Supporting Information

Discrimination of Native-like States of Membrane Proteins with Implicit Membrane-Based Scoring Functions

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Tables S1-S8

Table S1. Z-scores for each protein in decoy set 1 with different scoring functions with different membrane widths after application of the full scoring protocol.

Model	Membrane width [Å]	BRD7	fmr5	ltpA	RHOD	VATP
IMM1	23.1	4.19	2.65	2.34	3.89	2.46
	25.4	4.36	2.73	2.02	3.80	2.54
	27.0	4.10	2.48	2.74	3.26	2.62
	28.5	4.25	2.63	2.54	3.01	2.40
	30.4	4.10	2.82	2.18	2.50	2.12
IMM1-p36	23.1	4.39	4.72	2.28	4.33	3.12
	25.4	4.45	4.61	2.71	3.60	3.26
	27.0	4.22	4.22	2.55	3.84	3.33
	28.5	4.32	4.31	2.35	4.33	3.40
	30.4	4.50	4.87	2.07	3.75	3.44
GBSW	23.1	6.41	2.94	2.10	4.44	3.00
	25.4	5.61	2.75	2.14	4.37	3.31
	27.0	6.41	2.77	1.92	4.70	3.72
	28.5	5.45	3.17	2.07	4.82	3.73
	30.4	5.88	2.97	2.64	5.00	3.82
HDGBv2	23.1	6.51	3.73	2.35	5.07	3.65
	25.4	6.00	4.43	2.29	5.17	3.62
	27.0	5.98	3.75	2.69	5.31	4.02
	28.5	5.97	4.34	2.11	4.87	3.79
	30.4	5.99	4.30	2.37	4.79	3.66
HDGBv3	23.1	5.76	3.76	3.57	4.44	3.24
	25.4	6.04	3.90	2.47	4.67	3.67
	27.0	5.67	4.19	2.69	5.50	3.40
	28.5	5.69	4.27	2.44	5.41	3.53
	30.4	5.84	3.89	2.58	4.89	4.09
HDGBvdW	23.1	5.81	4.17	2.33	4.53	2.95
	25.4	5.77	4.27	1.99	4.94	2.93
	27.0	5.74	4.34	2.42	5.67	3.36
	28.5	5.29	4.57	2.18	5.04	3.09
	30.4	5.42	4.67	1.94	5.35	3.30

Table S2. Spearman's rank correlation coefficients between scores and RMSD$_1$ and RMSD$_2$ for each protein in decoy set 1 with different scoring functions with different membrane widths after application of the full scoring protocol.

		RMSD$_1$					RMSD$_2$				
Model	Membrane width [Å]	BRD7	fmr5	ltpA	RHOD	VATP	BRD7	fmr5	ltpA	RHOD	VATP
IMM1	23.1	0.26	0.28	0.10	0.32	0.47	0.31	0.30	0.28	0.41	0.42
	25.4	0.22	0.21	0.16	0.21	0.54	0.29	0.21	0.44	0.31	0.50
	27.0	0.26	0.24	0.14	0.24	0.50	0.34	0.24	0.40	0.34	0.47
	28.5	0.27	0.25	0.14	0.22	0.54	0.38	0.27	0.37	0.33	0.53
	30.4	0.30	0.21	0.18	0.15	0.45	0.42	0.25	0.40	0.24	0.46
IMM1-p36	23.1	0.23	0.32	0.11	0.10	0.49	0.29	0.34	0.31	0.21	0.47
	25.4	0.25	0.27	0.18	0.16	0.50	0.33	0.26	0.49	0.27	0.49
	27.0	0.25	0.32	0.16	0.19	0.62	0.32	0.33	0.52	0.29	0.59
	28.5	0.24	0.29	0.18	0.15	0.57	0.37	0.31	0.50	0.24	0.57
	30.4	0.29	0.30	0.19	0.18	0.51	0.42	0.32	0.48	0.27	0.55
GBSW	23.1	0.33	0.36	0.16	0.03	0.64	0.42	0.38	0.47	0.15	0.70
	25.4	0.24	0.37	0.15	0.05	0.61	0.31	0.38	0.45	0.14	0.68
	27.0	0.19	0.32	0.12	0.01	0.54	0.27	0.33	0.42	0.10	0.59
	28.5	0.21	0.37	0.15	0.03	0.54	0.28	0.38	0.43	0.13	0.60
	30.4	0.19	0.32	0.12	0.03	0.58	0.27	0.32	0.36	0.13	0.62
HDGBv2	23.1	0.24	0.27	0.14	0.06	0.60	0.30	0.27	0.34	0.17	0.65
	25.4	0.29	0.29	0.10	0.06	0.53	0.34	0.30	0.29	0.15	0.60
	27.0	0.26	0.29	0.12	-0.01	0.51	0.31	0.29	0.32	0.07	0.58
	28.5	0.27	0.25	0.12	-0.01	0.52	0.32	0.25	0.32	0.09	0.58
	30.4	0.28	0.26	0.13	0.03	0.51	0.33	0.26	0.31	0.12	0.57
HDGBv3	23.1	0.25	0.23	0.14	0.00	0.61	0.32	0.25	0.39	0.09	0.67
	25.4	0.31	0.26	0.19	-0.01	0.61	0.36	0.28	0.42	0.08	0.67
	27.0	0.21	0.33	0.12	0.07	0.58	0.25	0.34	0.34	0.15	0.63
	28.5	0.25	0.24	0.14	0.01	0.52	0.33	0.24	0.37	0.08	0.57
	30.4	0.25	0.31	0.14	0.05	0.47	0.31	0.33	0.35	0.13	0.53
HDGBvdW	23.1	0.14	0.11	0.04	0.03	0.50	0.19	0.14	0.30	0.11	0.55
	25.4	0.16	0.17	0.03	0.01	0.47	0.22	0.18	0.29	0.08	0.53
	27.0	0.16	0.19	0.06	-0.06	0.48	0.20	0.21	0.29	0.01	0.54
	28.5	0.19	0.21	0.04	-0.08	0.41	0.22	0.23	0.29	0.00	0.48
	30.4	0.14	0.20	0.02	0.10	0.36	0.18	0.21	0.22	0.15	0.43

Table S3. Average z-scores and Spearman's rank correlation coefficients with different membrane widths for different energy components: total energy (TOT), van der Waals (VDW) energy, electrostatic (ELEC) energy, and electrostatic solvation (GB) energy for decoys in set 1. ASP denotes the cavity and electrostatic terms for IMM1 and IMM1-p36, the cavity term for GBSW, HDGBv2 and HDGBv3, and the cavity and van der Waals terms for HDGBvdW.

		Z-scores					Correlation coefficients				
Model	Membrane width [Å]	TOT	VDW	ELEC	ASP	GB	TOT	VDW	ELEC	ASP	GB
IMM1	23.1	3.11	2.41	1.51	-0.59	-	0.28	0.24	0.11	-0.02	-
	25.4	3.09	2.16	1.47	-0.37	-	0.27	0.23	0.11	-0.05	-
	27.0	3.04	2.27	1.52	-0.48	-	0.27	0.24	0.12	-0.03	-
	28.5	2.97	2.04	1.77	-0.63	-	0.28	0.24	0.13	-0.02	-
	30.4	2.74	1.94	1.59	-0.42	-	0.26	0.24	0.15	-0.04	-
IMM1-p36	23.1	3.77	2.58	2.17	-0.64	-	0.25	0.24	0.08	0.02	-
	25.4	3.73	2.49	2.14	-0.50	-	0.27	0.23	0.15	-0.00	-
	27.0	3.63	2.40	2.17	-0.48	-	0.31	0.22	0.17	-0.01	-
	28.5	3.74	2.43	2.19	-0.44	-	0.29	0.21	0.18	-0.03	-
	30.4	3.72	2.70	2.12	-0.52	-	0.30	0.22	0.19	-0.00	-
GBSW	23.1	3.77	2.41	1.91	1.39	-1.42	0.30	0.31	-0.05	0.16	0.07
	25.4	3.64	2.51	1.59	1.28	-1.05	0.28	0.32	-0.05	0.14	0.07
	27.0	3.90	2.43	1.72	1.24	-1.13	0.24	0.32	-0.06	0.15	0.07
	28.5	3.85	2.33	1.49	1.13	-0.86	0.26	0.30	-0.09	0.14	0.12
	30.4	4.06	2.36	1.85	1.15	-1.18	0.25	0.32	-0.09	0.13	0.11
HDGBv2	23.1	4.26	2.53	1.45	1.24	-0.91	0.26	0.30	-0.02	0.30	0.02
	25.4	4.30	2.51	1.36	1.20	-0.83	0.25	0.28	-0.04	0.29	0.04
	27.0	4.35	2.53	1.37	1.25	-0.79	0.23	0.31	-0.01	0.30	0.01
	28.5	4.22	2.45	1.53	1.33	-0.98	0.23	0.31	-0.05	0.27	0.06
	30.4	4.22	2.63	1.20	1.17	-0.66	0.24	0.29	-0.07	0.27	0.08
HDGBv3	23.1	4.15	2.55	1.31	1.08	-0.75	0.25	0.28	-0.02	0.31	0.03
	25.4	4.15	2.34	1.55	1.28	-0.86	0.27	0.30	-0.01	0.29	0.02
	27.0	4.29	2.42	1.38	1.22	-0.70	0.26	0.32	-0.04	0.27	0.05
	28.5	4.27	2.37	1.51	1.26	-0.82	0.23	0.30	-0.03	0.28	0.04
	30.4	4.26	2.27	1.32	1.08	-0.59	0.25	0.30	-0.04	0.28	0.05
HDGBvdW	23.1	3.96	2.46	1.74	-2.06	-1.07	0.16	0.29	-0.05	-0.17	0.06
	25.4	3.98	2.68	1.29	-2.10	-0.69	0.17	0.28	-0.00	-0.16	0.01
	27.0	4.31	2.37	1.63	-2.16	-0.92	0.17	0.29	-0.04	-0.20	0.05
	28.5	4.03	2.60	1.25	-1.94	-0.61	0.15	0.29	-0.05	-0.18	0.06
	30.4	4.14	2.51	1.36	-1.96	-0.68	0.16	0.29	-0.01	-0.18	0.03

Table S4. RMSD_2 values in [Å] for top-scoring models of each protein in decoy set 1 with different scoring functions with different membrane widths after application of the full scoring protocol.

		Top-1					Top-10				
Model	Membrane width [Å]	BRD7	fmr5	ltpA	RHOD	VATP	BRD7	fmr5	ltpA	RHOD	VATP
IMM1	23.1	14.88	11.07	9.21	10.59	5.10	12.81	14.16	13.19	14.61	7.45
	25.4	14.77	11.01	15.30	10.52	4.79	13.43	14.39	13.64	15.08	6.18
	27.0	14.62	14.64	13.77	10.52	5.17	12.69	13.86	13.58	15.08	6.53
	28.5	14.66	14.41	9.50	10.61	7.47	12.96	13.37	13.53	14.56	6.67
	30.4	12.79	14.49	12.39	11.03	4.66	13.27	13.13	13.60	15.03	6.61
IMM1-p36	23.1	12.90	12.42	15.16	10.64	5.08	13.39	13.19	12.94	15.21	6.39
	25.4	12.76	10.50	13.79	10.57	4.83	13.46	13.76	13.94	14.79	6.05
	27.0	12.94	14.60	15.16	10.56	5.11	12.38	13.95	13.04	14.99	6.25
	28.5	14.71	14.54	13.85	10.63	5.41	12.94	12.86	14.33	14.96	6.37
	30.4	12.89	14.62	14.03	11.08	4.64	12.40	13.27	13.74	15.61	6.09
GBSW	23.1	14.67	14.66	13.67	17.57	5.39	12.01	14.17	13.12	15.00	6.63
	25.4	14.65	14.62	11.98	17.57	7.47	12.11	13.56	13.21	15.01	6.18
	27.0	11.65	14.63	11.95	17.59	5.35	12.31	13.56	13.55	15.32	6.33
	28.5	12.88	14.68	12.01	17.61	7.51	12.29	13.71	13.15	15.33	5.98
	30.4	11.74	14.68	11.94	17.58	7.50	11.81	13.36	13.39	15.23	5.74
HDGBv2	23.1	10.39	14.67	13.65	10.61	7.44	11.98	13.73	13.86	15.04	5.81
	25.4	13.36	14.67	13.68	13.93	7.47	12.39	13.78	14.25	15.76	5.70
	27.0	13.38	14.63	13.65	10.63	5.36	11.44	13.51	14.40	15.69	5.70
	28.5	10.22	14.67	15.22	15.32	5.32	11.80	13.66	14.64	15.47	5.44
	30.4	10.20	14.65	13.68	17.60	8.83	12.08	13.72	14.03	15.91	6.24
HDGBv3	23.1	11.43	14.58	15.21	16.92	7.52	11.72	13.36	13.68	15.52	5.48
	25.4	10.90	14.66	13.68	13.95	7.46	12.09	14.72	13.93	16.12	5.68
	27.0	13.36	14.64	15.27	15.33	5.33	11.58	13.36	14.20	15.73	5.92
	28.5	10.88	14.64	13.72	15.33	5.30	11.16	13.75	13.67	15.90	5.85
	30.4	13.36	14.65	15.25	17.60	7.46	11.86	13.06	13.97	15.45	6.70
HDGBvdW	23.1	10.27	13.49	15.34	13.98	5.36	12.70	14.38	14.24	15.75	5.79
	25.4	10.94	14.68	14.36	15.38	7.51	12.33	13.89	14.70	15.68	6.90
	27.0	10.86	10.97	13.79	15.44	5.27	12.11	13.86	14.37	15.68	6.03
	28.5	10.96	14.70	13.82	17.67	8.67	12.65	14.21	13.46	15.97	6.75
	30.4	11.46	14.68	13.71	14.05	5.28	12.13	13.63	14.84	15.35	6.47

Table S5. Z-scores for each protein in decoy set 2 with different scoring functions with different membrane widths after application of the full scoring protocol.

Model	Membrane width [Å]	BRD7	fmr5	ltpA	RHOD	VATP
IMM1	23.1	7.40	5.53	3.91	5.39	5.52
	25.4	7.15	5.79	3.73	5.36	5.84
	27.0	7.17	5.19	3.90	5.23	5.57
	28.5	7.44	5.54	3.95	4.92	5.52
	30.4	6.87	5.16	3.73	4.59	5.08
IMM1-p36	23.1	9.01	6.78	4.01	6.22	5.55
	25.4	9.17	6.90	4.08	5.83	6.08
	27.0	8.57	6.86	3.83	5.90	5.90
	28.5	8.44	6.36	3.63	5.90	5.45
	30.4	8.20	7.03	3.54	6.10	5.53
GBSW	23.1	7.68	6.93	4.07	5.83	6.66
	25.4	6.34	5.71	4.12	6.12	6.74
	27.0	7.10	5.81	3.82	5.90	6.75
	28.5	6.19	5.67	3.95	5.68	6.61
	30.4	6.75	5.63	4.01	5.46	6.39
HDGBv2	23.1	8.62	8.07	4.14	6.71	6.39
	25.4	8.02	8.58	4.06	6.71	6.34
	27.0	7.72	6.96	4.21	6.46	6.74
	28.5	7.84	7.87	3.85	6.43	6.38
	30.4	7.81	7.90	4.07	6.63	6.18
HDGBv3	23.1	7.54	8.11	4.63	6.03	6.96
	25.4	7.93	7.79	4.00	5.91	6.40
	27.0	7.63	8.23	4.13	6.32	6.08
	28.5	7.70	7.99	4.02	6.38	6.08
	30.4	7.30	7.24	4.07	6.25	6.38
HDGBvdW	23.1	9.10	7.02	4.29	5.95	6.25
	25.4	7.96	6.80	4.00	6.24	6.31
	27.0	7.74	7.03	4.37	6.28	6.11
	28.5	6.80	6.79	3.96	5.91	5.54
	30.4	7.18	7.03	4.08	5.88	5.60

Table S6. Spearman's rank correlation coefficients between scores and RMSD$_1$ and RMSD$_2$ for each protein in decoy set 2 with different scoring functions with different membrane widths after application of the full scoring protocol.

		RMSD$_1$					RMSD$_2$				
Model	Membrane width (Å)	BRD7	fmr5	ltpA	RHOD	VATP	BRD7	fmr5	ltpA	RHOD	VATP
IMM1	23.1	0.65	0.08	0.72	0.67	0.38	0.65	0.10	0.71	0.65	0.11
	25.4	0.65	0.09	0.75	0.67	0.41	0.65	0.11	0.75	0.66	0.20
	27.0	0.71	-0.02	0.77	0.72	0.40	0.70	-0.01	0.77	0.72	0.34
	28.5	0.73	0.01	0.78	0.70	0.44	0.72	0.03	0.79	0.70	0.41
	30.4	0.70	-0.08	0.79	0.70	0.45	0.71	-0.07	0.77	0.70	0.46
IMM1-p36	23.1	0.46	0.24	0.73	0.68	0.44	0.48	0.25	0.73	0.67	0.03
	25.4	0.48	0.22	0.80	0.71	0.47	0.48	0.24	0.80	0.70	0.24
	27.0	0.51	0.20	0.80	0.74	0.41	0.50	0.21	0.80	0.73	0.36
	28.5	0.56	0.22	0.80	0.73	0.47	0.56	0.22	0.80	0.73	0.44
	30.4	0.57	0.22	0.82	0.72	0.50	0.58	0.23	0.82	0.72	0.48
GBSW	23.1	0.65	0.10	0.82	0.77	0.53	0.64	0.11	0.81	0.76	0.37
	25.4	0.65	0.07	0.87	0.81	0.48	0.64	0.08	0.86	0.80	0.50
	27.0	0.68	0.05	0.82	0.81	0.51	0.67	0.06	0.81	0.81	0.51
	28.5	0.68	0.11	0.85	0.82	0.50	0.66	0.11	0.85	0.82	0.61
	30.4	0.67	0.10	0.83	0.79	0.51	0.64	0.10	0.84	0.79	0.70
HDGBv2	23.1	0.60	0.39	0.77	0.69	0.52	0.59	0.40	0.76	0.67	0.45
	25.4	0.60	0.37	0.77	0.76	0.53	0.60	0.37	0.75	0.75	0.51
	27.0	0.63	0.32	0.77	0.75	0.50	0.63	0.33	0.76	0.75	0.59
	28.5	0.64	0.33	0.76	0.76	0.56	0.65	0.32	0.75	0.75	0.57
	30.4	0.60	0.27	0.74	0.74	0.52	0.60	0.28	0.72	0.73	0.58
HDGBv3	23.1	0.61	0.35	0.81	0.74	0.51	0.61	0.36	0.79	0.74	0.53
	25.4	0.66	0.35	0.78	0.78	0.50	0.65	0.35	0.77	0.77	0.54
	27.0	0.69	0.26	0.79	0.81	0.54	0.69	0.26	0.77	0.80	0.65
	28.5	0.61	0.33	0.76	0.80	0.57	0.60	0.34	0.74	0.79	0.65
	30.4	0.61	0.29	0.80	0.78	0.57	0.62	0.29	0.79	0.77	0.67
HDGBvdW	23.1	0.62	0.32	0.81	0.78	0.46	0.62	0.32	0.80	0.77	0.56
	25.4	0.58	0.24	0.78	0.80	0.51	0.58	0.24	0.76	0.79	0.66
	27.0	0.66	0.33	0.75	0.82	0.41	0.66	0.33	0.75	0.82	0.65
	28.5	0.58	0.34	0.76	0.79	0.53	0.59	0.34	0.75	0.78	0.72
	30.4	0.59	0.33	0.78	0.76	0.53	0.59	0.32	0.77	0.75	0.73

Table S7. RMSD$_2$ values in [Å] for top-scoring models of each protein in decoy set 2 with different scoring functions with different membrane widths after application of the full scoring protocol.

		Top-1					Top-10				
Model	Membrane width [Å]	BRD7	fmr5	ltpA	RHOD	VATP	BRD7	fmr5	ltpA	RHOD	VATP
IMM1	23.1	1.57	3.03	1.56	2.72	4.54	3.01	6.29	2.32	3.02	4.38
	25.4	1.82	3.13	1.59	2.49	3.77	3.09	6.42	1.98	2.64	3.49
	27.0	1.70	3.28	1.62	1.65	2.00	3.08	6.77	2.04	2.47	2.52
	28.5	1.68	2.99	1.58	1.67	1.80	2.86	6.34	2.07	2.11	2.10
	30.4	1.97	3.26	1.77	1.90	1.32	3.26	7.23	2.07	2.78	1.77
IMM1-p36	23.1	2.37	3.05	1.57	3.15	4.51	4.16	5.51	2.70	3.71	4.41
	25.4	3.00	2.16	1.39	2.80	3.80	3.81	4.69	2.07	2.90	3.60
	27.0	1.73	1.79	1.45	1.76	2.11	4.56	4.87	2.62	2.74	2.63
	28.5	1.74	3.02	1.51	1.69	1.87	3.39	5.19	2.56	2.26	1.86
	30.4	2.09	3.27	1.80	1.90	1.31	3.83	5.67	2.21	2.47	1.84
GBSW	23.1	1.59	1.60	1.77	1.94	1.85	2.90	6.12	2.10	2.31	1.87
	25.4	1.68	6.20	1.72	1.68	1.88	3.00	6.30	2.05	2.47	1.93
	27.0	2.86	1.59	1.48	1.62	1.80	2.67	5.80	2.04	2.57	1.78
	28.5	1.59	1.60	1.50	1.70	1.81	2.41	6.44	2.12	2.23	1.78
	30.4	1.63	1.58	1.52	1.58	1.74	3.10	6.55	2.02	2.40	1.95
HDGBv2	23.1	1.73	1.61	1.57	1.67	1.89	3.69	6.17	2.15	2.58	1.89
	25.4	1.73	3.01	1.50	1.61	1.78	3.49	5.58	2.51	2.54	1.78
	27.0	1.74	1.60	1.57	1.62	1.80	3.20	5.42	2.15	2.11	1.82
	28.5	1.73	1.56	1.76	1.96	1.79	2.96	5.04	2.09	2.46	1.84
	30.4	1.74	4.06	1.54	1.61	1.76	3.56	5.77	2.55	2.48	1.90
HDGBv3	23.1	1.66	1.66	1.49	1.94	1.82	2.79	5.59	2.52	2.49	1.81
	25.4	1.57	1.61	1.57	1.95	1.77	3.27	4.96	2.52	2.58	1.96
	27.0	1.65	1.62	1.87	1.58	1.79	3.62	5.30	2.16	2.09	1.78
	28.5	1.59	6.24	1.75	1.60	1.84	3.07	5.04	2.17	2.09	1.80
	30.4	1.64	1.58	1.58	1.59	1.77	3.51	4.97	2.52	2.21	1.84
HDGBvdW	23.1	1.64	1.64	1.63	1.59	1.95	3.72	4.24	2.21	2.67	2.07
	25.4	1.68	1.63	1.59	1.99	1.87	3.61	5.42	2.10	2.39	2.00
	27.0	1.67	1.64	1.62	1.61	1.87	3.37	4.73	2.68	2.58	2.05
	28.5	1.68	1.61	1.59	1.64	1.90	3.96	4.24	2.39	2.12	1.95
	30.4	2.01	3.37	1.55	1.65	1.80	4.11	3.75	2.56	2.40	1.98

Table S8. Average z-scores and Spearman's rank correlation coefficients with different membrane widths for different energy components as in Table S4 but for decoy set 2.

		Z-scores					Correlation coefficients				
Model	Membrane width [Å]	TOT	VDW	ELEC	ASP	GB	TOT	VDW	ELEC	ASP	GB
IMM1	23.1	5.55	5.00	3.48	-4.15	-	0.50	0.36	0.30	-0.15	
	25.4	5.57	4.95	3.55	-3.83	-	0.52	0.38	0.32	-0.13	
	27.0	5.41	5.10	3.61	-3.86	-	0.52	0.37	0.34	-0.13	
	28.5	5.48	4.84	3.71	-3.75	-	0.53	0.35	0.36	-0.13	
	30.4	5.09	4.69	3.48	-3.50	-	0.51	0.38	0.39	-0.17	
MM1-p36	23.1	6.32	4.95	4.42	-4.90	-	0.51	0.32	0.32	-0.13	
	25.4	6.41	4.97	4.55	-4.65	-	0.54	0.31	0.32	-0.09	
	27.0	6.21	4.96	4.22	-4.38	-	0.53	0.32	0.35	-0.11	
	28.5	5.96	4.82	4.18	-4.23	-	0.56	0.33	0.37	-0.11	
	30.4	6.08	5.22	4.14	-4.38	-	0.57	0.28	0.44	-0.12	
GBSW	23.1	6.23	4.51	2.82	4.65	-2.46	0.57	0.34	0.41	0.25	-0.35
	25.4	5.80	4.42	2.62	4.27	-2.23	0.57	0.34	0.41	0.28	-0.34
	27.0	5.88	4.58	2.73	4.19	-2.27	0.57	0.33	0.34	0.26	-0.25
	28.5	5.62	4.46	2.49	3.86	-1.93	0.59	0.37	0.34	0.25	-0.22
	30.4	5.65	4.46	2.85	3.69	-2.34	0.58	0.38	0.37	0.27	-0.25
HDGBv2	23.1	6.79	4.98	2.35	2.70	-1.74	0.59	0.37	0.34	0.28	-0.26
	25.4	6.74	4.94	2.11	2.68	-1.54	0.61	0.35	0.37	0.27	-0.28
	27.0	6.42	4.94	2.26	2.74	-1.64	0.60	0.35	0.37	0.26	-0.27
	28.5	6.47	4.91	2.29	2.83	-1.70	0.61	0.37	0.36	0.30	-0.27
	30.4	6.52	5.24	2.04	2.55	-1.43	0.57	0.37	0.33	0.30	-0.24
HDGBv3	23.1	6.65	4.93	2.29	2.47	-1.63	0.60	0.38	0.34	0.26	-0.25
	25.4	6.41	4.70	2.40	2.76	-1.72	0.61	0.38	0.36	0.26	-0.24
	27.0	6.48	5.07	2.19	2.64	-1.48	0.62	0.38	0.33	0.29	-0.22
	28.5	6.44	5.07	2.30	2.77	-1.62	0.61	0.36	0.33	0.26	-0.21
	30.4	6.25	4.69	2.09	2.42	-1.36	0.61	0.40	0.39	0.31	-0.28
HDGBvdW	23.1	6.52	5.61	2.67	-5.76	-1.95	0.60	0.37	0.36	-0.32	-0.27
	25.4	6.26	5.78	2.23	-5.73	-1.57	0.58	0.38	0.37	-0.31	-0.26
	27.0	6.30	5.40	2.70	-5.65	-1.94	0.59	0.40	0.34	-0.35	-0.23
	28.5	5.80	5.53	2.20	-5.51	-1.54	0.60	0.39	0.33	-0.33	-0.22
	30.4	5.96	5.50	2.34	-5.36	-1.59	0.60	0.37	0.34	-0.34	-0.23