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Supplemental Information

Assembly Mechanism of Mucin and von Willebrand Factor Polymers

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	MUC2 D1D2D3CysD1 (EMDB-10517) (PDB 6TM2)
Data collection and processing	
Magnification	105,000x
Voltage (kV)	300
Electron exposure (e–/Å^2)	40.6
Defocus range (μm)	-1 to -2
Pixel size (Å)	0.85
Symmetry imposed	C2
Initial particle images (no.)	1,430,962
Final particle images (no.)	178,136
Map resolution (Å)	2.95
FSC threshold	0.143
Map resolution range (Å)	2.2 to 7.2
Refinement	
Initial model used (PDB code)	*Ab initio*, PDB IDs 6RBF and 6TM6
Model resolution (Å)	2.7 (6RBF) and 1.6 (6TM6)
Map sharpening *B* factor (Å^2)	Auto-estimated in Phenix
Model composition	
Non-hydrogen atoms	18,530
Protein residues	2,41
Waters	40
Ligands	30
B factors (Å^2)	
Protein	40.0
Waters	18.9
Ligands	75.4
R.m.s. deviations	
Bond lengths (Å)	0.009
Bond angles (°)	1.38
Validation	
MolProbity score	1.71
Clashscore	3.27
Poor rotamers (%)	0
Ramachandran plot	
Favored (%)	88.4
Allowed (%)	11.2
Disallowed (%)	0.4

Table S1. Cryo-EM data collection, refinement and validation statistics, related to Figure 3

Muc2 Cys 1	Muc2 Cys 2	VWF Cys 1	VWF Cys 2
37	169	35	162
59	206	57	200
67	166	65	159
218	255	210	255
225	250	225	250
237	275	237	275
257	263	257	263
265	291	265	291
295	329	295	329
308	321	308	321
312	351	312	348
331	345	331	342
353	375	350	372
370	387	367	384
373	382	370	379
391	528	388	524
413	563	410	559
435	443	432	440
574	619	570	613
588	614	584	608
601	639	595	633
621	627	615	621
629	654	623	648
661	698	652	687
674	688	665	679
678	718	669	707
700	712	689	701
720	742	709	731
740	749	729	738
759	800	767	808
768	796	776	804
784	820	792	827
802	814	810	821
822	844	829	851
839	856	846	863
842	851	849	858
860	992	867	996
882	1027	889	1031
891	989	898	993
909	916	914	921

Muc2 Cys 1	Muc2 Cys 2	VWF Cys 1	VWF Cys 2	
1037	1080	1046	1089	
1052	1075	1060	1084	
1062	1102	1071	1111	
1082	1090	1091	1099	
1092	1117	1101	1126	
1108	**1137**		**1149**	**1169**
1121	1163	1130	1173	
1145	1187	1157	1196	
1167	1181	1177	1190	
extra VWF disulfides:		304	325	
		418	521	
		661	683	
		788	799	

Table S2. Disulfide bonds in MUC2 and VWF, related to Figure 3 and Figure 5
Numbers are according to the precursor sequences in UniProt (MUC2: Q02817; VWF: P04275). Each row shows disulfides that are homologous between MUC2 and VWF. In bold is a pair of disulfides that share one conserved cysteine but a second divergent cysteine. Additional disulfides predicted in VWF due to close apposition of the corresponding residues in the homology model are listed as "extra VWF disulfides." The VWF disulfide assignment is consistent with previous reports of Cys767-Cys808, Cys776-Cys804, and Cys810-Cys821 (Marti et al., 1987) and the TIL´/E´ disulfides (Shiltagh et al., 2014).

	CysD1 (PDB 6TM6)
Data collection	
Space group	$P2_12_12$
Cell dimensions	
a, *b*, *c* (Å)	54.88, 57.86, 27.47
α, β, γ (°)	90, 90, 90
Resolution (Å)	15.23 - 1.63 (1.689 - 1.63)*
R_{sym} or R_{merge}	0.0753 (0.344)
I / σI	37.8 (3.6)
Completeness (%)	94.9 (65.6)
Redundancy	22.9 (7.5)
Refinement	
Resolution (Å)	1.63
No. reflections	10,882 (737)
R_{work} / R_{free}	0.174 / 0.211
No. atoms	860
Protein	747
Ligand/ion	2
Water	111
B-factors	25.7
Protein	24.6
Ligand/ion	21.4
Water	33.0
R.m.s deviations	
Bond lengths (Å)	0.006
Bond angles (°)	0.97

Table S3. Crystallographic data collection, phasing and refinement statistics, related to Figure 6

Asterisk indicates the highest-resolution shell, and data in parentheses correspond to this shell.