

Physics-based protein structure prediction and design using the confinement method

Arijit Roy, Justin L. MacCallum, Alberto Perez, and Ken A. Dill

Laufer Center for Physical and Quantitative Biology
Stony Brook University
Stony Brook, NY 11794-5252.

October 19, 2012

Abstract

The calculation of free energy differences is of central importance in the simulation of biochemical systems. The computation of the free energy difference between pairs of macromolecule with large conformational change is particularly a difficult task and computationally expensive with existing methods. In this work, an improved version of the confinement approach is used to calculate absolute free energies of bio molecular systems. The method does not require a reaction coordinate or transition path. It is fast to compute. We show that the method correctly picks out the state of lowest free energy of a pair of structures having similar sequence but different fold. We also show using models from CASP9 that the method picks out native-like structures from misfolded or decoys, provided at least one good structure is in the input set.

1 Introduction

In computational structural biology there are numerous cases where free energy between well defined states are necessary. Examples ranges from

small to large conformational change of protein due to ligand binding, change of pH etc^{1, 2, 3}. Free energy also play an important role in case of protein folding. The ground breaking work of Christian B. Anfinsen and coworkers showed that the native structures of small globular proteins have a unique, thermodynamically stable native structure with their conformation at the global free energy minimum⁹. Regardless of the starting point or unfolding it by changing different condition most proteins will finally assume the same structure. It is very important for proteins to achieve their native conformation since defects in protein folding may be the molecular cause of a range of human genetic disorder. For example a misfolded protein known as prion when enters any healthy organism it converts properly folded protein into misfolded one. Thus, Free energy can also act as a scale to identify between the misfolded and the native state of the protein. These observations further give free energy a special importance in structural biology.

However, the theoretical calculation of conformational free energy change become difficult if the states of interest are very different¹. In such scenario timescale involved in such transformation may be beyond timescale of direct classical molecular dynamics simulation. Generally, in order to calculate free energy a pathway or reaction coordinate is created with the intermediate structures. Method like umbrella sampling⁵, thermodynamic integration⁶ along with classical MD can suffer from overlap problem and require large computational effort. The idea of reaction coordinate became more complicated in case of protein folding. As free energy landscape of the protein folding is rough^{7, 8} it can be trapped in a energy well during its visit in the conformational space. Even with the advanced method like replica exchange molecular dynamics the three dimensional structure may be trapped in a local minima for a considerable time. Due to various reasons it can also be misfolded and trapped in a local energy minima. And one can mistakenly identify the misfolded state as the native state (give the example of human pin1ww domain from Benout Roux and Klaus Schultan).

Calculation of free energy has been successfully attempted by a number of groups^{1, 11 - 13}, . In recent years methods like Reference system method¹¹, Decativated Morphing¹², Orthogonal Space Random Work, Confinement Method have came out for calculation of free energy method.

Some of the groups relies on one of the great strength of free energy calculation, that it is a state function and thus it is independent of path.

In this work we have applied the confinement method which was originally devoled by Tyka et. al.¹⁴ and Cecchini et. al.¹⁵. The free energy is a state function and thus it can be independent of path. Confinement method relies on this fact and uses a thermodynamic cycle where first, non-harmonic degrees of freedom are removed by applying a series of restraint to the system. Then the free energy of the remaining harmonic system is obtained using a normal mode calculation and combined with the non-harmonic part to give the total absolute free energy. Previously, this method was applied to calculate the conformational free energy of a 16 amino acid residue peptide, known as BHP. We have first reproduced that known result. Then we have applied this method to larger proteins for the first time. The free energy of conformation of pair of proteins with similar sequence but completely different fold was calculated. Encouraged by the result, we applied the method of different targets of CASP9 competition.

2 Results and Discussion

2.1 The confinement method produces correct results in control experiments

As a first step, we performed several control experiments to verify that our implementation of the confinement method produces results compatible with previous calculations reported in the literature.

The method has previously been applied to a 16 amino acid residue β -hairpin from protein G, known as BHP¹⁵. We calculated the free energy difference between two different conformations of the peptide: (1) the native conformation, called bhp1, with a two-stranded β -sheet; and (2) a conformation, called bhp3, which has a three-stranded β -sheet. Analysis of long (4 μ s) equilibrium simulations^{15, 17} shows that bhp1 is the more favorable configuration by 1.8 kcal/mol. Using the confinement method, we obtain a value 1.7 kcal/mol, which is in good agreement with the equilibrium simulations and with previous calculations using the confinement method¹⁵ (see Supporting Information for further details).

Previous applications of the confinement method have focused on relatively short peptides, up to 17 residues in length. In this work we apply the confinement method to larger proteins. On that direction, We first test the confinement method for a chameleon sequence and found that it can correctly pick out the prefential structure of the chameleon sequence. Another of the applications we explore in the present work is the re-scoring, or metaprediction, of structures submitted during the Critical Assessment of Structure Prediction (CASP) experiment (described in detail later). We computed the relative free energies of predictions submitted during CASP9 10, with the expectation that the most native-like prediction will have the lowest free energy. As a control, for several targets we also calculated the relative free energy of the experimental structure (once it was available from the PDB). As Table 4 shows, in most cases, the confinement method correctly assigns a lower free energy to the experimentally determined structure than to any of the decoys.

[Table 1 about here.]

2.2 The confinement method correctly predicts the structural preferences of chameleon sequences

In general, proteins with similar sequences tend to have similar structures. This idea is the basis of comparative modeling and fold recognition in protein structure prediction. There are, however, examples—often referred to as chameleon sequences—of proteins with similar sequences that have remarkably different structures. Orban and co-workers have designed a series of 56-residue proteins (based on Protein G) that adopt one of two different folds depending on small changes in sequence (see Figure 4). Sequences that adopt a mixed alpha/beta structure similar to Protein G are denoted as “GB”, while sequences that form a three-helix bundle are denoted as “GA”. One pair of sequences (GA88/GB88) are 88 percent identical and differ in seven positions. Another pair (GA95/GA95) are 95 percent identical and differ in three positions. The last pair (GA98/GB98) differ only in a single tyrosine to alanine mutation.

The fact such small changes in sequence can lead to such dramatic changes in structure is rather remarkable. Accurately predicting the structural pref-

erences of these structures presents a serious challenge for computational methods^{18 – 21}.

We initially approached this problem by making a model of each sequence with the same backbone structure as its partner chameleon sequence. For example, we took the sequence of GA88 and built a model with the same overall structure as GB88. We then used the confinement method to assess the free energy difference between the experimentally determined structure of GA88 and the model (with the GA88 sequence and the GB88 structure). The confinement method was able to predict the conformational preferences correctly for all six sequences (data not shown). There is, however, a serious problem with this analysis: we are comparing an experimentally determined structure with a computer generated model. It might be possible that we were able to make correct predictions simply because artefacts of our modeling procedure always lead to the model having a higher free energy than the experimental structure.

To avoid this potential problem, we instead computed the relative free energy two different structural models for each sequence. One model is based on the GA structure and the other on the GB structure (see Supporting Information for details on the modeling procedure). This is a much more realistic test of the confinement method's ability to accurately calculate relative free energies.

The results of these calculations are presented in Figure 4. The confinement method identifies the correct structure for all five sequences. One of the hypothesis for fold switching of chameleon sequence is that the structural transitions require states with diminished stability. It is widely believed that if the free energy of the native state and the alternative state is within a range of -5Kcal/Mol then it can quickly change fold when the stability of the native state decreases. The stability of the native state can decrease for a number reason ranging from chemical modification, breaking of disulphide bond or mutation as in this case. The free energy differences, that came out from our calculation ranges from around 2.9 to 5.7 kcal/mol, which is consistent with the above hypothesis^{19, 20}.

[Figure 1 about here.]

2.3 The confinement method correctly identifies the most native-like predictions from a subset of CASP predictions

Arijit: we need a global table of success, rather than individual tables. The simplest form would have 3 columns: name of the PDB, number of structures tested, percent of success of picking 1st model

This method is particularly well suited to pick out the native/native like structure from misfolded or decoys. We have tested this using different models from CASP (critical assessment of structure prediction). CASP is a blind test world wide competition in which different groups apply their methods to predict the 3D structure of proteins given their sequence. This is done with a strict 3 week limit on each target (3 day for servers) and each group is allowed to submit 5 possible structures (ranked from better to worst). In our role as assessors during the CASP8 and CASP9²³ competition we observed no correlation at all between the ordering of structures submitted by the groups and the real ranking compared to an experimental model²⁴. The consequences of this go beyond those five structures; the deeper meaning is that groups producing ensembles of structures are generating structures that are better than the ones they submit, but they do not know about it. In fact, when querying different groups after the results were known, most groups agree that this is the case. Beyond the CASP problem, this reflects on the modelers ability to correctly rank order models in many different environments, from structures for drug design leads to designing more stable proteins or peptide mimetics such as peptoids. One of the main culprits of this lack of accuracy is the fact that ranking is often done via a potential energy function, which in many cases lacks an entropy component. Other initiatives including knowledge based potentials do use some sort of free energy to rank order, but its accuracy is not enough. Our method provides a physics based solution to this problem. We have tried two experiments centered on CASP. First we tried to rank order some structures from the previous CASP9 experiment. Our second test was to participate as a metapredictor group in CASP10. In both methods, our ranking is determined as a free energy measure, and it is compared with the ranking given by a geometrical comparison between native and submitted models called GDT_TS (Global distance test score²⁵). GDT_TS represent the average percentage of residues that are in close proximity in two structures

optimally superimposed using four different distance cutoffs (1, 2, 4 and 8).

We have chosen the initial models on which to test the methods based on server groups that have traditionally done good in past CASP events. There is a high correlation between the structures that are chosen for this method and its predictive accuracy. In particular, when GDT_TS scores are below 50, it is difficult for us to say anything about the models. Our approach is simple, with every subset of structures we choose, we use the confinement method in a pairwise procedure, and then rank the structures. In all cases, we have calculated the free energy with respect to the native structure either obtained from NMR or x-ray crystallography but we do not need to make comparisons to native in order to do rank ordering.

2.3.1 CASP9

The question that we want to answer here is whether we can distinguish between native structure and the submitted models? First we choose a protein BVU3908 from *Bacteroides vulgatus* whose PDB id and CASP target code are 2L01 and T0559 respectively. The native structure of this 69 residue protein was solved using NMR. The best predictor group for this target was "BAKER-ROSETTASERVER". We initially checked similarity between the models submitted by "BAKER-ROSETTASERVER" and discarded two of them from the analysis on the basis of being too similar to some of the other models. The GDT_TS score and rmsd values as shown in Figure 5 indicate that the model 1 was predicted correctly, whereas the order of model 3 and 5 was wrong. The main difference between the model 3 and the rest of the model is that the orientation of first alpha helix of model 3 is opposite. On the other hand, as shown in Figure 5 confine and release method not only can differentiate the native structure from the submitted models , it can also correctly rank all the models.

To further test the method we have taken the example of protein BT2368 from *Bacteroides thetaiotaomicron*. The PDB id of this 74 amino acid residue protein is 2L02 and CASP target code is T0560. We have compared the free energy difference between the native structure and the two of the five submitted models from the group "Splicer". The remaining three models are discarded as again they are similar to the rest of the models.

The comparison of GDT_TS score as shown in Figure 7 and published in final CASP result is only for models with residues 3 to 66. In order to keep consistency, we have also do our analysis with models and crystal structure consisting residues 3 to 66. As expected, the native state is identified correctly, and the two other models is ranked in the correct order.

Our next test was between models from the best submissions of different groups. For this purpose we have chosen the x-ray crystallographic structure of fas apoptosis inhibitory protein molecule whose pdb id and CASP target codes are 3MX7 and T0540 respectively. This protein contain 90 amino acid residues with 8 beta strands. We have chosen best models from groups "LTB" and "Mufold" for our analysis, which are labelled as Model 1 and Model 2 in Figure 8. As presented in Figure 8 we found that this method is able to correctly order the models which matches with the GDT_TS score.

There are however some instances where the method can fail, specially when GDT scores are very close. We have found this for an engineered protein from Asr4154 protein (PDB ID: 2L09 and CASP Target T0538). This protein contains 54 amino acid residues with three alpha helixes and two very short beta strand. The model that is closest to the native structure was generated by the group PconsR with a GDT_TS value of 96.23. We have also considered one model from group "Shell" (GDT_TS = 90.09) and "FOLDIT" (GDT_TS = 86.32) for our analysis along with the native crystal struture. The models from PconsR, Shell and FOLDIT are labelled as model 1, model 2 and model 3 respectively in Figure 6. As presented from Figure 6, one can found that the model from PconsR has lowest free energy value, making it a more stable structure. Although ranking of the other models remain consistent, it may happen that the theoretical model produced by the group "PconsR" much more stable than the crystal structure. This is particularly difficult target for rank ordering as all the models those are considered for this calculation are within RMSD values of 2.6 Å.

2.3.2 What can we say about low resolution models?

We mentioned earlier that our predictive abilities are greatly decreased with low model qualities. It is better to have atleast one good model to pick out the native/native like structures from the rest of the decoy. In oorder to test

this hypothesis we performed another test with target T0531 of CASP9, in which we compared the crystal structure to five models from the MUFOLD server. The pdb id of this extracellular domain of the jumping translocation breakpoint protein is 2KJX and the CASP target code is T0531. Looking at Figure 9 shows: 1.) native is correctly identified as expected and 2.) Surprisingly there is a high level of correlation between the GDT ranking and the free energy ranking, only two structures with GDT_TS score less than 35 are ordered incorrectly. It is worth to note that models 2 and 3 have the same GDT and very different free energies, meaning that the actual ordering could change a lot²⁶.

2.3.3 Difficulty in CASP Experiments

It is often difficult to model CASP targets using confinement and release method. There are many cases, where the sequence of a particular target are trimmed during actual result presentation. This is illustrated with the crystal structure of the leucine zipper domain of cGMP dependent protein kinase I (pdb id: 3NMD and CASP9 code: T0605) as shown in Figure 10. The actual CASP 9 target consisted of 72 amino acid residues, but as only 18-66 amino acid residues could be detected in actual crystal structure of this protein, the final result was trimmed with respect to that crystal structure with 49 amino acid residues which consist of a single alpha helix. The amino acid residues 18 and 66 are shown in three models submitted by the group "Baker". It is important to note that blind prediction of model ranking on the basis of free energy can be hugely affected in such scenario as the only major difference between those models are the trimmed parts, specially the region consisting residues 1-18.

2.3.4 Can confinement method perform better quality assessment in protein structure prediction ?

A part of CASP experiment is dedicated to the assessment of the quality of predicted model²⁴. Most of the top performing group in this category use consensus approaches for quality assessment²⁷. A review of CASP9 quality assessment also pointed out that the method which are based on clustering technique perform much better compare to those methos

which are based on analysis of individual model²⁴. In this background we try to answer, whether confinement method can do better quality assessment compare to the best performing group (MUFOLD-WQA) in this category. We have again picked up the CASP target T0538 to answer this question. We have chosen the Model 3 submitted by PconsR (GDT_TS = 96) and model 5 from the MULTICOM-NOVEL (GDT_TS = 83). Both are server predicted model and they were further used for quality assessment by the group MUFOLD-WQA²⁷. It is important to note that the model from PconsR was most accurate predicted model for this target and the model from MULTICOM-NOVEL was predicted as best by the quality assessment experiments of MUFOLD-WQA. Our free energy analysis we have shown that model from Pconsr is better than the model from MULTICOM-NOVEL ($\Delta\Delta G(Model_Pconsr - Model_MULTICOM-NOVEL) = -8.2 Kcal/Mol$), which matches well with the GDT_TS score. On the other hand the MUFOLD-WQA predicted the ranking in the reverse order. There is no doubt that the consensus approaches can predict the model quality in a faster manner. But we expect that confinement approach can predict the model quality in a relatively expensive but much accurate way.

Further Analysis is going on Target 560.

2.3.5 CASP10

We participated in CASP10 as a metapredictor group. Given the tight schedule of the CASP competition, we only attempted proteins under 100 residues in length. Our main problem during this part of the competition. was that proteins were trimmed from the actual calculation.

3 Conclusion

Proteins are essential parts of organisms and participate in virtually every process within living cells. In order to understand different functions of proteins, detect diseases caused by them and design more efficient drugs it is often useful to have the three dimensional structure of the protein. Experimental studies using NMR and X-ray crystallography is

not enough to detect large number of structures. In recent past there are number of studies directed towards understanding protein structure using theoretical tools. Experimentally, it is relatively easy to identify the native structure from the data obtained from x-ray crystallography or NMR. On the other hand using theoretical tools it is often difficult to identify the native structure using both physics based methods and knowledge based method. In order to rank structure from the available data, some groups use clustering algorithms and the structure of the most populated cluster is picked out as the most probable structure. However, it may happen that the structure may be trapped and spend most of its time in a kinetic trap, which may give a wrong interpretation of the clustering result. On the other hand, some groups also depend on potential energy function to pick out their best structure. In this paper, we have used a free energy method to identify the native/native like structure. First, we have tested this method for a chameleon sequence, which has a 95 percent sequence identity but one of them has a 3α structure and another one has $4\beta + \alpha$ structure. Using the current method, we can find that the native structure always has most stable structure. We have also tested this method for different targets of CASP experiments. We found that in most cases, it can pick out the native/native like structure in terms of lowest free energy value.

However, there may be some limitation of this method in terms of size of the protein molecule. The normal mode analysis may not be accurate for proteins larger than 100 amino acid residues. This can be approximated by removing the hydrogen molecules from the system. The method can be also give wrong result if all the models in the decoy are very poor. It may also be difficult to rank structures if all the structures are very close to the native structure. But that does not matter at all as our main aim is to differentiate between the good and the bad structure. In this article we have extensively tested this method using examples from CASP experiment. This method can be computationally expensive in actual CASP experiment if one want rank thousands of submitted models in CASP experiments. However, in real life experiment with a particular target this method can give accurate result. The important fact about Confinement method is that all the part of the calculation can be done independently. We have mostly carried out our calculation with Amber program²⁸ in GPU computer. With an average 56 residue we found that it takes only 4 hours to complete 20 ns of the confinement step. So, with available computer power this method will

be easy to use.

This method can be further used for calculating free energy due to very large conformational change. Another application may be for the case of ligand binding. It can also be used to distinguish the most stable structure during protein design. Another, important application may be to study the protein folding kinetics, specially to study the phi value analysis.

4 Method

The confinement method has been described in details in ref. by Tyka et.al. and Cecchini et. al. Here we briefly describe the methodology. We compute free energy ΔG_{AB} between A and B conformation of the protein. For this purpose we use a thermodynamic cycle.

1. We minimized both the conformation. These minimized conformation(A* and B*) are the restrained conformation of that state
2. Backbone dihedral angle of the whole protein is restrained by a harmonic potential to define the configurational state.
3. In order to calculate the free energy $\Delta G_{A,A*}$ and $\Delta G_{B,B*}$ A and B are gradually transformed in A* and B* by applying a harmonic restraint potential to all atom. For this purpose around 21 simulation were run each of 20 ns with increasing harmonic restraint potential from 0.00005 to 81.92 until the free and the restrained state overlap well. The final restrained state was chosen so high so that the rotational contribution of the protein frozen out and only remaining contribution remain that of vibrational free enrgy. The fluctuation from the reference structure was recorded and the free energy is calculated using a numerical approach developed by Tyka et. al.
4. Finally the thermodynamic cycle is closed by calculating the free energy between the final restrained state using normal mode analysis.

In all the calculation amber 10 program is used with ff99SB with GB/SA implicit solvent.

[Figure 2 about here.]

[Figure 3 about here.]

[Figure 4 about here.]

[Figure 5 about here.]

[Figure 6 about here.]

[Figure 7 about here.]

[Figure 8 about here.]

[Figure 9 about here.]

[Figure 10 about here.]

References

- [1] Meirovitch, H. Recent developments in methodologies for calculating the entropy and free energy of biological systems by computer simulation. *Current Opinion in Structural Biology*, 2007, 17, 181-186.
- [2] Chipot, C.; Shell, M.S.; Pohorille, A. Introduction, in Chipot, C., Pohorille, A., editors. *Free Energy Calculations: Theory and Applications in Chemistry and Biology*. Springer Series in Chemical Physics, vol. 86. Berlin and Heidelberg: Springer; 2007, p. 132.
- [3] Jorgensen, W.L. The many roles of computation in drug discovery, *Science* 2004, 303, 18138.
- [4] Gilson, M.K.; Zhou, H.X. Calculation of protein-ligand binding affinities. *Annu Rev Biophys Biomol Struct.* (2007) 36, 21-42.

- [5] Torrie, G. M.; Valleau, J. P. iNonphysical sampling distributions in Monte Carlo free-energy estimation: Umbrella sampling (1977) *J. Comput. Phys.* 23, 187
- [6] Tironi, I.G.; van Gunsteren, W.F. A molecular-dynamics simulation study of chloroform. *Mol. Phys.* (1994) 83, 381-403.
- [7] Dill, K.A.; H.S. Chan. From Levinthal to Pathways to Funnels: The "New View" of Protein Folding Kinetics. *Nature Structural Biology* 4, 10-19 (1997)
- [8] Dill, K.A.; Ozkan, S.B.; Shell, M.S.; Weikl, T.R. The protein folding problem. *Annual Review of Biophysics* (2008), 37, 289-316.
- [9] Anfinsen. C.B. Principles that Govern the Folding of Protein Chains. *Science* (1973) 181, 223-230.
- [10] Christ, C.D.; van Gunsteren, W.F. Enveloping distribution sampling: A method to calculate free energy differences from a single simulation, *J. Chem. Phys.* (2007), 126, 184110.
- [11] Ytreberg, F.; Zuckerman, D. Simple estimation of absolute free energies for biomolecules. *J. Chem. Phys.* 2006, 124, 104105.
- [12] Park, S.; Lau, A.; Roux, B. Computing conformational free energy by deactivated morphing. *J. Chem. Phys.* 2008, 129, 134102
- [13] Zheng, L.; Chen, M.; Yang, W. Random walk in orthogonal space to achieve efficient free-energy simulation of complex systems, *Proc. Natl. Acad. Sci.* 2008, 105 (51), 20227.
- [14] Tyka, M.; Clarke, A.; Sessions, R. An Efficient, Path-Independent Method for Free-Energy Calculations. *J.Phys.Chem. B* 2006, 110, 17212-17220.
- [15] Cecchini, M., Krivov, S.V., Spicthy, M., Karplus, M. Calculation of free-energy differences by confinement simulations. Application to peptide conformers. *J. Phys. Chem. B* 113, p. 9728-9740 (2009).
- [16] Strajbl, M.; Sham, Y.Y.; Vill, J.; Chu, Z.-T.; Warshel, A. Calculations of Activation Entropies of Chemical Reactions in Solution. (2000) 104, 4578-4584.

- [17] Krivov, S.; Karplus, M. Hidden complexity of free energy surfaces for peptide (protein) folding Proc. Natl. Acad. Sci. U.S.A. 2004, 101, (41), 14766.
- [18] Alexander, P.A.; He, Y.; Chen, Y.; Orban, J. Bryan, P. The design and characterization of two proteins with 88% sequence identity but different structure and function. Proc. Natl. Acad. Sci. 2007, 104 (29), 11963-11968.
- [19] He, Y.; Chen, Y.; Alexander, P.A.; Orban, J. NMR structures of two designed proteins with high sequence identity but different fold and function. Proc. Natl. Acad. Sci. 2008, 105 (38), 14412-14417.
- [20] Alexander, P.A.; He, Y.; Chen, Y.; Orban, J. Bryan, P. A minimal sequence code for switching protein structure and function. Proc. Natl. Acad. Sci. 2009, 106(50), 21149-21154.
- [21] Shortle, D. One sequence plus one mutation equals two folds. Proc. Natl. Acad. Sci. 2009, 106(50), 21011-21012.
- [22] Sheffler, W.; Baker, D. RosettaHoles: Rapid assessment of protein core packing for structure prediction, refinement, design, and validation. Protein Science. 2009, 18(1), 229-239.
- [23] MacCallum, J.; Prez, A.; Schnieders, MJ.; Hua, L.; Jacobson, M.P.; Dill, K.A. Assessment of protein structure refinement in CASP9. Proteins, 2011, 79, 74-90.
- [24] Kryshtafovych, A.; Fidelis, K; and Tramontano, A. Evaluation of model quality predictions in CASP9. Proteins, 2011, 79, 91106
- [25] Zemla, A. LGA: a method for finding 3D similarities in protein structures. Nucleic Acids Res 2003, 31, 33703374.
- [26] Perez, A.; Yang, Z.; Bahar, I.; Dill, K.A.; MacCallum, J.L.; FlexE: Using Elastic Network Models to Compare Models of Protein Structure. J. Chem. Theory Comput., 2012, 8, 3985-3991.
- [27] Wang, Q.; Vantasin, K.; Xu, D.; Shang, Y. MUFOld-WQA: A new selective consensus method for quality assessment in protein structure prediction. Proteins, 2011, 79: 185195.

- [28] Case, D.A.; Cheatham, III, T.E.; Darden, T.; Gohlke, Luo, H.R.; Merz, Jr., K.M.; Onufriev, A; Simmerling, C.; Wang, B.; R. Woods, R. The Amber biomolecular simulation programs. *J. Computat. Chem.* (20005) 26, 1668-1688.

123456789012345678901234567890123456789012345678901234567890123456
GA88:TTYKLILNLQAKEEAIKELVDA**GIAEKYIKL**IANAKTVEGVWTL**KDEIL**TFTVTE
GB88:TTYKLILNLQAKEEAIKELVDA**ATAEKYFKLY**ANAKTVEGVWTV**YKDETK**TFTVTE
GA95:TTYKLILNLQAKEEAIKE**LVDAGTAEKYIKL**IANAKTVEGVWTL**KDEIK**TFTVTE
GB95:TTYKLILNLQAKEEAIKE**AVDAGTAEKYFKL**IANAKTVEGVWTV**YKDEIK**TFTVTE
GB98:TTYKLILNLQAKEEAIKE**AVDAGTAEKYFKL**IANAKTVEGVW**TAKDEIK**TFTVTE

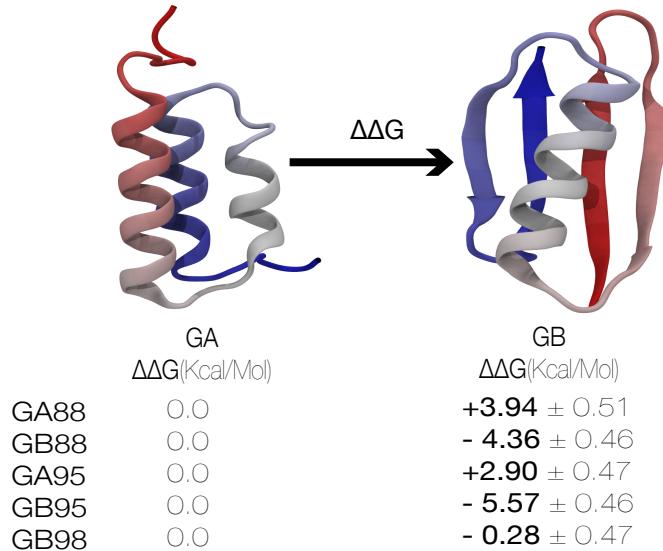


Figure 1: The confinement method correctly predicts the structural preferences of six chameleon sequences. (A) The six sequences used in this study. (B) Each sequence adopts either a Protein G-like fold (denoted GB) or a three-helix bundle fold (denoted GA). The relative free energies of the two folds are reported for each sequence.

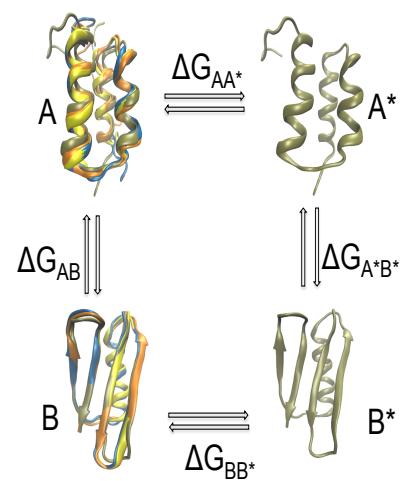


Figure 2: Graphical representation of the thermodynamic cycle involving confinement method.

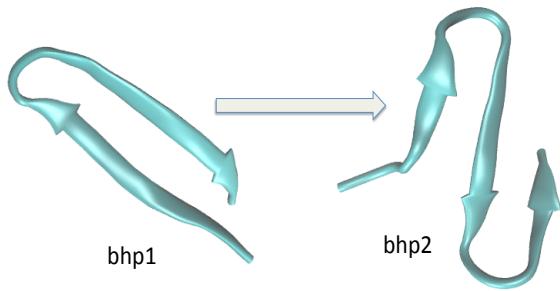


Figure 3: Two conformations from β hairpin from protein G, bhp1 and bhp2. The two stranded β sheet, bhp1 is the native structure and the three stranded β sheet is known as bhp3.

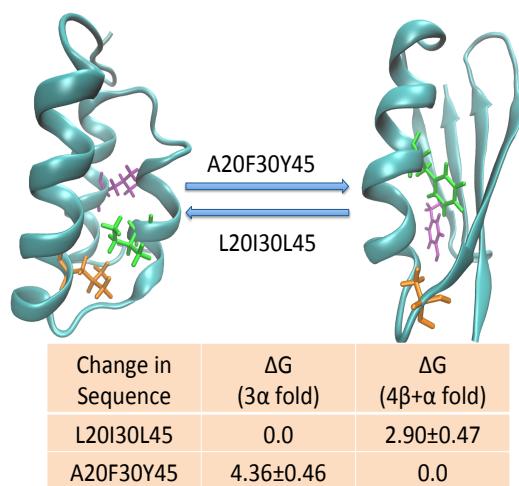


Figure 4: Two protein with 95 % similar sequence but different folds

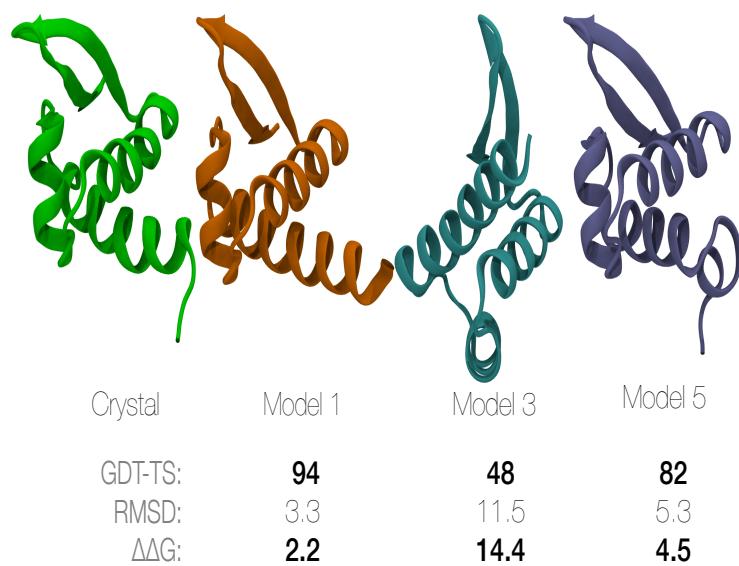


Figure 5: The native and three submitted model structure, along with their GDT_TS, RMSD and relative Free energy values of protein BVU3908 from *Bacteroides vulgatus* (PDB id: 2L01 and CASP code: T0559).

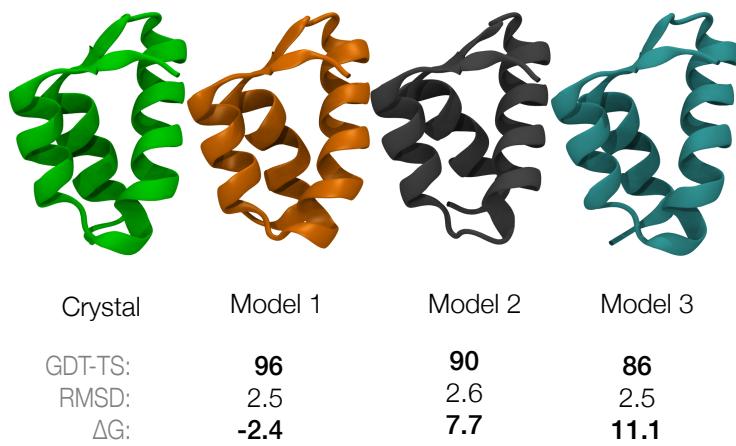


Figure 6: The native and three model structure of engineered protein from Asr4154 protein (PDB ID: 2L09 and CASP code:T0538). The model 1,2 and 3 are from the group PconsR, Shell and FOLDIT respectively.

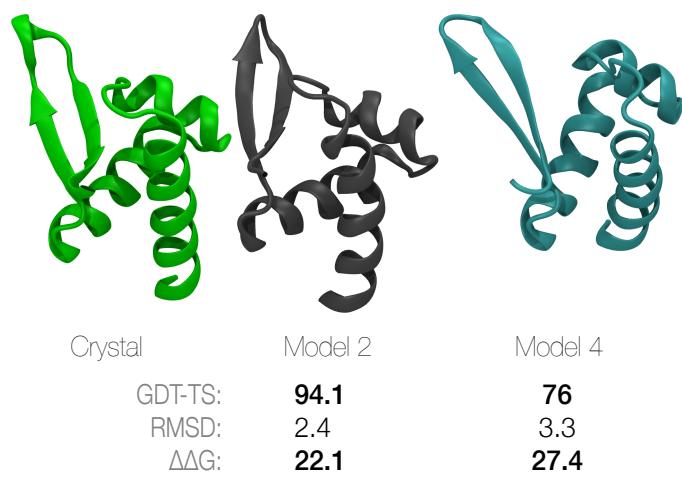


Figure 7: Native and two model structure of protein BT2368 from *Bacteroides thetaiotaomicron* (pdb id: 2L02 and CASP code: T0560). The two models were from the group "Splicer".

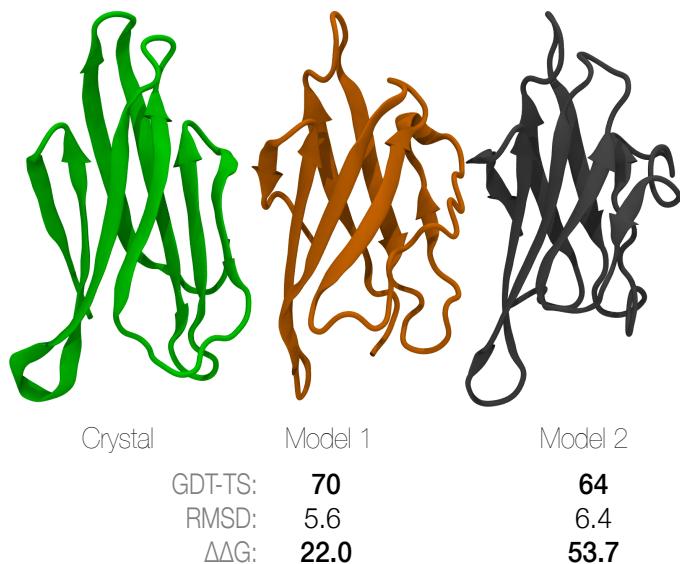


Figure 8: X-ray crystallographic structure and two submitted models of fas apoptosis inhibitory protein (pdb id: 3MX7 and CASP code: T0540). Model 1 and Model 2 in this analysis were submitted by the group LTB and MUFOLD respectively.

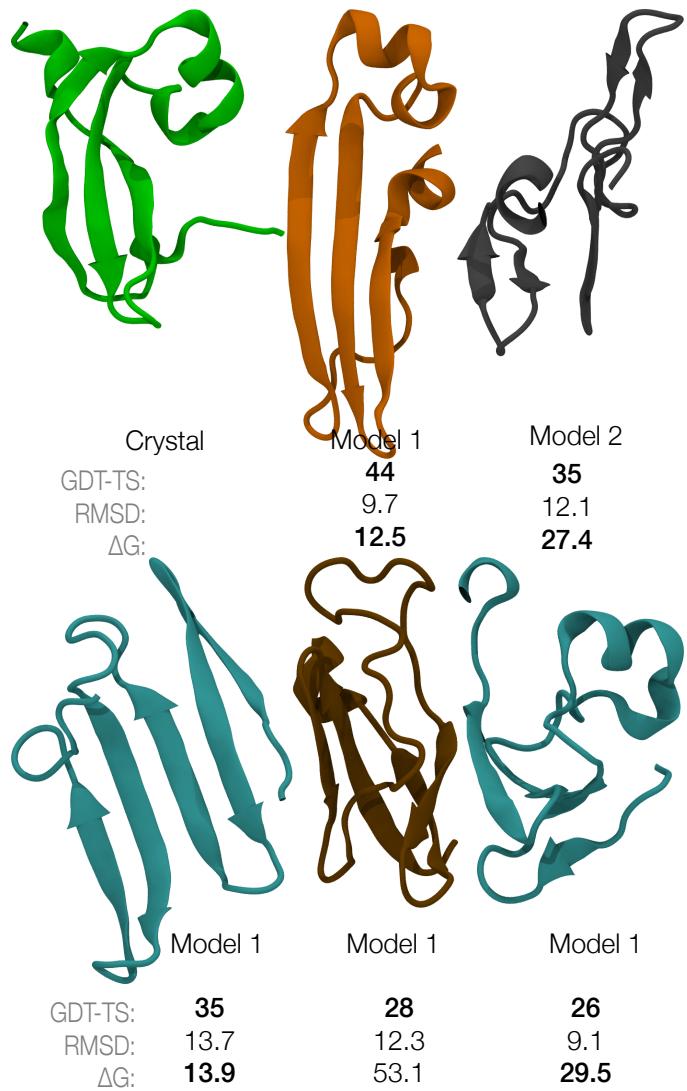


Figure 9: The native structure and 5 models of extracellular domain of the jumping translocation breakpoint protein (pdb id: 2KJX and the CASP code: T0531).

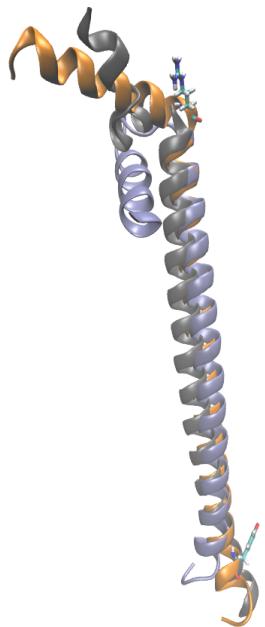


Figure 10: Three models of the leucine zipper domain of cGMP dependent protein kinase I (original pdb id: 3NMD and CASP target: T0605). The original target sequence of this protein was 72 residues. However only residues 3 to 66 is only kept during result announcement as that part can be found from crystallographic analysis. The region 3 to 66 are almost identical in all the 3 models

CASP Target	PDB Identifier	$\Delta\Delta G_{native \rightarrow best decoy}$ (kcal/mol)
T0531	2KJX	12.49 ± 0.70
T0538	2L09	-2.48 ± 0.47
T0540	3MX7	22.00 ± 0.49
T0559	2L01	2.24 ± 0.24
T0560	2L02	22.15 ± 0.49

Table 1: The confinement method assigns a more favorable free energy to the experimentally determined structure than to computer-generated predictions. For each target, we examined as many as five predictions submitted by CASP participants. Positive $\Delta\Delta G$ values indicate that the experimental structure is predicted to be more favorable than any of the decoys.