SUPPORTING INFORMATION

EVALUATION AND OPTIMIZATION OF A FORCE FIELD FOR CRYSTALLINE FORMS OF MANNITOL AND SORBITOL

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Table S1.
Evaluation and sensitivity analysis of the non-bonded *homo*-parameters of the GROMOS53A5/53A6 force field. The table shows the % deviation in the cell lengths of the simulated crystal structure from the experimental values for the original force field and when each of the individual force field parameters (A & B) are incremented by 5%. The cell angle deviations in all cases were less than 0.5%.

		α-mannitol			β-mannitol			δ-mannitol		
Interaction	Parameter	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		4.27	3.07	-2.34	-0.72	6.02	-0.32	1.21	0.10	4.12
CH1	A	4.61	3.34	-2.31	-0.67	6.29	-0.13	1.37	0.06	4.32
	B	4.12	2.92	-2.37	-0.76	5.84	-0.46	1.15	0.12	3.92
CH2	A	4.30	3.17	-1.99	-0.64	6.16	-0.10	1.20	0.28	4.16
	B	4.19	2.96	-2.51	-0.77	5.88	-0.45	1.21	0.02	4.05
HO	A	9.11	8.62	-3.28	5.88	11.27	-0.63	4.18	-5.33	29.64
	B	3.15	1.18	-2.11	-2.02	4.50	-0.05	-0.14	-0.39	1.57
OH	A	4.50	3.49	-2.26	-0.44	6.37	-0.27	1.48	0.17	4.79
	B	4.05	2.81	-2.45	-0.85	5.77	-0.47	1.11	0.06	3.84

		A-sorbitol			E-sorbitol			Γ-sorbitol		
Interaction	Parameter	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		-0.58	2.68	0.33	4.59	1.59	-1.11	3.11	1.65	0.65
CH1	A	-0.40	2.74	0.47	4.84	1.71	-1.05	3.25	2.14	0.78
	B	-0.66	2.68	0.24	4.32	1.52	-1.00	3.00	1.53	0.59
CH2	A	-0.43	2.73	0.39	4.81	1.66	-1.16	3.27	1.66	0.70
	B	-0.57	2.66	0.26	4.39	1.55	-1.09	3.03	1.58	0.63
HO	A	1.55	8.52	5.95	9.33	7.62	-0.58	5.94	2.11	7.99
	B	-1.52	1.75	-0.90	3.93	0.34	-1.29	2.21	0.32	-0.69
OH	A	-0.33	2.91	0.60	4.83	1.84	-1.08	3.28	2.37	0.79
	B	-0.81	2.57	0.19	4.29	1.42	-1.10	2.95	1.36	0.52

Table S2.
Evaluation and sensitivity analysis of the non-bonded *hetero*-parameters of the GROMOS53A5/53A6 force field. The table shows the % deviation in the cell lengths of the simulated crystal structure from the experimental values for the original force field and when each of the individual force field parameters (A & B) are incremented by 5%. The cell angle deviations in all cases were less than 0.5%.

		α-mannitol			β-mannitol			δ-mannitol		
Interaction	Parameter	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		4.27	3.07	-2.34	-0.72	6.02	-0.32	1.21	0.10	4.12
OH – OH	A	4.43	3.28	-2.54	-0.47	6.23	-0.39	1.46	0.15	4.57
	B	4.16	2.93	-2.38	-0.86	5.86	-0.30	1.13	0.07	3.95
OH – CH1	A	4.53	3.30	-2.40	-0.67	6.26	-0.22	1.30	0.08	4.51
	B	4.09	2.92	-2.35	-0.77	5.86	-0.42	1.15	0.13	3.89
OH – CH2	A	4.30	3.17	-2.16	-0.68	6.18	-0.14	1.20	0.12	4.22
	B	4.19	2.94	-2.52	-0.76	5.86	-0.48	1.21	0.06	4.01
OH – HO	A	7.96	8.18	-2.90	6.04	10.52	-2.32	3.41	-4.80	28.30
	B	3.63	1.50	-2.03	-2.02	4.81	0.41	-0.04	-0.48	1.97
CH1 – CH1	A	4.40	3.18	-2.26	-0.65	6.14	-0.30	1.32	0.05	4.18
	B	4.20	2.98	-2.44	-0.77	5.94	-0.31	1.18	0.12	4.07
CH1 – CH2	A	4.27	3.18	-2.24	-0.66	6.16	-0.13	1.22	0.17	4.12
	B	4.25	2.93	-2.51	-0.77	5.90	-0.35	1.21	0.07	4.10
CH1 – HO	A	6.39	3.67	-3.58	-0.96	6.24	0.52	1.76	-0.51	5.69
	B	3.78	2.93	-1.94	-0.71	5.85	-0.52	1.11	0.19	3.76
CH2 – CH2	A	4.27	3.03	-2.20	-0.73	6.01	-0.26	1.20	0.23	4.13
	B	4.24	3.04	-2.44	-0.73	6.00	-0.35	1.21	0.06	4.11
CH2 – HO	A	4.04	2.95	-1.69	-0.64	6.36	0.19	1.35	0.13	4.42
	B	4.23	2.96	-2.57	-0.77	5.84	-0.51	1.18	0.07	4.07
HO – HO	A	4.30	3.12	-2.36	-0.70	6.14	-0.27	1.21	0.11	4.14
	B	4.26	3.05	-2.35	-0.73	6.00	-0.32	1.21	0.10	4.11

		A-sorbitol			E-sorbitol			Γ-sorbitol		
Interaction	Parameter	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		-0.58	2.68	0.33	4.59	1.59	-1.11	3.11	1.65	0.65
OH – OH	A	-0.46	2.83	0.55	4.73	1.70	-1.15	3.24	1.89	0.84
	B	-0.58	2.65	0.20	4.48	1.49	-1.08	3.00	1.50	0.60
OH – CH1	A	-0.41	2.77	0.41	4.65	1.76	-1.09	3.27	2.27	0.67
	B	-0.67	2.66	0.26	4.38	1.51	-1.02	3.00	1.46	0.58
OH – CH2	A	-0.44	2.79	0.37	4.74	1.60	-1.13	3.21	1.54	0.72
	B	-0.61	2.65	0.25	4.39	1.57	-1.08	3.04	1.63	0.60
OH – HO	A	2.32	8.91	3.63	9.28	7.02	-0.80	4.72	6.03	5.79
	B	-1.43	1.82	-0.64	4.05	0.57	-1.13	2.36	0.39	-0.55
CH1 – CH1	A	-0.52	2.68	0.40	4.79	1.59	-1.14	3.18	1.64	0.83

	B	-0.56	2.70	0.28	4.47	1.59	-1.06	3.10	1.68	0.61
CH1 – CH2	A	-0.50	2.71	0.38	4.71	1.60	-1.11	3.25	1.55	0.71
	B	-0.61	2.69	0.29	4.47	1.58	-1.06	3.03	1.67	0.65
CH1 – HO	A	-0.70	2.49	1.76	3.81	2.29	-0.93	3.18	1.96	1.12
	B	-0.69	2.68	0.14	4.47	1.44	-1.09	2.72	2.19	0.90
CH2 – CH2	A	-0.53	2.66	0.34	4.72	1.60	-1.21	3.20	1.78	0.60
	B	-0.58	2.70	0.31	4.49	1.59	-1.06	3.08	1.65	0.64
CH2 – HO	A	-0.34	2.73	0.53	5.19	1.66	-1.12	3.30	1.38	0.92
	B	-0.60	2.61	0.23	4.34	1.55	-1.07	2.99	1.30	0.63
HO – HO	A	-0.55	2.67	0.34	4.59	1.60	-1.07	3.19	2.51	0.56
	B	-0.59	2.68	0.32	4.58	1.58	-1.12	3.13	1.53	0.67

Table S3.
Evaluation and sensitivity analysis of the non-bonded *homo*-parameters of the AMBER95 force field. The table shows the % deviation in the cell lengths (a, b, and c) and cell angles (α, β, and γ) of the simulated crystal structure from the experimental values for the original force field and when each of the individual force field parameters (ε & σ) are incremented by 5%.

		α-mannitol			β-mannitol			δ-mannitol		
Interaction	Parameter	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81
CT	ε	-0.79	-1.88	-0.98	0.22	-0.14	-2.51	-8.40	2.07	-4.80
	σ	-0.90	-1.30	-0.35	0.11	0.45	-1.77	-8.19	2.51	-6.93
H1	ε	-0.79	-1.75	-0.86	0.22	-0.10	-2.42	-8.34	2.08	-4.78
	σ	-0.63	-1.13	-0.11	0.14	0.52	-1.30	-7.84	2.44	-4.32
HO	ε	-0.78	-1.80	-0.92	0.22	-0.15	-2.43	-8.41	2.12	-4.80
	σ	-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81
OH	ε	-0.58	-1.74	-0.88	0.50	-0.08	-2.56	-8.12	2.17	-0.75
	σ	3.05	0.35	0.27	4.46	1.89	-1.95	-4.00	-1.27	1.43

Interaction	Parameter	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)
Unoptimized		-0.02	0.00	0.02	0.04	4.86	-0.30	0.00	-11.62	-0.06
CT	ε	0.01	0.00	0.04	0.00	-0.02	0.00	0.04	-11.60	-0.12
	σ	0.00	0.00	-0.02	-0.01	4.59	0.17	-0.19	-17.91	0.44
H1	ε	0.00	0.00	-0.01	0.01	-0.01	0.00	-0.02	-11.59	0.15
	σ	-0.01	0.00	-0.04	-0.04	0.05	0.03	0.03	-11.71	0.00
HO	ε	-0.01	0.00	0.00	0.02	0.02	-0.01	-0.09	-11.61	-0.04
	σ	-0.02	0.00	0.02	0.04	4.86	-0.30	0.00	-11.62	-0.06
OH	ε	0.03	0.00	0.04	0.00	-0.03	0.03	-0.06	-5.56	-0.01
	σ	0.01	0.01	-0.04	-0.01	0.00	-1.67	0.01	-5.82	-0.01

		A-sorbitol			E-sorbitol			Γ-sorbitol		
Interaction	Parameter	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)
Unoptimized		-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.03	-1.97
CT	ε	-1.64	2.66	-2.69	-1.72	-0.68	0.27	0.28	-0.05	-1.88
	σ	-1.13	3.16	-2.76	-1.79	-0.21	0.54	0.91	0.96	-2.21
H1	ε	-1.61	2.64	-2.57	-1.70	-0.57	0.31	0.32	0.01	-1.86
	σ	-1.00	2.70	-1.94	-1.15	0.10	0.41	0.93	1.10	-1.82
HO	ε	-1.66	2.63	-2.61	-1.74	-0.56	0.29	0.26	0.04	-2.01
	σ	-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.04	-1.97
OH	ε	-1.53	2.83	-2.51	-1.41	-0.67	0.32	0.57	-0.49	-1.26
	σ	0.93	5.55	-0.13	2.60	0.94	1.71	1.83	-0.20	2.94

Interaction	Parameter	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)
Unoptimized		0.01	0.00	-0.01	0.01	-1.89	0.00	-0.63	0.04	0.11
CT	ε	-0.01	0.00	0.00	-0.02	-1.94	0.02	-1.40	-0.05	0.05
	σ	0.00	0.00	0.00	0.02	-2.39	-0.04	0.54	-0.07	0.12
H1	ε	-0.01	0.00	0.00	0.00	-1.93	0.00	-1.31	-0.10	0.05
	σ	0.01	0.00	0.00	0.00	-2.13	0.00	-0.68	-0.26	-0.03
HO	ε	0.00	0.00	0.00	0.00	-1.88	0.02	-0.58	0.06	0.08
	σ	0.01	0.00	-0.01	0.01	-1.89	0.00	-0.66	0.04	0.10
OH	ε	0.00	0.00	0.00	-0.01	-1.99	0.03	-1.79	0.21	0.08
	σ	0.00	-0.01	-0.01	0.01	-1.94	0.01	0.22	-0.01	0.00

Table S4.
Sensitivity analysis of the dihedral energy force constants of the AMBER95 force field. The table shows the % deviation in the cell lengths (a, b, and c) and cell angles (α, β, and γ) of the simulated crystal structure from the experimental values when the dihedral force constants are incremented.

		α-mannitol			β-mannitol			δ-mannitol		
Torsion	Change	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81
-CT-CT-	-10%	-0.82	-1.77	-0.93	0.21	-0.05	-2.48	-8.42	4.91	-4.72
	-20%	-0.85	-1.71	-0.94	0.20	-0.03	-2.46	-8.53	2.03	-4.67
	-40%	-0.90	-1.66	-1.02	0.13	0.05	-2.49	-8.68	2.15	-4.52
-CT-OH-	-10%	-0.65	-1.76	-1.01	0.21	-0.15	-2.42	-8.35	2.10	-4.78
	-20%	-0.54	-1.78	-1.13	0.19	-0.07	-2.15	-8.33	2.11	-4.77
	-40%	-0.27	-1.70	-1.34	0.15	-0.01	-1.28	-8.19	2.09	-7.23
Torsion	Change	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)
Unoptimized		-0.02	0.00	0.02	0.04	4.86	-0.30	0.00	-11.62	-0.06
-CT-CT-	-10%	0.01	0.00	0.05	-0.01	0.01	0.01	3.69	-11.59	-14.91
	-20%	0.00	0.00	0.02	-0.02	-0.04	0.01	0.09	-11.54	-0.08
	-40%	0.01	0.00	0.02	0.01	-0.01	0.01	0.01	-11.55	0.04
-CT-OH-	-10%	0.02	0.00	0.03	0.02	-0.01	0.01	0.06	-11.62	-0.06
	-20%	-0.07	0.00	0.02	-0.02	-4.89	-0.28	-0.16	-11.60	-0.05
	-40%	-0.02	-0.01	0.02	0.00	9.66	-0.02	0.02	-17.99	0.10

		A-sorbitol			E-sorbitol			Γ-sorbitol		
Torsion	Change	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.03	-1.97
-CT-CT-	-10%	-1.68	2.62	-2.55	-1.73	-0.69	0.23	0.31	0.00	-1.90
	-20%	-1.71	2.60	-2.50	-1.78	-0.58	0.25	0.43	-0.18	-1.85
	-40%	-1.77	2.53	-2.39	-2.04	-0.35	0.33	0.42	0.07	-2.14
-CT-OH-	-10%	-1.63	2.63	-2.63	-1.62	-0.64	0.29	0.32	-0.02	-2.11
	-20%	-1.68	2.64	-2.58	-1.54	-0.69	0.28	0.10	0.13	-2.25
	-40%	-1.73	2.64	-2.52	-1.30	-0.87	0.13	0.08	-0.30	-1.99
Torsion	Change	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)	α (%)	β (%)	γ (%)
Unoptimized		0.01	0.00	-0.01	0.01	-1.89	0.00	-0.63	0.04	0.11
-CT-CT-	-10%	0.00	0.00	-0.01	0.01	-1.97	0.02	-1.38	0.31	-0.01
	-20%	-0.01	0.01	0.00	-0.03	-2.01	0.06	-1.44	0.23	-0.20
	-40%	0.00	0.00	0.00	-0.01	-2.01	0.02	-0.50	0.33	0.06

-CT-OH-	-10%	0.00	0.00	0.00	0.00	-1.86	0.00	-0.29	0.44	-0.03
	-20%	-0.01	0.00	0.01	-0.01	-1.90	0.02	-0.19	0.18	0.11
	-40%	-0.01	0.00	0.01	0.01	-1.85	-0.01	0.24	0.30	-0.17

Table S5.
Sensitivity analysis of the non-bonded *hetero*-parameters of the AMBER95 force field. The table shows the % deviation in the cell lengths of the simulated crystal structure from the experimental values for the original force field and when each of the individual force field parameters (ε & σ) are incremented by 5%.

		α-mannitol			β-mannitol			δ-mannitol		
Interaction	Parameter	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81
OH – OH	ε	-0.55	-1.72	-0.91	0.51	-0.06	-2.53	-8.11	2.96	-0.74
	σ	2.68	-0.08	-0.87	4.38	1.43	-3.58	-4.35	-1.29	0.43
OH – CT	ε	-0.81	-1.81	-0.95	0.22	-0.12	-2.51	-8.39	2.10	-4.77
	σ	-0.77	-0.54	-0.12	0.08	1.17	-1.47	-8.37	2.37	-3.65
OH – H1	ε	-0.73	-1.80	-0.82	0.25	-0.12	-2.35	-8.27	2.08	-4.72
	σ	0.13	-1.50	0.66	0.38	0.48	0.30	-7.63	-0.47	1.57
OH – HO	ε	-0.77	-1.78	-0.90	0.23	-0.12	-2.46	-8.37	2.21	-4.79
	σ	-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81
CT – CT	ε	-0.81	-1.81	-0.89	0.23	-0.14	-2.21	-8.35	2.04	-4.81
	σ	-0.84	-1.86	-0.88	0.21	-0.10	-2.53	-8.29	5.03	-4.86
CT – H1	ε	-0.79	-1.80	-0.89	0.23	-0.14	-2.13	-8.37	2.11	-4.81
	σ	-0.93	-1.73	-0.54	0.17	0.16	-1.99	-8.10	2.63	-7.41
CT – HO	ε	-0.77	-1.78	-0.89	0.26	-0.11	-2.23	-8.37	2.15	-4.82
	σ	-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81
H1 – H1	ε	-0.78	-1.75	-0.91	0.23	-0.08	-2.49	-8.39	2.18	-4.77
	σ	-0.99	-1.30	-0.92	0.11	0.26	-2.44	-8.23	2.34	-4.88
H1 – HO	ε	-0.77	-1.78	-0.89	0.25	-0.15	-2.21	-8.38	2.16	-4.81
	σ	-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81
HO – HO	ε	-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81
	σ	-0.77	-1.78	-0.89	0.24	-0.15	-2.16	-8.37	2.17	-4.81

		A-sorbitol			E-sorbitol			Γ-sorbitol		
Interaction	Parameter	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)	a (%)	b (%)	c (%)
Unoptimized		-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.03	-1.97
OH – OH	ε	-1.54	2.81	-2.52	-1.36	-0.64	0.28	0.33	-0.10	-1.57
	σ	0.12	5.24	-0.35	2.44	-0.13	1.44	1.33	-1.12	3.00
OH – CT	ε	-1.63	2.66	-2.69	-1.72	-0.67	0.26	0.39	-0.25	-1.74
	σ	-1.15	3.48	-2.44	-1.98	0.27	0.51	1.23	1.87	-2.73
OH – H1	ε	-1.58	2.65	-2.60	-1.63	-0.57	0.27	0.46	-0.25	-1.66
	σ	-0.68	2.92	-1.73	-0.97	0.48	0.48	2.07	0.39	-2.01
OH – HO	ε	-1.66	2.63	-2.58	-1.70	-0.54	0.28	0.30	0.04	-2.01
	σ	-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.04	-1.97
CT – CT	ε	-1.64	2.64	-2.65	-1.66	-0.65	0.23	0.23	0.03	-1.98
	σ	-1.47	2.77	-2.96	-1.71	-0.68	0.26	0.30	0.17	-2.13

CT – H1	ε	-1.66	2.63	-2.57	-1.66	-0.65	0.25	0.27	0.01	-1.98
	σ	-1.39	2.59	-2.22	-1.51	-0.46	0.49	0.85	-0.39	-1.43
CT – HO	ε	-1.66	2.64	-2.58	-1.69	-0.55	0.27	0.21	0.08	-1.97
	σ	-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.04	-1.97
H1 – H1	ε	-1.66	2.64	-2.55	-1.70	-0.52	0.28	0.24	-0.01	-1.87
	σ	-1.54	2.55	-2.32	-1.50	-0.35	0.25	0.37	0.57	-1.96
H1 – HO	ε	-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.03	-1.96
	σ	-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.04	-1.97
HO – HO	ε	-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.04	-1.97
	σ	-1.66	2.63	-2.57	-1.69	-0.55	0.27	0.25	0.04	-1.97