# The Prodigious Hydrogen Bonds with Sulfur and Selenium in Molecular Assemblies, Structural Biology and Functional Materials

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## The rise of S/SeCHBs: Milestones and Methods



*Figure S1:* Schematic timeline of evolution of significant events relating to sulfur/selenium centered H-bonds (S/SeCHBs)<sup>1-67</sup>, ranging from explorations on the unique nature and occurrence of these H-bonds<sup>3,21–26,68–71</sup> to their applicability in engineered natural systems as well as materials.(see main text for references)

The significant milestones enunciated above have been achieved through an arsenal of techniques perfected over the years by the researchers working in this arena. It is interesting to have an idea of the methods and the model complexes that were employed to answer the *critica quaestiones* pertaining to the nature of various kinds of S/SeCHBs, as detailed in Fig S2 and Table S1.



Figure S2: Graphical Representation of the communion of various methodologies adopted for detection and prediction of H-bonds with sulfur and selenium: (A) Gas phase resonant ion-dip infrared (RIDIR) spectra of N-phenylacetamide (NPAA) and pyridone (2PY) and their complexes with dimethyl sulphide (DMS) and dimethylselenide (DMSe) to probe N-H···S and N-H···Se Hbond, respectively. Reproduced with permission from ref.<sup>56</sup> Copyright (2017) American Chemical Society. (B) Benzene- $(H_2S)_n$  clusters subjected to electronic (resonant two-photon ionization combined with mass spectrometry) and ionization depletion IR spectra for probing S-H··· $\pi$ interactions. Reproduced with permission from ref.<sup>72</sup> Copyright (2019) American Chemical Society., (C) Fourier Transform Microwave spectroscopy of  $H_2S$  dimer and several isotopomers for evidence of S-H···S hydrogen bonds by study of Ka = 1 transitions. Reproduced with permission from ref.<sup>59</sup>, Copyright (2018) Wiley Publishers., (D) High-Resolution Zero Kinetic-Energy *Photoelectron-Spectroscopy (ZEKE-PE) spectra of p-chlorophenol-H<sub>2</sub>S complex for determination* of O-H···S H-bond dissociation energy. Adapted with permission from ref.<sup>70</sup> Copyright (2015) American Chemical Society. (E) Gibbs Energy determination at room level for -O-H•••O/S/Se Hbond formation in alcohol-dimethylselenide complex - The figure shows pressure of the complex versus the product of the donor and acceptor pressures, for complexes with TFE donor. Reproduced with permission from ref.<sup>62</sup> Copyright (2019) American Chemical Society. (F) Thioamide-N-H. H-bonds in solution investigated through concentration dependent NMR spectroscopy. Reproduced with permission from ref.<sup>57</sup> Copyright (2017) American Chemical Society., (G) Electron density topology analysis through plot of reduced density gradient against

the sign of the second eigenvalue of the electron-density Hessian matrix for the  $Fe(CO)_4H_2$ ...DMS dimer to study Fe-H. S H-bond. Reproduced with permission from ref.<sup>73</sup> Copyright (2019) American Chemical Society. (H) N-H···S H-bonds in NMFA-DMS complexes as revealed by colored isosurfaces of the reduced electron density gradient (3D-NCI-plot), following the NCI-plot topological analysis of the electron density at the MP2/aug-cc-pVDZ. Reproduced with permission from ref.<sup>51</sup> Copyright (2015) American Chemical Society. (I) Electrostatic potential plot drawn at an isosurface of 0.074 a.u. for S-H···S H-bond in 2-mercaptobenzoic acid and its (J) 2D deformation density and Laplacian plot of the interaction region. Reproduced with permission from ref.<sup>74</sup> Copyright (2017) International Union of Crystallography. (K) The plots of donoracceptor interacting natural bond orbitals (NBO) i.e. overlap of p-type sulfur/oxygen/nitrogen lone pair and N-H  $\sigma^*$  for the amide-N-H···S=C H-bond complex of 6-thioguanosine monophosphate (6thio-GMP) and NUDT15 (PDB-5LPG). Reproduced with permission from ref.<sup>57</sup> Copyright (2017) American Chemical Society. (L) Contribution of different components of interaction energy (Electrostatics, polarisation, dispersion, repulsion) in various complexes of indole conformers, as obtained from SAPT analysis. Adapted with permission from ref.<sup>75</sup> Copyright (2017) Royal Society of Chemistry.

## Probing the Nature and Strength of S/SeCHBs

It has been established that the strength of conventional hydrogen bonds (with nitrogen/oxygen as donor and acceptor) varies between 4-15 kcal/mol (16.74 kJ/mol-62.76 kJ/mol). These depend on the type of model systems studied. From various studies<sup>17,18,23,24,51,56,57,73,76-78</sup>, it has been proved that the strength of S/SeCHBs and conventional H-bonds in similar systems are comparable.

## **Table S1: Model Systems and Methodologies**

(The absolute values of various energies (corrected for BSSE and/or ZPE, wherever applicable) have been indicated within parenthesis. The given range of values are considered from calculations from different levels of theory/conformations/environment/intra or inter-H-bonding modes. Wherever possible, the corrected energy values (e.g BSSE, ZPE) have been given)

Interaction	Systems Studied	Methods		
N-H···S	Dimethylamine-dimethylsulfide <sup>47</sup> , (3-	FTIRS, AIM, NBO, EDA, R2PI,		
	methyl)Indole-Me <sub>2</sub> S <sup>23</sup> (18.11-19.08	FDIRS, NBO, Normal Coordinate		
	kJ/mol), N-methylformamide (NMFA)/N-	Analysis		

	phenylacetamide (NPAA)- Me <sub>2</sub> S <sup>51</sup> (30-40			
	kJ/mol) Zinc enzyme model complex <sup>33</sup>			
O-H···S	<i>para</i> -cresol·Me <sub>2</sub> S/MeSH/EtSh <sup>77</sup> (17.07-	R2PI, FDIRS, AIM, EDA (KR, NVS,		
	19.66 kJ/mol), thiomalondialdehyde and	NEDA), NBO, Ab-initio, Gas phase		
	thioacetylacetone derivatives <sup>79</sup> (40.0-42.1	FTIR		
	kJ/mol), Alcohol-ethylene sulphide			
	complex <sup>80</sup> (20.2-27.2 kJ/mol)			
C-H···S	Complexes of 1,2,4,5-tetracyanobenzene	LIF, FDIR spectroscopy, Ab-initio		
	with various sulfur containing solvents <sup>81</sup>			
	(5.73-27.82 kJ/mol)			
	$CH_4/C_2H_4/C_2H_2\cdots SH_2^{82}$	Ab-initio, DFT, AIM		
	2,3-thienyl- and phenyl- or 2,3-dithienyl-			
	substituted propenoic acid aggregates <sup>83</sup>	IR spectroscopy, Ab-initio		
	(9.6-9.8 kJ/mol)			
S-H···O	$H_2S$ -MeOH dimer <sup>21</sup> (6.65-14.06 kJ/mol),	Ab-initio, vibrational energy analysis		
	$H_2S$ -Et <sub>2</sub> O/Bu <sub>2</sub> O/1,4-dioxane complex <sup>71</sup> (0.5	IR Predissociation and VUV		
	kJ/mol -17.70 kJ/mol),	spectroscopy Microwave		
	thiomalondialdehyde and	spectroscopy, AIM, NBO		
	thioacetylacetone derivatives <sup>79</sup> (20.3-25.4			
	kJ/mol)			
	3-mercaptopropionic acid <sup>26</sup>			
S-H···N	Thiolimin tautomers of thioaminoacrolein <sup>42</sup>	High-level ab-initio, NBO, AIM		
	(16.08 kJ/mol-27.19 kJ/mol),			
	H <sub>2</sub> S: ammonia/aliphatic amines			
	complex <sup>43</sup> (7.37-15.72 kJ/mol)			
S-H···S	Ethane-1,2-dithiol <sup>84</sup> ,	Electron Diffraction,		
	2 and 3-mercaptobenzoic acid <sup>74</sup> (9.1, 6.9	X-ray diffraction, Multipole		
	kJ/mol)	modelling, DFT		
	Substituted (Z)-N-(Thionitrosomethylene)-	DFT, NBO, AIM		
	thiohydroxylamine Systems (23.64 kJ/mol-			
	31.35 kJ/mol)			
	$C_2H_4\cdots H_2S$ and $C_6H_5CCH\cdots H_2S^{45,85}$	Microwave spectroscopy		
S-H… <b>π</b>	[Benzene]-H <sub>2</sub> S clusters <sup>72</sup>	IR, Electronic Spectroscopy		

	Indole/3-methyl-indole- H <sub>2</sub> S <sup>76</sup> (20.46	FDIRS, R2PI, EDA		
	kJ/mol-21.63 kJ/mol)			
	Cysteine SH-aromatic interactions (8.34-	PDB analysis, Ab-initio calculations		
	15.5 <sup>86</sup> )			
N-H…Se	Amine adducts of chiral selones <sup>30</sup> , 2-	<sup>1</sup> H- <sup>77</sup> Se HMQC NMR, IR/UV double		
	pyridone/NPAA/NMFA- Me <sub>2</sub> Se complex <sup>56</sup>	resonance spectroscopy, NBO, NCI		
	(29.5-50.4 kJ/mol)			
O-H…Se	p-substituted phenol-SeH <sub>2</sub> complexes <sup>52,87</sup>	NBO, NRT, QTAIM, DFT		
	(4-15 kJ/mol (neutral), 32-57 kJ/mol	(B3LYP/6-311+G*), NICS, PDI,		
	(charged)) peri-substituted naphthalenes <sup>88</sup> ,	ATI, FTIR Spectroscopy		
	selenosalicylaldehyde <sup>89</sup> , Hydrated 6-			
	selenoguanine tautomers <sup>48</sup> (28.62-47.28			
	kJ/mol) Alcohol-dimethylselenide			
	complex <sup>62</sup> , 2-(Methylseleno)ethanol <sup>35</sup>			
C-H···Se	$Q_3$ CH···SeH <sub>2</sub> complex (Q =Cl, F, H) <sup>60</sup>	NBO, AIM, Normal Mode analysis,		
	(3.97-10.58 kJ/mol), Aldols of chiral N-	<sup>1</sup> H- <sup>77</sup> Se HMQC NMR and XRD,		
	acyl selones <sup>34</sup> Diselenocin <sup>15</sup>	Solid Phase IR, <sup>1</sup> H NMR		
Se-H…N	p-substituted pyridine-SeH <sub>2</sub>	NBO, NRT, AIM		
	complexes <sup>63</sup> (10-15 kJ/mol), 3-imino-			
	propeneselenol <sup>46</sup> (39.35- 41.03 kJ/mol)			
Se-H…O	Selenoacetic acid <sup>90</sup> , Tautomer of hydrated	FTIR, Raman, UV spectra, <sup>1</sup> H- <sup>77</sup> Se		
	6-selenoguanine <sup>48</sup> (29.20-32.17 kJ/mol), 2-	NMR, Ab-initio, vibrational energy		
	selenoformyl-3-thioxo-propionaldehyde91	analysis, AIM, NBO		
	(5.71-11.77 kJ/mol)			
S-H···Se	Selenal tautomer of 3-mercapto	TD-DFT, AIM, NBO		
	propeneselenal <sup>92</sup> (31.45-46.37 kJ/mol)			
Se-H…S	Thial tautomer of 3-mercapto			
	propeneselenal <sup>92</sup> (31.69-45.87 kJ/mol)			
Se-H…Se	Selenophenol <sup>53</sup> (3.2 kJ/mol)			

(FDIRS- fluorescence dip infrared spectroscopy, FTIR- Fourier Transform IR spectroscopy,

R2PI - resonant two-photon ionization, LIF-Laser Induced Fluorescence, DFT- Density

Functional Analysis, AIM – Atoms-in-molecules theoretical calculations, NBO-Natural Bond Orbital Analysis, EDA- Energy Decomposition Analysis, NICS- Nucleus Independent Chemical Shifts, PDI- para delocalization index, NRT- Natural Resonance Theory)

# **Drug-Biomolecule Interactions**

# Table S2 : Interactions between approved sulfur-containing drugs with biomolecules

PDB ID	Drug	Biomolecule	Donor ··· Acceptor
1I2W	Cefoxitin	Beta-Lactamase from Bacillus	CB <sub>ALA</sub> ··· S1 <sub>1Q1</sub> (Chain A, B)
		Licheniformis BS3	
1IYP	Cephalothin	Toho-1 Beta-Lactamase	CB <sub>PRO</sub> Chain A
			S19 <sub>CEP</sub>
			CB <sub>ASN</sub> ··· S19 <sub>CEP</sub>
2C5W	Cefotaxime	Penicillin-Binding Protein 1A(PBP-	CB <sub>TRP</sub> ··· S1 <sub>CEF</sub> (Chain A)
		1A) (Acyl-Enzyme Complex) from	
		Streptococcus Pneumoniae	
3VSL		Penicillin-Binding Protein 3 (PBP3)	CD <sub>PRO</sub> <sup></sup> S2 <sub>CEF</sub> (Chain A)
		from Methicillin-resistant	
		Staphylococcus aureus (MRSA)	
2ZQA		beta-lacta Toho-1	CB <sub>PRO</sub> Chain A
		E166A/R274N/R276N triple mutant	S2 <sub>CEF</sub>
5NZY		(E-coli)	CB <sub>ASN</sub> <sup></sup> S <sub>SO4</sub>
5ZQD		DNA cross-link repair protein 1A	CG <sub>PRO</sub> ··· S1 <sub>CE3</sub> (Chain A)
		Penicillin-Binding Protein D2 from	CE2 <sub>PHE</sub> ···· S2 <sub>CEF</sub>
		Listeria monocytogenes	(Chain A, B, C, E, G)
3Q1F	Piperacillin	CTX-M-9 S70G	CB <sub>LEU</sub> ··· SAI <sub>YPP</sub> (Chain B)
		TP domain from Chlamydia	
6I1G		trachomatis Penicillin-Binding	CB <sub>ASP</sub> <sup></sup> S <sub>JPP</sub> (Chain A)
		Protein 3	

4DKI	Ceftobiprole	PBP2A from Methicillin-resistant	CB <sub>GLN</sub> ··· SBE <sub>RB6</sub> (Chain B)
		Staphylococcus aureus (MRSA)	
5TX9		S. aureus penicillin binding protein 4	CB <sub>SER</sub> <sup></sup> SAS <sub>RB6</sub> (Chain A &
		(PBP4) mutant (E183A, F241R)	B)
5TXI		wild-type S. aureus penicillin binding	
		protein 4 (PBP4)	CB <sub>SER</sub> ··· SAS <sub>RB6</sub> (Chain A &
6G88		Enterococcus Faecium D63r	B)
		Penicillin-Binding protein 5	
		(PBP5fm)	CG <sub>GLN</sub> ··· SBE <sub>RB6</sub> (Chain A, B
			& C)
			CE2 <sub>TYR</sub> ··· SBE <sub>RB6</sub> (Chain B)
4JF4	Meropenem	OXA-23 β-lactamase	CB <sub>SER</sub> ··· S14 <sub>MER</sub> (Chain A &
4N91		β-lactamase PenP_E166S	B)
			CB <sub>ALA</sub> ··· SAK <sub>DWZ</sub> (Chain B)
4ML1	Oxacillin	Class D β-lactamase OXA-1 K70D	CZ2 <sub>TRP</sub> ··· SAR <sub>1S6</sub> (Chain D)
4R1G	Cloxacillin	peptidoglycan glycosyltransferase	CB <sub>TYR</sub> <sup></sup> S1 <sub>CFU</sub> (Chain A & B)
		from Atopobium parvulum	
4RA7	Nafcillin	peptidoglycan glycosyltransferase	CB <sub>TYR</sub> ···· S1 <sub>NXU</sub>
		from Atopobium parvulum	
5TY2		S. aureus penicillin binding protein 4	CB <sub>SER</sub> ···· SAS <sub>NFF</sub>
		(PBP4) mutant (E183A, F241R)	
5CGX	Cefoxitin	Fox-4 cephamycinase mutant Y150F	CE2 <sub>PHE</sub> ··· S1 <sub>1S7</sub> Chain A
6PT5		Class D Beta-lactamase OXA-48	CZ2 <sub>TRP</sub> S1 <sub>1S7</sub>
5TB8,	Lamivudine	Human DNA Polymerase Beta	CA <sub>PHE</sub> ···· S3' <sub>1RZ</sub> (Chain A)
5TBC	(Triphosphate)		
6G3V	Famotidine	Human carbonic anhydrase I	CE1 <sub>HIS</sub> ··· S <sub>F09</sub> (Chain B)
6I1F	Amoxicillin	TP domain from Chlamydia	CB <sub>ASP</sub> <sup></sup> S4 <sub>AXL</sub> (Chain A & B)
		trachomatis Penicillin-Binding	
		Protein 3	
6MKF	Imipenem	penicillin binding protein 5 (PBP5)	CG <sub>GLU</sub> S <sub>SO4</sub> (Chain A)
		from Enterococcus faecium	
6P54	Ceftriaxone	transpeptidase domain of PBP2 from	CA <sub>GLY</sub> <sup></sup> S2 <sub>CEF</sub> (Chain B)
		Neisseria gonorrhoeae	

6UN1	Temocillin	Pseudomonas aeruginosa PBP3	CE2 <sub>TYR</sub> ··· S1 <sub>TJ7</sub> (Chain A)
4ACS	Azathioprine	Glutathione transferase (GST) A2-2	SG2 <sub>GSH</sub> ··· O(H) <sub>TYR</sub>

#### More examples of S/SeCHBs in crystal structures and their applications

Sulfur and selenium centered H-bonds have been exploited in crystal engineering for design of three-dimensional stacked, channel, interpenetrated and tubular architectures.<sup>31,36,49,54,55,61,64,93</sup> Some examples from the Cambridge Structural Database corresponding to several kinds of S/SeCHBs have been presented in Fig S3. This also includes attractive features like host-guest formations<sup>16,94</sup>, layered packing features<sup>28</sup> and finite chain of cooperative/anti-cooperative H-bonds in co-crystals.<sup>37</sup> These can be particularly useful when such assembling of molecular units can be manipulated with an intention of targeting specific functionalities. For example, Thomas et al.<sup>53</sup> observed participation of S-H…S and Se-H…Se H-bonds in crystal structure organization (as seen in Fig S3(G) could lead to the formation of intriguing organic alloys of thiophenol and selenophenol. Another study shows the importance of the C-H···S H-bonds in the intersheet stability in crystals of Bis(ethylenedithio)tetrathiafulvalene (BDET-TTF)<sup>29</sup>; usually employed in the doping of superconducting materials as well as in development of organic light emitting diodes. Several S/SeCHBs are known to confer stability to metal complexes that are not only significant from their synthetic utility but also for optical/thermal properties.<sup>58</sup> This is illustrated by how complexes of iridium and rhodium with 2-aminoethanethiolate are known to yield dimeric structures bridged by triple S-H···S H-bonds. One of these H-bonds is converted to a covalent S-S disulphide bond on controlled oxidation, a feature that is being actively explored for creation of such coordination spheres in future.<sup>65</sup> It was also reported in a resonance Raman spectroscopic study of a synthesized dioxomolybdenum(VI) complex that the Mo<sup>VI</sup>=O bond with the oxo groups could be stabilised by the *trans* effect of the two N-H…S H-bonded thiolate ligands.<sup>95</sup>As seen in thiolate complexes, nickel complexes with xanthate ions or ligands, like the complex (Et<sub>4</sub>N)[N-(carbamoylmethyl)ethylxanthate)], often exhibit the presence of N-H···S as well as C-H···S H-bonds. This trait of sulfur in xanthates to act as H-bond acceptor, can be exploited to induce formation of its metal complexes.<sup>39</sup> Another excellent example of the usage of a combined N-H…S and C-H…S H-bonded interaction network was noted from a recent study by Ushakov et al.<sup>96</sup> on layered nanocrystals of MoS<sub>2</sub>. The interlinking of the layers through the afore-mentioned H-bonds formed by alkyldiammonium ions was responsible for stability of these sheets.

(A) N-H <sup></sup> S	(B) O-H <sup></sup> S	(C) S-H <sup></sup> S	(D) C-H <b></b> S
CSD ID: LINJOK	CSD ID: XIYGIY	CSD ID: DAPLAJ	CSD ID : LIRYIV
(E) N-H <sup></sup> Se	(F) O-H <sup>…</sup> Se	(G) S-H <sup></sup> Se/ Se-H <sup></sup> S	(H) C-H <sup></sup> Se
GGG G			
CSD ID: PHSEAZ11	CSD ID: GABTEJ	CSD ID: JUJNEJ	CSD ID : IPAKIV
(I) S-H <sup>…</sup> N	(J) S-H <b></b> O	(K) Se-H <sup>…</sup> O	(L) Se-H <sup>…</sup> Se
CSD ID: YIRGEM	CSD ID: RONVAR01	CSD ID: VUTTEK	CSD ID : HUCJUL

*Figure S3: Various types of supramolecular architectures like connected helices, stacked sheets, columns, host-guest structures, zig-zag/wavy ribbons, etc are sustained by different types of S/SeCHBs in crystal structures of (A) 5,5-dimethyldecahydro-3H-1,2,4-benzotriazepine-3-thione*<sup>97</sup>, *(B) 4-nitrobenzoic acid dimethyl sulfoxide solvate*<sup>66</sup>, *(C) 1-(Hydrogen sulfido)-tetra-µH-nido-decaborane*<sup>44</sup>, *(D) bis(2-(1H-Benzimidazol-2-yl)phenyl)disulphide acetone solvate*<sup>41</sup>, *(E) 10H-phenoselenazine*<sup>67</sup>, *(F) 2,3-Dimethyl-4-(phenylseleno)phenol*<sup>38</sup>, *(G) organic alloy of benzenethiol and benzeneselenol*<sup>53</sup>, *(H) (selanyldicyclohex-1-ene-2,1-diyl)dimethanol*<sup>98</sup>, *(I) Ethyl (E)-3-anilino-2-cyano-3-mercaptoacrylate*<sup>99</sup>, *(J) 2-Hydroxythiobenzoic acid*<sup>100</sup>, *(K) 17-Oxapentacyclo[6.6.5.0*<sup>2,7</sup>.0<sup>9,14</sup>.0<sup>15,19</sup>]nonadeca-2,4,6,9,11,13-hexaene-1-selenol<sup>101</sup>, *(L) trans-bis(2-(1)-methylamino)propyliminomethyl)-4,6-dihydroselenophenolato-N,N',O)-zinc(ii)*<sup>102</sup>

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