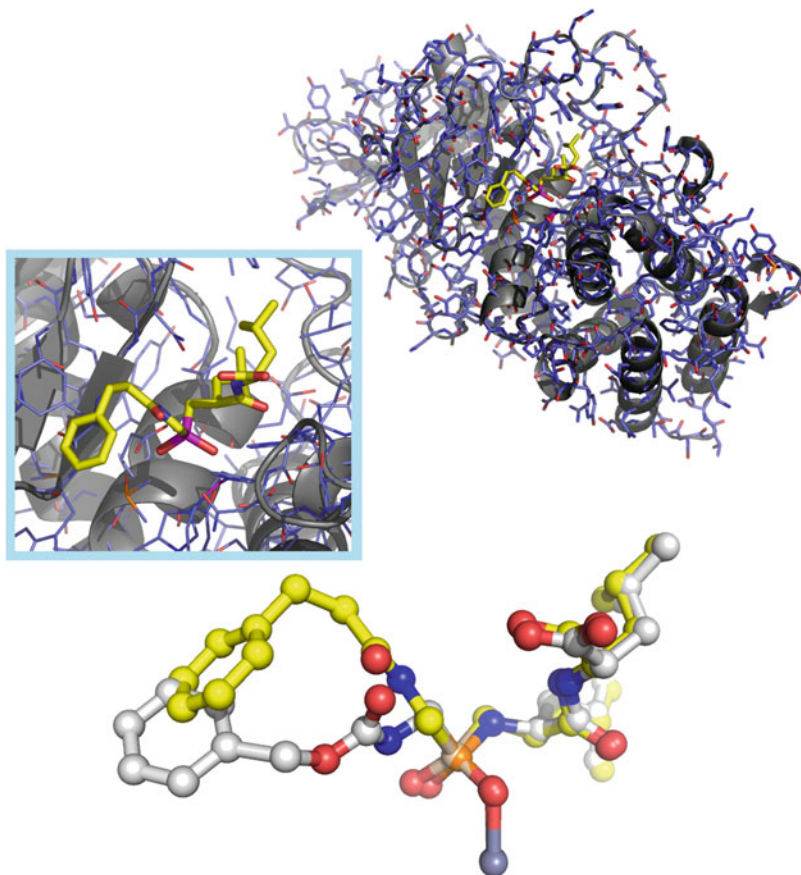
**Fig. 10** Silanediol inhibitors by analogy: known inhibitors (*left*) and their silane analogs (*right*)

inhibits thermolysin with a very similar IC<sub>50</sub> of 40 nM. A crystal structure of **42** bound to thermolysin has been obtained; see Fig. 11.

A single example of a silanediol aspartic protease inhibitor has been studied, compound **44**, prepared by analogy to HIV protease inhibitor **43** [78]. Carbinol **43** inhibits the HIV protease with an IC<sub>50</sub> of 0.38 nM, and silanediol **44** is sevenfold less potent, 2.7 nM. Side-by-side testing of **43** and **44** and the similarly potent and commercial HIV inhibitor indinavir [79] found that they all cross cell membranes with equal efficiency, as determined by their ability to prevent infection of cells by the HIV virus. These studies demonstrated that silanediol **44** has drug-like properties [78].

Syntheses of silanediols **42** and **44** followed paths similar to the preparation of **24** (Fig. 8), using enantiomerically pure lithium reagents **45** and **46**. While effective, this strategy was not efficient nor was it readily scalable. More efficient and catalytic methods have been developed recently and have been utilized for the silanediols that have followed the examples described below.

A crystal structure of silanediol **42** (PDB #1Y3G) bound to the active site of thermolysin found that the silanol oxygens are arrayed about the active site zinc in precisely the same way that the phosphorous oxygens are for the related phosphinamide **41a** (PDB #5TMN) (Fig. 11) [80]. Phosphinic acid **41** and

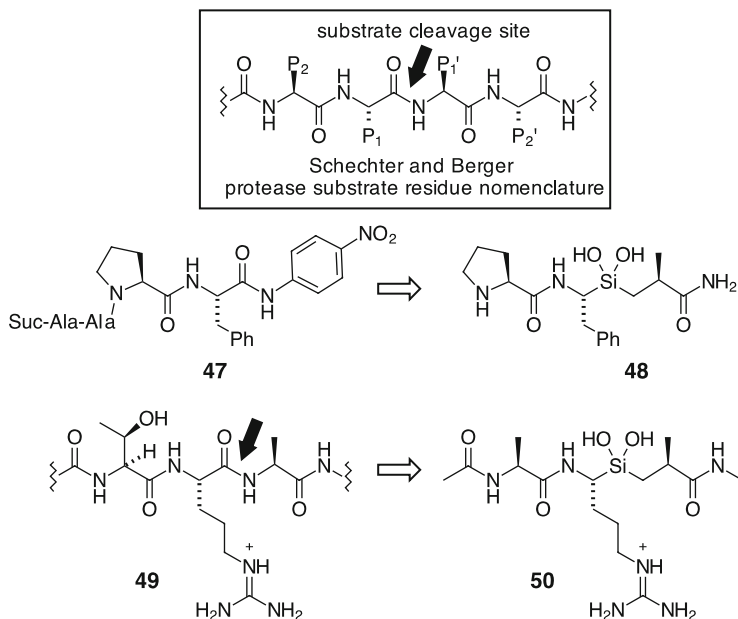


**Fig. 11** Crystal structure of silanediol **42** bound to thermolysin (PDB #1Y3G) and its overlay with **41b** also bound to thermolysin (PDB #5TMN). Silanediol **42** in yellow and **41b** in light gray. The overlay also shows the active site zinc in dark gray illustrating that they each touch the zinc in the same way

phosphinamide **41a** are both 10 nM inhibitors of thermolysin, but only the latter has been crystallized at the active site of thermolysin [75, 76, 81].

#### 2.1.4 Inhibition of Serine Proteases

Two of the more recent subjects of investigation are **48** and **50** (Fig. 12). Both of these structures target serine proteases, which are fundamentally different from the metallo- and aspartic proteases targeted initially. Metalloproteases have an active site zinc ion to coordinate with and activate an amide carbonyl. This zinc ion also delivers the water nucleophile (see inhibitors **23**, **24**, **41**, and **42**). Aspartic proteases have two aspartic acid residues at the active site, delivering the nucleophilic water



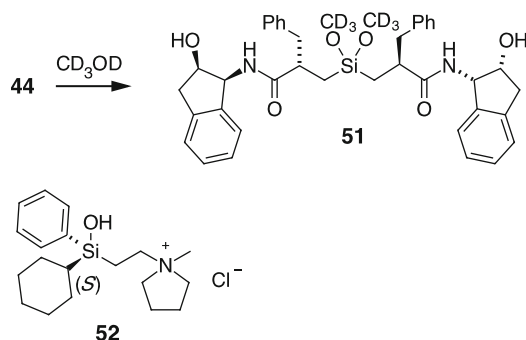
**Fig. 12** Protease substrate residue definitions and silanediol inhibitors by substrate analogy

molecule and stabilizing the hydrated carbonyl by hydrogen bonding (inhibitors **43** and **44**).

In contrast to the metallo- and aspartic proteases, serine proteases use a serine residue of the enzyme as the nucleophile. This reaction leads to departure of the amine portion of the peptide substrate, leaving the carbonyl esterified to the serine residue. In a second step, water hydrolyzes the ester, freeing the acid and regenerating the active site. Many serine protease inhibitors have electrophilic functionality that interact with the serine alcohol, but only carry recognition groups on one side of the active site nucleophile [82]. Using the Schechter and Berger descriptors [83], only the non-prime residues are represented in many serine protease inhibitors (Fig. 12). To adequately protect the silanediol moiety from oligomerization, we desired substitution at both  $P_1$  and  $P_1'$  sites to provide steric shielding. From the perspective of protease inhibitor selectivity – a major consideration in protease inhibitor design [84] – accessing recognition centers on both sides of the enzyme active site can be advantageous.

For the classic serine protease chymotrypsin, an enzyme that requires an aromatic side chain at  $P_1$  for substrate recognition, we modeled the silanediol inhibitor after the chromogenic substrate **47** and utilized a methyl group at  $P_1'$  (Fig. 12) [85]. Silanediol **48** was found to inhibit chymotrypsin with an  $IC_{50}$  of 107 nM [85].

A medically important serine protease, Factor XIa, was chosen as a second test case for study. Silanediol **50** was prepared as a potential inhibitor of Factor XIa, which is a key component of the coagulation cascade [86]. Silanediol **50** is a mimic of Factor IX, the substrate for Factor XIa, which is cleaved between Ala<sup>146</sup> and



**Fig. 13** Hydroxyls on silicon rapidly exchange with water and alcohols as evidenced by substitution by deuterio-methanol in **44** and the racemization of **52** in the presence of water

Arg<sup>145</sup> (**49**). The P<sub>1</sub> guanidinium ion of **49** is required for recognition by Factor XIa [87].

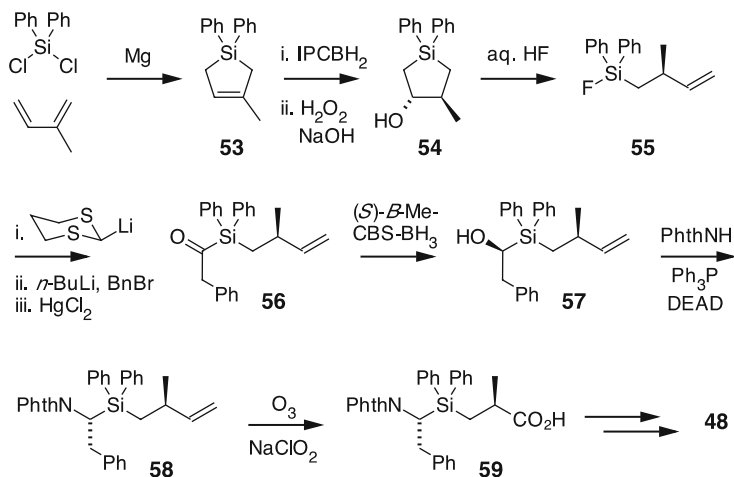
Electrophilic coordination to an active site serine nucleophile by a silanediol is inherently different from hydrogen bonding of the silanediol group in an aspartic protease active site or zinc ion coordination in metalloproteases. There was, however, ample experimental evidence for this kind of electrophilic role for silanols. We had observed a rapid exchange of silanediol hydroxyls by two equivalents of methanol-*d*<sub>4</sub> when **44** was dissolved in this solvent (Fig. 13) [71]. Additional evidence for rapid exchange of hydroxyls in silanols came from the work of Tacke. For example, enantiomerically pure silanediol **52** was found to be stable in aprotic solvents, but when exposed to aqueous solutions **52** rapidly racemized [88].

### 2.1.5 Second- and Third-Generation Silanediol Syntheses

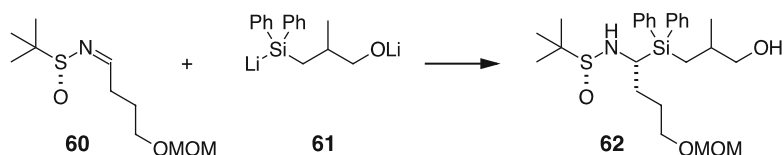
Initially, syntheses of **48** and **50** used an approach similar to that used earlier (Fig. 8), but these syntheses were superseded by better techniques for assembly and control of the two stereogenic centers flanking the silanediol [89, 90]. In all cases, a diphenylsilane was carried through the synthesis sequence and hydrolyzed to the silanediol by strong acid as the last step.

The synthesis of **59**, precursor of inhibitor **48**, began with cycloaddition of dichlorodiphenylsilane and isoprene to yield dihydrosilole **53** (Fig. 14). This reaction can easily produce hundreds of grams in a single run [91]. Asymmetric hydroboration of **53** with pinene-derived isopinocampylborane gave **54** in >90% ee [85, 92]. Warming **54** with aqueous HF leads to Peterson-like fragmentation and formation of fluorosilane **55** with the methyl stereogenic center in place. Fluorosilanes are relatively moisture insensitive and also react efficiently with nucleophiles [93]. Conversion of fluorosilane **55** to ketone **56** was followed by asymmetric reduction of the ketone using stoichiometric CBS-borane reagent to give **57** with >90% diastereoselectivity [94]. Mitsunobu inversion of the alcohol by phthalimide installed the amine in **58** with the correct stereochemistry. Oxidative





**Fig. 14** The stereogenic centers of **59** were installed using asymmetric hydroboration reagents

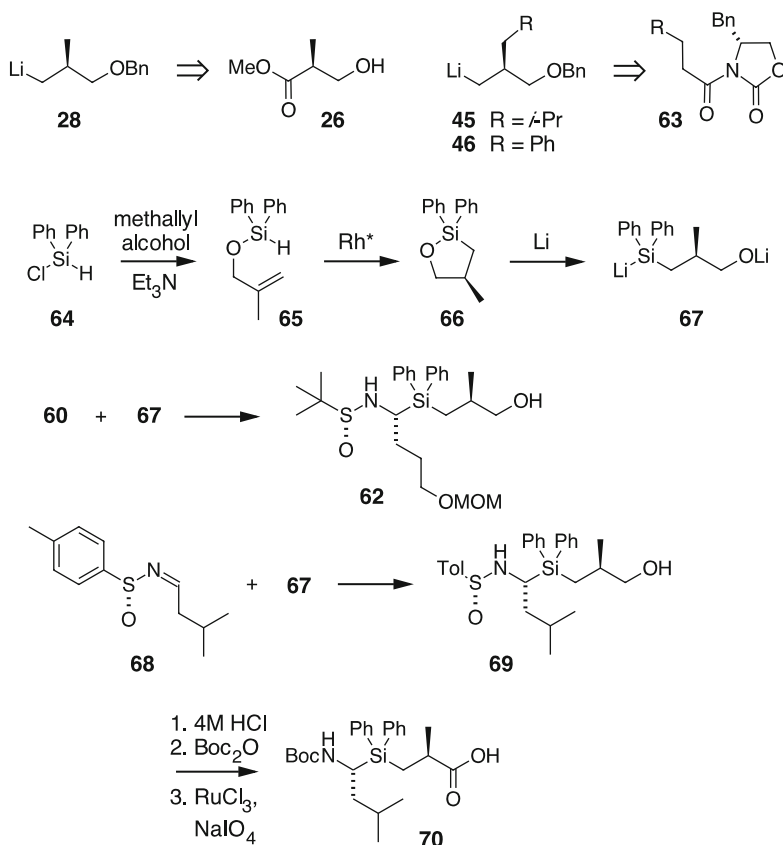


**Fig. 15** Using the Skrydstrup protocol, silyllithium reagent **61** added to sulfinimine **60** to give **62** with complete stereocontrol

cleavage of the alkene then gave the amino acid **59** full control of both stereocenters. Conversion of **59** to **48** then followed standard protocols [85].

A direct and efficient method for preparation of the  $\alpha$ -aminosilane group with control of enantioselectivity was introduced by Nielsen and Skrydstrup using silyllithium reagents and sulfinimines [72]. This method was applied to the synthesis of silanediol precursor **62** (Fig. 15). Silyllithium reagent **61** added to the enantiomerically pure **60** to give **62** with excellent diastereocontrol [90]. Use of racemic **61** demonstrated that the methyl stereogenic center does not influence the diastereoselectivity of the reaction with **60**.

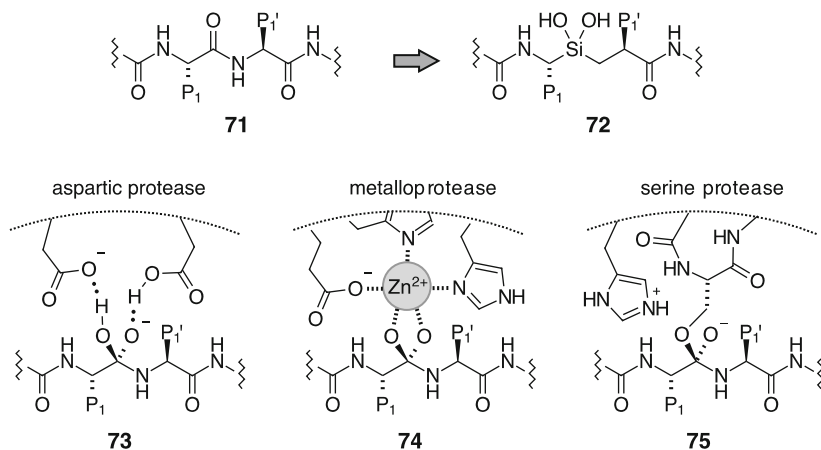
The coupling of Davis–Ellman sulfinimines [95] with silicon nucleophiles by Skrydstrup was an excellent solution for stereocontrol to the  $\alpha$ -aminosilane stereogenic center, but the stereochemistry of the  $\beta$ -silyl acid portion of these inhibitors (see **61** in Fig. 15) was in need of a better solution as well. The asymmetric hydroboration approach for control of this stereocenter, illustrated in Fig. 14 via **53**, was limited by the lack of readily available 2-substituted-1,3-dienes [96]. In the original syntheses of the inhibitors shown in Fig. 8, an enantiomerically pure lithium reagent was used, either prepared from the Roche ester **26** or using Evans chiral auxiliary technology **63** (Fig. 16).



**Fig. 16** Asymmetric hydrosilylation, reductive opening of **66**, and addition to sulfinimines yield advanced silaneol intermediates rapidly and with complete control of stereochemistry

One of the most efficient methods for forming Si–C bonds is hydrosilylation [97–100]. Intramolecular hydrosilylation has been extensively studied, but the asymmetric transformation of **65** into **66**, needed for our efforts, had only been achieved with low enantioselectivity [101, 102]. In a survey of commercially available rhodium ligands, it was found that (*S,S*)-diethylferrotane gave >90 % ee for this transformation and a similarly high enantioselectivity for homologs of **65** carrying groups other than methyl. A second breakthrough was the discovery that treatment of **66** with lithium directly and quantitatively generated the dianion **67**. In a reaction similar to that shown in Fig. 15, addition of **67** to sulfinimine **60** gave **62** in good yield and with complete control of stereochemistry (Fig. 16). Coupling of **67** and **68** gave **69**. Hydrolysis of the sulfonamide **69**, protection of the amine with a Boc group, and oxidation of the alcohol to an acid completed the preparation of key intermediate **70** in short order [103].

The combination of intramolecular hydrosilylation, direct reductive opening of the silyl ether, and coupling of the resulting silyl anion with a sulfinimine (Fig. 16)



**Fig. 17** First-generation silanediol protease inhibitors by substitution of the hydrated amide with a methylene silane group and the active sites of three protease classes for which silanediols are effective inhibitors

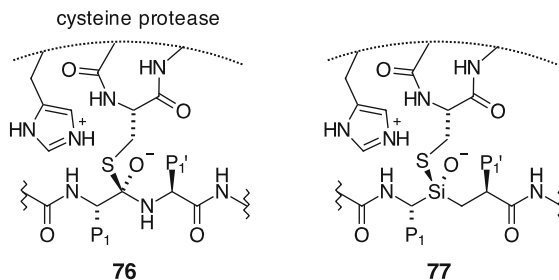
has proven to be a very efficient way to assemble the core components of the silanediol precursors such as **62** and **70**. Compound **70** can be directly coupled with amino acids and hydrolyzed to the silanediol, providing protease inhibitor candidates. Challenges remain, however. The key intermediate for assembly of Factor XIa inhibitor **50** (Fig. 12) is the readily prepared **62** (Fig. 16). The conversion of **62** to **50**, however, was a hard slog, requiring extensive functional group manipulation and illustrating the opportunities for improvement that remain [90].

### 3 Summary and Future Prospects

Silanediols embedded in a peptide-like structure were conceived as mimics of the tetrahedral intermediate of amide hydrolysis, with the potential for inhibiting protease enzymes. Starting with a protease substrate, **71** (Fig. 17), a first-generation inhibitor can be designed by replacing the scissile amide bond with a methylene-silanediol unit, e.g., **72**. This concept has been tested for three of the four classes of protease enzymes and found to be very effective.

#### 3.1 Mechanistic Considerations and Future Challenges

Aspartic proteases, enzymes that contain two aspartic acids at the active site, mediate proteolysis through hydrogen bonding, **73** (Fig. 17). The aspartic acid units are generally considered to have one ionized and one unionized at the active



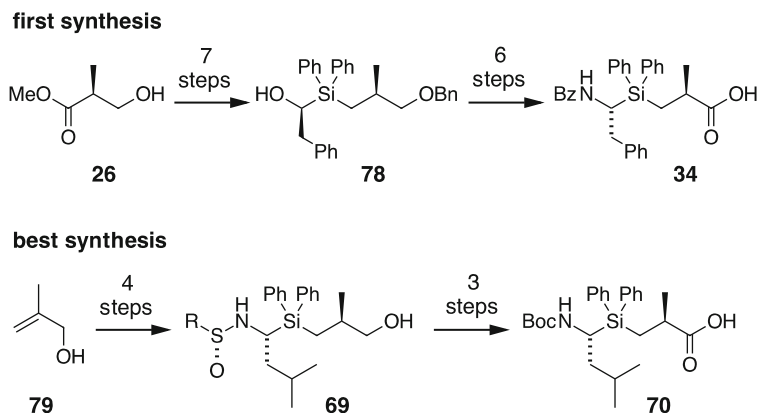
**Fig. 18** Cysteine proteases utilize a nucleophilic sulfur to hydrolyze amides. Inhibition of this important class of proteases by silanediols has not been demonstrated

site, and these stabilize the amide hydrate [104]. A silanediol replacement of this hydrated peptide is expected to readily interact with the active site carboxylic acids because silanols are outstanding hydrogen bond donors and acceptors [44, 45, 105, 106]. This potential has been evaluated using the HIV protease, taking advantage of the  $C_2$  symmetry of the enzyme with a  $C_2$  symmetric inhibitor **44** (Fig. 10). Inhibitor **44** was prepared by analogy to a published inhibitor (**43**) that contained a hydroxyethylene replacement for the amide bond. This silanediol-for-carbinol switch, without reoptimization, gave an effective inhibitor with an  $IC_{50}$  under 3 nM. More importantly, this study found that the silanediol was as effective as the commercial drug indinavir at crossing cell membranes and protecting cells from infection [78]. Additional examples of silanediol-based inhibitors of aspartic proteases would be desirable.

Two metalloprotease enzymes have been potently inhibited by silanediols. Metalloproteases have a zinc ion, held at the active site by a glutamate and two histidine ligands, **74**. This zinc ion stabilizes the amide hydrate by coordination to the geminal hydroxyl groups of the hydrated carbonyl. Silanols can ligate and chelate metal ions [107–109]. Silanediol **42** (Fig. 10) was prepared as an analog of a phosphinic acid **41** and phosphinamide, **41a**, and was found to inhibit the metalloprotease thermolysin with an  $IC_{50}$  of 40 nM. Moreover, both **41a** and **42** were examined by X-ray spectroscopy and found to coordinate to the zinc active site with precisely the same arrangement of their two oxygen atoms. An additional example of metalloprotease inhibition by a silanediol is the 4 nM inhibition of ACE by silanediol **24** (Fig. 10). This silanediol was patterned after the ketone inhibitor **23a** and its presumed inhibitor form, the ketone hydrate **23** (Fig. 7).

These metallo- and aspartic protease inhibitors bind to the active site of the enzyme through noncovalent interactions. In contrast, most inhibitors of serine proteases incorporate an electrophilic group that covalently engages the active site serine. In the case of silanediol inhibitors **48** and **50**, the electrophilic group is a silanediol. A crystal structure of these inhibitors bound to the active sites and demonstrating the covalent attachment of the silane to the serine nucleophile has not yet been achieved.

The fourth class of proteases is the cysteine proteases [110], for which inhibition by a silanediol has not been examined (Fig. 18). The use of silanediols for these



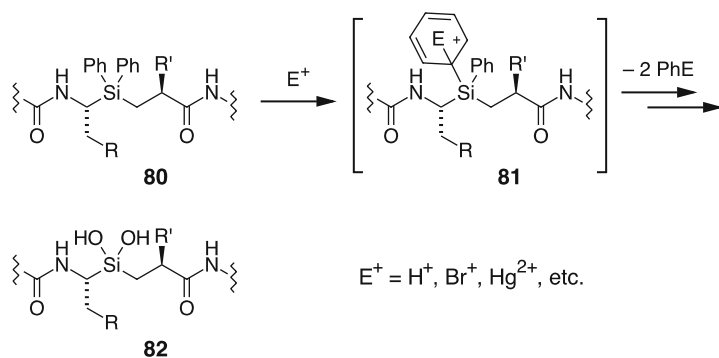
**Fig. 19** Comparison of two routes to advanced silanediol precursors **34** and **70**

important targets implies the formation of a silicon–sulfur bond, e.g., **77** [111]. Should the strength of the bond of the enzyme thiol to silicon be important, the lower bond strength for Si–S relative to Si–O (see **79**) may limit the use of silanediols as inhibitors of these enzymes.

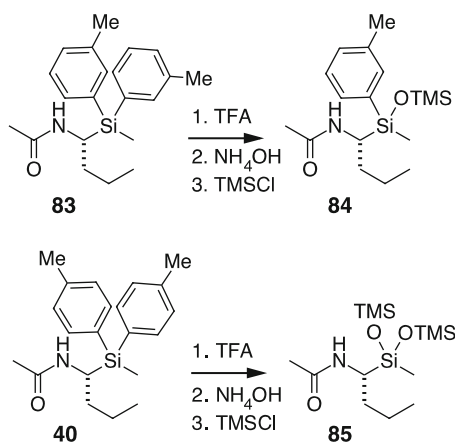
For all of the potential inhibitors discussed, the specificity and potency of the inhibition may, in large part, be determined by the side chain substituents that flank the central silicon atom (see Fig. 12). On the other hand, the silanediol imparts a polarity that lies somewhere between a phosphinic acid and a carbinol. This intermediate polarity has the potential to produce bioactive substances with useful log P values [112].

Preparation of silanediols as protease inhibitors, assembling the functionality and stereogenic centers in a general and efficient way, can now be routinely accomplished, but some targets remain a challenge. The original path to a silanediol required many functional group transformations, from the Roche ester **26** to the penultimate product **34** (Fig. 19). In the currently most efficient path, a 2-substituted allyl alcohol is converted to an intermediate like **69** in three steps, requiring only exchange of nitrogen substituents and oxidation of the primary alcohol. This route enjoys full control of stereochemistry using asymmetric hydrosilylation and a Davis–Ellman sulfinimine. Despite these advances, incorporation of the guanidine functional group for Factor XIa inhibitor **50** (Fig. 12) required many functional group manipulations [90].

An additional synthesis challenge is optimization of the ultimate deprotection step. There have been contributions from several labs [113], modifying the phenyl groups on silicon with a goal of avoiding the use of triflic acid in the deprotection. A variety of electrophiles can be utilized for this transformation, including bromine and mercury (Fig. 20) [114]. Protons are the most desirable of these; bromine can add to alkenes and activated aromatics, and mercury is a toxic heavy metal that has the potential to complicate enzyme assays if it is not fully removed from the inhibitor product.



**Fig. 20** The challenges of silanediol deprotection and the use of electrophiles other than protons



**Fig. 21** Skrydstруп's substituted phenyl silanes allow the use of milder acid for hydrolysis, particularly for *para* substitution

The most successful of the efforts to optimize the acid deprotection procedure has been from the Skrydstруп lab and the addition of methyl substituents to the phenyl groups (Fig. 21) ([73]; for the use of methoxy substitution to promote ease of protodesilylation reactions, see [115] and references therein). This work beautifully illustrates the utility of having electron-donating substitution appropriately placed. Methyl groups at the *meta* position (**83**) do not adequately facilitate aryl hydrolysis (see Fig. 9), but *para* substitution allows for removal of both toluene groups using only trifluoroacetic acid, which is far more mild than triflic acid.

The future of silanediols as pharmaceutical agents will also require a detailed understanding of the pharmacokinetics of these silanediols in peptide-like environments. Much is left to explore!

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# Selenium-Based Drug Design

Sheldon W. May

**Abstract** The biochemistry, pharmacology and epidemiology of selenium and selenium-containing compounds continue to be subjects of considerable interest from the viewpoint of public health. Selenium has a long history of association with human health and disease, and we now recognize that this element is an essential nutrient that is critical to key cellular processes. We now know that the selenoproteins constituting the human selenoproteome are encoded by 25 genes in the human genome, and much progress is being made in our understanding of selenium metabolism and the health effects of selenium metabolites in normal and disease states. The idea that selenium-containing dietary supplements might be effective in preventing disease has gone through both optimistic and pessimistic phases in recent years, and the future prospects for such a nutritional approach are unclear at the present time. In contrast, a significant number of promising efforts are underway that are aimed at designing and developing pharmaceutical agents that are selenium-based or that target specific aspects of selenium metabolism. This chapter focuses on some of these efforts to develop new selenium-based anticancer, antioxidant, antihypertensive, antiviral, immunosuppressive, and antimicrobial agents. While most of the efforts that entail designed organoselenium compounds – as opposed to inorganic selenium metabolites – are still at the preclinical stage, evidence is emerging that selenium-based compounds can operate via several beneficial biochemical and pharmacological mechanisms. Since our understanding of the biology, biochemistry and pharmacology of selenium and selenoproteins is rapidly expanding, we can anticipate that the coming years will bring further development of new selenium-based pharmaceutical agents with therapeutic potential against human diseases.

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## Contents

1	Introduction .....	88
2	Phenylaminoalkyl Selenides .....	90
3	Ebselen and BXT-51072 .....	96
4	Selenazolidine Prodrugs .....	98
5	Selenium-Carrier Conjugates .....	99
6	Targeting the Thioredoxin–Thioredoxin Reductase System .....	101
7	Selenium-Containing Metabolites .....	103
8	Diaryl Diselenides .....	106
9	Selenium Versus Sulfur in Drug Design .....	107
10	Conclusions and Perspectives .....	109
	References .....	111

## 1 Introduction

The biochemistry, pharmacology, and epidemiology of selenium and selenium-containing compounds continue to be a subject of considerable interest, particularly from the viewpoint of public health. Selenium has a long history of association with human health and disease [1, 2], and specific populations have historically suffered from certain diseases that are now recognized to be associated with selenium deficiency. A widely known example is Keshan disease, which is characterized by congestive heart failure [3, 4]; healers in Keshan, China, where the disease was discovered, have traditionally treated it with the common herb, *Astragalus*, several species of which accumulate selenium from the soil. Ironically, *Astragalus* may be the very plant seen by Marco Polo in the “Succuir” district of China; the explorer describes how beasts of burden unaccustomed to the area would feast on this plant, thereby causing the animals to become so ill that their hooves dropped off [5]. Polo’s description fits what is now known to be an equestrian form of selenosis. Thus, in retrospect, it is likely that even this very early report underscores the critical importance of managing the proper dose and molecular form of selenium when considering therapeutic applications.

It is worth noting that the notion that selenium may exert a protective effect against human cancer was actually discussed in the mainstream scientific literature more than four decades ago [6, 7]. Early geographical studies suggested an inverse correlation between selenium levels and cancer incidence, and cancer mortality rates were found to be significantly lower in US counties with intermediate or high

selenium levels as compared to counties with low selenium levels [8]. Similarly, low selenium concentrations were found in the sera of patients with pancreatic carcinoma and in the plasma of breast cancer patients, and selenium compounds have exhibited antitumorogenic activities in a number of animal studies over the years [5].

Turning to the present time, we now know that selenium (as selenocysteine) is an essential component of the active sites of the enzymes glutathione peroxidase and mammalian thioredoxin reductase and is also present in a variety of other mammalian selenoproteins [9–13]. Both glutathione peroxidase and thioredoxin reductase catalyze reactions that are essential to the protection of cellular components against oxidative and free radical damage. In epidemiological studies, a low concentration of selenium in plasma was identified as a risk factor for several diseases including cancer, cardiovascular disease, osteoarthritis, and AIDS [3, 14–19]. In the United States, the National Academies of Science Institute of Medicine has issued a dietary reference intake report on selenium and other antioxidants [20], with the current recommended dietary allowance (RDA) for selenium being 55 micrograms for adult men and women. It should be noted that symptoms of selenosis appear when dietary levels of selenium exceed 1 milligram/day, whereas a selenium dietary intake below 1 microgram/kg can lead to selenium deficiency diseases such as the aforementioned Keshan disease.

Over the past three decades, there have been a number of efforts aimed at designing and developing pharmaceutical agents that are selenium based or that target specific aspects of selenium metabolism (for some relevant reviews, see [5, 9–12, 21]). These efforts have focused on the design of selenium-based antihypertensive, anticancer, antiviral, immunosuppressive, and antimicrobial agents. There has also been much interest in the development of organoselenium compounds capable of reducing oxidative tissue damage and edema. This chapter will focus on some of the more promising of these efforts to develop new selenium-based therapeutic agents.

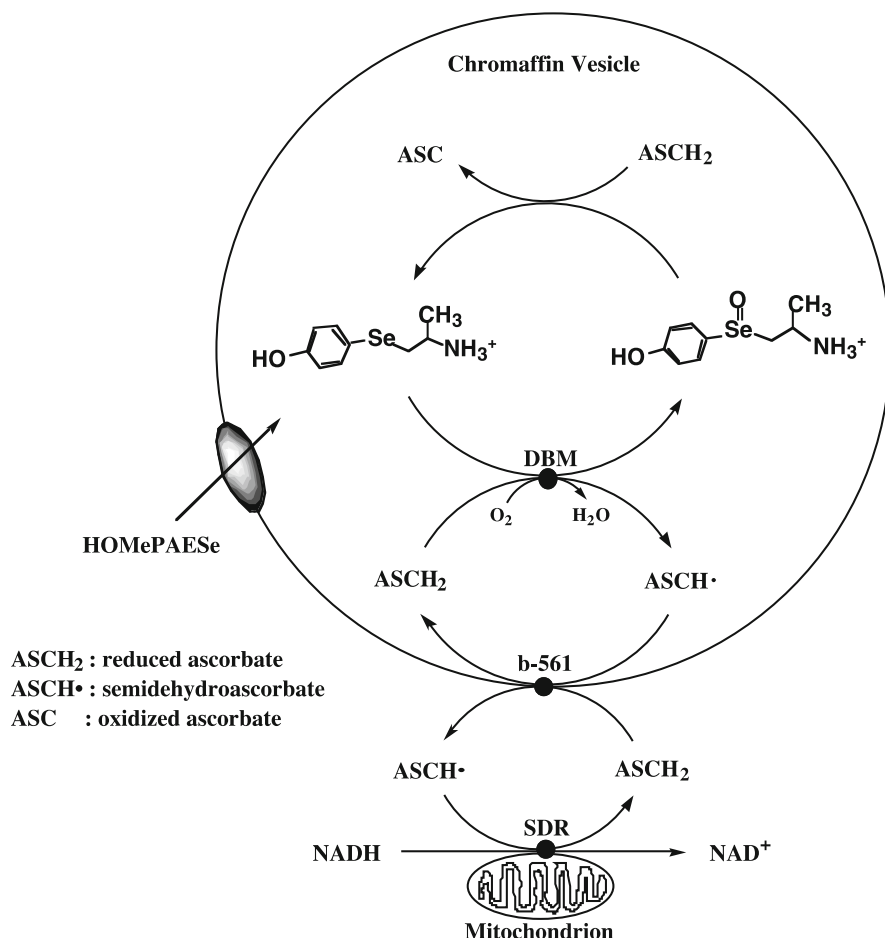
It is very important to mention at the outset that concurrent with these drug design and development efforts, some findings that looked initially quite promising emerged from nutritional trials and epidemiological studies. In 1996, Clark and coworkers [22] reported that their long-term, double-blind, placebo-controlled study demonstrated significant reductions in incidences of lung, colorectal, and prostate cancers in patients receiving daily 200 microgram oral doses of “selenium yeast.” Subsequently, a prospective study of 33,737 men reported [14] that individuals with the highest selenium levels had only about one-third the likelihood of developing advanced prostate cancer as did individuals with low selenium levels, and similar results were reported in other prospective cancer studies (see, e.g., van den Brandt et al. [15]). In view of findings such as these, the Selenium and Vitamin E Cancer Prevention Trial (SELECT) was launched [23] by the National Cancer Institute. SELECT was designed to be a very large, randomized, placebo-controlled trial of selenium (200 µg/day L-selenomethionine) and/or vitamin E (400 IU/day racemic  $\alpha$ -tocopheryl acetate) supplementation for a minimum of 7 years (maximum of 12 years) focusing on the prevention of prostate cancer by these agents.

Unfortunately, SELECT was discontinued since an independent review of the data being collected showed that selenomethionine and vitamin E, taken together or alone, were not preventing prostate cancer [24, 25]. Nevertheless, despite this disappointing result, there still remains much interest from a nutritional perspective in the development of effective selenium supplementation protocols, if only the proper selenium formulation and dosage could be identified (see, e.g., the “post-SELECT” perspective by Ledesma et al. [24]). A detailed discussion of epidemiological and nutritional aspects of selenium supplementation is beyond the scope of this review.

## 2 Phenylaminoalkyl Selenides

This author’s laboratory has developed a family of phenylaminoalkyl selenides [26–31] and we have shown that these selenides possess the ability to propagate a cycle that depletes reduced ascorbate within adrenergic vesicles. Initially, dopamine- $\beta$ -monooxygenase (DBM) present within the vesicle converts these selenides to the corresponding selenoxides; however, the product selenoxides are then nonenzymatically reduced back to the selenides, with the concomitant and stoichiometric oxidation of reduced ascorbate present in the vesicle to fully oxidized ascorbate. This selenide/ascorbate cycle is a localized process since DBM is present only in these vesicles and reduced ascorbate does not cross the vesicle membrane. While adrenergic vesicles possess a cytochrome b561-dependent ascorbate recycling system, this native system can only recycle semidehydroascorbate, which is generated during DBM turnover, and cannot recycle the fully oxidized ascorbate produced by the nonenzymatic selenoxide/ascorbate reaction. Thus, the net result of selenide processing in the vesicle is the effective local depletion of reduced ascorbate – an essential cofactor for DBM – and the consequent diminution of norepinephrine production. We demonstrated this turnover-dependent ascorbate depletion process both *in vitro* and in chromaffin granule ghosts, and we confirmed cellular and vesicular uptake of the selenides. Moreover, as predicted on the basis of the redox potentials of selenoxides versus sulfoxides, we showed that while sulfur-containing analogs undergo DBM-catalyzed sulfoxidation, they are not capable of propagating such a cycle of ascorbate depletion. Thus, it is clear that the ability of phenylaminoalkyl selenides to effect turnover-dependent depletion of local reduced ascorbate is a direct consequence of the redox chemistry of the selenium moiety present in these compounds (Fig. 1).

The pharmacological testing of phenylaminoethyl selenide (PAESe) confirmed that this compound exhibits dose-dependent antihypertensive activity when administered *i.p.* to spontaneously hypertensive rats, and we have provided evidence that the adrenergic nerve terminal is indeed the pharmacological site of action of PAESe *in vivo*. However, as is true for other peripherally acting pharmacological agents, the CNS permeability of PAESe is a significant concern, since undesirable side effects can often result from CNS penetration. Moreover, it is highly desirable from



**Fig. 1** Dopamine  $\beta$ -monoxygenase-catalyzed selenoxidation of 4-hydroxyphenyl-2-methyl-2-aminoethyl selenide (HOMePAESE), followed by nonenzymatic recycling of the selenoxide product. This results in the *local* depletion of reduced ascorbate within the chromaffin vesicle even in the presence of the b-561-dependent ascorbate recycling system, since the native b561 system can only recycle the semidehydroascorbate generated during DBM turnover but not the fully oxidized ascorbate produced by the nonenzymatic selenoxide/ascorbate reaction

a therapeutic perspective that pharmacological agents used to treat chronic diseases such as hypertension be orally active. We therefore proceeded to develop a PAESE derivative that would exhibit both restricted CNS permeability and oral antihypertensive activity [32].

Briefly, our approach was as follows: First, we employed inductively coupled plasma/mass spectroscopic (ICP/MS) analysis of plasma samples to determine the pharmacokinetic parameters for our selenide compounds. Next, an oxidative procedure for the digestion and processing of tissue samples was then developed in

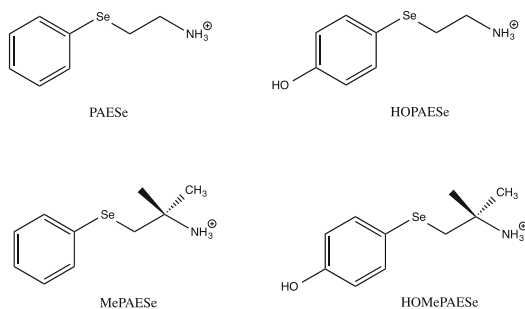


order to obtain ICP/MS data on the tissue distributions of selenium-containing metabolites following the administration of selenide compounds. The results clearly demonstrated that the aromatic-ring hydroxylation of the selenides results in a marked reduction in brain levels of selenium-containing metabolites. We also demonstrated that  $\alpha$ -methylation abolishes the activity of the enzyme MAO toward these compounds and markedly enhances their oral activity; since the intestinal mucosa possesses a considerable amount of MAO, resistance to MAO-catalyzed degradation is an essential characteristic for drugs to exhibit good oral bioavailability. Finally, we investigated the comparative effects of PAESE derivatives on locomotor activity and operant behavior. The results fully corroborated our analytical data, thus confirming the pharmacological relevance of the ICP/MS results and providing a compelling basis for drug design. On the basis of these biochemical, pharmacological, inductively coupled plasma/mass spectrometry, and behavioral studies, we successfully demonstrated that the novel compound (*S*)-4-hydroxyphenyl-2-methyl-2-aminoethyl selenide (HOMePAESE) exhibits both restricted CNS permeability and oral antihypertensive activity [32]. Indeed, this compound is the first orally active selenium-based antihypertensive agent ever reported (Fig. 2).

We carried out a series of experiments designed to probe the hemodynamic mechanism of action of these phenylaminoethyl selenide antihypertensives [33]. In these experiments, a noninvasive pulsed Doppler ultrasound probe was used to measure peak blood flow velocity in the aortic arch from the right second intercostal space. PAESE was found to increase peak aortic blood flow velocity (+44%), heart rate (+16%), and blood flow acceleration (+105%), while decreasing left ventricular ejection time (LVET) (−37%) concomitant with a decrease in mean arterial pressure (−54%). These results were compared with the known vasodilator, hydralazine, which had similar effects on mean arterial pressure (MAP) and peak velocity but caused an increase in LVET (+42%) and a decrease in heart rate (−18%). Taken together, these results indicate that PAESE decreases blood pressure via a decrease in peripheral resistance, which overcomes an initial increase in heart rate and acceleration to give a net decrease in mean arterial pressure.

More recent work in the author's laboratory has focused on elucidating and harnessing the redox cycling and antioxidant activity of phenylaminoethyl selenides [34–37]. We established that PAESE reacts rapidly with many cellular

**Fig. 2** Structures of phenylaminoethyl selenides investigated in the author's laboratory. It is noteworthy that the compound (*S*)-4-hydroxyphenyl-2-methyl-2-aminoethyl selenide (HOMePAESE) exhibits both restricted CNS permeability and oral antihypertensive activity



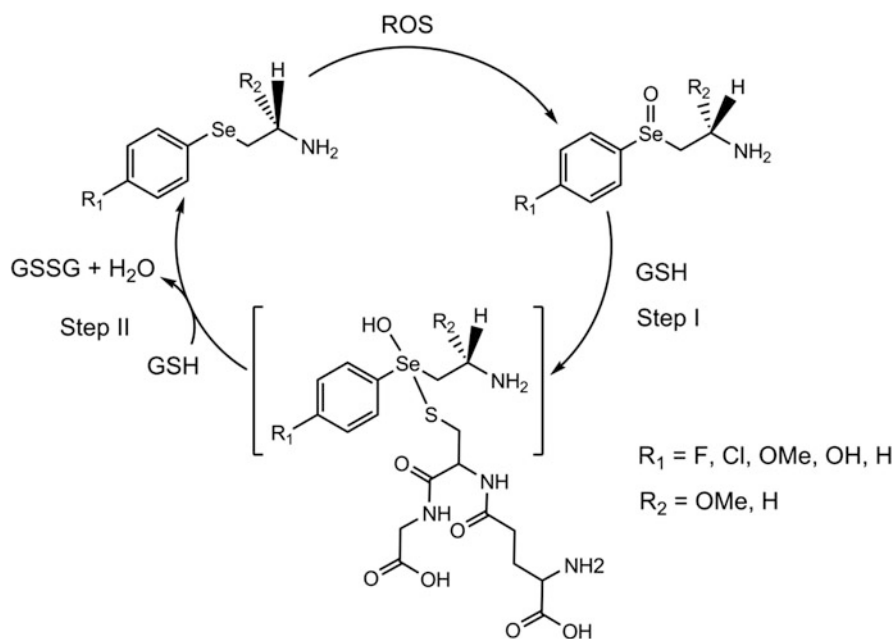
oxidants, with the selenoxide product generated from this antioxidant activity being readily recycled back to the selenide by cellular reductants such as ascorbate and glutathione with no complex side reactions. One of the most predominant of such cellular oxidants is peroxynitrite, a powerful oxidizing and nitrating agent formed from a diffusion-controlled reaction between nitric oxide and superoxide in endothelial cells, macrophages, and neutrophils. Reactions of peroxynitrite with cellular components have been linked to oxidative stress and inflammatory tissue damage, as, for example, in atherosclerosis and ischemia–reperfusion injury. Peroxynitrite also reacts readily with DNA where it causes base modification and induction of double- and single-strand breaks. We showed that phenylaminoalkyl selenides protect plasmid DNA from peroxynitrite-mediated damage by scavenging this powerful cellular oxidant and forming phenylaminoethyl selenoxides as the sole selenium-containing product. Moreover, on the basis of kinetic studies, potentiometric titrations, cyclic voltammetry, and MatLab simulations, we demonstrated that glutathione-based selenoxide redox cycling enhances these protective effects of the selenides against peroxynitrite-induced DNA damage.

The above results provide support for the idea that exogenously supplied or metabolically generated organoselenium compounds, capable of propagating a selenium redox cycle, might supplement natural cellular defenses against the oxidizing agents generated during metabolism. While several such organoselenium compounds are under active investigation as potential therapeutic agents, the chemical characterization of reaction intermediates involved in selenium redox cycling has been problematical. Among the proposed selenium intermediates in the redox reactions of organoselenium compounds are species such as selenenic and seleninic acids, selenones, spirodioxaselenanonanes, and thiol-seleninates. Thus, for example, evidence has been reported for the formation of a thiol-seleninate intermediate in the reactions between ebselen oxide and certain thiols [38, 39] and for a spirodioxaselenanonane intermediate in the reaction between di(3-hydroxypropyl) selenide and *tert*-butyl hydroperoxide [40]. The reactivity and instability of some tetra-coordinate selenium compounds, coupled with fast reaction rates for the reactions of organoselenium compounds with oxidants or with reducing agents such as thiols, have made it difficult for several investigators to clearly characterize thio-selenurane-like intermediates (see Cowan et al. [36] for further discussion of this point).

Work in the author's laboratory has provided direct evidence that the reaction between phenylaminoalkyl selenoxides and glutathione (GSH) proceeds through the intermediacy of a thio-selenurane species [36]. The results of stopped-flow kinetic experiments were consistent with a rapid and stoichiometric initial reaction of GSH with selenoxide to generate a kinetically detectable intermediate, followed by a slower reaction of this intermediate with a second molecule of GSH to produce the final selenide and GSSG products. Flow injection ESI-MS and ESI-MS/MS experiments confirmed that the reaction intermediate is indeed a thio-selenurane. Final structural characterization of the thio-selenurane intermediate was obtained from the analysis of the daughter ions produced in flow injection ESI-MS/MS experiments. These results elucidate the chemical nature of the redox cycling of

phenylaminoalkyl selenides and represent, to our knowledge, the first evidence for the intermediacy of a thioselenurane species in the reaction of thiols with selenoxides. Previously, Kumar et al. [38] had proposed the formation of a thioselenurane in the reaction between benzenethiol and a substituted phenyl benzyl selenoxide, since they observed via ESI-MS a cyclization product that could arise from such a species; however, they were unable to obtain any structural evidence for this proposed intermediate (Fig. 3).

Hydrogen peroxide, produced in living cells by oxidases and by other biochemical reactions, plays an important role in cellular processes such as signaling and cell cycle progression [41, 42]. Nevertheless, hydrogen peroxide is capable of inducing damage to cellular components, and it can be converted through Fenton chemistry to even more reactive molecules, such as hydroxyl and peroxide radicals. Indeed, oxidative stress – the cellular state arising from overproduction of hydrogen peroxide and other reactive oxygen species (ROS) – has been linked to cellular pathologies ranging from DNA and cellular membrane damage to more complex disorders such as inflammatory diseases and cancer [43]. In experiments carried out in the author's laboratory [37], we made use of peroxalate nanoparticle methodology to achieve chemiluminescent imaging of hydrogen peroxide consumption by phenylaminoethyl selenides. Further, we demonstrated that phenylaminoethyl selenides decrease lipopolysaccharide (LPS)-induced oxidative stress in human



**Fig. 3** Identification of a thioselenurane intermediate in the reaction between phenylaminoalkyl selenoxides and glutathione

embryonic kidney cells. We also encapsulated PAESE within poly(lactide-co-glycolide) nanoparticles, and we showed that these selenide-loaded nanoparticles exhibit antioxidant activity in a mammalian cell line. Taken together, these results significantly enhance the attractiveness of phenylaminoethyl selenides as potential agents for supplementing cellular defenses against reactive oxygen species.

Anthracyclines such as doxorubicin (DOX) and daunorubicin are widely used anticancer agents that are effective in the treatment of acute leukemia, non-Hodgkin's lymphomas, and breast, ovarian, and lung cancers [44]. However, the clinical use of anthracycline is limited by severe dose-limiting cardiotoxicities, such as cardiomyopathy and congestive heart failure. This cardiotoxicity is now generally believed to result primarily from the generation of reactive free radicals such as superoxide anion, hydroxyl radical, and peroxynitrite [45, 46]. Dexrazoxane, a potent iron chelator that interrupts anthracycline-iron-mediated free radical generation, is in clinical use to decrease this free radical-associated toxicity of DOX [47, 48]. However, dexrazoxane is known to cause myelosuppression, and recent studies suggest that its use may lead to acute myeloid leukemia and myelodysplastic syndrome. The FDA has noted (<http://www.fda.gov/Drugs/DrugSafety/ucm263729.htm>) that the European Medicines Agency has announced restrictions on dexrazoxane usage to certain types of patients [48].

In collaboration with the laboratory of Dr. Robert Arnold, we have carried out a series of studies [49] aimed at determining the potential of PAESE to mitigate anthracycline-induced cardiotoxicity. First, we determined the effects on the growth of human prostate carcinoma (PC-3) cells of combined administration of PAESE with DOX, vincristine, or *tert*-butyl hydroperoxide (TBHP). DOX and vincristine are, of course, used clinically as anticancer drugs, whereas *tert*-butylhydroperoxide is a potent oxidizing agent known to exert oxidative-mediated cytotoxicity on PC-3 cells. We found that while PAESE had little effect on the activities of DOX or vincristine, the selenide significantly decreased the cytotoxic effect of TBHP in a dose-dependent manner. Moreover, using the cell-permeable indicator, CM-H<sub>2</sub>DCFDA, we showed that PAESE decreased the formation of intracellular reactive oxygen species from either TBHP or DOX. We then proceeded to determine the effect of PAESE on the antitumor activity of DOX in an *in vivo* xenograft tumor model of human prostate cancer in NCr nude mice. We found that PAESE did not alter DOX antitumor activity and also showed evidence of direct antitumor activity relative to controls. Most importantly, PAESE decreased DOX-mediated infiltration of neutrophil and macrophages into the myocardium, which are early signs of cardiotoxicity. In addition, recent experiments in H9C2 cells have shown that concomitant treatment with PAESE significantly reduced DOX-mediated expression of ANP and MHC- $\beta$ , which are markers of cardiac hypertrophy (unpublished observations). These findings suggest that selenides such as PAESE may be quite attractive agents for mitigating the cardiotoxicity associated with clinical use of DOX and related anticancer drugs.

### 3 Ebselen and BXT-51072

Ebselen (2-phenyl-1,2-benzisoxolin-3[2H]-one) is an organoselenium compound that has been shown to mediate the reduction of hydroperoxides by thiol compounds such as glutathione, thereby modeling the enzymatic activity of the selenoenzyme, glutathione peroxidase [50]. Many researchers have carried out a number of chemical, biochemical, mechanistic, and pharmacological studies on ebselen and its chemical analogs, and a commentary providing historical perspective on the early research and development of ebselen has recently been published [51]. Over the years, a key rationale underlying much of this interest in ebselen has been the possibility that selenium redox cycling in ebselen or its derivatives might supplement natural cellular defenses against oxidizing agents. However, it has now become quite clear that the redox cycle of ebselen consists of multiple reaction pathways with several intermediates and by-products [52–55]. Moreover, several investigations have shown that ebselen is an inefficient catalyst due to deactivating pathways, where unreactive intermediates hinder the regeneration of the original compound [54, 56–58]. In contrast, as noted above, stopped-flow kinetic and ESI-MS/MS results in this author's laboratory have demonstrated that the redox cycling of phenylaminoethyl selenides is a rapid and efficient two-step process, with initial formation of a thioselenurane intermediate followed by complete regeneration of the original selenide (Fig. 4).

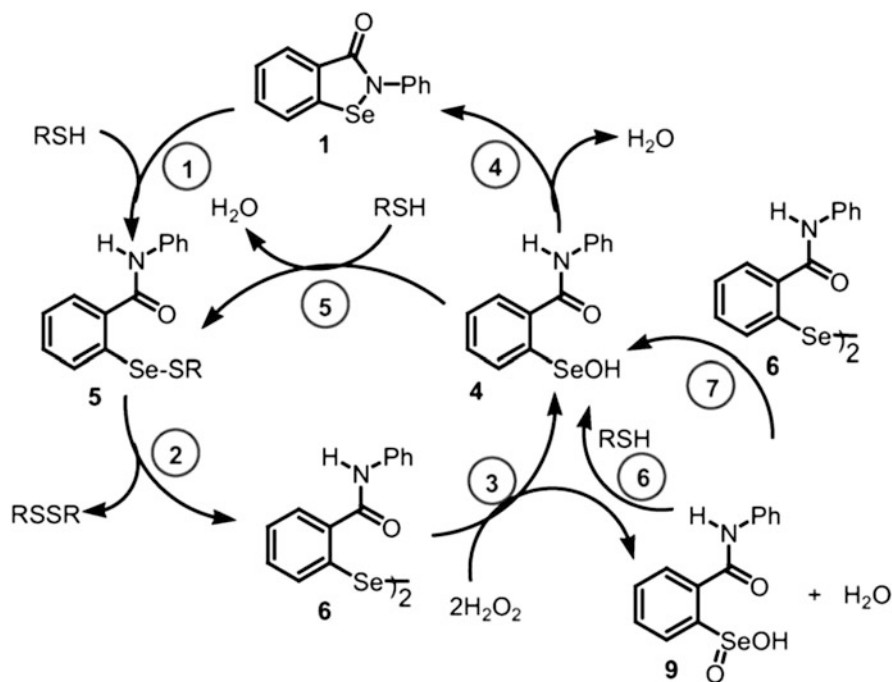


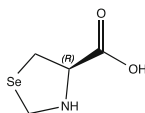
Fig. 4 Mechanism for the GPx activity of ebselen as proposed by Sarma and Mugesh [54]

Several years ago, a clinical trial was undertaken in Japan to assess whether ebselen is capable of protecting against the oxidative tissue damage which occurs following acute ischemic stroke [59]. The results of this trial showed that the most significant improvement was achieved in patients who started a 14-day course of ebselen treatment within 24 h of stroke onset; however, these benefits were statistically significant when evaluated after 1 month but not after 3 months. Subsequently, recruitment was announced for a phase III trial in Japan, sponsored by the Daiichi Pharmaceutical Company, to test the efficacy of ebselen in patients with acute cerebral infarction (cortical infarction). According to the Web site <http://www.strokecenter.org/trials/TrialDetail.asp?trialName=list/trialPage298.htm>, 394 patients were enrolled in this placebo-controlled, double-blind, randomized, multicenter trial, with enrollment to be completed by November 2002. Unfortunately, results from this trial have never been posted on this Web site, and this author could not find any publications in the open scientific literature reporting results from this trial. In their recent commentary on the early research and development of ebselen [51], Parnham and Sies state that the results of the trial were submitted for registration to the Japanese regulatory authority (MHLW), but the reviewers considered the drug efficacy to be insufficient for approval. According to media reports (see, e.g., <http://www.bbsrc.ac.uk/news/health/2013/130114-n-new-drug-bipolar-disorder.aspx>), researchers in Oxford have begun a small study in healthy volunteers to test whether ebselen has lithium-like effects on brain function in humans; if successful, these researchers reportedly plan to move on to a small phase II trial in people with bipolar disorder.

Ebselen has been investigated in animal models in a number of laboratories for other possible pharmacological activities. For example, Kono et al. [60] reported that twice-daily treatment of rats with 50 mg/kg ebselen significantly reduces early alcohol-induced liver injury, as measured by liver enzyme assays, inflammation, and liver necrosis. Another example is the report of Moussaoui et al. [61] that ebselen, when administered before, during, and after injections of 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP), prevents both neuronal loss and clinical symptoms in a primate MPTP model of Parkinson's disease. More recently, Chew et al. [62] studied the antiatherosclerotic and renoprotective effects of ebselen in diabetic apolipoprotein E/GPx1-double knockout mice that had been injected with streptozotocin. They found that that ebselen reduced atherosclerosis and that it also prevented the changes in renal structure and function and the inflammatory responses associated with nephropathy in the diabetic mice. These findings are reminiscent of the earlier work of Chander et al. [63], who reported that ebselen improved renal outcomes in the Zucker diabetic fat rat. Ebselen been reported to protect neuronal cells in the ventroposterior nucleus of stroke-prone renovascular hypertensive rats against damage resulting from a cerebral cortical infarction [64]. Along these lines, Yamagata and coworkers [65] have reported that ebselen exhibits protective effects against neurodegeneration induced by hypoxia and reperfusion in stroke-prone spontaneously hypertensive rats.



Based on these considerations, Roberts and coworkers [70–72] pioneered the development of selenazolidine-4(*R*)-carboxylic acids as prodrug forms of selenocysteine for potential use in therapeutic applications.



selenazolidine-4(*R*)-carboxylic acid

These prodrugs are condensation products of selenocysteine and carbonyl compounds, and contain selenazolidine rings with various substituents; they are designed to release selenocysteine either enzymatically or through spontaneous hydrolysis. The selenazolidines were found to be much less toxic than sodium selenite in cultured lung fibroblast cells; this is as expected since organoselenium compounds have generally been perceived as being less toxic than inorganic selenium species. Treatment of these cells with selenazolidines increased cellular glutathione peroxidase activity, and a clear stereochemical preference was observed, with the prodrugs of *L*-selenocysteine being more active than the *D*-enantiomers in increasing glutathione peroxidase activity. Overall, the selenazolidines exhibited comparable chemopreventive activity to selenocysteine, with decreased cytotoxicity and greater biological selenium availability than sodium selenite or selenomethionine.

As discussed below, many cancers are known to overexpress thioredoxin reductase, and knockdown of thioredoxin reductase can enhance the sensitivity of cancer cells to anticancer agents. Accordingly, Poerschke and Moos [73] extended the earlier work of Roberts by utilizing a lentiviral microRNA delivery system to knockdown thioredoxin reductase expression in human lung adenocarcinoma cells and then examining the cytotoxic activities of the selenazolidine prodrugs, 2-butylselenazolidine-4(*R*)-carboxylic acid and 2-cyclohexylselenazolidine-4-(*R*)-carboxylic acid. They found that thioredoxin reductase knockdown increased the cytotoxicity of selenazolidines in these adenocarcinoma cells via a mechanism involving mitochondrial dysfunction and caspase-independent activation of the apoptosis-inducing factor.

## 5 Selenium-Carrier Conjugates

In a series of US patents [74–76], Spallholz and Reid described the methodology for preparing selenium-carrier conjugates which could then be specifically targeted for delivery to tumors or to sites of pathogenic infection. The underlying rationale of this methodology is the idea of utilizing specific organoselenium compounds to



generate superoxide and other free radicals in a localized environment. Selenium Ltd. (<http://www.selenbio.com>), a company established in 2004 based on the work of these investigators, claims to have developed the necessary technology for covalently attaching selenium-containing molecules to antibodies, peptides, polymers, and drugs. Thus, for example, selenium-modified humanized antibodies and proteins have been used to effectively kill human prostate, colorectal, and lymphatic cancer cells in tissue culture, with the operative mechanism being the generation of superoxide by the antibody-linked organoselenium compound at the target site which induces apoptosis and destroys the tumor cell. Similarly, an organoselenium-labeled CD-4 peptide directed against the HIV-1 virus destroyed the virus before it was able to infect T cells, with 95% of a virulent isolate of HIV being inactivated in 2 h.

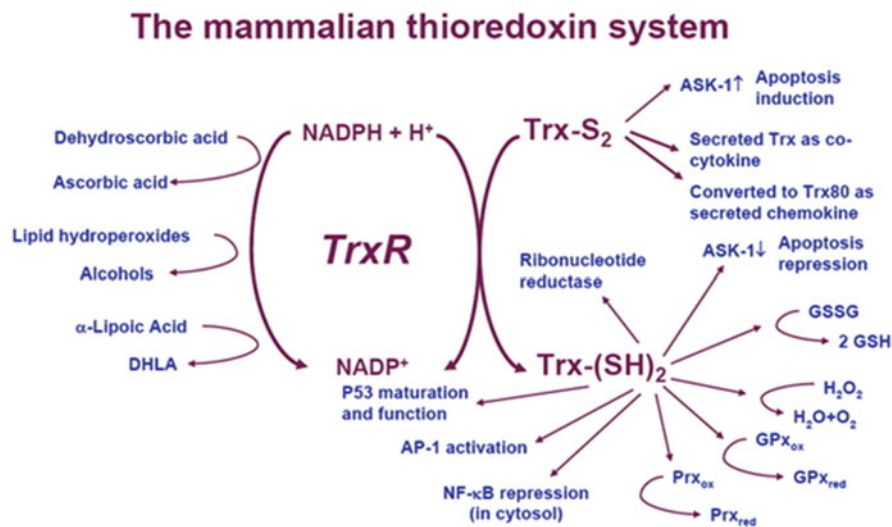
Another potential use for selenium-carrier conjugates is in the treatment of infections caused by bacteria, especially in a biofilm. Tran et al. [77] examined the ability of an organoselenium–methacrylate polymer (Se-MAP) to block biofilm formation by both *Pseudomonas aeruginosa* and *Staphylococcus aureus*. These bacteria were chosen since they cause a major share of wound infections and because drug-resistant forms of these bacteria have become a serious problem in the treatment and management of such infections. The results showed that 0.2% (wt/wt) Se in Se-MAP, covalently attached to cellulose disks, completely inhibited *P. aeruginosa* and *S. aureus* biofilm formation. The authors surmise that inhibition of biofilm formation is due to damage to bacterial cell walls and DNA by superoxide, which is generated via selenium-mediated thiol oxidation. The authors also found that the Se-MAP coating is stable and not cytotoxic to mammalian cells. Thus, they suggest that the application of Se-MAP-coated gauze to the debrided tissues of burn wounds may prevent the development of biofilms and facilitate wound healing. This approach might also be used for dental applications [78] and to combat infections in hospitals caused by catheters and other medical implants.

Kunstelj et al. [79] have patented the idea of producing a water-soluble polymer possessing a reactive selenium group (e.g., PEG coupled to selenocysteine or selenocystamine). The polymer is then reacted with a pharmaceutically active agent such as granulocyte colony-stimulating factor (G-CSF) to form a conjugate through linkage of the polymer's Se moiety to a Cys of the pharmaceutically active agent via an –Se–S– bond. The inventors visualize the use of this type of conjugate for the treatment of diseases such as neutropenia. Miki et al. [80] have patented an approach for inhibiting tumor cell growth that entails the administration of a selenium-containing prodrug while also administering directly to the tumor an expression system for an enzyme for which the prodrug is a substrate. Thus, for example, SeMet is administered together with a vector for expression of methionine lyase, such that the vector preferentially replicates in rapidly proliferating cells or is under control of a promoter that is operable selectively in tumor tissue, thus conferring specificity for tumor cells. The lyase cleaves the prodrug at the C–Se bond, thus liberating a toxic form of selenium (presumably  $RSe^-$ ) at the site of the tumor in an amount sufficient to inhibit tumor cell growth.

## 6 Targeting the Thioredoxin–Thioredoxin Reductase System

A number of investigators have been pursuing the development of compounds that target the mammalian selenoenzyme, thioredoxin reductase (TrxR), which catalyzes the NADPH-dependent reduction of the redox protein, thioredoxin (Trx). The Trx/TrxR system functions as a donor of reducing equivalents for enzymes such as ribonucleotide reductase, which is essential for DNA synthesis, and protein disulfide reductase, which is critically involved in thiol/disulfide redox regulation (Fig. 5). Therefore, the inhibition of TrxR would be expected to be highly detrimental to the growth of tumor cells, especially since the levels of both TrxR and Trx have been found to be elevated in tumor cell lines, and expression profiles of thioredoxin family proteins correlate with cell proliferation, survival, and tumor grade [81–84]. Moreover, knockdown of thioredoxin reductase in murine lung carcinoma cells reversed the malignant phenotype and decreased tumor growth and metastasis [85].

As mentioned above, Poerschke and Moos [73] have reported that knockdown of thioredoxin reductase in human lung adenocarcinoma cells using a lentiviral microRNA delivery system increased the cytotoxicity of selenazolidines in these adenocarcinoma cells. In earlier work, Powis and coworkers [86] found that certain organoselenium and organotellurium compounds, primarily of the diaryl chalcogenide type, were inhibitors of TrxR and also growth inhibitors of cultured tumor cells; these compounds, with one exception, did not inhibit glutathione reductase. Subsequently, these investigators reported [87] that water-soluble organotellurium



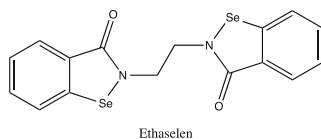
**Fig. 5** The mammalian thioredoxin–thioredoxin reductase (Trx/TrxR) system is linked to many cellular processes (from [http://biochem.mbb.ki.se/Arner/research/img/Trx\\_TrxR.jpg](http://biochem.mbb.ki.se/Arner/research/img/Trx_TrxR.jpg))

compounds of the diaryl telluride, alkyl aryl telluride, and dialkyl telluride types are very potent inhibitors of TrxR, and these tellurides inhibited the growth of MCF-7 and HT-29 human cancer cells in culture at the 5–10 micromolar level; however, their hydrophilicity did seem to restrict cellular uptake.

In 2002, Holmgren and coworkers reported [88] that ebselen is an excellent substrate for human TrxR. They showed that TrxR, in the presence of thioredoxin, catalyzes a very rapid reduction of ebselen to ebselen selenol, with NADPH serving as the electron donor. The reduced ebselen can, in turn, react rapidly with hydrogen peroxide (peroxidase activity), thus setting up a catalytic cycle whereby hydrogen peroxide and lipid peroxides can be eliminated. Since TrxR and Trx are present in all cells throughout the body, the authors proposed that this peroxidase activity provides a mechanistic explanation for the antioxidant and anti-inflammatory effects of ebselen and, in particular, for its activity in protecting cells against ischemic tissue damage. They further stated that their results “demonstrate that the mechanism of action of ebselen may be predominantly via the thioredoxin system rather than via glutathione.” Recently, Lu and Holmgren [89] have pointed out that the absence of a glutathione-based antioxidant system in pathogenic bacteria such as *Helicobacter pylori*, *Mycobacterium tuberculosis*, and *S. aureus* makes the bacterial thioredoxin-based antioxidant system essential for the survival of such organisms under conditions of oxidative stress. They therefore conclude that the inhibition of TrxR accounts for ebselen’s antibacterial activity in such organisms.

This issue of the relationship between the thioredoxin-based and glutathione-based antioxidant systems, and the possibility of cross talk between these systems, is very relevant to the findings of Casagrande et al. [90], who showed that Trx undergoes glutathionylation in human T cell blasts that had been exposed to oxidative stress. Glutathionylation, which was shown by MALDI-TOF mass spectrometry to occur on rhTrx’s Cys72 residue, abolished the ability of Trx to act as a disulfide reductase in the presence of TrxR and NADPH. The authors conclude that their finding of Trx regulation by glutathionylation indicates that cross talk exists between the thioredoxin and the glutathione systems.

With the recognition that many tumor cells exhibit a high level of expression of Trx and TrxR, which renders such cells more resistant to apoptosis and chemotherapy, there is obviously considerable interest in the clinical evaluation of TrxR inhibitors as potential anticancer agents. Ethaselen (1,2-[bis(1,2-benzisoseleazolone-3(2H)-ketone)]ethane), a novel organoselenium compound developed by Zeng and coworkers [91], is the first selenium-containing inhibitor of mammalian TrxR1.



Ethaselen

Ethaselen specifically targets the catalytically essential cysteine–selenocysteine (Cys–Sec) redox pair at the C-terminal active site of mammalian TrxR thereby

inhibiting the enzyme, and this leads to an accumulation of oxidized Trx and increased levels of reactive oxygen species. Etheselen exhibits anticancer activity with low toxicity in tumor cells and in animal models, and inhibition of cancer cell growth by ethaselen correlates with TrxR1 inactivation in several tumor cell lines. As of June 2014, recruitment was underway in China for a phase 1c single-arm study of ethaselen for the treatment of non-small cell lung cancer in patients who had previously received more than two lines of standard treatment (clinicaltrials.gov identifier: NCT02166242). Reportedly, ethaselen has now entered phase II clinical trials – presumably in China – targeting gastric, lung, and colon cancers (see Li et al. [92]).

It should be noted that a number of non-selenium-based anticancer drugs undergoing clinical evaluation are thought to target the Trx/TrxR system. Among these are PX-12 (1-methylpropyl 2-imidazolyl disulfide) for patients with advanced gastrointestinal cancers (phase Ib) [93] and motexafin gadolinium, in combination with doxorubicin (phase I) for patients with advanced solid tumors [94] and in combination with pemetrexed (phase II) for second-line treatment of patients with non-small cell lung cancer [95]. In addition, a number of well-established chemotherapeutic agents are known inhibitors of the Trx system (see Mahmood et al. [96] and references therein).

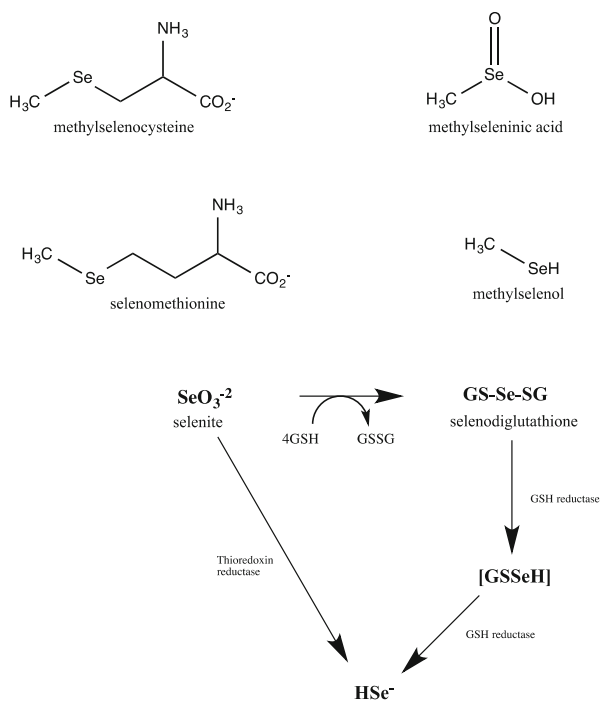
## 7 Selenium-Containing Metabolites

Several years ago, Combs [97, 98] pointed out that a number of selenium compounds had been found to be antitumorigenic in a variety of animal models at intakes that are substantially greater than those associated with maximal expression of the known selenocysteine-containing enzymes. This supports the view that the antitumorigenic effects seen in selenium supplementation studies arise at least in part from enhanced production of specific Se-containing metabolites, not just from maximal expression of selenoenzymes. Combs proposed a two-stage model in which selenium supplementation of individuals with low, nutritionally deficient, natural intakes of this element enhances the activities of protective selenoenzymes, whereas selenium supplementation of individuals who are not selenium deficient results in the beneficial buildup of antitumorigenic selenium metabolites. At about the same time, Ganther [99] reemphasized that alterations in selenoenzyme activity had failed to explain the anticancer effects of selenium, and therefore mechanisms involving low-molecular-weight selenium metabolites must also be involved. In subsequent years, a number of low-molecular-weight selenium-containing compounds known – or, quite often, simply postulated – to be formed in the course of selenium metabolism have been studied for possible therapeutic potential (see [100, 101] for recent reviews).

In this author's view, it stands to reason that the specific metabolic state of a particular cell, tissue, or organ should sensitively affect the bioactivity of a given selenium supplement or metabolite. Thus, for example, as recently mentioned by

Zeng and coworkers [91], the well-studied chemopreventive selenium compounds selenite, selenodiglutathione, and methylseleninate are all substrates of mammalian TrxR1, and the product selenium metabolites formed from these compounds play important roles in selenium-induced cytotoxicity and apoptosis in cancer cells. Therefore, the degree to which TrxR1 activity is upregulated or downregulated in a given metabolic situation or disease state would be expected to have a very significant effect on the steady-state levels of these bioactive product metabolites. In this regard, Weekley and Harris recently published [101] an excellent comprehensive review of the current evidence for the various metabolic pathways of common dietary selenium compounds, such as selenite, selenomethionine, methylselenocysteine, and selenocysteine. They conclude that dietary selenium compounds should be considered prodrugs, whose biological activity depends on the activity of the various metabolic pathways in, and the redox status of, cells and tissues. Obviously, such factors will need to be considered carefully when selecting selenium compounds for future trials of disease prevention and treatment by selenium supplementation.

As stated at the outset, a full discussion of the numerous studies on nutritional and epidemiological aspects of selenium metabolites and supplements is beyond the scope of this review. Nevertheless, a few illustrative examples will be mentioned here (Fig. 6).



**Fig. 6** Structures of some selenium metabolites

The initial step in metabolism of inorganic selenite ( $\text{SeO}_3^{2-}$ ) is its reaction with glutathione to form selenodiglutathione (GS-Se-SG), which is subsequently reduced enzymatically to hydrogen selenide ( $\text{HSe}^-$ ). Selenodiglutathione has been extensively studied by many investigators and shown to be a potent carcinostatic agent in animals and an inhibitor of cell growth and inducer of apoptosis in tumor cells [102–104]. Spyrou et al. [105] have shown that both selenodiglutathione and selenite inhibit the binding of the transcription factor AP-1 to DNA nuclear extracts of 3B6 lymphocytes. Selenodiglutathione is also a facile substrate for the thioredoxin reductase system and glutathione reductase [106] and was found to inhibit human thioredoxin by oxidation of structural thiol groups [107]. It should be noted that there are numerous published studies reporting anticancer effects of inorganic selenite itself, and it is possible that some chemoresistant malignant cells may exhibit enhanced sensitivity to selenite [108]. One promising study in *human patients* was reported by Asfour et al. [109], who found that administering high doses of sodium selenite along with standard chemotherapy increased apoptosis of lymphoma cells in adult patients with non-Hodgkin's lymphoma.

The methylated selenium metabolites methylselenocysteine and methylseleninic acid inhibit the progression and metastasis of cancer and increase survival in the transgenic adenocarcinoma of prostate mouse model [110]. Methylseleninic acid reduces the spontaneous metastasis of Lewis lung carcinoma in mice [111] and also increases the apoptosis potencies of the topoisomerase I inhibitor 7-ethyl-10-hydroxycamptothecin, the topoisomerase II inhibitor etoposide, or the microtubule inhibitor paclitaxel/taxol, in cell lines of advanced human metastatic prostate cancer against which standard chemotherapeutic treatments have limited efficacy [112]. Methylselenocysteine, which is found in foods such as garlic, onions, and broccoli, has been shown in combination with tamoxifen to inhibit MCF-7 breast cancer xenografts in nude mice through elevated apoptosis and reduced angiogenesis [113]. Methylselenocysteine and methylseleninic acid are cleaved metabolically to produce methylselenol ( $\text{MeSe}^-$ ); Ganther and coworkers [114] have shown that the production of this monomethylated selenium metabolite is a key step in cancer chemoprevention by compounds such as methylselenocysteine and methylseleninic acid. Methylselenocysteine has recently been called “a promising antiangiogenic agent for overcoming drug delivery barriers in solid malignancies for therapeutic synergy with anticancer drugs” [115].

Selenomethionine is the form of selenium used in the National Cancer Institute's SELECT trial and in a number of other selenium supplementation studies. Selenomethionine is capable of binding to methionine t-RNA and becoming incorporated into proteins in place of methionine [116]. Selenomethionine at micromolar concentration was found to inhibit growth of three human tumor cell lines, whereas growth inhibition of normal diploid fibroblasts required millimolar concentrations [117]. Thus, at least in these cell lines, cancer cells apparently exhibit greatly enhanced sensitivity to the growth inhibitory effects of selenomethionine. Mice treated orally or topically with selenomethionine were found to have significantly lowered UV irradiation-induced skin damage and reduced incidence of skin cancer

[118]. Frenkel and Caffrey [119] have reported that two selenium compounds, selenite and selenomethionine, are able to reduce the induction of resistance by ovarian cancer cells or xenografts to the chemotherapeutic agents melphalan or cisplatin. Similarly, selenomethionine and selenite were found to prevent the induction of resistance to the antitumor agent cisplatin in mice bearing tumors derived from human ovarian cells [120]. These are interesting findings, since the development of drug resistance is considered to be a major cause for the failure of chemotherapy in several types of cancer.

A clever approach to selenium-based gene-directed enzyme prodrug therapy for cancer was devised by Miki et al. [121]. Their strategy exploits the toxic prooxidant property of methylselenol, which is released from selenomethionine by cancer cells that had been transduced with the adenoviral-delivered methionine  $\alpha,\gamma$ -lyase gene. In these cells, the cytotoxicity of the selenomethionine prodrug was increased up to 1,000-fold compared with nontransduced cells. A strong bystander effect occurred due to methylselenol release from the transduced cells and uptake by surrounding tumor cells. Methylselenol damaged the mitochondria via oxidative stress and caused cytochrome c release into the cytosol, thereby activating the caspase cascade and apoptosis. These investigators also reported that treatment using their prodrug approach inhibited tumor growth in rodents and significantly prolonged their survival.

## 8 Diaryl Diselenides

In a series of nutritional and behavioral studies, diphenyl diselenide compounds were found to improve memory in a rodent model of Alzheimer's-type sporadic dementia, thereby ameliorating learning performance in these animals [122]. In subsequent studies, these investigators investigated the molecular mechanism of neuroprotection by *p,p'*-methoxyl-diphenyl diselenide in cortical neurons exposed to amyloid- $\beta$  (A $\beta$ ) peptide as well as in A $\beta$ -infused mice [123]. The diselenide compound was found to prevent A $\beta$ -induced cell death associated with the inhibition of caspase-3 and caspase-9 activities, poly(ADP-ribose) polymerase cleavage, and JNK activation. In addition, oral administration of the diselenide at 5 mg/kg for 5 days rescued memory impairment in mice that had been exposed to A $\beta$  fragment via intracerebroventricular infusion. Taken together, these findings are both timely and noteworthy, given the intense current interest in developing new approaches for the treatment of Alzheimer's disease.

Diaryl diselenides have also been investigated as potential anti-inflammatory agents. Shin et al. [124] reported that bis-(3-hydroxyphenyl) diselenide inhibits LPS-stimulated iNOS and COX-2 expression in RAW 264.7 macrophages. The diselenide compound also significantly reduced the release of TNF- $\alpha$ , interleukin (IL)-1 $\beta$ , and IL-6, and the authors provided evidence that these activities are due to the downregulation of NF- $\kappa$ B binding activity. In addition, disubstituted diaryl diselenides have been found to reduce carrageenan-induced paw edema in rats

[100], and there is a report [125] that diphenyl diselenide produces a significant peripheral antinociceptive (i.e., analgesic) effect via a mechanism that is unlike the activation of opioid, dopaminergic D2, or muscarinic cholinergic receptors.

It should be noted that in a recent review article, Nogueira and Rocha [126] refer to diphenyl diselenides as “Janus-faced” molecules, since the interaction of diphenyl diselenide with thiols can give rise to either toxic or beneficial effects. In truth, this appellation could apply as well to a number of other organoselenium compounds (see below).

## 9 Selenium Versus Sulfur in Drug Design

Although selenium and sulfur are members of the same periodic table group, there are important differences between the chemical properties of these two elements (see Iwaoka and Arai [127] and references therein for a detailed comparison). Selenium has a lower electronegativity and larger atomic radius than sulfur. Bond dissociation energies for C–Se, Se–H, and Se–Se covalent bonds are 58, 67, and 44 kcal/mol, respectively, whereas the corresponding values for sulfur are 65, 88, and 63 kcal/mol. Thus, organoselenium compounds should be more reactive than organosulfur compounds; selenols are more reactive than thiols and Se–Se bonds can be more easily cleaved than S–S bonds. Importantly, the ability of selenoxides to act as mild oxidizing agents has been recognized for decades [128].

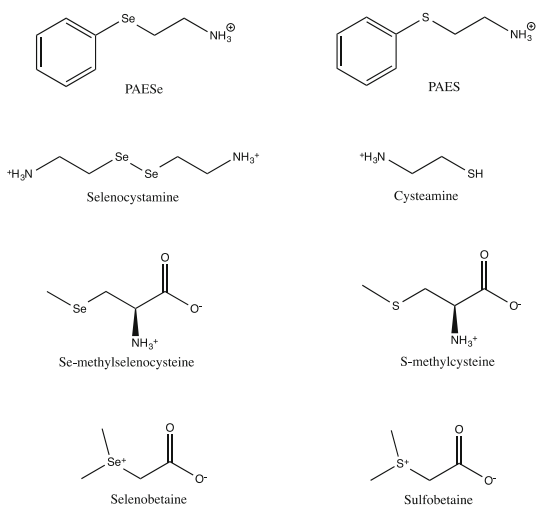
The differences between selenium and sulfur can be very significant from the perspective of drug design. One illustrative example is provided by work carried out in this author’s laboratory on the markedly differing effects of selenide versus sulfide compounds on norepinephrine production in adrenal chromaffin granules [26–29]. Both phenylaminoethyl selenide and its sulfur cognate, phenylaminoethyl sulfide, are readily taken up into chromaffin granules, where they undergo facile DBM-catalyzed heteroatom oxygenation to produce the corresponding selenide or sulfoxide product, respectively. However, only the selenoxide product has the ability to propagate a turnover-dependent redox cycle that results in local depletion of reduced ascorbate within the chromaffin vesicle. In contrast, the sulfoxide product formed enzymatically from phenylaminoalkyl sulfide is not capable of propagating such a redox cycle, and depletion of reduced ascorbate in the chromaffin granule consequently does not occur with the sulfide compound. We demonstrated [34] on the basis of potentiometric titrations that these findings are fully consistent with the redox potentials of the phenylaminoethyl selenoxides, which range from +410 to +480 mV (depending on the ring substituents) at the pH of the chromaffin granule milieu. Cyclic voltammetry experiments confirmed that the peak potentials for the reductive waves, *E<sub>pc</sub>*, for sulfoxides are ca. 500 mV lower than the *E<sub>pc</sub>* for the corresponding phenylaminoethyl selenoxides.

More than two decades ago, Ip and Ganther [104] compared the cancer chemopreventive efficacy in a rat mammary tumor model of three pairs of selenium and sulfur analogs; the compounds tested were selenocystamine/cysteamine,



Se-methylselenocysteine/S-methylcysteine, and selenobetaine/sulfobetaine. In all cases, the selenium compounds were found to be far more active in chemoprevention than their structurally similar sulfur cognates, and the authors concluded that selenium compounds may both prevent cellular transformation and delay or inhibit the expression of malignancy after carcinogen exposure. More recently, Xiao and Parkin [129] investigated the effects of 27 selenium compounds and 16 structurally related organosulfur compounds on phase II enzyme activity induction (a chemopreventive mechanism) in murine hepatoma cells, and identified nine highly active species, all of which were organoselenium compounds (Fig. 7).

The issue of the relative activities of organoselenium versus organosulfur compounds as antioxidants has been discussed by a number of investigators. For example, Steinmann et al. [130] found that the reactions of selenocysteine and selenogluthathione with tyrosyl radicals in *N*-Ac-Tyr-NH<sub>2</sub> and in insulin proceed orders of magnitude more rapidly than the reactions of the corresponding sulfur analogs. These authors point out that the effective concentration of a selenocysteine residue in the microenvironment of a selenoprotein is much higher than its concentration in the aqueous compartments of the cell, so a protective function that entails repair of radical damage to neighboring residues can be envisioned for selenocysteine. Similarly, phenylaminoethyl selenides have been found to be much more effective in protecting pUC19 DNA against peroxyntirite-induced damage than the corresponding sulfur analogs [34]. Iwaoka and Arai [127] have expressed the view that “progress in selenium biology [*has*] allowed researchers in biological chemistry to expand their research arena from sulfur to selenium.” While this statement is quite evidently true, there are likely major differences between the mechanisms that underlie the biological activities of organoselenium versus organosulfur compounds, and this must certainly be kept in mind when extrapolating to selenium from the large body of information that has accumulated over the



**Fig. 7** Selenium compounds and their sulfur analogs

years about the biology of sulfur compounds. It is reasonable to expect that relevant mechanistic details will continue to be further elucidated in future investigations.

## 10 Conclusions and Perspectives

Selenium has a long history of association with human health and disease. We now recognize that this element is an essential nutrient that is critical to key cellular processes and to the activities of a number of important enzymes. Great strides have been made over the past few years in our understanding of the biochemistry of selenium metabolism, and these efforts have been facilitated by structural determinations of low-concentration metabolites using advanced separation and mass spectral techniques. With regard to selenoproteins, we now know that the selenoproteins constituting the human selenoproteome are encoded by 25 genes in the human genome [13], and very significant progress is being made in characterizing selenoproteins and their physiological functions. As discussed by Labunsky et al. in their excellent and very recent review [131], selenoproteins not only function as antioxidant enzymes but also in diverse cellular processes such as thyroid hormone function, selenophosphate synthesis, protein folding, and protein degradation. However, the biological functions of approximately half of the human selenoproteins still remain unknown [84]. Over the coming years, we can anticipate that research efforts will be directed at answering important questions about selenoprotein function and the mechanisms by which these functions are linked to the health effects of dietary selenium and selenium metabolites in normal and disease states.

The idea that selenium-containing dietary supplements could be effective in preventing disease has gone through both optimistic and pessimistic phases. It has been recognized for decades that a deficiency of dietary selenium in certain populations is linked to cancer, cardiovascular disease, and various other disorders. Approximately 20 years ago, the Associated Press, Reuters, the New York Times, newspapers and media in many cities, and numerous Internet sites all enthusiastically reported the results of large epidemiological studies indicating that higher selenium levels are associated with a reduced risk of advanced prostate cancer. The subsequent failure of the very large and expensive SELECT trial a decade later greatly dampened the initial enthusiasm for the notion that simple dietary selenium supplementation could be an effective approach for cancer prevention. Some subsequent “postmortem” analyses of perceived flaws in the SELECT protocols did mitigate this disappointment to some extent, but it seems unlikely that government funding would be provided in the foreseeable future for any large-scale selenium supplementation trials similar to SELECT. As recently noted by Weekley and Harris [101], “with regards to the connection between selenium supplementation and disease prevention and treatment, there is an astounding gap between the

efficacy observed in laboratory studies and the mixed results of clinical trials. . .choice of selenium supplement speciation [*sic*] in laboratory and clinical studies may explain some of this efficacy gap.” Another concern that also needs to be addressed in any future long-term supplementation protocol is the possibility of long-term dietary selenium toxicity. As well stated by Nogueira and Rocha [100], a balance must be struck in supplementation studies between nutritional requirements and the potential toxicological consequences of over- or under-selenium intake. Clearly, careful attention needs to be paid to the proper formulation and dosage of selenium dietary supplements.

Dietary supplementation on the one hand and the development of new therapeutic entities on the other are quite different matters. Glutathione peroxidase (GPx) was the first mammalian enzyme whose activity was clearly shown to be dependent on selenium. Since this selenoenzyme plays such an essential role in cellular defense against detrimental oxidants, a very strong impetus emerged for the development of selenium-containing small-molecule “GPx mimics” as potential therapeutic agents against disease states known to be associated with oxidative stress. In this regard, Roberts and coworkers [70] state as follows: “GPx activity has been previously observed to plateau with increased selenium administration, even as chemoprevention increases. . .this is one reason that it is no longer thought to play an important role in selenium-mediated chemoprevention.” In this author’s opinion, it is very unlikely that this statement holds true for all classes of selenium-based compounds. As detailed in this review, many current efforts continue to focus on compounds that modulate the glutathione-based – as well as the thioredoxin-based – antioxidant systems. Nevertheless, a general concern regarding the disappointing clinical outcomes to date of therapy with *natural* antioxidants in general must be kept in mind. As stated by Murphy [132], “a large number of well-conducted clinical trials have been carried out using several different antioxidants on a range of pathologies with little improvement in clinical outcome for the patients.” Clearly, as Murphy himself concludes, more sophisticated drug design efforts are needed in the development of new chemical entities as antioxidants. It should be clear from the work described in this review that a number of such efforts with selenium-based compounds are underway.

In conclusion, it is quite evident that a number of selenium-based molecules with therapeutic potential are under development. While most of the efforts that entail *designed* organoselenium compounds – as opposed to inorganic selenium metabolites – are still at the preclinical stage, evidence is emerging that selenium-based compounds can operate by several biochemical and pharmacological mechanisms. Since our understanding of the biology, biochemistry, and pharmacology of selenium and selenoproteins is rapidly expanding, we can anticipate that the coming years will bring further development of new selenium-based pharmaceutical agents with therapeutic potential against human diseases.

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# Selenium-Functionalized Molecules (SeFMs) as Potential Drugs and Nutritional Supplements

Rob Abdur and Zhen Huang

**Abstract** Selenium (Se) is an essential element to humans and animals. Since its diverse functions were discovered, its importance has been more and more revealed. After the discovery of selenium as a key component of many proteins, significant research efforts have been focused on its therapeutic and nutritional potentials and possible impacts on human and animal health. To date, 25 selenoprotein genes have been identified in humans and animals, where selenium exists in the form of an amino acid, selenocysteine (Sec). Sec incorporation into selenoproteins occurs through a unique process by recognizing UGA stop codon via the Sec-charged tRNA for delivering Sec into proteins. Most selenoproteins are antioxidant proteins and play critical roles in maintaining redox balance in living systems by removing reactive oxygen species (ROS) and/or reactive nitrogen species (RNS). These reactive species are major threats to bio-macromolecules, such as DNAs, RNAs, proteins, lipids, and carbohydrates. They may cause molecular oxidation and DNA damage/mutation, alter gene expression patterns, weaken the immune system, and even lead to neurological disorders and other pathological conditions. As potential drugs and/or nutritional supplements, selenium-functionalized molecules (SeFMs) have shown benefits in preventing and/or treating many diseases, such as cancer, cardiovascular diseases, thyroid diseases, diabetes, AIDS, rheumatoid arthritis (RA), and neurodegenerative diseases. These promising results and therapeutic potentials of SeFMs have attracted tremendous attention from academia and pharmaceutical and biotech industries. However, further fundamental research and investigation are required to discover the ideal chemical, biochemical, and biological forms of selenium, appropriate dosages, and mechanisms of the selenium biological actions, since the tolerance window of selenium in humans may be limited.

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## Contents

1	Introduction .....	120
2	Naturally Occurring Selenium Proteins .....	124
3	Naturally Occurring Selenium Nucleic Acids .....	128
4	Artificially Seleno-Modified Nucleosides and Nucleotides and Selenium Nucleic Acids (SeNA) .....	128
5	Selenium Deficiency and Diseases .....	130
5.1	Thyroid Health .....	130
5.2	Cardiovascular Disease .....	133
5.3	SeFMs for Diabetes Treatment .....	134
5.4	Rheumatoid Arthritis .....	135
5.5	SeFMs for Cancer Prevention and Treatment .....	136
5.6	SeFMs for HIV Treatment .....	137
5.7	SeFMs for Tropical Disease Treatment .....	139
5.8	SeFMs for Neurodegenerative Disease Treatment .....	140
6	SeFMs in Clinical Trials .....	142
7	Conclusion and Perspective .....	144
	References .....	144

## 1 Introduction

Selenium is an essential trace element for humans and animals. It was discovered in 1817 by Jöns Jakob Berzelius (a Swedish physician and chemist), when he was trying to uncover the etiology of a mysterious disease among workers at a  $\text{H}_2\text{SO}_4$  plant in Gripsholm (Sweden). The reason that selenium research has become an intense field of research is because this trace element with nutritional importance has unique sets of biological activities. During early years of the twentieth century, selenium was reported as a toxic element that was manifested by feeding livestock forage grown in seleniferous soil. The first evidence of selenium essentiality in living systems appeared in the middle of the twentieth century. Selenium was reported as a nutritional factor in the formation of formic dehydrogenase in *E. coli* and *Aerobacter aerogenes* bacteria [1] and in prevention of exudative diathesis in chicks [2]. Around the same time, Klaus Schwarz and Calvin M. Foltz reported that selenium could prevent liver necrosis in rats fed with torula yeast grown in a selenium-rich medium [3]. Soon thereafter, selenium deficiency was implicated as a factor for the development of several diseases, such as white muscle disease of calves, lambs and foals, and exudative diathesis of poultry. In the late 1960s, epidemiological surveys in different parts of the United States suggested an inverse correlation between the incidences of certain cancers (particularly breast

cancer) and the selenium content of the plants growing in different regions. It took about 15 years after the establishment of selenium essentiality in human health to determine one biological role of selenium. The real excitement appeared in 1973 when selenium was found as a natural part of a redox enzyme, glutathione peroxidase (GPx) [4]. Subsequently, two other selenium-containing redox enzymes, formate dehydrogenase [5] and glycine reductase of *Clostridium thermoaceticum* (belonging to the glutathione peroxidase family), were identified [6]. Analysis of the glycine-reductase complex labeled with  $^{75}\text{Se}$  found an oxygen-labile chromophore, which implied the ionized -SeH group of the selenocysteine (Sec) residue [7]. Later, many other studies confirmed the existence of selenium in selenoproteins in the chemical form of selenocysteine [8, 9]. Sec is a cysteine (Cys) analog that differs from Cys by only one atom (selenium versus sulfur), and yet this switch dramatically influences the important aspects of the enzyme reactivity [10]. As Sec is invariably recognized by a codon and has its unique Sec-tRNA and other translation factors, Sec is referred as the 21st amino acid. Besides the glutathione peroxidase family, type 1 iodothyronine deiodinase (a Sec-containing enzyme), which catalyzes the hepatic conversion of thyroxine (T4) to triiodothyronine, was reported in the late 1980s [11, 12].

The puzzle of how selenium incorporates into the amino acid Sec and how Sec is stably co-translated into selenoprotein became clear in 1986. The mRNA sequences of glutathione peroxidase (*gpx*) of mouse [13] and formate dehydrogenase (*fdhF*) of *E. coli* [14] revealed an in-frame UGA codon (termination codon), which encodes for Sec. Simultaneously, another *cis*-acting element called Sec-insertion sequence (SECIS) element was identified at the 3'-untranslated region of mRNA, which forms the secondary structure and helps Sec-tRNA<sup>Sec</sup> to get position at the UGA codon [15, 16]. To date, 25 selenoproteins (Table 1) have been identified and characterized with various functions, such as hormone metabolism, selenium transport, antioxidant/redox properties, anti-inflammatory properties, etc. In every selenoprotein, the Sec residue invariably occupies the core position of the active site and plays very diverse but crucial role in enzymatic catalysis. Besides Sec, another selenium-containing amino acid (selenomethionine, Se-Met) also presents in proteins of all genera. But the incorporation of Se-Met into proteins is not regulated as Sec. Se-Met is randomly incorporated into protein in place of Met, and its incorporation rate depends on the availability of Se-Met during protein synthesis. Se-Met replaces methionine (Met) by charging with the same methionine tRNA (tRNA<sup>Met</sup>), which is efficiently recognized by all translational factors [54, 55]. The stably incorporated Se-Met does not significantly alter the protein structure, but may influence the activity of enzymes, if Se-Met replaces Met in the vicinity of the active site.

The natural occurrence of selenium is also reported in certain tRNAs from bacteria, archaea, and eukaryotes. The modified 5-methylaminomethyl-2-selenouridine (mnm5Se2U) has been reported to commonly occupy at the wobble position of the anticodons of tRNA<sup>Glu</sup>, tRNA<sup>Gln</sup>, and tRNA<sup>Lys</sup> [56–59]. It is thought to play a critical role in fine-tuning of codon–anticodon base pairing by positioning the Se-modified nucleotide at the first position of the anticodon. The proposed

**Table 1** Lists of 25 human selenoproteins identified to date

Entry	Selenoprotein	Short name	Main function	Subcellular or body localization
1	Deiodinase type 1	DIO1	To transform the prohormone thyroxine ( $T_4$ , 3,5,3',5'-tetraiodothyronine) to the active hormone ( $T_3$ , 3,3',5-triiodothyronine), convert $T_4$ to 3,3',5'-triiodothyronine ( $rT_3$ ), convert $T_3$ to 3,3'-diiodothyronine ( $T_2$ ), and convert $rT_3$ to $T_2$ . It can deiodinate both rings	ER (endoplasmic reticulum) membrane, plasma membrane [17, 18]
2	Deiodinase type 2	DIO2	To transform $T_4$ to $T_3$ and convert $rT_3$ to $T_2$ . It can only deiodinate the outer ring	Brain and other tissues [19]
3	Deiodinase type 3	DIO3	To transform $T_4$ to $rT_3$ and convert $T_3$ to $T_2$ . It can only deiodinate the inner ring	Cell and endosome membrane [20]
4	Glutathione peroxidase 1	GPx1/cGPx	To provide antioxidant environment (detoxification of hydrogen peroxide)	Cytoplasm and nucleus [21]
5	Glutathione peroxidase 2	GPx2/GI (gastrointestinal)-GPx2	To provide antioxidant environment (detoxification of hydrogen peroxide)	Cytoplasm [22, 23]
6	Glutathione peroxidase 3	GPx3	Detoxification of hydrogen peroxide	Skeletal muscle other tissues [24]
7	Glutathione peroxidase 4	GPx4/PH (phospholipid hydroperoxidase)-GPx	To provide antioxidant environment and protect against lipid peroxidation, redox signaling, and regulatory processes, such as inhibiting lipoxigenases and apoptosis	Cytoplasm, mitochondria, nucleus and cell membranes [25, 26]
8	Glutathione peroxidase 6	GPx6	Detoxification of hydrogen peroxide	Secreted, found only in olfactory epithelium and embryonic tissues [27, 28]
9	Thioredoxin reductase 1	TRxR1	Ubiquitous cytoplasmatic housekeeping enzyme, reduction of thioredoxin and other substrates	Cytoplasm, mitochondria, nucleus [29]
10	Thioredoxin reductase 2	TRxR2	Reduction of thioredoxin, disulfide bond isomerization, thioredoxin/glutaredoxin/glutathione reductase	Mitochondrial [30, 31]
11	Thioredoxin reductase 3	TRxR3	Reduction of thioredoxin, defense against oxidative stress	Mitochondrial, nucleus cytoplasm [32]

12	Selenoprotein H	SeH	Redox-sensing DNA-binding protein, antioxidant defense, and phase II detoxification	Overexpressed in brain, specific location unknown [33]
13	Selenoprotein I	SeI	Unknown	An integral membrane protein [34]
14	Selenoprotein K	SeK	Antioxidant defense, calcium regulation, ER-associated protein degradation	Membrane ER [35, 36]
15	Selenoprotein M	SeM	Thiol disulfide oxidoreductase, formation of disulfide bonds, calcium responses	ER, highly expressed in the brain [37, 38]
16	Selenoprotein N	SeN	Essential for muscle regeneration and satellite cell maintenance	ER membrane [39]
17	Selenoprotein O	SeO	Redox-dependent activity/specific function unknown	Unknown [40]
18	Selenoprotein P	SePP	Se transport and delivery, modulate metal ion-mediated A $\beta$ aggregation, reactive oxygen species (ROS) production, and neurotoxicity	Secreted [41–43]
19	Selenoprotein S	SePS/SeS	Inflammatory response, regulation cytokine production, protection against ER-stress-induced apoptosis	Plasma and ER membrane protein [44, 45]
20	Selenoprotein T	SeT	Intracellular Ca <sup>2+</sup> mobilization and neuroendocrine secretion	Plasma membrane/Golgi/ER [46]
21	Selenoprotein V	SeV	Redox-related function	Unknown/seminiferous tubules of the testes [34]
22	Selenoprotein W	SeW	Antioxidant, redox metabolism	Cytoplasm, cell membrane [47, 48]
23	Selenophosphate synthetase 2	SPS2	Conversion selenide to selenophosphate	Unknown [49, 50]
24	15 kDa	SeP15	Form complex with UDP-glucose:glycoprotein glucosyltransferase 1, prevent transport of improperly folded glycoproteins out of the ER	ER [51, 52]
25	Thioredoxin glutathione reductase	TGR	Testis-specific enzyme; it can reduce glutathione disulfide, while its specific function unknown	ER [53]

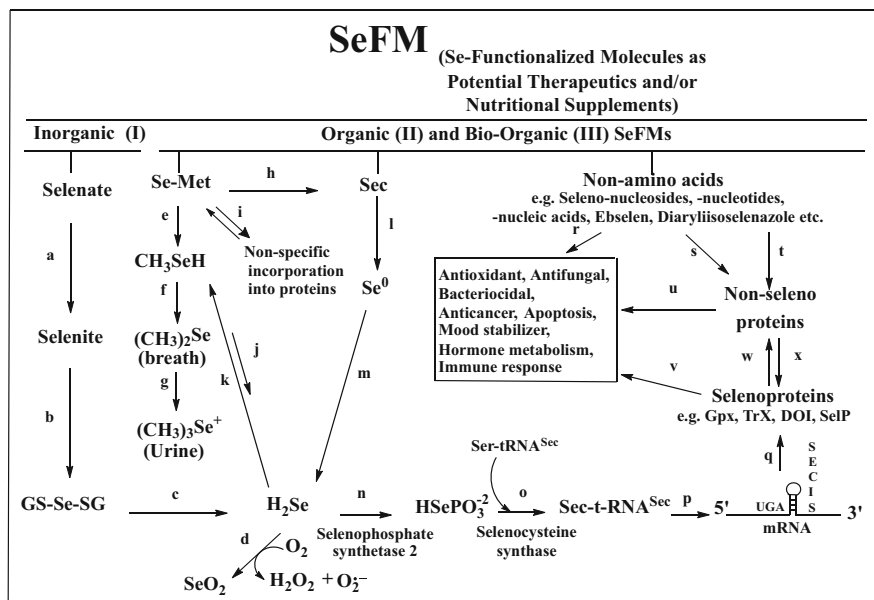


selenium function at the wobble position is supported by the recent research from Zhen Huang and co-workers [60–62]. In addition, the selenium introduction as a heavy atom via Se-Met into protein provides a magnificent tool to solve the phase problem in X-ray crystal structure determination of proteins. In the structure determination, selenium acts as a suitable resonance center for anomalous dispersion in MAD and SAD experiments, which require synchrotron radiation with precise beam wavelength control [63–68]. For nucleic acid structure studies, Zhen Huang and co-workers have developed selenium nucleic acids [61, 62, 68–72] to derivatize nucleic acids and protein–nucleic acid complexes for nucleic acid–protein X-ray crystallography [68].

The selenoproteins have a wide range of pleiotropic effects, ranging from antioxidant and anti-inflammatory properties to the production of active thyroid hormone. In the past 10 years, a large number of research projects have been dedicated to discover the disease-associated polymorphism in selenoprotein genes. Selenium is an essential microelement because of its participation in many important enzymes, and its deficiency hampers or reduces the activities of many enzymes essential for proper physiological functions. The two most notable classes of selenoproteins are antioxidants and deiodinases. The roles of antioxidant proteins are to scavenge or neutralize reactive oxygen species (ROS) and reactive nitrogen species (RNS) from the body, where they are continuously generated during normal metabolic and respiratory processes. These ROS and RNS are the major oxidation threats to bio-macromolecules, and they or their by-products may also cause alkylation of DNA, RNA, proteins, lipids, and/or many other biomolecules, which are potentially linked with many diseases, such as cardiovascular diseases, cancers, AIDS, neurodegenerative diseases, thyroid diseases, rheumatoid arthritis, etc. Selenoproteins have been reported to prevent these diseases by removing ROS and RNS. Selenium supplementation may help to maintain a proper level of selenoproteins, thereby reducing the threat of ROS and/or RNS in plasma and preventing many deadly diseases. Selenoproteins have a number of biological functions in oxidoreductions, redox signaling, antioxidant defense, thyroid hormone metabolism, and immune responses. This review focuses on the recent advancement and a few pathological conditions and/or diseased states that may be prevented by or even cured with selenium-functionalized molecules (SeFM; Fig. 1).

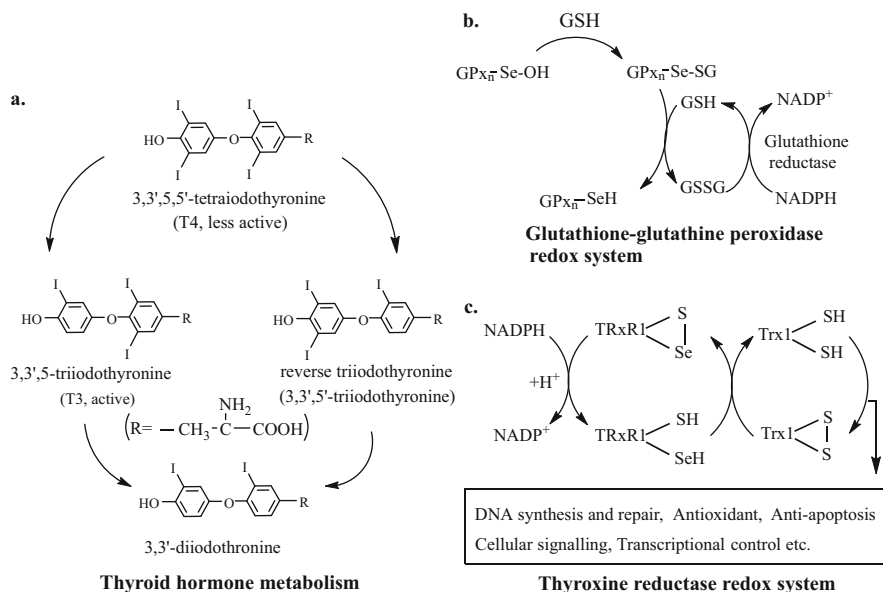
## 2 Naturally Occurring Selenium Proteins

Twenty-five selenoproteins have been identified in humans with different functions in different subcellular locations (Table 1). Selenoproteins are mostly enzymes that constitute two major metabolic pathways (Fig. 2), namely, redox metabolism and thyroid hormone metabolism (discussed later). The selenoproteins with redox activities are ubiquitous and help to maintain redox balance along with other pathways in the body. The selenoprotein GPx operates with a small ubiquitous



**Fig. 1** Potential metabolic mechanisms of Se-functionalized molecules (SeFMs) in the human body. SeFM enters the body in inorganic (I), organic (II), and/or bio-organic (III) forms. Selenium inorganic forms (selenate and selenite taken as supplements) are converted into hydrogen selenide (less reactive) through several reductions (*a–c*). The hydrogen selenide is phosphorylated and converted into selenophosphate by selenophosphate synthetase enzyme in an ATP-driven process (*n*). The highly active selenium donor (selenophosphate) donates selenium functionality to the serine-charged tRNA<sup>Sec</sup>, catalyzed by selenocysteine synthase, and produces Sec-tRNA<sup>Sec</sup>. The Sec-tRNA<sup>Sec</sup> is positioned on an in-frame UGA codon of an mRNA containing SECIS secondary hairpin structure during translation process (*q*), generating selenoproteins. The most common forms of the organic seleno-compounds are Sec and Se-Met, which are derived from the hydrolysis of proteins ingested as diet. Se-Met can be readily incorporated into proteins nonspecifically (*i*). Sec, which can be formed from Se-Met by the *trans*-selenization process (*h*) and derived from hydrolysis of selenoproteins, undergoes several chemical transformations and forms hydrogen selenide via elemental selenium (*l* and *m*). Methylation of the hydrogen selenide could readily occur and produces methyl selenol (CH<sub>3</sub>SeH) (*k*), which can also be formed from Se-Met (*e*). Further methylation of methyl selenol (CH<sub>3</sub>SeH) produces dimethyl selenide [(CH<sub>3</sub>)<sub>2</sub>Se] and trimethyl selenonium ion [(CH<sub>3</sub>)<sub>3</sub>Se<sup>+</sup>], which are excreted from the body through the breath and urine, respectively. The non-amino acid selenium compounds (including organic and bio-organic SeFMs) may also act as potential drugs and/or nutritional supplements [73, 74] in order to supply selenium for maintaining the proper level of selenoproteins and producing beneficial physiological effects [75, 76]

peptide called glutathione (GSH) and forms one of the major pathways to neutralize or reduce reactive oxygen species (ROS) and reactive nitrogen species (RNS), which are generated continuously during metabolic and respiratory processes. In the GSH–GPx redox system, the sulfur-containing peptide glutathione (GSH) is a cofactor and acts as a reducing substrate in the peroxidase reaction. During the GPx catalytic cycle, the selenenic acid form (GPx–Se–OH) reacts with GSH and



**Fig. 2** General catalytic mechanisms of human selenoproteins. Selenoproteins constitute two major classes of enzymes: deiodinases (**a**) and antioxidants (**b** and **c**). Deiodinases are responsible for converting the less-active thyroid hormones T<sub>4</sub> into active form T<sub>3</sub>. Among the several redox systems in humans, glutathione–glutathione peroxidase (**b**;  $n = 1, 2, 3, 4,$  or  $6$ ) and thioredoxin–thioredoxin reductase (**c**) redox systems are very important for detoxification of ROS in the body. In the glutathione–glutathione peroxidase redox system, glutathione is a cofactor and acts as a reducing substrate. During the catalytic cycle, oxidized di-glutathione is reduced by the enzyme, glutathione reductase. Thioredoxin–thioredoxin reductase (**c**) system can also detoxify ROS, but this system has broader substrate specificity

generates GPx–selenenyl-sulfide adduct (GPx–Se-SG). Subsequently, the adduct reacts with an additional GSH to regenerate the active selenol (GPx–SeH), which reduces a peroxide molecule (Fig. 2) [77, 78]. Another selenoprotein family, involved in redox defense system, consists of thioredoxin, thioredoxin reductase, and peroxiredoxin. This is also a major redox pathway and plays a diverse role in metabolism with broader substrate specificity. This powerful system is involved in many central intracellular and extracellular processes, including cell proliferation, the redox regulation of gene expression and signal transduction, protection against oxidative stress, anti-apoptotic functions, growth factor and co-cytokine effects, and regulation of the redox state of the extracellular environment [79, 80] (Fig. 2).

Selenium in proteins exists as amino acid selenocysteine (Sec) and selenomethionine (Se-Met). The presence of selenium atom in proteins confers many advantages in protein functionality. Selenium belongs to the same elemental family (VI A) as oxygen and sulfur in the periodic table. Although the selenium atom (atomic radius, 1.16 Å) is bigger than oxygen (atomic radius, 0.73 Å) and sulfur (atomic radius, 1.02 Å) atoms, their chemical and electronic properties are closely related. As a result of this functional similarity with oxygen and sulfur, but

bigger atomic size on the other hand, incorporation of selenium into biomolecules offers many unique and important advantages. Due to the larger electron density, one of the major advantages is that selenium can exist in multiple oxidation states, such as elemental selenium (0), selenide ( $-2$ ), selenite ( $+4$ ), and selenate ( $+6$ ), which largely depend on the chemical properties of the environment. The reactivity of a selenoprotein arises from the selenol ( $-SeH$ ) side chain of the Sec residue. This SeH functionality provides unique properties to selenoprotein over other residues in the protein. The  $pK_a$  value of the SeH group in Sec is lower ( $pK_a$  5.2), compared to the SH group in Cys ( $pK_a$  8.5). As a result of lower  $pK_a$ , the SeH side chain is more acidic and remains deprotonated at physiological pH, which makes the SeH a more powerful reductant and stronger nucleophile. Most of the selenoproteins are enzymes, and their Sec residues are conveniently located in or near an active site in the close proximity with Cys residue. The catalytic function of a selenoprotein enzyme is dependent on the interplay or shuttling of electrons among SeH, SH groups, and cofactors (if any).

On the other hand, selenium in Se-Met exists as  $-Se-CH_3$  side chain, and proteins containing Se-Met do not completely depend on the Se function for their activity. Se-Met is an essential amino acid, and it cannot be synthesized de novo in humans. It must be ingested in the form of Se-Met or protein containing Se-Met. Plants and microorganisms can introduce selenium in place of sulfur during Met biosynthesis. In eukaryotes, if Se-Met is available, it can be charged onto  $tRNA^{Met}$ , which is recognized by all other translational components and stably incorporated into proteins in place of Met. Se-Met incorporation into protein is random, and it depends on the availability of Se-Met [81–83]. Se-Met does not significantly alter the protein structure, but may influence the activity of enzymes, if Se-Met replaces Met in the vicinity of the active site. In contrast, Sec may remain in the free form and cannot be introduced into protein readily. It is incorporated into protein via a specific translational control process, which is unique in relation to the standard protein translation [84]. The Sec incorporation into selenoproteins is discovered in all three domains of life: bacteria, archaea, and eukarya [85]. The pathway for selenocysteine incorporation into protein in archaea and eukarya is very similar to *E. coli*. Selenoprotein synthesis in *E. coli* begins with the acylation of the 3'-end of a special  $tRNA^{Sec}$  (encoded by *selC* gene) with L-serine by seryl-tRNA ligase, thus producing seryl-tRNA<sup>Sec</sup> (Ser-tRNA<sup>Sec</sup>) [86]. The  $tRNA^{Sec}$  has many unique and unusual features, such as formation of *O*-phosphoseryl-tRNA [87], its anticodon (UCA) suppressing UGA termination codon [88], longer in size (90 nucleotides in eukaryotes), relatively fewer base modifications [89, 90], and the unique cloverleaf model with a long extra arm [91]. The serine residue on the Ser-tRNA<sup>Sec</sup> is converted into Sec and forms Sec-tRNA<sup>Sec</sup> in two-step reactions by the pyridoxal 5'-phosphate-dependent enzyme, selenocysteine synthase (product of *selA* gene, EC 2.9.1.1). In the first step, a Schiff base is formed between  $\alpha$ -amino group of serine and carbonyl of pyridoxal 5'-phosphate, followed by 2,3-elimination of a water molecule to yield enzyme-bound dehydroalanyl-tRNA<sup>Sec</sup> intermediate. In the second step, nucleophilic addition of monoselenophosphate to the double bond of the dehydroalanyl residue produces selenocystyl-tRNA<sup>Sec</sup> [92–95]. The highly

active Se donor (monoselenophosphate) is formed by transferring  $\gamma$ -phosphate of ATP to hydrogen selenide, which is catalyzed by selenophosphate synthetase (product of *selD*) [96]. Once Sec-tRNA<sup>Sec</sup> is formed, the Sec-tRNA<sup>Sec</sup> is recognized by a *cis*-acting element, Sec-insertion sequence (SECIS), a secondary structure on the selenoproteins mRNA that helps in docking Sec-tRNA<sup>Sec</sup> at UGA codon and directs selenocysteine incorporation into protein [97–99]. A Sec-specific elongation factor (product of *selB* gene) binds to Sec-tRNA<sup>Sec</sup> and SECIS and guides the incorporation of Sec onto nascent selenoprotein [100–102]. In archaea and eukarya, *O*-phosphoseryl-tRNA<sup>Sec</sup> kinase phosphorylates the hydroxyl group of serine on seryl-tRNA<sup>Sec</sup> [103, 104], and the resulting *O*-phosphoseryl-tRNA<sup>Sec</sup> is subsequently converted to selenocysteinyl-tRNA<sup>Sec</sup> by Sec synthetase.

### 3 Naturally Occurring Selenium Nucleic Acids

The natural occurrence of selenium in certain tRNAs was also reported in bacteria [59, 105], archaea [58, 106], mammals [107], and plants [108]. The discovery of the presence of naturally occurring selenium in tRNAs further provides the evidence at the molecular level for the nutritional role of selenium in life. It is not clear whether selenium can be directly incorporated into nucleosides naturally. Nonetheless, the presence of seleno-modified uridine residue (5-methylaminomethyl-2-selenouridine, mnm<sup>5</sup>Se<sup>2</sup>U) in tRNAs was reported, and mnm<sup>5</sup>Se<sup>2</sup>U occupies the wobble (first) position of the anticodon of the tRNAs for glutamate (tRNA<sup>Glu</sup>), glycine (tRNA<sup>Gln</sup>), and lysine (tRNA<sup>Lys</sup>) in bacteria [56, 59, 109]. This modified nucleoside is thought to play a critical role in the fine-tuning of codon–anticodon base pairing by positioning the Se modification at the first position of the anticodon. In the anaerobic microorganism, *Clostridium sticklandii*, the most prominent selenium-containing tRNA was identified as the major glutamate-accepting species in the bulk tRNA preparation. It has been proposed that the presence of selenium in this tRNA<sup>Glu</sup> is essential for its aminoacylation activity [58, 106, 110].

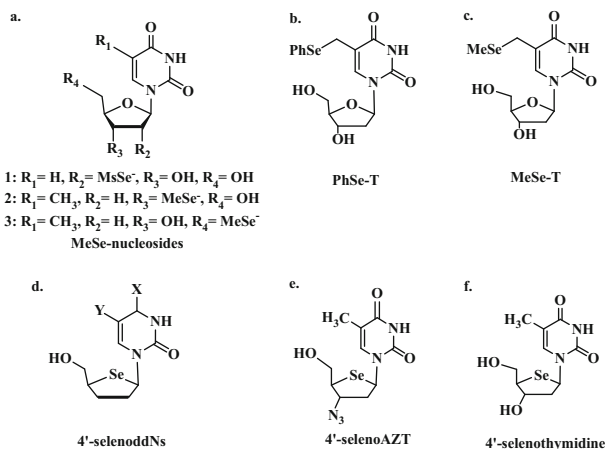
### 4 Artificially Seleno-Modified Nucleosides and Nucleotides and Selenium Nucleic Acids (SeNA)

The presence of the Se modification in natural tRNA has encouraged Huang and co-workers to pioneer and incorporate the selenium functionalities at various selected positions of RNA and DNA, namely, selenium-derivatized nucleic acids (SeNA) [68–71, 111–115]. Their experimental data have demonstrated that nucleic acid oxygen in various positions can be stably replaced with selenium for structure and function studies, especially the facilitation of phase solution, crystallization, and high-resolution structure determination in X-ray crystallography. Their studies

imply that selenium functionalities on nucleobases might improve the accuracy and efficiency of translation, RNA transcription, and even DNA replication by enhancing base-pair interaction, selectivity, and fidelity. For instance, the biochemical study of RNase H with the Se-modified DNA/RNA duplexes showed that the Se-modified nucleobase functionality can enhance the enzyme turnover rate by manyfold [68]. The supporting evidence from X-ray crystallographic structures has revealed that as a larger atom, the selenium functionality causes local unwinding of DNA/RNA substrate duplex. The Se-functionalized DNA acts as a guiding sequence shifting the scissile phosphate of the RNA substrate closer to the active site, therefore further activating the attacking nucleophilic water molecule [68]. Previously, it has been reported that the selenium-modified nucleic acids can resist nuclease digestion [116–118]. Thus, this Se-atom-specific mutagenesis (SAM) has opened a new research area to further explore and design nucleic acid-based novel therapeutics as well as nutritional supplements.

Therapeutic nucleosides, nucleotides, and nucleic acids can be used to block or interfere with specific pathological processes or pathways. The most common targets of these therapeutics are cancers and viruses. The potential oligonucleotide therapeutics, such as small interference RNAs (siRNA), antisense DNAs, or CRISPR-RNA (crRNA) [119, 120], are based on sequence complementarity to the target RNAs (such as mRNAs) or DNAs (such as genomic DNA). This is an intensely advanced area, because the short oligonucleotides can target a specific RNA very precisely and hydrolyze the RNA by Dicer–Argonaute system [121–125] or target a specific DNA by crRNA and Cas system [119, 120, 126]. Potential application of the Se functionalities in short oligonucleotides could offer additional benefits to the oligonucleotides by improving the base-pair stability, selectivity, and fidelity, by enhancing the catalytic rate, and by conferring resistance to nuclease digestion. However, extensive *in vivo* research is needed in order to take full advantage of all Se modifications, especially the Se-nucleobase functionalities [61, 68, 72, 127].

As we know, nucleoside analogs are a major class of chemotherapeutic agents that disrupt DNA and/or RNA synthesis (or repair) in targeting malignant cancer cells or viruses. Because the proliferative status of a malignant cell is higher than that of a normal cell, the malignant cell always maintains an elevated concentration of nucleosides. Thus, the malignant cells are generally more sensitive to modified nucleoside agents disrupting nucleic acid synthesis. However, research on the Se-modified therapeutic nucleosides is limited; few Se-modified nucleosides have been investigated to target cancers and viruses. Recently, after pioneering and developing selenium nucleic acids (SeNA) for the function and X-ray crystal structure studies [68–71, 111–115], Huang and co-workers have also investigated several Se-modified nucleosides for anticancer activity against various tumor cell lines. They reported that the MeSe nucleosides have relatively fine solubility in aqueous solution, have anticancer effects, and can generally inhibit cancer cell growth (Fig. 3). Among them, 5'-Se-thymidine (**3** in Fig. 3a) is more active than the other Se nucleosides against these prostate cancer cell lines [128]. Recently, Kim and co-workers [129] reported the synthesis of two Se-modified nucleosides:



**Fig. 3** Chemical structures of selenium-modified nucleosides used as anticancer and antiviral therapy. (a) Among these three MeSe nucleosides, compound 3 was more effective as cytotoxic agent. (b) and (c) PhSe-T and MeSe-T mediate apoptosis induced by p38 pathway. (d) 4'-SelenodN, (e) 4'-seleno-AZT, and (f) 4'-selenothymidine; they are inhibitors of reverse transcriptase

5-phenylselenenyl-methyl-2'-deoxyuridine (5-PhSe-T) and 5-methylselenenyl-methyl-2'-deoxyuridine (5-MeSe-T). They have been evaluated for the cytotoxic effect on human cancer cells (Fig. 3b and c). Their caspase activity study suggested that these nucleoside derivatives induced apoptosis by interfering with caspase-2 and caspase-3 pathways and, to a lesser extent, caspase-8 pathway. Another study on HL-60 cells by the same group suggested that the apoptosis induced by 5-PhSe-T and 5-MeSe-T is attributed to p38 pathway. This p38 pathway served as a link between ROS generation and DNA damage/caspase activation [129]. Moreover, several other Se-modified nucleosides have been investigated against HIV as potent inhibitors of reverse transcriptase (Fig. 3d-f) [130].

## 5 Selenium Deficiency and Diseases

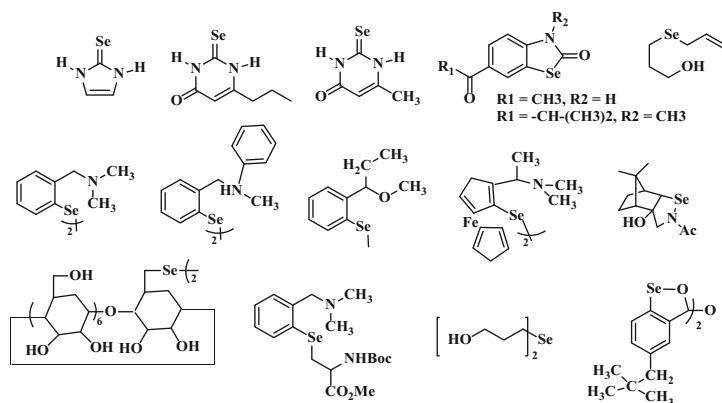
### 5.1 Thyroid Health

The role of selenium in thyroid function has been established for a long time. In thyroid gland, the amount of selenium per gram of the tissue is the highest among all organs in human body [131, 132]. As an essential micronutrient, selenium is as important as iodine for the production of thyroid hormone thyroxine (or triiodothyronine,  $T_3$ ) and the maintenance of thyroid hormone homeostasis [133]. Thyroid peroxidase (TPO) is the major enzyme produced by the thyroid gland [134, 135], and it is a heme-containing oxidoreductase that catalyzes stepwise

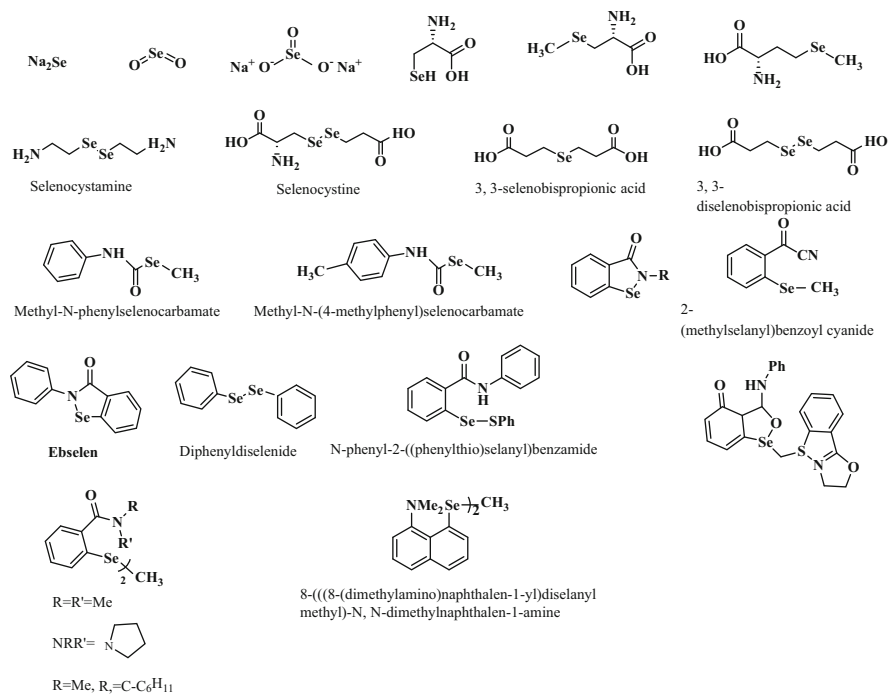
iodination of the tyrosine residue on thyroglobulin to produce thyroxine or 3,3',5,5'-tetraiodothyronine (T4). The selenoenzyme iodothyronine deiodinase converts inactive thyroxine (T4) to its more active 3,5,3'-triiodothyronine form (T3) by removing one iodine atom [136, 137]. Three isozymes of the selenoproteins, iodothyronine deiodinase, types 1, 2, and 3 (DIO1, DIO2, and DIO3), have been characterized and cloned [20, 138, 139]. The expression and function of these isozymes are tightly regulated in a tissue-specific manner and represent a new family of eukaryotic selenoproteins. Two other seleno-enzymes, the antioxidant enzyme (such as glutathione peroxidase) and the redox enzyme (such as thioredoxin reductase), are present in thyroid glands in order to maintain proper environment for thyroid activity [140]. The role of glutathione peroxidase in the gland is to protect the thyroid cells from oxidative damage by catalyzing the reduction of  $H_2O_2$  with the help of thiol co-substrates, such as glutathione (GSH). The human TRxR also plays important roles in detoxifying ROS in the thyroid gland [132, 141, 142]. Therefore, adequate supply of both iodine and selenium is necessary for thyroid homeostasis and thyroid health. One of the most common thyroid diseases is hyperthyroidism, also called Graves' disease, often referred to as an overactive thyroid. Hyperthyroidism is a condition where the thyroid gland produces and secretes excessive amounts of thyroid hormones that circulate in the blood [143]. A number of studies have demonstrated an increase in oxidative stress and generation of ROS in Graves' disease and also reported an increased production of malondialdehyde found in urine [144].

In Graves' disease, the balance between intracellular and extracellular oxidants and antioxidants appears to be disturbed, and overall GPx activity has been reported to be diminished [145]. In treating hyperthyroidism, methimazole (MMI), propylthiouracil (PTU), and methyl thiouracil (MTU) are the commonly prescribed drugs for adult and pediatric patients. Recently, the FDA has issued a warning that use of PTU is associated with a higher risk for clinically serious or fatal liver injury compared to MMI in both adult and pediatric patients. There are also clinical study reports on the resistance of MMI in patients with hyperthyroidism in spite of good compliance [146]. In recent years there have been renewed interest is grown in developing selenium analogs of antithyroid drugs, such as, MMI (MSeI), PTU (PSeU), and MTU (MSeU) (Fig. 6). Besides toxicity and drug resistance, there are several other initial assumption was made for the selection of the selenium analog over thiol containing compounds. Selenium is a better nucleophile than sulfur; therefore, the seleno-compound may exhibit higher inhibitory effect toward ID-1, compared to the sulfur drug. As these compounds are anticipated to react with the selenenyl iodide intermediate of ID-1, the formation of Se–Se bond may occur more readily than the formation of Se–S bond [147]. In addition, the seleno-compounds may have a significant effect in neutralizing  $H_2O_2$ . There are a few other low-molecular-weight seleno-compounds listed in Fig. 4 that were designed and synthesized by several different groups to mimic Gpx activity as ebselen. These compounds are generated either by modifying the basic structure of ebselen or by incorporating some structural features of the native enzyme. The synthetic GPX mimics reported in the literature include benzoselenazolinones, selenenamide,





**Fig. 4** Chemical structures of SeFMs for the treatment of thyroid diseases



**Fig. 5** SeFMs investigated for antioxidant activity, including ROS scavenging for the treatment of cardiovascular disease

diaryl selenide, various diselenides, hydroxyalkyl selenides, a selenocysteine derivative, and a selenenate ester (Fig. 4).

Selenium deficiency is implicated in several other thyroid diseases. Chronic lymphocytic thyroiditis is the most common thyroid autoimmune disease where iodine supply is insufficient. Administration of selenium in the form of selenomethionine or sodium selenite along with levothyroxine substitution therapy improves the pathogenic conditions [148, 149]. The thyroid disease myxoedematous cretinism is also found to associate with selenium deficiency. Myxoedematous cretinism is characterized by the persistence of hypothyroidism despite of supplement with iodine. It has been reported that supplementation with iodine alone has no effect, but when together with selenium, it improves the pathogenic condition of myxoedematous cretinism [150].

## 5.2 Cardiovascular Disease

Cardiovascular disease (also called heart disease) is the number one disease causing death and disability worldwide [151, 152]. There are diverse causes for cardiovascular disease, but the main causes are arteriosclerosis and hypertension [153]. The manifestation and progression of arteriosclerosis involve the triad: hyperlipidemia, oxidative stress, and inflammation [154]. Hyperlipidemia is the condition of elevated level of low-density lipoprotein (LDL) in the blood, which is eventually deposited in adipose tissues. Lipids are the primary targets for oxidative modification (oxidative stress consequence) enzymatically or by free radicals, because they are the main repository of oxidizable olefinic or double bond [155]. Subsequently, these oxidized lipids activate an NF $\kappa$ B-like transcription factor and induce the expression of genes containing NF $\kappa$ B binding sites, which initiate the production of various cytokines [156, 157] involved in inflammation. The inflammatory response leads to the development of the fatty streak and atherosclerotic plaque. Many studies have clearly demonstrated that selenium can greatly reduce cardiovascular risks (such as arteriosclerosis, myocardial hypertrophy, etc.) and help to maintain cardiac health by enhancing antioxidant role of selenoproteins, especially glutathione peroxidases. These cardioprotective effects are thought to confer through the antioxidant actions of selenoprotein enzymes, which directly limit the levels of ROS (such as hydrogen peroxide, H<sub>2</sub>O<sub>2</sub>) and reverse the oxidative damages to lipids and proteins [158–160]. It is generally accepted that the GPx level is decreased by the instability of GPx mRNA at low selenium intakes [161, 162].

In the glutathione–GPx redox system, the sulfur-containing peptide glutathione (GSH) is a cofactor and acts as a reducing substrate in the reduction of peroxidases. During the GPx catalytic cycle, the selenenic acid of GPx reacts with GSH to generate GPx–selenenyl-sulfide adduct (GPx–Se–SG). Subsequently, the adduct reacts with an additional GSH to generate the active selenol (GPx–SeH), which in turn reduces peroxide [77, 78]. Another selenoprotein family, involved in redox

defense system, consists of thioredoxin, thioredoxin reductase (TRxR), and peroxiredoxin, which play a pivotal role in both hematopoiesis and heart function. Among three types of TRxR in humans, the cytosolic TRxR1 and mitochondrial TRxR2 are required for protecting heart from ROS or free radical-mediated damages [163, 164]. The primary function of the TRxR system in normal cell is to keep thioredoxin (Trx) in reduced state, serve as a redox regulator for cell signaling, and contribute to the antioxidant defense to cells [165, 166].

SeFMs as potential therapeutics and nutritional supplements have been reported to prevent cardiovascular risks and/or to treat cardiovascular diseases. Some SeFMs (Fig. 5) have been studied for preventing or treating cardiovascular diseases by many research laboratories. Though the exact mechanisms of actions for these compounds are not clear, it has been proposed that the cardioprotective effects may be attributed to the antioxidant defense [167]. One particular organo-seleno-compound, diphenyl diselenide (DPDS), has been reported to inhibit human LDL oxidation, and this phenomenon was related to the thiol-peroxidase activity [168]. Another SeFM, ebselen (2-phenyl-1,2-benzisoselesazol-3(2*H*)-one), has been investigated for a long time and is a nontoxic organo-seleno-compound that has anti-inflammatory, anti-atherosclerotic, and cytoprotective properties. Ebselen acts by mimicking the active site of GPx, and it is also an excellent scavenger of peroxynitrite. Moreover, it inhibits activities of cyclooxygenase and lipoxygenases at the micromolar concentrations [169, 170].

### 5.3 *SeFMs for Diabetes Treatment*

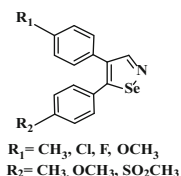
Diabetes mellitus (DM) affects over 170 million people worldwide, with more than 90% of the patients suffering from type 2 diabetes (T2D) [171]. T2D is a heterogeneous metabolic disorder characterized by increased blood sugar level resulting from the resistance of liver, skeletal muscle, and fat tissue to insulin. These conditions cause dyslipidemia, hyperglycemia, and an increase in insulin secretion by pancreatic beta cells for compensation of the poor insulin response by major target tissues [172–175]. T2D is a major risk factor for the incidence of cardiovascular disease characterized by arteriosclerosis and hypertension [153, 176, 177]. In the United States, 12.9% of the adults older than 20 have T2D, of which 39.8% remain undiagnosed [178, 179]. The relationship between glucose metabolism and selenium status in the body is conflicting [180]. In spite of the antioxidant effect of many selenoproteins in maintaining redox balance in the cellular system, some studies indicate a deleterious effect of selenium in T2D. A cross-sectional study on almost 9,000 American adults, along with other analysis, showed a positive link between high selenium levels and T2D [181, 182]. A similar study performed on 7,182 women from Northern Italy has indicated that the increased dietary selenium intake is associated with an increased risk of T2DM [183]. It has also been suggested that selenium impairs hepatic insulin sensitivity through opposite regulation of ROS [184].

In the insulin signaling pathway, binding of insulin to its receptors initiates a signaling cascade with a mild oxidative burst, where  $H_2O_2$  acts as secondary messenger [180]. In turn,  $H_2O_2$  oxidizes redox-regulated Cys residues, therefore leading to the deactivation of tyrosine phosphatase 1B (PTP-1-B) and tensin homolog protein (PTEN). PTP-1B deactivates insulin receptor substrate (IRS), whereas PTEN inhibits phosphatidylinositol 3-kinase (PI3K). This results in overall stimulation of the signaling pathway for glucose uptake [185–187]. The selenoproteins (such as glutathione peroxidase 1) reduce  $H_2O_2$ ; therefore, the presence of antioxidant proteins produces an inhibitory action on the signaling cascade [188, 189]. However, it has been observed that insulin combined with selenium significantly decreased blood glucose levels and maintained the expression of insulin receptor substrate (IRS-1), phosphatidylinositol-3 kinase (PI3K), and glucose transporter 4 (GLUT4) in skeletal muscles of diabetic rats [190]. This experimental result indicates that the relation between insulin and selenium still remains a challenging mystery, which requires more investigation.

#### 5.4 Rheumatoid Arthritis

Rheumatoid arthritis (RA) is an autoimmune condition with unknown etiology. It is characterized by chronic inflammatory polyarthritis with progressive erosion of tissues within and surrounding the joints. It affects 1% of the population and is associated with significant morbidity and increased mortality [191]. Recent studies indicate a possible role of selenium on the etiology and disease progression of RA. Clinical data shows that patients with RA have a lower level of selenium in serum, compared to healthy controls [192, 193]. The exact mechanism is unknown, but it is assumed that selenium deficiency affects the signaling pathway of nuclear factor kappa-B (NF- $\kappa$ B), which is correlated with interleukin-6 and TNF- $\alpha$  production [194, 195]. Recently, diaryl isoselenazole compounds (4,5-diaryl isoselenazoles) have been reported (Fig. 6) as multiple target nonsteroidal anti-inflammatory drugs (MTNSAIDs) for the inhibition of inflammatory processes [196]. This SeFM could be a safe alternative as a nonsteroidal anti-inflammatory drug (NSAID), which is associated with serious side effects, such as hypertension, gastrointestinal hemorrhage, ulceration, and kidney failure [197]. The mechanism of NSAIDs is to inhibit cyclooxygenase enzymes (COX-1 and COX-2), which catalyze the biotransformation of arachidonic acid to the prostaglandins [198, 199]. But the new class MTNSAIDs (4,5-diaryl isoselenazoles) have been

**Fig. 6** Diaryl isoselenazole, a new class of SeFMs with dual COX/LO inhibition property



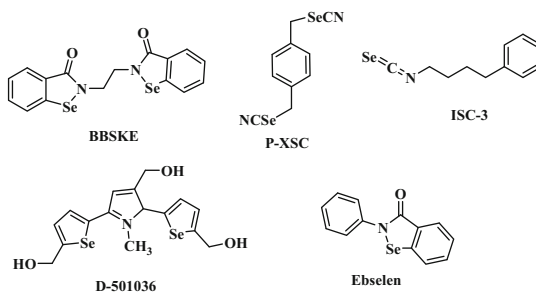
described as dual COX/LO inhibitors with potential radical scavenging by the selenium moiety. This compound is related to the well-known SeFM ebselen with a variety of beneficial properties, such as antioxidant function, radical inactivation, and lipid peroxidase inhibition.

## 5.5 *SeFMs for Cancer Prevention and Treatment*

Cancer is becoming an increasingly deadly disease, and there are seven million deaths occurring around the globe each year. According to World Cancer Research Fund and American Institute for Cancer Research, 40% of all cancer can be prevented by the combination of appropriate diets and physical activities. Therefore, cancer management becomes an ideal approach for reduction of cancer mortality by preventing, delaying, or even reversing cancer incidence. Since the initial discovery of selenium as an essential element in humans, the nutritional aspect of selenium has become an intense field of research for connecting the possible role of selenium in cancer prevention. Extensive epidemiological and specific studies have started after the identification of selenoproteins decades ago. Since then, many selenol compounds have been examined, and some have demonstrated potential clinical and molecular role in cancer prevention. A few selenol compounds have been found very effective against many types of cancers, such as lung cancer [200], bladder cancer [201], colorectal cancer [202], liver cancer [203], esophageal cancer [204], gastric–cardiac cancer [205], thyroid cancer [206], and prostate cancers [202, 207–210]. The pivotal role of selenium in cancer prevention is the antioxidant defense, which protects the cells against ROS. Both inorganic forms (such as sodium selenite:  $\text{Na}_2\text{SeO}_3$ ) and organic forms of selenium (such as selenocysteine or selenomethionine) have shown effectiveness in antioxidant defense [76]. Several mechanisms have been proposed for the selenium-mediated anticancer effects. The major mechanisms are (1) the reduction of DNA damage [211, 212], oxidative stress [213–218], and inflammation [219], (2) induction of phase II conjugating enzymes that detoxify carcinogens [220, 221], (3) Se incorporation into selenoproteins, (4) alteration in DNA methylation status of tumor suppressor genes [222–224], and (5) induction of apoptosis and kinase modulation [225–227].

In addition to chemopreventive and anticarcinogenic properties, several seleno-compounds have been reported to halt progression and metastasis of various types of cancers [228–230]. Among them, prostate cancer has been studied most extensively with SeFMs. Administration of oral capsules of sodium selenate to patients with prostate cancer significantly boosts the activity of the protein PP2A phosphatase and impedes tumor neovascularization and angiogenesis [231]. Selenium effect has also been examined in ovine pulmonary adenocarcinoma (OPA), as an animal model for studying lung cancer, by treating animals with sodium selenate [232]. Selenium at higher concentration suppresses expression of TrxR in tissues with lung cancer and causes rapid cell death [233]. The possible mechanism is due

**Fig. 7** Examples of seleno-compounds with cytotoxic effect on cancer cells. The Se nucleoside analogs for cancer chemotherapy are in Fig. 3



to an impaired function of SBP2 (SECIS binding protein 2), therefore reducing TrxR production and activity [234]. Methylselenol, a selenium metabolite, has been reported to induce cell cycle arrest in G1 phase and mediate apoptosis via inhibiting extracellular-regulated kinase 1/2 (ERK1/2) pathway and c-Myc expression [235].

More SeFMs are listed in Fig. 7, and they have been examined as cytotoxic agents with anticancer properties. A clinical trial report revealed that the administration of 1,4-phenylenebis(methylene)selenocyanate (*p*-XSC) to 40 patients with end-stage cancers has increased predicted survival time in 76% of these cases [236]. The cytotoxic effect of this compound is thought to function by modulating TrxR activity through mitochondrial dysfunction [237]. Another selenol derivative cytotoxic compound acting by Akt3 signaling modulation is isoselenocyanate-4 (ISC-4, similar to ISC-3 in Fig. 7) with a four-carbon alkyl chain. Topical application of ISC-4 on xenografted melanoma mice resulted in reducing tumor cell expansion and development by 80% and increasing apoptosis rates by threefold [238]. Another heterocyclic selenium compound, 1,2-[bis(1,2-benzisoxazolone-3-(2H)-ketone)]ethane (BBSKE), has been reported to induce apoptosis of the tongue cancer Tca8113 cells by activating caspase-3 pathway. BBSKE is structurally related to ebselen, a thioredoxin reductase inhibitor (Fig. 7) [239].

## 5.6 SeFMs for HIV Treatment

HIV belongs to the retrovirus family. It carries a single copy of genomic RNA and RNA genes required for reproduction and pathogenesis. The HIV infection process begins with attachment of viral protein gp120 to the specific type of CD4 receptor and a co-receptor on the surface of the CD4 cell. Upon its entry into cells, the viral RNA genome is reversely transcribed into DNA (cDNA) by reverse transcriptase (viral protein), followed by integration of the double-stranded DNA into the host genome. The picture of the HIV-infected population is dire. According to the recent estimates from UNAIDS, there were 35.3 million people living with HIV in 2012, which was up from 29.4 million in 2001. HIV is a leading cause of death worldwide, and the number one cause of death by disease in Africa. Sub-Saharan Africa is most heavily affected by HIV and AIDS than any other regions in the world. An

estimated 22.9 million people live with HIV in this region, which is approximately two-thirds of the total number. In 2012, 1.6 million deaths were caused by AIDS worldwide. Though enormous research has been performed on many aspects of HIV/AIDS, critical research on nutritional aspect (especially micronutrient) on HIV epidemic has not been done thoroughly. There are growing concerns on why HIV infection, disease progression, and mortality rates are much higher in the underdeveloped areas in the world. Recently, a randomized clinical trial on the effect of micronutrient supplementation on HIV-infected ART (antiviral treatment) has been reported. It has been found that the combined supplementation with selenium and vitamins B, C and E largely improved the CD4 cell counts of the HIV-infected patients. A supplement containing multivitamins and selenium was found to be safe. The supplement significantly reduced the risk of immune decline and morbidity, if the supplement treatment was started in the early stages of HIV infection [240].

The HIV-infected individuals are immunocompromised. The mechanisms on why vitamins and selenium exert immune stimulatory effects are not fully elucidated, but the role of each micronutrient has been documented. The role of selenium in HIV infection, activation, and disease progression has been investigated in human and animal models extensively [241]. Like many other pathological conditions, oxidative stress is also a potent inducer of HIV activation and DNA damage to the infected cells [242]. The antioxidant properties of selenoproteins are assumed to play an important regulatory role in immune response [243, 244]. Since HIV infection causes the inflammatory response, many inflammatory cytokines are elevated during HIV infection [245], which include tumor necrosis factor- $\alpha$  (TNF $\alpha$ ), interferon- $\alpha$ , and various interleukins (IL-1, IL-4, IL-6, IL-10) [246]. Elevation of TNF $\alpha$  was related with viral activation, a high level of free radicals, and DNA damage [242].

Oxidative stress is also reported to upregulate the activation of viral replication through the actions of nuclear factor kappa-B (NF $\kappa$ B) [247, 248]. All of these free radical productions lead to body-wide inflammation and depletion of primary antioxidants that cells use to protect themselves against free radicals. In addition, various free radicals generated from inflammatory response cause hypermutation of the viral genome, which lead to the generation of HIV with new pathogenesis. Several identified selenoproteins can decrease the viral replication by mitigating the oxidative stress. It has been found that the levels of selenoproteins that are expressed in T cells, including thioredoxin reductase, glutathione peroxidase, and phospholipid hydroperoxide glutathione peroxidases, are increased in the presence of selenium supplements [249–253]. Unlike some Se-containing compounds used as potential antioxidant supplements, several Se-modified nucleosides have been reported as potential antiviral agents. The 2',3'-dideoxy-4'-selenonucleosides [254] and 4'-seleno-AZT [255], which are bioisosteric analogs of 2',3'-dideoxynucleosides (ddNs) and AZT, have been reported as potential inhibitors of HIV reverse transcriptase (Fig. 3).

## 5.7 SeFMs for Tropical Disease Treatment

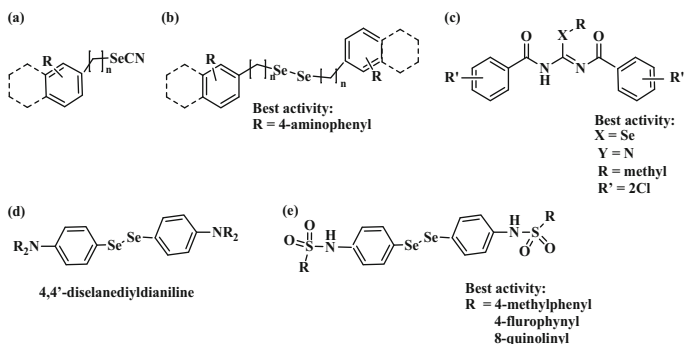
Tropical diseases refer to diseases that occur solely or principally in the tropics, such as tuberculosis, malaria, leishmaniasis, schistosomiasis, onchocerciasis, lymphatic filariasis, Chagas disease, African trypanosomiasis, and dengue [256, 257]. As a result of selenium functionality being a natural component of antioxidants and redox proteins in mammals, many experiments have been designed to observe the effect of selenium on tropical diseases as a preventive agent and cure. Among the different diseases that constitute tropical disease, only tuberculosis (TB) and leishmaniasis are discussed here in relation to potential selenium drugs.

Leishmaniasis is a tropical disease, prevalent in the Southeast Asia and East Africa. It occurs all over the world, but the form of leishmaniasis is different from one region to another [258, 259]. Leishmaniasis is caused by several species of flagellated protozoa belonging to the genus *Leishmania* in the *Trypanosomatidae* family, whose members are characterized by the presence of the kinetoplast, a unique form of mitochondrial DNA [260]. Leishmaniasis can be caused by over 20 *Leishmania* species, and it is transmitted to humans through the bite of infected female phlebotomine sand flies [261, 262]. The World Health Organization (WHO) estimates that leishmaniasis results in two million new cases a year and threatens 350 million people in 88 countries. There are 12 million people currently infected worldwide [261, 263]. Recently, the trace element selenium has been identified as a protective agent against oxidative damage caused by *Leishmania* infection [264, 265]. The biochemical pathways that constitute the cellular targets for selenium are still under investigation.

A class of compounds, which were originally developed as anticancer drugs, has been found very effective as antiprotozoal agents (Fig. 8) [265–268]. These seleno-compounds were synthesized and reported as potential antileishmanial drugs by Carmen Sanmartín's laboratory. It has also been reported that between the selenocyanide (Fig. 8a) and diselenide (Fig. 8b) derivatives, the diselenide compound with aryl ring substitution (especially with 4-aminophenyl) showed better cytotoxic effects, compared to selenocyanide [265]. Another class of imidothiocarbamate and imidoselenocarbamate compounds (Fig. 8c) has been synthesized and tested against leishmaniasis. Among various substitutions, the imidoselenocarbamate compound (especially with X = Se, Y = N, R = methyl, and R' = 2Cl groups) was very effective as an antileishmaniasis agent [264]. In 2013, the same laboratory has synthesized and tested a new class of compounds for the treatment of leishmaniasis. The new compound was designed based on the 4,4'-diselanediyldianiline (Fig. 8d) with sulfonamide moieties bound to different rings (Fig. 8e) [269]. Their data suggest that compounds with R group, such as 4-methylphenyl, 4-fluorophenyl, or 8-quinoliny, exhibit high leishmanicidal activity and low cytotoxicity, which are required for antileishmanial drugs.

Tuberculosis (TB) is a highly infectious disease. The etiological agent of TB is *Mycobacterium tuberculosis*. The notoriety of this highly infectious disease is rested on the fact that the *Mycobacterium tuberculosis* could develop multidrug-resistant (MDR) and extensively drug-resistant (XDR) strains within





**Fig. 8** Selenium containing antiprotozoal agents. (a) Selenocyanide, (b) Diselenide derivatives (best cytotoxic effect with aryl ring substitution with 4-aminophenyl), (c) Imidothiocarbamate and imidoselenocarbamate compounds (among various substitutions, X = Se, Y = N, R = methyl, R' = 2Cl was shown very effective), (d) 4,4'-diselenediyl dianiline (e) 4,4'-diselenediyl dianiline with sulfonamide moieties bound to different rings

the long treatment regimen [270]. The bacteria have evolved drug resistance mechanisms through a persistent phenotype and mutations in drug target genes [271]. Recently, a new target, the antigen 85 (Ag85) protein family consisting of Ag85-A, Ag85-B, and Ag85-C, has been identified. Ag85 has mycoloyl transferase activity, which produces an envelope lipid called trehalose dimycolate (TDM) and cell wall with arabinogalactan-linked mycolic acids, and it is required for cell wall synthesis [272–274]. The organoselenium compound ebselen has been reported to inactivate the Ag85 activity by covalently linking with a cysteine residue located near the mycoloyl transferase active site. Mutational and crystal structure studies indicate that linking ebselen to the cysteine residue disrupts the hydrogen bonding network within the active site that is essential for enzymatic activity [275]. Tuberculosis often coincides with nutritional deficiencies. The effect of selenium on tuberculosis has also been explored in the nutritional aspect. It has been reported that a 2-month intervention with vitamin E and selenium supplementation reduced oxidative stress and improved the outcome in patients undergoing TB chemotherapy [276, 277].

## 5.8 SeFMs for Neurodegenerative Disease Treatment

Free radicals or, more generally, reactive oxygen species are generated continuously during the process of normal oxidative metabolism. There is growing evidence that free radicals play an important role in onset and progression of several neurodegenerative diseases. Those diseases include cerebral ischemia, Parkinson's disease, Huntington's disease, epilepsy, amyotrophic lateral sclerosis, Down's syndrome, and Alzheimer's disease (AD) [278–281]. Among these neurodegenerative diseases, Alzheimer's disease (AD) is among the most pressing health

concerns. The pathology of AD is characterized by the formation of large insoluble plaques made of misfolded amyloid beta ( $A\beta$ ) protein. Amyloid beta ( $A\beta$ ) protein is a short peptide that is a proteolytic by-product of the transmembrane protein amyloid precursor protein (APP), whose function is unclear, but thought to be involved in neuronal development [282, 283]. The experimental data suggests that beta-amyloid aggregation and toxicity are probably caused by the cellular oxidative stress, which plays a key role in the conversion of soluble to insoluble beta-amyloid, suggesting that the oxidative stress is primary to the beta-amyloid cascade [284, 285].

The effect of selenium on neurodegenerative diseases has been investigated. It has been found that the brain is enriched with selenium and its level declines with age, which may be linked to cognitive impairment and AD development. Administration of selenium in a rat model of acute dementia is found to reduce tau phosphorylation and improve memory loss, which implies the neuroprotective role of selenium [37, 286]. It has also been reported that selenium could attenuate  $A\beta$ -induced neuronal death by reducing amyloidogenic  $\beta$ - and  $\gamma$ -secretase activities [286]. Gene knockdown experiments have revealed a potent effect of glutathione peroxidase 4, which protects cells against lipid hydroperoxide damage, the characteristic feature of neurodegenerative disease and AD [287]. A number of studies suggest that GPx4 is an antioxidant enzyme possessing broader substrate specificity than other glutathione peroxidases. It accepts many reductant substrates in addition to glutathione and reacts with a wide array of organic and inorganic peroxides [25, 288, 289]. The neuroprotective role of SelP protein has also been investigated. SelP protects neuronal cells from  $A\beta$ -induced toxicity, suggesting a neuroprotective role for SelP in preventing neurodegenerative disorders in AD [290, 291]. Consistently, several studies have demonstrated the significantly lower Se levels (micronutrient status) in plasma, erythrocytes, and nails in AD patients [292]. The therapeutic effect of *p,p'*-methoxyl-diphenyl diselenide [(MeOPhSe)<sub>2</sub>], a SeFM, against streptozotocin (STZ)-induced sporadic dementia of Alzheimer's type (SDAT) in rats has been evaluated [293]. Several interesting observations from (MeOPhSe)<sub>2</sub> supplementation on SDAT rats have been reported. The results indicate that dietary supplementation with (MeOPhSe)<sub>2</sub> reverts STZ-induced memory impairment in rats and also reverts oxidative stress in the STZ group by decreasing reactive species and tyrosine nitration levels and enhancing nonprotein thiol levels [294]. The dietary supplementation with (MeOPhSe)<sub>2</sub> has also shown to normalize acetylcholinesterase (AChE) activity, which was reported to enhance by STZ injection, but did not revert the deficit in cerebral energy metabolism caused by STZ [293, 295].

Huntington's disease (HD) is also a fatal neurodegenerative disorder caused by CAG-repeat expansion encoding a polyglutamine tract in the huntingtin (Htt) protein characterized by motor and psychiatric disturbances and cognitive decline leading to dementia [296, 297]. In HD neurodegeneration, an increase in intracellular reactive oxygen species (ROS) and caspase-3 activity has been reported. Oxidative stress from ROS is primarily implicated to the impaired activity of the major endogenous glutathione redox system. This impaired system causes oxidative damage and formation of 8-hydroxydeoxyguanosine (8-OH-dG) [298, 299] as

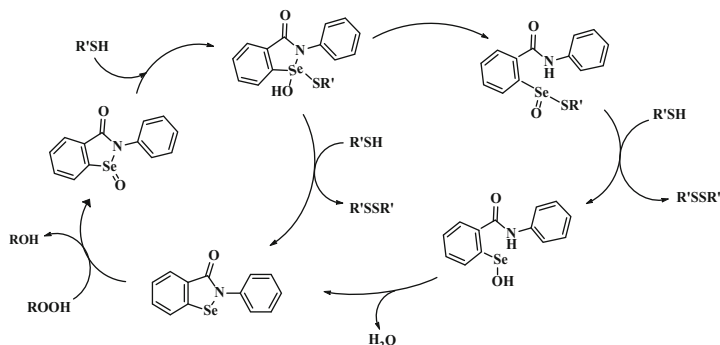
a DNA oxidative damage marker, malondialdehyde (MDA) [300] as a lipid peroxidation marker, and protein oxidation [301]. The role of antioxidant defense by glutathione peroxidases in HD has been demonstrated via genome-wide screening, two suppressors of Htt encode glutathione peroxidases, and their overexpression could ameliorate the toxicity of a mutant Htt fragment in yeast [302]. Moreover, studies indicated that mGPx1 overexpression and ebselen treatment mimicking GPx activity can lower the ROS production and significantly reduce caspase-3/caspase-7 activation.

Selenium supplementation and therapeutics have also been examined in treating bipolar disease. Recently, ebselen has been examined as a potential drug for bipolar disease. They reported ebselen as an effective drug candidate inhibiting inositol monophosphatase (IMPase) activity and acting as a lithium mimetic in mouse models of bipolar disorder [303]. Lithium has been used as the most effective mood stabilizer for the treatment of bipolar disorder, but it is toxic at only twice the therapeutic dosage and has many undesirable side effects [304, 305]. The selenium moiety of ebselen irreversibly inhibits IMPase by forming a selenylsulfide (–Se–S–) bond with the cysteine residue, which is conserved in both human and mouse isoforms. It has also been demonstrated that ebselen permeates blood–brain barrier and inhibits endogenous inositol monophosphatase in mouse brain with no selenium toxicity at pharmacological dosage.

Epilepsy, which affects about 2–3% of the general population, is a common chronic neurological disorder with various etiological factors [306]. Several causes have been suggested to be responsible for idiopathic epilepsy, such as imbalances in trace elements [307] and genetic reasons, including mutations in ion and non-ion channel genes [308, 309] and mutations in genes involved in the antioxidant system [310]. The impaired antioxidant system, which generates oxidative stress by producing free radicals, has been implicated as a leading cause to seizures or the risk of their recurrence in idiopathic epilepsy [311, 312]. A control case study suggests that the Se and Zn levels are significantly decreased in patients with epilepsy and there are no significant differences in gender or age, which implies the possible cause for impaired antioxidant system in epilepsy patients [313].

## 6 SeFMs in Clinical Trials

After discovery of several selenocysteine-containing key enzymes in humans and vertebrates, tremendous attention has been paid to evaluate synthetic Se compounds for pharmaceutical applications. Among many Se compounds that have been studied, ebselen is studied and tested most extensively for its therapeutic value in many pathological conditions. Ebselen [2-phenyl-1,2-benzoisoselenazol-3(2*H*)-one] was first synthesized in 1924. In 1984, it was first reported that ebselen has the properties of thiol peroxidase and antioxidant and acts by mimicking glutathione peroxidase (GPx; Fig. 9) [315, 316]. Since then, a large number of research articles have been published: approximately 1000 ebselen-related publications may be found in the NCBI database. Due to its properties as antioxidant [317, 318] and



**Fig. 9** Mechanism of glutathione peroxidase-like activity of ebselen. R = polyunsaturated phospholipids, cholesterol esters, cholesterol, or any other organic hydroperoxide or hydrogen. R' = glutathione, dihydrolipoate, *N*-acetylcysteine, or thiol protein residue [314]

anti-inflammatory [319, 320] and its low toxicity in vivo [321], ebselen was first clinically tested for using in the stroke treatment by Daiichi Pharmaceuticals, Japan, in 1997 [322]. Unfortunately, it was not authorized (as harmokisane) for registration by MHLW, the Japanese regulatory authority in therapeutics [323]. Ebselen has a broad range of biological activities due to the GPx-like activity, which catalyzes the reduction of hydrogen peroxide and other hydroperoxides by utilizing glutathione and a variety of other thiols [324]. Ebselen can also reduce the peroxynitrite ( $\text{ONOO}^-$ ) to nitrite, thereby diminishing harmful effect of peroxynitrite to cellular constituents in host, when the concentration of peroxynitrite is too high [325]. Ebselen is in the National Institutes of Health Clinical Collection, a chemical library of bioavailable drugs considered clinically safe but without proven use.

Ebselen was studied clinically for treating the late stages of development of stroke. The pathological condition of stroke involves a variety of destructive mechanisms, which include oxygen radical generation [326], lipid peroxidation [326], calcium overload [327, 328], and the generation of inflammatory mediators [329–331]. In vitro and animal studies showed that Ebselen can mimic glutathione peroxidase, react with peroxynitrite, and inhibit acute ischemic stroke-related enzymes, such as cyclooxygenase [332], lipoxygenases [169], NO synthases [333, 334], NADPH oxidase [335–337], and H(+)/K(+)-ATPase [317].

Ebselen is the most characterized for its high bioavailability. It can readily cross the blood–brain barrier and also produce promising results in clinical trials for noise-induced hearing loss (NIHL) along with stroke. NIHL is manifested by the acute exposure to loud noise, which affects several structural elements in auditory hair cells, including cell membrane and intracellular biochemical pathways [338]. Loud noise can reduce GSH and increase the level of oxidized glutathione in the inner ear, therefore leaving it prone to mediated cell damages, which also overwhelm resident detoxification and other antioxidant mechanisms [339, 340]. Intriguingly, GPx activity, which regenerates reduced GSH, has been

reported to decrease following noise exposure. Therefore, administration of ebselen improves NIHL conditions by mimicking GPx activity [341–343].

## 7 Conclusion and Perspective

Because it is a natural part of proteins and tRNAs, selenium is an essential trace element for living systems. Many selenoproteins (such as GPx, TRxR, and Sel proteins) modulate the redox status and systems. Therefore, selenium deficiency will lead to insufficient and/or nonfunctional selenoprotein production, which disrupts the balance of cellular redox systems, thereby resulting in pathological conditions, such as cardiovascular disease, thyroid disease, cancer, neurological disease, depression, diabetes, pancreatitis, and tropical diseases. Furthermore, the deiodinase selenoprotein family is responsible for maintaining a circulating level of thyroid hormone. As an atypical element, selenium has been successfully incorporated into numerous potential therapeutic agents. Approximately 30,000 research articles on selenium have been published and deposited into the NCBI database, indicating the importance of selenium in human health. However, the tolerance range of elemental selenium in humans is narrow: from 55 µg/day (the adequate intake level) to 400 µg/day (the tolerable upper intake level). Epidemiological and pharmacological studies and randomized clinical trials should be conducted to further investigate the link between Se supplement intake and health benefits.

Clearly, selenium function in living systems and its effects on human health are essential. As selenium naturally occurs in protein and tRNA via replacement of oxygen or sulfur atom(s), we predict that the selenium functionality may also present in genomic DNA to assist genome functions, including DNA condensation and accuracy and efficiency of DNA replication and RNA transcription. Thorough research is required to discover and fully understand the selenium functionalities in living organisms. Moreover, selenium-atom-specific modification (SAM) will transform the design of potential oligonucleotide therapeutics via antisense DNA, siRNA, miRNA, and crRNA strategies, by improving the molecular specificity and substrate cleavage efficiency [68].

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# Index

## A

Acetylcholinesterase (AChE), 141  
African trypanosomiasis, 139  
Alzheimer's disease (AD), 106, 140  
Alzheimer's-type sporadic dementia (SDAT), 106, 141  
3-Aminophenyl boronic acid (3-APBA), 18  
4-Aminophenyl boronic acid (4-APBA), 18  
Amyloid- $\beta$  (A $\beta$ ) peptide, 106, 141  
Amyloid precursor protein (APP), 141  
Angiotensin-converting enzyme (ACE), 61, 70  
Anthracyclines, 95  
Antibacterial agents, 11  
Antibiotics,  $\beta$ -lactam, 10  
Anticancer agents, 3, 87  
Anticoagulant agents, 12  
Antihypertensives, 87, 92  
Antimicrobials, 87  
Antioxidants, 87  
Antiviral agents, 87  
Apoptosis, 4, 6, 15, 53, 100, 130, 136  
Arteriosclerosis, 133  
Aspartic proteases, 72  
*Astragalus* spp., 88  
Atazanavir, 66  
Autoinducer-2 (AI-2), 11  
Autotaxin (ATX) inhibitors, 3, 7

## B

Benzoselenazolinones, 131  
Bexarotene, 29  
Bioisosterism, 29  
1,2-[Bis(1,2-benzisoseleazolone-3-(2H)-ketone)]ethane (BBSKE), 137

Bisboronic acid, 15  
  sensors, 15  
BODIPY, 17  
Boronic acid, 1  
Boron neutron capture therapy (BNCT), 14  
Boronolectin-MS tag conjugation, 16  
Bortezomib, 1, 3, 8, 66, 67  
Bourgeonal, 55  
2-Butylselenazolidine-4(R)-carboxylic acid, 99  
BXT-51072 (4,4-dimethyl-2,3-dihydro-1,2-benzoselenazine), 96

## C

Camphorsulfonic acid, 32  
Cancer prevention, SeFMs, 136  
Carbohydrate binders/receptors, 14  
Carbon/silicon switch, 29  
Cardiovascular diseases (CVD), 12, 133  
Caspase, 130  
CD-4, 100  
Cell surface carbohydrates, 2  
Cephalosporinase, 10  
Cerebral ischemia, 140  
Chagas disease, 139  
Chemosensors, 1  
Chymotrypsin, 61, 73  
Cisobitan, 62  
Clavulanic acid, 10  
*Clostridium sticklandii*, 128  
2-Cyclohexylselenazolidine-4-(R)-carboxylic acid, 99  
Cyclooxygenases, 135  
Cypermethrin, 63

**D**

Daunorubicin, 95  
 Davis–Ellman sulfinimines, 75  
 Dengue, 139  
 Dexrazoxane, 95  
 Diabetes, 19, 134  
 Diagnostics, 1  
 Diaryl diselenides, 106  
 Diaryl isoselenazoles, 135  
 Diazaborines, 10  
 Dideoxynucleosides (ddNs), 138  
 2,3-Dideoxy-40-selenonucleosides, 138  
 Difluorodiphenylsilane, 69  
 Dihydrobenzoxaboroles, 11  
 Diisobutylsilanediol, 65  
 Dimethylsilanediol, 65  
 Dipeptidyl peptidase activity (DPP), 5  
 Diphenyl diselenides, 106  
 Diphenylsilanes, 68  
 Disila-bexarotene, 29, 30, 45  
 DNA, 119  
 Dopamine- $\beta$ -monooxygenase (DBM), 90  
 Dopamine reuptake inhibition, 34  
 Down's syndrome, 140  
 Doxorubicin (DOX), 95  
 Drug and supplement, 119  
 Drug design, 29

**E**

Ebselen oxide, 93  
 Ebselen (2-phenyl-1,2-benzisoseleniazol-3  
 [2H]-one), 87, 96, 102, 125,  
 131–140  
 Enzyme inhibitors, 61  
 Epilepsy, 140, 142  
 Esfenvalerate, 63  
 Essential elements, 119  
 Ethaselen (1,2-[bis(1,2-benzisoselenazolone-3  
 (2H)-ketone)]ethane), 102  
 7-Ethyl-10-hydroxycamptothecin, 105  
 Etofenprox, 63  
 Extracellular-regulated kinase 1/2 (ERK1/2),  
 136

**F**

Factor XIa, 61, 73  
 Fexofenadine, 53  
 Fibroblast activation protein (FAP) inhibitors,  
 3, 5  
 Fluorosilanes, 74  
 Flusilazole, 63

Formate dehydrogenase, 121  
 Fosinoprilate, 66

**G**

Glucose, 19  
 Glutathione, 87, 102, 125, 143  
 Glutathione peroxidase, 89, 121, 131,  
 138, 141  
 Glutathionylation, 102  
 Glycine reductase, 121  
 Glycosyltransferase, 17  
 Granulocyte colony-stimulating factor  
 (G-CSF), 100

**H**

Haloperidol, 29, 37  
 Harmokisane, 143  
 Hepatitis C, 8  
 Histone deacetylase (HDAC) inhibitors, 3, 6  
 HIV, 15, 61, 66, 100, 130, 137  
 protease, 66, 71, 78  
 SeFMs, 137  
 Huntington's disease, 140, 141  
 Hydrolase inhibitor, 61  
 Hydrosilylation, 61  
 Hydroxyalkyl selenides, 133  
 8-Hydroxydeoxyguanosine (8-OH-dG), 141  
 4-Hydroxyphenyl-2-methyl-2-aminoethyl  
 selenide (HOMePAESE), 91  
 Hyperthyroidism (Graves' disease), 131  
 Hypoxia-induced factor-1 $\alpha$  (HIF-1 $\alpha$ ), 3, 6

**I**

Imaging mass spectrometry, 1  
 Indinavir, 71  
 Inflammatory bowel disease (IBD), 97  
 Inositol monophosphatase (IMPase), 142  
 Insulin, 135  
 receptor substrate (IRS-1), 135  
 Iodothyronine deiodinase, 121, 131

**K**

Kappa-B (NF $\kappa$ B), 138  
 Keshan disease, 88

**L**

$\beta$ -Lactamases, 10  
 Lectin mimics, 15



Leishmaniasis, 139  
Lewis, sialyl, 2  
Lymphatic filariasis, 139  
Lysophosphatidic acid (LPA), 7

## M

Malaria, 139  
MALDI-IMS, 1, 16  
Malondialdehyde (MDA), 142  
Metallohydrolase, 10  
Metalloproteases, 70, 72  
Metastasis, 136  
Methimazole (MMI), 131  
Methoxyl-diphenyl diselenide, 106  
5-Methylaminomethyl-2-selenouridine, 121  
1-Methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP), 97  
Methylseleninate, 104  
Methylseleninic acid, 105  
Methylselenocysteine, 104  
Methylselenol, 105  
5-Methylselenenyl-methyl-2'-deoxyuridine (5-MeSe-T), 130  
Methyl thiouracil (MTU), 131  
Motexafin gadolinium, 103  
Multiple target nonsteroidal antiinflammatory drugs (MTNSAIDs), 135  
Murine double minute 2 protein (MDM2)/p53 inhibitors, 3, 6  
Mycolic acids, 140  
Myxoedematous cretinism, 133

## N

Neurodegenerative diseases, SeFMs, 140  
Neutron capture therapy (NCT), 2  
Niguldipine, 53  
Noise-induced hearing loss (NIHL), 143  
Nonsteroidal anti-inflammatory drugs (NSAID), 135  
NS3 protease inhibitors, 9  
Nucleic acids, 119  
Nucleosides, selenium-derivatized, 119, 128  
Nucleotides, 119, 128

## O

Okoumal, 55  
Onchocerciasis, 139  
Organoselenium compounds, therapeutic use, 87

Organoselenium–methacrylate polymer (Se-MAP), 100  
Organosulfur compounds, 107

## P

Panamesine, 53  
Parkinson's disease, 140  
Penicillinase, 10  
Peptide boronates, 4  
Peroxyxynitrite, 93, 143  
Phantolide, 55  
Phenylaminoalkyl sulfide, 107  
Phenylaminoethyl selenides (PAESe), 87, 90  
1,4-Phenylenebis(methylene)selenocyanate (*p*-XSC), 136  
Phosphatidylinositol 3-kinase (PI3K), 135  
Propyl thiouracil (PTU), 131  
Prostate cancer, 136  
Protease inhibitors, 4, 61  
Proteasome inhibitors, 3  
Protein disulfide reductase, 101  
Protodesilylation, 68  
PX-12 (1-methylpropyl 2-imidazolyl disulfide), 103  
Pyrethrin, 63

## Q

Quartz crystal microbalance (QCM), 18

## R

Reactive nitrogen species (RNS), 119, 124  
Reactive oxygen species (ROS), 94, 119, 124, 141  
Retinoic acid, 50  
Retinoid agonist, 45  
Rheumatoid arthritis (RA), 135  
Rhubafuran, 55  
RNA, 119  
Roundup, 62

## S

SAR, 29  
Saxagliptin, 13  
Schistosomiasis, 139  
Se-atom-specific mutagenesis (SAM), 129, 144  
Secretase, 141  
Selenazolidine-4(*R*)-carboxylic acids, 99  
Selenazolidines, 87, 98

- Selenenamide, 131  
Selenium, 87  
    functionalization/modification, 119  
    nucleic acids, 128  
Selenium-based drugs, 87  
Selenium-carrier conjugates, 99  
Selenium-containing metabolites, 87, 103  
Selenium-functionalized molecules (SeFMs),  
    119  
4'-Seleno-AZT, 138  
Selenobetaine/sulfobetaine, 108  
Selenocysteine, 89, 99, 119–136, 142  
Selenodiglutathione, 104  
Selenomethionine, 98, 121, 126  
Selenoproteins, 87, 89, 124  
Selenosis, 88  
Serine protease, 66, 72  
Serotonin/noradrenaline reuptake inhibitor, 29,  
    32  
Sila-drugs, 29  
Silafluofen, 63  
Sila-haloperidol, 29, 30, 37  
Silanediols, 61, 65, 67  
    peptidomimetics, 68  
Silanols, 64  
Silanones, 65  
Sila-substitution, 31  
Sila-venlafaxine, 29, 30, 32  
Silicon, 29  
Siloxanes, 64  
Silyl anion, 61  
Silyllithium, 75  
Sitagliptin, 13, 66  
Sodium selenate, 136  
Spirodioxaselenanonanes, 93  
Streptozotocin, 141  
Sulbactam, 10  
Sulfinimines, 61, 75  
Surface plasmon resonance (SPR), 18
- T**  
Talabostat, 13  
Tamibarotene, 49  
Tamoxifen, 105  
Tazobactam, 10  
Terfenadine, 53  
*tert*-Butyl hydroperoxide (TBHP), 95  
Tetraiodothyronine, 131  
Thermolysin, 61, 71  
Thiazolidinedione, 8  
Thiolseleninates, 93  
Thioredoxin reductase, 87, 89, 101  
Thrombin inhibitors, 12  
Thromboembolic diseases, 12  
Thyroid peroxidase (TPO), 130  
Thyroxine, 121, 130  
Topoisomerase I inhibitor, 105  
Trehalose dimycolate (TDM), 140  
Triiodothyronine, 121, 130  
Tropical diseases, 139  
Trypanosomiasis, 139  
TTNPB, 50  
Tuberculosis, 102, 139  
Tyrosine phosphatase 1B, 135
- V**  
Velcade, 1, 4  
Venlafaxine, 29  
Vildagliptin, 13  
Vincristine, 95