Building blocks of protein structures – Physics meets Biology

Tatjana Škrbić[1,2], Amos Maritan[3], Achille Giacometti[2], George D. Rose[4], Jayanth R. Banavar[1]

1. Department of Physics and Institute for Fundamental Science, University of Oregon, Eugene, OR 97403, USA
2. Dipartimento di Scienze Molecolari e Nanosistemi, Università Ca' Foscari Venezia, Campus Scientifico, Edificio Alfa, via Torino 155, 30170 Venezia Mestre, Italy
3. Dipartimento di Fisica e Astronomia, Università di Padova and INFN, via Marzolo 8, 35131 Padova, Italy
4. T. C. Jenkins Department of Biophysics, Johns Hopkins University, 3400 N. Charles Street, Baltimore, MD 21218-2683, USA

Abstract

The native state structures of globular proteins are stable and well-packed indicating that self-interactions are favored over protein-solvent interactions under folding conditions. We use this as a guiding principle to derive the geometry of the building blocks of protein structures – α-helices and strands assembled into β-sheets – with no adjustable parameters, no amino acid sequence information, and no chemistry. There is an almost perfect fit between the dictates of mathematics and physics and the rules of quantum chemistry. Our theory establishes an energy landscape that channels protein evolution by providing sequence-independent platforms for elaborating sequence-dependent functional

diversity. Our work highlights the vital role of discreteness in life and has implications for the creation of artificial life and on the nature of life elsewhere in the cosmos.

Proteins (1-40) [we apologize that we have only included a limited selection of papers], the molecular machines of life, are formidably complex (41). They have myriad degrees of freedom, an astronomical number of possible sequences for even a moderate length chain, and are stabilized by thousands of interactions, both intra-molecular and with solvent. Yet, many proteins adopt their native conformation spontaneously under physiological conditions (5). The native state structures of globular proteins are space-filling and maximize self-interaction (6,7,9). The folded structures (21,26,32,35) are modular and built on scaffolds of α-helices (2) and strands of β-sheet (3), the only two conformers that can be extended indefinitely without steric interference while providing hydrogen-bonding partners for their own backbone polar groups (4,10,28). Proteins are digital molecules: nature's exclusion of α-β hybrid segments (27) – part α-helix, part β-strand – is built into proteins at the covalent level and restricts the topology of single domain proteins to a few thousand distinct folds at most (8,14,20).

Helices are ubiquitous in biomolecular structures. They are also found in everyday life, e.g. a garden hose (or a flexible tube) is often wound into a helix. Figure 1a is a sketch of a segment of a protein helix shown with a tube envelope. A uniform, flexible, self-avoiding solid tube, whose axis is a line, is a geometrical generalization of a sphere. A sphere is a region carving out space around a point, its center. Analogously, all points within the tube are at a distance from the tube axis smaller than or equal to the tube thickness, which is measured by the tube radius, Δ. A flexible tube is an extended object with uniaxial symmetry and is not plagued by symmetry conflicts, unlike the simple model of a chain of tethered spheres for which the uniaxial symmetry inherent to a chain clashes with the spherical symmetry of the constituent objects.

Here we model a protein as a discretized tube with a set of equally spaced points, analogous to the C_α atoms along the protein backbone, defining its axis. The coordinates of these points are described using two angles: θ and μ (see Figure 2). The simplest repeating geometry of the axis of a tube of radius Δ is a helix of pitch P, wrapped around a straight cylinder of radius R, taken to be the helix radius. The helix is parameterized by a variable t and is defined by

$$\mathbf{r}(t) = (R\cos(t), R\sin(t), Pt/(2\pi)). \quad (1)$$

As t advances by an integer multiple of 2π, the helix repeats periodically along the z-axis, with an increment equal to the pitch. The helical tube geometry is characterized by three dimensionless quantities Δ/R, $\eta=P/(2\pi R)$, and ε_0, the rotation angle between successive points along the axis. Our initial goal parallels the seminal work of Pauling et al. (2), who sought rotation angles that allowed for the optimal placement of hydrogen bonds in a helix. The crucial difference here is that we do not need to invoke quantum chemistry, covalent bonds, the planarity of peptide bonds or hydrogen bonds.

We seek to maximize the self-interaction of a *continuum* tube (42-47) by winding the tube as tightly as possible, subject to the excluded volume constraint that the tube cannot penetrate itself. We ensure local space-filling of the helix by equating the tube radius to the local radius of curvature (Fig 1c), which, in turn, is equal to $R(1+\eta^2)$ (46) yielding:

$$\Delta = R(1+\eta^2). \quad (2)$$

The successive turns of a space-filling helix need to be parallel and alongside each other (Figure 1e). The square of the distance between a reference point in the continuum helix (denoted by $t_0=0°$) and an arbitrary point t is given by

$$d^2 = R^2 [2(1-\cos t)+\eta^2 t^2]. (3)$$

We determine the parameter value t_{min} for which d^2 is a minimum and set this minimum distance equal to the square of the tube diameter, $4\Delta^2$, thereby ensuring non-local space-filling (Figure 1f). The minimization condition is

$$\sin t_{min}+\eta^2 t_{min} = 0, (4)$$

and the distance constraint is

$$4\Delta^2 = R^2[2(1-\cos t_{min})+\eta^2 t_{min}^2]. (5)$$

We solve Equations (2, 4, and 5) simultaneously to obtain the unique geometry of the continuum space-filling helix (Figure 1c,e,f): $\eta\sim0.4$, $\Delta/R\sim1.16$, and $t_{min}\sim302°$.

The idealized continuum tube does not take into account discreteness, a common ingredient to all matter, which is crucial at small length scales. A unique benefit of discreteness is the emergence of a second building block (besides the space filling helix): a two dimensional strand with a zig-zag tube axis (Figure 3a), the rotation angle ε_0 of 180°, and $\mu=180°$. The existence of two building blocks is *required* for the rich diversity of topologically distinct folds, necessary for the versatile functioning of the molecular machines. A helix is defined by a repeat of (θ,μ)-values and a planar strand by a repeat of $\mu=180°$. For repeat μ-values close to 180°, one obtains a twisted planar strand, a geometrical feature often observed in protein structures.

Figure 1g shows the space-filling discrete helix with η~0.4 and Δ/R~1.16, the geometrical characteristics of the continuum space-filling helix. The discretization requires the specification of the rotation angle ε_0 between successive points that retains the space-filling conditions for the discrete case. This choice of ε_0 is made (in direct analogy with the continuum case) by requiring that the distance between points i (analogous to t_0=0°) and i+m with integer m (analogous to t_{min}) is equal to the tube diameter and the angles (i-1,i,i+m) and (i,i+m,i+m+1) are both equal to 90° (analogous to the minimization condition). The smallest value of m for which these conditions are satisfied is m=3 and ε_0~99.8° (the ratio of the distance to the tube diameter is found to be 1.00… and both the angles are 90.0…° for this value of ε_0). Upon defining the length scale to match the mean C_α-C_α distance along the protein backbone of 3.81Å, the tube radius is found to be Δ~2.63Å. Using these basic results, one may derive many attributes of the space-filling discrete helix, which are in excellent accord with the α-helix building block of protein structures (see Figures 4-5, Table 1).

A space-filling helix maximizes self-interaction through local interactions, whereas the non-local interactions of strands assembled into sheets leads to space-filling. We build on the insights gained from the helix analysis to make predictions of the geometrical arrangements for strand pairing (Figure 3b-c). First, the strands need to be in phase with each other mimicking the behavior of adjoining turns in the continuum helix, placed parallel to and alongside each other. Second, there are two distinct ways (Figures 3b-c) of accomplishing space-filling of assembled strands corresponding to anti-parallel and parallel β-sheet hydrogen bonding patterns, first predicted by Pauling and Corey (3) based on hydrogen bonding. The space-filling packing requires that the distances (i,j) in Figure 3b (anti-parallel arrangement) and (i,M_j) in Figure 3c (parallel arrangement), which are measures of the closest approach of two parallel tube segments, both ought to be $2\Delta \sim 5.26$Å (see Figure 3d-e and Table 1).

In addition to helices and strands, chain turns are needed to inter-connect these building blocks. In proteins, the most abundant turns are β-turns, tight, four-residue segments that approximately reverse the overall chain direction (13). β-turns are tightly wound like an α-helix, and therefore are predicted to have similar θ-angles as in the α-helix (Figure 4).

Figure 4b shows the (θ,μ) coordinates for 4 classes of residues: those that participate in α-helices, parallel β-sheets, anti-parallel β-sheets, and β-turns. The black X marks the coordinates of the predicted space-filling helix. Unsurprisingly, α-helix μ-values (49.7 ± 3.9)° are a bit lower than the theoretical prediction of 52.4° because the distance between a hydrogen-bonded donor and acceptor (N-H···O=C) can be less than their summed van der Waals radii. Of course, an ideal tube is unaffected by such chemical particulars. Nevertheless, the predicted μ value for an ideal tube is remarkably close to 50°, the average μ value for Pauling's α-helix (2), with 3.6 residues per turn. As predicted, the tight turns predominantly have a θ value close to that of the α-helix. The β strands are twisted with a μ angle around 180° and have a spread of θ angles.

The accord between our prediction and structural data from the protein data bank underscores the consilience (48) between mathematics and physics on one hand and quantum chemistry on the other and show how self-interaction is maximized through a space-filling arrangement of individual helices and sheets (Figure 6). The large but finite number of protein native state folds (8,14,20) sculpted by geometry and symmetry (24,25) is reminiscent of the restriction of the number of space groups of Bravais lattices of three-dimensional crystals to exactly 230 due to periodicity and space-filling requirements (49).

Our theory shows convincingly that structure-space and sequence-space of proteins are separable, yielding sequence-independent forms (22) that are Platonic and immutable, and not subject to Darwinian evolution. Sequences can then populate these forms resulting in the evolution of the functional diversity of life. The evolution (40,50,51) of biological macromolecules can be framed as a random walk in an inordinately vast sequence space, with selection guided by "fitness". Our formalism imposes an important constraint on protein evolution. A consequence is that the repertoire of possible folds is generated from pre-sculpted α-helices and β-strands, and, of necessity, accessible folds are mix-and-match constructs of these fundamental forms. This diversity of structural scaffolds provides a platform for elaborating functional diversity.

In seminal work, Anfinsen (5) demonstrated that proteins fold rapidly and reproducibly into their native state structures. This naturally led to the text book wisdom (35) that *the amino acid sequence of a protein determines its three-dimensional structure* leading to much effort in finding the energy minimum of a many-body complex system of a protein in its solvent with a huge number of degrees of freedom and with myriad interactions. Subsequent work by Matthews (16) and others showed that protein structure is nevertheless *very tolerant of amino acid replacement.*

Our results here conclusively demonstrate a simple two-step process for understanding proteins. First, a menu of putative native state structures is created without regard to amino acid sequence and chemistry. In the second step, a given protein selects its native state from this menu. Thus the horrendous problem of working out the native state structure of a given protein from knowledge of its sequence by finding, from scratch, the conformation, which minimizes the net energy of myriad imperfectly known microscopic interactions, is replaced by the much simpler task of finding the best fit of the sequence to one among the library of geometrically sculpted folds determined in a sequence-independent and chemistry-independent manner. This best-fit process, also exploited in the threading algorithm (15), is where the role of the amino acid sequence becomes paramount. Indeed, in an influential series of papers (12,17-19), it has been highlighted that the amino acid side chains must be able to fit into the native state fold with minimal frustration thereby creating a landscape akin to a folding funnel.

Some 80 years ago, Bernal (1) wrote – *Any effective picture of protein structure must provide at the same time for the common character of all proteins as exemplified by their many chemical and physical similarities, and for the highly specific nature of each protein type. It is reasonable to believe, though impossible to prove, that the first of these depends on some common arrangement of the amino acids*. Indeed, our work here shows that the common character of all proteins originates from an appropriate tube-like geometrical description of just the backbone C_α atoms, which are common to all proteins, and results in the library of native state folds sculpted by geometry and symmetry, without a need for sequence specificity or chemistry. *The highly specific nature of each protein type* then arises from its distinctive amino acid side-chains and their fit to one of the folds from the library. For a protein, the folded structure is central to its functionality. The situation is loosely analogous to a restaurant in which the chef (geometry and symmetry) creates a menu of items (the library of putative native state folds) that customers (protein sequences) can order from (fold into). The chef does not cater to the individual tastes of the customers. Rather, all patrons of the restaurant are satisfied picking an item from the menu. As in proteins, the total number of patrons can vastly exceed the number of menu items. If, in fact, the menu of protein structures itself evolved, then one would be confronted by an almost impossible situation for evolution and natural selection in which a protein and its interacting partners would have to co-evolve their structures synergistically in order to maintain function. This situation is deftly avoided by the geometrically determined native state folds providing a fixed backdrop for evolution to shape protein sequences and functionalities.

Richard Feynman, in a lecture entitled *There's Plenty of Room in the Bottom: An Invitation to Enter a New Field of Physics* at the annual American Physical Society Meeting at Caltech on December 29, 1959, suggested that tiny, nanoscale machines could be constructed by manipulating individual atoms. Proteins are precisely such machines (21,26,32,35). Indeed, proteins as well as macroscopic machines establish a stable framework that can accommodate moving parts, which perform a function. Proteins are nature's implementation of the abstract forms presented here, a diversity of stable forms deduced entirely from mathematical considerations. These predictions – independent of any chemistry – have implications for life elsewhere in our cosmos (52) suggesting that there is no absolute need for carbon chemistry for life to exist. We look forward to other implementations in the lab, raising the prospect of powerful interacting machines, potentially leading to artificial life (53).

In summary, underlying life's evolving complexity (41) is a sequence-independent energy landscape with thousands of stable minima — a landscape formed from nature's scaffold building blocks, a protein grammar. In both natural and artificial languages, a grammar is a finite set of rules that can generate an a large number of syntactically correct sentences or strings. The discretized tube model establishes an immutable grammar of life and "*from so simple a beginning, endless*" – protein sequences and functionalities – "*most beautiful and most wonderful have been, and are being, evolved*" (54).

PDB analysis: We have carried out a quantitative comparison between our predictions and protein structure. To develop a working set for comparison, Richardsons' Top 8000 set of high-resolution, quality-filtered protein chains (resolution < 2Å, 70% PDB homology level) [see the web site: http://kinemage.biochem.duke.edu/databases/top8000.php] was further filtered to exclude all structures with missing backbone atoms, yielding a working set of 4416 structures (listed in Table 2). The working set was cross-checked against 478 proteins having a more stringent homology cutoff of 20%, taken from the Pisces database (23); 205 entries are in common to both sets. Almost all bond lengths ($C_{\alpha(i)}$-$C_{\alpha(i+1)}$ distance) (~99.7%) in the working set are clustered around 3.81Å, as expected for a *trans* peptide. Those remaining have shorter bonds, ~2.95Å, predominantly from *cis* residues. For purposes of comparison, a fixed bond length of 3.81Å is used. Hydrogen bonds were identified using DSSP (11). Hydrogen-bonded conformers extracted from the working set include 3595 helices, 8473 antiparallel pairs, 4639 parallel pairs, and 58,820 turns. Helices were identified as 12-residue segments with intra-helical hydrogen bonds (N_i-H•••O_{i-4} and O_i•••H-N_{i+4}) at each residue. Antiparallel strand pairs were identified by three inter-pair hydrogen bonds at (i,j), (i+2,j-2), and (i-2,j+2), i ∈ strand1, j ∈ strand2. To avoid possible end effects, only (i,j) residue pairs were used. Parallel strand pairs were identified by four inter-pair hydrogen bonds between (i,j-1), (i,j+1), (i+2,j+1), and (i-2,j-1), i ∈ strand1,

$j \in$ strand2, and again only the i-th residue was retained. Double-counting was assiduously avoided. β turns were identified by hydrogen bonds between (i,i+3) with no helical residues among the 4. The (θ,μ)-values were then recorded for points i+1 and i+2 in the turns.

References

1. Bernal, J. D. Structure of Proteins. *Nature* **143**, 663-667 (1939).
2. Pauling, L., Corey, R. B. & Branson, H. R. The structure of proteins: two hydrogen-bonded helical configurations of the polypeptide chain. *Proc. Natl. Acad. Sci. USA* **37**, 205-210 (1951).
3. Pauling, L. & Corey, R. B. The pleated sheet, a new layer configuration of polypeptide chains. *Proc. Natl. Acad. Sci. USA* **37**, 251-256 (1951).
4. Ramachandran, G. N. & Sasisekharan, V. Conformation of polypeptides and proteins. *Adv. Prot. Chem.* **23**, 283-438 (1968).
5. Anfinsen, C. B. Principles that govern the folding of protein chains. *Science* **181**, 223-230 (1973).
6. Richards, F. M. The Interpretation of Protein Structures: Total Volume, Group Volume Distributions and Packing Density. *J. Mol. Biol.* **82**, 1-14 (1974).
7. Finney, J. L. Volume Occupation, Environment and Accessibility in Proteins. The Problem of the Protein Surface. *J.Mol. Biol.* **96**, 721- 732 (1975).
8. Levitt, M. & Chothia, C. Structural patterns in globular proteins. *Nature* **261**, 552-558 (1976).
9. Richards, F. M. Areas, volumes, packing, and protein structure. *Annu. Rev. Biophys. Bioeng.* **6**, 151-176 (1977).

10. Kim, P. S. & Baldwin, R. L. Specific intermediates in the folding reactions of small proteins and the mechanism of protein folding. *Annu. Rev. Biochem.* **51**, 459-489 (1982).

11. Kabsch, W. & Sander, C. Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features. *Biopolymers* **22**, 2577-2637 (1983).

12. Gō, N. The consistency principle in protein structure and pathways of folding. *Adv. Biophys.* **18**, 149-164 (1984).

13. Rose, G. D., Gierasch, L. M. & Smith, J. A. Turns in peptides and proteins. *Adv. Protein Chem.* **37**, 1-109 (1985).

14. Chothia, C. One thousand families for the molecular biologist. *Nature* **357**, 543–544 (1992).

15. Jones, D. T., Taylor, W. R. & Thornton, J. M. A new approach to protein fold recognition. *Nature* **358**, 86-89 (1992).

16. Matthews, B. W. Structural and genetic analysis of protein stability. *Annu. Rev. Biochem.* **62**, 139–160 (1993).

17. Bryngelson, J. D., Onuchic, J. N., Socci N. D. & Wolynes, P. G. Funnels, pathways, and the energy landscape of protein folding: a synthesis. *Proteins* **21**, 167-195 (1995).

18. Wolynes, P. G., Onuchic, J. N. & Thirumalai D. Navigating the folding routes. *Science* **267**, 1619-1620 (1995).

19. Dill, K. A. & Chan, H. S. From Levinthal to pathways to funnels. *Nat. Struct. Biol.* **4**, 10-19 (1997).

20. Przytycka, T., Aurora, R. & Rose, G. D. A protein taxonomy based on secondary structure. *Nat. Struct. Biol.* **6**, 672-682 (1999).

21. Tanford, C. & Reynolds, J. *Nature's Robots: A History of Proteins* (Oxford University Press, 2001).

22. Denton M. & Marshall, C. Laws of form revisited. *Nature* **410**, 417 (2001).

23. Wang, G. & Dunbrack, R. L., Jr. PISCES: a protein sequence culling server. *Bioinformatics* **19**, 1589-1591 (2003).

24. Banavar, J. R., Hoang, T. X., Maritan, A., Seno, F. & Trovato, A. Unified perspective on proteins: A physics approach. *Phys. Rev. E* **70**, 041905 (2004).

25. Hoang, T. X., Trovato, A., Seno, F., Banavar, J. R. & Maritan, A. Geometry and symmetry presculpt the free-energy landscape of proteins. *Proc. Natl. Acad. Sci. USA* **101**, 7960-7964 (2004).

26. Lesk, A. M. *Introduction to Protein Science: Architecture, function and genomics* (Oxford University Press, 2004).

27. Fitzkee, N. C. & Rose, G. D. Steric restrictions in protein folding: an alpha-helix cannot be followed by a contiguous beta-strand. *Protein Sci.* **13**, 633-639 (2004).

28. Rose, G. D., Fleming, P. J., Banavar, J. R. & Maritan, A. A backbone-based theory of protein folding. *Proc. Natl. Acad. Sci. USA* **103**, 16623-16633 (2006).

29. Dill, K.A., Ozkan, S. B., Shell, M. S. & Weikl, T. R. The protein folding problem. *Annu. Rev. Biophys.* **37**, 289–316 (2008).

30. Shaw D. E., Maragakis, P., Lindorf-Larsen, K., Piana, S., Dror, R. O., Eastwood, M. P., Bank, J. A., Jumper, J. M., Salmon, J. K., Shan, Y. & Wriggers W. Atomic-Level Characterization of the Structural Dynamics of Proteins. *Science* **340**, 341-346 (2010).

31. Bitbol, A.-F., Dwyer, R. S., Colwell, L. J. & Wingreen, N. S. Inferring interaction patterns from protein sequences. *Proc. Natl. Acad. Sci. USA* **113**, 12180-12185 (2016).

32. Bahar, I., Jernigan R. L. & Dill, K. A. *Protein Actions* (Garland Science, Taylor & Francis Group, 2017).

33. Rocks, J. W., Pashine, N., Bischofberger, I., Goodrich, C. P., Liu, A. J. & Nagel, S. R. Designing allostery-inspired response in mechanical networks. *Proc. Natl. Acad. Sci. USA* **114**, 2520-2525 (2017).

34. Runnels, C. M., Lanier, K. A., Williams, J. K., Bowman, J. C., Petrov, A. S., Hud, N. V. & Williams, L. D. Folding, assembly, and persistence: The essential nature and origins of biopolymers. *J. Mol. Evol.* **86**, 598-610 (2018).

35. Berg. J. M., Tymoczko, J. L., Gatto, G. J. Jr & Stryer, L. *Biochemistry, Ninth edition* (Macmillan Learning, 2019).

36. Leman, J. K. et al. (2020). Macromolecular modeling and design in Rosetta: recent methods and frameworks. *Nat. methods* **17**, 665-680 (2020).

37. Dobson, C. M., Knowles, T. P. J. & Vendruscolo M. The Amyloid Phenomenon and Its Significance in Biology and Medicine. *Cold Spring Harb. Perspect. Biol.* **12**, a033878 (2020).

38. Fantini, M., Lisi, S., De Los Rios, P., Cattaneo, A. & Pastore, A. Protein Structural Information and Evolutionary Landscape by In Vitro Evolution. *Mol. Biol. Evol.* **37**, 1179-1192 (2020).

39. Merritt, H. I., Sawyer, N. & Arora, P. S. Bent into shape: Folded peptides to mimic protein structure and modulate protein function. *Peptide Sci.* **112**, e24145 (2020).

40. Bowman, J. C., Petrov, A. S., Frenkel-Pinter, M., Penev, P. I. & Williams, L. D. Root of the Tree: The Significance, Evolution, and Origins of the Ribosome, *Chem. Rev.* **120**, 4848−4878 (2020).

41. Goldenfeld N. & Kadanoff, L. P. Simple Lessons from Complexity. *Science* **284**, 87-89 (1999).

42. Maritan, A., Micheletti, C., Trovato, A. & Banavar, J. R. Optimal shapes of compact strings. *Nature* **406**, 287-290 (2000).

43. Stasiak, A. & Maddocks, J. H. Best packing in proteins and DNA. *Nature* **406**, 251-252 (2000).

44. Przybyl, S. & Pieranski, P. Helical close packings of ideal ropes. *Eur. Phys. J. E* **4**, 445-449 (2001).

45. Snir, Y. & Kamien, R. D. Entropically Driven Helix Formation. *Science* **307**, 1067 (2005).

46. Snir, Y. & Kamien, R. D. Helical tubes in crowded environments. *Phys. Rev. E* **75**, 051114 (2007).

47. Olsen, K. & Bohr, J. The generic geometry of helices and their close-packed structures. *Theor. Chem. Acc.* **125**, 207-215 (2010).

48. Wigner, E. P. Unreasonable Effectivness of Mathematics in the Natural Sciences. *Commun. Pure Appl. Math.* **13**, 1-14 (1960).

49. Chaikin, P. & Lubensky, T. *Principles of Condensed Matter Physics* (Cambridge University Press, 2000).

50. Dawkins R. *The Blind Watchmaker* (W. W. Norton & Company, London, 1986).

51. Goldenfeld, N. & Woese, C. Biology's next revolution. *Nature* **445**, 369 (2007).

52. Davis, P. *The Eerie Silence: Renewing Our Search for Alien Intelligence* (Mariner Books, 2011).

53. Levy, S. *Artificial Life: The Quest for a New Creation* (Penguin Books, 1993).

54. Darwin, C. *On the Origin of Species* (John Murray, London, 1859).

Acknowledgements: We are indebted to Pete von Hippel for his warm hospitality and to him, Jeremy Berg, and Brian Matthews for stimulating comments. **Funding:** This project received funding from the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie Grant Agreement No 894784. The contents reflect only the authors' view and not the views of the European Commission. Support from the University of Oregon (through a Knight Chair to JRB), NSF (GDR), University of Padova through "Excellence Project 2018" of the Cariparo foundation (AM), MIUR PRIN-COFIN2017 *Soft Adaptive Networks* grant 2017Z55KCW and COST action CA17139 (AG) is gratefully acknowledged. The computer calculations were performed on the Talapas cluster at the University of Oregon.

Author contributions: JRB, AM and TŠ developed the ideas for the calculations, and all the authors participated in exploring the consequences of the theory. TŠ carried out the calculations under the guidance of JRB. JRB and GDR wrote the paper. All authors reviewed the manuscript.

Emails: tskrbic@uoregon.edu, amos.maritan@pd.infn.it, achille.giacometti@unive.it, grose@jhu.edu, banavar@uoregon.edu

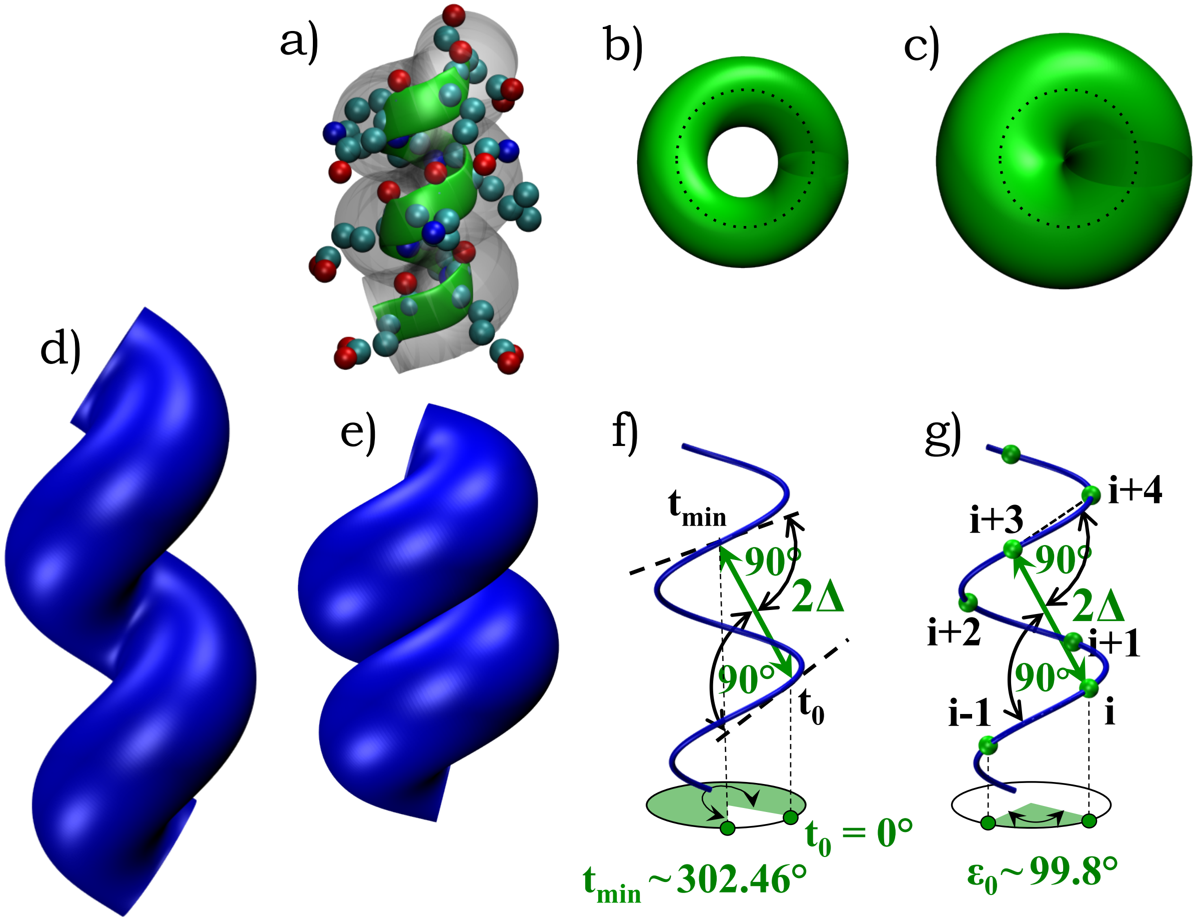

Figure 1: Optimal geometry of space-filling helix. (a) A segment of ten residues of a helix from phage T4 lysozyme protein 1L56 (residues 61-70). The green ribbon represents the helical trace formed by the C_α atoms, the spheres denote the heavy backbone and side-chains atoms in the helix, and the transparent tube is a guide to the eye. (b-c) show top-views of two continuum helices, both with a helix pitch P to helix radius R ratio $\eta=(P/2\pi R)\sim 0.4$ and a local radius of curvature of the helix, $R_{local}=R(1+\eta^2)\sim 1.16R$. The tube radii Δ in the two cases are different: $\Delta/R_{local}=1/2$ and 1 respectively. (b) When Δ is less than R_{local}, there is empty space in the interior. When Δ is bigger than R_{local}, the turn is too tight leading to a kink, as is sometimes observed in a garden hose (not shown). (c) The sweet spot occurs when $\Delta=R_{local}$, leading to maximization of the *local* self-interaction. (d-e) shows side views of two helices with η-values of 0.8 and ~0.4

respectively. In both cases, Δ has been chosen to be the local radius of curvature of the latter helix ~1.16R. (d) When η is larger than ~0.4, there is empty space between successive turns and the *non-local* self-interaction is not maximized. In the other limit of small η (not shown), successive turns of the tube overlap and this is forbidden sterically. (e) A Goldilocks situation here is when η is tuned just right to ~0.4 yielding (Δ/R)~1.16 for a continuum space-filling helix maximizing both local and non-local self-interaction. The top and side views of the optimal continuum helix are shown in (c) and (e) respectively. (f) and (g) show how these results can be captured analytically (see text) for a continuum and a discrete tube respectively.

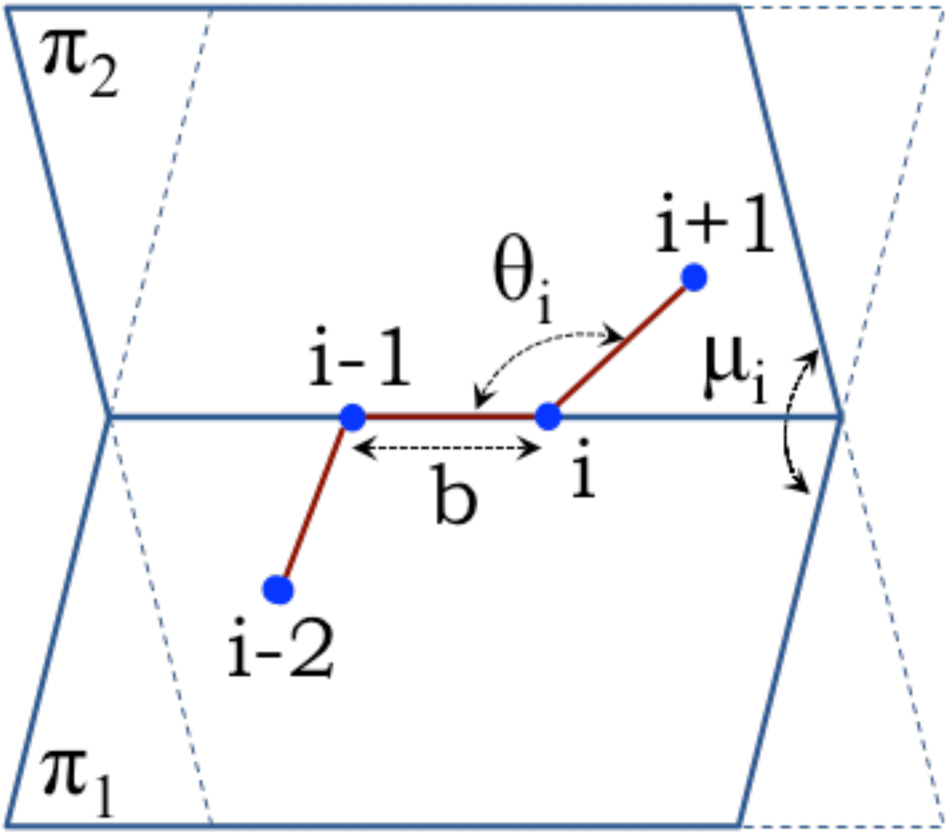

Figure 2: Coordinate system at discrete location i along tube axis. The bond length b, assumed here to be a constant, is the distance between successive points. The angle θ_i is the angle subtended at i by points (i-1) and (i+1) along the tube axis. μ_i is the dihedral angle between the planes π_1 and π_2 formed by [(i-2),(i-1),i] and [(i-1),i,(i+1)] respectively or equivalently the angle between the binormals in a Frenet reference frame at points (i-1) and i. Knowledge of the coordinates of the previous three points (i-2,i-1,i) and the variables (θ_i, μ_i) are sufficient to uniquely specify the coordinates of the point (i+1).

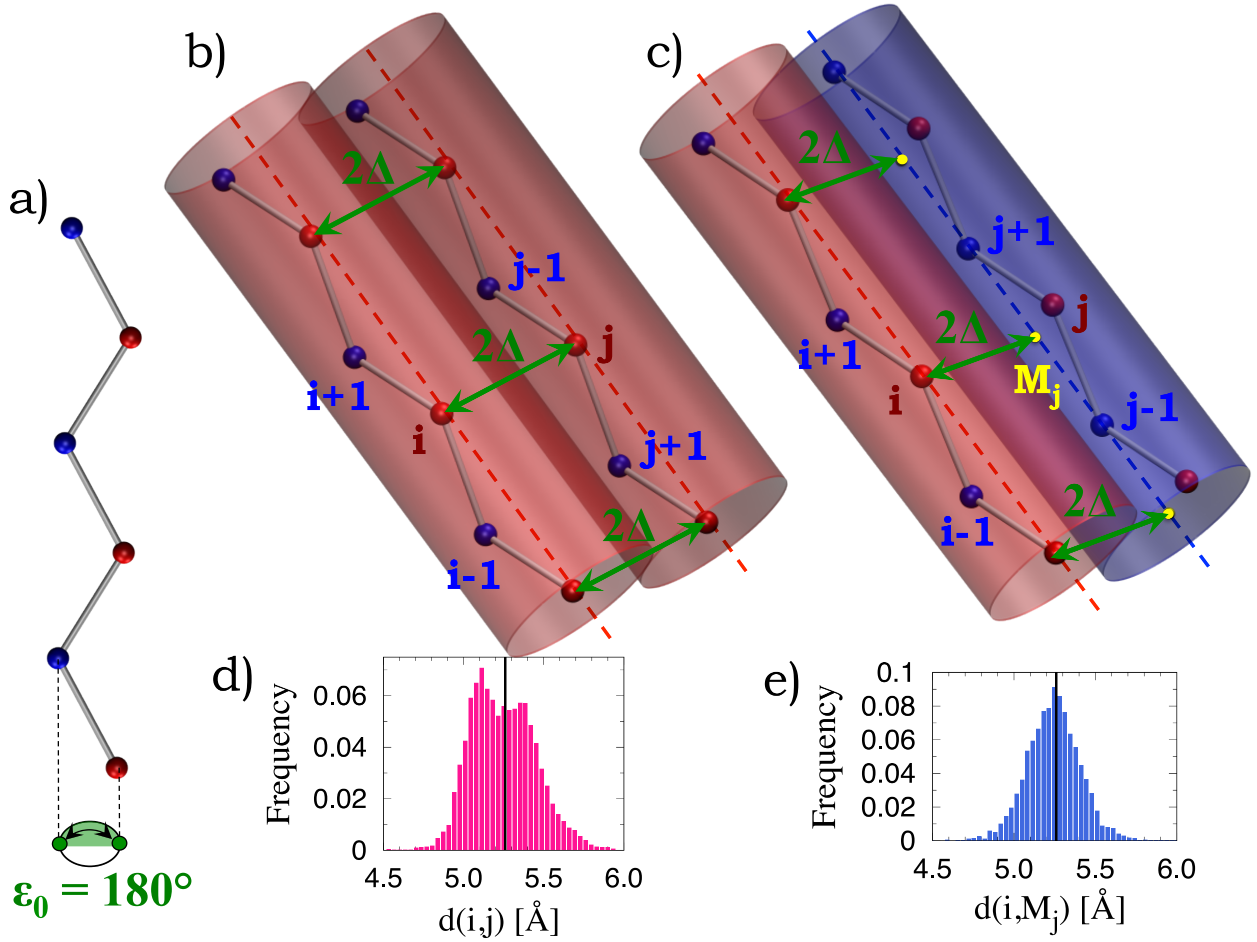

Figure 3: Optimal packing of strands. (a) A single two dimensional zig-zag strand (with a rotation angle of 180°) lying in the plane of the paper. This planarity can only occur for a

discrete tube and is forbidden for a tube in the continuum. Alternate points along a strand are colored red and blue. There are two equivalent choices for a straight tube axis, one lying along the line of blue points (the blue axis) or the line of red points (red axis). Two distinct space-filling arrangements for strand packing are shown corresponding to (b) red axis-red axis (or equivalently blue axis-blue-axis – not shown) packing and (c) red axis-blue axis (or equivalently blue axis-red axis – not shown) packing. The two cases correspond to anti-parallel and parallel β-sheets with distinct distance constraints. The yellow point M_j lies midway between the blue points j-1 and j+1. The maximization of self-interaction dictates that the distances (i,j) in (b) and (i,M_j) in (c) ought to be $2\Delta \sim 5.26$Å to ensure space filling. (d) and (e) show the histograms of the distances (i,j) and (i,M_j) in the interior of anti-parallel and parallel β-sheets in protein structures. The black vertical lines show the theoretical prediction of $2\Delta \sim 5.26$Å. The mean values of both histograms are the same as the theoretical prediction (see Table 1).

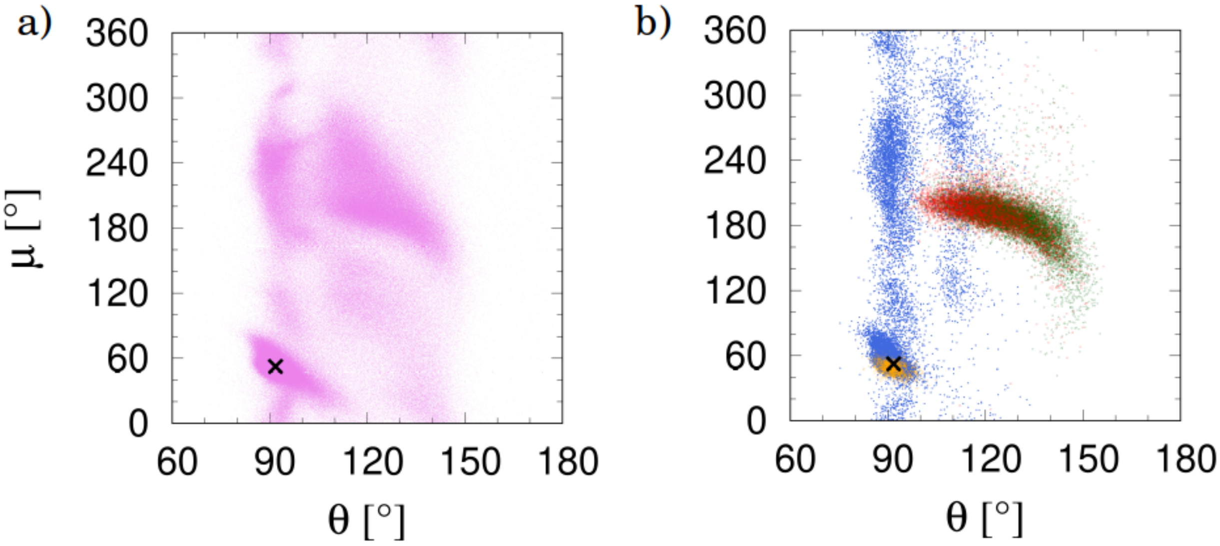

Figure 4: Two views of the local structure representation of proteins. a) (θ, μ) plot of the PDB data set (see Table 2) comprising 4416 proteins and 972,519 residues. Here, the local conformations of residues are shown in the (θ,μ) plane. For strands, a μ-value that deviates from ~180° is the signature of a twisted strand, which is still locally planar. The plot shows chiral symmetry breaking, i.e., the points are not symmetrically placed around μ=180°. Our simplified analysis does not attempt to account for this. b) (θ, μ) coordinates of random samples of 12000 points each from the interior of α-helices (orange); anti-parallel (green) and parallel (red) β-sheets; and β-turns (the two interior sites of (i,i+3) hydrogen-bonded residues with no helical residues) (blue). The tight turns have θ-values similar to those of helices. Unlike for helices and turns, the θ-values of strands are not constrained. The black X in both panels shows our prediction of the geometry of space-filling helices.

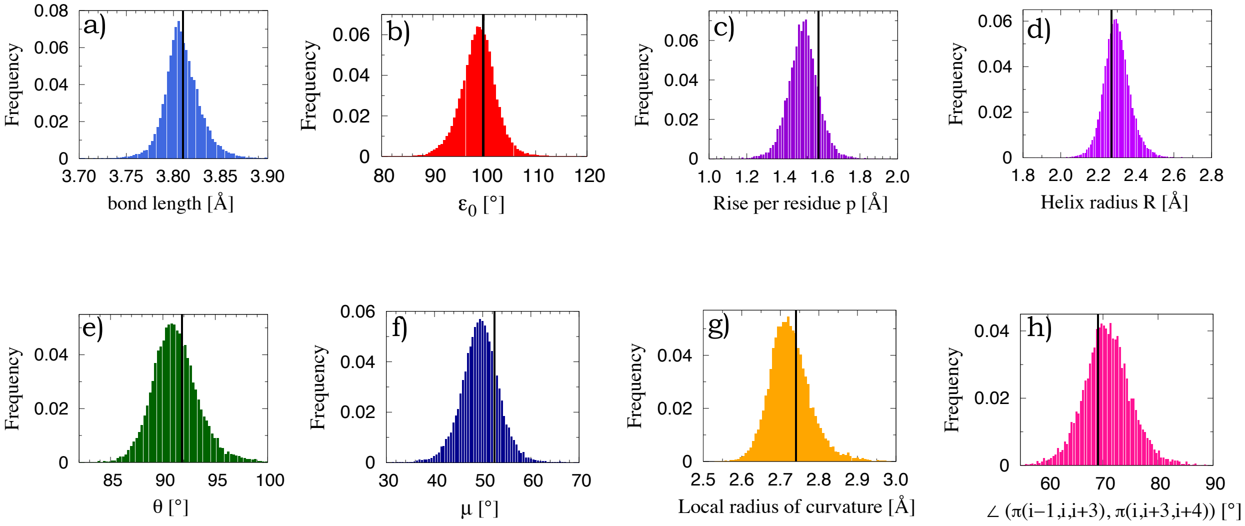

Figure 5: Distribution of α-helix characteristics. (a) Distribution of the experimentally determined bond lengths (consecutive C_α-C_α distances). The bond length in the theory was chosen to be the mean bond length of 3.81Å and sets the characteristic length scale. The other panels show the distributions of (b) the rotation angle, (c) the rise per residue, (d) the helix radius, (e) θ, (f) μ, (g) the local radius of curvature, and (h) the dihedral angle between the planes defined by the points (i-1,i,i+3) and (i,i+3,i+4) in Figure 1g. The triangles formed by the two triplets ought to be congruent but they are not co-planar. The black line in each of the panels (except the first) shows the zero parameter theoretical prediction. Overall, there is excellent accord between theory and observations from protein structures.

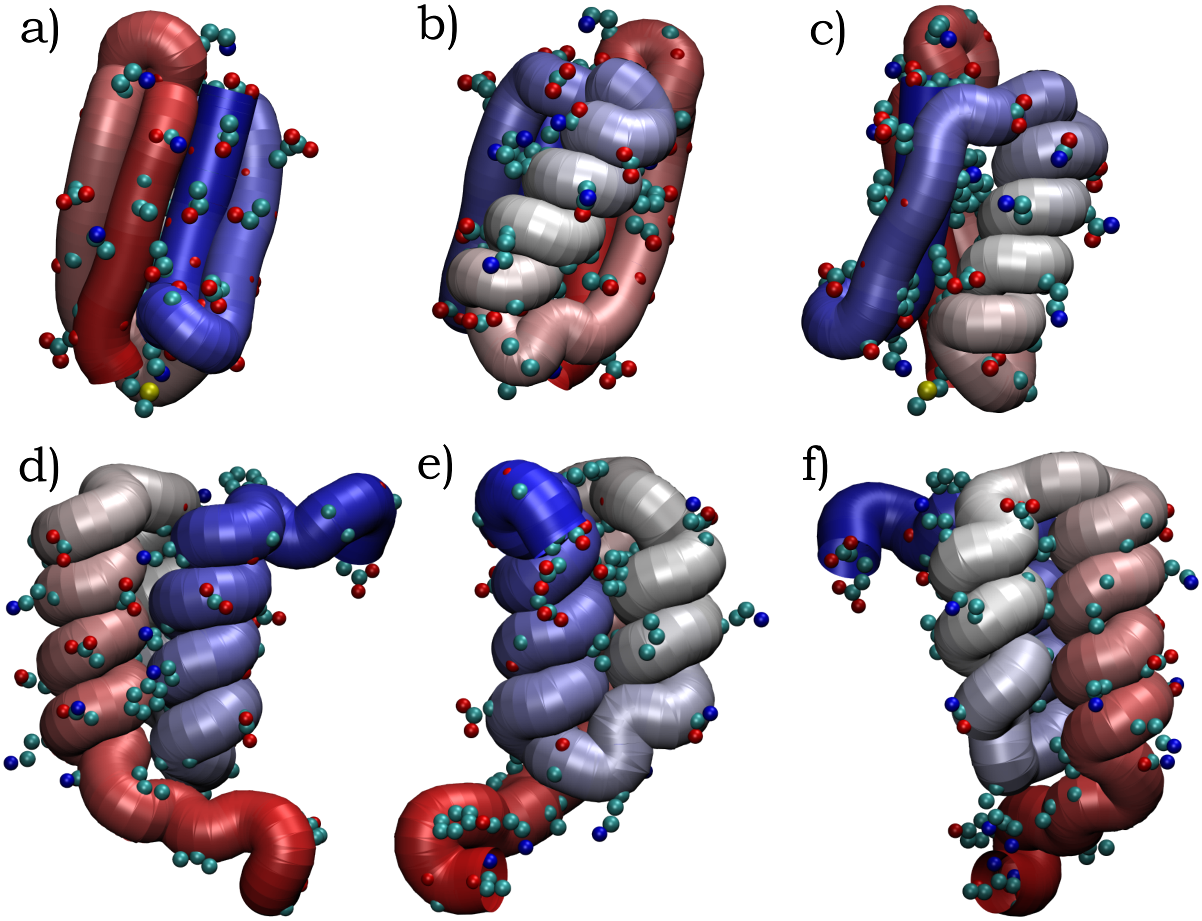

Figure 6: Consilience between mathematics and biochemistry. The figure shows three views each of two short proteins. (a-c) is the 56-residue long protein 3GB1 comprising 4 strands assembled into sheets along with a single helix. (d-f) is a protein of the same length, 2KDL, comprised of a three-helix bundle. Each panel shows a uniform tube, with the theoretically predicted radius of 2.6Å, whose axis passes through the C_α atoms. The sole exception is the β-sheet (for which hydrogen bonding was identified using DSSP (11)), where every other C_α atom is considered (as explained in Figures 3b and c). The tube color varies continuously from red to blue (via grey) as its axis moves from the N-terminal to the C-terminal. The heavy atoms of the side chains sticking outside the tube are shown. The maximization of the self-interaction through space-filling is evident.

Continuum tube diameter from theory 2Δ=5.26… Å		
Quantity	**Theory**	**PDB data**
HELIX		
Rotation angle ε [°]	99.8	99.1 ± 3.4
Number of residues per turn	3.61	3.63 ± 0.13
Helix radius R [Å]	2.27	2.30 ± 0.07
Rise per residue p [Å]	1.58	1.51 ± 0.08
Helix pitch P [Å]	5.69	5.47 ± 0.49
Pitch to radius ratio $\eta = P/(2\pi R)$	0.400	0.377 ± 0.046
$\angle(\pi(i-1,i,i+3), \pi(i,i+3,i+4))$ [°]	69.1	70.0 ± 4.4
Local radius of curvature [Å]	2.74	2.73 ± 0.05
θ [°]	91.8	91.3 ± 2.2
μ [°]	52.4	49.7 ± 3.9
SHEET		
Type I β-sheet: parallel		
θ [°]	flexible	121 ± 10
μ [°]	~180	191 ± 17
$d(i,M_j)$ [Å]	2Δ=5.26	5.26 ± 0.16
Type II β-sheet: antiparallel		
θ [°]	flexible	127 ± 10
μ [°]	~180	186 ± 20
$d(i,j)$ [Å]	2Δ=5.26	5.26 ± 0.20

Table 1: Quantitative comparison between theory and data from the Protein Data Bank (PDB). We choose the bond length to match the experimentally determined mean distance between successive C_α atoms of 3.81 ± 0.02Å. The chain is defined by discrete points denoted by 1,2,3,…,i,… d(i,j) is the distance between the points i and j. The angle $\angle(\pi(i,j,k), \pi(l,m,n))$ is the dihedral angle between the two planes formed by the sites (i,j,k) and (l,m,n). M_j is defined to be the geometrical center of the points j-1 and j+1. The agreement between theory and data is striking considering that the theory is parameter-free.

Table 2: PDB codes of the 4416 proteins used in our analysis.

16pk_A
1a1i_A
1a2p_B
1a2y_A
1a2y_B
1a2z_C
1a34_A
1a3a_A
1a4i_B
1a73_A
1a7d_A
1a7t_B
1a88_A
1a8q_A
1a8s_A
1a92_C
1ab1_A
1aba_A
1afb_3
1ag9_B
1agy_A
1ah7_A
1aho_A
1aii_A
1ako_A
1aky_A
1aoh_B
1aoz_A
1arb_A
1ast_A
1atg_A
1atl_B
1atz_B
1aun_A
1avb_A
1awd_A
1aye_A
1b0b_A
1b16_A
1b1c_A
1b2s_F
1b37_B
1b3a_B
1b4f_B
1b5e_A
1b63_A
1b66_A
1b67_A
1b8a_B
1b8d_K
1b8p_A
1b93_A
1bas_A
1baz_A
1bdo_A
1beh_A
1bf6_A
1bgf_A
1bgp_A
1iqc_C
1iqq_A
1iqz_A
1irq_A
1isp_A
1isu_A
1it2_B
1itw_D
1itx_A
1iu8_B
1iue_B
1iuz_A
1iv3_D
1iv9_A
1iwd_A
1ix1_B
1ixg_A
1iy8_C
1iyb_A
1iye_C
1iyn_A
1izc_A
1ize_A
1j05_B
1j0h_B
1j0p_A
1j1y_A
1j24_A
1j27_A
1j2j_B
1j2r_A
1j30_B
1j34_A
1j34_B
1j3w_C
1j48_A
1j71_A
1j75_A
1j77_A
1j7d_A
1j7g_A
1j8e_A
1j8u_A
1j9l_A
1ja9_A
1jae_A
1jak_A
1jat_A
1jay_B
1jcd_A
1jcv_A
1jd0_B
1jd1_C
1jd5_A
1jdh_B
1jdl_A
1jek_A
1jev_A
1jf8_A
1pnc_A
1pnd_A
1pp0_C
1psr_A
1ptq_A
1puc_A
1puf_B
1pvm_A
1pvx_A
1pxv_B
1pyo_B
1pzs_A
1q08_B
1q0q_A
1q0r_A
1q1r_B
1q1u_A
1q2h_A
1q4u_B
1q5m_B
1q5z_A
1q6o_A
1q7l_A
1q7l_B
1q8f_A
1qau_A
1qav_A
1qaz_A
1qb5_E
1qb7_A
1qba_A
1qcx_A
1qd1_B
1qd2_A
1qd9_C
1qdd_A
1qfv_B
1qgi_A
1qgj_A
1qgu_D
1qh5_B
1qhf_A
1qho_A
1qhq_A
1qhv_A
1qj5_B
1qjc_B
1qjw_B
1qkk_A
1ql0_B
1ql3_B
1qlw_A
1qmy_C
1qnj_A
1qnn_C
1qnp_A
1qnx_A
1qoz_B
1qre_A
1w0p_A
1w0u_A
1w1h_C
1w2c_A
1w2i_B
1w3i_A
1w3w_A
1w3y_A
1w4s_A
1w4t_A
1w4v_B
1w4x_A
1w53_A
1w5r_B
1w66_A
1w6s_C
1w6s_D
1w70_A
1w8o_A
1w8u_A
1w99_A
1w9p_A
1w9s_A
1wa3_A
1wb0_A
1wb6_B
1wba_A
1wbe_A
1wbh_B
1wbi_H
1wbj_A
1wbj_B
1wc2_A
1wc9_A
1wcf_A
1wcg_B
1wck_A
1wd3_A
1wdd_S
1wdy_A
1wf3_A
1whi_A
1wka_A
1wko_A
1wkq_B
1wkr_A
1wku_B
1wkx_A
1wld_A
1wlg_B
1wlz_C
1wm2_A
1wma_A
1wmd_A
1wmh_A
1wmw_A
1wmz_D
1wn2_A
1wny_A
2buw_B
2bv2_B
2bv4_A
2bw0_A
2bw8_A
2bwf_A
2bwl_A
2bwr_B
2c0c_A
2c0h_A
2c0r_B
2c0z_A
2c1d_D
2c1s_A
2c1v_B
2c29_F
2c2n_A
2c2p_A
2c2u_A
2c3n_C
2c41_F
2c42_B
2c4e_A
2c4f_T
2c4j_D
2c4n_A
2c53_A
2c6q_B
2c6u_A
2c6z_A
2c78_A
2c7p_A
2c81_A
2c82_B
2c8h_D
2c92_D
2c95_B
2c9q_A
2cal_A
2car_B
2cb5_A
2cb8_A
2cbz_A
2cc6_A
2cch_B
2ccq_A
2ccw_A
2cdn_A
2cf7_C
2cfe_A
2cg7_A
2cgq_A
2chc_B
2cia_A
2ciu_A
2ciw_A
2cj3_A
2cj4_A
2cjj_A
2hwn_D
2hxm_A
2hxp_A
2hxs_A
2hxt_A
2hy5_A
2hy5_B
2hy7_A
2hyk_A
2hyv_A
2hzl_B
2hzy_B
2i0q_A
2i1n_A
2i24_N
2i2q_A
2i3f_A
2i49_A
2i4a_A
2i5r_B
2i5v_O
2i61_A
2i62_D
2i6v_A
2i7c_C
2i7d_A
2i7f_B
2i8t_B
2i9a_D
2i9i_A
2iax_A
2ib8_A
2ibj_A
2ibl_A
2ibp_B
2ic6_A
2ic7_B
2idl_B
2if6_A
2ifc_C
2ig8_A
2igi_A
2igp_A
2igv_A
2igx_A
2ih5_A
2ihd_A
2ii2_A
2iid_A
2ijh_A
2ijq_A
2ijx_D
2imf_A
2imi_B
2imq_X
2in8_A
2inc_A
2inc_B
2ior_A
2rc3_A
2rc8_B
2rci_A
2rcq_A
2rcv_E
2rcz_B
2rdh_C
2rdq_A
2rdu_A
2rdz_A
2ree_A
2reg_A
2rem_B
2rer_A
2rfg_A
2rfm_B
2rh2_A
2rh3_A
2rhi_A
2rhk_C
2ri0_B
2ri7_A
2ri9_A
2rik_A
2riq_A
2rji_A
2rjw_A
2rk3_A
2rk5_A
2rkl_A
2rkq_A
2rku_A
2rky_C
2sak_A
2sec_I
2sga_A
2sn3_A
2tnf_B
2uuy_B
2uv4_A
2uvj_A
2uvo_B
2uw1_A
2uwa_A
2uyt_A
2uyw_A
2uyz_A
2uyz_B
2uz1_D
2uzc_C
2v09_A
2v0h_A
2v0s_A
2v0u_A
2v1o_B
2v1q_A
2v1w_B
2v25_A
2v27_A
2zk9_X
2zkd_B
2zl6_B
2znd_A
2znr_A
2zoo_A
2zpd_A
2zpo_A
2zpu_A
2zqe_A
2zqm_A
2zqn_B
2zs0_A
2zs0_D
2zs1_B
2zs1_C
2zsi_A
2ztl_C
2zu1_B
2zu2_A
2zux_B
2zuy_A
2zw2_A
2zwd_A
2zwj_A
2zwn_A
2zwu_A
2zx2_A
2zxj_B
2zxy_A
2zya_B
2zyh_B
2zyo_A
2zzd_E
2zzd_J
2zzj_A
2zzr_A
2zzs_O
2zzv_B
3a02_A
3a03_A
3a04_A
3a07_A
3a09_A
3a0y_B
3a16_C
3a1c_A
3a21_A
3a2q_A
3a2v_I
3a2z_A
3a39_A
3a3d_B
3a3v_A
3a40_X
3a4r_A
3a4u_A
3a4w_B
3a57_A
3euf_D
3eul_A
3eun_A
3eup_B
3evf_A
3evk_D
3evy_B
3ew0_A
3ew1_D
3ewi_A
3exe_D
3exr_A
3ey6_A
3eye_A
3eyi_A
3eyp_B
3ezi_B
3f0y_C
3f17_A
3f1l_A
3f1p_A
3f1p_B
3f2e_A
3f2u_A
3f3q_A
3f3x_A
3f47_A
3f4m_A
3f4s_A
3f52_A
3f5l_B
3f5o_G
3f6o_A
3f6q_A
3f6q_B
3f6y_A
3f74_B
3f75_A
3f75_P
3f7l_A
3f7q_A
3f8m_B
3f97_A
3f9b_A
3f9r_A
3fas_B
3fb9_A
3fbg_A
3fbl_A
3fd7_B
3fde_B
3fdl_A
3fdq_A
3fdr_A
3fe0_A
3fe7_A
3fev_A
3ff5_B
3ff7_C
3kl0_B
3kl6_B
3klq_A
3klr_A
3kmt_C
3kmv_D
3knb_B
3knv_A
3kp8_A
3kpb_D
3kq0_A
3kqi_A
3kqr_A
3kre_A
3krs_A
3kru_A
3kse_D
3ksh_A
3ksv_A
3ksx_A
3kt9_A
3ktz_A
3ku3_B
3kus_B
3kuv_A
3kwe_A
3kxt_A
3kyj_A
3kz5_A
3kz7_A
3kzj_A
3kzu_B
3l07_B
3l0f_A
3l0l_B
3l18_A
3l1e_A
3l2c_A
3l32_A
3l39_A
3l3u_A
3l41_A
3l42_A
3l46_A
3l4p_A
3l4r_A
3l5l_A
3l6g_A
3l6n_A
3l77_A
3l7h_B
3l7t_B
3l8e_B
3l8w_A
3l91_A
3l91_B
3l9a_X
3l9f_D
3l9s_A

1bhp_A
1bj7_A
1bkp_A
1bn8_A
1bq8_A
1bqb_A
1bqk_A
1brt_A
1bs3_B
1bs9_A
1bsg_A
1bue_A
1bx4_A
1bx7_A
1bxu_A
1bxy_A
1byi_A
1c02_A
1c0p_A
1c1d_A
1c1k_A
1c1l_A
1c1y_A
1c1y_B
1c4q_B
1c52_A
1c5e_A
1c75_A
1c7j_A
1c7k_A
1c7n_F
1cc8_A
1ccw_B
1cf3_A
1cg5_A
1cg5_B
1chd_A
1cip_A
1cjc_A
1cjw_A
1cka_A
1clc_A
1cnv_A
1cnz_B
1coj_A
1cpq_A
1cqm_B
1cru_B
1cs6_A
1ctj_A
1cuo_A
1cxy_A
1cyd_D
1cyo_A
1cz9_A
1cza_N
1czf_A
1czn_A
1d02_B
1d0d_A
1d2n_A
1d4o_A
1jfl_B
1jfr_A
1jfu_A
1jfx_A
1jg1_A
1jhd_A
1jhf_A
1jhg_A
1jhj_A
1jhs_A
1ji1_A
1jid_A
1jif_A
1jke_C
1jkg_A
1jkx_A
1jl1_A
1jl7_A
1jlj_A
1jlt_A
1jlt_B
1jm1_A
1jnr_C
1jnr_D
1jo0_A
1jo8_A
1jpe_A
1jq5_A
1jqe_A
1jr8_A
1jsd_B
1jt2_A
1ju2_A
1jub_B
1juv_A
1jvw_A
1jwq_A
1jy2_N
1jy2_R
1jy3_P
1jyh_A
1jyo_B
1k07_A
1k0i_A
1k0m_A
1k1e_K
1k20_A
1k2e_A
1k4i_A
1k4m_C
1k5c_A
1k5n_A
1k66_B
1k6a_A
1k6d_B
1k7c_A
1k7i_A
1k94_A
1k9u_B
1ka1_A
1kaf_A
1kao_A
1qrp_E
1qs1_A
1qsa_A
1qsg_A
1qt9_A
1qtn_A
1qtw_A
1qu1_D
1qve_B
1qw9_B
1qwd_A
1qwg_A
1qwk_A
1qwm_B
1qwz_A
1qxy_A
1qy6_A
1qz9_A
1r0r_E
1r12_A
1r17_A
1r1p_A
1r1t_B
1r26_A
1r29_A
1r2m_A
1r2r_B
1r3q_A
1r45_B
1r55_A
1r6d_A
1r6j_A
1r6x_A
1r77_B
1r7j_A
1r87_A
1r88_B
1r89_A
1r8h_D
1r8s_A
1r9d_A
1r9h_A
1r9l_A
1ra0_A
1rc9_A
1rdo_2
1rfs_A
1rfy_B
1rg8_B
1rgx_C
1rgz_A
1rh6_B
1rh9_A
1rhc_A
1rie_A
1rjd_A
1rkd_A
1rki_A
1rkq_A
1rku_A
1rl0_A
1rlh_A
1wo8_D
1wod_A
1wog_E
1woq_B
1wor_A
1wpa_A
1wpn_B
1wpu_A
1wq8_A
1wqj_B
1wqj_I
1wr8_B
1wrd_A
1wri_A
1wrm_A
1ws8_A
1wst_A
1wt6_A
1wta_A
1wte_A
1wtj_A
1wto_A
1wu9_B
1wui_S
1wur_B
1wve_D
1wvf_A
1wwz_B
1wy1_A
1wy2_B
1wyx_B
1wz3_A
1wz8_A
1wzd_B
1x0c_A
1x0l_A
1x1i_A
1x1n_A
1x1o_B
1x2i_A
1x2t_C
1x38_A
1x3o_A
1x3x_B
1x46_A
1x54_A
1x6i_A
1x6x_X
1x8d_C
1x91_A
1x9i_A
1x9u_A
1xcr_A
1xd3_C
1xdw_A
1xeo_A
1xes_B
1xfk_A
1xg0_B
1xg2_A
1xg2_B
1xg4_A
2cjl_B
2cjp_A
2cjs_C
2ckf_D
2ckk_A
2cks_A
2cm4_A
2cmj_B
2cmt_A
2cn3_B
2cnz_A
2cov_I
2cs7_A
2cu5_A
2cvd_D
2cve_A
2cvi_B
2cwd_A
2cwi_B
2cwr_A
2cws_A
2cxn_B
2cyg_A
2cz4_A
2czd_A
2czq_B
2d0i_B
2d16_A
2d1c_A
2d1x_A
2d1y_C
2d29_A
2d37_A
2d3d_A
2d3n_A
2d4n_A
2d4p_A
2d4v_C
2d5b_A
2d5c_A
2d5k_C
2d5w_B
2d5z_B
2d68_B
2d69_A
2d6m_A
2d73_A
2d7t_H
2d7t_L
2d81_A
2d8d_B
2dc1_B
2dc3_A
2dc4_B
2ddb_C
2ddx_A
2de3_A
2de6_A
2de6_F
2dep_A
2dfb_A
2dfd_C
2ioy_B
2ip2_B
2ip6_A
2ipr_B
2iq7_A
2iqj_A
2iru_B
2is8_A
2is9_A
2it1_A
2iu5_A
2ium_A
2ivf_A
2ivf_B
2ivn_A
2ivx_A
2ivy_A
2iw0_A
2iw1_A
2iw2_B
2iwk_A
2iwz_A
2ix4_B
2ixc_A
2ixd_B
2ixk_A
2ixm_A
2izz_B
2j1s_A
2j23_A
2j27_A
2j2j_F
2j3x_A
2j5g_A
2j5i_F
2j5y_A
2j5z_C
2j6a_A
2j6b_A
2j6f_A
2j6i_A
2j6l_F
2j73_B
2j7j_A
2j7z_A
2j8b_A
2j8g_A
2j8h_A
2j8k_A
2j8m_A
2j8w_A
2j9c_B
2j9o_B
2j9w_A
2ja2_A
2jab_C
2jaf_A
2jb0_A
2jba_B
2jbv_A
2jc4_A
2jc5_A
2v2g_C
2v33_B
2v36_D
2v3g_A
2v3s_A
2v4n_A
2v4v_A
2v5i_A
2v5j_A
2v5z_A
2v6a_O
2v6k_B
2v6u_A
2v7w_C
2v84_A
2v89_A
2v8i_A
2v8u_A
2v9m_A
2v9t_B
2v9v_A
2vac_A
2vap_A
2vb1_A
2vba_D
2vbk_A
2vc3_A
2vc8_A
2ve8_E
2veb_A
2vfk_A
2vfq_A
2vg1_B
2vg3_C
2vgp_D
2vha_B
2vi8_A
2vig_A
2vj0_A
2vjp_B
2vjv_B
2vk8_C
2vkj_A
2vkl_A
2vkv_A
2vla_A
2vlf_B
2vlu_A
2vmc_A
2vn4_A
2vn6_A
2vn6_B
2vng_A
2vnk_C
2vnl_A
2vnz_X
2vo4_A
2vo8_A
2vo9_B
2voc_A
2voz_A
2vpg_A
3a5p_D
3a5r_A
3a6r_B
3a72_A
3a7l_A
3a7n_A
3a8g_B
3a8u_X
3a9b_A
3a9f_A
3a9j_A
3a9l_B
3a9q_N
3a9s_B
3aa0_A
3aa6_B
3aaf_B
3aal_A
3aam_A
3ab6_A
3aba_A
3abf_E
3aci_A
3act_B
3acx_A
3adg_A
3ado_A
3aey_A
3afm_A
3afv_A
3ag3_C
3ag3_E
3ag7_A
3agn_A
3ah2_A
3ahc_A
3ahn_A
3ahx_D
3ahy_A
3ahz_A
3ai3_C
3aia_A
3aj7_A
3ajo_A
3ajx_C
3ak2_B
3ak8_H
3akb_A
3akh_A
3alf_A
3alu_A
3amn_B
3ans_B
3ap9_A
3apa_A
3apr_E
3b34_A
3b42_A
3b4u_B
3b4w_A
3b51_X
3b5g_B
3ff9_B
3fg0_F
3fgd_A
3fh2_A
3fhg_A
3fid_A
3fil_B
3fiq_A
3fju_B
3fkb_E
3fkc_A
3fke_A
3flg_A
3flv_A
3fn5_A
3fp5_A
3fpc_A
3fpf_A
3fpk_B
3fpr_D
3fpu_B
3fpw_A
3fq3_C
3fqm_A
3frq_A
3frr_A
3fs7_A
3ft1_C
3ftd_A
3fv3_G
3fv9_G
3fvb_B
3fvh_A
3fwa_A
3fwy_A
3fx4_A
3fx7_A
3fy1_B
3fy3_A
3fym_A
3fza_A
3fzy_B
3g00_A
3g0e_A
3g0m_A
3g1l_A
3g1p_B
3g1v_A
3g20_B
3g21_A
3g2b_A
3g2s_B
3g46_B
3g48_A
3g5k_D
3g5w_C
3g6m_A
3g7n_B
3g7w_A
3g8h_A
3g98_B
3g9m_B
3l9u_A
3l9y_B
3las_B
3lat_A
3lbe_D
3lbf_C
3lbl_A
3lbm_B
3lcc_A
3lcm_A
3ld3_A
3ldd_A
3le0_A
3le3_A
3le4_A
3let_A
3lf6_B
3lfh_F
3lfj_B
3lfk_C
3lg5_A
3lgi_A
3lgn_A
3lhq_A
3lhr_B
3lid_B
3lim_D
3liy_A
3ljw_B
3lke_A
3lkt_B
3lkt_Q
3llb_A
3llu_A
3lny_A
3log_C
3lp6_C
3lpc_A
3lpe_B
3lpe_G
3lpw_B
3lqw_A
3lr4_A
3lrt_A
3ls0_A
3ls9_A
3ltj_A
3luc_A
3lum_D
3lvf_P
3lw6_A
3lwg_B
3lwz_A
3lx3_A
3lxr_A
3lxr_F
3lxy_A
3ly0_B
3ly7_A
3lz5_A
3lzo_B
3lzw_A

1d4t_A
1d5l_B
1d5t_A
1d7o_A
1daa_B
1dbf_A
1dbw_B
1dci_C
1deu_A
1dfu_P
1dgf_A
1dhn_A
1dj0_B
1djr_G
1dk8_A
1dl5_B
1dlf_H
1dlf_L
1dlj_A
1dlw_A
1dly_A
1dm1_A
1doi_A
1dok_A
1dp7_P
1dpj_A
1dpt_A
1dqg_A
1dqi_A
1dqp_A
1dqz_A
1ds1_A
1dsx_C
1dsz_A
1dtd_B
1duv_H
1dxe_B
1dxj_A
1dxy_A
1dys_B
1dzk_A
1e0w_A
1e25_A
1e29_A
1e2w_B
1e3d_B
1e4c_P
1e4m_M
1e4v_A
1e59_A
1e5k_A
1e5m_A
1e6i_A
1e6y_B
1e7l_B
1e7s_A
1e9g_A
1eaj_B
1eao_A
1ear_A
1eb6_A
1eco_A
1kap_P
1kaz_A
1kdg_B
1kdj_A
1kdo_B
1keq_B
1kew_A
1kfw_A
1kg2_A
1kgc_D
1khi_A
1khq_A
1kid_A
1kjv_A
1klx_A
1km9_A
1kms_A
1kmt_A
1kng_A
1knt_A
1koe_A
1kol_B
1kop_A
1kp6_A
1kpt_A
1kpu_B
1kq1_B
1kq3_A
1kqp_A
1kqr_A
1krh_A
1krn_A
1ks8_A
1ku1_A
1kug_A
1kvd_C
1kve_D
1kw6_B
1kwf_A
1kwg_A
1kzq_A
1l2p_A
1l2t_B
1l3p_A
1l5o_A
1l5w_B
1l6r_A
1l6w_B
1l7l_A
1l9l_A
1l9x_A
1lb6_A
1lc3_A
1lc5_A
1lcl_A
1lcp_A
1le6_A
1lgt_A
1lj5_A
1lj9_B
1ljo_A
1lk5_B
1rlk_A
1rm6_A
1rm6_B
1rm6_C
1roc_A
1rp0_B
1rqj_A
1rro_A
1rtq_A
1rtt_A
1ru0_B
1ru4_A
1rv9_A
1rwh_A
1rwj_A
1rwr_A
1rwy_B
1rwz_A
1rx0_C
1ry9_C
1ryi_B
1ryo_A
1ryp_I
1ryp_J
1ryp_K
1ryp_Z
1rzh_H
1rzh_L
1rzh_M
1s1d_B
1s2o_A
1s3c_A
1s57_B
1s5m_A
1s5u_D
1s69_A
1s9r_A
1sa3_A
1sat_A
1sau_A
1sbp_A
1sd5_A
1sdi_A
1sds_A
1seg_A
1sen_A
1sf9_A
1sff_C
1sfs_A
1sg4_C
1sgw_A
1sh7_B
1sh8_B
1shu_X
1skz_A
1smo_A
1sn2_B
1snn_A
1stm_B
1svb_A
1svd_M
1svf_B
1xg7_B
1xgs_A
1xiw_A
1xiw_C
1xiw_H
1xk4_H
1xk4_I
1xky_B
1xkz_B
1xlq_C
1xm8_A
1xmk_A
1xmp_B
1xmt_A
1xng_B
1xnk_A
1xo7_B
1xoc_A
1xov_A
1xph_A
1xpp_C
1xqo_A
1xre_A
1xrk_B
1xs5_A
1xso_B
1xsz_A
1xt5_A
1xtt_C
1xty_B
1xu1_D
1xu1_T
1xvg_C
1xvg_E
1xvo_A
1xvx_A
1xw6_A
1xwt_A
1xwv_A
1xww_A
1xx1_C
1xxq_D
1xyz_A
1y0h_A
1y0m_A
1y1p_A
1y1x_A
1y20_A
1y2t_B
1y37_A
1y43_B
1y4j_B
1y4w_A
1y51_A
1y5i_B
1y60_E
1y66_C
1y6i_A
1y7p_B
1y7t_B
1y7w_A
1y80_A
2dg1_C
2dga_A
2dge_B
2dgk_A
2dho_A
2dkj_A
2dko_A
2dm9_B
2dp6_A
2dp9_A
2dpf_D
2dqa_A
2dql_A
2dr1_B
2dri_A
2drm_B
2ds2_D
2ds5_A
2dsj_B
2dsn_B
2dsx_A
2dt4_A
2dtj_A
2dtx_A
2dur_A
2dvm_B
2dvx_B
2dwu_A
2dxe_B
2dy0_A
2dy1_A
2dyj_B
2dyr_K
2dyu_A
2dze_A
2e0q_A
2e0t_A
2e11_B
2e1n_B
2e1z_A
2e27_L
2e2o_A
2e3a_A
2e3z_B
2e42_A
2e4t_A
2e5f_A
2e5y_B
2e6f_A
2e6u_X
2e7u_A
2e7z_A
2e85_A
2e8e_A
2e9m_A
2e9y_B
2ea3_A
2eab_A
2ebb_A
2ebo_C
2ecs_A
2ecu_A
2jcb_A
2jcq_A
2jda_A
2jdd_A
2jdf_A
2jdk_D
2je6_B
2je8_B
2jek_A
2jep_B
2jft_A
2jg6_A
2jh1_A
2jhf_B
2jhq_A
2ji7_A
2jik_A
2jjc_A
2jjf_A
2jjn_A
2jjs_C
2jk9_A
2jkb_A
2jkg_A
2jkh_A
2jl1_A
2jlp_A
2jlq_A
2lis_A
2mnr_A
2nml_A
2nmx_A
2nn8_A
2nnr_A
2nnu_A
2no4_A
2npt_D
2nql_B
2ns1_B
2nsf_A
2nsz_A
2nt4_A
2ntp_A
2nug_B
2nuh_A
2nuk_A
2nuw_A
2nw2_B
2nx0_A
2nx4_C
2nxb_B
2nyb_A
2nz7_A
2nzh_A
2o07_B
2o0b_A
2o1c_B
2o1k_B
2o20_F
2o28_A
2o2c_C
2o2p_D
2vpj_A
2vq4_A
2vqg_D
2vri_A
2vrs_C
2vsv_A
2vtc_B
2vuj_A
2vun_B
2vuo_A
2vv6_D
2vve_A
2vvp_B
2vvt_B
2vvw_A
2vw8_A
2vwf_A
2vwr_A
2vws_C
2vx5_A
2vxn_A
2vxq_A
2vxt_I
2vxt_L
2vxy_A
2vyo_A
2vyq_A
2vyw_A
2vyx_C
2vzc_A
2vzm_A
2w0p_B
2w15_A
2w1j_B
2w1p_A
2w1r_A
2w1v_A
2w20_A
2w2b_B
2w2j_A
2w2k_A
2w31_B
2w39_A
2w3g_A
2w3j_A
2w3p_B
2w3v_A
2w3x_A
2w40_A
2w43_A
2w47_A
2w4c_A
2w4f_A
2w4i_F
2w50_B
2w5q_A
2w70_A
2w7n_A
2w7w_B
2w83_C
2w86_A
2w8x_A
3b5l_B
3b5m_B
3b5n_A
3b5n_B
3b5n_D
3b5n_K
3b64_A
3b6i_A
3b76_A
3b7e_A
3b7s_A
3b84_A
3b8f_C
3b8i_E
3b8z_B
3b9c_C
3b9d_A
3b9w_A
3ba1_A
3baa_A
3bal_B
3bbb_D
3bc1_B
3bc9_A
3bd1_A
3bd2_A
3bec_A
3beo_A
3ber_A
3bex_A
3bf7_B
3bfk_B
3bfo_B
3bfq_G
3bfv_A
3bg8_A
3bgo_P
3bh4_A
3bh7_A
3bh7_B
3bj1_C
3bje_A
3bkb_A
3bkj_H
3bkr_A
3bkt_A
3bl6_A
3bmb_B
3bmw_A
3bmx_B
3bn6_A
3bnj_A
3bo6_B
3bod_A
3boe_A
3boi_A
3bom_C
3bom_D
3bov_A
3bp5_A
3bpj_B
3bpv_A
3g9x_A
3ga3_A
3ga4_A
3gad_F
3gah_A
3gbe_A
3gbs_A
3gc6_A
3gcz_A
3gd6_A
3gd8_A
3gdc_A
3gdl_B
3ge3_A
3ge3_E
3gfu_A
3gg7_A
3gg9_B
3ggw_C
3ggy_A
3gh6_A
3gha_A
3gip_A
3gir_A
3gk7_B
3gkb_C
3gkj_A
3gkm_A
3gkr_A
3gkt_A
3gkv_B
3gl0_A
3glr_A
3glv_B
3gmf_A
3gmg_A
3gmi_A
3gms_A
3gmv_X
3gmx_B
3gn9_C
3gne_A
3gnr_A
3go2_A
3go6_A
3goc_B
3goe_A
3gon_A
3gox_B
3gp3_D
3gp4_B
3gpg_B
3gqh_A
3gqj_A
3grh_A
3grn_A
3gru_A
3gsh_A
3gt5_A
3gv6_A
3gvf_A
3gvg_B
3m07_A
3m0f_A
3m0j_A
3m0m_B
3m1h_B
3m21_D
3m3g_A
3m4d_A
3m5l_A
3m5q_A
3m66_A
3m6b_A
3m6z_A
3m73_A
3m7o_A
3m7q_B
3m8j_A
3m8o_H
3m8o_L
3m8t_B
3m8u_A
3m91_C
3m9q_B
3mab_A
3mao_A
3maz_A
3mb4_B
3mb5_A
3mbg_B
3mbk_B
3mbx_H
3mcb_B
3md1_A
3md7_A
3md9_A
3mdm_A
3mds_B
3mdu_A
3meb_B
3mf7_A
3mgn_B
3mh9_A
3mhs_B
3mhy_C
3mi4_A
3mil_A
3mjo_B
3mjv_B
3mkh_B
3mlb_A
3mm5_B
3mm6_A
3mmg_A
3mmh_B
3mmw_D
3mn1_C
3mos_A
3moy_A
3mpc_A
3mpz_B
3mq2_B
3mqd_A

1edg_A
1edq_A
1eej_B
1egw_B
1eis_A
1ej0_A
1ej2_A
1ejb_A
1ekj_C
1ekx_A
1elk_A
1elr_A
1elu_A
1elw_A
1enf_A
1eo6_B
1ep0_A
1eq9_B
1es5_A
1esw_A
1eu3_A
1euh_C
1euv_A
1euv_B
1evh_A
1ex2_B
1ext_A
1eyh_A
1eyl_A
1eyv_A
1ez3_B
1ezg_B
1ezm_A
1f08_B
1f0k_B
1f0y_B
1f1m_C
1f1u_A
1f39_A
1f3u_G
1f46_B
1f4p_A
1f5j_A
1f5v_A
1f60_A
1f60_B
1f7l_A
1f8m_C
1f94_A
1f9f_D
1fcz_A
1fd3_A
1fe0_B
1fec_B
1feh_A
1fj2_B
1fk5_A
1flj_A
1fm0_D
1fm4_A
1fn9_A
1fob_A
1lkp_A
1llf_B
1llm_C
1lo6_A
1lq9_A
1lqa_A
1lqv_A
1lqx_A
1lr7_A
1lrh_A
1ls6_A
1ls9_A
1lst_A
1lt1_H
1lua_C
1lvw_B
1lw6_E
1lw6_I
1lwb_A
1lwd_B
1ly2_A
1m0d_C
1m0s_B
1m0u_A
1m15_A
1m1n_E
1m1n_F
1m1r_A
1m2d_B
1m2h_A
1m2t_B
1m2x_D
1m3u_C
1m40_A
1m4i_A
1m4j_A
1m55_A
1m5t_A
1m6j_B
1m70_D
1m7a_B
1m7g_A
1m7j_A
1m7s_D
1m8s_A
1m93_B
1m9z_A
1mb4_A
1mc2_A
1md6_A
1me4_A
1mex_L
1mfa_H
1mg4_A
1mgq_C
1mgr_A
1mgt_A
1mhn_A
1mhx_A
1mi3_B
1mix_A
1mj5_A
1sw5_B
1swy_A
1sxq_B
1sxr_A
1sy7_B
1syy_A
1szh_A
1szn_A
1szo_K
1t00_A
1t06_A
1t0b_D
1t0f_B
1t0f_C
1t0p_B
1t0t_X
1t1g_A
1t1j_B
1t1v_B
1t2d_A
1t2h_B
1t2w_C
1t3q_A
1t3q_B
1t3y_A
1t4b_B
1t61_C
1t61_E
1t6c_A
1t6g_D
1t6u_L
1t6v_N
1t7q_B
1t7r_A
1t8h_A
1t8k_A
1t8t_B
1t8z_C
1t92_B
1t9i_B
1ta3_A
1ta3_B
1ta9_B
1tag_A
1taw_B
1tbf_A
1tc5_B
1tca_A
1ten_A
1tez_B
1tf1_A
1tf4_A
1tg0_A
1tg7_A
1tgr_A
1tgx_B
1th7_H
1thg_A
1thm_A
1thx_A
1thz_A
1tjy_A
1y8a_A
1y9l_A
1y9w_B
1y9z_B
1yac_B
1yar_D
1yar_N
1yb0_B
1yb5_A
1ybi_B
1ybk_D
1ybz_A
1yd3_A
1ydy_A
1yfn_C
1yfu_A
1yif_A
1yii_A
1ykd_A
1yki_B
1yn3_B
1yn8_E
1yn9_A
1ynb_C
1ynh_B
1ynp_B
1yo3_A
1yoa_A
1yoc_B
1yon_A
1yp1_A
1yph_D
1yph_E
1yq2_C
1yqd_A
1yqe_A
1yqw_B
1yqw_Q
1yqz_A
1yrk_A
1ys1_X
1ysl_B
1yt3_A
1ytq_A
1yu0_A
1yuz_B
1yw5_A
1ywm_A
1yxy_A
1yya_A
1yzf_A
1yzl_A
1yzm_A
1yzq_A
1yzx_A
1z06_A
1z08_C
1z0j_A
1z0j_B
1z0s_C
1z1s_A
1z2a_A
2eeo_B
2eey_A
2efr_B
2efv_A
2egd_B
2egj_A
2egv_A
2eh6_A
2ehg_A
2ehq_A
2eht_A
2ehz_A
2ei5_B
2eiq_B
2eix_A
2eiy_B
2eja_B
2ejn_B
2ejw_A
2ejx_A
2ekp_A
2eky_C
2elc_B
2end_A
2eo4_A
2eq6_B
2erf_A
2erw_A
2ery_B
2esl_A
2et1_A
2etb_A
2etx_A
2eu7_X
2eut_A
2ev1_A
2evb_A
2ewh_A
2ewt_A
2ex0_B
2ex2_A
2exh_D
2exv_A
2ez9_A
2f0c_A
2f23_B
2f2b_A
2f51_A
2f5g_B
2f5t_X
2f5v_A
2f60_K
2f6e_A
2f6u_A
2f7b_A
2f91_A
2f99_C
2f9i_D
2f9n_B
2fao_B
2fb5_A
2fba_A
2o36_A
2o37_A
2o4a_A
2o4t_A
2o4v_B
2o5f_B
2o5g_A
2o5u_A
2o6f_A
2o6p_A
2o6s_A
2o74_F
2o7i_A
2o90_A
2o9c_A
2o9s_A
2oaa_B
2obi_A
2obl_A
2ocg_A
2ode_D
2odf_E
2odk_C
2oe3_A
2oeb_A
2ofc_A
2ofk_A
2og1_A
2oh5_A
2ohw_B
2oif_B
2oiz_B
2oj6_C
2okl_B
2okm_A
2okq_A
2ol1_B
2olm_A
2oln_A
2olp_A
2olr_A
2omy_B
2omz_A
2on5_A
2oo1_B
2op3_A
2op6_A
2opc_A
2opg_B
2oqb_A
2or7_A
2os5_A
2os9_B
2osa_A
2otu_E
2oui_A
2ous_A
2ov0_A
2ow9_B
2ows_A
2ox0_A
2ox4_H
2w8y_B
2w91_A
2w98_B
2w9h_A
2w9r_A
2wa2_B
2waa_A
2wb6_A
2wbf_X
2wbs_A
2wc8_B
2wci_A
2wcj_A
2wco_A
2wcr_A
2wcu_A
2wdc_A
2wds_A
2wdu_B
2we5_C
2wei_A
2wf6_A
2wfc_C
2wfh_B
2wfj_A
2wfo_A
2wfz_A
2wge_A
2wgp_B
2wh7_A
2whg_B
2wi8_A
2wiy_A
2wj5_A
2wje_A
2wjn_C
2wjn_L
2wjn_M
2wk0_A
2wkk_C
2wkx_A
2wl1_A
2wm3_A
2wm8_A
2wmf_A
2wn3_C
2wnp_F
2wns_A
2wnv_F
2wnx_A
2wny_B
2woe_C
2wol_A
2wot_A
2wp7_A
2wpq_C
2wpv_D
2wpv_E
2wqi_D
2wqk_A
2wqr_A
2wsb_C
3bpw_A
3bpz_D
3bqp_B
3br8_A
3bs1_A
3bs2_A
3bs9_B
3bsy_B
3buv_B
3bv6_D
3bvk_F
3bwh_A
3bwu_D
3bx4_A
3bx4_B
3bxe_B
3by4_A
3byb_B
3byp_A
3bzz_B
3c05_A
3c05_D
3c0i_A
3c1o_A
3c2u_A
3c3y_B
3c4s_A
3c5a_A
3c5e_A
3c5j_A
3c5k_A
3c68_B
3c6w_A
3c70_A
3c7f_A
3c7t_A
3c7x_A
3c8e_A
3c8i_A
3c8o_A
3c8p_A
3c97_A
3c9a_B
3c9h_B
3c9u_B
3c9x_A
3c9z_A
3ca7_A
3cai_A
3cb0_D
3cb6_A
3cbq_A
3cbx_A
3ccd_B
3ce6_A
3ce7_A
3cfc_H
3cfz_A
3cg1_A
3cgi_C
3chj_A
3chm_A
3gvo_A
3gw9_C
3gwa_A
3gwc_D
3gwh_B
3gwi_A
3gwk_E
3gwm_A
3gwn_A
3gx8_A
3gxb_A
3gxr_B
3gzg_A
3gzh_A
3gzk_A
3gzx_A
3gzx_B
3h01_A
3h04_A
3h09_B
3h0o_A
3h0u_C
3h12_B
3h1g_A
3h1s_B
3h34_A
3h3n_X
3h4n_A
3h4x_A
3h55_B
3h5i_A
3h5j_B
3h5l_B
3h62_B
3h6p_B
3h6p_C
3h78_A
3h7h_A
3h7h_B
3h7i_A
3h7r_A
3h7u_A
3h81_C
3h87_B
3h87_D
3h8g_C
3h8t_A
3h8x_A
3h91_A
3h9c_A
3h9e_O
3ha9_A
3hc4_L
3hcj_A
3hcn_B
3hd4_A
3hdf_B
3hdl_A
3he5_C
3he5_D
3he8_B
3hef_B
3mqh_D
3ms5_A
3msu_B
3msx_B
3mte_A
3mtr_B
3mu7_A
3muj_B
3muz_3
3mwc_A
3mwf_A
3mwj_A
3mx6_B
3mxn_A
3mxn_B
3mxu_A
3myb_A
3mzv_B
3n08_A
3n0i_B
3n10_B
3n11_A
3n1e_B
3n1f_D
3n1s_M
3n22_A
3n2n_E
3n37_A
3n3s_A
3n4i_B
3n4j_A
3n5a_A
3n5b_B
3n72_B
3n79_A
3n98_A
3n9g_H
3n9i_B
3n9u_B
3n9u_C
3nbk_A
3ncl_A
3ndd_A
3ndh_B
3ndj_A
3ndo_A
3nfu_A
3nfw_B
3ng7_X
3ngf_A
3ngh_A
3ngj_A
3ngp_A
3ni0_A
3ni2_A
3nis_B
3nj2_A
3nje_B
3njn_C
3nn1_A
3no0_A
3no7_A

1fp2_A
1fpo_B
1fqt_B
1fr3_A
1frb_A
1fsg_A
1ftr_A
1fus_A
1fw4_A
1fx4_A
1fxl_A
1fxo_G
1fz1_B
1g01_A
1g0o_C
1g12_A
1g1s_B
1g1t_A
1g29_2
1g2o_C
1g2q_A
1g2r_A
1g3k_B
1g4i_A
1g5a_A
1g61_A
1g6a_A
1g6c_B
1g6g_A
1g6h_A
1g6u_B
1g8a_A
1g8i_B
1g8k_A
1g8k_D
1g94_A
1g97_A
1g9g_A
1g9o_A
1ga6_A
1gai_A
1gbg_A
1gbs_A
1gci_A
1gcq_C
1gde_B
1gee_E
1geg_G
1ges_B
1gk6_A
1gk7_A
1gk9_A
1gk9_B
1gl2_A
1gl2_B
1gl2_C
1gl2_D
1gmu_C
1gmy_A
1gn0_A
1gnl_A
1gnt_A
1mk0_A
1mkk_A
1mla_A
1mlw_A
1mn8_B
1mo0_B
1mo9_A
1mof_A
1moq_A
1mpg_B
1mpl_A
1mug_A
1mv8_C
1mvf_A
1mvf_D
1mvo_A
1mxg_A
1mxr_A
1my5_A
1my6_B
1mz4_A
1mz9_A
1mzy_A
1n08_B
1n0q_B
1n13_G
1n1j_A
1n1j_B
1n3y_A
1n5w_D
1n63_C
1n63_E
1n71_C
1n7e_A
1n7s_A
1n7s_B
1n7s_C
1n7s_D
1n82_B
1n83_A
1n8f_B
1n9l_A
1na0_A
1na5_A
1nb9_A
1nbc_B
1nbu_D
1nc5_A
1ndd_A
1ne7_C
1nep_A
1nf8_A
1nff_B
1nfv_N
1ng6_A
1nh2_A
1nh2_B
1nhc_E
1nhk_L
1nki_B
1nkp_D
1nln_A
1tke_A
1tn4_A
1to4_A
1toa_B
1tov_A
1tp5_A
1tp6_A
1tp9_B
1tqh_A
1tr0_J
1tsf_A
1tt2_A
1tt8_A
1tu1_B
1tu7_B
1tu9_A
1tua_A
1tuh_A
1tuk_A
1tvn_B
1txg_B
1ty9_A
1tzw_A
1tzy_C
1tzy_F
1u07_A
1u09_A
1u11_A
1u1w_B
1u2b_A
1u2h_A
1u2p_A
1u2w_B
1u3i_A
1u53_A
1u55_A
1u5d_B
1u5f_A
1u60_B
1u6e_A
1u6r_B
1u6t_A
1u6z_B
1u84_A
1u8f_Q
1u8v_C
1u8y_B
1u9k_A
1ua4_A
1ua6_L
1uai_A
1uas_A
1ub3_A
1uc4_A
1uc4_G
1uca_A
1ucr_B
1ucs_A
1udc_A
1ueb_A
1uek_A
1uf5_A
1z2n_X
1z2u_A
1z3e_A
1z3e_B
1z3q_A
1z47_A
1z4j_A
1z4r_A
1z6n_A
1z6o_D
1z6o_M
1z76_B
1z7x_W
1z8o_A
1z96_A
1zbf_A
1zch_A
1zcz_A
1zd0_A
1zd8_A
1zdy_A
1zem_A
1zgd_B
1zhh_A
1zhq_A
1zhv_A
1zhx_A
1zi9_A
1zja_A
1zjc_A
1zjj_B
1zk4_A
1zk7_A
1zkc_A
1zke_B
1zkk_B
1zkl_A
1zl0_B
1zlm_A
1zm8_A
1zn8_A
1zo2_A
1zoi_B
1zos_C
1zps_B
1zpw_X
1zq9_B
1zr0_D
1zr3_B
1zr6_A
1zs4_D
1zsw_A
1zsx_A
1zt5_A
1zu3_A
1zuo_A
1zuu_A
1zuy_A
1zv1_A
1zwh_A
1zwz_A
1zx6_A
2fbd_A
2fbn_A
2fbq_A
2fc3_A
2fcb_A
2fcr_A
2fcw_A
2fcw_B
2fd5_A
2fdn_A
2fdv_A
2fdx_A
2fe3_A
2fe5_A
2fe8_A
2ff4_A
2ffu_A
2ffy_B
2fgo_A
2fgr_A
2fhf_A
2fhz_A
2fhz_B
2fi1_A
2fi9_A
2fj8_A
2fl4_A
2flh_B
2fli_A
2fm6_A
2fma_A
2fmm_C
2fmp_A
2fn3_A
2fn4_A
2fn9_B
2fne_A
2fnu_A
2fo3_A
2fp1_A
2fp7_A
2fq3_A
2fqw_A
2fr2_A
2fr5_C
2frg_P
2ft0_A
2ftx_B
2fu0_A
2fu4_A
2fuk_A
2fvh_A
2fvv_A
2fvy_A
2fwh_A
2fyg_A
2fyx_A
2fzp_A
2fzv_B
2fzw_B
2g2n_C
2g2s_A
2ox6_B
2oxc_A
2oxg_A
2oxg_Y
2oxn_A
2oy2_F
2oy7_A
2oya_B
2oyn_A
2oyp_A
2ozf_A
2ozl_A
2ozn_A
2ozn_B
2p02_A
2p09_A
2p0f_A
2p1g_B
2p1m_B
2p39_A
2p3h_A
2p49_B
2p4e_P
2p4k_A
2p51_A
2p54_A
2p57_A
2p5k_A
2p5y_A
2p65_A
2p68_A
2p6h_B
2p6w_A
2p6z_A
2p74_A
2p8b_A
2p9x_D
2pa1_A
2pa6_B
2pa7_B
2pbc_C
2pbd_P
2pbi_C
2pbi_D
2pbp_A
2pc8_A
2pcj_B
2pcn_A
2pdr_B
2pfz_A
2pg0_B
2pgo_A
2ph3_A
2phn_A
2pi6_A
2pie_A
2piy_B
2pjz_A
2pk3_A
2pk8_A
2pkf_A
2pko_A
2wt1_A
2wta_A
2wtg_A
2wtm_C
2wto_A
2wu9_A
2wue_A
2wuh_A
2wuk_A
2wut_A
2wv3_A
2wvf_A
2wvg_F
2wvv_A
2ww2_B
2ww5_A
2wwe_A
2wwf_C
2wwk_T
2wwx_A
2wwx_B
2wx9_A
2wy3_B
2wy4_A
2wy7_Q
2wy8_A
2wya_A
2wyq_A
2wz9_A
2wzm_A
2wzx_A
2x0k_A
2x18_E
2x1b_A
2x23_B
2x2o_A
2x32_A
2x3h_C
2x3m_A
2x49_A
2x4d_A
2x4k_B
2x4l_A
2x5c_B
2x5f_B
2x5h_B
2x5x_A
2x5y_A
2x6w_A
2x7b_A
2x7k_A
2x7m_A
2x8h_A
2x8r_A
2x8s_A
2x8x_X
2x96_A
2xb4_A
2xbk_A
2xbl_A
2xbp_A
2xc2_A
3ci7_A
3cij_A
3cin_A
3cip_G
3civ_A
3cjp_B
3cjs_B
3ckf_A
3cl5_A
3cla_A
3cls_D
3cm0_A
3cmj_A
3cmy_A
3cnk_B
3cnm_A
3cnu_A
3cou_A
3cp5_A
3cp7_B
3cpq_B
3cpt_A
3cq5_B
3cql_A
3cqt_A
3cry_A
3csk_A
3ct1_A
3ctg_A
3ctk_A
3ctp_B
3ctz_A
3cu4_A
3cu9_A
3cui_A
3cvb_A
3cwn_B
3cwv_A
3cx5_E
3cx5_F
3cx5_G
3cx5_I
3cx5_O
3cxk_A
3cxz_A
3cy4_A
3cyi_A
3cz1_B
3czf_B
3czt_X
3czz_B
3d03_B
3d0n_A
3d0o_A
3d1b_C
3d1g_A
3d1k_A
3d2q_A
3d2w_A
3d30_A
3d32_A
3d34_A
3hf5_C
3hfo_A
3hfw_A
3hg3_B
3hgb_A
3hgm_A
3hgu_A
3hh7_A
3hh8_A
3hhi_B
3hht_B
3his_A
3hjb_A
3hje_A
3hjr_A
3hjs_A
3hl5_B
3hlx_A
3hm5_A
3hmc_A
3hms_A
3hnb_M
3hnx_A
3hol_A
3hpc_X
3hr0_A
3hra_A
3hrx_A
3hs3_A
3hsh_A
3hss_B
3ht1_A
3ht5_A
3huh_A
3hup_B
3hv2_B
3hvi_A
3hvu_C
3hvv_A
3hx9_A
3hxa_F
3hxs_B
3hxw_A
3hz2_A
3hzb_E
3i0w_A
3i1a_A
3i1u_A
3i24_A
3i26_D
3i2z_A
3i31_A
3i33_A
3i35_A
3i36_A
3i3f_B
3i3g_A
3i45_A
3i47_A
3i48_B
3i4o_B
3i4s_A
3noj_A
3nok_A
3nol_A
3noo_B
3nqx_A
3nr1_A
3ns2_A
3ns6_B
3nsl_F
3nsx_B
3nsz_A
3nt1_B
3ntk_A
3nua_A
3nv1_A
3nvs_A
3nvw_J
3nwo_A
3nxb_B
3ny3_A
3ny7_A
3nye_A
3nyk_A
3nyt_A
3nzn_B
3o07_A
3o0a_B
3o0d_C
3o0g_D
3o1g_A
3o1k_B
3o1n_A
3o1p_A
3o26_A
3o2e_A
3o3m_C
3o3m_D
3o3u_N
3o4h_A
3o4r_B
3o4v_B
3o5v_B
3o70_A
3o79_A
3o7b_A
3o83_B
3o85_B
3o8m_A
3o9z_A
3oa3_B
3oaj_A
3oam_A
3obu_A
3ocu_A
3od9_A
3odg_A
3ofk_C
3og9_B
3ogn_B
3ogr_A
3oid_C
3oig_A

1gny_A
1go3_N
1goi_B
1gp6_A
1gpe_A
1gpi_A
1gpu_A
1gq1_A
1gq8_A
1gql_B
1gqv_A
1gtf_I
1gtv_A
1gtz_D
1gu2_A
1gu7_B
1gud_A
1gug_D
1gui_A
1gv5_A
1gvj_A
1gvn_D
1gwe_A
1gwi_B
1gwu_A
1gxn_A
1gxu_A
1gxy_A
1gy6_A
1gy7_C
1gyh_C
1gyo_A
1gyv_A
1gyy_B
1gzc_A
1gzw_B
1h03_P
1h0h_B
1h16_A
1h1n_A
1h1y_A
1h2b_B
1h2c_A
1h2e_A
1h2s_A
1h2s_B
1h4a_X
1h4g_A
1h4p_A
1h4r_A
1h5b_B
1h5q_L
1h5v_A
1h64_Q
1h6f_A
1h6l_A
1h6u_A
1h6w_A
1h72_C
1h75_A
1h7e_B
1h8p_B

1nls_A
1nnf_A
1nnh_A
1nns_A
1nnw_B
1noa_A
1nof_A
1nog_A
1nox_A
1npy_B
1nq6_A
1nq7_A
1nqu_B
1nr0_A
1nr4_G
1nsc_B
1nth_A
1ntv_A
1nty_A
1nvm_C
1nvm_F
1nw2_H
1nwa_A
1nwp_A
1nww_A
1nwz_A
1nxc_A
1nxj_A
1nxm_A
1nyk_B
1nyt_C
1nza_A
1o04_E
1o0e_B
1o1z_A
1o26_C
1o4k_A
1o4s_A
1o4t_A
1o4v_A
1o4y_A
1o5u_A
1o5x_A
1o7e_B
1o7i_A
1o7j_C
1o7q_B
1o7z_B
1o82_A
1o8s_A
1o8x_A
1o91_C
1o98_A
1o9i_D
1o9r_E
1oa2_C
1oa8_A
1oaa_A
1oai_A
1oal_A
1oao_A
1oaq_H

1ufb_C
1ufi_B
1ufy_A
1ug6_A
1ugi_E
1ugp_B
1ugx_A
1uha_A
1uhe_A
1uhk_B
1ui0_A
1uiw_C
1uj0_A
1uj2_A
1uj8_A
1uk7_A
1ukf_A
1ukm_A
1ukm_B
1uku_A
1ukz_A
1ulk_A
1ulr_A
1umd_C
1umd_D
1umk_A
1umz_A
1uow_A
1uoy_A
1uqx_A
1uqz_A
1urn_C
1urr_A
1urs_A
1us5_A
1use_A
1usf_B
1usg_A
1uso_A
1usq_B
1uti_A
1uu4_A
1uuq_A
1uuy_A
1uv4_A
1uvq_A
1uw4_C
1uw4_D
1uwc_A
1uwf_A
1uwk_B
1uwz_A
1uxx_X
1uxy_A
1uy1_A
1uyx_A
1uz3_A
1v05_A
1v08_B
1v0z_B
1v2z_A
1v30_A

1zxt_B
1zxx_A
1zz0_A
1zzg_B
1zzk_A
1zzo_A
1zzw_A
256b_B
2a07_K
2a0n_A
2a14_A
2a15_A
2a26_C
2a28_A
2a2n_C
2a2r_B
2a40_E
2a4v_A
2a4x_A
2a53_C
2a5d_A
2a61_C
2a6s_B
2a6x_A
2a70_A
2a7l_B
2a8n_A
2a9i_A
2a9s_A
2aa1_B
2aal_C
2aan_A
2ab0_A
2abk_A
2abw_B
2acf_D
2ad6_A
2ad6_D
2ae2_A
2aen_E
2aex_A
2ag4_B
2ag5_B
2agd_B
2ahf_A
2ahn_A
2aib_A
2akz_B
2anv_A
2any_A
2ap1_A
2apg_A
2aqm_A
2aqp_A
2ar1_A
2arc_B
2asd_A
2asu_B
2at8_X
2atb_A
2atv_A
2au7_A

2g30_A
2g45_D
2g5x_A
2g64_A
2g6f_X
2g76_A
2g7o_A
2g84_A
2g8o_B
2g9f_A
2ga4_D
2gag_A
2gag_B
2gag_C
2gas_A
2gb4_B
2gbt_A
2gbw_E
2gc4_L
2gdq_B
2gdz_A
2gec_A
2gey_D
2gf3_B
2gf9_A
2gg6_A
2gh0_B
2gh0_D
2gh9_A
2gha_A
2gia_B
2gib_B
2giy_A
2gj3_A
2gjd_C
2gke_A
2gkm_B
2gkr_I
2gl5_A
2gmy_E
2gn4_B
2gnc_A
2gok_A
2gom_A
2gou_A
2gpe_B
2gqt_A
2gqw_A
2grc_A
2grr_B
2gsd_A
2gso_B
2gte_A
2gtr_A
2gu3_A
2gud_B
2gui_A
2guv_C
2guy_A
2gw4_D
2gwm_A
2gxg_A

2pkt_A
2plt_A
2pmk_A
2pmr_A
2pn6_A
2pn8_B
2pnd_A
2pnx_A
2pny_A
2poi_A
2pok_B
2por_A
2pos_D
2ppp_A
2ppt_B
2pqm_B
2pqr_B
2pqr_D
2pqx_A
2pr5_A
2psd_A
2psp_B
2pst_X
2pth_A
2ptt_B
2ptz_A
2pu3_A
2pu9_A
2pu9_B
2pv2_A
2pvb_A
2pve_B
2pvq_A
2pwy_A
2pxx_A
2py4_A
2pyw_A
2pz0_B
2pze_B
2pzh_B
2q0l_A
2q20_B
2q28_A
2q2a_D
2q2h_A
2q35_A
2q5c_A
2q62_G
2q73_C
2q86_B
2q87_A
2q88_A
2q8n_C
2q8r_G
2q9u_A
2qa9_E
2qac_A
2qap_A
2qb7_A
2qc5_A
2qd6_A
2qdx_A

2xcb_A
2xce_F
2xcj_A
2xcz_A
2xda_A
2xde_A
2xdg_A
2xdj_F
2xdp_A
2xdw_A
2xe4_A
2xed_A
2xet_B
2xeu_A
2xev_A
2xf2_A
2xfd_A
2xfv_A
2xh2_C
2xhi_A
2xhn_A
2xi8_A
2xij_A
2xio_A
2xkg_A
2xkr_A
2xla_A
2xlk_A
2xm5_A
2xmx_A
2xn4_A
2xn6_A
2xov_A
2xpp_A
2xqu_A
2xs4_A
2xsu_A
2xt2_A
2xts_A
2xts_B
2xtt_B
2xu3_A
2xu8_B
2xvm_B
2xvs_A
2xvx_A
2xws_A
2xwt_C
2xxj_D
2xxl_B
2xy2_A
2xz2_A
2xzi_A
2y2z_A
2y39_A
2y3q_B
2y3v_D
2y3z_A
2y5p_C
2y7b_A
2y88_A
2y8m_A

3d3b_A
3d3z_A
3d43_B
3d47_A
3d4i_A
3d4u_B
3d6r_A
3d79_A
3d7a_B
3d8t_A
3d95_B
3d9t_A
3d9x_C
3d9y_A
3da0_C
3dac_A
3dai_A
3dan_A
3daq_A
3dau_A
3dc5_C
3dcn_A
3del_B
3deo_A
3dfg_A
3dgb_A
3dgp_A
3dgp_B
3dgt_A
3dha_A
3dhi_B
3dhi_C
3dho_C
3die_A
3dj9_A
3djh_C
3djl_A
3djo_A
3dk9_A
3dkc_A
3dkm_A
3dkr_A
3dl0_A
3dlm_A
3dm8_A
3dme_B
3dmg_A
3dmi_A
3dmo_A
3dnf_B
3dpg_B
3dqg_A
3dr0_C
3dr4_B
3dra_A
3drf_A
3drw_B
3drz_B
3ds4_B
3dsk_A
3dso_A
3dt9_A

3i4z_B
3i57_B
3i5c_B
3i5r_A
3i5x_A
3i6c_A
3i6t_B
3i7u_B
3i8s_C
3i94_A
3i96_A
3i98_E
3i9q_A
3ia2_F
3ia4_D
3ian_A
3iar_A
3iav_A
3ib7_A
3ich_A
3id1_A
3id7_A
3ida_A
3idw_A
3ie4_A
3ie5_A
3iei_C
3iev_A
3iez_B
3ife_A
3ig9_C
3igz_B
3ihw_A
3ihz_B
3ii7_A
3iij_A
3iiu_M
3ij3_A
3ijl_A
3ik7_D
3ilo_A
3ils_A
3ilw_A
3im1_A
3im9_A
3imh_A
3inz_B
3iof_A
3ioh_A
3ioq_A
3iox_A
3ip4_A
3ip8_A
3ipc_A
3ipf_A
3ipw_A
3iq3_A
3iql_A
3irp_X
3irs_A
3irv_A
3is3_A

3oiu_A
3oj7_A
3ojs_A
3ol0_A
3ol3_A
3omc_B
3omt_A
3onr_I
3oo8_A
3ooi_A
3op8_A
3opk_A
3oq2_A
3oqy_B
3orh_C
3orv_B
3orv_D
3ose_A
3osm_A
3oti_B
3ouf_B
3ovp_B
3oyy_B
3p0t_A
3p1f_A
3p1g_A
3p2n_A
3p2t_A
3p3c_A
3p3e_A
3p3g_A
3p3o_A
3p48_A
3p4t_A
3p5h_A
3p73_A
3p73_B
3p7y_A
3p97_C
3p9c_A
3p9p_A
3p9x_A
3pb6_X
3pbf_A
3pc3_A
3pcv_A
3pd2_B
3pd7_A
3pdn_A
3pel_B
3pew_A
3pf2_A
3pfg_A
3pfs_A
3pg6_C
3pgx_A
3phs_A
3phx_B
3pjp_B
3pk0_A
3pkv_A
3plf_D

1h8u_A
1h97_B
1h98_A
1h9m_A
1h9s_B
1hbn_C
1hbn_E
1hc9_B
1hd2_A
1hdo_A
1hfe_L
1hfe_T
1hfo_E
1hfs_A
1hh8_A
1hj8_A
1hjs_B
1hl7_B
1hle_A
1hlq_C
1hm6_B
1hml_A
1hmt_A
1hnj_A
1hp1_A
1hpg_A
1hq0_A
1ht6_A
1ht9_B
1hw1_B
1hx0_A
1hx1_B
1hx6_C
1hxh_D
1hxr_B
1hz4_A
1hz6_C
1hzj_A
1hzo_A
1hzt_A
1i0l_A
1i0r_A
1i0v_A
1i1n_A
1i24_A
1i27_A
1i2t_A
1i4u_A
1i6m_A
1i77_A
1i7h_A
1i7k_A
1i8a_A
1i8f_F
1i8k_B
1i8o_A
1i9c_A
1iap_A
1iby_B
1idp_A
1ig3_A
1igq_A
1oaq_L
1obo_A
1oc2_B
1oc8_A
1ock_A
1ocy_A
1odm_A
1odt_H
1oe2_A
1off_A
1ofl_A
1ofs_C
1ofs_D
1ofw_A
1ofz_A
1ogd_D
1ogm_X
1oh0_A
1oh4_A
1oh9_A
1ohp_B
1oi6_B
1ojk_A
1ojq_A
1ojx_C
1ok0_A
1okt_A
1on3_A
1ong_A
1oni_C
1onj_A
1ooe_A
1oot_A
1oqj_A
1oqv_C
1orn_A
1orr_A
1os6_A
1osy_B
1oth_A
1ou8_B
1ouw_C
1ov3_A
1ow3_A
1owf_A
1ox0_A
1oxj_A
1oxs_C
1oyg_A
1oz9_A
1ozn_A
1ozw_B
1p0f_B
1p1j_A
1p1m_A
1p1x_B
1p28_B
1p3c_A
1p6o_B
1p71_A
1p99_A
1pa2_A
1v33_A
1v37_A
1v4p_C
1v4x_B
1v54_A
1v54_J
1v54_V
1v55_D
1v55_L
1v58_B
1v5d_A
1v5f_A
1v5i_B
1v6s_A
1v70_A
1v7p_C
1v7r_A
1v7z_F
1v8c_C
1v8f_A
1v8h_A
1v93_A
1v96_B
1v98_A
1v9f_A
1vbi_A
1vbu_A
1vbw_A
1vc4_B
1vcd_A
1vcl_A
1vd1_A
1vd6_A
1ve1_A
1vef_B
1vf1_A
1vfr_B
1vfy_A
1vg8_C
1vh5_A
1vht_B
1vhw_A
1vi6_B
1vim_A
1vj2_A
1vjk_A
1vjw_A
1vk5_A
1vkc_A
1vke_F
1vki_A
1vkk_A
1vl1_A
1vl7_A
1vlc_A
1vlj_A
1vm9_A
1vmb_A
1vmf_C
1vmj_A
1vp2_A
1vp6_C
2avd_B
2avk_A
2axq_A
2axw_B
2ayd_A
2b0a_A
2b0t_A
2b1k_A
2b3f_D
2b3h_A
2b49_A
2b4z_A
2b5a_A
2b5h_A
2b5w_A
2b6n_A
2b7r_A
2b82_A
2b9w_A
2ba2_C
2bay_E
2bba_A
2bbe_A
2bcg_G
2bcg_Y
2bcm_B
2bcr_A
2bd0_D
2bek_D
2bem_A
2beq_D
2bez_C
2bf6_A
2bfw_A
2bgs_A
2bh8_B
2bii_B
2bjd_B
2bjf_A
2bji_A
2bjq_A
2bk9_A
2bka_A
2bkf_A
2bkl_B
2bkm_B
2bko_A
2bkr_A
2bkx_A
2bky_B
2bky_Y
2bl0_A
2bl0_B
2bl8_B
2blf_A
2blf_B
2bme_B
2bmo_A
2bmo_B
2bnm_B
2bo1_A
2bo4_F
2gyq_B
2gz1_B
2gz4_A
2gze_A
2gze_B
2gzg_B
2h17_A
2h1c_A
2h1v_A
2h2b_A
2h2r_B
2h2z_A
2h3h_A
2h3l_A
2h54_B
2h62_A
2h64_B
2h6f_A
2h6f_B
2h6n_A
2h6u_G
2h88_A
2h88_B
2h88_D
2h88_P
2h8e_A
2h8g_B
2h9b_A
2h9h_A
2ha8_B
2hax_B
2haz_A
2hba_A
2hbv_A
2hc8_A
2hc9_A
2hd9_A
2hda_A
2he0_A
2he2_A
2he4_A
2hek_B
2heu_B
2hew_F
2hf9_A
2hfn_H
2hgx_B
2hhv_A
2hin_B
2hjv_A
2hke_B
2hl7_A
2hlc_A
2hls_A
2hlv_A
2hmq_D
2hor_A
2hos_B
2hq6_A
2hqh_C
2hqs_H
2hqy_A
2qed_A
2qee_F
2qev_A
2qf4_B
2qfa_A
2qfa_B
2qfa_C
2qfe_A
2qg1_A
2qgy_B
2qhl_B
2qho_B
2qhs_A
2qia_A
2qif_A
2qih_B
2qim_A
2qkh_A
2qkp_C
2qlt_A
2qmc_A
2qmc_D
2qmm_A
2qmq_A
2qn0_A
2qnw_A
2qo4_A
2qpn_B
2qpw_A
2qq4_B
2qqi_A
2qrl_A
2qrw_I
2qsa_A
2qsk_A
2qsq_B
2qt7_B
2qub_I
2qud_A
2qul_C
2quo_A
2quy_H
2qv5_A
2qvb_A
2qvo_A
2qvu_B
2qwc_A
2qwl_A
2qwo_B
2qx8_B
2qxi_A
2qy1_B
2qy9_A
2qzt_B
2r0b_A
2r0h_C
2r16_A
2r1j_R
2r2y_A
2r31_A
2r37_A
2r5o_B
2yay_A
2ygs_A
2yqu_B
2yrr_B
2ysk_A
2yva_B
2yve_A
2yvi_A
2yvo_A
2yvt_A
2yw2_A
2yw3_A
2ywd_A
2ywj_A
2ywk_A
2yxm_A
2yxn_A
2yxo_B
2yxw_A
2yxz_A
2yyv_B
2yyy_A
2yz1_B
2yzc_D
2yzh_C
2yzt_A
2z0a_B
2z0j_E
2z0m_A
2z0t_C
2z0x_A
2z1a_A
2z1c_B
2z2f_A
2z38_A
2z3g_D
2z3v_A
2z4u_A
2z66_B
2z6n_A
2z6o_A
2z6r_A
2z6w_A
2z72_A
2z79_B
2z7f_E
2z7f_I
2z84_A
2z8f_A
2z8l_A
2z8q_A
2z8u_B
2z8x_A
2z9v_B
2za0_A
2zbo_A
2zbt_B
2zc8_A
2zd1_A
2zdh_A
2zdo_B
2zdr_A
3dtb_A
3dvw_A
3dwg_A
3dwg_C
3dwv_B
3dxt_A
3dy0_A
3dzw_A
3e05_B
3e0i_A
3e13_X
3e17_B
3e2d_A
3e3u_A
3e4g_A
3e4w_B
3e55_A
3e6j_A
3e6s_F
3e6z_X
3e7d_A
3e7h_A
3e7r_L
3e8m_B
3e8t_A
3e96_B
3e9t_B
3ea3_B
3ea6_A
3eaz_A
3ebh_A
3ec0_B
3edf_A
3edv_A
3ee4_A
3eeh_A
3ees_A
3ef4_A
3ef6_A
3efy_A
3eg4_A
3egg_D
3ego_B
3egw_C
3ehg_A
3ehw_B
3ei9_B
3eif_A
3ej9_B
3ej9_C
3eja_A
3ejf_A
3ejg_A
3eju_A
3eki_A
3elw_A
3elx_A
3em1_A
3emi_A
3emw_A
3enb_A
3enk_B
3isa_B
3iso_A
3isq_A
3it4_B
3it4_C
3iu5_A
3iu7_A
3iux_A
3iwt_A
3ix3_B
3ixq_D
3jpz_B
3jqj_C
3jql_A
3jqu_A
3jqy_C
3jr0_B
3js4_B
3js5_A
3js8_A
3jsl_B
3jsy_B
3jte_A
3jtm_A
3jtz_A
3ju2_A
3juu_A
3jva_F
3jxo_A
3jxs_A
3jxy_A
3jyo_A
3jzy_A
3k01_A
3k1h_A
3k26_A
3k2w_E
3k31_A
3k3c_D
3k3k_A
3k3v_A
3k62_A
3k6f_A
3k6i_A
3k6v_A
3k6y_A
3k7f_B
3k7i_B
3k7p_B
3k89_A
3k8d_A
3k8u_A
3k8w_A
3k9o_A
3k9w_A
3kbf_A
3kcc_A
3kcg_H
3kci_A
3kcp_A
3kda_A
3ke4_A
3plw_A
3plx_B
3pmc_B
3pmd_A
3pms_A
3pmt_A
3pna_A
3po0_A
3po8_A
3pqa_B
3pr9_A
3prp_A
3psm_A
3pua_A
3pvi_B
3pxl_A
3q0h_A
3q12_C
3q1x_A
3q20_B
3q23_B
3q2e_A
3q3u_A
3q49_B
3q4t_A
3q4u_A
3q5y_A
3q62_B
3q6d_B
3q6l_A
3q8g_A
3q93_B
3qan_C
3qat_B
3qby_A
3qc7_A
3qds_B
3qe1_A
3qgz_A
3qh4_A
3qhz_M
3qk8_C
3qki_B
3qmd_A
3qp4_A
3qqi_B
3qry_A
3qu1_B
3qug_A
3qxc_A
3qy1_B
3qyj_A
3qzb_A
3r0p_B
3r1i_A
3r1w_C
3r3r_A
3r3s_C
3r6f_A
3sil_A
4ubp_A
4ubp_B

1ihj_B
1iib_B
1ijb_A
1ijt_A
1ijx_C
1ijy_B
1ikt_A
1io0_A
1iom_A
1ioo_B
1iq6_B
1pam_B
1pcf_C
1pdo_A
1pe9_B
1pfb_A
1pgv_A
1pj5_A
1pk3_B
1pkh_A
1pl3_A
1pl8_D
1vph_E
1vps_A
1vq3_B
1vqe_A
1vsr_A
1vyf_A
1vyo_A
1vzi_B
1vzy_B
1w0d_A
1w0n_A
2bo9_C
2bo9_D
2boo_A
2bpd_B
2bpq_A
2bqx_A
2br9_A
2bsj_A
2bt6_A
2bt9_A
2buu_A
2hra_A
2hrv_B
2hsa_A
2ht9_B
2hta_A
2hu9_A
2hur_B
2hv8_A
2hv8_E
2hvm_A
2hvw_C
2r6j_B
2r75_1
2r8e_E
2r8o_A
2r8q_A
2r99_A
2r9f_A
2ra3_B
2ra4_A
2ra6_B
2rbk_A
2zex_A
2zez_B
2zfc_B
2zfd_A
2zfz_D
2zgq_A
2zhj_A
2zhn_A
2zhz_C
2zib_A
2zjd_C
3enu_A
3eoi_A
3epr_A
3eqn_B
3er6_A
3era_B
3erj_A
3erx_B
3esg_B
3esl_B
3eu9_C
3kef_B
3keo_B
3kfa_A
3kff_A
3kg0_C
3kgr_A
3kgz_B
3kh7_A
3kij_C
3kki_A
3kkq_A
4vub_A
5pal_A
6cel_A
6rxn_A
7fd1_A
7rsa_A
8abp_A