Appendix A

Results of Pairwise Surface Alignment

This appendix contains the numerical results from Chapter 5.

In this appendix, two types of tables are given. The tables of the first type present the numbers of initial transformations used for the computation of pairwise alignments. In the tables of the second type, the rms (root mean square) distances w.r.t. to the computed pairwise alignments are presented.

The tables which contain the rms distances have to be read as follows. The reference molecule is given in the first column, and each row contains the results of the pairwise alignments with the reference molecule's experimental conformer. Every table entry contains two values, each of which measures the rms distance of the aligned query molecule to its experimental conformer. While the first value is the rms distance of the pairwise alignment with the highest score, the second value gives the smallest rms distance of any of the 10 top-ranked alignments.

In order to allow to quickly grasp the main information given by each table, the following colors were used for highlighting:

- green: rms distances between 1.0 and 2.0 Å.
- blue: rms distances between 2.0 and 4.0 Å.
- red: rms distances above 4.0 Å.

For a detailed discussion of the tables we refer the reader to Section 5.6.

A.1 Thermolysin Inhibitors

A.1.1 Experimental Conformers

Table A.1: Experiment T1 and T3: Number of initial transformations.

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	10728	7922	3111	3128	7202	4665	4817
1TLP	10728	–	10149	3290	3420	8926	5600	5921
1TMN	7922	10149	–	2666	2747	7186	4554	4672
3TMN	3111	3290	2666	–	1252	2336	1608	1772
5TLN	3128	3420	2747	1252	–	2566	1761	1728
4TMN	7202	8926	7186	2336	2566	–	4436	4494
5TMN	4665	5600	4554	1608	1761	4436	–	3453
6TMN	4817	5921	4672	1772	1728	4494	3453	–

Table A.2: Experiment T2: Number of initial transformations.

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	10827	10916	3024	3890	7954	7338	6343
1TLP	10827	–	11191	3369	4043	7062	7574	6942
1TMN	10916	11191	–	3205	4114	7952	7936	7287
3TMN	3024	3369	3205	–	1367	2476	2371	2076
5TLN	3890	4043	4114	1367	–	3642	2782	2736
4TMN	7954	7062	7952	2476	3642	–	6372	6055
5TMN	7338	7574	7936	2371	2782	6372	–	6465
6TMN	6343	6942	7287	2076	2736	6055	6465	–

Table A.3: Rms distances (in Å) of surface alignment with atom-based initial transformations (experiment T1a).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.40/0.40	0.17/0.17	0.25/0.25	0.86/0.57	0.43/0.43	0.66/0.66	0.95/0.95
1TLP	0.55/0.55	–	0.95/0.69	0.89/0.89	0.56/0.56	0.85/0.85	1.00/1.00	1.14/1.14
1TMN	0.24/0.24	0.91/0.56	–	0.43/0.43	0.54/0.54	0.78/0.48	1.09/0.67	0.67/0.67
3TMN	0.37/0.37	1.25/0.77	0.48/0.48	–	1.29/0.98	0.75/0.75	0.63/0.63	0.85/0.78
5TLN	0.62/0.62	0.77/0.77	0.53/0.53	1.27/1.11	–	0.72/0.72	1.03/1.03	0.62/0.62
4TMN	0.38/0.38	0.86/0.86	0.56/0.56	0.37/0.37	0.71/0.71	–	0.31/0.31	0.51/0.51
5TMN	0.67/0.51	0.85/0.85	0.88/0.48	0.57/0.57	0.64/0.64	0.32/0.32	–	0.18/0.18
6TMN	0.53/0.53	0.88/0.88	0.57/0.57	0.74/0.70	0.54/0.54	0.53/0.53	0.18/0.18	–

Table A.4: Rms distances (in Å) of surface alignment with atom-based initial transformations (experiment T1b).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.77/0.65	0.28/0.28	0.38/0.38	4.84/4.75	0.75/0.53	1.65/0.65	1.84/0.65
1TLP	0.67/0.67	–	1.34/0.77	0.45/0.45	4.85/4.85	1.18/1.01	1.17/1.10	0.98/0.98
1TMN	–	0.39/0.39	1.33/0.75	0.89/0.71	5.33/4.84	0.91/0.31	2.05/0.46	1.61/0.20
3TMN	0.76/0.38	0.56/0.56	1.19/0.96	–	4.17/1.70	7.68/7.25	1.13/1.13	10.26/1.03
5TLN	7.37/1.54	8.11/5.85	7.53/5.72	3.56/1.91	–	8.11/0.74	8.29/0.85	8.63/0.60
4TMN	0.35/0.35	1.09/0.97	0.64/0.59	6.44/5.71	6.41/0.80	–	1.75/0.31	1.82/0.19
5TMN	0.88/0.88	0.96/0.92	1.72/0.47	0.59/0.59	5.98/0.59	1.85/0.31	–	0.46/0.46
6TMN	1.01/0.66	0.77/0.77	1.35/0.21	2.87/0.64	5.51/1.03	1.89/0.19	0.45/0.45	–

Table A.5: Rms distances (in Å) of surface alignment with atom-based initial transformations (experiment T1c).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.69/0.69	0.37/0.37	0.34/0.34	0.40/0.40	0.32/0.32	0.85/0.85	0.69/0.69
1TLP	0.71/0.71	–	0.68/0.68	0.92/0.92	6.62/0.71	1.08/1.08	1.00/1.00	0.85/0.85
1TMN	0.37/0.37	0.67/0.38	–	0.35/0.35	0.38/0.38	0.55/0.55	0.44/0.44	0.57/0.57
3TMN	0.36/0.36	1.22/1.22	0.43/0.43	–	0.86/0.86	1.00/1.00	0.70/0.70	1.30/1.30
5TLN	0.61/0.61	7.94/0.67	0.41/0.41	0.75/0.75	–	1.54/1.54	1.45/1.45	0.97/0.97
4TMN	0.32/0.32	0.94/0.94	0.39/0.39	0.63/0.63	0.95/0.95	–	0.52/0.52	0.42/0.42
5TMN	0.82/0.82	0.83/0.83	0.33/0.33	0.60/0.60	0.89/0.89	0.53/0.53	–	0.23/0.23
6TMN	0.72/0.72	0.68/0.68	0.54/0.54	0.97/0.97	0.72/0.72	0.45/0.45	0.23/0.23	–

Table A.6: Rms distances (in Å) of surface alignment with atom-based initial transformations (experiment T1d).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.55/0.55	0.36/0.36	0.59/0.58	0.72/0.72	0.24/0.24	1.17/0.99	1.51/0.68
1TLP	0.42/0.42	–	0.52/0.52	0.89/0.50	0.82/0.82	0.80/0.80	0.92/0.92	0.99/0.99
1TMN	0.42/0.42	0.54/0.54	–	1.81/0.68	0.58/0.58	0.66/0.66	0.61/0.61	0.64/0.64
3TMN	0.33/0.33	1.47/0.86	2.75/0.96	–	5.12/4.33	10.13/3.97	3.57/3.57	3.93/3.67
5TLN	1.13/0.98	1.01/0.94	0.75/0.75	4.19/4.19	–	0.97/0.75	1.03/1.03	0.60/0.60
4TMN	0.37/0.37	0.88/0.88	0.56/0.56	11.38/2.38	0.71/0.71	–	0.71/0.53	0.57/0.57
5TMN	0.34/0.34	0.82/0.82	0.56/0.56	2.51/2.51	0.73/0.73	0.73/0.52	–	0.26/0.26
6TMN	1.02/0.42	0.96/0.94	0.58/0.58	2.89/1.21	0.49/0.49	0.62/0.62	0.26/0.26	–

Table A.7: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment T2a).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.38/0.38	0.32/0.32	0.42/0.42	1.05/1.01	0.49/0.49	1.63/0.47	0.49/0.49
1TLP	0.40/0.40	–	0.96/0.56	0.87/0.87	0.79/0.79	0.82/0.82	1.07/1.07	1.08/1.08
1TMN	0.17/0.17	0.92/0.57	–	0.43/0.43	0.54/0.54	0.57/0.57	0.56/0.56	0.64/0.64
3TMN	0.33/0.33	1.27/1.27	0.47/0.47	–	1.74/1.36	0.81/0.81	0.64/0.64	0.86/0.82
5TLN	0.87/0.87	0.85/0.85	0.53/0.53	1.84/1.34	–	0.75/0.75	1.53/0.66	0.67/0.67
4TMN	0.31/0.31	0.84/0.84	0.45/0.45	0.52/0.52	0.72/0.72	–	0.31/0.31	0.52/0.52
5TMN	0.60/0.60	0.89/0.89	0.46/0.46	0.56/0.56	0.89/0.89	0.31/0.31	–	0.20/0.20
6TMN	0.78/0.78	0.82/0.82	0.55/0.55	0.74/0.74	0.54/0.54	0.54/0.54	0.20/0.20	–

Table A.8: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment T2b).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.37/0.37	0.68/0.39	0.20/0.20	4.82/1.54	0.65/0.65	2.69/0.67	1.79/0.39
1TLP	0.41/0.41	–	1.34/0.84	0.60/0.44	4.85/4.85	1.19/0.87	1.17/1.02	0.98/0.98
1TMN	0.67/0.39	1.33/0.82	–	0.85/0.70	4.90/4.81	0.88/0.37	2.05/0.53	1.48/0.53
3TMN	0.15/0.15	0.88/0.59	1.17/0.68	–	4.09/3.37	8.17/7.53	0.86/0.86	9.68/1.71
5TLN	7.46/1.62	8.11/5.87	8.07/5.77	3.47/2.90	–	8.15/0.73	8.31/0.96	8.65/1.52
4TMN	0.87/0.64	1.09/0.60	0.61/0.59	6.40/6.08	6.41/0.80	–	1.80/0.23	1.79/0.71
5TMN	1.71/1.03	0.96/0.93	1.72/0.52	0.38/0.38	5.97/0.71	1.90/0.21	–	0.41/0.41
6TMN	1.32/0.40	0.77/0.77	1.23/0.47	2.16/0.96	5.49/0.85	1.87/0.58	0.40/0.40	–

Table A.9: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment T2c).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.73/0.73	0.37/0.37	0.36/0.36	0.55/0.55	0.37/0.37	0.77/0.77	0.64/0.64
1TLP	0.71/0.71	–	0.66/0.66	5.57/0.82	7.07/0.76	1.13/1.13	1.00/1.00	0.87/0.87
1TMN	0.37/0.37	0.65/0.65	–	0.41/0.41	0.37/0.37	0.52/0.52	0.47/0.47	0.57/0.57
3TMN	0.38/0.38	6.39/1.17	0.44/0.44	–	2.08/1.23	0.82/0.82	1.23/1.23	1.33/0.77
5TLN	0.67/0.67	8.13/0.85	0.38/0.38	2.34/1.20	–	0.42/0.42	1.25/1.25	0.65/0.65
4TMN	0.34/0.34	1.06/0.54	0.38/0.38	0.39/0.39	0.48/0.48	–	0.49/0.49	0.54/0.54
5TMN	0.70/0.70	0.85/0.85	0.36/0.36	0.80/0.80	0.77/0.77	0.50/0.50	–	0.20/0.20
6TMN	0.81/0.81	0.72/0.72	0.52/0.52	0.92/0.92	0.54/0.54	0.56/0.56	0.20/0.20	–

Table A.10: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment T2d).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.73/0.73	0.37/0.37	0.36/0.36	0.55/0.55	0.37/0.37	0.77/0.77	0.64/0.64
1TLP	0.35/0.35	–	0.54/0.54	0.84/0.54	0.77/0.77	0.88/0.88	0.93/0.93	0.76/0.76
1TMN	0.32/0.32	0.54/0.54	–	1.51/1.01	0.57/0.57	0.86/0.39	0.56/0.56	0.85/0.85
3TMN	0.70/0.59	1.21/1.00	2.46/1.65	–	5.61/4.29	10.03/7.15	3.65/1.76	9.19/1.97
5TLN	0.78/0.78	0.98/0.98	0.74/0.74	4.54/3.42	–	0.91/0.91	0.92/0.63	0.50/0.50
4TMN	0.54/0.54	0.98/0.92	0.66/0.47	11.23/5.99	0.90/0.74	–	0.85/0.51	0.57/0.57
5TMN	1.53/0.49	0.83/0.83	0.52/0.52	2.45/1.60	0.65/0.65	0.88/0.48	–	0.25/0.25
6TMN	0.35/0.35	0.79/0.79	0.77/0.73	6.00/1.05	0.41/0.41	0.62/0.62	0.25/0.25	–

Table A.11: Rms distances (in Å) of atom alignment with atom-based initial transformations (experiment T3).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.54/0.54	0.28/0.28	0.31/0.31	6.79/0.91	0.37/0.37	0.57/0.57	0.58/0.58
1TLP	0.34/0.34	–	0.62/0.62	0.85/0.85	0.74/0.74	0.80/0.80	0.93/0.93	0.91/0.91
1TMN	0.27/0.27	0.62/0.62	–	0.35/0.35	1.08/1.08	0.62/0.62	0.50/0.50	0.44/0.44
3TMN	0.35/0.35	1.15/1.15	0.48/0.48	–	6.60/1.15	1.36/1.36	0.94/0.47	0.87/0.50
5TLN	8.08/0.85	0.88/0.88	1.96/0.98	5.88/1.31	–	1.08/1.08	1.57/1.57	1.56/1.56
4TMN	0.28/0.28	0.76/0.76	0.41/0.41	0.70/0.70	0.62/0.62	–	0.47/0.47	0.52/0.52
5TMN	0.50/0.50	0.84/0.84	0.43/0.43	0.62/0.62	0.80/0.80	0.50/0.50	–	0.17/0.17
6TMN	0.49/0.49	0.82/0.82	0.42/0.42	0.66/0.58	0.75/0.75	0.58/0.58	0.17/0.17	–

A.1.2 Ensemble of Conformers

Table A.12: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment T4).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	0.90 /0.84	0.38 /0.38	0.25/0.25	2.56[a]/1.75	1.29 /0.53	0.96 /0.84	1.28 /0.68
1TLP	0.84 /0.84	–	0.56 /0.56	0.70/0.70	2.38[a]/2.38	9.57 /1.54	1.26 /1.26	1.11 /1.11
1TMN	0.52 /0.52	0.70 /0.70	–	0.34/0.34	1.73 /1.35	1.32 /0.54	0.38 /0.38	1.41 /0.57
3TMN	0.93 /0.93	4.56[b]/1.21	3.55[c]/0.77	–	7.16 /2.06	4.81[d]/4.81	2.72[d]/2.72	8.91 /7.27*
5TLN	2.73[f]/1.29	7.81 /1.00	0.57 /0.57	6.14/5.87*	–	8.03 /1.26	6.16[d]/0.97	6.86 /3.25[d]
4TMN	2.41[f]/0.53	0.84 /0.84	0.44 /0.44	5.55/0.97	6.56[g]/0.88	–	0.50 /0.50	2.54[d]/0.66
5TMN	2.03[f]/0.82	0.79 /0.79	1.47 /0.59	5.47/0.41	1.01 /1.01	4.69[d]/0.60	–	0.47 /0.47
6TMN	2.19[f]/0.59	0.80 /0.80	0.50 /0.50	5.70/0.62	2.75 /1.09	1.35 /0.62	0.43 /0.43	–

* Miss-alignment.
[a] Large rms is due to wrong orientation of the terminating imino-hydroxyl moiety.
[b] Large rms is due to wrong orientation of the terminating hydroxyl-ring moiety.
[c] Large rms is due to wrong orientation of the terminating aromatic ring moiety.
[d] Large rms is due to wrong orientation of benzyloxycarbonyl moiety.
[f] Large rms is due to wrong orientation of indole moiety.
[g] Wrong, but interesting "alternative" alignment.

Table A.13: Rms distances (in Å) of atom alignment with atom-based initial transformations (experiment T5).

	1THL	1TLP	1TMN	3TMN	5TLN	4TMN	5TMN	6TMN
1THL	–	4.19/0.77	0.36/0.36	0.32/0.32	5.22/4.68	1.22/0.57	0.92/0.92	0.92/0.92
1TLP	1.09/1.09	–	2.85/0.68	1.72/0.93	5.17/1.45	1.48/0.88	0.94/0.94	4.07/0.97
1TMN	0.59/0.59	0.70/0.70	–	0.37/0.37	1.55/1.55	1.29/0.58	0.55/0.55	0.73/0.73
3TMN	4.85/0.94	1.28/0.81	4.32/2.41	–	4.46/4.41*	7.34/7.31*	7.06/0.68	3.34/0.92
5TLN	6.77/3.55*	6.59/1.11	3.14/2.27	5.80/2.15	–	9.91/4.22*	3.81/1.57	5.17/3.74*
4TMN	2.98/0.56	0.86/0.86	0.46/0.46	8.00/1.92	6.76/6.36*	–	0.50/0.50	0.58/0.58
5TMN	2.24/1.19	1.20/0.77	2.74/0.52	1.79/0.62	1.38/1.17	4.52/0.79	–	0.44/0.44
6TMN	1.69/1.11	0.83/0.83	0.51/0.51	0.67/0.67	1.36/1.32	4.69/0.85	0.34/0.34	–

* Miss-alignment.

A.2 HIV-1 Protease Inhibitors

A.2.1 Experimental Conformers

Table A.14: Experiment H1 and H3: Number of initial transformations.

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	6888	2866	6222	7727	7801	5610
IDV	6888	–	1995	4441	5078	5358	3708
APV	2866	1995	–	2008	2317	2345	1659
NFV	6222	4441	2008	–	4212	4630	3554
RTV	7727	5078	2317	4212	–	6003	4386
LPV	7801	5358	2345	4630	6003	–	4558
TPV	5610	3708	1659	3554	4386	4558	–

Table A.15: Experiment H2a-d: Number of initial transformations.

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	2801	2451	2496	5455	4904	2923
IDV	2801	–	1137	1355	2600	2009	1015
APV	2451	1137	–	1219	2166	2005	1093
NFV	2496	1355	1219	–	2308	2117	1413
RTV	5455	2600	2166	2308	–	4099	2940
LPV	4904	2009	2005	2117	4099	–	2587
TPV	2923	1015	1093	1413	2940	2587	–

Table A.16: Experiment H2e: Number of initial transformations.

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	5249	4716	4766	10124	8721	5434
IDV	5249	–	2268	2517	4848	3884	2055
APV	4716	2268	–	2198	4147	3864	2098
NFV	4766	2517	2198	–	4430	3930	2518
RTV	10124	4848	4147	4430	–	7882	5430
LPV	8721	3884	3864	3930	7882	–	4737
TPV	5434	2055	2098	2518	5430	4737	–

Table A.17: Rms distances (in Å) of surface alignment with atom-based initial transformations (experiment H1a).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	0.75/0.72	0.72/0.31	0.50/0.49	1.42/0.45	0.86/0.45	0.91/0.28
IDV	0.80/0.80	–	0.63/0.63	0.52/0.45	0.68/0.68	0.69/0.53	0.91/0.74
APV	0.57/0.57	0.85/0.70	–	0.85/0.52	0.68/0.58	0.35/0.35	1.51/0.97
NFV	0.55/0.55	0.51/0.39	0.89/0.48	–	1.09/0.62	0.57/0.57	0.46/0.46
RTV	1.18/0.59	0.56/0.56	0.75/0.52	1.21/0.63	–	0.85/0.85	0.74/0.74
LPV	1.02/0.68	0.71/0.56	0.35/0.35	0.55/0.42	0.93/0.93	–	1.17/0.45
TPV	0.60/0.52	0.74/0.74	1.13/0.94	0.47/0.47	0.71/0.71	1.24/0.37	–

Table A.18: Rms distances (in Å) of surface alignment with atom-based initial transformations (experiment H1b).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	1.09/0.84	0.55/0.54	0.39/0.36	1.36/0.46	1.11/0.16	2.53/2.53
IDV	0.85/0.85	–	0.70/0.47	0.87/0.32	1.32/0.71	0.60/0.58	5.22/0.77
APV	1.39/0.77	0.90/0.52	–	0.95/0.61	0.92/0.43	0.71/0.33	5.16/1.15
NFV	1.02/0.75	0.80/0.32	0.94/0.61	–	1.56/0.68	0.71/0.62	1.00/1.00
RTV	1.32/0.87	1.23/0.68	0.83/0.40	1.66/0.58	–	1.22/0.62	5.22/0.76
LPV	1.17/0.36	0.64/0.60	0.65/0.31	0.66/0.41	1.34/0.57	–	0.86/0.86
TPV	6.11/2.38	6.60/0.66	5.45/1.00	0.93/0.49	6.72/0.72	0.91/0.91	–

Table A.19: Rms distances (in Å) of surface alignment with atom-based initial transformations (experiment H1c).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	1.65/0.78	0.72/0.72	0.62/0.62	0.60/0.60	2.14/0.83	1.23/0.98
IDV	1.70/0.83	–	1.47/1.08	1.19/0.65	0.61/0.61	1.26/0.59	3.13/1.63
APV	1.25/0.63	1.78/1.25	–	1.13/0.25	1.15/1.02	2.11/0.98	3.02/1.65
NFV	0.72/0.72	1.36/0.65	1.18/0.40	–	1.46/1.40	2.20/1.24	1.76/1.10
RTV	0.63/0.49	0.53/0.53	1.16/1.03	1.43/1.37	–	1.03/1.03	1.56/1.12
LPV	2.25/0.70	1.23/0.65	1.86/0.56	1.93/0.85	1.05/1.05	–	2.42/2.07
TPV	1.15/1.15	3.25/1.45	3.01/1.56	1.59/1.05	1.85/1.08	2.40/2.00	–

Table A.20: Rms distances (in Å) of surface alignment with atom-based initial transformations (experiment H1d).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	1.65/0.78	0.72/0.72	0.62/0.62	0.60/0.60	2.14/0.83	1.23/0.98
IDV	1.70/0.83	–	1.47/1.08	1.19/0.65	0.61/0.61	1.26/0.59	3.13/1.63
APV	1.25/0.63	1.78/1.25	–	1.13/0.25	1.15/1.02	2.11/0.98	3.02/1.65
NFV	0.72/0.72	1.36/0.65	1.18/0.40	–	1.46/1.40	2.20/1.24	1.76/1.10
RTV	0.63/0.49	0.53/0.53	1.16/1.03	1.43/1.37	–	1.03/1.03	1.56/1.12
LPV	2.25/0.70	1.23/0.65	1.86/0.56	1.93/0.85	1.05/1.05	–	2.42/2.07
TPV	1.15/1.15	3.25/1.45	3.01/1.56	1.59/1.05	1.85/1.08	2.40/2.00	–

Table A.21: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment H2a).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	0.90/0.90	1.33/0.56	0.97/0.72	1.94/1.01	1.31/0.88	6.38/0.67
IDV	1.47/0.52	–	0.74/0.74	0.59/0.59	1.00/0.89	0.84/0.83	1.28/1.28
APV	0.87/0.87	1.85/0.49	–	1.55/1.08	0.73/0.66	0.35/0.35	10.92/1.18
NFV	1.02/0.63	0.50/0.50	1.71/0.46	–	1.27/1.12	1.28/0.62	0.89/0.89
RTV	1.54/0.82	1.09/0.78	1.59/1.11	1.17/1.17	–	1.09/1.09	0.93/0.93
LPV	0.85/0.57	0.76/0.76	0.76/0.62	1.17/0.56	1.12/1.12	–	0.93/0.88
TPV	8.40/0.73	1.20/1.09	11.05/1.17	0.78/0.78	0.88/0.88	0.68/0.68	–

Table A.22: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment H2b).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	1.28/0.76	1.18/0.64	0.52/0.52	1.61/1.09	0.55/0.50	5.26/2.39
IDV	1.31/0.76	–	0.70/0.55	0.89/0.44	0.96/0.58	0.60/0.60	5.11/0.70
APV	1.12/0.80	0.90/0.58	–	1.25/0.62	1.26/0.49	0.62/0.73	5.18/0.90
NFV	0.64/0.62	0.82/0.41	1.24/0.66	–	1.59/0.82	0.69/0.51	1.00/0.96
RTV	1.31/0.56	0.94/0.60	1.09/0.43	1.69/0.71	–	1.27/0.58	5.24/0.93
LPV	0.56/0.46	0.64/0.64	0.65/0.74	0.49/0.64	1.35/0.55	–	0.87/0.87
TPV	6.01/2.84	6.56/0.69	5.33/0.97	0.94/0.94	6.70/0.84	0.95/0.95	–

Table A.23: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment H2c).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	1.47/0.68	0.74/0.74	0.62/0.62	1.95/0.51	2.21/0.79	1.65/0.94
IDV	2.48/1.01	–	1.14/1.43	1.07/1.07	0.70/0.70	1.31/0.78	5.90/2.10
APV	0.65/0.65	1.72/1.72	–	1.25/0.64	1.02/1.02	2.00/0.50	5.87/1.45
NFV	0.63/0.63	1.23/1.10	1.30/0.66	–	3.06/0.59	2.29/0.82	1.86/1.08
RTV	1.76/0.64	0.63/0.63	1.02/1.02	2.43/0.50	–	1.01/1.01	1.59/1.46
LPV	1.92/0.92	1.15/0.78	1.79/0.44	2.01/0.91	1.05/1.05	–	2.13/1.18
TPV	1.40/0.59	5.07/0.98	4.96/1.08	1.58/1.58	1.95/1.01	2.12/1.06	–

Table A.24: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment H2d).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	0.66/0.66	0.83/0.82	0.76/0.76	1.46/0.60	0.73/0.73	3.67/1.26
IDV	0.75/0.75	–	0.82/0.82	0.59/0.59	0.99/0.89	0.82/0.82	1.18/1.04
APV	1.00/0.72	0.86/0.86	–	1.68/0.65	1.17/1.17	0.73/0.28	5.26/1.26
NFV	0.75/0.75	0.50/0.50	1.56/0.60	–	0.98/0.26	1.28/0.86	2.09/0.89
RTV	1.48/0.63	1.07/0.78	1.29/1.29	1.18/0.92	–	1.09/1.09	2.04/1.80
LPV	0.85/0.84	0.78/0.78	0.76/0.28	1.17/0.85	1.12/1.12	–	0.44/0.44
TPV	3.87/1.22	1.07/0.98	5.57/1.09	2.15/0.78	1.97/1.97	0.42/0.42	–

Table A.25: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment H2e).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	0.84/0.84	0.69/0.56	0.66/0.66	1.16/0.63	0.73/0.73	0.68/0.60
IDV	1.02/1.02	–	0.67/0.63	0.66/0.66	0.65/0.65	0.68/0.61	1.02/0.77
APV	0.74/0.74	0.78/0.64	–	0.91/0.56	0.84/0.49	1.57/0.30	1.40/1.18
NFV	0.73/0.73	0.63/0.63	0.92/0.76	–	1.26/0.36	0.79/0.62	0.80/0.80
RTV	1.22/0.42	0.55/0.55	0.89/0.46	1.17/0.37	–	0.99/0.40	1.53/0.86
LPV	0.71/0.71	0.74/0.60	1.35/0.30	0.76/0.60	1.01/0.35	–	1.86/0.97
TPV	0.44/0.44	0.80/0.80	0.98/0.98	0.71/0.71	1.89/0.79	1.93/0.74	–

Table A.26: Rms distances (in Å) of atom alignment with atom-based initial transformations (experiment H3).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	0.88/0.80	0.79/0.25	0.57/0.57	1.35/0.58	0.85/0.58	6.59/0.86
IDV	0.91/0.79	–	0.81/0.65	0.58/0.58	1.14/0.80	0.79/0.64	6.51/0.93
APV	0.95/0.26	0.81/0.63	–	0.33/0.33	0.97/0.97	0.55/0.44	9.41/3.34
NFV	0.76/0.51	0.64/0.64	0.32/0.32	–	1.25/0.90	0.72/0.72	6.50/0.73
RTV	1.28/0.74	1.16/0.84	1.02/1.02	1.39/0.80	–	0.98/0.98	5.29/0.99
LPV	0.81/0.68	0.75/0.67	0.57/0.50	0.68/0.68	1.00/0.94	–	4.94/2.77
TPV	6.78/0.73	8.75/1.10	10.30/3.54	7.69/0.65	5.78/1.02	5.62/2.96	–

A.2.2 Ensemble of Conformers

Table A.27: Rms distances (in Å) of surface alignment with surface-based initial transformations (experiment H4).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	0.78/0.78	1.29/1.06	0.84/0.83	2.86/0.70	1.18/0.62	3.44/0.70
IDV	1.07/1.07	–	1.30/1.21	0.68/0.68	5.93/1.52	0.84/0.84	4.79/0.87
APV	0.81/0.81	1.97/0.55	–	0.93/0.75	5.16/0.92	0.53/0.53	5.38/4.62*
NFV	1.19/0.94	0.42/0.42	1.25/1.22	–	1.09/1.01	0.79/0.56	4.60/1.84[a]
RTV	1.45/1.03	0.61/0.61	1.61/0.98	0.80/0.58	–	1.22/1.22	5.98/1.06
LPV	1.68/1.00	2.78/0.55	1.27/1.12	1.27/0.83	1.14/1.14	–	5.90/1.45
TPV	2.59/2.59**	2.58/2.26**	6.56/1.65	5.85/2.86**	8.18/2.80	2.46/0.63	–

* Miss-alignment.
** Correct general position.
[a] Large rms is due to the wrong orientation of the terminating aromatic ring.

Table A.28: Rms distances (in Å) of atom alignment with atom-based initial transformations (experiment H5).

	SQV	IDV	APV	NFV	RTV	LPV	TPV
SQV	–	0.70/0.70	2.27/0.97	0.66/0.66	1.05/1.05	0.85/0.85	4.66/2.92*
IDV	1.01/1.01	–	4.02/1.67	0.66/0.66	7.64/0.85	0.75/0.75	5.17/4.86*
APV	0.82/0.82	6.93/0.98	–	1.12/0.77	1.24/1.24	0.68/0.56	5.78/3.91*
NFV	0.94/0.94	0.64/0.64	1.68/1.25	–	1.36/1.36	0.94/0.87	4.80/4.11*
RTV	1.41/0.86	1.18/0.77	1.37/1.37	1.38/1.21	–	1.06/1.06	4.92/3.57*
LPV	1.06/1.06	0.65/0.65	1.35/0.95	0.92/0.83	1.28/1.28	–	6.26/3.80*
TPV	6.22/4.56*	6.45/5.19*	6.56/2.65**	5.55/3.02*	6.10/5.30*	6.83/2.53**	–

* Miss-alignment.
** Correct general position.