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Protein Structure Validation and Refinement Using Amide Proton Chemical Shifts Derived from Quantum Mechanics

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Abstract

We present the ProCS method for the rapid and accurate prediction of protein backbone amide proton chemical shifts - sensitive probes of the geometry of key hydrogen bonds that determine protein structure. ProCS is parameterized against quantum mechanical (QM) calculations and reproduces high level QM results obtained for a small protein with an RMSD of 0.25 ppm (r = 0.94). ProCS is interfaced with the PHAISTOS protein simulation program and is used to infer statistical protein ensembles that reflect experimentally measured amide proton chemical shift values. Such chemical shift-based structural refinements, starting from high-resolution X-ray structures of Protein G, ubiquitin, and SMN Tudor Domain, result in average chemical shifts, hydrogen bond geometries, and trans-hydrogen bond (\(\delta_{\text{H}}\)) spin-spin coupling constants that are in excellent agreement with experiment. We show that the structural sensitivity of the QM-based amide proton chemical shift predictions is needed to obtain this agreement. The ProCS method thus offers a powerful new tool for refining the structures of hydrogen bonding networks to high accuracy with many potential applications such as protein flexibility in ligand binding.

Introduction

Chemical shifts hold valuable structural information that is being increasingly used in determining protein structure and dynamics[1]. This is made possible primarily by empirical chemical shift predictors such as SHIFTS, SPARTA, SHIFTX, PROSHIFT, and CamShift [2–7]. While these methods generally offer quite accurate predictions, the predicted chemical shifts of backbone amide protons (\(\delta_{\text{H}}\)) tend to be significantly less accurate than, for example, the proton on the \(\text{\(^{13}\)}\text{C}\) atom [8,9]. This is unfortunate since \(^{13}\text{N}-\text{HSQC}\) forms a large fraction of all protein NMR studies and \(\delta_{\text{H}}\) holds valuable information about the hydrogen bond geometry of the ubiquitous amide-amine hydrogen bonds that are key to protein secondary structure. Parker, Houk and Jensen [10] have proposed a \(\delta_{\text{H}}\)-predictor that was shown to offer significantly more accurate predictions, although this was only demonstrated for 13 \(\delta_{\text{H}}\)-values. The method suggests that there is an exponential dependence of \(\delta_{\text{H}}\) in the NH–O = C bond length (as suggested by Barfield [11] and Cornilescu et al. [12]) as well as a non-negligible contribution from cooperative effects in hydrogen bonding networks. This exponential dependence makes empirical parameterizations of \(\delta_{\text{H}}\)-predictors challenging since even small discrepancies between the structure used in the parameterization (usually an X-ray structure without explicitly represented hydrogens) and the solution-phase structural ensemble that gives rise to the experimentally observed \(\delta_{\text{H}}\)-values can have a significant effect. The method by Parker et al. addresses this problem by parameterization against \(\delta_{\text{H}}\)-values obtained by quantum mechanical (QM) calculations, and is similar in spirit to the QM-based \(\text{\(^{13}\)}\text{C}\)-carbon chemical shift predictor CheShift developed by Vila et al. [13,14]. Both studies noted that the QM-based chemical shift predictors tend to be more sensitive to small structural changes compared to popular empirical chemical shift predictors and therefore promises to be valuable tools in protein structure validation and refinement. Here we present several key advances in the use of backbone amide proton chemical shifts to refine and validate the geometry of the amide-amine hydrogen bonding network in proteins. First we present and validate the ProCS method which extends the QM-based backbone amide proton chemical shift predictor proposed by Parker et al. [10]. Second we present a computational methodology for using ProCS and experimental \(\delta_{\text{H}}\)-values to refine the hydrogen bond-geometries of proteins. This is accomplished by implementing ProCS in the Markov chain Monte Carlo (MCMC) protein simulation framework PHAISTOS [15], and using this in...
combination with a molecular mechanics (MM) force field. Third, we show for a number of small proteins that structural refinement against experimental $\delta_H$ values using ProCS leads to hydrogen bond geometries that are in closer agreement with high-resolution X-ray structures and experimental trans-hydrogen bond spin-spin coupling constants ($^{3}J_{NC}$) compared to using an energy function based on the empirical chemical shift predictor CamShift [7] or solely using a force field (OPLS-AA/L [16] with the GB/SA continuum solvent model [17]).

Results and Discussion

The ProCS method

The ProCS program uses a modified implementation of the formula developed by Parker et al. [10] where the amide proton chemical shift is approximated by a sum of additive terms:

$$\delta_{H} = \delta_{BB} + \Delta\delta_{1-HB} + \Delta\delta_{2-HB} + \Delta\delta_{1-HB} + \Delta{\delta}_{RC}$$

(1)

Here, $\delta_{BB}$ is a backbone term that depends on the $(\phi, \psi)$ torsion angles of the residue, $\Delta\delta_{1-HB}$ is due to a primary hydrogen bond directly to the amide proton in question, $\Delta\delta_{2-HB}$ is due to a secondary hydrogen bond to the carbonyl oxygen in the amide group, $\Delta\delta_{1-HB}$ is a small term that incorporates further polarization due to hydrogen bonding at the primary and/or secondary bonding partner and $\Delta{\delta}_{RC}$ describes magnetic perturbations due to ring currents in nearby aromatic side chains. ProCS calculates amide proton chemical shift values referenced to dimethyl-silapentane-sulfonate (DSS).

We have replaced the original $\delta_{BB}$ term, which was a crude 3-step function, by a scaled version of the $(\phi, \psi)$ backbone torsion angle hypersurface parametrized by Czinki and Császár [18]. The $\delta_{BB}$ term is given as

$$\delta_{BB} = 0.828 \cdot (ICS(\phi, \psi) + 0.77 \text{ ppm})$$

(2)

where $ICS(\phi, \psi)$ is the $n$-th order cosine series given in reference [16]. The scaling is necessary to account for differences in choice of basis set and molecular geometry optimization [19].

In the cases described by Parker et al., $\Delta{\delta}_{RC}$-values are obtained through the SHIFTS web-interface [3]. Since this would be impractical, we implemented the point-dipole [20,21] approximation given by:

$$\Delta{\delta}_{RC} = i \cdot B \cdot \frac{1 - 3 \cos^2(\theta)}{|\vec{r}|^3}$$

(3)

where $i$ is an intensity parameter which depends on the type of aromatic ring, $B$ is a constant of 30.42 ppm Å$^2$, $\vec{r}$ is the vector between the amide proton and the center of the aromatic ring and $\theta$ is the angle between $\vec{r}$ and the normal to the plane of the aromatic ring located on its center. The values of $i$ and $B$ are obtained from the parameter set by Christensen et al. [22].

The following expression for $\Delta\delta_{1-HB}$ was implemented for primary bonds to backbone amide carbonyl oxygen atoms:

$$\Delta\delta_{1-HB} = [4.81 \cos^2(\theta) + \sin^2(\theta)\{3.10 \cos^2(\rho) - 0.84 \cos(\rho) + 1.75\}]e^{-2.0 \text{ Å}^{-1}v_{OH}^{-1}(212.760 \text{ ppm})}$$

(4)

This formula originates from the works of Barfield [11] and is fitted to chemical shifts computed for model systems of hydrogen bonding between two formamide molecules. In order to treat hydrogen bonding to other oxygen atom types (carboxylic acids and alcohols as found in side chains and C-terminal), we carried out similar scans (see Section S2 and Fig. S4 in Supporting Information S1) over bond angles and lengths and stored these in lookup-tables from which the chemical shift perturbation due to any hydrogen bonding geometry can be interpolated. Hydrogen bonding to carboxylic acid oxygen atoms interaction were modeled by N-methyleacetamide/acetate dimers, while bonds to alcohols oxygen atoms were modeled by N-methyleacetamide/methanol dimers.

For non-hydrogen bonding amide protons, which are found primarily on the protein surface, $\Delta\delta_{1-HB}$ is approximated as the interaction between a water molecule and an N-methyleacetamide molecule. In this case, $\Delta\delta_{1-HB}$ is equal to 2.07 ppm for an energy minimized bonding geometry (see Section S3 and Fig. S5 in Supporting Information S1). The functional forms of $\Delta\delta_{1-HB}$ and $\Delta\delta_{1-HB}$ were kept as described in reference [10].

Reproducing QM chemical shifts

ProCS predictions result from several terms (Eq. 1) that are assumed to be additive. To test this additivity assumption we use density functional theory (DFT) and compute chemical shielding values (at the B3LYP/cc-pVTZ/PCM level) for the crystal structure of human parathyroid hormone, residues 1–34 at 0.9 Å resolution, PDB-code 1ET1 [23]. Chemical shift values for amide protons at the termini are excluded from the statistics presented in this section, since they do not participate in any hydrogen bonds in the crystal structure. Using the linear scaling method due to Jain et al. [24] similar DFT calculations reproduce experimental proton chemical shifts of a test set of 80 small to medium sized molecules to an RMSD of 0.13 ppm. [24]

ProCS reproduces the QM calculation with an RMSD of 0.25 ppm (Table 1) based on the same structure. ProCS is parameterized based on a number of DFT calculations (see Methods section) which have been shown to yield proton chemical shifts within 0.16 ppm of experimental values for small organic molecules [19]. Thus, the error from non-additivity is roughly the same as the expected deviation from experiment.

The chemical shifts predicted by empirical methods do not agree well with the DFT results, with RMSD values ranging from 0.56 to 0.70 ppm (see Table 1 and Fig. 1). The DFT chemical shifts span a relatively large range (5.8–9.3 ppm) while the empirically predicted chemical shifts span a very narrow range (up to 6.9–8.9 ppm for SPARTA+ - see Fig. 1). This indicates that the empirical methods are less sensitive to small differences in hydrogen bond geometry found in the X-ray structure.

Reproducing experimental chemical shifts from X-ray structures

The QM method used here reproduces small molecule $^1$H chemical shifts with an RMSD of 0.13 ppm [24]. The RMSD between the chemical shifts calculated by QM using the static X-Ray structure and the experimental data obtained in solution is 0.66 ppm. The main sources of this discrepancy are likely inaccuracies in the hydrogen bond lengths in the X-ray structure compared to solution, since there is an exponential dependence of the proton chemical shifts on this distance (Eq. 4), and/or the use of a single structure rather than a structural ensemble.

The corresponding RMSD to experimental data for ProCS (0.63 ppm) is similar to the QM RMSD and significantly larger than the 0.25 ppm RMSD between QM and ProCS, indicating

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that ProCS is sufficiently accurate to identify inaccuracies in the X-ray structure, and/or the effect of using a single structure rather than a structural ensemble. A similar comparison to experiment for 13 other proteins is given in Table 2 (PDB-codes: 1BRF, 1CEX, 1CY5, 1ET1, 1I27, 1IFC, 1IGD, 1OGW, 1PLC, 1RGE, 1RUV, 3LZT, 5PTI). The deviation from experiment for the empirical methods are significantly smaller than for ProCS with RMSD values ranging from 0.46 to 0.64 ppm (Table 2). A likely explanation for this is that the empirical methods are parameterized using X-ray structures. In order for these methods to produce low RMSD values relative to experiment they need to be insensitive to errors in protein structure.

Refining protein structures based on chemical shifts

If indeed the difference in experimental and computed chemical shifts reports on inaccuracies in the protein structure, then minimizing this difference can be used for structural refinement. To test this hypothesis we generate structural ensembles that minimizes the difference in computed and observed chemical shifts to the specified uncertainty in the chemical shift model and experimental values. We note that the resulting ensemble is not a dynamic ensemble but an ensemble that reflects experimentally measured amide proton chemical shifts. The simulation lengths are roughly equivalent to 6–10 ns of molecular dynamics simulations [25].

Refinement is accomplished using a Markov chain Monte Carlo (MCMC) technique described in detail in the Methods section. In short, the method involves Monte Carlo sampling of structural changes using a posterior distribution constructed using the OPLS-AA/L force field [16] with the GB/SA implicit solvent model [17] (referred to hereafter simply as “OPLS”) and amide proton chemical shifts differences from experiment computed using either CamShift or ProCS. We note that the resulting ensemble is a 1-to-1 correlation.

![Figure 1. Correlation between chemical shift predictions from five different NMR prediction methods and quantum mechanical chemical shifts for human parathyroid hormone, residues 1–37 (PDB code: 1ET1). Blue lines represent a 1-to-1 correlation.](doi:10.1371/journal.pone.0084123.g001)

Table 1. Correlation coefficients and RMSD between five chemical shift predictors, chemical shifts derived from quantum mechanics (B3LYP/cc-pVTZ/PCM) chemical shifts and experimental values.

<table>
<thead>
<tr>
<th>Data source</th>
<th>Exp’tl</th>
<th>Exp’tl</th>
<th>QM</th>
<th>QM</th>
</tr>
</thead>
<tbody>
<tr>
<td>ProCS</td>
<td>0.54</td>
<td>0.63</td>
<td>0.94</td>
<td>0.25</td>
</tr>
<tr>
<td>SHIFTX[5]</td>
<td>0.69</td>
<td>0.37</td>
<td>0.71</td>
<td>0.62</td>
</tr>
<tr>
<td>SPARTA[40]</td>
<td>0.69</td>
<td>0.42</td>
<td>0.68</td>
<td>0.56</td>
</tr>
<tr>
<td>CamShift[7]</td>
<td>0.64</td>
<td>0.32</td>
<td>0.59</td>
<td>0.66</td>
</tr>
</tbody>
</table>

*The crystal structure of human parathyroid hormone, residues 1–34 at 0.9 Å resolution (PDB-code 1ET1[23]) is used as input structure in all chemical shift calculations. doi:10.1371/journal.pone.0084123.t001

Table 2. Reproduction of experimental amide proton chemical shift values based on 13 X-ray structures with a crystallographic resolution of 1.35 Å or less.

<table>
<thead>
<tr>
<th>Method</th>
<th>&lt;(r)&gt;</th>
<th>(RMSD)&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>ProCS</td>
<td>0.58</td>
<td>1.13 ppm</td>
</tr>
<tr>
<td>SHIFTX[5]</td>
<td>0.71c</td>
<td>0.51 ppmc</td>
</tr>
<tr>
<td>SPARTA[40]</td>
<td>0.79</td>
<td>0.40 ppm</td>
</tr>
<tr>
<td>CamShift[7]</td>
<td>0.74</td>
<td>0.46 ppm</td>
</tr>
</tbody>
</table>

<:(r)> denotes the average correlation coefficient over the 13 structure. *(RMSD)> denotes the average root mean square deviation over the 13 structure. *For SHIFTX, three structures displayed over fitting behavior with r ≤ 0.99. These structures are excluded from the average values. doi:10.1371/journal.pone.0084123.t002

Figure 1. Correlation between chemical shift predictions from five different NMR prediction methods and quantum mechanical chemical shifts for human parathyroid hormone, residues 1–37 (PDB code: 1ET1). Blue lines represent a 1-to-1 correlation. doi:10.1371/journal.pone.0084123.g001
Table 3. Statistics for three different types of protein simulations.

<table>
<thead>
<tr>
<th>Structures*</th>
<th>ProCS</th>
<th>CamShift</th>
<th>Bond length</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$^1$H RMSD</td>
<td>$^1$H RMSD</td>
<td>deviation$^b$</td>
</tr>
<tr>
<td>Ubiquitin Ensembles: CamShift + OPLS</td>
<td>0.79 ppm</td>
<td>-</td>
<td>0.03 Å</td>
</tr>
<tr>
<td>Ubiquitin Ensembles: CamShift + OPLS</td>
<td>-</td>
<td>0.50 ppm</td>
<td>0.37 Å</td>
</tr>
<tr>
<td>Ubiquitin Ensembles: OPLS (no chemical shifts)</td>
<td>1.56 ppm</td>
<td>0.60 ppm</td>
<td>0.41 Å</td>
</tr>
<tr>
<td>1UBQ X-ray starting structure</td>
<td>1.22 ppm</td>
<td>0.51 ppm</td>
<td>-</td>
</tr>
<tr>
<td>SMN Tudor Domain Ensembles: ProCS + OPLS</td>
<td>0.93 ppm</td>
<td>-</td>
<td>0.09 Å</td>
</tr>
<tr>
<td>SMN Tudor Domain Ensembles: CamShift + OPLS</td>
<td>-</td>
<td>0.46 ppm</td>
<td>0.17 Å</td>
</tr>
<tr>
<td>SMN Tudor Domain Ensembles: OPLS (no chemical shifts)</td>
<td>1.47 ppm</td>
<td>0.61 ppm</td>
<td>0.22 Å</td>
</tr>
<tr>
<td>1MHN X-ray starting structure</td>
<td>1.09 ppm</td>
<td>0.65 ppm</td>
<td>-</td>
</tr>
<tr>
<td>Protein G Ensembles: ProCS + OPLS</td>
<td>0.69 ppm</td>
<td>-</td>
<td>0.06 Å</td>
</tr>
<tr>
<td>Protein G Ensembles: CamShift + OPLS</td>
<td>-</td>
<td>0.52 ppm</td>
<td>0.38 Å</td>
</tr>
<tr>
<td>Protein G Ensembles: OPLS (no chemical shifts)</td>
<td>1.54 ppm</td>
<td>0.68 ppm</td>
<td>0.37 Å</td>
</tr>
<tr>
<td>1PGB X-ray starting structure</td>
<td>1.21 ppm</td>
<td>0.55 ppm</td>
<td>-</td>
</tr>
</tbody>
</table>

*$^a$The ensembles are obtained from MCMC simulations using either OPLS-AA/L with the GB/SA solvent model (OPLS) force field energy or OPLS energy plus a chemical shift energy term from either ProCS or CamShift. Values are calculated over four runs on each of three protein structures, Ubiquitin, Protein G and SMN Tudor Domain, or their static X-ray structure.

*$^b$The mean bond length deviation denotes the mean absolute difference between the mean hydrogen bond length observed in the sampled structures to the mean hydrogen bond length observed in the corresponding X-ray structure noted below.

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chemical shifts energy term via ProCS to the OPLS force field stabilized the hydrogen bonds and also gave an improvement in the RMSD values to 0.14 Hz, which is close to that of the most accurate structural NMR ensembles of ubiquitin (see Table 4). For Protein G we obtained similar RMSD values: 0.20 Hz, 0.14 Hz and 0.18 Hz for the OPLS alone, OPLS+ProCS and the OPLS+CamShift simulations, respectively. In the SMN Tudor Domain simulation, the average $^{1}J_{NC}$ value of all three types of simulations were comparably close to experimental values 0.24, 0.24 and 0.23 Hz for OPLS alone, OPLS+ProCS and the OPLS+CamShift simulations, respectively. Thus, overall the coupling constants based on the ProCS refined ensembles are indeed in better agreement with experimental values indicating the refinement led to improved hydrogen bond geometries compared to using OPLS or OPLS+CamShift.

Impact on Q-factor

In this section we investigate how amide proton chemical shifts restraints affect back-calculated $^{1}D_{HN}$ residual dipolar couplings (RDCs) compared to experimental values for ubiquitin. RDCs are attractive in this regard since they report on structural features that are not related to hydrogen bonding conformations as studied intensively in the previous sections. The Q-factor is a qualitative measure for the agreement between back-calculated RDCs and the corresponding experimentally observed values [29].

We find, that for our Ubiquitin ensemble generated using the OPLS force field alone has a Q-factor of 0.29 while inclusion of chemical shifts only gives a very modest improvement of this figure to 0.27 for both CamShift and ProCS as chemical shift model. The same value calculated for the three X-ray structures 1UBQ, 1UBI and 1OGW are 0.22, 0.25 and 0.26, respectively. For six NMR-based ensembles the Q-factor is in the range 0.04–0.38, though in some cases the ensembles were refined against the RDCs (see Table 4). We observe no significant correlation ($P < 0.05$) between RMSDs for predicted chemical shifts or spin-spin couplings constant to their experimental values and the calculated Q-factor for the 12 cases presented in Table 4.

While amide proton chemical shifts have some dependence on the dihedral angles of the backbone, the dependence on the particular hydrogen bonding conformations is much larger in comparison. This is due to an exponential dependence on the hydrogen bond length.

The distribution from which we sample chemical shifts is constructed from a prior distribution based on the OPLS force field and a likelihood which contains information from experimental chemical shifts. We expect that structural features of the resulting ensemble, which are not local to the hydrogen bond geometry, will largely reflect the prior distribution, i.e. in this our case, the OPLS force field.

Computational efficiency

Executing the simulations on one core of a Intel Xeon X5560 running at 2.80 GHz with the 1UBQ structure, the average evaluation time of the three different energy-terms were OPLS-AA/L: 27 ms, CamShift 1.35: 4.7 ms, ProCS: 0.74 ms. Similar evaluation times were observed for the 1MHN and 1PGB simulations. Note that, in our implementation, the CamShift term calculates chemical shifts for six atoms per residue, even if those chemical shifts are not used to calculate the corresponding energy term. The OPLS and CamShift terms were implemented with a caching algorithm, so only the subset of parts of the chemical shift terms that change after a local Monte Carlo move were recomputed. This approach was not implemented for ProCS since the OPLS force field energy evaluation is by far the most computationally expensive step. Running on four cores, we obtained between 10 to 16 mio Monte Carlo iteration steps total per day, depending on the protein size and combination of energy terms.

Methods

Monte Carlo refinement of protein structure

We employ Markov chain Monte Carlo sampling from a Bayesian posterior distribution to perform protein structure refinements and simulations. MCMC simulations are attractive because no gradient expressions need to be derived for ProCS. Bayesian inference [30] provides a rigorous mathematical framework for the inference of protein structure from experimental data. It involves the construction of a posterior distribution, which consists of a prior distribution and a likelihood. The former brings in general information on protein structure, and in our case is

![Figure 2. Distribution of average hydrogen bond lengths throughout Monte Carlo simulations on Ubiquitin, Protein G and SMN Tudor Domain.](image-url)
based on the OPLS energy function. The latter brings in the experimental data, and is based on the difference between the back-calculated data from a simulated structure and the experimental data. Using PHAISTOS, we draw samples from the joint probability distribution, which is given by:

\[ p(x_j | \{ \sigma_i \}, I) \propto p(\{ \delta_i^{exp} \}|X, I)p(X|I) \quad (5) \]

where \( X \) represents a protein structure, \( \{ \delta_i^{exp} \} \) is experimental chemical shift data and \( I \) denotes prior information, such as sequence and knowledge about the uncertainties in the prediction model. The prior distribution \( p(X|I) \) is proportional to \( \exp\{-\beta E_{FF}\} \), where \( E_{FF} \) is the molecular mechanics force field potential energy and \( \beta = 1/k_B T \). \( p(\{ \delta_i^{exp} \}|X, I) \) denotes the probability of observing experimental data given a trial structure. Under the assumption that the error in the chemical shift prediction model follows a Gaussian distribution with some set of standard deviations \( \{ \sigma_i \} \), the expression for \( p(\{ \delta_i^{exp} \}|X, I) \) is:

\[ p(\{ \delta_i^{exp} \}|X, \{ \sigma_i \}) = \prod_{i=1}^{n} \left[ \frac{1}{2\pi\sigma_i^2} \exp \left\{ -\frac{(\Delta\delta_i)^2}{2\sigma_i^2} \right\} \right] \quad (6) \]

where \( \Delta\delta_i \) is the discrepancy between predicted and experimental data for the \( i \)-th nucleus of the data set in the trial structure, \( X \). This formulation of the posterior distribution assumes that the prior distribution on \( X \) is also a good prior distribution for the chemical shift differences, \( \Delta\delta_i \), otherwise an additional term would be required[31]. The set of standard deviations, \( \{ \sigma_i \} \) was assigned based on the primary bond type, since, for instance, the model for solvent exposed amide protons is much cruder than the amide-amide bonding model. \( \sigma_i \) was set to 0.3 ppm, for primary bonds to another backbone amide, 0.5 ppm to a side chain amide group, 0.8 ppm to a side chain alcohol or carboxylic acid group and 1.2 ppm for solvent exposed amide protons and other types of bond not included in the prediction model.

**Protein Structures and NMR data**

All protein structures used in this study were downloaded from the RCSB Protein Data Bank[32] (PDB) and protonated using PDB2PQR 1.5, [26,27] with PROPKA[33] to determine protonation states at the pH at which NMR data was recorded. Chemical shift data were obtained from the ReFeDB[34] or the Biological Magnetic Resonance Bank[35], and subsequently re-referenced through Shiftcor[34]. \( b_i J_{NC} \) spin-spin coupling constants for 1PGB, 1UBQ and 1MHN were obtained from references [28], [12] and [36], respectively.

**MCMC simulations**

MCMC simulations were carried out in PHAISTOS v1.0-rc1 (rev. 335) using the Metropolis-Hastings algorithm at 300 K. The simulations are initialized from the experimental crystal structures. Four independent trajectories were simulated for each protein structure. A total of 100 mio MC steps were taken for each trajectory for Protein G and the SMN Tudor Domain simulation.
and 85 mio MC steps for the Ubiquitin simulation. Structures were saved every 10,000 Monte Carlo step. The Monte Carlo move-set was composed of 25% CRISP backbone moves[25] and 75% uniform side chain moves. The force field energy was calculated using the OPLS-AA/L force field [16] with the GB/SA continuum solvent model [17]. The following crystal structures obtained from the PDB were used as starting structures in the simulations: 1PGB (Protein G), 1UBQ (Ubiquitin) and 1MHN

Figure 4. Reproducing experimental $h^3J_{NC}$ spin-spin coupling constants via different structural ensembles and experimental X-ray structures. Squares denote the average coupling constant observed for that hydrogen bond in the ensemble and error bars represent the standard deviation observed throughout the simulations. Crosses represent the spin-spin coupling constants calculated using the static experimental X-ray structure. Results from simulations on ubiquitin is displayed in A, SMN Tudor domain in B and Protein G in C. Left column displays simulations only the OPLS force field energy; second column is from OPLS plus the CamShift energy term; third column is for the simulation with only the OPLS force field energy. In the rightmost column $h^3J_{NC}$ are computed from the corresponding X-ray structure.

doi:10.1371/journal.pone.0084123.g004
Table 4. Statistics for selected ubiquitin ensembles and X-ray structures.a

<table>
<thead>
<tr>
<th>PDB-ID</th>
<th>(CamShift) 1H RMSD</th>
<th>(CamShift) 1H RMSD</th>
<th>(ProCS) RMSD</th>
<th>(ProCS) RMSD</th>
<th>R3JNC</th>
</tr>
</thead>
<tbody>
<tr>
<td>2KOX</td>
<td>0.29</td>
<td>0.84</td>
<td>0.68</td>
<td>0.86</td>
<td>0.12</td>
</tr>
<tr>
<td>2K39</td>
<td>0.34</td>
<td>0.82</td>
<td>0.98</td>
<td>0.77</td>
<td>0.13</td>
</tr>
<tr>
<td>2KNN</td>
<td>0.23</td>
<td>0.91</td>
<td>0.71</td>
<td>0.82</td>
<td>0.12</td>
</tr>
<tr>
<td>2NH2</td>
<td>0.44</td>
<td>0.74</td>
<td>1.35</td>
<td>0.64</td>
<td>0.14</td>
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<td>1XOQ</td>
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<td>0.81</td>
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<td>1D3Z</td>
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<td>0.77</td>
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<td>0.72</td>
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</tr>
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<td>1UBI</td>
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<td>1OGW</td>
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<td>0.84</td>
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<td>OPLS + ProCS</td>
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<td>0.79</td>
<td>0.17</td>
<td>0.98</td>
<td>0.14</td>
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<tr>
<td>OPLS + CamShift</td>
<td>0.32</td>
<td>0.79</td>
<td>0.17</td>
<td>0.98</td>
<td>0.14</td>
</tr>
<tr>
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<td>0.78</td>
<td>1.11</td>
<td>0.78</td>
<td>0.18</td>
</tr>
</tbody>
</table>

aChemical shifts RMSD and r values are calculated for the residues for which R3JNC spin-spin coupling constants have been measured. [12]

bERNS method/CHARMM22 + NOE + RDC [41]
OPLS/AA-L + NOE + RDC [42]
Backrub method/Rosetta all-atom energy + RDC [42]
MUMO method/CHARMM22 + NOE + RDC [43]
DER method/CHARMM22 + NOE + S* [44]
NOE + RDC [45]
X-ray 1.80 Å structure [46]
X-ray 1.80 Å structure [47]
X-ray 1.32 Å structure (synthetic protein with fluoro-LEU at residues 50 and 67) [48]
The methods presented here

(SMN Tudor Domain). Time evolution of Monte Carlo energy and chemical shift RMSDs are available in the Supplementary Information (Section S1, Figures S1–S3 of Supporting Information S1).

Back calculation of spin-spin coupling constants

R3JNC spin-spin coupling constants were calculated using the approximation by Barfield [11].

\[
R_{3JNC}(\theta, \rho, \sigma_{OH}) = \left[ -1.31 \cos^2(\theta) + 0.62 \cos^2(\rho) + 0.92 \cos(\rho) + 0.14 \right] \sin^2(\theta) e^{\frac{\rho}{2} - 1(r_{2OH} - 1.760A)} 1 Hz
\]

Here, the coupling depend on the \( \angle \text{H-O-C} \), \( \rho \), \( \angle \text{H-O=C} \), \( \theta \), and the hydrogen bonding distance, \( r_{2OH} \). From the MCMC ensembles, the mean R3JNC spin-spin coupling constant was calculated via Eqn. 7 and the standard deviation was calculated as the root mean square deviation from the mean. The R3JNC RMSD to experiment is then given as

\[
R_{3JNC} \text{RMSD} = \sqrt{\frac{\sum \left( R_{3JNC}^{\text{exp}} - \langle R_{3JNC} \rangle \right)^2}{N}}
\]

where \( \langle R_{3JNC}^{\text{calc,i}} \rangle \) is the average value over the ensemble for the \( i \)th coupling constant.

QM NMR calculations

All density functional theory (DFT) calculations of NMR isotropic shielding constants involved in the parametrization of ProCS were carried out in Gaussian 03 [37]. Data was obtained at the GIAO/B3LYP/6-311+G(d,p)/B3LYP/6-31+G(d) level of theory using the scaling technique by Rablen et al. [19].

The NMR calculation on the 1ET1 protein structure was carried out at the B3LYP/cc-pVTZ/PCM level of theory with a water-like dielectric constant of 78.3553. In this case shielding constants were converted to chemical shifts using the scaling factor obtained by Jain et al. [24], assuming that the value of the dielectric constant has a negligible contribution to the scaling factors.

Calculation of ubiquitin Residual Dipolar Couplings

Residual dipolar couplings were back-calculated from the structural ensembles using singular value decomposition to fit the alignment tensor [38]. Ensemble averaging was taken into account so that all structures simultaneously were fitted to a single alignment tensor [39]. The agreement to experimental values was calculated via the Q-factor:

\[
Q = \sqrt{\frac{\sum (RDC^{\text{exp}} - RDC^{\text{calc}})^2}{\sum (RDC^{\text{calc}})^2}}\]

Conclusions

ProCS is a QM-based backbone amide proton chemical shift (\( \delta_{HH} \)) predictor that can deliver QM quality chemical shift predictions for a protein structure in a millisecond. \( \delta_{HH} \)-values predicted using X-ray structures are in worse agreement with experiment, compared to those of the popular empirical chemical shift-predictors CamShift, SHIFTS, SHIFTX, and SPARTA+.
However the agreement with experiment can be significantly improved by refining the protein structures using an energy function that includes a force field and a solvation term (OPLS-AA/L with the GB/SA continuum solvent model) and a chemical shift term in the program PHAISTOS. This refinement also results in structures with predicted trans-hydrogen bond coupling constants ($^{3}J_{NC}$) in good agreement with experiment indicating that the refined protein structures reflect the structures in solution. Comparison of average hydrogen bond geometries to those of high-resolution (<1.35 Å) X-ray structures reveals that the structural refinement improves the predicted $\theta_{H}$-values through relatively small changes in the hydrogen bond geometry distribution.

Structural refinement without chemical shifts (i.e. using only the OPLS-AA/L + Generalized Born solvation energy) or combined with CamShift has relatively little effect on the predicted $\theta_{H}$-values, while the predicted $^{3}J_{NC}$ values are in slightly worse agreement with experiment compared to using X-ray structures or ProCS-refined structures. This is not surprising given the fact that CamShift and similar empirical methods were designed to be insensitive to relatively small changes in protein structure in order to offer robust chemical shift predictions based on X-ray structures of varying accuracy. Structural refinement based on other empirical shift predictors, such as SHAFTS, SHIFTX, and SPARTA+, were not tested mainly because an efficient interface to PHAISTOS requires a complete re-implementation of the method. However, based on our comparison to the QM-calculations (Table 1 and Fig. 1) we do not think the conclusions will be substantially different. Our data, and that of Vila et al. [14], suggests that QM-derived chemical shift predictors are sufficiently accurate to extract small changes in structure and dynamics from experimentally measured protein chemical shifts.

We are currently working on implementing a QM-based chemical shift prediction method for the remaining H, C, and N nuclei in a protein in ProCS (unfortunately, the source code of the CheShift method developed by Vila et al. for QM-based C chemical shift prediction is not available). The resulting ProCS/PHAISTOS interface should provide a powerful tool for chemical shift-based protein structure refinement.

The ensembles resulting from the simulations can be downloaded from DOI: http://dx.doi.org/10.5879/BILS/p000001

Implementations of ProCS and CamShift can be downloaded as separate modules for PHAISTOS under the terms of the GNU General Public License v3 from: http://github.com/jensengroup/

**Supporting Information**

Supporting Information S1  Section S1: Time evolution of energies and chemical shift RMSDs during MCMC simulation. Figures S1–S3: Details of Monte Carlo energies and chemical shift RMSDs over time for the presented simulations. Section S2: Parametrization of chemical shift contributions due to hydrogen bonding interactions to carboxylic acids and alcohols. Figure S4: Sketches showing the geometric parameters and the systems used in the modeling of chemical shift contributions due to hydrogen bonding. Section S3: Model for solvent exposed amide protons. Table S1: Chemical shift contributions due to hydrogen bonding to water molecules. Figure S5: Local minima of NMA-water dimer. (PDF)

**Author Contributions**

Conceived and designed the experiments: ASC KLL TH JHJ. Performed the experiments: ASC TEL MB WB. Analyzed the data: ASC TEL JHJ. Wrote the paper: ASC JHJ.

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**References**


