

## Supporting Information

### **Aqueous two-phase system formed by polyethylene glycol methyl ether 550 and choline-based ionic liquids: from phase diagrams to application in the extraction of proteins**

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**Table S1.** Experimental binodal mass fraction data for the system composed of PEGME 550 ( $w_1$ ) + [Ch]Cl ( $w_2$ ) + water ( $w_3$ ) at 298 K and 0.1 MPa.<sup>a</sup>

<b>100 <math>w_1</math></b>	<b>100 <math>w_2</math></b>	<b>100 <math>w_3</math></b>
28.63	38.91	32.46
26.79	41.72	31.49
25.05	44.38	30.57
23.75	46.35	29.90
22.51	48.30	29.20
21.42	50.02	28.56
20.37	51.49	28.13
19.53	52.85	27.63
18.71	54.13	27.16
17.76	55.61	26.63
17.08	56.64	26.28
16.30	57.90	25.80
15.57	59.04	25.39
14.97	60.01	25.02
14.33	61.06	24.61
13.79	62.01	24.20
13.20	62.97	23.83
12.66	63.93	23.41
12.48	64.29	23.24
12.05	64.95	23.00
11.65	65.59	22.77
11.19	66.36	22.44
10.81	67.06	22.13
10.42	67.74	21.84
10.08	68.25	21.66
9.76	68.86	21.38
9.47	69.4	21.13
9.14	70.02	20.84

<sup>a</sup>Standard uncertainties  $u$  are  $u(w_1, w_2 \text{ or } w_3) = 0.01 \%$  (m/m), and expanded uncertainties for 0.98 % confidence are  $U(T) = 1 \text{ K}$  and  $U(p) = 10 \text{ kPa}$ .

**Table S2.** Experimental binodal mass fraction data for the system composed of PEGME 550 ( $w_1$ ) + [Ch][DHC] ( $w_2$ ) + water ( $w_3$ ) at 298 K and 0.1 MPa.<sup>a</sup>

<b>100 <math>w_1</math></b>	<b>100 <math>w_2</math></b>	<b>100 <math>w_3</math></b>
60.12	17.86	22.02
50.91	26.41	22.68
43.93	32.99	23.08
40.05	36.85	23.10
34.79	42.01	23.20
31.23	45.50	23.27
29.05	47.72	23.23
26.74	50.04	23.23
23.97	53.34	22.70
21.75	55.64	22.61
19.80	58.06	22.13
17.98	60.17	21.85
16.42	62.10	21.48

<sup>a</sup>Standard uncertainties  $u$  are  $u(w_1, w_2 \text{ or } w_3) = 0.01 \%$  (m/m), and expanded uncertainties for 0.98 % confidence are  $U(T) = 1 \text{ K}$  and  $U(p) = 10 \text{ kPa}$ .

**Table S3.** Experimental binodal mass fraction data for the system composed of PEGME 550 ( $w_1$ ) + [Ch][HEPES] ( $w_2$ ) + water ( $w_3$ ) at 298 K and 0.1 MPa.<sup>a</sup>

<b>100 <math>w_1</math></b>	<b>100 <math>w_2</math></b>	<b>100 <math>w_3</math></b>
46.05	32.89	21.06
35.97	43.65	20.38
29.05	51.20	19.75
23.18	58.57	18.25
20.28	61.22	18.50

<sup>a</sup>Standard uncertainties  $u$  are  $u(w_1, w_2 \text{ or } w_3) = 0.01 \%$  (m/m), and expanded uncertainties for 0.98 % confidence are  $U(T) = 1 \text{ K}$  and  $U(p) = 10 \text{ kPa}$ .

**Table S4.** Experimental binodal mass fraction data for the system composed of PEGME 550 ( $w_1$ ) + [Ch][BIT] ( $w_2$ ) + water ( $w_3$ ) at 298.15 K and 0.1 MPa.<sup>a</sup>

<b>100 <math>w_1</math></b>	<b>100 <math>w_2</math></b>	<b>100 <math>w_3</math></b>
63.49	5.98	30.53
58.49	8.27	33.24
54.55	11.54	33.91
50.34	14.55	35.11
45.23	18.91	35.86
42.61	22.19	35.20
39.25	25.02	35.73
35.41	30.33	34.26
34.07	31.73	34.20
32.35	33.84	33.81
29.81	37.60	32.590

<sup>a</sup>Standard uncertainties  $u$  are  $u(w_1, w_2 \text{ or } w_3) = 0.01 \%$  (m/m), and expanded uncertainties for 0.98 % confidence are  $U(T) = 1 \text{ K}$  and  $U(p) = 10 \text{ kPa}$ .

**Table S5.** Partition coefficient ( $K_{BSA}$ ) and extraction efficiency on bottom phase ( $EE\%_{BSA}$ ) for the overall systems of ATPSs composed of PEGME 550 (45 wt%) and cholinium-based ionic liquids (40 wt%) at 298 K and 0.1 MPa.

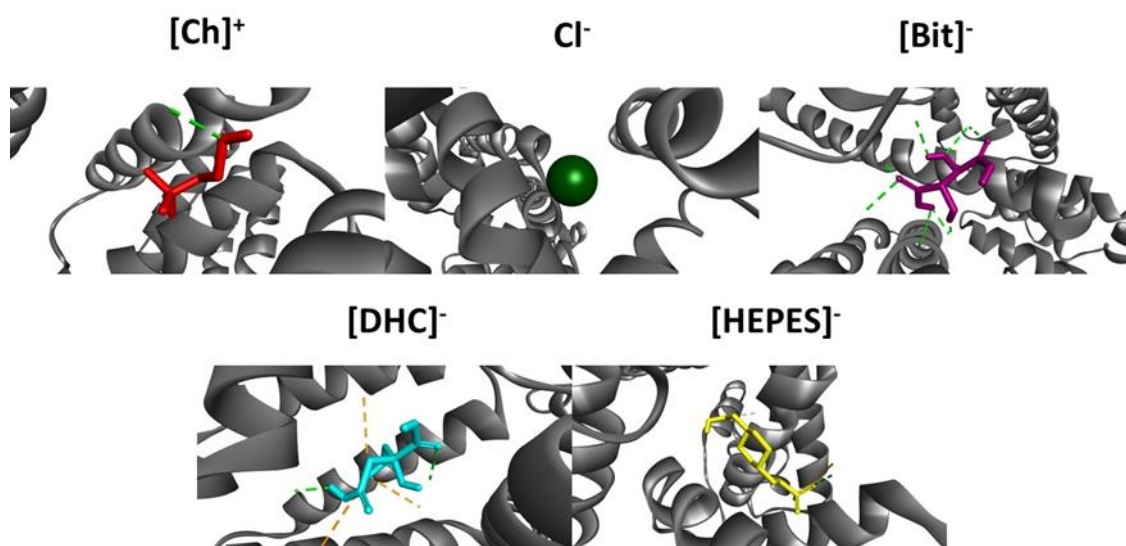
<b>Ionic Liquid</b>	<b><math>K_{BSA}</math></b>	<b><math>EE\%_{BSA}</math></b>
[Ch]Cl	$0.81 \pm 0.04$	$50.31 \pm 1.30$
[Ch][DHC]	$0.91 \pm 0.02$	$48.71 \pm 0.10$
[Ch][BIT]	$0.85 \pm 0.02$	$45.91 \pm 0.60$
[Ch][HEPES]	$0.950 \pm 0.004$	$42.21 \pm 0.51$

**Table S6.** Docking affinity and interacting atoms predicted by AutoDock Vina for BSA + ILs cation and anions

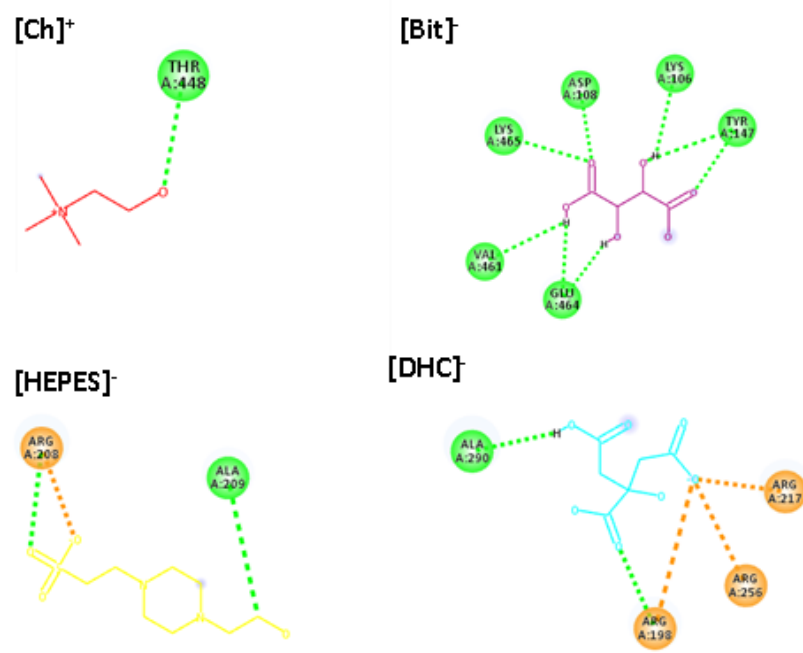
Compound	Affinity (kcal/mol)	Type of interaction	From	To	Distance (Å)
[Ch] <sup>+</sup>	-3.5	Hydrogen Bond	Threonine44	[Ch] <sup>+</sup>	2.50
Cl <sup>-</sup>	-1.3	-	-	-	-
[BIT] <sup>-</sup>	-4.8	Hydrogen Bond	AsparticAcid108	[BIT] <sup>-</sup>	2.02
			Tyrosine147		2.53
			Lysine465		2.73
			Lysine465		2.86
			Valine461		3.00
			[BIT] <sup>-</sup> GlutamicAcid 464		2.16
			[BIT] <sup>-</sup> 464		1.93
			Lysine106	2.48	
[DHC] <sup>-</sup>	-5.2	Electrostatic	Arginine198	[DHC] <sup>-</sup>	4.14
			Arginine217		5.13
			Arginine256		5.52
		Hydrogen Bond	Arginine198		2.49
		[DHCit] <sup>-</sup>	Alanine290		2.21
[HEPES] <sup>-</sup>	-4.9	Electrostatic	Arginine208	[HEPES] <sup>-</sup>	5.52
		Hydrogen Bond			2.83
		[HEPES] <sup>-</sup>	Alanine209	3.78	

**Table S7.** Docking affinity and interacting atoms predicted by AutoDock Vina for IgG + [Ch]Cl (cation and anion)

Compound	Affinity (kcal/mol)	Type of interaction	From	To	Distance (Å)
[Ch] <sup>+</sup>	-3.5	Electrostatic	[Ch] <sup>+</sup>	Aspartic Acid220	5.50
		Hydrogen Bond	Valine210	[Ch] <sup>+</sup>	2.66
Cl <sup>-</sup>	-1.1	-	-	-	-



**Figure S1.** Docking pose with the lowest absolute value of affinity (kcal mol<sup>-1</sup>) for BSA with: [Ch]<sup>+</sup> (■), Cl<sup>-</sup> (■), [BIT]<sup>-</sup> (■), [DHC]<sup>-</sup> (■), and [HEPES]<sup>-</sup> (■).



**Figure S2.** 3D molecular interaction diagrams of BSA with IL ions: ■ – hydrogen bond interactions; ■ – electrostatic interactions.