Supplementary Information

Hydrogen bond-mediated recognition of the chemical warfare agent soman (GD)

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Experimental details

The chemical warfare agent (CWA) soman (GD) was obtained in-house at Dstl and confirmed as >99% using standard methods. Deuterated solvents were purchased from Goss Scientific (Cheshire, UK) and used as received. Receptors **1-4** were prepared and characterised as reported previously.¹ NMR spectra were obtained on a JEOL Eclipse+ 500 instrument (operating at 500 MHz for ¹H and 202 MHz ³¹P spectra) or a JEOL Eclipse+ 300 instrument (operating at 300 MHz for ¹H and 121.5 MHz for ³¹P). ³¹P spectra were referenced externally using (MeO₃)P (δ 141.3 ppm).

Assessment of binding interactions



Figure S1. ³¹P NMR spectrum of GD. Solvent: MeCN- d_3 98%/DMSO- d_6 2%. T = 293 K



Figure S2. ¹⁹F NMR spectrum of GD. Solvent: MeCN- d_3 98%/DMSO- d_6 2%. T = 293 K.

	Receptor ¹ H NMR perturbations (ppm)			GD ³¹ P NMR shift perturbations (ppm)			
	urea	indole	amide				
2	0.05	0.10	0.06	0.04	0.05	0.05	0.05
3	0.09	0.09	0.13	0.02	0.02	0.02	0.02

Table S1. Table of ¹H and ³¹P NMR chemical shift perturbations for receptors **2** and **3** in MeCN- d_3 98%/DMSO- d_6 2%. [receptor] = [**GD**] = 5.5 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S3. Job plots analysis of receptor **2** plus GD in MeCN- d_3 98%/DMSO- d_6 2%, where x = amide, Δ = urea. [**2**] + [GD] = 5.5 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S4. Job plot analysis of receptor **3** plus GD in MeCN d_3 98%/DMSO- d_6 2%, where x= amide, Δ = urea. [**3**] +[GD] = 5.5 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S5. ¹H NMR titration binding curves for (left) receptor **2** and (right) receptor **3**, where + = indole protons, x = amide protons and Δ = urea. Solvent MeCN-*d*₃ 98%/DMSO-*d*₆ 2%; [Receptor]_{initial} = 1.75 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S6. Job plot analysis of receptor **2** plus GD in MeCNd₃ 95%/DMSO-d₆ 5%, where x= amide, Δ = urea. [**3**] +[GD] = 5.5 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S7. ¹H NMR titration binding curve for receptor **2** plus GD in MeCN- d_3 95%/DMSO- d_6 5% where + = indole protons. [Receptor]_{initial} = 1.75 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S8. ¹H NMR titration binding curve for receptor **2** plus GD in MeCN- d_3 97%/DMSO- d_6 3% where + = indole protons. [Receptor]_{initial} = 1.75 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S9. Region of the ¹H NMR spectra of receptors (left) **1** and (right) **4** in the absence (top) and presence (bottom) of equimolar concentrations of GD revealing downfield perturbations in indole, urea, amide and pendant indole proton environments. [receptor] = [GD] = 5.5×10^{-3} mol dm⁻³. T = 293 K.



Figure S10. Job plot analyses of receptor **1** plus GD, where + = indole, Δ = (urea). Solvent = MeCN- d_3 95%/DMSO- d_6 5%. [**1**] + [GD] = 5.5 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S11: ¹H NMR titration binding curve for receptor **1** plus GD in MeCN- d_3 95%/DMSO- d_6 5% where + = indole protons. [Receptor]_{initial} = 1.75 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S12. Job plot analysis of receptor **4** with GD, where x = amide, + = indole, Δ = urea. [**4**] + [GD] = 5.5 × 10⁻³ mol dm⁻³. T = 293 K.



Figure S13. ¹H NMR binding curve for receptor **4** plus GD in MeCN- d_3 95%/DMSO- d_6 5% where x = amide protons. [Receptor]_{initial} = 1.75 × 10⁻³ mol dm⁻³. T = 293 K.

MacSPARTAN '10 Quantum Mechanics Program: (x86/Darwin) build 10.0.1v4 Job type: Geometry optimization. Method: RBJLYP Basis set: 6-31G(D) Number of shells: 193 Number of basis functions: 559 Multiplicity: 1 SCF model: A restricted hybrid HF-DFT SCF calculation will be performed using Pulay DIIS + Geometric Direct Minimization Optimization: Step Energy Max Grad. Max Dist. Optimization: Step Energy Max Grad. Max Dist. 1 -1818.588643 0.043127 0.089850 2 -1818.618090 0.023993 0.111295 3 -1818.629290 0.008849 0.156100 4 -1818.63271 0.004939 0.145954 5 -1818.633786 0.003754 0.136318 6 -1818.634791 0.003505 0.125929 7 -1818.63528 0.003896 0.107583 2 - 1919. 6418000 0.023993 0.111295 - 1918. 632290 0.008849 0.145954 5 - 1918. 633786 0.003754 0.136318 6 - 1918. 633786 0.003754 0.136318 6 - 1918. 635628 0.004853 0.107893 9 - 1918. 636223 0.005151 0.102039 10 - 1918. 63623 0.005151 0.102039 11 - 1918. 638278 0.00456 0.110683 11 - 1918. 638278 0.00456 0.110683 11 - 1918. 638278 0.00456 0.101683 11 - 1918. 638278 0.00456 0.051957 15 - 1918. 639078 0.002395 0.108247 16 - 1918. 639078 0.002395 0.108247 16 - 1918. 639079 0.002395 0.108247 16 - 1918. 639079 0.003398 0.04493 19 -1918. 639079 0.003398 0.044493 19 -1918. 639079 0.003398 0.044493 19 -1918. 639070 0.003396 0.044959 21 - 1918. 639070 0.003295 0.020556 21 - 1918. 639079 0.003251 0.023547 15 - 1918. 639079 0.003254 0.05655 21 - 1918. 639079 0.002254 0.037676 27 - 1918. 640027 0.00425 0.033421 26 - 1918. 640027 0.00252 0.033421 26 - 1918. 640027 0.00252 0.037676 27 - 1918. 640027 0.00252 0.033123 31 - 1918. 640245 0.002670 0.03285 30 - 1918. 640247 0.00252 0.050135 31 - 1918. 640247 0.00252 0.050135 31 - 1918. 640247 0.00252 0.050135 31 - 1918. 640247 0.00252 0.050135 31 - 1918. 640247 0.00252 0.050135 31 - 1918. 640245 0.002267 0.013123 31 - 1918. 640245 0.002267 0.013123 31 - 1918. 640251 0.00252 0.012017 41 - 1918. 640252 0.00212 0.012618 32 - 1918. 640464 0.00252 0.012017 41 - 1918. 64065 0.002122 0.012618 42 - 1918. 64065 0.002122 0.012618 43 - 1918. 64065 0.002122 0.012618 44 - 1918. 64065 0.002122 0.012618 45 - 1918. 64062 0.000164 0.022435 55 - 1918. 64062 0.000164 0.022435 51 - 1918. 64062 0.000164 0.022435 51 - 1918. 64062 0.000174 0.022436 51 - 1918. 64062 0.000174 0.022456 51 - 1918. 640029 0.000591 0.425245 51 - 1918. 640029 0.00064 0.022435 51 - 1918. 640029 0.00064 0.022435 51 - 1918. 640029 0.00074 0.022586 51 - 1918. 640029 0.000740 0.022586 51 - 1918. 640029 0.000740 0.022585 51 - 1918. 640029 0.000740 0.022585 51 - 1918. 640029 0.000740 0.022585 51 - 1918. 640029 0.000740 0.022585 51 - 1918. 640029 0.000740 0.022586 51 - 1918. 6400

Table S1 DFT calculation of the structure of the 1.GD complex

References

1. P. A. Gale, J. R. Hiscock, C. Z. Jie, M. B. Hursthouse and M. E. Light, *Chem. Sci.* 2010, **1**, 215-220.