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Table S1: TALOS+ prediction of gp36 CHR-MPER backbone dihedral angles (PHI, PSI), estimated standard deviations of the prediction errors in PHI and PSI (DPHI, DPSI), TALOS+ database matching score (DIST), Wishart RCI chemical shift order parameter (S2), number of database triplets used to form the torsion angle predictions (COUNT, CS COUNT), classification of the prediction result (CLASS; **None** if no torsion prediction was made, **Good** if majority consensus in database matches, **Warn** if no consensus in database matches, **Dyn** if RCI S2 value indicates dynamic conformation).

Table S2: ^1H , ^{15}N and ^{13}C chemical shift of (^{15}N - ^{13}C)-labeled gp36-MPER in DPC/SDS 90:10 M/M mixed micelles.

Fig. S2: A) FPLC chromatogram ; B) HPLC chromatogram, obtained using gradient: 10-40 B in 20 min poi 40-70 B in 30 min, Buffer A: water + TFA 0.1%, Buffer B: Acetonitril + TFA 0.1%; C) SDS-PAGE of FPLC fractions (4-5), after cleavage (6) and HPLC fractions (7 KSI - 8 isotope labeled gp36-MPER).

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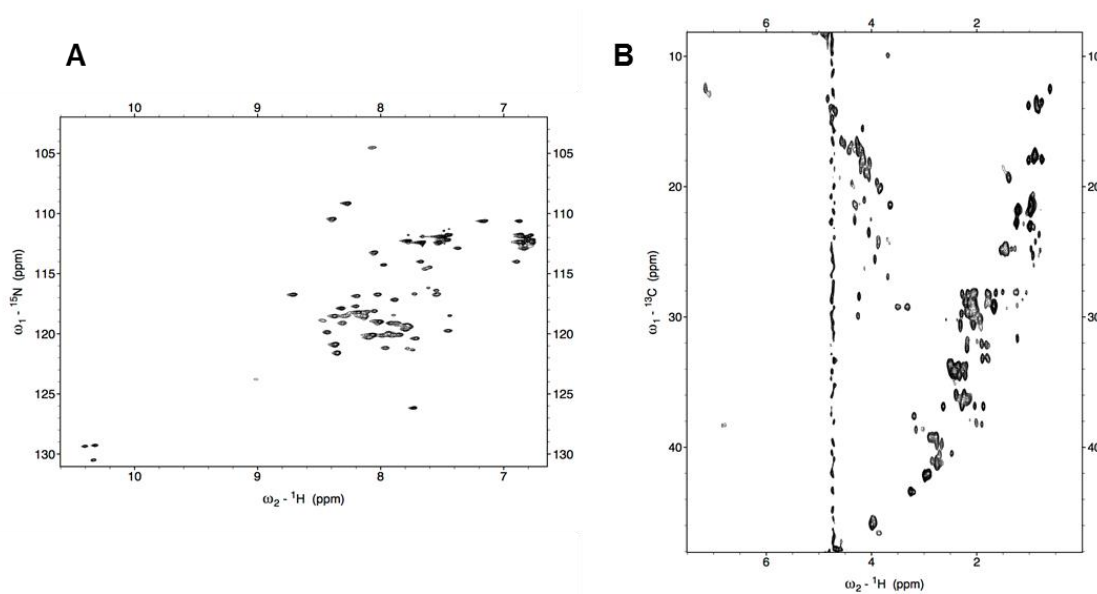


Table S1: TALOS+ prediction backbone dihedral angles of 0.5 mg (¹⁵N-¹³C)-labeled gp36 CHR-MPER acquired on Bruker 900 MHz in DPC/SDS 90:10 M/M mixed micelles, at pH 7.4 and at 300 K. Gp36 CHR-MPER backbone dihedral angles (PHI, PSI), estimated standard deviations of the prediction errors in PHI and PSI (DPHI, DPSI), TALOS+ database matching score (DIST), Wishart RCI chemical shift order parameter (S²), number of database triplets used to form the torsion angle predictions (COUNT, CS COUNT), classification of the prediction result (CLASS; **None** if no torsion prediction was made, **Good** if majority consensus in database matches, **Warn** if no consensus in database matches, **Dyn** if RCI S² value indicates dynamic conformation).

RESID	RESNAME	PHI (°)	PSI (°)	DPHI (°)	DPSI (°)	DIST	S ²	COUNT	CS_COUNT	CLASS
740	T	-59.27	-32.743	6.798	6.694	0.295	0.82	25	13	Strong
741	K	-64.099	-36.692	3.451	5.224	0.198	0.838	25	15	Strong
742	D	-69.767	-38.96	3.261	4.211	0.139	0.864	25	14	Strong
743	L	-64.344	-42.725	3.785	3.874	0.119	0.872	25	14	Strong
744	Q	-61.889	-42.434	2.942	3.434	0.118	0.88	25	14	Strong
745	Q	-64.923	-41.272	1.866	2.816	0.123	0.875	25	14	Strong
746	K	-65.752	-40.177	3.738	4.614	0.136	0.875	25	14	Strong
747	F	-67.009	-36.821	4.576	5.526	0.181	0.88	25	14	Strong
748	Y	-64.819	-33.798	3.675	6.293	0.265	0.865	25	14	Strong
749	E	-66.576	-34.207	6.072	6.355	0.479	0.837	25	13	Strong
750	I	-71.134	-33.281	8.714	9.908	0.685	0.823	10	12	Generous
751	I	-70.167	-33.55	12.121	10.156	0.628	0.839	25	12	Strong
752	L	-64.437	-41.439	3.934	4.164	0.499	0.867	25	13	Strong
753	D	-66.624	-39.424	4.273	3.586	0.333	0.88	25	13	Strong
754	I	-64.585	-41.763	3.305	3.019	0.218	0.87	25	14	Strong
755	E	-64.433	-37.712	3.857	7.155	0.188	0.85	25	14	Strong
756	Q	-66.81	-29.89	4.93	7.798	0.195	0.79	25	15	Strong
757	N	-72.646	-23.666	8.89	9.49	0.249	0.675	25	15	Strong
758	N	-83.381	-9.776	13.122	14.316	0.301	0.578	10	15	Dyn
759	V	-85.832	-17.811	11.078	12.641	0.347	0.549	7	15	Dyn
760	Q	-59.901	127.866	5.762	5.666	0.377	0.574	25	13	Dyn
761	G	80.971	4.017	10.068	14.434	0.67	0.596	25	13	Dyn
762	K	-119.08	32.449	13.865	27.416	1.519	0.584	5	13	Dyn
763	T	-81.612	138.095	27.123	13.574	-1.319	0.59	25	13	Dyn
764	G	87.54	4.72	9.69	15.78	1.065	0.652	25	12	Strong
765	I	-83.032	-23.771	21.661	19.913	0.665	0.732	6	12	Warn
766	Q	-64.897	-37.011	6.741	7.086	0.508	0.797	25	14	Strong
767	Q	-65.743	-40.861	4.731	5.737	0.497	0.798	25	14	Strong
768	L	-64.078	-40.361	4.498	4.57	0.558	0.792	25	13	Strong
769	Q	-67.642	-35.127	4.154	4.969	0.479	0.761	25	13	Strong

770	K	-67.202	-36.082	5.542	5.681	0.429	0.777	25	13	Strong
771	W	-70.467	-33.251	11.365	13.761	0.383	0.809	25	14	Strong
772	E	-63.52	-41.008	5.068	6.5	0.318	0.869	25	14	Strong
773	D	-67.762	-37.224	4.255	5.09	0.298	0.884	25	15	Strong
774	W	-64.26	-43.256	3.666	6.78	0.43	0.868	25	14	Strong
775	V	-65.844	-35.363	7.173	7.915	0.559	0.853	25	11	Strong
776	G	-65.321	-35.277	4.082	7.93	0.755	0.826	8	10	Warn
777	W	-65.683	-36.749	5.126	8.095	0.782	0.808	25	10	Strong
778	I	-79.538	-15.175	13.499	16.625	0.862	0.756	25	11	Strong
779	G	-72.287	-19.263	11.195	6.852	0.938	0.708	4	12	Warn
780	N	-95.479	-8.29	13.461	12.633	0.686	0.64	10	12	Generous
781	I	-70.999	136.664	6.686	11.093	0.799	0.627	25	9	Strong
782	P	-58.878	143.966	6.645	8.142	0.811	0.662	25	8	Strong
783	Q	-59.959	-34.931	3.728	5.313	0.996	0.72	25	8	Strong
784	Y	-74.76	-18.594	15.94	20.997	0.948	0.727	25	12	Strong
785	L	-65.858	-30.25	8.291	7.025	0.817	0.715	25	8	Strong

Table S2: ^1H , ^{15}N and ^{13}C chemical shift of 0.5 mg (^{15}N - ^{13}C)-labeled gp36-MPER acquired on Bruker 900 MHz in DPC/SDS 90:10 M/M mixed micelles. The final pH was 7.4. NMR experiments were recorded at 300 K.

Number Residue	Residue	HN	^{15}N	$^{13}\text{C}\alpha$	H α	$^{13}\text{C}\beta$	H β	H γ	Others
738	Q			54.736	4.752	30.450	2.615/2.311		
739	T	8.752	117.073	65.468	4.290	68.366	4.155		
740	K	8.387	120.983	58.262	4.217	32.055	1.851		
741	D	7.796	119.367	56.514	4.610	40.956	2.821		
742	L	7.741	120.066	58.351	4.020		1.677		QQ δ 0.924
743	Q	8.337	117.844	60.124	3.833	28.693	2.258		
744	Q	7.932	117.201	58.798	4.134	28.051	2.249		
745	K	7.929	118.588	58.332	4.177		1.983	1.559	Q δ 1.804
746	F	8.368	111.615	61.053	4.203	38.576	3.135		Q δ 7.111
747	Y	8.128	117.472	61.007	4.122	37.938	3.189		Q ϵ 7.115 C ϵ 1 92.892
748	E	8.088	117.921	58.059	4.010		2.081	2.337	
749	I	7.918	119.996	59.189	4.063		1.896	1.524	Q δ 1 0.793
750	I	7.831	118.343	60.388	3.825		1.919	1.266/1.011	Q δ 1 0.830
751	L	7.938	120.068	62.522	3.999		1.701		QQ δ 0.807
752	D	7.733	119.459	56.789	4.514	41.197	2.711		
753	I	8.003	120.007	64.227	3.876		1.906	1.080/0.894	
754	E	8.389	121.040	58.836	4.068	29.435	2.124		
755	Q	8.221	117.395	57.850	4.133	28.789	2.152		
756	N	8.127	116.880	54.230	4.663	39.125	2.807		
757	N	8.238	118.284	53.950	4.748	39.115	2.897/2.730		
758	V	8.047	119.072	63.518	4.042	32.100	2.195	0.955	
759	Q	8.405	121.028	56.755	4.255	28.856	2.104/2.017		
760	G	8.247	108.979	45.809	4.121				
761	K	8.136	120.069	57.020	4.188	33.020	1.830	1.335	
762	T	8.101	113.101	61.134	4.338	69.847	4.650		
763	G	8.437	110.298	45.914	3.963				
764	I	8.165	120.090	59.331	4.026		1.909	1.420/0.894	
765	Q	8.420	121.495	58.691	4.098	28.690	2.350/2.062		
766	Q	8.154	118.402	57.098	4.239	28.641	2.058		
767	L	7.877	119.893	62.603	4.322		1.738		QQ δ 0.807
768	Q	7.802	119.419	55.532	4.437		1.918/1.813	2.191	
769	K	7.619	116.117	57.040	4.182	33.064	1.841		
770	W	8.023	114.881	57.216	4.607		3.411		H ϵ 1 10.512 N ϵ 1 123.999
771	E	8.408	119.529	59.912	3.865	29.285	2.080		
772	D	8.148	118.450	56.963	4.354	40.357	2.677/2.293		
773	W	7.932	120.979	61.338	4.352	29.151	3.537/3.300		H δ 1 7.263 H ϵ 1 10.424 N ϵ 1 123.126
774	V	8.282	118.522	61.411	3.626		2.131	1.052/0.938	
775	R	8.097	119.012		4.231				
776	W	7.865	120.025	61.455	4.288		3.389		H ϵ 1 10.511
777	I	8.493	118.531	61.471	3.648		2.050	1.484/0.988	
778	G	8.073	104.570	46.587	3.853				

779	N	7.412	116.699	53.260	4.826	39.672	2.756/2.678	
780	I	7.800	121.083	60.065	3.783		2.101	1.663 Qδ1 0.904
781	P							2.042 Qδ 3.854
782	Q	7.946	119.632	65.547	3.985		2.021	
783	Y	7.939	119.882	57.352	4.260		3.154	Qε 7.149 Cε1 92.486
784	L	7.738	116.447	57.971	4.134		1.862	QQδ 0.872
785	K							
786	M							

Figure S2: A) FPLC chromatogram obtained using: binding buffer (10 mM Guanidine, 0,5 M NaCl, 20 mM Tris-HCl and 15mM Imidazole) and elution buffer (10 mM Guanidine, 0,5 M NaCl, 20 mM Tris-HCl and 50 mM Imidazole). The protein was purified using His-Trap™ HP column at 1 mL/min and AKTA purifier system. **B)** HPLC chromatogram, obtained using gradient: 10-40 B in 20 min then 40-70 B in 30 min, Buffer A: water + TFA 0.1%, Buffer B: Acetonitril + TFA 0.1%; the protein was purified using C18 Phenomenex™ column at 2 mL/min. **C)** SDS-PAGE of FPLC fractions (4-5), after cleavage (6) and HPLC fractions (7 KSI - 8 isotope labeled gp36 CHR-MPER).

