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# Perfluoroalkane Sulfonamides and Derivatives, a Different Class of PFAS: Sorption and Microbial Biotransformation Insights

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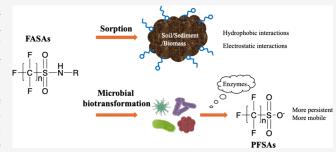
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ABSTRACT: Perfluoroalkane sulfonamides and their derivatives (FASAs), an emerging subclass of per- and polyfluoroalkyl substances (PFAS), have attracted increasing attention due to their widespread applications, environmental persistence, and potential biological toxicity. Unlike perfluoroalkyl acids (PFAAs), FASAs can be transformed by microorganisms in the environment, producing fluorinated intermediates that eventually form stable PFAAs. A key difference of FASAs is that their  $pK_a$ s enable them to exist as neutral species or zwitterions, unlike all other PFAS subclasses, which are all anions. Sorption processes regulate the bioavailability of FASAs to microorganisms for transformation,



driving the environmental transport and fate of FASAs. In this critical review, we provide a comprehensive overview of the classification, properties, and environmental fate of FASAs, with a focus on sorption and microbial transformation. We discuss recent advancements in understanding the sorption of FASAs onto soil, sediment, and microbial biomass, including key sorption descriptors and influencing factors. Additionally, we examine the microbial biotransformation of FASAs, detailing transformation pathways, key intermediates, transformation kinetics, and enzymes involved. Finally, we identify critical research gaps and propose future directions to advance the study of the sorption and biotransformation of FASAs in environmental systems. Mechanistic understanding of these processes is crucial for managing sites impacted with FASAs.

KEYWORDS: Perfluoroalkane sulfonamides, sorption, microbial biotransformation, PFAS, biotransformation enzymes

### 1. INTRODUCTION

Perfluoroalkane sulfonamides and their derivatives (FASAs) are an emerging class of perfluoroalkyl and polyfluoroalkyl substances (PFAS). FASAs have a perfluoroalkyl chain attached to a sulfonamide group, with possible additional Nsubstitutions (Table 1). A detailed list of FASAs, including their acronyms, CAS numbers, and chemical structures, is provided in Table S1 of the Supporting Information. FASAs have been used alongside other PFAS in various industrial and consumer products, such as aqueous film-forming foams (AFFF), 1,2 fabric protectors, 3 and firefighter turnout gear textiles. Notably, FASAs continue to be used today, with some serving as replacements for legacy PFAS. Some short-chain FASAs, including perfluorobutane sulfonamide (FBSA; subclass 1 in Table 1) and perfluorobutane sulfonamide ethanol (FBSE; subclass 2), have recently substituted perfluoroalkyl acids (PFAAs) in semiconductor manufacture. 5,6 N-Ethyl perfluorooctane sulfonamide (EtFOSA, subclass 1) has been extensively used as an active ingredient in the pesticide sulfluramid.<sup>7</sup> Glüge et al.<sup>8</sup> noted that three FASAs (potassium N-ethyl perfluorooctane sulfonamidoacetate (subclass 5), perfluorooctane sulfonamidoalkyl ammonium iodide (subclass 7), and perfluorooctane sulfonamidoalkyl ammonium chloride (subclass 7)) are among the PFAS with high usage frequency,

because they have more than ten assigned applications in commerce. With the recent availability of standards and advancements in suspect screening techniques, the detection frequency of FASAs in environmental and biological samples has increased.<sup>2,9–14</sup> Concerningly, FASAs exhibit a potential biological toxicity. FASAs were the only type of PFAS that influenced developmental, morphological, and behavioral outcomes in zebrafish embryos. 15,16 FOSA, MeFOSA, and FHxSA even showed higher toxicity than perfluorooctanesulfonate (PFOS).16 The sulfonamide group is associated with antimicrobial properties, a characteristic that has been exploited in the development of many nonfluorinated antibacterial agents.<sup>17</sup> Unlike PFAAs, which are anionic, FASAs can exist in protonated forms at environmentally relevant pH levels. This unique property and varying nonfluorinated moieties affect their environmental transport and fate, making them distinct from the majority of PFAS.

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Table 1. Subclass Structures for Nine FASAs and Their Main Uses<sup>8,19,a</sup>

Subclass	Chemical structure		Chemical name	Use
The blue	'A' represents alkyl length. F	For $n = 4, 6, 8, A = B$ (butane), $Hx$	(hexane), O (octane)	
	FO	where R=H,	Perfluoroalkyl sulfonamides (FASA)	Major raw material for surfactant and
1	F+C+nS-N-R F O	R=alkyl (methyl, ethyl),	N-alkyl FASA (MeFASA, EtFASA)	surface protection products
	F O R	where R=H,	Perfluoroalkane sulfonamidoethanols (FASE)	Major raw material for surfactant and
2	F+C+nS-N-OH	R=alkyl (methyl, ethyl),	N-alkyl FASE (MeFASE, EtFASE)	surface protection products
3	F+C+S-N_O	Where R=alkyl (methyl, ethyl),	N-Alkyl perfluoroalkane sulfonamidoethyl acrylates (FASAC)	Major raw material for surfactant and surface protection products
4	F+C+N-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N	Where R=alkyl (methyl, ethyl),	N-Alkyl perfluoroalkane sulfonamidoethyl methacrylates (FASMAC)	Major raw material for surfactant and surface protection products
5	F+C+n OH	where R=H,	Perfluoroalkane sulfonamidoacetic acids (FASAA)	Intermediate environmental transformation product
		Where R=alkyl (methyl, ethyl),	N-alkyl FASAA (MeFASAA, EtFASAA)	
6	$F + \begin{matrix} F & O \\ - & \parallel \\ - & \parallel \\ F & O \end{matrix} - \begin{matrix} N & N \\ - & \parallel \\ N & N \end{matrix}$		N-dimethyl ammonio propyl Perfluoroalkane sulfonamide (AmPr-FASA), also refered to as PFASAm	Functioning surfactants in AFFF-formulations
7	$F + C + S - N \longrightarrow N^{+}$ $F = 0$		N-trimethyl ammonio propyl Perfluoroalkane sulfonamide (TAmPr-FASA), also refered to as PFASAmS	Functioning surfactants in AFFF-formulations
8	F+C+S-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N-N	0	Perfluoroalkane sulfonamido amine oxides (PFASNO)	Functioning surfactants in AFFF-formulations
9	F+C+S-N-N+-F O	0	Perfluoroalkane sulfonamido betaine (PFASB)	Functioning surfactants in AFFF-formulations

<sup>&</sup>lt;sup>a</sup>This is not an exhaustive list but includes reported FASAs with commercial standards.

Sorption and microbial transformation affect the transport and fate of FASAs in the environment. Previous studies demonstrated that PFAA sorption to soil is controlled by hydrophobic and electrostatic interactions. PFAA adsorption increases with sediment organic matter content, solution ionic strength, and perfluoroalkyl chain length.<sup>20</sup> Perfluoroalkanesulfonates (PFSAs) show higher adsorption than perfluoroalkyl carboxylic acids (PFCAs) with comparable chain lengths. 21,22 Due to the different electrostatic charge (zwitterionic and neutral) compared to PFAAs (anionic) and diverse terminal functional groups of FASAs, their sorption mechanisms are expected to be more complex. To date, the sorption of FASAs in environmental media has been intermittently reported along with PFAAs data, and few dedicated studies on FASAs sorption exist. Beyond soils and aquifer solids, the sorption onto microbial biomass and biofilm can also influence the retention and transport of FASAs in environmental matrices.<sup>23</sup> PFAS sorption onto biomass has just started to be evaluated.<sup>24–26</sup>

PFAS are often considered biologically recalcitrant, although this primarily applies to PFAAs.<sup>27</sup> While some studies have reported PFAAs loss in various microbial cultures, the mechanisms continue to be debated and PFAAs remain biologically recalcitrant in most environmental settings. <sup>28–32</sup> In contrast, FASAs have been shown to undergo microbial transformation in natural environments, leading to the formation of terminal products—PFAAs, primarily

PFSAs.33-37 As a result, FASAs are designated as PFAS precursors. Unlike the more widely studied fluorotelomers (FTs), microbial transformation of FASAs yields PFSAs of the same perfluoroalkyl chain length, whereas fluorotelomers typically generate n to n-2 PFCAs. <sup>36,38</sup> FASAs have been reported to have greater recalcitrance compared to fluorotelomers, <sup>36</sup> but over the long term the transformation products formed appear to be more persistent and mobile.

Therefore, a comprehensive review of the sorption and microbial transformation of FASAs is crucial for understanding their transport and fate in the environment as well as for providing a theoretical foundation for the management of contaminated sites. Although previous reviews on the environmental fate of PFAS have included the microbial transformation pathways of some FASAs, 33,35-37 they have not focused on the role of sorption processes, evaluated their microbial transformation kinetics, or provided detailed explanations of the underlying microbial transformation mechanisms. Therefore, this review aims to (1) examine the literature on the sorption of FASAs onto soil and microorganisms, summarizing sorption descriptors and influencing factors, (2) review the microbial transformation of FASAs in environmental media, including transformation pathways, key intermediates, final products, and transformation kinetics, (3) identify and discuss microbial enzymes involved in the

Table 2. Reported log  $K_d$  and  $pK_a$  Values of FASAs and Some Reference PFASs<sup>a</sup>

Compounds	Speciation	pKa values	log Kd (mL/g)	pH condit ions	References
FASAs					
FBSA	$C_4F_9 - \overset{\circ}{\underset{-}{\overset{\circ}{=}}} - NH_2 \xrightarrow{\overset{\circ}{\underset{-}{\overset{\circ}{=}}}} C_4F_9 - \overset{\circ}{\underset{-}{\overset{\circ}{=}}} - NH$	6.27, 5.98 <sup>E</sup>	-0.5	3.4-8.3	Nguyen et al., 2020
FHxSA	$C_0F_{13} - \overset{\circ}{\underset{N}{\stackrel{\text{pka}}{=}}} \operatorname{C}_0F_{13} - \overset{\circ}{\underset{N}{\stackrel{\text{pka}}{=}}} \operatorname{C}_0F_{13} - \overset{\circ}{\underset{N}{\stackrel{\text{pka}}{=}}} \operatorname{NH}$	6.25	0.2	3.4-8.3	Nguyen et al., 2020
FOSA	$C_{\theta}F_{17}-\bigvee_{g}^{\bullet}-NH_{2}\xrightarrow{pka}C_{\theta}F_{17}-\bigvee_{g}^{\bullet}-NH$	6.2-6.52	1.2	3.4-8.3	Nguyen et al., 2020
105/1	0 8	0.2 0.32	1.79	3.2-8.6	Campos-Pereira et al., 2023
EtFOSA*	C <sub>0</sub> F <sub>17</sub> -S-NH	$9.0, 9.5^{E}$	3.21	2.9-6.1	Campos-Pereira et al., 2022
MeFOSAA	$C_0F_{\gamma}-\bigvee_{j=1}^{N}-N \qquad \bigcirc OH  \stackrel{2}{\Longrightarrow} C_0F_{\gamma}-\bigvee_{j=1}^{N}-N \qquad \bigcirc O$	2.92	1.46	5.7-7.0	Higgins et al., 2006
EtFOSAA	$C_0F_{\gamma} - \stackrel{Q}{\stackrel{-}{\stackrel{-}{\stackrel{-}{\stackrel{-}{\stackrel{-}}{\stackrel{-}{\stackrel{-}$	3.9	1.29	5.7-7.0	Higgins et al., 2006
AmPr-FHxSA	$C_0F_{13} = \begin{matrix} 0 \\ -S \\ -N \end{matrix} \\ \begin{matrix} N \\ N \end{matrix} \\ \begin{matrix} N \\ N \end{matrix} \\ \begin{matrix} N \\ N \\ N \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \begin{matrix} N \\ N \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \begin{matrix} N \\ N \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \begin{matrix} N \\ N \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \begin{matrix} N \\ N \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \begin{matrix} N \\ N \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \end{matrix} \\ \end{matrix} \end{matrix} \\ \begin{matrix} N \\ N \end{matrix} \\ \end{matrix} \\ \end{matrix} \end{matrix} \begin{matrix} N \\ N \\ N \end{matrix} \\ \end{matrix} \end{matrix} \begin{matrix} N \\ N \\ N \end{matrix} \\ \end{matrix} \end{matrix} \end{matrix} \begin{matrix} N \\ N \end{matrix} \end{matrix} \end{matrix} \end{matrix} \begin{matrix} N \\ N \end{matrix} \end{matrix} \end{matrix} \end{matrix} \begin{matrix} N \\ N \end{matrix} \end{matrix} \end{matrix} \end{matrix} \begin{matrix} N \end{matrix} \end{matrix} \end{matrix} \end{matrix} \begin{matrix} N \end{matrix} \end{matrix} \end{matrix} \end{matrix} \begin{matrix} N \end{matrix} \end{matrix} \end{matrix} \end{matrix}$	(pka1)3.57; (pka2)9.21	1.1	3.4-8.3	Nguyen et al., 2020
TAmPr-FHxSA	$C_0F_{13} = 0 \\ \begin{array}{c} 0 \\ -N \end{array} \\ \begin{array}{c} N \\ -N \end{array} \\ \begin{array}{c} \rho ka \\ N \\ -N \end{array} \\ \begin{array}{c} 0 \\ -N \\ -N \end{array} \\ \begin{array}{c} N \\ -N \\ -N \\ -N \end{array} \\ \begin{array}{c} N \\ -N \\ -N \\ -N \\ -N \end{array} \\ \begin{array}{c} N \\ -N \\$	3.28	1.3	3.4-8.3	Nguyen et al., 2020
PFOSB	$C_0F_{17}-\overset{Q}{\underset{\longrightarrow}{\circ}}-\overset{N}{\underset{\longrightarrow}{\circ}}\overset{\otimes}{\underset{\longrightarrow}{\circ}}\overset{N}{\underset{\longrightarrow}{\circ}}\overset{O}{\underset{\longrightarrow}{\circ}}\overset{pka1}{\underset{\longrightarrow}{\circ}}}C_0F_{17}-\overset{Q}{\underset{\longrightarrow}{\circ}}\overset{N}{\underset{\longrightarrow}{\circ}}\overset{N}{\underset{\longrightarrow}{\circ}}\overset{O}{\underset{\longrightarrow}{\circ}}\overset{pka2}{\underset{\longrightarrow}{\circ}}C_0F_{17}-\overset{Q}{\underset{\longrightarrow}{\circ}}\overset{N}{\underset{\longrightarrow}{\circ}}\overset{N}{\underset{\longrightarrow}{\circ}}\overset{O}{\underset{\longrightarrow}{\circ}}\overset{N}{\underset{\longrightarrow}{\overset{N}{\overset{N}{\underset{\longrightarrow}{\circ}}{\circ}}\overset{N}{\underset{\longrightarrow}{\overset{N}{\overset{N}{\overset{N}{\overset{N}{\overset{N}{\overset{N}{\overset{N}{\overset$	(pka1)2.26; (pka2)6.78	0.94-1.08	5.2-7.6	Mejia-Avendaño et al., 2020
Reference PFAS					
PFOAB	$C_7F_{15}-\overset{Q}{C}-\overset{Q}{N} \overset{\circ}{\nearrow} \overset{\longrightarrow}{\nearrow} $	(pka1)2.25; (pka2)7.79	0.48-0.81	5.2-7.6	Mejia-Avendaño et al., 2020
PFOAAmS	$C_7F_{15} \overset{\bigcirc}{C} \overset{\bigcirc}{C} \overset{\bigcirc}{H} \overset{\bigcirc}{N} \overset{\bigcirc}{\longleftarrow} C_7F_{15} \overset{\bigcirc}{C} \overset{\bigcirc}{C} \overset{\bigcirc}{N} \overset{\bigcirc}{N}$	7.71	1.51-1.69	5.2-7.6	Mejia-Avendaño et al., 2020
6:2 FTAB	$c_{ij}F_{13} \overset{\bigcirc}{\underset{0}{{{{{{{{}{{}{}{}{}{}{}{}{}}}}}$	(pka1)2.26-2.81; (pka2)11.12	0.67-0.91	5.2-7.6	Mejia-Avendaño et al., 2020
6:2 FtSaAm		(pka1)9.2; (pka2)10.7	0.25	3.4-8.3	Nguyen et al., 2020
C <sub>6</sub> F <sub>13</sub>	NH pka1 c <sub>0</sub> F <sub>13</sub>		2.81	5.2	Barzen-Hanson et al., 2017

"All p $K_a$  values in this table were estimated by modeling,  $^{39,42,43,47}$  except those marked with a superscript "E", which indicate experimentally determined values by 3M company. All log  $K_d$  values were experimentally determined,  $^{39-41,49}$  except for PFOSB, PFOAB, PFOAAMS, and 6:2 FTAB, which were calculated based on the Freundlich model due to the original experimentally determined values not being reported. Note: Organic carbon partition coefficient ( $K_{oc}$ ) is provided for EtFOSA as no reported  $K_d$  values were found.

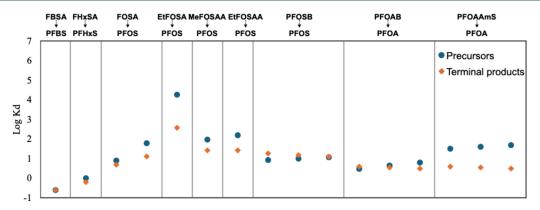
biotransformation of FASAs, and (4) highlight key knowledge gaps and propose opportunities for further research.

# 2. SORPTION OF FASAS

**2.1.**  $pK_a$  of FASAs. FASAs are different from other PFAS because the NH2 in the sulfonamide group can exist in protonated (neutral) or deprotonated forms (negatively charged) at environmentally relevant pHs. Additionally, some FASAs contain N-substitutions with charged head groups, such as carboxyl, trimethylammonium, and quaternary ammonium. This means that FASAs can be present as anions, cations, or zwitterions or neutral species under different environmental conditions. As such, the pH-dependent protonation and deprotonation processes of FASAs need to be considered to evaluate the sorption. In Table 2, we list the reported experimental and calculated  $pK_a$  values of FASAs and several reference PFAS. Most of these data were estimated based on various models, including SPARC, Chemicalize, and ACD/ Laboratories. 39,42,43,47 Only the p $K_a$  values of FHxSA and EtFOSA were obtained experimentally by 3M Company.<sup>4</sup> The p $K_a$  values of the sulfonamides range from 3.28 to 11.12 (Table 2). Based on computational estimates, Rayne et al. 18 indicated that alkylation of the parent perfluoroalkyl sulfonamides increases the  $pK_a$  compared to N-unsubstituted

FASAs: N-methyl (2–3 log increase), N-ethyl/ethanol (2–3 log increase), and N-acetate (1–2 log increase). The degree and proximity of branching of the perfluoroalkyl chain also increases the sulfonamide  $pK_a$ , up to a 3–4 log difference between isomers. The length of the perfluoroalkyl does not appear to have a significant effect on sulfonamide  $pK_a$  values. It is important to note that  $pK_a$  predictions have been based on nonfluorinated aromatic and alkyl-substituted sulfonamide experimental data. Thus, these predicted sulfonamide  $pK_a$  values still need to be validated experimentally.

**2.2. Sorption onto Soils and Sediments.** PFAS sorption to soils drives their transport and fate into the surface and groundwater. Theoretically, only PFAS not adsorbed by soil can infiltrate groundwater and be bioavailable to (micro)-organisms. The soil-water partition coefficient ( $K_d$ ) is extensively employed to quantify the sorption of PFAS and other organic contaminants in soils and is defined as the ratio of the PFAS soil concentration with respect to the aqueous concentration.  $K_d$  is a soil-specific parameter influenced by the organic carbon content (OC), clay composition, cation exchange capacity (CEC), and anion exchange capacity (AEC), among other soil properties. The variable electrostatic charge and diverse head functional groups of FASAs, make their adsorption mechanisms more complex than anionic



**Figure 1.** Comparison of log  $K_{\rm d}$  values between FASAs (blue circles) and their potential terminal transformation products (yellow diamonds). The two sets of data for FOSA are from different sources. The three sets of data for PFOSB, PFOAB, and PFOAAMS are three calculated log  $K_{\rm d}$  values at different liquid-phase concentrations based on the Freundlich model. Aside from the data for PFOSB, PFOAB, and PFOAAMS, all other data were obtained experimentally. The data for EtFOSA and matched PFOS represents log  $K_{\rm oc}$  values, as log  $K_{\rm d}$  values were not reported in the original literature.

PFSAs. We compiled  $\log K_d$  values of various FASAs along with reference PFAS (Table 2), including the amide analogs of PFOSB and PFOSAmS-perfluorooctane amido betaine (PFOAB) and N-trimethyl ammonio propyl perfluorooctane amido (PFOAAmS), as well as the fluorotelomer analog of PFOSB, 6:2 fluorotelomer sulfonamide alkylbetaine (6:2 FTAB), and the fluorotelomer analog of AmPr-FHxSA, 6:2 fluorotelomer sulfonamido amine (6:2 FtSaAm). The soil characteristics used in the referenced studies, including soil texture, CEC (cmol/kg), and anion exchange capacity (cmol/ kg), are summarized in Table S2 of the Supporting Information. To contextualize the change in sorption potential because of FASA transformation, we compared the log  $K_d$ values of FASAs with those of their potential terminal transformation products, PFAAs (Figure 1). The log  $K_d$  values of FASAs and their paired PFAAs are derived from the same study. $^{39-42,49}$  Overall, most FASAs exhibit  $K_{\rm d}$  values higher than those of their end products. This suggests that the microbial transformation of FASAs under natural conditions generates more mobile PFAS, likely leading to more widespread aqueous contamination.

Multiple studies have shown statistically significant positive correlation of OC values with the  $K_d$  values of FOSA, <sup>39,40</sup> FBSA,<sup>39</sup> and N-alkyl FASAAs (MeFOSAA, EtFOSAA).<sup>41</sup> This indicates that hydrophobic interactions play an important role in the sorption of anionic and neutral FASAs. In contrast, the cationic and zwitterionic FASAs have not shown significant correlation with  $K_d$  and OC values. <sup>39,42,43</sup> The  $K_d$  values of some cationic and zwitterionic FASAs (AmPr- and TAmPr-FHxSA) were dominantly and positively impacted by exchangeable sodium percentage (ESP) and CEC, 39,42 in agreement with zwitterionic fluorotelomer studies. 43,44 CEC reflects the capacity of soil to hold onto cations resulting from the negatively charged organic matter and clay particles through electrostatic interactions. The higher the CEC values, the more negatively charged the organic matter and clay sites are for the adsorption of cationic FASAs. In addition, the increase in the CEC value may extend the basal plane spacing of some clay minerals, providing more volume for sorption.<sup>4</sup> Although few studies have reported significant correlations between the combined content of silt and clay in soil and the K<sub>d</sub> values of certain PFAS, including FOSA (positively correlated) and 6:2 FTAB (negatively correlated), their

predictive strength was weak to moderate ( $R^2 = 0.52-0.57$ ).

pH not only affects the charge properties of the soil surface but also affects the charge state of FASAs, affecting the adsorption behavior of FASAs. For the FASAs and derivatives reviewed, the  $K_d$  values generally decrease with the increase in solution pH, but these effects depend on whether their p $K_a$ s were in the evaluated pH range (Table 2). MeFOSAA and EtFOSAA (p $K_a$  range 2.92–3.9) remain in anionic form within the tested pH range (5.7-7).<sup>41</sup> Then, the pH-induced change in K<sub>d</sub> values would instead impact the soil surface charge and/ or hydrophobicity. At low pH, soil OC is more protonated, which could decrease repulsion of anionic FASA moieties. 46 As pH increases, soil OC and clay minerals become progressively more negatively charged, causing electrostatic repulsion of anionic FASAs and reducing sorption. For FASAs with  $pK_a > 1$ 6, the increase in pH has a greater impact on reducing adsorption, as higher pH leads to deprotonation of FASAs, enhancing electrostatic repulsion with the soil. 39,43 Nguyen et al.<sup>39</sup> observed that the most drastic changes in  $K_d$  values of FBSA, FHxSA, and FOSA were apparent when the solution pH increased from approximately 5 to 7. Within this range, these FASAs may be rapidly ionized from neutral molecules into anions. Similarly, a drastic reduction in  $K_d$  for PFOSB was observed between pH 5.4 and 7.6, 42 which corresponds to its sulfonamide pKa. In addition, Kd values of zwitterionic AmPr-FHxSA (p $K_{a1}$  3.57, p $K_{a2}$  9.21) and TAmPr-FHxSA (p $K_a$  3.28) showed high sensitivity to changes in pH between  $\sim$ 7 and 8. $^{39}$ However, their predicted  $pK_a$  values did not indicate deprotonation of the sulfonamides between pH ~7 and 8, which may suggest inaccurate  $pK_a$  predictions. PFOAB, PFOAAmS, and 6:2 FTAB did not exhibit strong pHdependent adsorption within the studied pH range (4-7),<sup>42</sup> probably because their  $pK_as$  fall outside environmentally relevant pHs.

The perfluorocarbon chain, molecular weight, functional groups, and charge exhibit important impact on the sorption behavior of FASAs. The  $K_{\rm d}$  values of FBSA, FHxSA, and FOSA increase sequentially, suggesting increased hydrophobic interactions with the increasing perfluoroalkyl chain.<sup>39</sup> PFOSB showed stronger sorption than PFOAB,<sup>42</sup> which is consistent with stronger PFSA sorption compared to PFCAs. This could be due to the presence of one additional carbon atom and larger molar volume of the sulfone group in

sulfonamide compared to that of the carbonyl in amides. EtFOSA, an eight-carbon analog, was found to show stronger sorption in soil than FOSA, 49 which indicated the addition of an ethyl group to the -SO<sub>2</sub>-NH- headgroup appeared to have enhanced sorption. Relatively minor differences in sorption were observed between N-MeFOSAA and EtFO-SAA;<sup>41</sup> the additional N-alkyl carbon had little impact on sorption. Additional sorption studies involving N-alkyl FASAAs (i.e., N-butyl-FOSAA) and N-alkyl FASAs (i.e., MeFOSA) may contribute to an enhanced understanding of the impact of N-atom substituents on the sorption of these compounds via sulfonamide  $pK_a$ . Comparing FASAs with reference PFAS with identical fluorinated carbon chains, the  $K_d$ values were highest for cationic species, followed by zwitterionic species, and lowest for anionic species (AmPrand TAmPr-FHxSA > 6:2 FTAB > FHxSA > PFHxA). This is in good agreement with findings in perfluoroalkyl amides (PFOAAmS > PFOAB) $^{42}$  and FTs (6:2 FtSaAm > 6:2 FTAB > 6:2 fluorotelomer sulfonate (6:2 FTS)), 43 which indicates the electrostatic interaction is an important mechanism in the adsorption process of all of these polyfluorinated compounds.

2.3. Sorption by Bacteria (Biosorption) of FASAs and Sulfonamide Antibiotics. The sorption of PFAS onto microbial biomass and biofilm can influence the retention and transport of PFAS in environmental matrices.<sup>23</sup> However, microbial adsorption of PFAS has just started to be evaluated. 24-26 Previous batch biosorption studies have evaluated sorption of PFAAs. 23,25,50-52 The molecular structure of PFAS, solution chemistry, and cell membrane structure can affect the magnitude of the PFAS sorption. Some research indicated that bacteria showed stronger adsorption with long-chain PFAS compared to short-chain PFAS, 52 and bacterial sorption was greater for PFOS than for perfluorooctanoic acid (PFOA), 25,52 which aligns with findings from PFAS sorption studies in soil.<sup>39</sup> The hydrophobic components in the cell membrane (e.g., phospholipids), along with the extracellular polymeric substances (EPS, composed of polysaccharides, proteins, and lipids)<sup>53</sup> produced by the cells, may provide hydrophobic and electrostatic PFAS binding sites. 26,54 Butzen et al. reported that PFOS sorption onto bacteria varied with pH, with greater sorption at pH ~4 compared to pH 6.25 As pH increases, binding sites (such as peptides) on the cell surface deprotonate and repel anionic PFAS. Bacteria have negative-bulk charges at neutral pHs their isoelectric point (pI) ranges from pH 2-5—and Grampositive bacteria have a wider pI range compared to Gramnegative 55,56 Based on differences in cell membrane composition, these two groups are hypothesized to exhibit different adsorption capacities, but studies have yielded contradictory results to date. A study suggested that Gramnegative bacteria show a stronger PFAS sorption capacity because of higher lipid content stemming from the double membrane bilayer.<sup>52</sup> However, another study found greater sorption of PFAS by Gram-positive bacteria.<sup>25</sup> With an outward-facing and thicker peptidoglycan, more peptide sorption sites have been hypothesized<sup>57</sup> to increase PFOS sorption in Gram-positive bacteria. Lastly, Dai et al.<sup>23</sup> found no significant difference in PFAS sorption capacity between different Gram-stain bacteria. Bacteria can retain PFAS through sorption onto cell surfaces and uptake into the cell interior. Butzen et al.<sup>25</sup> suggested PFOS bacterial sorption was rapid and completely reversible, indicating that biosorption is likely a cell surface phenomenon within the test period (80 h).

On the other hand, studies showed inactivated bacteria retained PFAS significantly less than active bacteria.  $^{52,58}$  Presentato et al.  $^{59}$  reported that two *Pseudomonas* sp. strains were able to accumulate PFHxS within the cells in a short period ( $\sim\!15$  days), indicating the incorporation of PFAS into the cells. Studies on animal cells have shown that passive diffusion and protein-facilitated transport are the primary mechanisms for PFAS uptake into cells.  $^{60-63}$ 

Certain nonfluorinated sulfonamide antibiotics, including sulfamethoxazole (SMX), sulfadimethoxine (SDM), and sulfamonomethoxine (SMM), are adsorbed onto wastewater activated sludge. At the experimental pH 6.8, the sorption affinity of sulfonamide antibiotics to activated sludge followed the order of SDM (p $K_a$  6.3) > SMM (p $K_a$  6.0) > SMX (p $K_a$  5.7), which is consistent with the order of p $K_a$  values of the  $-\mathrm{SO}_2-\mathrm{NH}-$  moiety. <sup>64,65</sup> In addition, Pi et al. <sup>66</sup> reported that the fluorescence intensity of certain hydrophobic amino acids (such as the aromatic amino acids tryptophan and tyrosine) in EPS significantly decreased after adsorbing sulfonamide antibiotics. Based on these observations, it is reasonable to hypothesize that both p $K_a$  and hydrophobicity significantly influence the sorption behavior of FASAs, with EPS likely playing a critical role in this process.

EPS is known to decrease bacterial pI<sup>55</sup> and thus possibly increase sorption capacity for PFAS. PFAS sorbed can create a feedback loop for EPS production. For example, PFAAs have been shown to induce EPS-production in Rhodococcus jostii as a stress response mechanism.<sup>67</sup> So far, no studies have directly investigated the interactions between bacterial surfaces and EPS with FASAs. Ruyle et al.<sup>24</sup> reported large and rapid losses of 3 FASAs (AmPr-FHxSA, TAmPr-FHxSA, and FHxSA) from the aqueous phase in bioactive microcosms, indicating rapid sorption onto cells (<1 day). Faster biosorption of AmPr-FHxSA and TAmPr-FHxSA was reported compared to FHxSA. Considering the findings of biosorption literature on PFAAs and nonfluorinated sulfonamide antibiotics, we hypothesize that FASAs may exhibit more complex adsorption behavior due to their diverse head groups and charge properties, as well as pH gradients that drive microbial metabolism across cell membranes. Additionally, the sulfonamide nitrogen may act as an electron donor, forming hydrogen bonds with electron acceptor groups on the cell surface (such as amide, amine, or hydroxyl groups), thereby stabilizing the sorption process.<sup>68</sup> Elucidating biosorption mechanisms of sulfonamide PFAS is crucial to evaluate their bioavailability for microbial transformation.

#### 3. MICROBIAL BIOTRANSFORMATION

The adsorption of FASAs onto solid-phase media hinders their microbial transformation. Additionally, the high surface activity of PFAS can promote self-aggregation and enrichment at the air—water interface, further reducing its bioavailability to microorganisms. Solower microbial biotransformation kinetics have been reported for electrochemical fluorination-derived (ECF) PFAS compared to fluorotelomers because the alpha and beta nonfluorinated carbons with respect to the perfluoroalkyl chain can serve as oxidizable moieties. Despite the slower kinetics, decades of application of FASAs to the environment can yield substantial transformation. Microbial transformation kinetics are crucial to predicting the long-term fate of these precursors. We examined the microbial transformation rates of FASAs by comparing their first-order half-lives ( $t_{1/2}$ , Table 3). Additionally, we summarized their

Table 3. Reported Microbial Biotransformation of FASAs and Their Test Conditions with Product Yields<sup>a</sup>

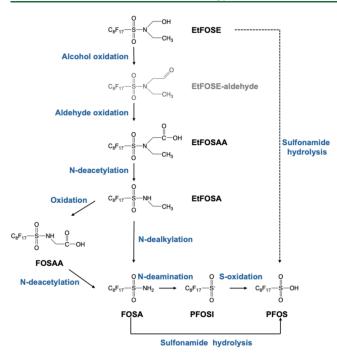
		PFAS initial				
Compound	Incubation conditions	concentrations	Duration	$t_{1/2}$ (days)	Mass balance and transformation products (mol %)	References
EtFOSE	WWTP activated sludge, aerobic, 28 $\pm$ 2 $^{\circ}\mathrm{C}$	2.38 mg/L	35 d	2-3	Mass balance 100.6 ± 16.3%, EtFOSAA (34.9%), FOSAA (48.9%), FOSA (5%), PFOSI (3.5%), PFOS (7%), EtFOSA (0.1%)	Lange et al., 2000
EtFOSE	WWTP activated sludge, aerobic, 25 °C	$1.5 \pm 0.05$ mg/L	96 h	3	EtFOSAA (23 $\pm$ 5.0%), PFOSI (5.3 $\pm$ 0.8%)	Boulanger et al., 2005
EtFOSE	WWTP activated sludge, aerobic, 30 °C	0.1 mg/L	10 d	0.71 ± 0.05	Mass balance 111%, EtFOSAA (66%), EtFOSA (1%), FOSAA (7%), FOSA (18%), PFOSI (1%), PFOS (7%)	Rhoads et al., 2008
EtFOSE	Marine sediments, aerobic, 25 °C	0.0625 mg/L	120 d	44	Mass balance 84%, EtFOSAA (31%), EtFOSA (1.7%), PFOS (0.44%), FOSAA (0.43%), FOSA (0.21%)	Benskin et al., 2013
EtFOSE	Marine sediments, aerobic, 4 °C	0.0625 mg/L	120 d	160	Mass balance 95%, EtFOSAA (39%), PFOS (12%), EtFOSA (6.4%), FOSAA (2.8%), FOSA (2.8%),	Benskin et al., 2013
EtFOSE	Acidic forest silt loam (pH = 5.5, OC 2.4%), aerobic, $22 \pm 2$ °C	3.7 μg/g	210d	26	Mass balance 97 $\pm$ 12%, EtFOSAA, FOSSA, FOSA, PFOS (1.06%)	Zhang et al., 2017
EtFOSE	Agricultural loam (pH = 7.8, OC 2.6%), aerobic, $22 \pm 2$ °C	3.7 μg/g	180d	31	Mass balance 102 $\pm$ 3%, EtFOSAA, FOSSA, FOSA, PFOS, PFOS (5.49%)	Zhang et al., 2017
EtFOSE	Anaerobic digester sludge, 20–26 °C (1010 mg/L)	1010 mg/L	108 d	1860	Mass balance 92%, EtFOSAA (1.7%), PFOSI (0.3%)	Lange et al., 2017
n-EtFOSE	Soil, aerobic, 22 °C	$2.696 \ \mu g/g$	105 d	9.6	Mass balance 60–83%, n-FOSAA (49%), n-FOSA (0.47%), n-FOSAA (3.6%), n-FOSA (12%), and n-PFOS (7.9%)	Liu et al., 2019
br-EtFOSE	Soil, aerobic, 22 °C	$2.696 \ \mu {\rm g/g}$	105 d	8.7	br-EtFOSAA,br-PFOS, br-FOSAA, br-FOSA	Liu et al., 2019
MeFBSE	Anaerobic digester sludge, 20– $26~^{\circ}\mathrm{C}$	976 mg/L	108 d	35.8	Mass balance 122% (92–122%), MeFBSAA (57%), PFBSI (40%)	Lange et al., 2017
EtFOSA	WWTP activated sludge, aerobic, 30 °C	0.1 mg/L	10 d	0.24	Mass balance 73%, FOSA (55%), FOSAA (2%), PFOSI (2%), PFOS (41%)	Rhoads et al., 2008
EtFOSA	Soil, aerobic	1.62 mg/L	182 d	$13.9 \pm 2.1$	Mass balance 71%, FOSA (30.3%), FOSAA (34.2%), EtFOSA (2.21%), PFOS (4%)	Mejia- Avendaño et al., 2015
EtFOSA	Slurry from wetland, aerobic, 30 °C	$0.47 \ \mu g/g$	91 d	0.51	Mass balance 99.7-131.4%, FOSAA, FOSA, PFOS (85.1%)	Yin et al., 2018
EtFOSAA	WWTP activated sludge, aerobic, 30 °C	0.1 mg/L	10 d	0.025	Mass balance 62%, EtFOSA (1%), FOSAA (5%), FOSA (18%), PFOS (10%)	Rhoads et al., 2008
FOSAA	WWTP activated sludge, aerobic, 30 °C	0.1 mg/L	10 d	$0.11 \pm 0.04$	Mass balance 72%, FOSA (38%), PFOSI (2%), PFOS (21%)	Rhoads et al., 2008
FOSA	WWTP activated sludge, aerobic, 30 °C	0.1 mg/L	10 d	0.02	Mass balance 83%, PFOSI (2%), PFOS (38%)	Rhoads et al., 2008
PFOSI	WWTP activated sludge, aerobic, 30 °C	0.1 mg/L	10 d	$0.25 \pm 0.02$	Mass balance 86%, PFOS (78%)	Rhoads et al., 2008
PFOSAmS	Soil, aerobic, 22 °C	2.827 μg/g	180 d	no significant change	Mass balance 73.1%, PFOSAm (10%), FOSA (<0.005%), PFOS (0.3%)	Mejia- Avendaño et al., 2016
PFOSNO	Soil, aerobic	1.998 $\mu g/g$	90 d	15	Mass balance 15−16%, FOSAA, FOSA, PFOS(~2%)	Chen et al., 2020
PFOSAm	Soil, aerobic, 22 °C	$2.0~\mu\mathrm{g/g}$	90 d	47.5	FOSAA (0.001%), FOSA (0.8%), PFOS (0.27%)	Liu et al., 2021
PFOSB	Soil, aerobic, 22 °C	$1.8~\mu\mathrm{g/g}$	90 d	675	FOSAA (0.064%), FOSA (0.52%), PFOS (1.5%)	Liu et al., 2021
AmPr- FHxSA	Amended AFFF-impacted soil, $30^{\circ}\text{C}$	0.097 mg/L	70 d	27.4	FHxSA (~40%), PFHxS (1-5.4%)	Cook et al., 2022
AmPr- FHxSA	Slurry,19 °C/29 °C, pH 6.0-7.2	6851 mg/L	45 d/ 60 d		FHxSA, PFHxS	Ruyle et al., 2023
AmPr- FHxSA	Slurry,19 °C/29 °C, pH 6.0-7.2	47501 mg/L	45 d/ 60 d		FHxSA, PFHxS	Ruyle et al., 2023
FHxSA	Slurry,19 °C/29 °C, pH 6.0-7.2	28729 mg/L	45 d/ 60 d		PFHxS	Ruyle et al., 2023

<sup>&</sup>lt;sup>a</sup>Standard deviation for  $t_{1/2}$  is reported whenever available.

transformation pathways (Figures 2 and 3) and major intermediates (Table 3) expected to persist in the environment at high levels. Finally, we reviewed the reported enzymes involved in microbial precursor transformation to hypothesize biochemical mechanisms of FASAs transformation.

**3.1.** Aerobic and Anaerobic Microbial Transformation of EtFOSE. EtFOSE is aerobically biotransformed into PFOS via intermediates, including EtFOSAA, EtFOSA, FOSAA, FOSA, and PFOSI, which all can be quantified by LCMS.<sup>70–76</sup> The aerobic microbial transformation half-life

range of EtFOSE is <1 day to 160 days depending on the matrix and conditions. In general, the transformation rate of EtFOSE follows activated sludge > soil > marine sediments, which could be attributed to aerobic microbial density and activity in different media. Incubation conditions (e.g., temperature, pH) are expected to impact transformation rates and product yields. In a study of the transformation of EtFOSE in different soils, EtFOSE was transformed slightly faster in acidic soils, but PFOS yields in alkaline soils were four to five times higher than in acidic soils.<sup>75</sup> It was hypothesized



**Figure 2.** Microbial transformation pathways of EtFOSE. <sup>70–76</sup> Structures in gray are undetected, predicted intermediates. The solid line represents the primary pathways, and the dashed line represents the secondary pathways.

that varied soil properties resulted in differences in microbial communities and bioavailability of major intermediates, based on their  $pK_as$ . It has been demonstrated that the biotransformation half-lives of branched and linear EtFOSE show no significant difference.<sup>76</sup>

There are two main pathways for microbial transformation of EtFOSE (Figure 2): the primary pathway is a series of Nalkyl oxidations and N-dealkylations to yield FOSA, which can accumulate in the environment. The sulfonamide group in FOSA is hydrolyzed to yield PFOS, but with reported lower yields. Although a parallel transformation pathway leading to FOSE (N-deethylation) has been observed in fish, 77 FOSE has not been quantified in studies of microbial transformation due to unavailable analytical standards and its volatility. Zhang et al. 75 confirmed that the proposed pathway including FOSE did not fit the previous experimental data well. Previous studies have consistently demonstrated that EtFOSE can be transformed into EtFOSAA rapidly, accumulating and then remaining or slightly decreasing. EtFOSAA is considered the major intermediate, with yields ranging from 23% to 66%. Other persistent intermediates include FOSAA and FOSA, which are consistent with frequent reporting of coexistence of these substances with PFOS in soils, sludge, and landfill leachates. 78,79 However, PFOS accumulates relatively slowly during the incubation (maximum yield of 12% from EtFOSE after 120 d)<sup>73</sup> and even shows a continuously increasing trend at the end of the incubation duration, indicating the long-term accumulation of PFOS in the environment. In a microbial transformation study of EtFOSA by wetland microcosms, 80 an unexpectedly high yield of PFOS was reported at 85.1 mol % after 91 days of aerobic incubation. Meanwhile, the microbial community shifted to Methylocaldum, methanotrophs which are obligately aerobic and are able to utilize methane as their sole carbon and energy source.<sup>81</sup> Previous studies have shown that methanotrophs have a broad substrate profile and can

cometabolize certain recalcitrant chemicals, like chlorinated ethenes.  $^{82}$ 

Some studies have reported microbial transformation behaviors of major intermediates of EtFOSE to identify the bottlenecks in PFOS yields. <sup>72,74,80</sup> FOSAA and FOSA are frequently identified as major intermediates from EtFOSAA and EtFOSA biotransformation. <sup>72,74,80</sup> Combined with the evidence that EtFOSAA is the main intermediate of EtFOSE, <sup>70,73,75</sup> it can be inferred that carboxylic acids are difficult to transform due to their oxidation state. Therefore, the removal of the N-acetic acid group and the hydrolysis of the sulfonamide are the major rate-limiting step.

Notably, Lange<sup>83</sup> reported the extremely slow transformation of EtFOSE with the half-life time of 1860 d in anaerobic digestion sludge. In contrast, MeFBSE exhibited a significant loss in anaerobic sludge with a half-life of 35.8 days and produced MeFBSAA (57%) and PFBSI (40%). This study suggested the potential for the anaerobic transformation of short-chain precursors and the formation of short-chain PFAAs. Currently, there is no evidence of abiotic transformation of FASAs in sterile environmental media.

**3.2. Cationic and Zwitterionic N-alkylamine FASAs.** These cationic and zwitterionic N-alkylamine FASAs possess relatively large molecular weights and tertiary or quaternary amine moieties. Due to the diverse functional groups, they exhibit more complex microbial transformation compared to EtFOSE and EtFOSA. In studies of microbial transformations of cationic and zwitterionic *N*-alkyl amine-containing FASAs, large gaps in mass balance remain, with recoveries ranging from 15% to 73.1%, indicating unquantified and unidentified transformation intermediates. High-resolution mass spectrometry under full scan mode has been applied to identify anticipated biotransformation intermediates based on suspect lists, <sup>24,36,84</sup> as well as biodegradation prediction simulators (e.g., EnviPath, CATALOGIC).

We reviewed the microbial transformation pathways of cationic and zwitterionic ammonium-containing FASAs based on limited previous literature (Figure 3, Table 2). PFOSAmS, PFOSNO, and PFOSB can transform into PFOSAm at a relatively rapid rate through N-demethylation, N-oxide reduction, and N-deacetylation, which could be the major initial steps of these three precursors. Cook et al.84 also detected perfluorohexane sulfonamidoalkyl amine oxide (PFOHxNO) among the transformation products of the sixcarbon homologue (AmPr-FHxSA) of PFOSAm, which suggests the occurrence of N-oxidation of tertiary amines. PFOSAm could then undergo sequential N-demethylation and oxidation removal of ammonium, eventually forming polyfluoroalkyl sulfonamide aldehyde (PFOSAm-3); the aldehyde can also be directly generated from the parent compounds (PFOSAmS and PFOSNO) through the oxidative removal of the ammonium group. Subsequently, polyfluoroalkyl sulfonamide aldehyde undergoes sequential oxidation and hydrolysis in several steps to eventually form PFOS, which resembles the previously reported biotransformation process in the aerobic soil of EtFOSA.<sup>74</sup> FOSAA and FOSA are frequently detected as major transformation intermediates of these ammoniumcontaining FASAs, as well as key intermediates of EtFOSE and EtFOSA. This is consistent with the fact that FOSAA and FOSA (as well as shorter-chain homologues) are frequently detected and present at high levels in PFAS-contaminated sites. 5,85 The six-carbon homologue, AmPr-FHxSA was

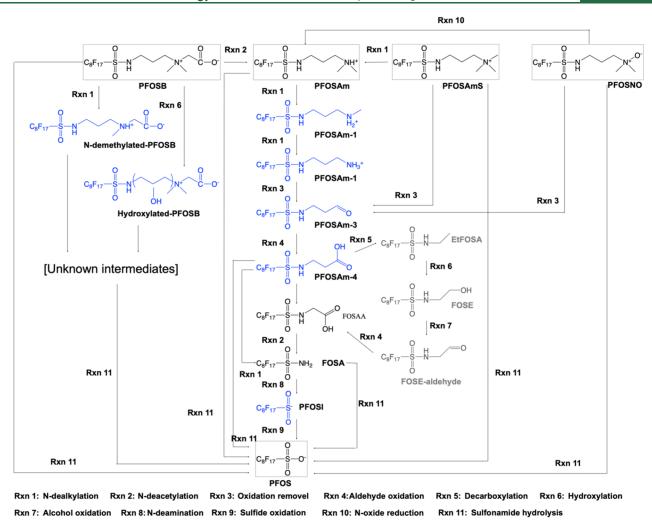


Figure 3. Microbial transformation pathways of cationic and zwitterionic amine-containing FASAs. Structures in blue are identified by suspect screening. Structures in gray are undetected, predicted intermediates. 24,84,86–88

demonstrated to undergo similar microbial transformation processes as PFOSAm under aerobic conditions.<sup>84</sup>

Another pathway for PFOSAmS, PFOSNO, PFOSB, and PFOSAm is to generate PFOS through direct sulfonamide bond hydrolysis. Although previous literature only listed the direct hydrolysis pathways of PFOSAmS, PFOSNO, and PFOSAm, based on analogous reasoning, we included the direct hydrolysis of PFOSB in this review. Rayne et al. 89 indicated that abiotic hydrolysis at the S-N bond of Nunsubstituted FASAs appears unlikely under environmentally relevant conditions. However, N-ethanol and N-acetate moieties in perfluoroalkyl sulfonamido ethanols and acetates may self-attack the S-N bond and induce hydrolysis, leading to the formation of PFOS. In addition, as for transformation intermediates of PFOSB, Liu et al.87 detected hydroxylsubstituted betaines and demethylated betaine, which suggest other two transformation pathways of PFOSB. However, the subsequent transformation processes of these hydroxylated or N-demethylated compounds are unknown.

Compared with the microbial transformation of neutral precursors (EtFOSE and EtFOSA) in aerobic soil ( $t_{1/2}$ : 9.6–31 d), these cationic and zwitterionic precursors ( $t_{1/2}$ : ~47.5 d) exhibit higher resistance to microbial transformation except for PFOSNO ( $t_{1/2}$ : 15 d). The presence of cationic groups significantly increases the electrostatic attraction to negatively

charged soil particles. Both factors contribute to a decrease in microbial bioavailability.

The half-lives of FASAs are longer than those of their amide analogs with the same number of fluorinated carbons. Specifically, the observed  $t_{1/2}$  values follow the trends PFOSB > PFOAB, PFOAAmS > PFOSAmS, N-dimethyl ammonio propyl perfluorooctane amido (PFOAAm) > PFOSAm and PFOSNO > perfluorooctane sulfonamido amine oxide (PFOANO). We hypothesize that the higher persistence of sulfonamides could be due to their stronger sorption to soil, resulting from a longer perfluoroalkyl chain and a bulkier sulfonyl group compared to corresponding amides, which in turn reduces their bioavailability for transformation. Additionally, the sulfonamide group is more resistant to hydrolytic cleavage than the amide group,  $^{84}$  which could result in slow biotransformation kinetics of sulfonamides in microbial hydrolytic reactions.

The difference in microbial transformation rates between eight-carbon cationic and zwitterionic FASAs derived with varying N-alkyl substitutions is notable. When evaluating their stability in aerobic soil, their  $t_{1/2}$  values exhibit a distinct pattern, quaternary amine  $\approx$  propyl betaine  $\gg$  tertiary amine > amine oxide, <sup>87</sup> which is consistent with the ranking in corresponding amides. Thus, terminal N-substitutions exert significant influence on the biotransformation rates of these

Table 4. Reported Enzymes Involved in Biotransformation and Defluorination of PFAS

ı							
Enzymes/proteins	Encoded gene	Function	PFAS sub- strate	Products	Source microor- ganisms	Research method	References
Alkanesulfonates-binding protein	SsuA	Alkanesulfonate assimilation/uti- lization					
Alkanesulfonates ABC transporter ATP-bind- ing protein	SsuB	Alkanesulfonate assimilation/uti- lization		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
Alkanesulfonate monoox- ygenase	SauD	Alkanesulfonate assimilation/uti- lization	6:2 FTS	<ul><li>6:2 FTUA, 5:3 FTCA, PFHxA, PFPeA, fluoride ion</li></ul>	Dietzia aurantiaca J3	Identifying upregulated proteins in the presence of 6:2 F13 compared to sulfate through genome sequencing and annotation	Méndez et al., 2022
alkanesulfonate permease protein	SsuC	Alkanesulfonate assimilation/uti- lization					
nitrilotriacetate monooxy- genase component B	ntaA-MoB	Amino acid catabolism					
alkane monooxygenase	RHA1_ro02534	Defluorination	6:2 FTOH, 6:2 FTS				
cytochrome P450	RHA1_ro00377	Defluorination	6:2 FTOH, 6:2 FTS	6:2 FTCA, Perfluoroheptanoic acid (PFHpA),	Rhodococcus jostii	Examining the expression levels of presumptive enzymes at	Yang et al.,
haloacid dehalogenases	RHA1_ro00230	Defluorination	6:2 FTOH, 6:2 FTS	6:2 F1UA, a-OH 5:3 F1CA, fluoride ion (from 6:2 FTS)	RHA1	different growing substrates, heterologous gene expression and in vitro assays	2022
alkanesulfonate monooxy- genase	RHA1_ro01768	Desulfonation	6:2 FTS				
toluene dioxygenase		Transformation	6:2 FtTAoS	6:2 FTS, PFHxA, PFPeA, PFBA	microorganisms in AFFF-impacted soil	Examining the presumptive genes in the BTEX amended enrichments	Olivares et al., 2022
nitrilotriacetate monooxy- genases	ntaA(ISGA 1218 and 1222)	Desulfonation	6:2 FTS	6:2 FTCA. 6:2 FTUA	Gordonia sp. strain NB4-1Y	Identifying differentially expressed proteins in the presence of 6:2 FTS compared to sulfate	Hamme et al., 2013
alkane hydroxylase	alkB	Transformation	6:2 PAPs	6:2 FTOH, 6:2 FTCA, 6:2 FTUA, PFHxA, fluoride ion	microorganisms in activated sludge	Examining the presumptive genes in the activated sludge enrichments	Lewis et al., 2016
haloacid dehalogenases	PZP66635.1, WP_011137954.1	Defluorination	PFOA	Fluoride ion	Delftia acidovorans	Heterologous gene expression	Harris et al., 2022
Fluc family F <sup>-</sup> channel	crcB1 and crcB2	Functional fluo- ride exporter		Fluoride ion, (CF <sub>3</sub> ) <sub>2</sub> CFCF=CHCOO <sup>-</sup> ,	Acetohacterium	Identifying upregulated genes in the presence of PFMeUPA compared to nonspiked control; Heterologous gene expression in E. coli	Yu et al
caffeoyl-CoA reductase	car operon (car- ABCDE)	Reductive de- fluorination	PFMeUPA	(CF <sub>3</sub> ) <sub>2</sub> CF(CHFCH <sub>2</sub> COO <sup>-</sup> , (CF <sub>3</sub> ) <sub>2</sub> CF(CHF) <sub>2</sub> COO <sup>-</sup>	bakii	Caffeate competitive inhibition of PFMeUPA defluorination; Molecular docking of caffeoyl-CoA and perfluorinated acyl-CoA with CarC	2024

precursors. The presence of a quaternary amine group significantly enhances the persistence of PFOSAmS and PFOSB. As a permanently cationic moiety, the quaternary amine group likely exhibits strong adsorption to soil, thereby reducing the bioavailability. In contrast, the amine oxide group imparts high reactivity to PFOSNO, resulting in its rapid biotic and abiotic transformations in soil. The microbial stability ranking also shows that the formation of a precursor to the tertiary amines (PFOSAm or PFOAAm) can be a rate-limiting step, as in the cases of quaternary ammonium and betaine compounds.

Most studies have focused only on the aerobic microbial transformation of N-alkyl amine-containing FASAs, with no significant loss of FASAs observed in sterilized controls. Unexpectedly, Chen et al. 88 found that in sterile soils, the concentrations of PFOSNO were significantly decreased, accompanied by production of FOSAA and FOSA at very low yields, which indicated the possibility of abiotic transformation of amine oxides. However, the production of PFSAs has only been observed in live soils.  $^{24,84,88}$ 

**3.3. Cationic/Zwitterionic FT-Derivatives.** Cationic and zwitterionic fluorotelomer derivatives, including 6:2 fluorotelomer sulfonamido amine oxide (6:2 FTNO), 6:2 FtSaAm, and 6:2 FTAB, are discussed in comparison with their FASA analogues PFOSNO, PFOSAm, and PFOSB, respectively. Overall, the microbial recalcitrance ranking of 6:2 FT sulfonamide-containing PFAS follows the order 6:2 FTAB  $\gg$  6:2 FtSaAm > 6:2 FTNO, 90 which aligns with the resistance order observed for FASAs with different *N*-alkyl substitutions 87

Fang et al. 90 reported rapid microbial transformation of 6:2 FTNO in aerobic sludge, with a half-life of 1.2 days. This aligns with the rapid loss of PFOSNO and PFOANO observed in aerobic soil, attributed to the high reactivity of the amine oxide. 87,88 However, unlike the pronounced and extensive abiotic transformation of PFOSNO and PFOANO in sterilized soil, 88 the abiotic transformation of 6:2 FTNO in sludge was found to be negligible. 90 6:2 FTNO underwent a series of biotransformation reactions, including N-demethylation, deamination, hydroxylation, oxidation, and decarboxylation, ultimately forming 6:2 fluorotelomer sulfonamide (6:2 FTSAm). Further transformation products like 6:2 FTS and short-chain PFAAs were not detected. 90 This contrasts with the microbial transformation of PFOSNO and PFOANO in soil, which leads to the formation of PFOS and PFOA.88 6:2 FTSAm appeared to be resistant to hydrolysis in aerobic

6:2 FtSaAm was proposed to be a primary intermediate product of 6:2 FTNO, with an estimated microbial transformation half-life of 11.5 days in activated sludge. 90 D'Agostino et al. reported that 6:2 FtSaAm was biotransformed in aerobic sludge, yielding 6:2 fluorotelomer alcohol (6:2 FTOH), 5:3 fluorotelomer carboxylic acid (5:3 FTCA), and short-chain PFAAs, including perfluorohexanoic acid (PFHxA), perfluorobutanoic acid (PFPeA), and perfluorobutanoic acid (PFBA). 6:2 FTOH is a critical intermediate for various fluorotelomer-based precursors. 91,92 Due to the high reactivity of its hydroxyl group, it undergoes oxidative defluorination, ultimately forming PFCAs with shorter fluorinated chains than the parent compound. This is a significant difference from the biotransformation products of FASAs, which have not been observed to undergo microbial partial defluorination and ultimately form PFSAs instead of

PFCAs. Notably, 6:2 FtSaAm was found to be transformed into 6:2 FTSAm and 6:2 FTS through abiotic processes in sterilized sludge.

Overall, 6:2 FTAB exhibited a strong recalcitrance to microbes. In the activated sludge reported by Fang et al., the concentration of 6:2 FTAB showed no significant reduction after 100 days of aerobic incubation. D'Agostino et al. 93 reported that in aerobic activated sludge, 6:2 FTAB underwent microbial transformation to produce small amounts of 6:2 FTSAm, 6:2 FTOH, 5:3 FTCA, PFHxA, PFPeA, and PFBA (total molar yield≈ 3%). Similar to 6:2 FtSaAm, 6:2 FTAB underwent abiotic transformation in sterilized sludge to form 6:2 FTSAm (molar yield ≈5%). Interestingly, in petroleum hydrocarbon-amended soil, 6:2 FTAB decreased rapidly, with an estimated half-life of 31 days, and the accumulation of 6:2 fluorotelomer unsaturated acid (6:2 FTUA) and 5:2 ketone was observed.<sup>94</sup> However, no accumulation of PFCAs was detected, due to the slow conversion of 6:2 FTAB to PFCAs or the irreversible adsorption of certain transformation intermediates.94

**3.4. Enzymes Involved.** The limited research on microbial enzymes involved in PFAS biotransformation has focused on fluorotelomers. PFAS biotransformation has focused on fluorotelomers. No studies have reported on enzymes involved in the microbial transformation of FASAs (enzymes in animals, plants, and humans are outside the scope of this review). Therefore, this study focuses on the previously reported microbial enzymes involved in the transformation and degradation of PFAS, their presumed roles, and research methods (Table 4), aiming to provide background and strategies for future research on the biotransformation enzymes of FASAs.

Many oxygenases have been targets for emerging contaminants, including some PFAAs precursors, due to their broad substrate range and proven activity against various persistent organic pollutants. Alkanesulfonate monooxygenase, alkane monooxygenase, nitrilotriacetate monooxygenase, alkane hydroxylase, and cytochrome P450 were found to be upregulated and involved in the biotransformation of 6:2 FTS, 6:2 polyfluoroalkyl phosphates (6:2 PAPs), and 6:2 FTOH. 95,96,98,103 Furthermore, heterologous gene expression experiments in E. coli confirmed that cytochrome P450 and alkane monooxygenase possess defluorination activity toward 6:2 FTOH. 96 Crude enzymes of alkanesulfonate monooxygenase (gene: Ssu D and SsuE) were shown to desulfonate 6:2 FTS and produce sulfite. 96 It is noteworthy that the Ssu operon (SsuABC, SsuD, and SsuE) is known to be expressed by certain bacteria to utilize organosulfonates as sulfur sources for growth under sulfur-limiting conditions, 104 which is consistent with the biotransformation of 6:2 FTS by various bacteria under sulfur-limited conditions. 95-97 However, neither of these above-mentioned strains exhibiting desulfonation of 6:2 FTS is able to grow with PFOS or PFHxS as the sole sulfur source. 95,97 In addition to these monooxygenases, Olivares et al. 91 reported the presence of toluene dioxygenase in AFFFimpacted soils, which may be involved in the biotransformation of 6:2 fluorotelomer thioacetic acid sulfonate (6:2 FtTAoS). Moreover, some fluorinated aromatics, fluorinated olefins, and a short-chain ether PFAS (1,1,1,2-tetrafluoro-2trifluoromethoxy-4-iodobutane) were shown to induce toluene dioxygenase in Pseudomonas putida F1. 105 The transformation and defluorination activity of dioxygenases toward PFAS still needs further validation.

Haloacid dehalogenases are another class of enzymes that have been found to be involved in the microbial transformation of PFAS. Yang et al. Feported that the expression of haloacid dehalogenase in *Rhodococcus jostii* RHA1 was upregulated during the transformation of 6:2 FTOH and 6:2 FTS. Additionally, enzyme inhibition tests and heterologous expression further confirmed that this haloacid dehalogenase exhibits defluorination activity on 6:2 FTOH. Furthermore, Harris et al. Finteriore introduced a gene (PZP66635.1) encoding haloacid dehalogenases from *Delftia acidovorans* into a plasmid for expression in *Escherichia coli*. The results showed that fluorine ions were detected in the transformed *E. coli* samples incubated with PFOA, although the levels were not significantly different from those in the control group without PFOA.

Recently, a few studies reported the reductive defluorination of  $\alpha$ , $\beta$ -unsaturated per- and polyfluorocarboxylic acids by *Acetobacterium* species under anaerobic conditions.  $^{100,106,107}$  Yu et al.  $^{100}$  were the first to demonstrate that the Fluc family F<sup>-</sup> channels encoded by crcB1 and crcB2 are involved in transporting fluoride ions out of the cell, a process essential for cellular defluorination activity.  $^{108}$  Fluoride is toxic to cells as it inactivates essential enzymes, including ATPases, which directly generate energy, and pyrophosphatase, which is critical for maintaining a phosphate source to biosynthesize ATP.  $^{108}$  Furthermore, Yu et al. reported that caffeoyl-CoA reductase can reduce the  $\alpha$ , $\beta$ -unsaturated bond in (E)-perfluoro-4-methylpent-2-enoic acid (PFMeUPA, (CF<sub>3</sub>)<sub>2</sub>CFCF=CFCOOH) in a manner similar to its reduction of caffeate, leading to defluorination.  $^{100}$ 

In contrast to fluorotelomers, the final products of microbial transformation of FASAs are PFSAs rather than PFCAs. This indicates that the microbial metabolism of FASAs does not involve desulfonation but involves sulfonamide hydrolysis and assimilation of N-substituents. PFSA yields from N-alkylamine FASAs have been associated with methanotrophy<sup>80,84</sup> and nitrification,<sup>24</sup> both microbial processes that involve wellknown cometabolic oxygenase (such as methane monooxygenase, ammonium monooxygenase). 109-113 Methane monooxygenase has been proven to be capable of oxidizing alkanes, alkenes, alicyclics, aromatics, ethers, heterocyclics, chlorinated solvents, and ammonia. 114 A recent study reported that in parallel with the biotransformation of C6-FASAs (FHxSA, PFHxSAm, and PFHxSAmS), there was an increase in the total abundance of nitrifying taxa (such as Nitrososphaeria and Nitrospina) and nitrate concentrations,<sup>24</sup> suggesting associations between nitrification and FASAs biotransformation. There is ample evidence of cometabolism of nonfluorinated sulfonamides in the natural and built environment, 109-113,115,116 although the hydrolysis of the sulfonamide bond is not usually detected. Certain sulfonamide monooxygenases and flavin reductases have been reported to be involved in the initial cleavage reaction of sulfonamides, leading to the breakdown of an S-N bond and the production of sulfur dioxide. 117,118 It is possible that the perfluorocarbon chain adjacent to the sulfonamide group appears to largely hinder sulfonamides hydrolysis. Direct hydrolysis of the sulfonamide bond in N-alcohol or N-carboxylated FASAs has been proposed as an alternate pathway to PFSAs 36,119 and supported by lower activation energy required than for FASA hydrolysis.<sup>24</sup> The NH<sub>2</sub> moiety in FASAs is not a great leaving group, so bacterial hydrolases likely use metals (i.e., Zn<sup>2+</sup>) or acid to mediate the conjugation of glutathione with the

substrate, releasing NH<sub>2</sub>. Indeed, glutathione<sup>120</sup> and N-glucuronidation<sup>121</sup> of FASAs have been reported during in vivo transformations in mouse models but have not been evaluated in microbial systems. Yet, bacterial glutathione transferases are well-known enzymatic systems mediating xenobiotic detoxification and oxidative stress. A systematic evaluation of the specific enzymatic activity linked to FASA biotransformation is needed.

Currently, enzymes involved in biotransformation are mainly identified through differential expression of genes or proteins in microbial communities when exposed to PFAS. Heterologous gene expression or purified enzyme activity assays can further verify the enzymatic ability to transform FASAs based on increases of PFSAs in the medium. In vitro tests in which biological enzymes and PFAS are coincubated can directly display the conversion and kinetic characteristics of certain enzymes to the PFAS substrate. Computational methods, including molecular docking, molecular dynamics, and quantum mechanics/molecular mechanics, can help predict the binding affinity of FASAs, 123-127 before experimental validation.

#### 4. RESEARCH GAPS AND PROSPECTS

FASAs differ from fluorotelomers in their diverse charged properties and antibacterial characteristics. This review examined the sorption and microbial transformation of FASAs to clarify their complex environmental fate. Compared with fluorotelomers, FASAs exhibit stronger sorption onto soil and greater resistance to microbial transformation. Despite the slow transformation, the terminal end products, PFSAs, become more mobile. Therefore, the introduction of FASAs into the environment poses longer-term and more widespread pollution issues. Several gaps remain regarding sorption descriptors, biotransformation pathways, and enzymes involved. We suggest the following research directions.

- (1) Experimental  $pK_a$  and biosorption descriptors. Due to the complex speciation changes of certain FASAs,  $pK_a$ s significantly influence their adsorption behaviors and microbial bioavailability. However, the  $pK_a$  values of FASAs in current studies are mostly predicted by models trained with nonfluorinated compounds. Therefore, experimentally determined  $pK_a$  values are necessary for future research to characterize the speciation of FASAs in real environmental media. In addition, the sorption of FASAs by bacteria should be investigated in future research to get a comprehensive understanding of the extent of microbial biosorption in the environment.
- (2) The fate of short-chain FASAs and their transformation under anoxic conditions. At present, most studies focus on the fate of C8 FASAs. However, with the gradual phase-out of long-chain PFAS, C6 and C4 FASAs have become more frequently detected in various applications. This has resulted in a significant data gap regarding the sorption and transformation of these short-chain FASAs in environmental media. Additionally, the microbial transformation of FASAs under anoxic conditions also warrants attention. These efforts will contribute to a better understanding of the fate and transport of FASAs in subsurface environments.
- (3) Identification of enzymes responsible for biotransformation of FASAs. Current studies on the biotransformation of FASAs have only focused on biotransformation

reactions, lacking identification of the microorganisms and enzymes involved in the biotransformation. Simplified microcosms (such as enrichment, pure strains, and cell-derived active mixtures) can be used to test the degradability on FASAs. Additionally, it is essential to elucidate the mechanisms of microbial transformation of FASAs (whether through cometabolism) and identify key biomarkers, including involved enzymes. These efforts will contribute to developing effective remediation strategies for FASAs-impacted sites.

# ASSOCIATED CONTENT

# Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acs.est.5c00906.

The names, acronyms, CAS numbers, and structures of FASAs and their reference compounds and soil characteristics from studies on FASAs adsorption (PDF)

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#### Notes

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