Supplementary Information For

Identification of perrhenate-binding peptides by phage display

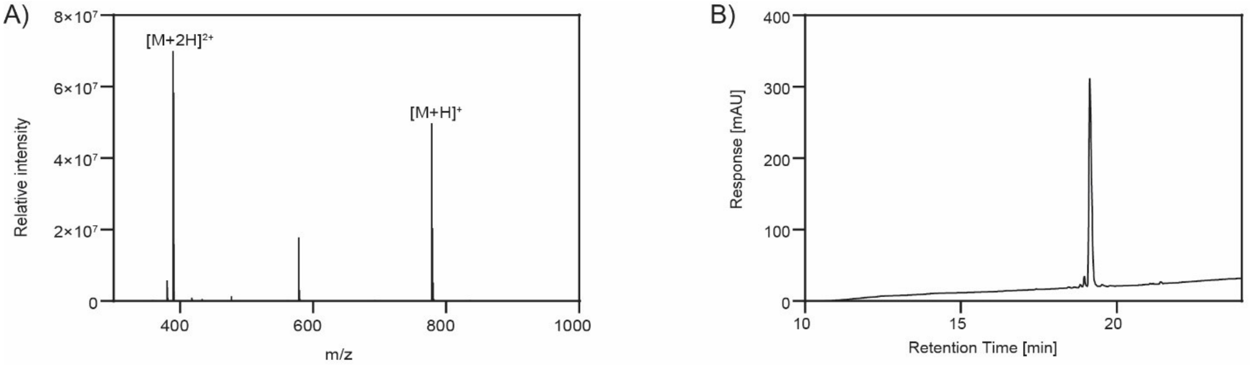
Supplementary Table S1: Results from rounds of biopanning. Peptide sequences highlighted in red are were identified multiple times either in different rounds of selection or the same round.

3rd round	4th round	6th round
TNSAIAK	AFYANPL	KMISILW
GKSIGSW	TMHRDPR	KMISTLS
HTPMHGW	VVHTYGV	KMISTIS
TSTSVHR	AYMVVNT	KMIYTIS
LPPPCAP	VVNFHSR	GKSIGSW
VIVGRSP	QQSNMAS	KAIHLQK
AATHLQN	CFASAPR	KMISTLW
NPYTGYS	AYMVVNT	KMISTIS
QSTKDVQ	GTWKSLK	TKDPQRT
NGPYRAA	KMISTIS	GKSIGSW
NILTTYP	HENLFDS	TATHLQK
KMISTIS	GVQPTTR	KMISTIS
TLHRSMP	TSTSVHR	
IGKVSFA	YKHNDAL	

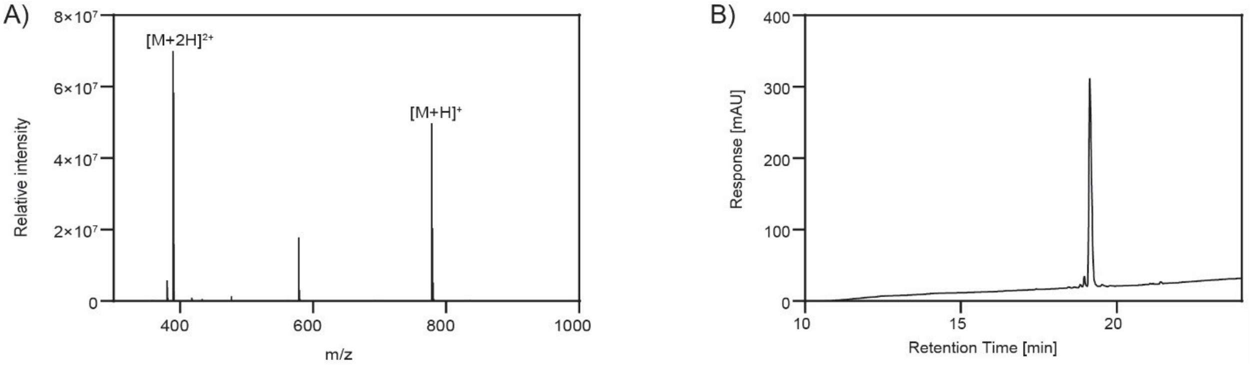
Supplementary Table2: Identified peptides and their corresponding scrambled peptides. ST.b1 and ST.b2 are arbitrarily generated peptides containing acidic residues.

Name	Peptide	Name	Scrambled peptides
ST1	KMISTIS	ST1.sc	IMTSKSI
ST2	KMISTLS	ST2.sc	LKISMTS
ST3	KMIYTIS	ST3.sc	MYKITSI
ST4	KMISILW	ST4.sc	LMIWKSI
ST5	KMISTLW	ST5.sc	LMKWTIS
ST6	GKSIGSW	ST6.sc	SGIWSKG
		ST.b1	ADVQPDV
		ST.b2	VQPAQVD

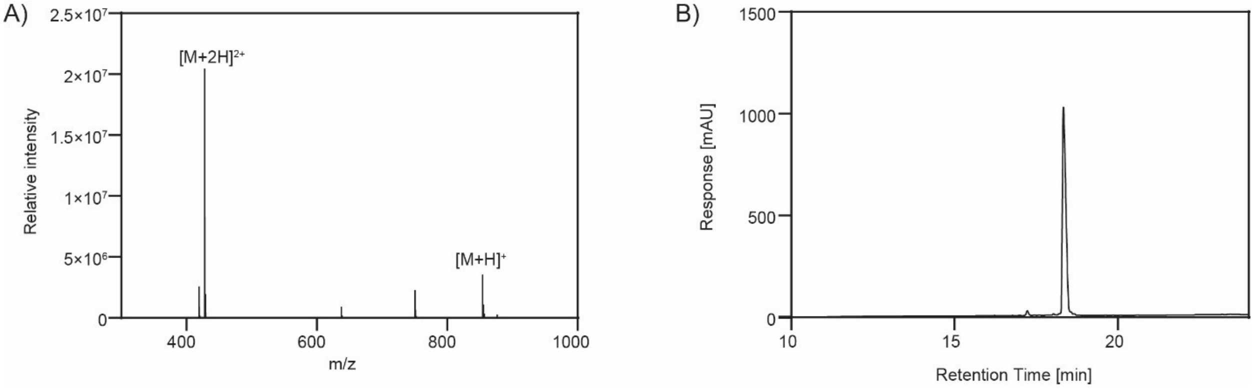
Supplementary Figure S1. Characterization of ST1. A) High resolution mass spectrum. [M+H] expected m/z: 778.4491, [M+H] measured m/z: 778.4511, Δppm: 3. B) HPLC chromatogram of purified ST1.



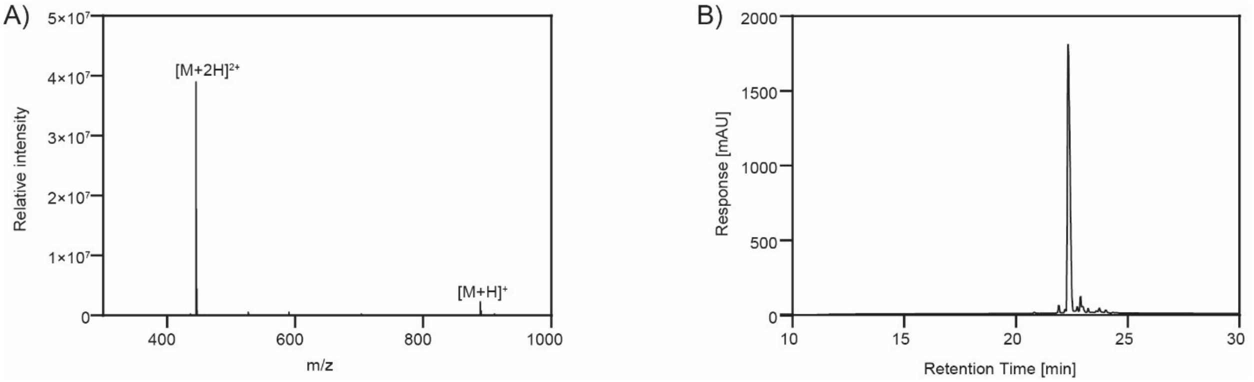
Supplementary Figure S2. Characterization of ST2. A) High resolution mass spectrum. [M+H] expected m/z: 778.4491, [M+H] measured m/z: 778.4511, Δppm: 3. B) HPLC chromatogram of purified ST2.



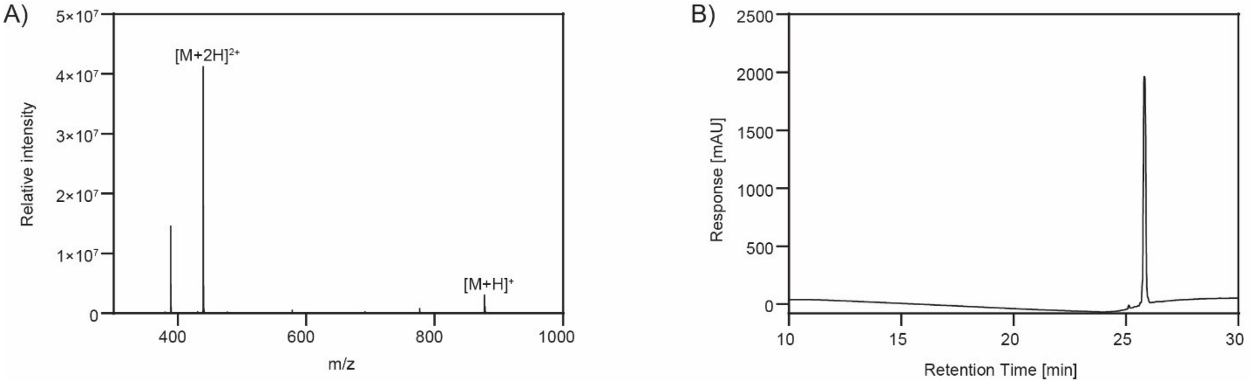
Supplementary Figure S3. Characterization of ST3. A) High resolution mass spectrum. [M+H] expected m/z: 854.4804, [M+H] measured m/z: 854.4897, Δppm: 11. B) HPLC chromatogram of purified ST3.



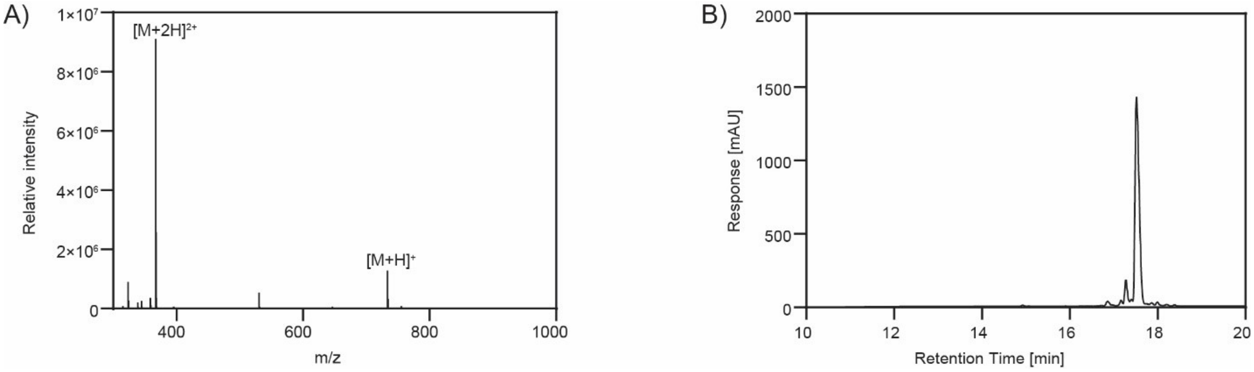
Supplementary Figure S4. Characterization of ST4. A) High resolution mass spectrum. [M+H] expected m/z: 889.5328, [M+H] measured m/z: 889.5438, Δppm: 12. B) HPLC chromatogram of purified ST4.



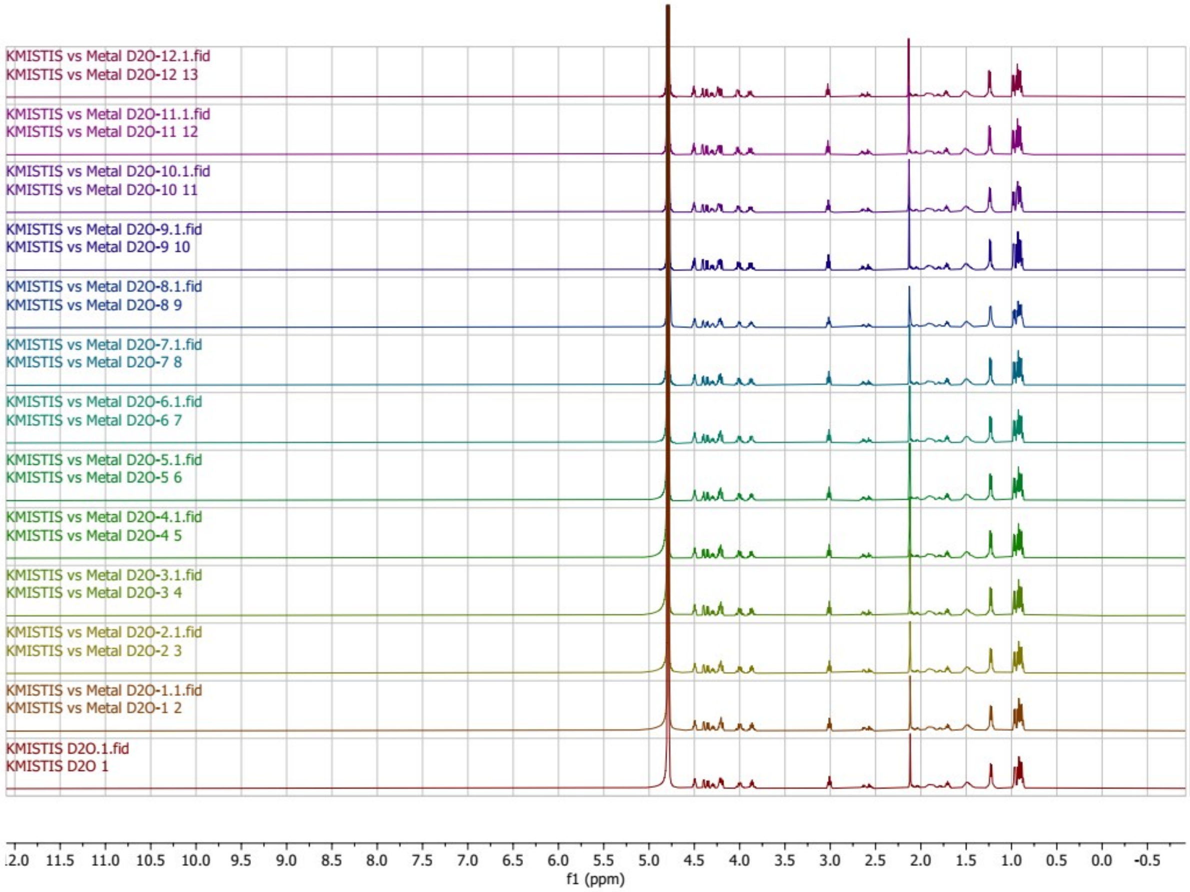
Supplementary Figure S5. Characterization of ST5. A) High resolution mass spectrum. [M+H] expected m/z: 877.4964, [M+H] measured m/z: 877.5079, Δppm: 13. B) HPLC chromatogram of purified ST5.



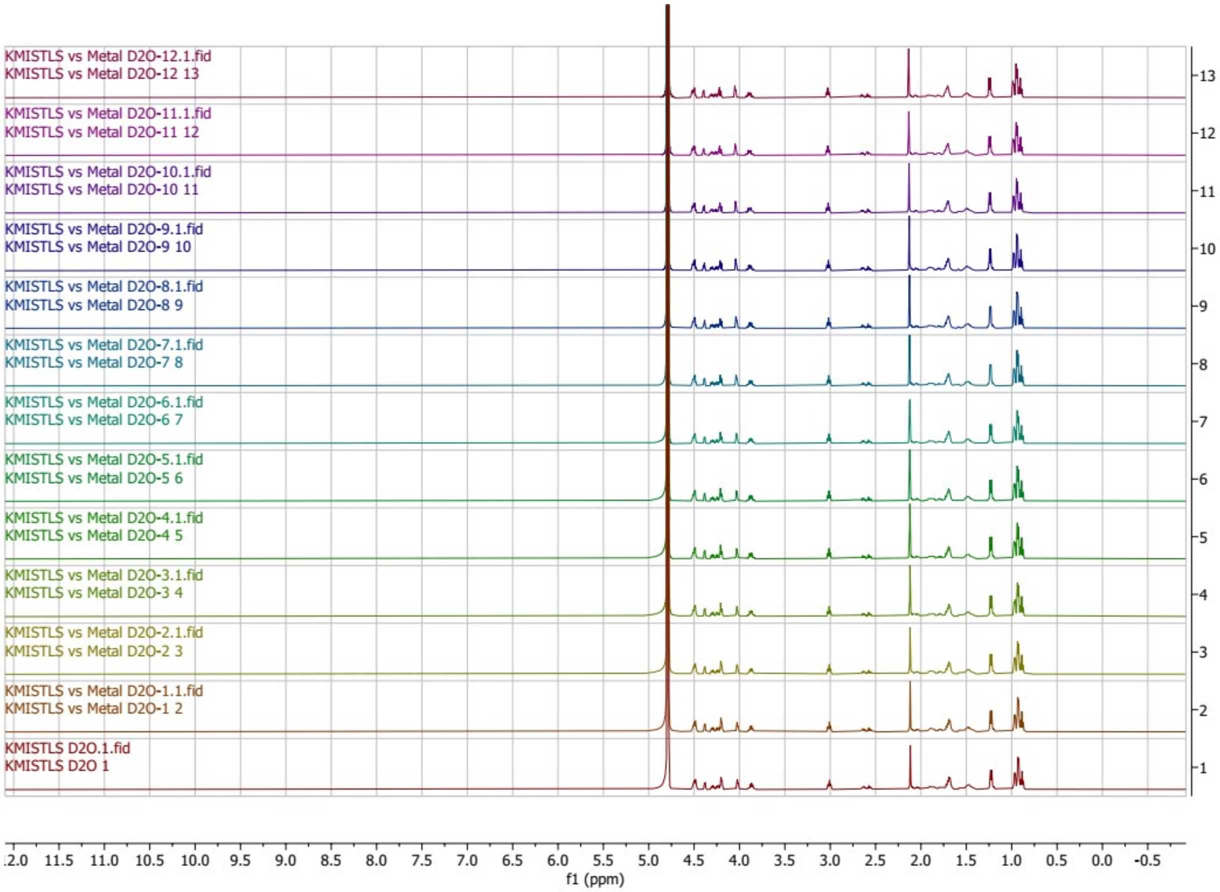
Supplementary Figure S6. Characterization of ST6. A) High resolution mass spectrum. [M+H] expected m/z: 733.3991, [M+H] measured m/z: 733.3991, Δppm: 16. B) HPLC chromatogram of purified ST6.



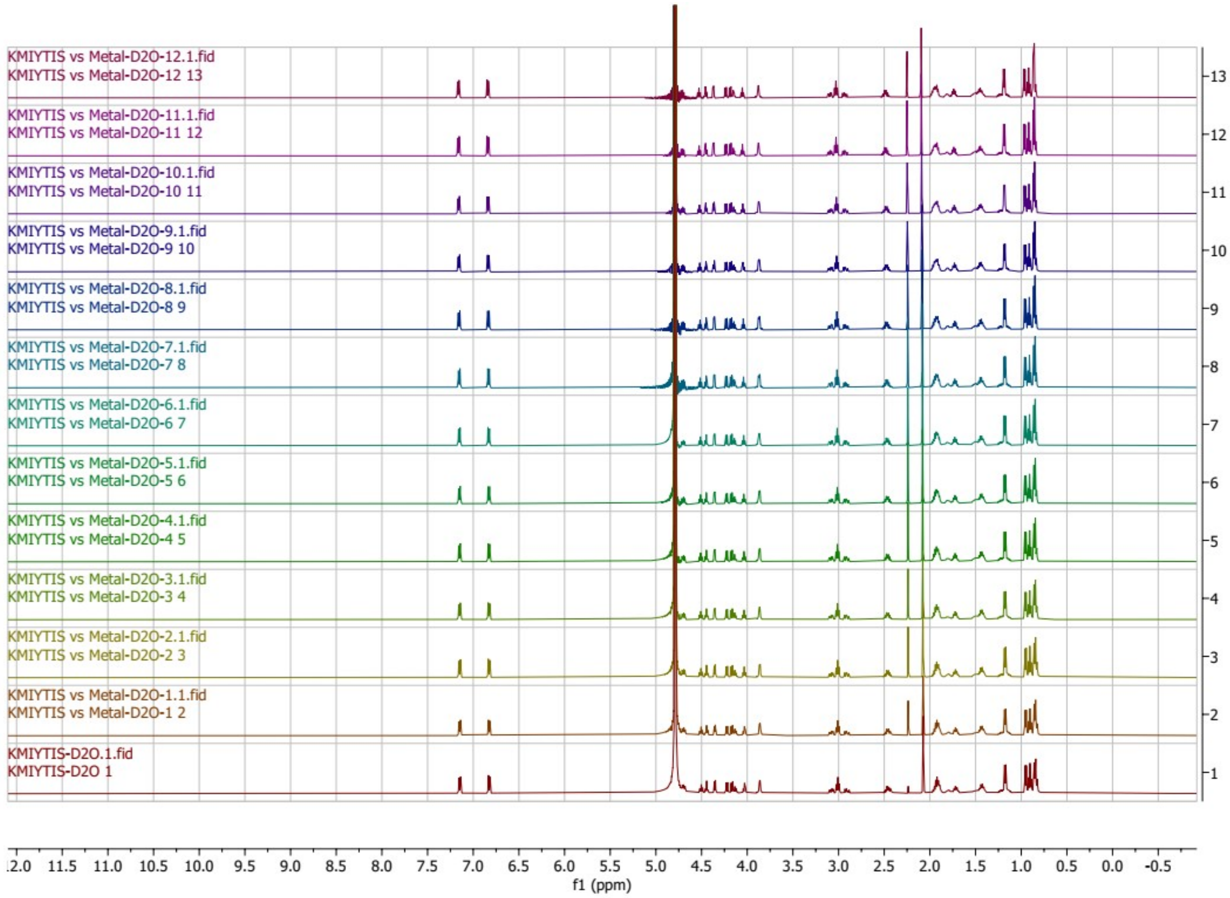
Supplementary Figure S7. NMR titration of ST1.



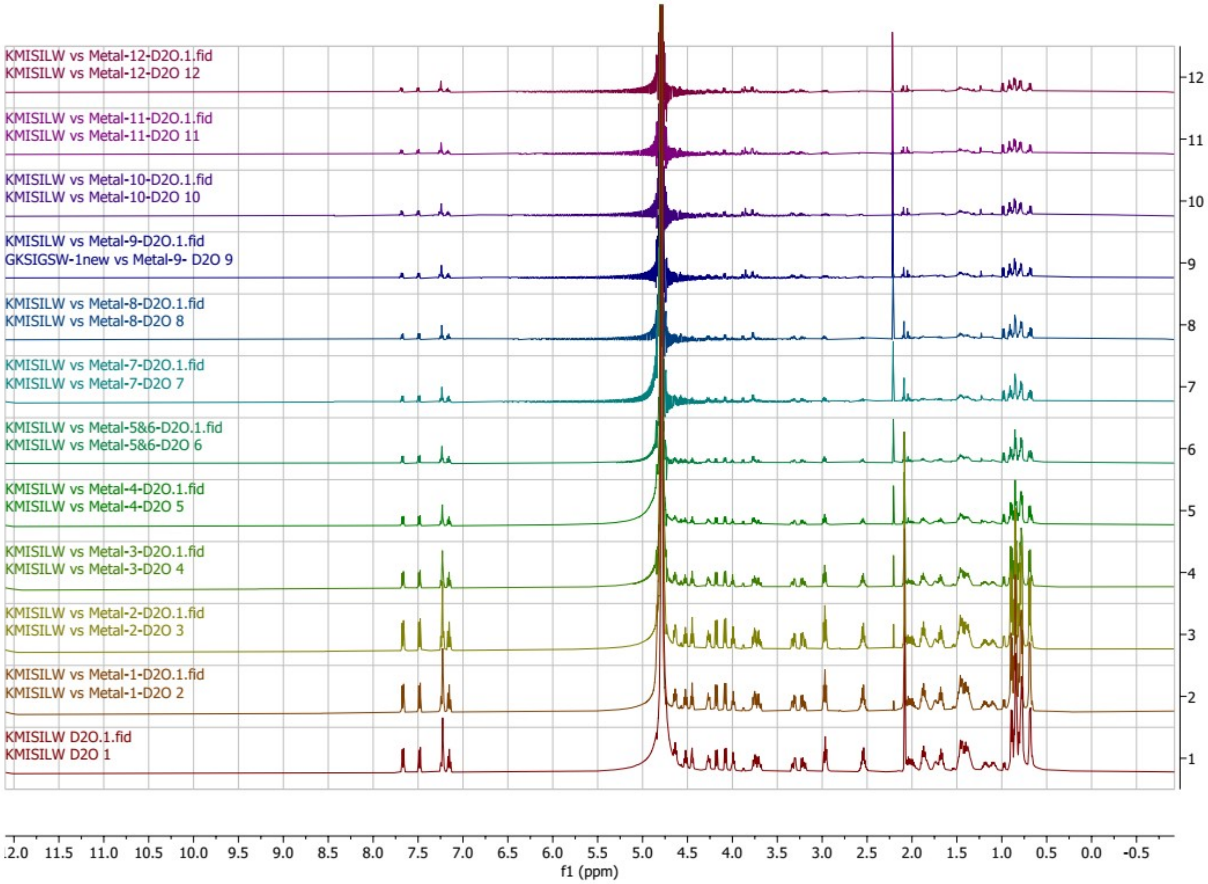
Supplementary Figure S8. NMR titration of ST2.



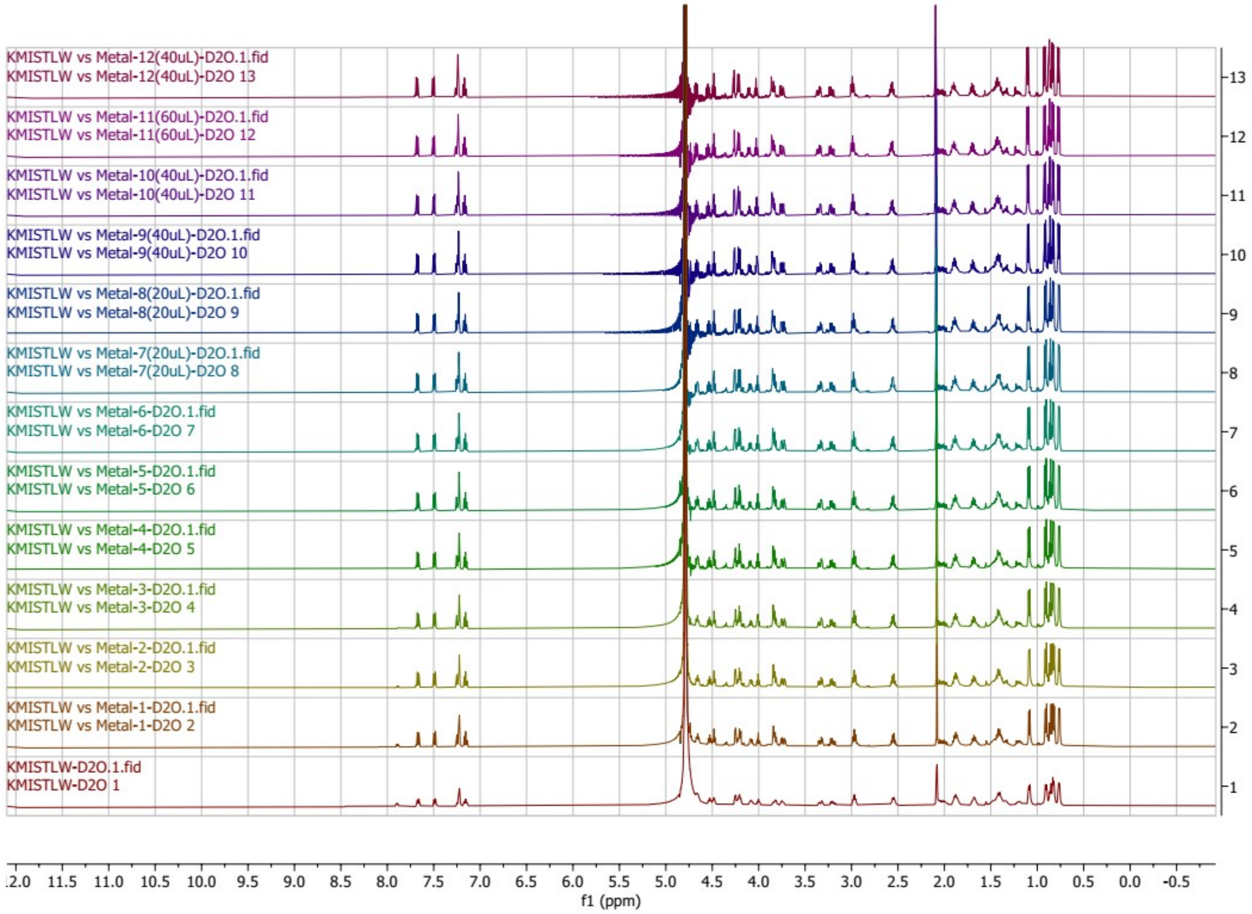
Supplementary Figure S9. NMR titration of ST3.



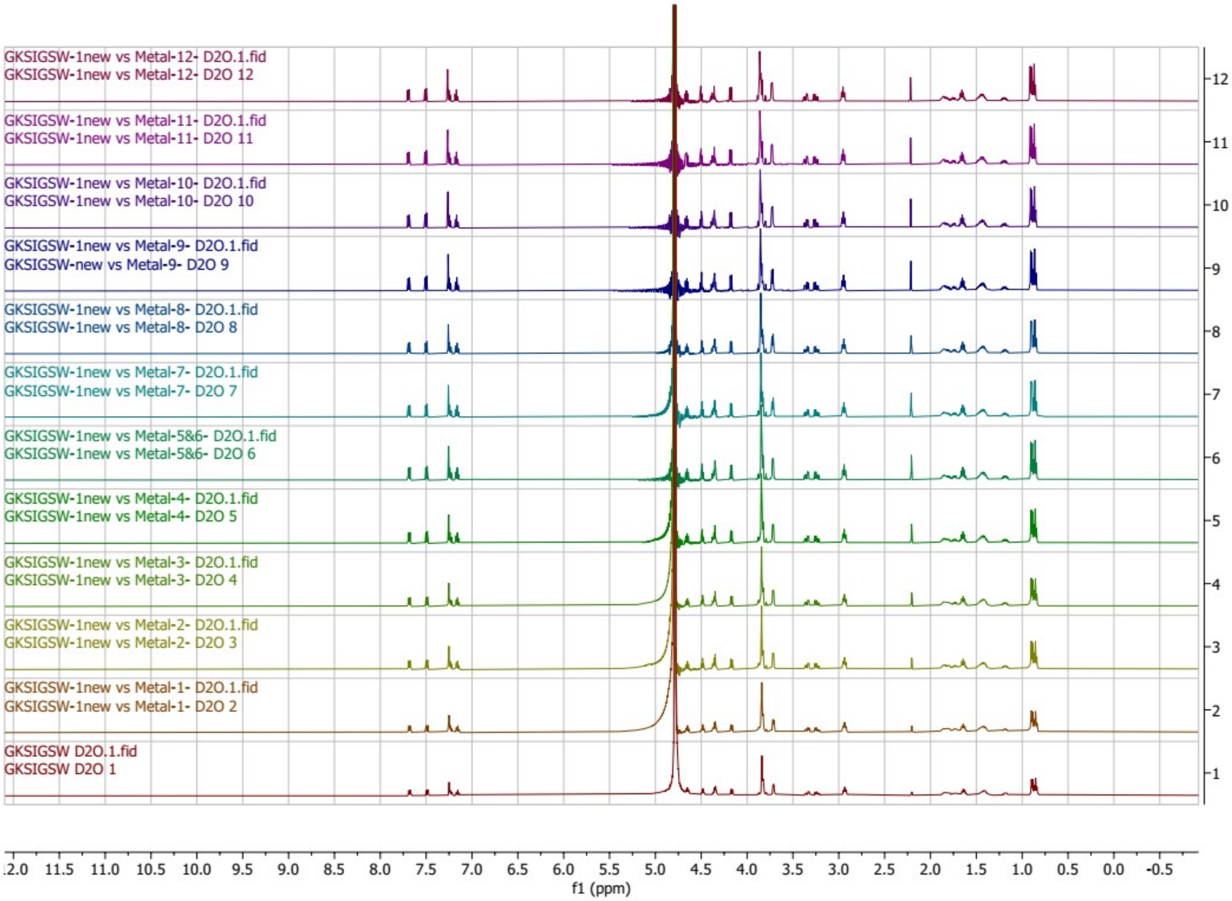
Supplementary Figure S10. NMR titration of ST4.



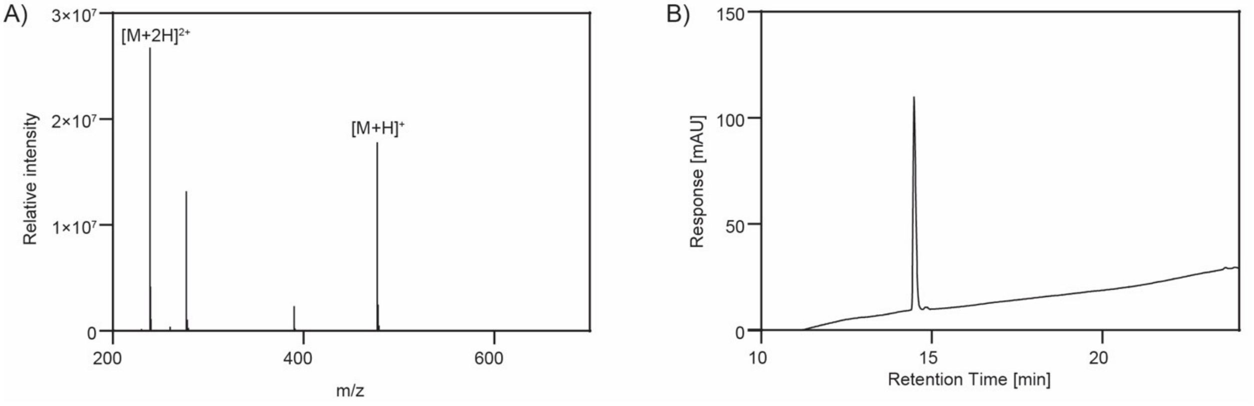
Supplementary Figure S11. NMR titration of ST5.



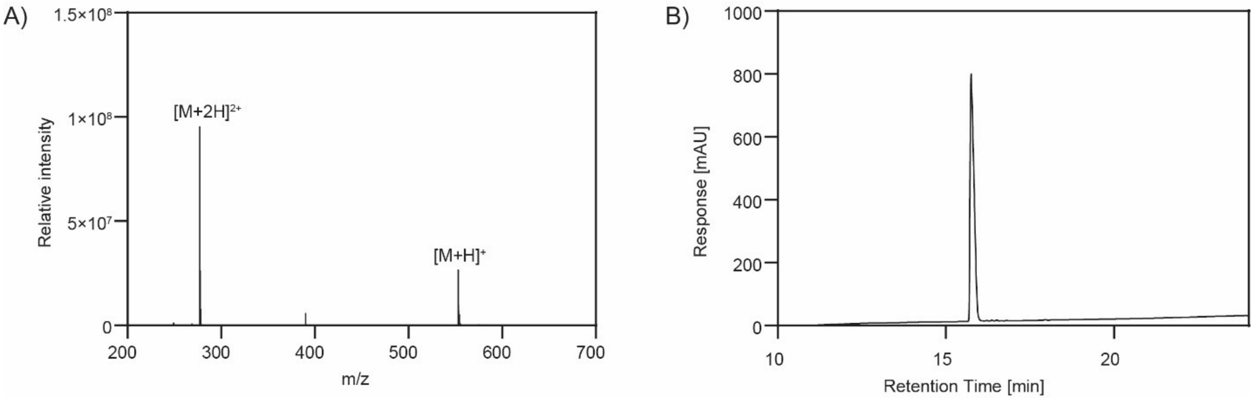
Supplementary Figure S12. NMR titration of ST6.



Supplementary Figure S13. Characterization of KMIS. Top) High resolution mass spectrum. [M+H] expected m/z: 477.2854, [M+H] measured m/z: 477.2899, Δppm: 9. Bottom) HPLC chromatogram of purified KMIS.



Supplementary Figure S14. Characterization of KMIY. Top) High resolution mass spectrum. [M+H] expected m/z: 553.3167, [M+H] measured m/z: 553.3190, Δppm: 4. Bottom) HPLC chromatogram of purified KMIS.



Supplementary Figure S15. Standard curves for metal salts at various maximum wavelengths. Errors bars, ± the standard deviation of three replicate measurements at each concentration, are not visible as they are smaller than the data points. A) NaI at 235 nm. B) $NaNO_2$ at 235 nm. C) $NaReO_4$ at 230 nm. D) Na_2CrO_4 at 372 nm. E) NH_4NO_3