

Amber ff15ipq

Torsion Parameter Fitting

ff14ipq

The torsion parameters of the Amber ff14ipq force field were fit by matching the relative molecular mechanical energies of a set of ~62,000 conformations of di-, tri-, and tetrapeptides to their relative quantum mechanical energies calculated at the MP2/cc-pvTZ level.

The fitting set included dipeptide conformations (ACE-XXX-NME), many of which were obtained from the Simmerling group. These included conformations with backbone ϕ and ψ angles corresponding to alpha helix and beta sheet secondary structures, as well as comprehensive sampling of ϕ and ψ at 20° intervals. In addition, conformations sampling the χ_1 and χ_2 side chain dihedrals at 20° intervals were used.

The set also included tripeptide conformations (ACE-{GLY, ALA, SER}-XXX-NME or ACE-XXX-{GLY, ALA, SER}-NME); these sampled the backbone ϕ and ψ at 15° intervals.

Finally the set included tripeptide conformations (ACE-ALA-ALA-ALA-NME and ACE-GLY-GYL-GLY-NME), sampling ϕ and ψ at 10° intervals.

ff15ipq

For ff15ipq, which includes updates to the charges and Lennard-Jones radii, an initial set of torsions has been fit using the same ~62000 conformations used for ff14ipq. To these were added an additional ~1500 conformations of the ACE-ALA-PRO-ALA-NME tetrapeptide obtained from Dave Cerutti.

Refinement of the torsion parameters will be carried out using an iterative cycle: conformations will be generated using version i of the force field, and the quantum mechanical energies of these conformations incorporated into the fitting of version $i+1$. If version i of favors conformations that are unfavorable according to the quantum model, this will be reflected in version $i+1$. Currently my plan is to run ~30000 conformations, split into four iterations:

Iteration 1

- Dipeptides: 23 systems including all side chain protonation states; 250 conformations each, except for CYM and LYN which are new additions to the fitting set and will include 1000 conformations
- Tetrapeptides: ALAALAALA, GLYGLYGLY, and ALAPROALA; 250 conformations each
- Di-dipeptide: CYX-CYX 1000 conformations
- Total: 9000 conformations

Iteration 2

- Tripeptides: 51 systems of form GLYXXX and XXXGLY including all side chain protonation states; 100-125 conformations each
- Tetrapeptides: ALAALAALA, GLYGLYGLY, and ALAPROALA; 250 conformations each
- Di-dipeptide: CYX-CYX, 250 conformations
- Total: 6100-7275 conformations

Iteration 3

- Tripeptides: 51 systems of form ALAXXX and XXXALA including all side chain protonation states; 100-125 conformations each
- Tetrapeptides: ALAALAALA, GLYGLYGLY, and ALAPROALA; 250 conformations each
- Di-dipeptide: CYX-CYX, 250 conformations
- Total: 6100-7275 conformations

Iteration 4

- Tripeptides: 51 systems of form SERXXX and XXXSER including all side chain protonation states; 100-125 conformations each
- Tetrapeptides: ALAALAALA, GLYGLYGLY, and ALAPROALA; 250 conformations each
- Di-dipeptide: CYX-CYX 250 conformations
- Total: 6100-7275 conformations

Progress

A table of the completed and planned calculations follows. ALA, GLY, and SER, which are included in tripeptides and therefore present in a much larger number of systems, are listed separately. Systems that were part of the fitting set of ff14ipq are listed in upper case, while new systems added for ff15ipq are listed in lower case. The first iteration of calculations is underway; systems in italics are planned as part of this iteration, while systems in bold are complete.

RES	SOLO	PRE	POST	PRE/POST	RESTRAINED
ALA	ALAALA ALAALAALA	ALAARG alaash alaasn ALAASP alacym ALACYS alaglh ALAGLN ALAGLU ALAGLY alahid ALAHIE alahip ALAILE ALALEU alalyn ALALYS ALAMET ALAPHE ALAPRO ALASER ALATHR ALATRP ALATYR ALAVAL	ARGALA ashala ASNALA ASPALA cymala cysala glhala GLNALA GLUALA GLYALA hidala hieala hipala ileala leuala lynala lysala metala pheala proala serala thrala trpala tyrala valala	alaproala	
GLY	GLYGLY GLYGLYGLY	GLYALA GLYARG glyash GLYASN GLYASP glycym GLYCYS glyglh GLYGLN GLYGLU glyhid GLYHIE glyhip GLYILE GLYLEU glylyn GLYLYS GLYMET GLYPHE GLYPRO GLYSER GLYTHR GLYTRP GLYTYR GLYVAL	ALAGLY ARGGLY ashgly ASNGLY aspgly cymgly CYSGLY glhgly GLNGLY GLUGLY hidgly HIEGLY hipgly ILEGLY LEUGLY lyngly lysgly metgly phegly PROGLY SERGLY thrgly TRPGLY TYRGLY valgly		
SER	<i>ser</i> serser	SERALA SERARG serash SERASN SERASP sercym sercys serglh SERGLN SERGLU SERGLY serhid SERHIE serhip SERILE SERLEU serlyn serlys SERMET SERPHE SERPRO serthr sertrp SERTYR serval	ALASER ARGSER ashser ASNSER ASPSER cymser CYSSER glhser GLNSER gluser GLYSER hidser hieser hipser ileser leuser lynser lysser metser pheser proser thrser trpser tyrser valser		SER_ALPHA SER_BACKBONE SER_BETA

RES	SOLO	ALA	GLY	SER	RESTRAINED
ARG	ARG	ALAARG ARGALA	GLYARG ARGGLY	SERARG ARGSER	ARG_ALPHA ARG_BACKBONE
ASH	ash	alaash ashala	glyash ashgly	serash ashser	ASH_ALPHA ASH_BACKBONE ASH_BETA
ASN	asn	alaasn ASNALA	GLYASN ASNGLY	SERASN ASNSER	ASN_ALPHA ASN_BACKBONE ASN_BETA
ASP	asp	ALAASP ASPALA	glyasp aspgly	serasp ASPSER	ASP_ALPHA ASP_BACKBONE ASP_BETA
CYM	cym	alacym cymala	glycym cymgly	sercym cymser	
CYS	cys	ALACYS	GLYCYS CYSGLY	sercys CYSSER	CYS_ALPHA CYS_BACKBONE CYS_BETA
CYX	<i>cyxcyx</i>				CYX_ALPHA_CHI CYX_ALPHA_DISULF CYX_CHI CYX_DISULF
GLH	GLH	alaglh glhala	glyglh glhgly	serglh glhser	GLH_ALPHA GLH_BACKBONE
GLN	GLN	ALAGLN GLNALA	GLYGLN glngly	SERGLN GLNSER	GLN_ALPHA GLN_BACKBONE
GLU	<i>GLU</i>	ALAGLU GLUALA	GLYGLU GLUGLY	SERGLU gluser	GLU_ALPHA GLU_BACKBONE
HID	hid	alahid hidala	glyhid hidgly	serhid hidser	HID_ALPHA HID_BACKBONE HID_BETA
HIE	hie	ALAHIE hieala	GLYHIE HIEGLY	SERHIE hieser	HIE_ALPHA HIE_BACKBONE HIE_BETA

HIP	hip	alahip hipala	glyhip hipgly	serhip hipser	HIP_ALPHA HIP_BACKBONE HIP_BETA
ILE	<i>ile</i>	ALAILE ileala	GLYILE ILEGly	SERILE ileser	ILE_ALPHA ILE_BACKBONE ILE_BETA
LEU	<i>leu</i>	ALALEU leuala	GLYLEU LEUGly	SERLEU leuser	LEU_ALPHA LEU_BACKBONE LEU_BETA
LYN	<i>lyn</i>	alalyn lynala	glylyn lyngly	serlyn lynser	
LYS	LYS	ALALYS lysala	GLYLYS lysgly	serlys lysser	LYS_ALPHA LYS_BACKBONE
MET	<i>MET</i>	ALAMET metala	GLYMET metgly	SERMET metser	MET_ALPHA MET_BACKBONE
PHE	<i>phe</i>	ALAPHE pheala	GLYPHE phegly	SERPHE pheser	PHE_BACKBONE
PRO	<i>pro</i>	ALAPRO proala ALAPROALA	GLYPRO PROGLY	SERPRO proser	
THR	<i>thr</i>	ALATHR thrala	GLYTHR thrgly	serthr thrser	THR_ALPHA THR_BACKBONE THR_BETA
TRP	trp	ALATRP trpala	GLYTRP TRPGly	sertrp trpser	TRP_ALPHA TRP_BACKBONE TRP_BETA
TYR	tyr	ALATYR tyrala	GLYTYR TYRGly	SERTYR tyrser	TYR_ALPHA TYR_BACKBONE TYR_BETA
VAL	val	ALAAVAL valala	GLYVAL valgly	serval valser	VAL_ALPHA VAL_BACKBONE VAL_BETA