

# SUPPORTING INFORMATION

## Local Protein Structure Refinement via Molecular Dynamics Simulations with locPREFMD

*Michael Feig*<sup>1,2\*</sup>

<sup>1</sup>Department of Biochemistry and Molecular Biology and

<sup>2</sup>Department of Chemistry, Michigan State University,

East Lansing, Michigan 48824, United States

\*Email: feig@msu.edu

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Modified CMAP parameters.

**Table S1:** Bond force field terms that were modified from the standard CHARMM36 force field. Modified values (equilibrium bond distance and/or force constant) are given in bold with the original force field values given in parentheses. CHARMM atom types are given in parentheses below the atom names.

Residue(s)	Atoms	Minimum [ $\text{\AA}$ ]	Force constant [kcal/mol/ $\text{\AA}^2$ ]
PRO	N-C (N-C)	1.329 (1.30)	560.0 (260.0)
ALA/ARG/ASN/ASP/CYS/ GLN/GLU/GLY/HSD/HSE/ HSP/ILE/LYS/MET/PHE/ SER/THR/TRP/TYR/VAL	N-C (NHI-C)	1.329 (1.345)	570.0 (370.0)

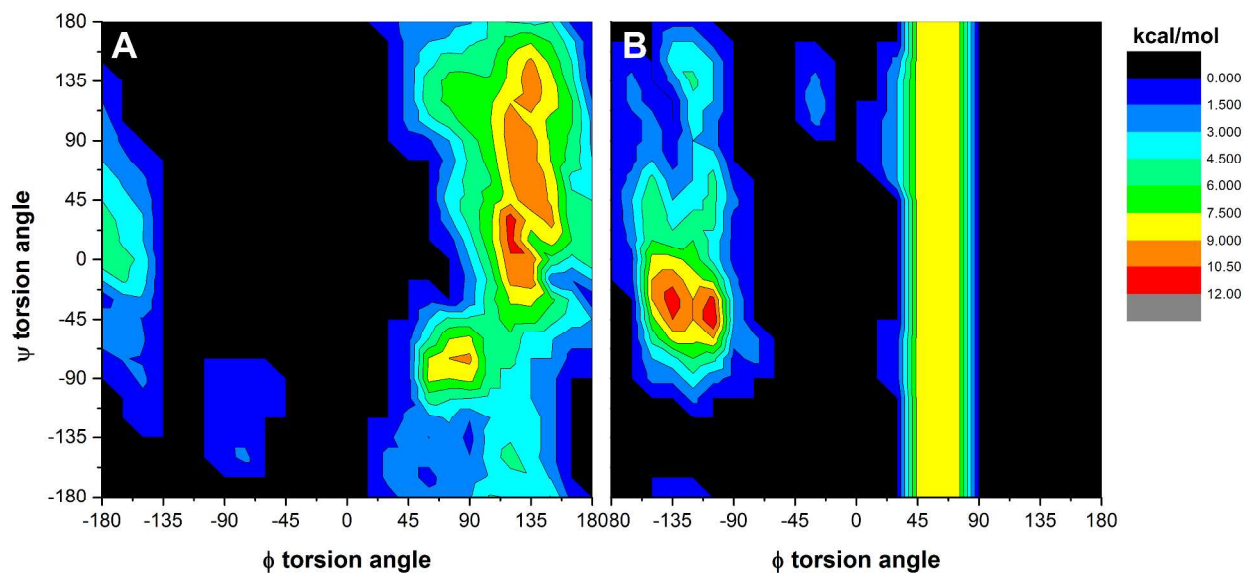
**Table S2:** Angle force field terms that were modified from the standard CHARMM36 force field. Modified values (equilibrium angle and/or force constant) are given in bold with the original force field values given in parentheses. CHARMM atom types are given in parentheses below the atom names.

Residue(s)	Atoms	Minimum [degrees]	Force constant [kcal/mol/degrees <sup>2</sup> ]
PHE/TYR	CA-CB-CG (CT1-CT2-CA)	110.5 (107.5)	151.8 (51.8)
ASN/GLN	CA-CB-CG (CT1-CT2-CC)	110.0 (108.0)	152.0 (52.0)
HSD/HSE/HSP	CA-CB-CG (CT1-CT2-CPH1)	113.0	158.35 (58.35)
ALA/ARG/ASN/ASP/CYS/ GLN/GLU/HSD/HSE/HSP/ ILE/LYS/MET/PHE/SER/ THR/TRP/TYR/VAL	N-C-CA (NH1-C-CT1)	116.5	180.0 (80.0)
ARG/ASN/CYS/GLN/HSD/ HSE/HSP/LYS/MET/PHE/ SER/TRP/TYR	N-CA-CB (NH1-CT1-CT2)	110.5 (113.5)	170.0 (70.0)
HSD	NR2-CPH1-CPH1 (NR1-CPH1-CPH1)	106.0	230.0 (130.0)
HSE	ND1-CG-CD2 (NR2-CPH1-CPH1)	108.0 (110.0)	230.0 (130.0)
HSD/HSE/HSP	NE2-CE1-ND1 (NR2-CPH2-NR1)	110.5 (112.5)	230.0 (130.0)

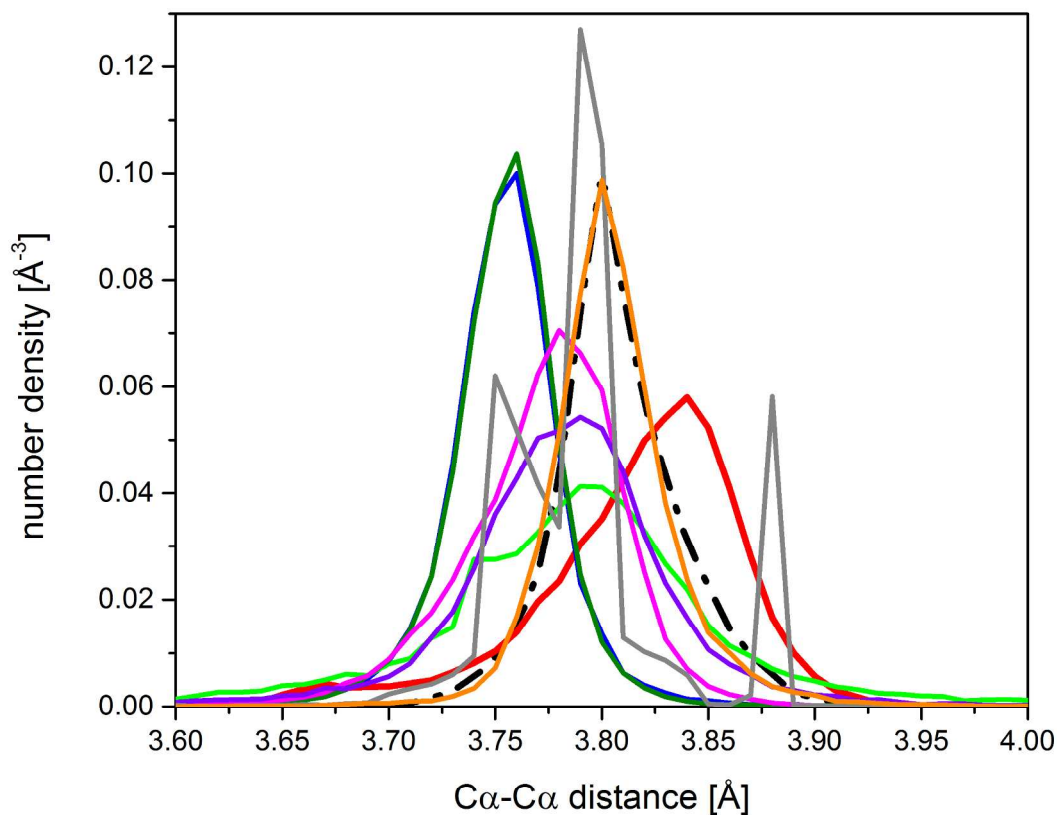
ASP/GLU	N-CA-CB <i>(NH1-CT1-CT2A)</i>	110.5 <i>(113.5)</i>	170.0 <i>(70.0)</i>
ASP	CA-CB-CG <i>(CT1-CT2A-CC)</i>	110.0 <i>(108.0)</i>	152.0 <i>(52.0)</i>

**Table S3:** Additional improper torsion terms to maintain sidechain ring planarity.

Residue(s)	Atoms	Minimum	Force constant [kcal/mol/degrees <sup>2</sup> ]
HIS/HSD/HSE/HSP	CG-CD2-ND1-CB	0	30.0
PHE/TYR	CG-CD1-CD2-CB	0	30.0



**Figure S1:** Difference between the CMAP used here as a function of  $\phi$  and  $\psi$  backbone torsion angles (in degrees) compared to the standard CHARMM force field for non-proline/non-glycine residues (A; left) and proline residues (B; right).



**Figure S2:** Radial distribution of  $C\alpha$ - $C\alpha$  distances in subsequent residues normalized by spherical shell volumes as a function of distance for CASP11 server targets. The distribution from the native PDB structures (black dashed line) is compared with model 1 (TS1) server predictions from Zhang-Server (red), Rosetta (orange), TASSER-VMT (grey), RaptorX (violet), HHPredX (green), MULTICOM-CONSTRUCT (dark green), FFAS-3D (blue), and nns (magenta).

Modified CMAP entry to be used in CHARMM parameter file (also available upon request from the author):

```

CMAP
! alanine map
C   NH1  CT1  C   NH1  CT1  C   NH1  24
! phi = -180.0
  0.126790  0.768700  0.971260  1.250970  2.121010
  2.720430  2.089440  2.789790  2.780870  2.288474
  1.501130  0.900520  0.827670  0.821447  0.913223
  0.891106  0.766446  0.204200  0.204589  0.246991
 -0.835350 -1.222656 -0.951542 -0.036650

! phi = -165.0
 -0.127133  1.377090  1.577020  1.872290  2.398990
  2.486630  3.236754  3.529070  3.886456  3.543400
  2.558676  2.000440  1.009477  0.135306  0.420090
  0.602140  0.599128  0.501241  0.101780 -0.861434
 -0.640168 -0.207701 -1.076344 -1.122030

! phi = -150.0
  0.084069  1.420317  1.624350  2.047200  2.853910
  3.816410  4.221416  3.285454  3.257466  3.863293
  2.525720  1.815886  1.583256  0.006154  0.551995
  0.890683  0.554215  0.027243  0.068512 -0.225016
 -0.765479 -1.283444 -1.293226 -0.816303

! phi = -135.0
  0.927992  1.521370  2.242218  2.546305  3.111384
  2.918410  2.460813  2.187970  2.058314  1.852278
  0.115935 -1.183897 -1.995479 -2.278329 -1.959136
 -1.340467 -0.932949  0.021790  0.313725 -0.517358
 -1.152891 -0.983285 -0.566518 -0.442565

! phi = -120.0
  1.357468  1.959160  2.698894  3.037857  3.698960
  3.558453  2.639296  2.773853  2.719664  1.627997
  0.705667 -0.785637 -2.118268 -2.628489 -1.803113
 -0.425969 -0.062320  0.439040  0.910952 -0.546994
 -0.968118 -0.856791 -0.250116  0.449309

! phi = -105.0
  2.045006  2.544424  2.818030  3.088582  3.370620
  3.551568  3.073520  2.903794  2.956634  2.124759
  0.906487 -0.823628 -2.090819 -2.241579 -1.456524
  0.206160  0.082195  0.771710  1.040241 -0.124647
 -0.316550 -0.164333  0.314474  0.733747

! phi = -90.0
  1.451735  2.748481  3.638185  4.156796  4.450028
  4.344157  3.780200  3.898724  3.335030  2.440579
  0.912671 -0.606502 -1.511772 -1.620864 -0.962798
 -0.020653  0.415153  0.908250  0.459433  0.145910
 -0.071054  0.017622  0.280839  0.748823

! phi = -75.0
  1.378160  3.345958  4.352424  4.063543  4.814070
  4.700796  4.980310  4.212293  3.536425  1.693809
  0.095172 -0.682452 -0.123614 -0.427765 -0.598368
  0.226352  0.423308  0.301999  0.551890  0.191719

```



	-0.253585	-0.190548	-0.253412	0.468922	
! phi = -60.0					
	0.237754	1.229980	1.716960	3.168570	4.208190
	5.391860	5.276080	3.673107	2.272295	-0.482789
	-0.406695	-0.038919	-0.357600	-0.823341	-0.173146
	0.139806	0.267796	0.322420	0.309664	-0.666399
	-0.948631	-1.534365	-1.479968	-0.204264	
! phi = -45.0					
	-1.184837	0.078060	2.347410	4.211350	5.376000
	5.389940	4.380200	2.461506	1.123713	0.107016
	0.007574	-0.149443	-0.797230	-0.582210	0.082910
	0.271580	-0.045570	0.379430	0.247770	-0.890956
	-1.582430	-1.954532	-1.980965	-2.000433	
! phi = -30.0					
	-1.174720	1.067030	4.180460	6.741610	6.070770
	4.806470	2.783340	1.320806	0.765978	-0.008448
	0.276860	-0.707140	1.314360	1.522590	1.915550
	2.223490	0.194290	0.534000	0.331780	-1.595147
	-2.849141	-3.550465	-3.277369	-2.655135	
! phi = -15.0					
	0.293590	5.588070	3.732620	3.217620	3.272450
	2.517320	1.588700	1.381760	0.856410	0.655170
	1.616970	0.846920	0.511070	0.740760	1.021020
	1.616580	-0.342400	0.181770	-0.613920	-2.558037
	-3.786839	-3.807325	-3.155346	-1.749204	
! phi = 0.0					
	2.832310	0.787990	0.323280	0.479230	0.628600
	0.976330	1.238750	1.671950	1.645480	2.520340
	1.606970	0.776350	0.119780	0.070390	0.121170
	-1.569230	-1.213010	-1.846360	-2.744510	-3.792530
	-3.934880	-3.615930	-2.675750	-0.924170	
! phi = 15.0					
	-0.778340	-1.912680	-2.052140	-1.846280	-1.047430
	0.183400	1.682950	2.223500	1.358370	2.448660
	1.436920	0.678570	-0.237060	-0.535320	-0.790380
	-2.182580	-3.251140	-4.195110	-4.269270	-3.908210
	-3.455620	-2.773970	1.755370	0.313410	
! phi = 30.0					
	-2.163810	-1.483730	-1.441809	-1.400349	-1.125083
	0.336200	1.428450	1.394630	0.970370	2.462720
	1.522430	0.553620	-0.407380	-1.482950	-3.613920
	-4.159810	-4.709721	-4.496271	-3.764540	-2.959140
	-1.963850	-1.071260	-1.599580	-2.445320	
! phi = 45.0					
	-1.821496	-1.836549	-1.365327	0.534377	0.984725
	1.362000	1.814380	1.754110	1.502370	1.903420
	0.770220	-0.416420	-3.286310	-3.875270	-4.611550
	-5.287977	-5.146239	-4.038627	-1.865450	-0.368170
	-0.860490	-1.416560	-1.666490	-1.595217	
! phi = 60.0					
	-1.353683	-1.984416	-0.317412	0.240143	2.257890
	5.922610	8.668070	8.038130	6.895330	4.632470
	-1.041450	-3.218100	-3.915080	-4.568574	-5.096776
	-5.526955	-5.005312	-3.777879	-1.540678	0.508820

1.756430	1.640810	0.451845	-0.342810	
! phi = 75.0				
0.248733	0.641080	1.010583	2.539656	3.836063
5.423710	8.017140	9.013120	7.070910	3.692809
-2.305650	-3.420580	-4.484960	-4.807237	-3.001264
-1.787739	-1.740525	-1.619378	-0.685150	1.151360
2.170739	2.725589	1.736732	0.620673	
! phi = 90.0				
1.120840	1.177830	1.128430	1.277730	2.407900
5.303260	8.582510	9.036900	7.086270	3.074070
-0.593220	-1.828560	-2.211800	-2.294328	-1.617221
-0.763953	0.272995	0.911450	1.158306	2.473413
2.099325	2.769822	2.157300	1.651694	
! phi = 105.0				
2.850640	2.092420	3.445020	3.828490	4.005520
4.884820	5.485850	4.818470	4.257670	3.682330
2.514400	0.481110	0.053510	0.165400	0.171130
0.728240	1.912230	1.802110	2.034640	2.715990
2.600554	2.086721	2.274630	2.410940	
! phi = 120.0				
2.469230	2.916650	4.540250	4.150330	4.763520
5.038890	4.758480	5.313530	5.333050	4.872770
4.366270	4.508260	4.124810	4.034830	4.724320
4.700200	4.510620	4.185650	4.361620	4.847490
4.444320	4.004260	4.415720	3.751230	
! phi = 135.0				
2.111250	3.168960	3.322790	4.006920	4.316660
4.086270	3.939170	3.625340	3.166360	4.830310
4.469470	4.946030	4.112560	4.915580	4.047310
4.996740	4.996730	4.842690	4.886620	4.300540
5.094620	5.442210	5.163570	4.183510	
! phi = 150.0				
2.757590	2.403620	2.023920	2.362390	2.634520
3.264920	3.361360	3.948420	3.073680	3.483560
3.152820	3.835120	3.762860	3.093660	3.744830
3.390070	3.783930	3.190630	3.115420	3.042280
4.125570	4.028550	3.026100	2.937910	
! phi = 165.0				
0.210590	-0.071500	0.378890	0.543310	1.277880
1.641310	1.698840	2.519950	2.631950	2.588670
1.436530	0.835240	-0.563830	-0.408350	-0.889450
-0.141750	-0.194970	1.666490	1.843450	2.555000
2.548722	1.746995	1.751289	1.814368	

```

!proline map
C   N   CP1  C   N   CP1   C   NH1 24
! phi = -180.0
  2.973500  3.348200  3.062900  2.113400  1.040500
  0.770600  0.785200  0.263300 -0.479000 -0.583000
 -0.463800 -0.292600  0.000000  0.259100  0.177100
 -0.151200 -0.173500  0.211700  0.348900 -0.135600
 -0.950000 -1.256600 -0.292800  1.560000

! phi = -165.0
  5.674100  6.011400  5.562700  4.467300  3.390800
  3.008800  2.848600  2.311200  1.661400  1.468400
  1.142700  2.437400  3.113200  4.799500  5.589100
  5.869000  5.016100  4.328500  4.232900  3.547600
  3.647200  3.422700  3.517100  4.339800

! phi = -150.0
  6.752800  6.973200  6.444300  5.389800  4.438600
  4.046000  5.832800  6.442400  8.303500 10.010000
 11.838100 12.162200 11.778300 10.362800 10.603600
 10.546200  9.702100  7.837200  6.549500  5.849600
  4.099200  3.031800  4.060200  5.624800

! phi = -135.0
  8.627800  8.153400  7.342500  5.893500  4.799200
  4.433400  6.551500  8.442800 10.222200 11.276300
 12.190000 12.152300 11.932900 10.274900  9.830800
  8.988600  7.588500  6.211000  5.918000  4.292100
  3.495500  5.449800  8.617700  9.311700

! phi = -120.0
  9.115600  8.477200  7.754300  6.585000  5.537900
  6.964300  8.929000 10.421200 10.336100 10.257800
 10.769300 11.359900 12.018000 12.055500 11.217600
  9.726100  8.512200  8.820200  8.716700  8.872300
  8.066800  9.094600  9.284900  9.931500

! phi = -105.0
  9.249700  9.483000  8.668500  7.525300  7.003200
  6.834600  8.822100 10.287600 12.320600 14.640300
 14.464800 12.100300 10.537600 10.885600 10.842000
 10.248700 10.540200 10.652400  9.196700  8.625400
  8.710100  8.581700  9.651500  9.192800

! phi = -90.0
  9.335600  9.208000  8.564600  8.010200  7.885100
  8.212200  9.737100  9.429100  9.306500  9.474200
  9.651300  9.484700  9.195300  9.295000  8.407200
  8.529900  7.242000  6.227500  6.347300  6.449700
  6.404700  6.579300  7.391700  8.570700

! phi = -75.0
 10.955200 11.455400 11.173300 10.428700 10.062400
 10.044500  9.279600  8.965100  7.361500  5.102700
  6.267600  7.871600  8.009800  7.104500  6.616400
  6.733700  7.504000  8.664700  9.282800  8.795900
  7.872500  7.612400  8.498100  9.894000

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! phi = -60.0
  8.422900  8.529200  8.608500  9.306400 10.239400
 11.025900 11.510800  9.283500  7.566000  6.624600
   7.038700  8.222400  8.786400  8.512000  8.103500
   7.988200  8.192900  8.291000  8.055600  7.436800
   6.651800  6.317000  6.802500  7.746300

! phi = -45.0
   6.913200  7.937400  8.610800  9.316600  9.388500
   9.408400  8.828800  7.297900  5.456400  4.742700
   5.793100  7.118800  7.565400  7.598500  7.438700
   7.512500  7.878100  8.082200  7.642700  6.320500
   4.680400  3.830500  4.215800  5.435200

! phi = -30.0
   5.466700  7.116000  8.908800  8.347200  7.413500
   7.047000  6.031600  4.193100  2.674800  3.023700
   4.485300  5.451700  6.214900  6.422600  6.229300
   6.191100  6.488900  6.646400  5.833400  5.751300
   4.719800  3.064900  2.955800  3.860800

! phi = -15.0
   3.061500  5.603800 12.179500  6.295200  5.323400
   4.826500  3.705600  2.461500  2.291600  3.145900
   3.562100  4.443600  5.337500  5.728800  5.694800
   5.641600  5.943300  6.169000  4.759500  2.569400
   1.357100  1.669800  3.212300  5.031900

! phi = 0.0
   8.085900  8.051100  5.023600  3.450800  2.836100
   2.192500  1.566200  1.456300  2.039300  1.945200
   2.188400  2.921300  3.467500  3.543500  3.374500
   3.472300  4.069900  3.615600  2.082200  0.958600
   0.792600  1.494200  2.794900  4.853100

! phi = 15.0
   6.639500  5.177400  3.252300  1.952700  1.078400
   0.888300  1.505400  2.442300  2.178600  1.578600
   1.777400  2.395400  2.820200  2.795200  2.662400
   2.917100  2.562100  2.557900  2.322300  2.631400
   2.051200  2.555600  3.039100  4.915000

! phi = 30.0
   7.548800  5.095500  2.747000  0.955200  0.444500
   1.318700  3.733300  4.223200  3.565500  2.150900
   2.394400  2.939300  3.266000  3.210000  3.113400
   2.491300  3.978300  3.815300  4.522700  5.055600
   5.199900  5.327600  5.474200  7.977800

! phi = 45.0
   8.000000  8.000000  8.000000  8.000000  8.000000
   8.000000  8.000000  8.000000  8.000000  8.000000
   8.000000  8.000000  8.000000  8.000000  8.000000
   8.000000  8.000000  8.000000  8.000000  8.000000
   8.000000  8.000000  8.000000  8.000000

! phi = 60.0
   8.000000  8.000000  8.000000  8.000000  8.000000
   8.000000  8.000000  8.000000  8.000000  8.000000
   8.000000  8.000000  8.000000  8.000000  8.000000
   8.000000  8.000000  8.000000  8.000000

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