OMP	No. of β-strands	Molecular weight* (kDa)	Function
tOmpA	8	18.875	Adhesin/invasin/evasin
PagP	8	19.110	Acyl transferase
OmpT	10	35.284‡	Protease
OmpF	16	37.216	Porin
tBamA	16	43.240	Insertase/secretase

Supplementary Table 1: Model OMPs investigated have a range of functions, sizes and number of β-strands. *Molecular weight of the mature OMP sequences, lacking their cleavable N-terminal signal sequences. ‡ Molecular weight for the OmpT construct used here including an N-terminal hexahistidine tag and a TEV protease cleavage site.

OMP	OMP:Skp ratio	k_1 ($x10^{-3}$ s^{-1})	k_2 ($x10^{-3}$ s^{-1})
tOmpA	OMP alone	15.7 ± 0.6	N/A
	1:1	11.1 ± 1.4	1.3 ± 0.1
	1:2	No folding	No folding
PagP	OMP alone	3.8 ± 0.8	0.8 ± 0.1
	1:1	1.2 ± 0.3	0.1 ± 0.02
	1:2	No folding	No folding
OmpF	OMP alone	10.5 ± 0.6	0.5 ± 0.2
	1:2	1.8 ± 0.2	N/A
	1:4	No folding	No folding
tBamA	OMP alone	12.8 ± 2.4	1.6 ± 0.3
	1:2	7.6 ± 0.6	1.4 ± 0.4
	1:4	No folding	No folding

Supplementary Table 2: Measured rate constants for OMP folding into liposomes after pre-incubation with varying molar ratios of Skp. Data are shown as the mean ± the standard deviation of the rate constants obtained from three separate folding experiments, each using independently prepared batches of liposomes. For each batch of liposomes at least three folding transients were fitted globally to obtain the rate constants shown. N/A: The kinetic traces for the condition were adequately described by a single exponential.

Complex	Expected Mass (Da)	Observed Mass (Da)
Skp	47,075	47,125 ± 10
1:1 Skp:tOmpA	65,818	65,898 ± 12
1:1 Skp:PagP	66,185	66,208 ± 15
1:1 Skp:OmpT	82,355	83,304 ± 20
2:1 Skp:OmpT	129,430	130,542 ± 14
1:1 Skp:OmpF	84,220	84,210 ± 18
2:1 Skp:OmpF	131,295	131,337 ± 11
1:1 Skp:tBamA	90,315	90,183 ± 5
2:1 Skp:tBamA	137,390	137,303 ± 8

Supplementary Table 3: Observed and expected masses for the complexes studied. For mass measurements, mass spectrometry conditions were optimised empirically for each sample to decrease peak widths, by increasing the cone voltage and trap collision energy, (typically 100 V and 40 V, respectively), relative to the gentler conditions used to acquire IMS data.

Skp		1:1 Skp:tOmpA		1:1 Skp: PagP		1:1 Skp:OmpT		1:1 Skp:OmpF	
z	**CCS**	***z***	**CCS**	***z***	**CCS**	***z***	**CCS**	***z***	**CCS**
13	36.4 ± 0.2	15	45.6 ± 0.1	15	45.8 ± 0.3	17	51.4 ± 0.8	17	51.8 ± 0.3
13	37.9 ± 0.6	16	46.1 ± 0.3	16	45.8 ± 0.1	18	53.0 ± 0.4	18	52.8 ± 0.6
14	37.1 ± 0.2	17	46.5 ± 0.6	17	45.8 ± 0.2	19	53.9 ± 0.7	19	54.2 ± 0.2
14	38.8 ± 0.3	18	47.3 ±0.2			20	57.1 ± 0.2	20	55.1 ± 0.2
15	39.3 ± 0.6								
16	40.8 ± 0.6								

1:1 Skp:tBamA		2:1 Skp:OmpT		2:1 Skp:OmpF		2:1 Skp:tBamA	
z	**CCS**	***z***	**CCS**	***z***	**CCS**	***z***	**CCS**
18	54.2 ± 0.3	22	71.7 ± 0.04	22	71.2 ± 0.5	22	72.8 ± 0.2
19	55.6 ± 0.8	23	72.7 ± 0.03	23	72.1 ± 0.9	23	74.1 ± 0.1
20	57.4 ± 0.6	24	74.4 ± 0.02	24	73.4 ± 0.4	24	75.5 ± 0.5
		25	76.2 ± 0.4	25	75.1 ± 0.1	25	75.7 ± 0.3
				26	76.9 ± 0.6	26	78.20 ± 0.1

Supplementary Table 4: Experimentally determined modal collision cross-sections (CCSs) (nm^2) for the observed charge states (*z*) of Skp and the Skp assemblies. CCS values are shown as mean ± standard deviation of three independent measurements.

Protein(s)	Calculated CCS from simulation (nm^2)	CCS measured by IMS-MS (nm^2)
tOmpA alone	19.0 ± 0.06	-
tBamA alone	37.9 ± 0.9	-
1:1 Skp-tOmpA (*in vacuo*)	43.7 ± 1.2	45.6 ± 0.1
2:1 Skp:tBamA (*in vacuo*)	74.4 ± 1.4	72.8 ± 0.2
Skp (*in vacuo*)	37.3 ± 1.9	37.9 ± 0.6
1:1 Skp-tOmpA (H_2O)	56.5 ± 0.3	-
2:1 Skp:tBamA (H_2O)	101.2 ± 6.0	-

Supplementary Table 5: Comparison of CCS values from MD simulations and IMS-MS measurements. CCS values from IMS-MS are shown as the mean ± standard deviation of the modal value of the lowest charge state ion from three independent measurements. CCS values from the simulations are the mean ± standard deviation for the endpoint structures at 100 ns from three independent simulations. For globular assemblies, the error between measured CCS values and those computed from atomic coordinates is below 3% (Benesch, J.L. & Ruotolo, B.T. *Curr Opin Struct Biol* **21** 641-9, 2011).