

**Supplementary Table 1**

Protein	Oligomerisation State	Max. Charge State	Spectral Resolution of Maximum Charge State (FWHM)	Theoretical Average Monomer Mass (Da)	Theoretical Average Complex Mass (Da)	Measured Average Mass (Da)	Standard Deviation ( $\pm$ Da)	<b>Error (Da)</b>	Previously Reported Measured Average Mass (Da)	Previously Reported Standard Deviation ( $\pm$ Da)	<b>Previously Reported Error (Da)</b>
chemokine receptor (CCR5)	Monomer	12	3008	43839.09	43839.09	43852.95	0.12	<b>13.86</b>	-	-	-
semiSWEET	Dimer	8	2503	13084.32	26168.64	26167.77	0.21	<b>-0.87</b>	-	-	-
OmpF	Trimer	23	3358	37084.10	111252.29	111252.27	3.30	<b>-0.02</b>	111294	30	<b>42<sup>21</sup></b>
AmtB	Trimer	17	2462	42263.38	126790.15	126788.12	0.12	<b>-2.03</b>	126696	25	<b>-94<sup>12</sup></b>
ELIC	Pentamer	30	1903	37133.20	185665.99	185679.90	2.14	<b>13.92</b>	185829	44	<b>163<sup>14</sup></b>

**Supplementary Table 2**

	Charge State 25+	1 Ligand Bound		2 Ligands Bound		
		CsA	CDL	2CsA	1CDL 1CsA	2CDL
P1	5672.81	<b>5720.91</b> (5720.30)	<b>5722.48</b> (5722.11)	<b>5769.02</b> ( <b>5768.54</b> )	<b>5770.58</b> ( <b>5770.30</b> )	5772.14
P2	5675.7	5723.80	5725.37	<b>5771.91</b> ( <b>5771.75</b> )	<b>5773.47</b> ( <b>5773.35</b> )	<b>5775.03</b> ( <b>5775.03</b> )
P3	5679.06	5727.16	5728.73	5775.27	5776.83	5778.39

## Supplementary Table Legends

Supplementary Table 1 – Measured masses for membrane proteins in Figure 1a complete with experimental resolution of peak corresponding to the maximum charge state, mass error and comparison with previously published data.

Supplementary Table 2 - Assignment of species in Figure 1c and Supplementary Figure 6. Measured  $m/z$  of 25+ Pg-p P1-3 and expected  $m/z$  for addition of all combinations of ligands. Experimental  $m/z$  of assigned peaks are given in parentheses highlighted in bold.