

## Supporting Information

# Probing the Effect of Conformational Constraint on Phosphorylated Ligand Binding to an SH2 Domain using Polarizable Force Field Simulations

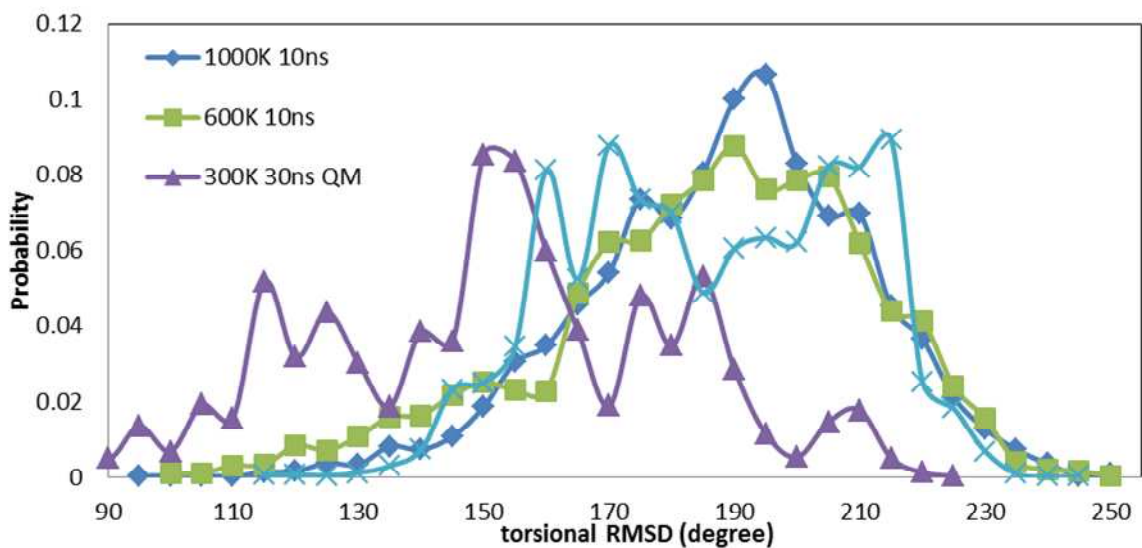
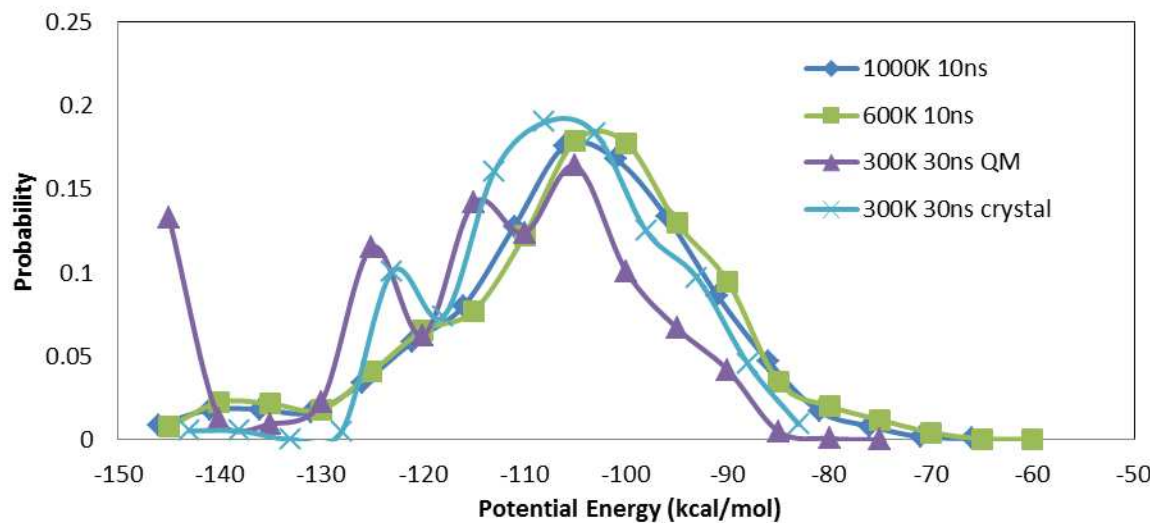
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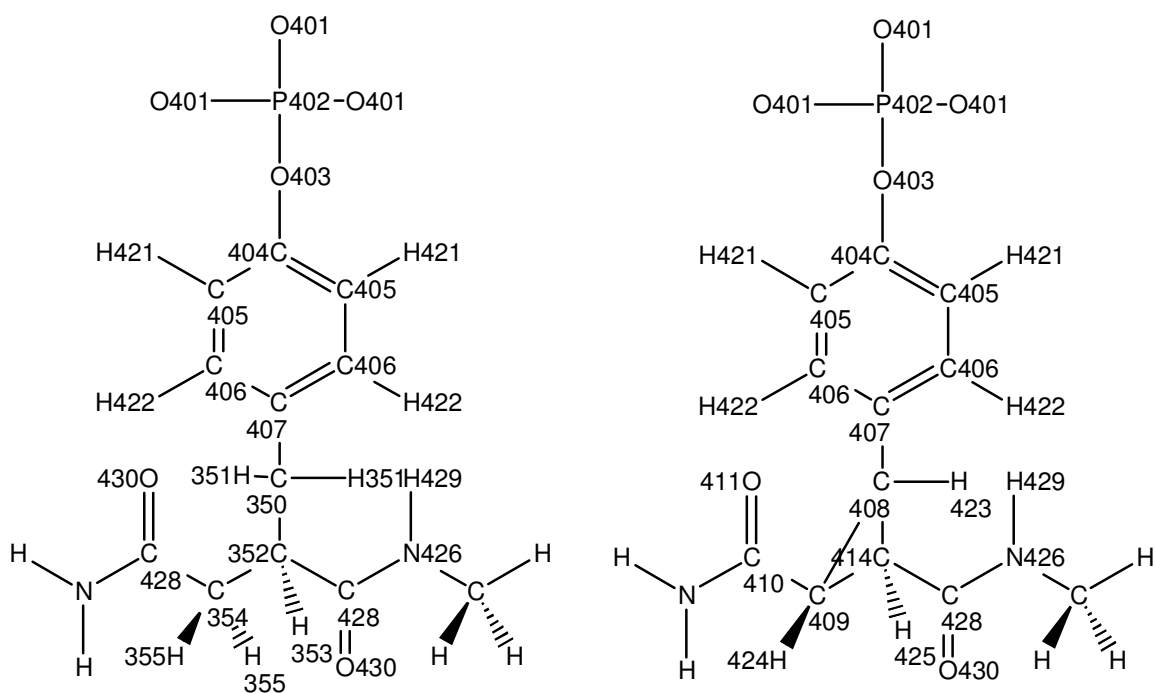
**Temperatures in Replica Exchange Molecular Dynamics Simulations (in K)**

260.00, 265.25, 270.59, 276.01, 281.76, 287.35, 293.03, 298.79, 304.63, 310.54, 316.57,  
322.69, 328.90, 335.21, 341.63, 348.14, 354.75, 361.46, 368.27, 375.18, 382.20, 389.33,  
396.57, 403.92, 411.38, 418.96, 426.66, 434.49, 442.43, 450.50, 458.68, 467.00, 475.45,  
484.03, 492.74, 501.59, 510.58, 519.71, 528.98, 538.39, 547.93, 557.64, 567.50, 577.52,  
587.69, 598.03, 608.03 and 619.03.

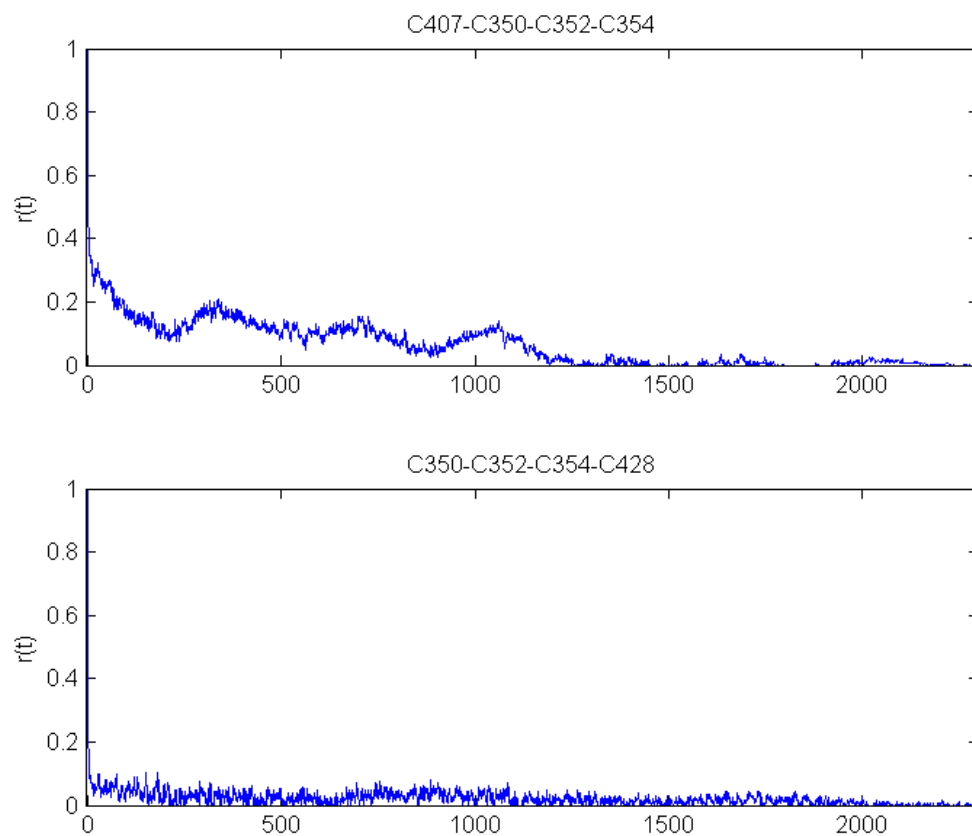


**Figure S1.** Potential energy distributions of configurations sampled at different temperatures (300 K, 600 K and 1000 K) and with different simulation length (10 ns and 30 ns). QM optimized structure and the structure taken from complex crystal structure are as the starting points for repeated simulations. The frames are sampled every 2 ps, and then minimized with a convergence of 0.1 kcal/mol/Å. Thus the conformational distributions we are examining are for 0K, even though the simulations have been done at high temperatures to accelerate the sampling process. The dihedral angles are measured

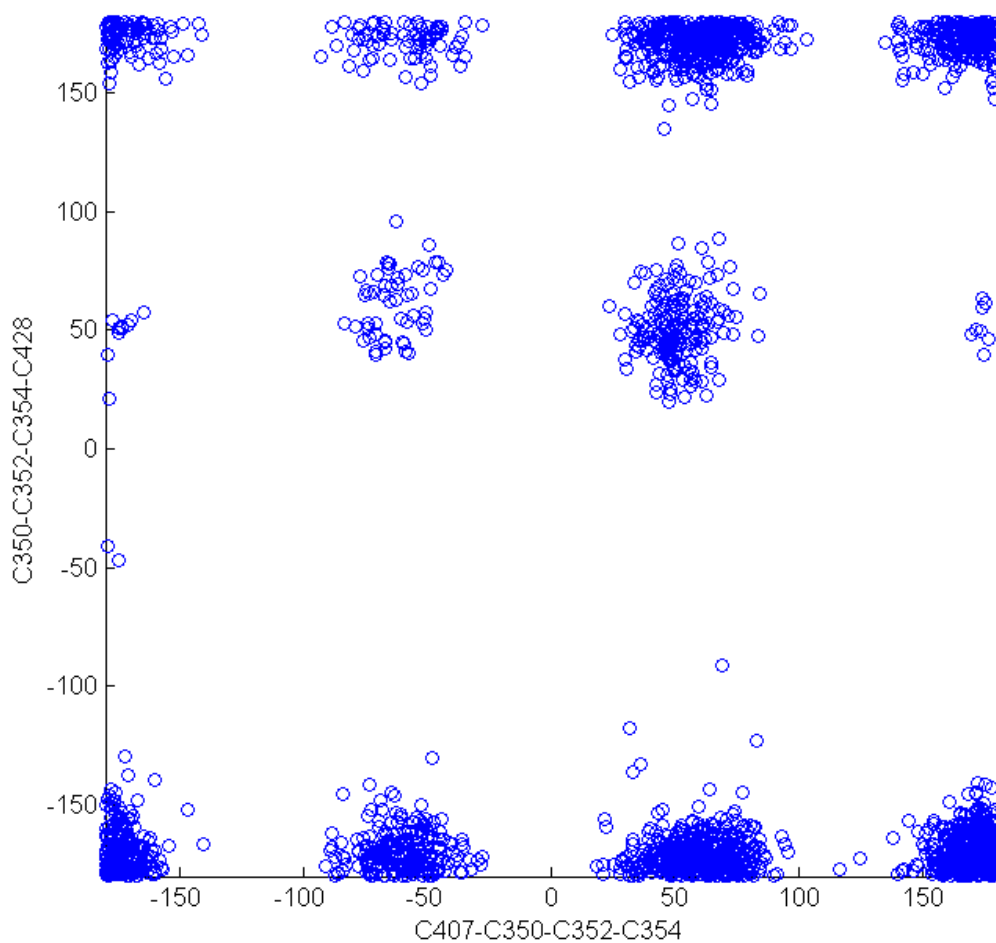
from 0~360 degree (instead of 0~180 degree) in order to capture all the different orientations. The QM optimized structure is selected as the reference to calculate torsional RMSDs for all snapshots.



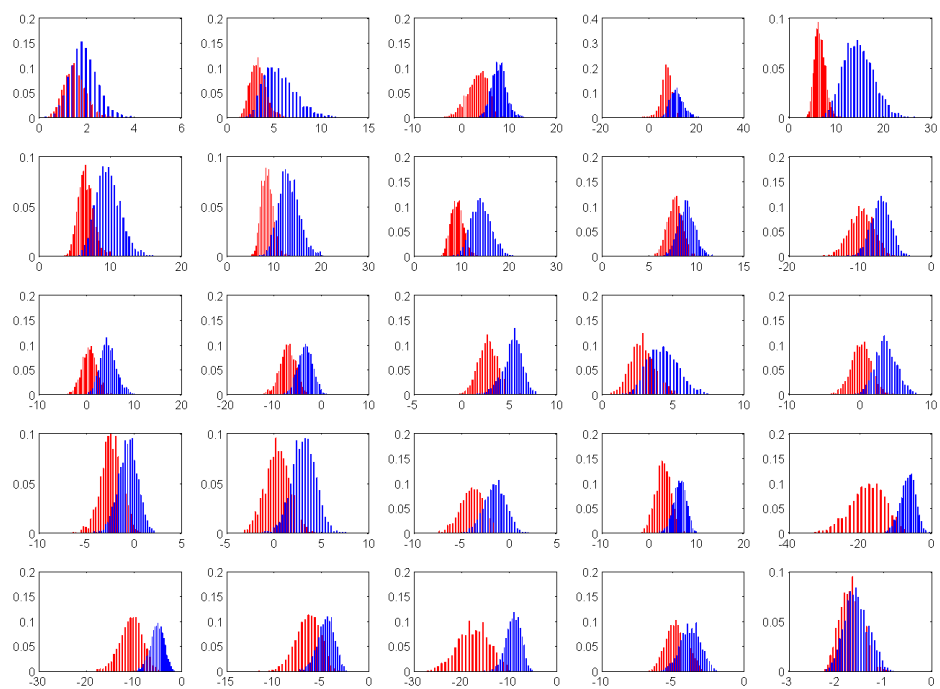
**Figure S2.** Atom types of model compounds used for parameterization. Parameters for C428, O430, N426 and H429 are transferred from AMOEBA PRO.



**Figure S3.** Autocorrelation of dihedral angle C407-C350-C352-C354 and C350-C352-C354-C428 of fpYVN in solvent from REMD simulation at 298 K.

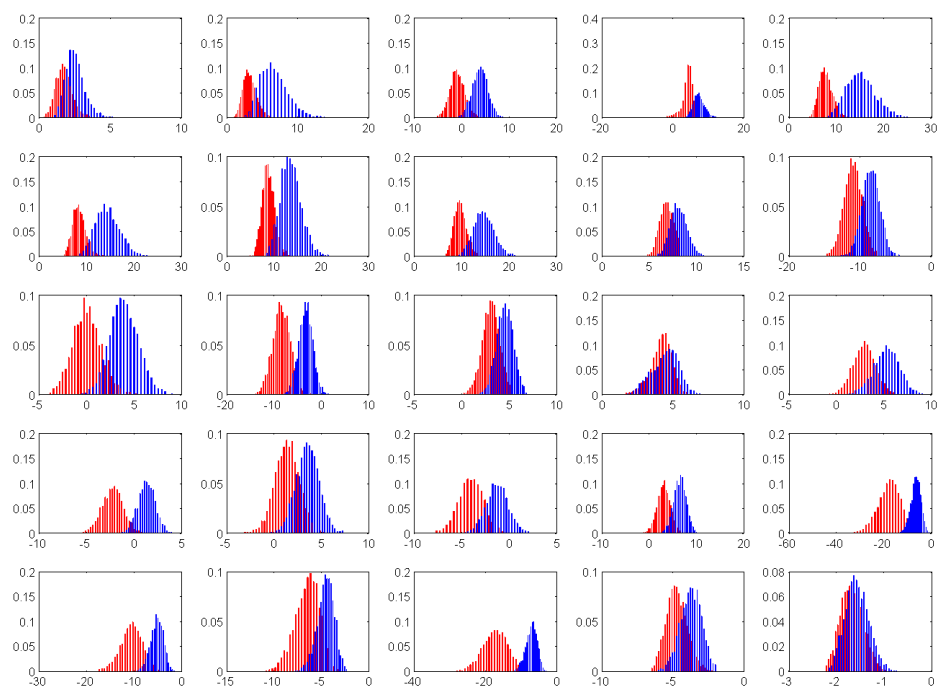


**Figure S4.** Conformational distribution of dihedral angle C407-C350-C352-C354 and C350-C352-C354-C428 of fpYVN in solvent from REMD simulation at 298 K.

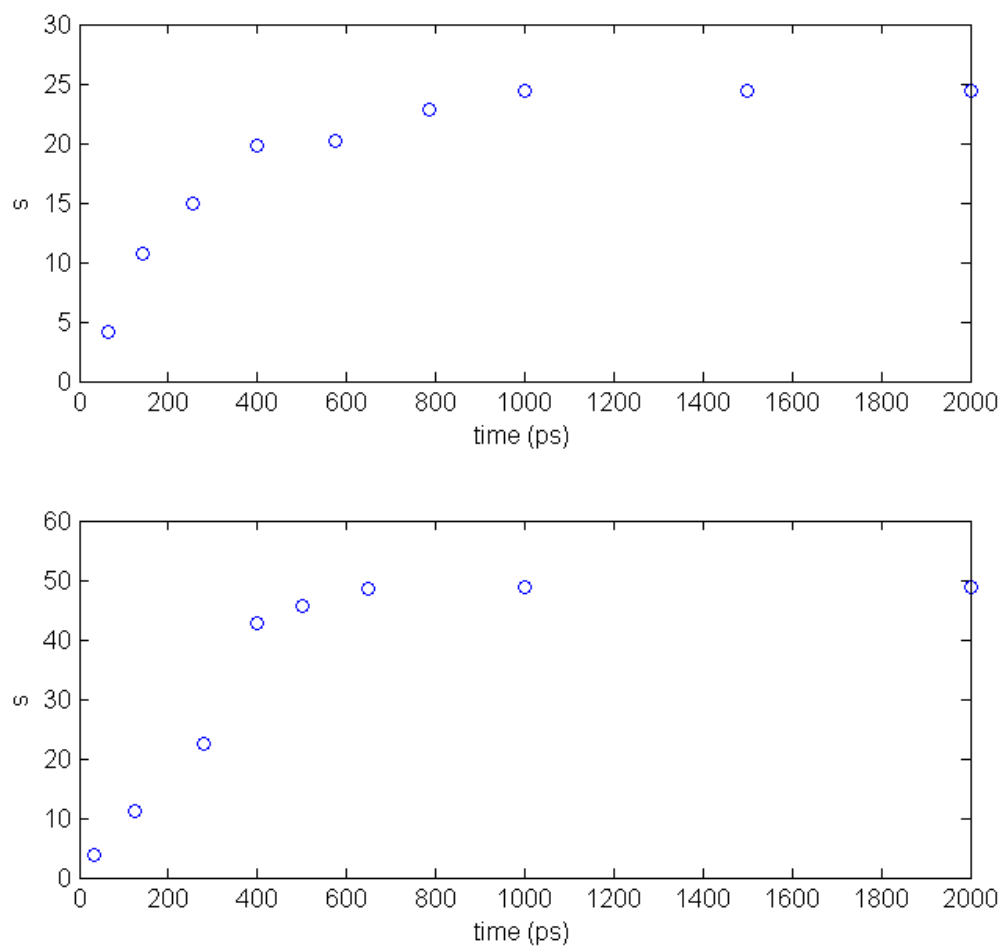


**Figure S5.** Overlap of potential energy differences calculated forward (blue) and backward (red) of perturbation from fpYVN to cpYVN in water. The X-axis represents the potential energy difference, and the Y-axis shows the probability.





**Figure S6.** Overlap of potential energy differences calculated forward (blue) and backward (red) of perturbation from fpYVN to cpYVN in solvated complex. The X-axis represents the potential energy difference, and the Y-axis shows the probability.



**Figure S7.** Statistical inefficiency of the free energy calculations for fpYVN->cpYVN in water (upper panel) and fpYVN in solvated complex (lower panel) at 298K.

#	complex		solvent		$\Delta\Delta G$
	$\Delta G_{complex}$	deviation	$\Delta G_{solvent}$	deviation	
26	24.392	0.000	26.670	0.000	-2.278
25	24.367	-0.025	26.645	-0.025	-2.278
24	24.467	0.075	26.595	-0.070	-2.128
23	24.524	0.132	26.508	-0.162	-1.984
22	24.385	-0.007	26.469	-0.201	-2.084
21	25.428	1.036	27.035	0.365	-1.607
20	24.685	0.293	26.897	0.227	-2.212
13	26.034	1.642	27.032	0.362	-0.998

**Table S1.** The dependence of relative binding free energy (fpYVN->cpYVN) at 298K on the number of intermediate steps in the alchemical calculation (energy in kcal/mol). Every 2<sup>nd</sup> (13 steps total), 4<sup>th</sup> (20 steps), 5<sup>th</sup> (21 steps), 6<sup>th</sup> (22 steps), 7<sup>th</sup> (23 steps), 10<sup>th</sup> (24 steps), 13<sup>th</sup> (23 steps with the middle step skipped) step is skipped respectively.

**Force Field Parameters of the Model Compounds in Figure S2**

#atom #atom type #atom class #atom name #description #atomic number #mass

#connectivity

atom	401	401	O	" O401 "	8	15.999	1
atom	402	402	P	" P402 "	15	30.974	4
atom	403	403	O	" O403 "	8	15.999	2
atom	404	404	C	" C404 "	6	12.011	3
atom	405	404	C	" C405 "	6	12.011	3
atom	406	404	C	" C406 "	6	12.011	3
atom	407	404	C	" C407 "	6	12.011	3
atom	408	405	C	" C408 "	6	12.011	4
atom	409	406	C	" C409 "	6	12.011	4
atom	410	407	C	" C410 "	6	12.011	3
atom	411	408	O	" O411 "	8	15.999	1
atom	414	406	C	" C414 "	6	12.011	4
atom	423	414	H	" H423 "	1	1.008	1
atom	424	415	H	" H424 "	1	1.008	1
atom	425	415	H	" H425 "	1	1.008	1
atom	350	350	C	" C350 "	6	12.011	4
atom	354	354	C	" C354 "	6	12.011	4
atom	352	352	C	" C352 "	6	12.011	4
atom	351	351	H	" H351 "	1	1.008	1
atom	355	355	H	" H355 "	1	1.008	1
atom	353	353	H	" H353 "	1	1.008	1

#vdw #atom cluass #diameter #epsilon #scaling factor for H

vdw	401		3.360	0.1120	
vdw	402		4.450	0.3900	
vdw	403		3.405	0.1120	
vdw	404		3.800	0.0910	
vdw	405		3.820	0.1010	
vdw	406		3.820	0.1010	
vdw	407		3.820	0.1060	
vdw	408		3.300	0.1120	
vdw	414		2.960	0.0240	0.92
vdw	415		2.960	0.0240	0.92
vdw	350		3.820	0.1010	
vdw	354		3.820	0.1010	
vdw	352		3.820	0.1010	
vdw	351		2.960	0.0240	0.92
vdw	355		2.960	0.0240	0.92
vdw	353		2.960	0.0240	0.92

#bond #atom class 1 #atom class 2 #force constant #bond length

bond	401	402	775.0	1.4924
bond	402	403	450.0	1.8897
bond	403	404	465.0	1.2769
bond	404	404	680.0	1.3975

bond	404	405	385.0	1.4997		
bond	405	406	385.0	1.5059		
bond	405	414	400.0	1.0795		
bond	406	407	385.0	1.4955		
bond	406	406	385.0	1.5116		
bond	406	415	400.0	1.0740		
bond	407	408	680.0	1.2059		
bond	350	404	385.0	1.5128		
bond	350	352	385.0	1.5486		
bond	350	351	400.0	1.0864		
bond	354	417	385.0	1.5253		
bond	352	354	385.0	1.5639		
bond	354	355	400.0	1.0826		
bond	352	417	385.0	1.5287		
bond	352	353	400.0	1.0844		
#angle	#atom	class 1	#atom class 2	#atom class 3	#force constant	#equilibrium angle
angle	401	402	401	89.88	117.42	
angle	401	402	403	75.86	99.34	
angle	402	403	404	95.30	122.17	
angle	403	404	404	60.00	121.93	
angle	404	404	404	60.00	119.99	
angle	404	404	413	32.00	119.09	
angle	404	404	405	60.00	121.69	
angle	404	405	406	60.00	122.94	
angle	404	405	414	38.00	116.06	
angle	406	405	406	60.00	60.25	
angle	406	405	414	38.00	111.42	
angle	405	406	407	60.00	123.48	
angle	405	406	406	60.00	59.87	
angle	405	406	415	38.00	115.50	
angle	406	406	407	60.00	119.61	
angle	407	406	415	38.00	113.15	
angle	406	406	415	38.00	115.00	
angle	406	407	408	60.00	121.75	
angle	350	404	404	60.00	120.79	
angle	352	350	404	60.00	110.70	
angle	351	350	404	38.00	111.43	
angle	351	350	352	38.00	108.50	
angle	351	350	351	34.50	106.14	
angle	352	354	417	60.00	111.73	
angle	355	354	417	38.00	108.50	
angle	352	354	355	38.00	110.23	
angle	355	354	355	34.50	107.53	
angle	354	417	419	60.00	119.10	
angle	354	417	416	60.00	117.10	
angle	350	352	354	60.00	114.08	

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angle 350 352 417 60.00 111.41
angle 350 352 353 38.00 107.12
angle 354 352 417 60.00 111.33
angle 353 352 354 38.00 106.83
angle 353 352 417 38.00 105.49
angle 352 417 419 60.00 123.74
angle 352 417 416 60.00 114.38
#stretch bend #atom class #force constant1 #force constant2 #force constant3
strbnd 402 7.20 4.30 0.00
strbnd 403 14.40 0.00 0.00
strbnd 404 38.00 0.00 0.00
strbnd 405 18.70 18.70 0.00
strbnd 406 18.70 18.70 0.00
strbnd 407 18.70 18.70 0.00
strbnd 350 18.70 11.50 0.00
strbnd 354 18.70 11.50 0.00
strbnd 352 18.70 11.50 0.00
#out of plane #atom class 1 #atom class 2 #force constant
opbnd 404 403 1.60
opbnd 404 404 0.80
opbnd 404 405 1.60
opbnd 407 406 0.65
opbnd 407 408 0.65
opbnd 404 350 0.20
opbnd 417 354 0.20
opbnd 417 419 0.20
opbnd 417 416 0.20
opbnd 417 352 0.20
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angle #nth fold
torsion 413 404 404 413 0.000 0.0 1 4.070 180.0 2 0.000 0.0 3
torsion 404 404 404 405 -0.610 0.0 1 4.210 180.0 2 0.000 0.0 3
torsion 413 404 404 405 0.000 0.0 1 6.100 180.0 2 0.000 0.0 3
torsion 404 404 405 406 -3.034 0.0 1 1.393 111.0 2 1.590 0.0 3
torsion 404 404 405 414 0.000 0.0 1 0.000 180.0 2 -0.090 0.0 3
torsion 404 405 406 407 0.180 0.0 1 0.170 180.0 2 0.520 0.0 3
torsion 404 405 406 406 0.180 0.0 1 0.170 180.0 2 0.520 0.0 3
torsion 404 405 406 415 0.000 0.0 1 0.000 180.0 2 0.340 0.0 3
torsion 406 405 406 407 0.180 0.0 1 0.170 180.0 2 0.520 0.0 3
torsion 406 405 406 415 0.000 0.0 1 0.000 180.0 2 0.340 0.0 3
torsion 414 405 406 407 0.000 0.0 1 0.000 180.0 2 0.340 0.0 3
torsion 414 405 406 406 0.000 0.0 1 0.000 180.0 2 0.340 0.0 3
torsion 414 405 406 415 0.000 0.0 1 0.000 180.0 2 0.300 0.0 3
torsion 405 406 406 407 0.180 0.0 1 0.170 180.0 2 0.520 0.0 3
torsion 405 406 406 415 0.000 0.0 1 0.000 180.0 2 0.340 0.0 3
torsion 407 406 406 405 0.180 0.0 1 0.170 180.0 2 0.520 0.0 3

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torsion	415	406	406	415	0.000	0.0	1	0.000	180.0	2	0.300	0.0	3
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torsion	406	406	407	408	0.000	0.0	1	0.000	180.0	2	0.000	0.0	3
torsion	406	406	407	409	0.000	0.0	1	0.000	180.0	2	0.000	0.0	3
torsion	415	406	407	408	-3.300	0.0	1	2.510	180.0	2	1.180	0.0	3
torsion	415	406	407	409	0.000	0.0	1	0.000	180.0	2	0.800	0.0	3
torsion	404	404	404	350	-0.610	0.0	1	4.210	180.0	2	0.000	0.0	3
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torsion	351	350	352	354	0.000	0.0	1	0.000	180.0	2	0.500	0.0	3
torsion	351	350	352	417	0.000	0.0	1	0.000	180.0	2	0.180	0.0	3
torsion	351	350	352	353	0.000	0.0	1	0.000	180.0	2	0.299	0.0	3
torsion	352	354	417	419	0.000	0.0	1	0.000	180.0	2	0.000	0.0	3
torsion	352	354	417	416	0.000	0.0	1	0.000	180.0	2	0.000	0.0	3
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torsion	355	354	417	416	0.000	0.0	1	0.000	180.0	2	-0.010	0.0	3
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torsion	353	352	354	417	0.000	0.0	1	0.000	180.0	2	0.500	0.0	3
torsion	350	352	354	355	0.000	0.0	1	0.000	180.0	2	0.500	0.0	3
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torsion	424	416	417	354	-1.000	0.0	1	2.000	180.0	2	2.000	0.0	3
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torsion	350	352	417	419	-3.000	0.0	1	0.000	180.0	2	0.000	0.0	3
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torsion	353	352	417	416	0.000	0.0	1	0.000	180.0	2	0.000	0.0	3
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polarize	401	0.837	402										
polarize	402	1.828	401	403									
polarize	403	0.837	402										
polarize	404	1.334	405										
polarize	405	1.334	404	406	421								

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polarize 406 1.334 405 407 422
polarize 407 1.334 406
polarize 408 1.334 409 414 415 423
polarize 409 1.334 408 414 424
polarize 410 1.334 411 444
polarize 411 0.837 410
polarize 414 1.334 408 409 425
polarize 423 0.496 408
polarize 424 0.496 409
polarize 425 0.496 414
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polarize 354 1.334 355
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polarize 351 0.496 350
polarize 355 0.496 354
polarize 353 0.496 352
#multipole #atom type #local frames #monopole,dipole,quadrupole
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-0.21597
0.00000 -0.20175
0.10909 0.00000 0.41772
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0.02795 0.00000 0.29813
0.12864
0.00000 -0.01112
0.16427 0.00000 -0.11752
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0.15410 0.00000 0.04551
0.08581
0.00000 0.13303
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-0.02058
0.00000 0.15420
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-0.05282
0.00000 -0.39415
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multipole 406 405 -407 0.15385
0.15153 0.00000 0.52078
-0.72529
0.00000 -0.95398

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				-0.01560	0.00000	1.67927
multipole	407	406	-406	-0.14822		
				0.06758	0.00000	-0.44854
				0.49878		
				0.00000	-0.50762	
				-0.84078	0.00000	0.00884
multipole	408	407	409	-0.01053		
				0.25957	0.00000	-0.42521
				0.61143		
				0.00000	-0.42324	
				-0.39716	0.00000	-0.18819
multipole	409	410	408	-0.12452		
				0.26921	0.00000	-0.05962
				-0.34013		
				0.00000	-0.52238	
				-0.54093	0.00000	0.86251
multipole	410	411	444	0.75664		
				0.16992	0.00000	0.40025
				0.37203		
				0.00000	0.26442	
				0.01882	0.00000	-0.63645
multipole	411	410	444	-0.77899		
				-0.04005	0.00000	-0.15258
				-0.24470		
				0.00000	0.13023	
				-0.07153	0.00000	0.11447
multipole	414	415	408	-0.27531		
				0.06593	0.00000	0.02909
				0.11429		
				0.00000	-0.12510	
				-0.60512	0.00000	0.01081
multipole	423	408	407	0.05149		
				-0.01080	0.00000	-0.00337
				0.02311		
				0.00000	-0.13107	
				-0.03020	0.00000	0.10796
multipole	424	409	408	0.08718		
				-0.05374	0.00000	0.08463
				-0.02788		
				0.00000	-0.22397	
				0.11821	0.00000	0.25185
multipole	425	414	408	0.08030		
				-0.12310	0.00000	-0.17009
				-0.13346		
				0.00000	0.23636	
				-0.05699	0.00000	-0.10290

multipole	428	430	354	0.85068		
				-0.01685	0.00000	0.27745
				0.29463		
				0.00000	-0.41598	
				-0.00743	0.00000	0.12135
multipole	428	430	352	0.85068		
				-0.01685	0.00000	0.27745
				0.29463		
				0.00000	-0.41598	
				-0.00743	0.00000	0.12135
multipole	430	428	352	-0.77770		
				-0.01897	0.00000	-0.21786
				-0.61542		
				0.00000	0.33936	
				0.00866	0.00000	0.27606
multipole	430	428	354	-0.77770		
				-0.01897	0.00000	-0.21786
				-0.61542		
				0.00000	0.33936	
				0.00866	0.00000	0.27606
multipole	350	407	352	-0.07300		
				0.54428	0.00000	-0.21148
				0.55213		
				0.00000	-0.40597	
				-0.31298	0.00000	-0.14616
multipole	354	428	352	-0.12505		
				0.35636	0.00000	0.12083
				0.85801		
				0.00000	-0.71012	
				-0.17159	0.00000	-0.14789
multipole	352	428	350	-0.42976		
				0.05048	0.00000	0.10288
				0.24143		
				0.00000	-0.23770	
				-0.12466	0.00000	-0.00373
multipole	351	350	407	0.03751		
				-0.00850	0.00000	-0.09826
				-0.15828		
				0.00000	0.18088	
				-0.03180	0.00000	-0.02260
multipole	355	354	428	0.08131		
				0.03321	0.00000	-0.08398
				0.10608		
				0.00000	0.13680	
				0.09275	0.00000	-0.24288
multipole	353	352	350	0.07719		

-0.02946	0.00000	0.06650
0.06868		
0.00000	0.22176	
-0.26490	0.00000	-0.29044

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