Building blocks of protein structures – Physics meets Biology

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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

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

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

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

and the distance constraint is

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

We solve Equations (2, 4, and 5) simultaneously to obtain the unique geometry of the continuum space-filling helix (Figure 1c,e,f): η~0.4, Δ/R~1.16, and t_{min}~302°.

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 μ=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 μ=180°. For repeat μ-values close to 180°, one obtains a twisted planar strand, a geometrical feature often observed in protein structures.

91 Figure 1g shows the space-filling discrete helix with η~0.4 and Δ/R~1.16, the geometrical
92 characteristics of the continuum space-filling helix. The discretization requires the specification
93 of the rotation angle ε_0 between successive points that retains the space-filling conditions for the
94 discrete case. This choice of ε_0 is made (in direct analogy with the continuum case) by requiring
95 that the distance between points i (analogous to t_0=0°) and i+m with integer m (analogous to t_{min})
96 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
97 90° (analogous to the minimization condition). The smallest value of m for which these
98 conditions are satisfied is m=3 and ε_0~99.8° (the ratio of the distance to the tube diameter is
99 found to be 1.00… and both the angles are 90.0…° for this value of ε_0). Upon defining the length
100 scale to match the mean C_α-C_α distance along the protein backbone of 3.81Å, the tube radius is
101 found to be Δ~2.63Å. Using these basic results, one may derive many attributes of the space-
102 filling discrete helix, which are in excellent accord with the α-helix building block of protein
103 structures (see Figures 4-5, Table 1).
104
105 A space-filling helix maximizes self-interaction through local interactions, whereas the non-local
106 interactions of strands assembled into sheets leads to space-filling. We build on the insights
107 gained from the helix analysis to make predictions of the geometrical arrangements for strand
108 pairing (Figure 3b-c). First, the strands need to be in phase with each other mimicking the
109 behavior of adjoining turns in the continuum helix, placed parallel to and alongside each other.
110 Second, there are two distinct ways (Figures 3b-c) of accomplishing space-filling of assembled
111 strands corresponding to anti-parallel and parallel β-sheet hydrogen bonding patterns, first
112 predicted by Pauling and Corey (3) based on hydrogen bonding. The space-filling packing
113 requires that the distances (i,j) in Figure 3b (anti-parallel arrangement) and (i,M_j) in Figure 3c

114 (parallel arrangement), which are measures of the closest approach of two parallel tube segments,
115 both ought to be 2Δ~5.26Å (see Figure 3d-e and Table 1).
116
117 In addition to helices and strands, chain turns are needed to inter-connect these building blocks.
118 In proteins, the most abundant turns are β-turns, tight, four-residue segments that approximately
119 reverse the overall chain direction (13). β-turns are tightly wound like an α-helix, and therefore
120 are predicted to have similar θ-angles as in the α-helix (Figure 4).
121
122 Figure 4b shows the (θ,μ) coordinates for 4 classes of residues: those that participate in α-helices,
123 parallel β-sheets, anti-parallel β-sheets, and β-turns. The black X marks the coordinates of the
124 predicted space-filling helix. Unsurprisingly, α-helix μ-values (49.7 ± 3.9)° are a bit lower than
125 the theoretical prediction of 52.4° because the distance between a hydrogen-bonded donor and
126 acceptor (N-H⋯O=C) can be less than their summed van der Waals radii. Of course, an ideal
127 tube is unaffected by such chemical particulars. Nevertheless, the predicted μ value for an ideal
128 tube is remarkably close to 50°, the average μ value for Pauling's α-helix (2), with 3.6 residues
129 per turn. As predicted, the tight turns predominantly have a θ value close to that of the α-helix.
130 The β strands are twisted with a μ angle around 180° and have a spread of θ angles.
131
132 The accord between our prediction and structural data from the protein data bank underscores the
133 consilience (48) between mathematics and physics on one hand and quantum chemistry on the
134 other and show how self-interaction is maximized through a space-filling arrangement of
135 individual helices and sheets (Figure 6). The large but finite number of protein native state folds
136 (8,14,20) sculpted by geometry and symmetry (24,25) is reminiscent of the restriction of the

137 number of space groups of Bravais lattices of three-dimensional crystals to exactly 230 due to
138 periodicity and space-filling requirements (49).
139
140 Our theory shows convincingly that structure-space and sequence-space of proteins are separable,
141 yielding sequence-independent forms (22) that are Platonic and immutable, and not subject to
142 Darwinian evolution. Sequences can then populate these forms resulting in the evolution of the
143 functional diversity of life. The evolution (40,50,51) of biological macromolecules can be
144 framed as a random walk in an inordinately vast sequence space, with selection guided by
145 "fitness". Our formalism imposes an important constraint on protein evolution. A consequence is
146 that the repertoire of possible folds is generated from pre-sculpted α-helices and β-strands, and,
147 of necessity, accessible folds are mix-and-match constructs of these fundamental forms. This
148 diversity of structural scaffolds provides a platform for elaborating functional diversity.
149
150 In seminal work, Anfinsen (5) demonstrated that proteins fold rapidly and reproducibly into their
151 native state structures. This naturally led to the text book wisdom (35) that *the amino acid*
152 *sequence of a protein determines its three-dimensional structure* leading to much effort in
153 finding the energy minimum of a many-body complex system of a protein in its solvent with a
154 huge number of degrees of freedom and with myriad interactions. Subsequent work by Matthews
155 (16) and others showed that protein structure is nevertheless *very tolerant of amino acid*
156 *replacement.*
157
158 Our results here conclusively demonstrate a simple two-step process for understanding proteins.
159 First, a menu of putative native state structures is created without regard to amino acid sequence

160 and chemistry. In the second step, a given protein selects its native state from this menu. Thus
161 the horrendous problem of working out the native state structure of a given protein from
162 knowledge of its sequence by finding, from scratch, the conformation, which minimizes the net
163 energy of myriad imperfectly known microscopic interactions, is replaced by the much simpler
164 task of finding the best fit of the sequence to one among the library of geometrically sculpted
165 folds determined in a sequence-independent and chemistry-independent manner. This best-fit
166 process, also exploited in the threading algorithm (15), is where the role of the amino acid
167 sequence becomes paramount. Indeed, in an influential series of papers (12,17-19), it has been
168 highlighted that the amino acid side chains must be able to fit into the native state fold with
169 minimal frustration thereby creating a landscape akin to a folding funnel.
170
171 Some 80 years ago, Bernal (1) wrote – *Any effective picture of protein structure must provide at*
172 *the same time for the common character of all proteins as exemplified by their many chemical*
173 *and physical similarities, and for the highly specific nature of each protein type. It is reasonable*
174 *to believe, though impossible to prove, that the first of these depends on some common*
175 *arrangement of the amino acids*. Indeed, our work here shows that the common character of all
176 proteins originates from an appropriate tube-like geometrical description of just the backbone
177 C_α atoms, which are common to all proteins, and results in the library of native state folds
178 sculpted by geometry and symmetry, without a need for sequence specificity or chemistry. *The*
179 *highly specific nature of each protein type* then arises from its distinctive amino acid side-chains
180 and their fit to one of the folds from the library. For a protein, the folded structure is central to its
181 functionality. The situation is loosely analogous to a restaurant in which the chef (geometry and
182 symmetry) creates a menu of items (the library of putative native state folds) that customers

183 (protein sequences) can order from (fold into). The chef does not cater to the individual tastes of
184 the customers. Rather, all patrons of the restaurant are satisfied picking an item from the menu.
185 As in proteins, the total number of patrons can vastly exceed the number of menu items. If, in
186 fact, the menu of protein structures itself evolved, then one would be confronted by an almost
187 impossible situation for evolution and natural selection in which a protein and its interacting
188 partners would have to co-evolve their structures synergistically in order to maintain function.
189 This situation is deftly avoided by the geometrically determined native state folds providing a
190 fixed backdrop for evolution to shape protein sequences and functionalities.
191
192 Richard Feynman, in a lecture entitled *There's Plenty of Room in the Bottom: An Invitation to*
193 *Enter a New Field of Physics* at the annual American Physical Society Meeting at Caltech on
194 December 29, 1959, suggested that tiny, nanoscale machines could be constructed by
195 manipulating individual atoms. Proteins are precisely such machines (21,26,32,35). Indeed,
196 proteins as well as macroscopic machines establish a stable framework that can accommodate
197 moving parts, which perform a function. Proteins are nature's implementation of the abstract
198 forms presented here, a diversity of stable forms deduced entirely from mathematical
199 considerations. These predictions – independent of any chemistry – have implications for life
200 elsewhere in our cosmos (52) suggesting that there is no absolute need for carbon chemistry for
201 life to exist. We look forward to other implementations in the lab, raising the prospect of
202 powerful interacting machines, potentially leading to artificial life (53).
203
204 In summary, underlying life's evolving complexity (41) is a sequence-independent energy
205 landscape with thousands of stable minima — a landscape formed from nature's scaffold

206 building blocks, a protein grammar. In both natural and artificial languages, a grammar is a finite
207 set of rules that can generate an a large number of syntactically correct sentences or strings. The
208 discretized tube model establishes an immutable grammar of life and "*from so simple a*
209 *beginning, endless"* – protein sequences and functionalities – *"most beautiful and most*
210 *wonderful have been, and are being, evolved"* (54).
211
212 **PDB analysis:** We have carried out a quantitative comparison between our predictions and
213 protein structure. To develop a working set for comparison, Richardsons' Top 8000 set of high-
214 resolution, quality-filtered protein chains (resolution < 2Å, 70% PDB homology level) [see the
215 web site: http://kinemage.biochem.duke.edu/databases/top8000.php] was further filtered to
216 exclude all structures with missing backbone atoms, yielding a working set of 4416 structures
217 (listed in Table 2). The working set was cross-checked against 478 proteins having a more
218 stringent homology cutoff of 20%, taken from the Pisces database (23); 205 entries are in
219 common to both sets. Almost all bond lengths ($C_{\alpha(i)}$-$C_{\alpha(i+1)}$ distance) (~99.7%) in the working set
220 are clustered around 3.81Å, as expected for a *trans* peptide. Those remaining have shorter bonds,
221 ~2.95Å, predominantly from *cis* residues. For purposes of comparison, a fixed bond length of
222 3.81Å is used. Hydrogen bonds were identified using DSSP (11). Hydrogen-bonded conformers
223 extracted from the working set include 3595 helices, 8473 antiparallel pairs, 4639 parallel pairs,
224 and 58,820 turns. Helices were identified as 12-residue segments with intra-helical hydrogen
225 bonds (N_i-H•••O_{i-4} and O_i•••H-N_{i+4}) at each residue. Antiparallel strand pairs were identified by
226 three inter-pair hydrogen bonds at (i,j), (i+2,j-2), and (i-2,j+2), i ∈ strand1, j ∈ strand2. To avoid
227 possible end effects, only (i,j) residue pairs were used. Parallel strand pairs were identified by
228 four inter-pair hydrogen bonds between (i,j-1), (i,j+1), (i+2,j+1), and (i-2,j-1), i ∈ strand1,

229 j ∈ strand2, and again only the i-th residue was retained. Double-counting was assiduously
230 avoided. β turns were identified by hydrogen bonds between (i,i+3) with no helical residues
231 among the 4. The (θ,μ)-values were then recorded for points i+1 and i+2 in the turns.
232
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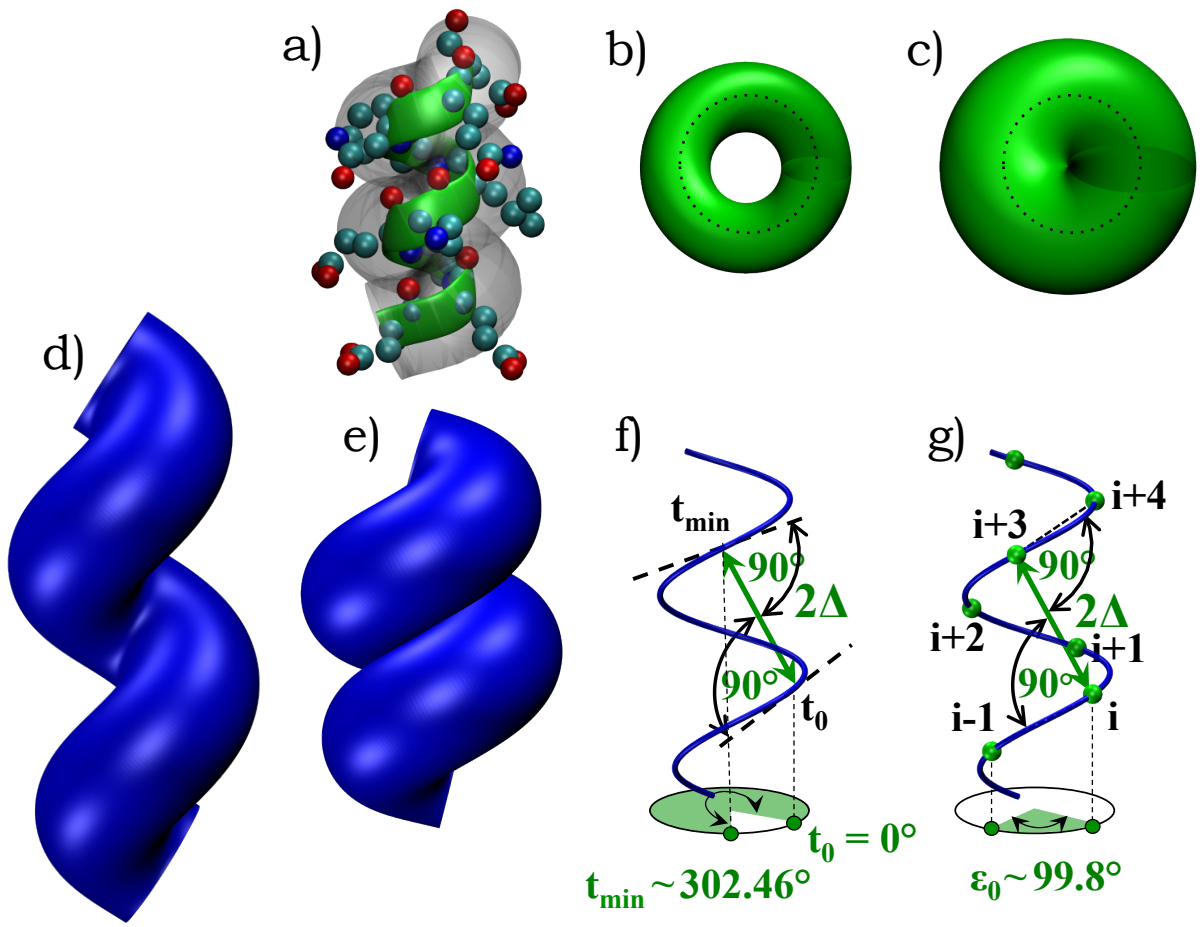

Figure 1: Optimal geometry of space-filling helix. (a) A segment of ten residues of a helix from phage T4 lysozyme protein 1L56 (residues 61-70). The green ribbon represents the helical trace formed by the C_α atoms, the spheres denote the heavy backbone and side-chains atoms in the helix, and the transparent 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 $\eta=(P/2\pi R)\sim0.4$ and a local radius of curvature of the helix, $R_{local}=R(1+\eta^2)\sim1.16R$. 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, Δhas 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.

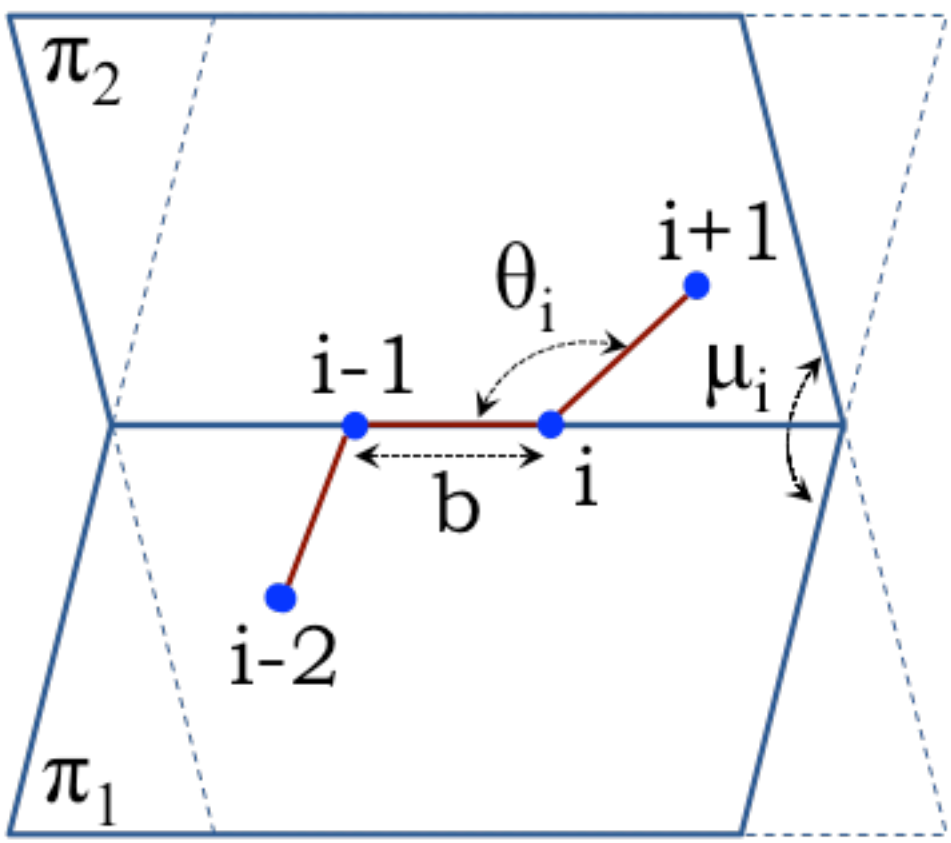

Figure 2: Coordinate system at discrete location i along tube axis. The bond length b, assumed here to be a constant, is the distance between successive points. The angle θ_i is the angle subtended at i by points (i-1) and (i+1) along the tube axis. μ_i is the dihedral angle between the planes π_1 and 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).

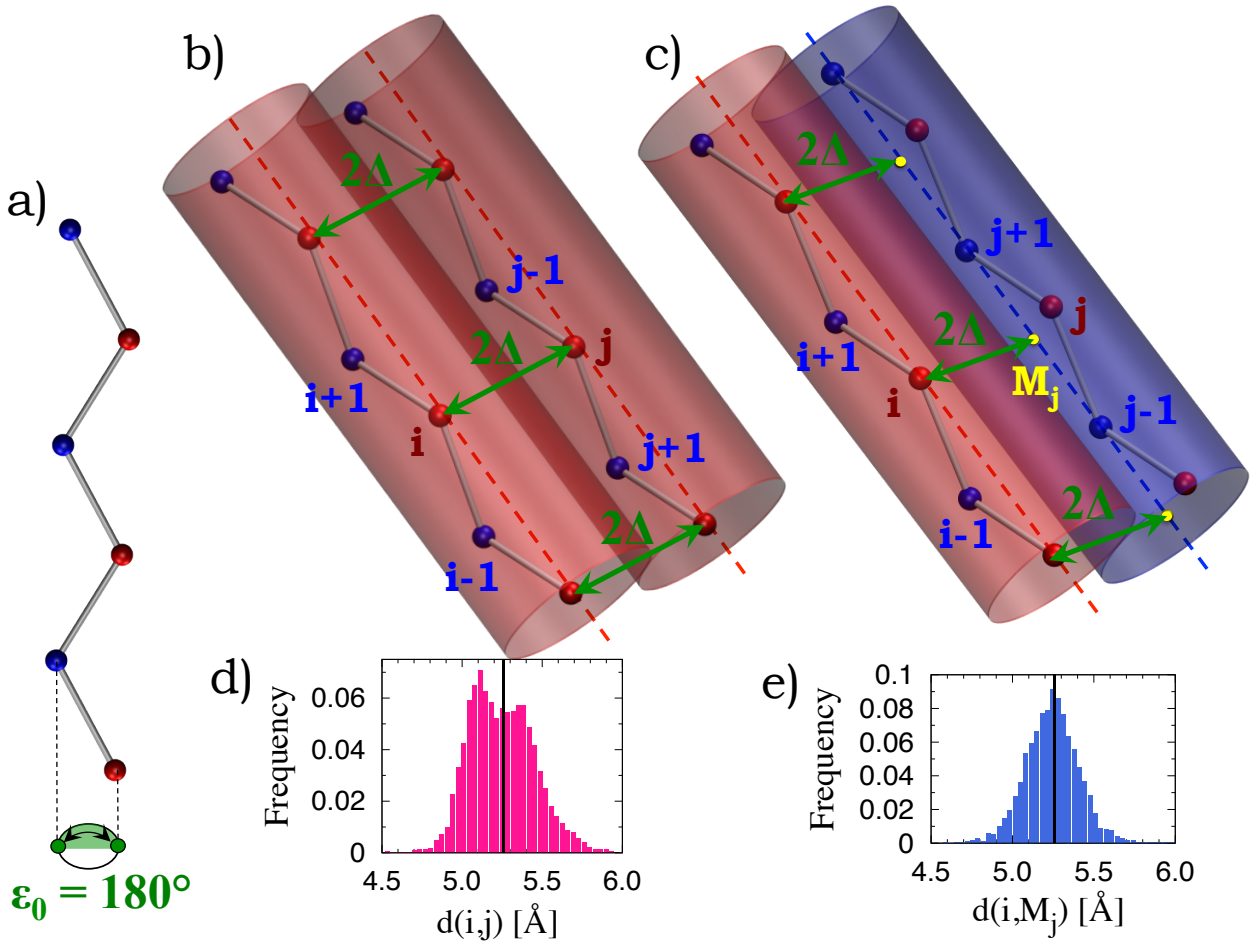

Figure 3: Optimal packing of strands. (a) A single two dimensional zig-zag strand (with a rotation angle of 180°) lying in the plane of the paper. This planarity can only occur for a

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

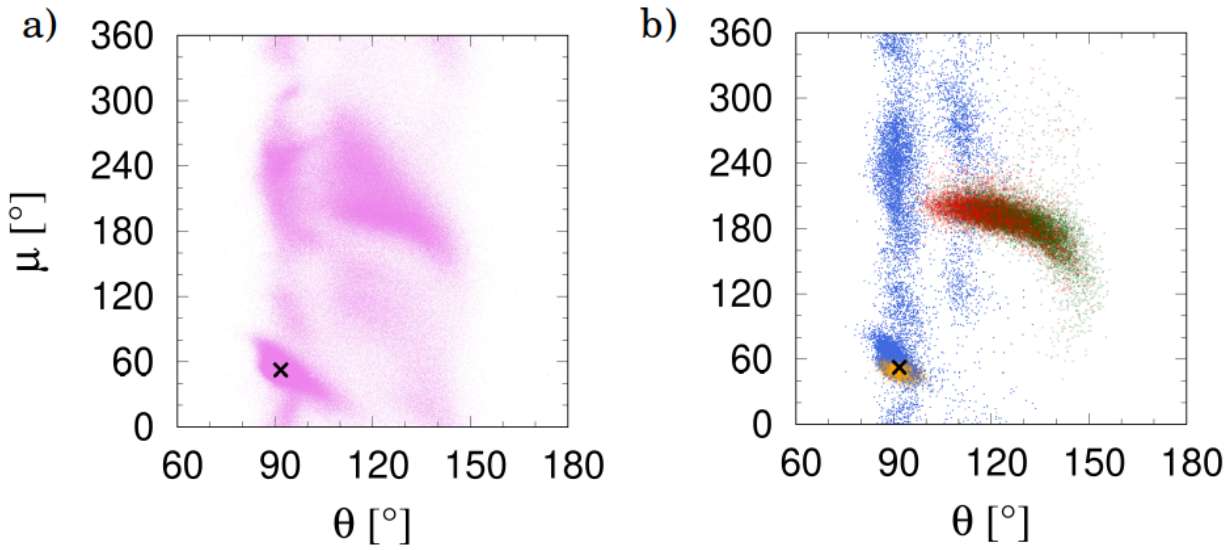

Figure 4: Two views of the local structure representation of proteins. a) (θ, μ) plot of the PDB data set (see Table 2) comprising 4416 proteins and 972,519 residues. Here, the local conformations of residues are shown in the (θ,μ) plane. For strands, a μ-value that deviates from ~180° is the signature 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.

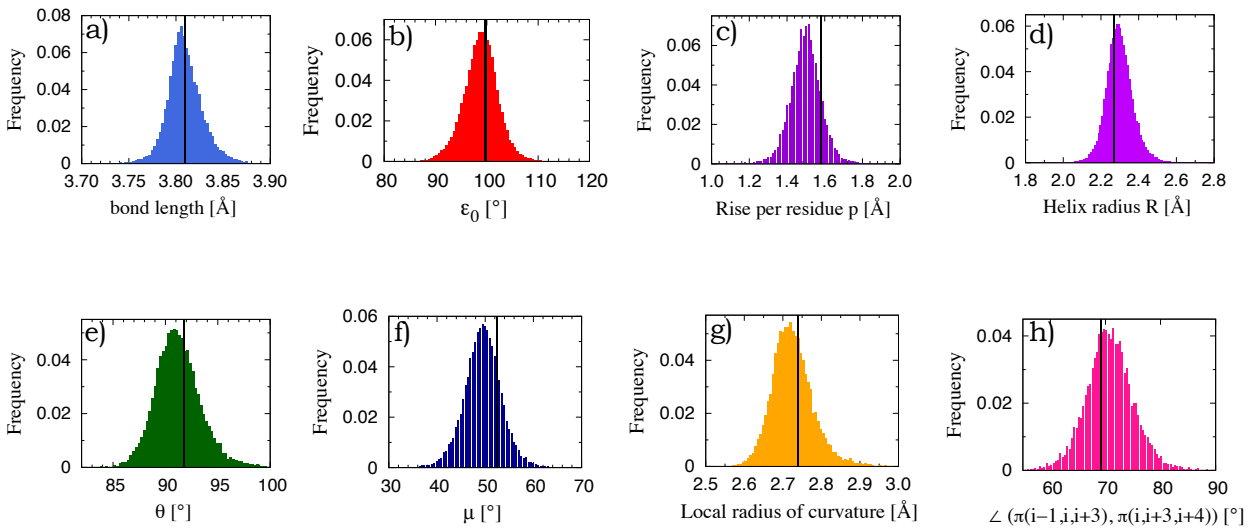

Figure 5: Distribution of α-helix characteristics. (a) Distribution of the experimentally determined bond lengths (consecutive C_α-C_α distances). The bond length in the theory was chosen to be the mean bond length of 3.81Å and sets the characteristic length scale. The other panels show the distributions 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.

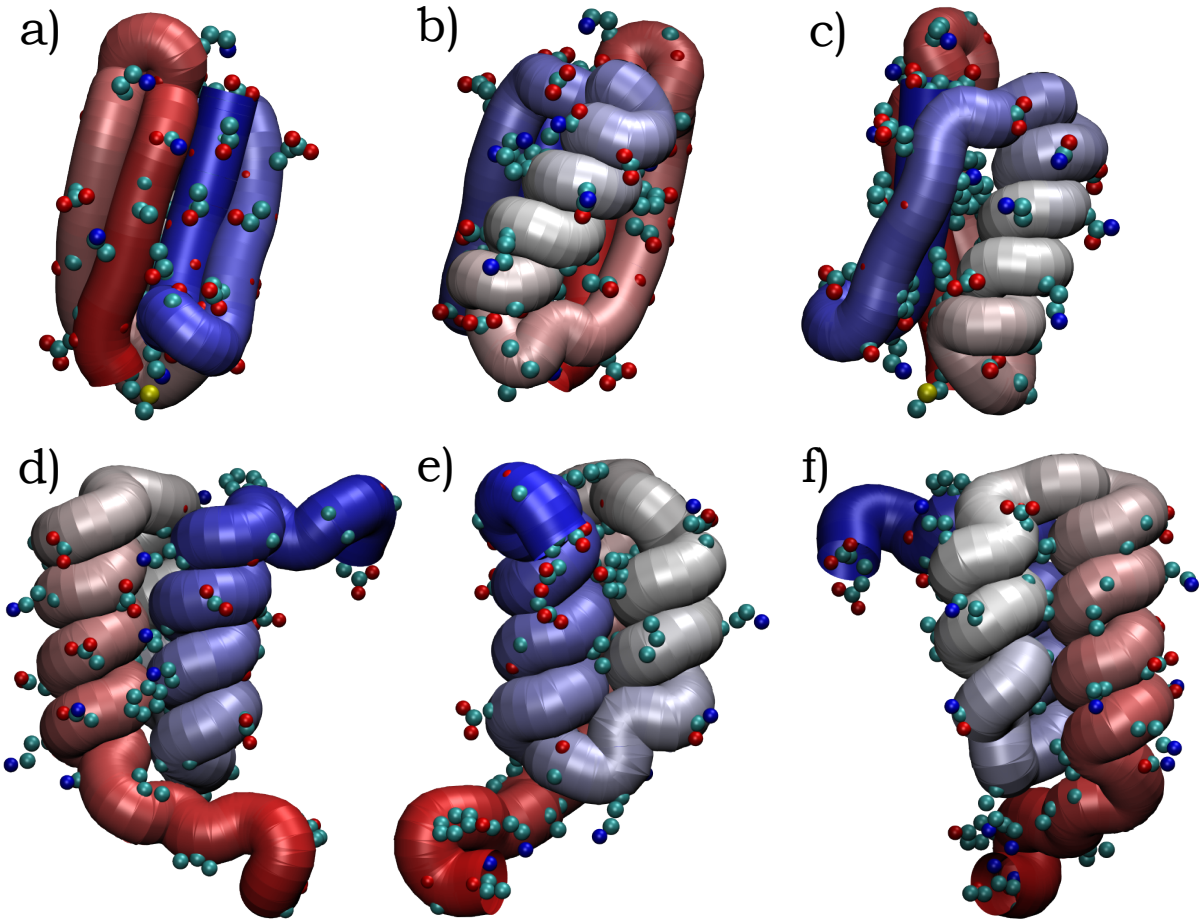

Figure 6: Consilience between mathematics and biochemistry. The figure shows three views each of two short proteins. (a-c) is the 56-residue long protein 3GB1 comprising 4 strands assembled into sheets along with a single helix. (d-f) is a protein of the same length, 2KDL, comprised of a three-helix 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 η= P/(2πR)	0.400	0.377 ± 0.046
∠ (π(i-1,i,i+3), π(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 ∠(π(i,j,k), π(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	1iqc_C	1pnc_A	1w0p_A	2buw_B	2hwn_D	2rc3_A	2zk9_X	3euf_D	3kl0_B
1a1i_A	1iqq_A	1pnd_A	1w0u_A	2bv2_B	2hxm_A	2rc8_B	2zkd_B	3eul_A	3kl6_B
1a2p_B	1iqz_A	1pp0_C	1w1h_C	2bv4_A	2hxp_A	2rci_A	2zl6_B	3eun_A	3klq_A
1a2y_A	1irq_A	1psr_A	1w2c_A	2bw0_A	2hxs_A	2rcq_A	2znd_A	3eup_B	3klr_A
1a2y_B	1isp_A	1ptq_A	1w2i_B	2bw8_A	2hxt_A	2rcv_E	2znr_A	3evf_A	3kmt_C
1a2z_C	1isu_A	1puc_A	1w3i_A	2bwf_A	2hy5_A	2rcz_B	2zoo_A	3evk_D	3kmv_D
1a34_A	1it2_B	1puf_B	1w3w_A	2bwl_A	2hy5_B	2rdh_C	2zpd_A	3evy_B	3knb_B
1a3a_A	1itw_D	1pvm_A	1w3y_A	2bwr_B	2hy7_A	2rdq_A	2zpo_A	3ew0_A	3knv_A
1a4i_B	1itx_A	1pvx_A	1w4s_A	2c0c_A	2hyk_A	2rdu_A	2zpu_A	3ew1_D	3kp8_A
1a73_A	1iu8_B	1pxv_B	1w4t_A	2c0h_A	2hyv_A	2rdz_A	2zqe_A	3ewi_A	3kpb_D
1a7d_A	1iue_B	1pyo_B	1w4v_B	2c0r_B	2hzl_B	2ree_A	2zqm_A	3exe_D	3kq0_A
1a7t_B	1iuz_A	1pzs_A	1w4x_A	2c0z_A	2hzy_B	2reg_A	2zqn_B	3exr_A	3kqi_A
1a88_A	1iv3_D	1q08_B	1w53_A	2c1d_D	2i0q_A	2rem_B	2zs0_A	3ey6_A	3kqr_A
1a8q_A	1iv9_A	1q0q_A	1w5r_B	2c1s_A	2i1n_A	2rer_A	2zs0_D	3eye_A	3kre_A
1a8s_A	1iwd_A	1q0r_A	1w66_A	2c1v_B	2i24_N	2rfg_A	2zs1_B	3eyi_A	3krs_A
1a92_C	1ix1_B	1q1r_B	1w6s_C	2c29_F	2i2q_A	2rfm_B	2zs1_C	3eyp_B	3kru_A
1ab1_A	1ixg_A	1q1u_A	1w6s_D	2c2n_A	2i3f_A	2rh2_A	2zsi_A	3ezi_B	3kse_D
1aba_A	1iy8_C	1q2h_A	1w70_A	2c2p_A	2i49_A	2rh3_A	2ztl_C	3f0y_C	3ksh_A
1afb_3	1iyb_A	1q4u_B	1w8o_A	2c2u_A	2i4a_A	2rhi_A	2zu1_B	3f17_A	3ksv_A
1ag9_B	1iye_C	1q5m_B	1w8u_A	2c3n_C	2i5r_B	2rhk_C	2zu2_A	3f1l_A	3ksx_A
1agy_A	1iyn_A	1q5z_A	1w99_A	2c41_F	2i5v_O	2ri0_B	2zux_B	3f1p_A	3kt9_A
1ah7_A	1izc_A	1q6o_A	1w9p_A	2c42_B	2i61_A	2ri7_A	2zuy_A	3f1p_B	3ktz_A
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1aii_A	1j05_B	1q7l_B	1wa3_A	2c4f_T	2i6v_A	2rik_A	2zwd_A	3f2u_A	3kus_B
1ako_A	1j0h_B	1q8f_A	1wb0_A	2c4j_D	2i7c_C	2riq_A	2zwj_A	3f3q_A	3kuv_A
1aky_A	1j0p_A	1qau_A	1wb6_B	2c4n_A	2i7d_A	2rji_A	2zwn_A	3f3x_A	3kwe_A
1aoh_B	1j1y_A	1qav_A	1wba_A	2c53_A	2i7f_B	2rjw_A	2zwu_A	3f47_A	3kxt_A
1aoz_A	1j24_A	1qaz_A	1wbe_A	2c6q_B	2i8t_B	2rk3_A	2zx2_A	3f4m_A	3kyj_A
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1bxy_A	1jkx_A	1qxy_A	1ws8_A	2cve_A	2ivx_A	2v89_A	3aa6_B	3fp5_A	3let_A
1byi_A	1jl1_A	1qy6_A	1wst_A	2cvi_B	2ivy_A	2v8i_A	3aaf_B	3fpc_A	3lf6_B
1c02_A	1jl7_A	1qz9_A	1wt6_A	2cwd_A	2iw0_A	2v8u_A	3aal_A	3fpf_A	3lfh_F
1c0p_A	1jlj_A	1r0r_E	1wta_A	2cwi_B	2iw1_A	2v9m_A	3aam_A	3fpk_B	3lfj_B
1c1d_A	1jlt_A	1r12_A	1wte_A	2cwr_A	2iw2_B	2v9t_B	3ab6_A	3fpr_D	3lfk_C
1c1k_A	1jlt_B	1r17_A	1wtj_A	2cws_A	2iwk_A	2v9v_A	3aba_A	3fpu_B	3lg5_A
1c1l_A	1jm1_A	1r1p_A	1wto_A	2cxn_B	2iwz_A	2vac_A	3abf_E	3fpw_A	3lgi_A
1c1y_A	1jnr_C	1r1t_B	1wu9_B	2cyg_A	2ix4_B	2vap_A	3aci_A	3fq3_C	3lgn_A
1c1y_B	1jnr_D	1r26_A	1wui_S	2cz4_A	2ixc_A	2vb1_A	3act_B	3fqm_A	3lhq_A
1c4q_B	1jo0_A	1r29_A	1wur_B	2czd_A	2ixd_B	2vba_D	3acx_A	3frq_A	3lhr_B
1c52_A	1jo8_A	1r2m_A	1wve_D	2czq_B	2ixk_A	2vbk_A	3adg_A	3frr_A	3lid_B
1c5e_A	1jpe_A	1r2r_B	1wvf_A	2d0i_B	2ixm_A	2vc3_A	3ado_A	3fs7_A	3lim_D
1c75_A	1jq5_A	1r3q_A	1wwz_B	2d16_A	2izz_B	2vc8_A	3aey_A	3ft1_C	3liy_A
1c7j_A	1jqe_A	1r45_B	1wy1_A	2d1c_A	2j1s_A	2ve8_E	3afm_A	3ftd_A	3ljw_B
1c7k_A	1jr8_A	1r55_A	1wy2_B	2d1x_A	2j23_A	2veb_A	3afv_A	3fv3_G	3lke_A
1c7n_F	1jsd_B	1r6d_A	1wyx_B	2d1y_C	2j27_A	2vfk_A	3ag3_C	3fv9_G	3lkt_B
1cc8_A	1jt2_A	1r6j_A	1wz3_A	2d29_A	2j2j_F	2vfq_A	3ag3_E	3fvb_B	3lkt_Q
1ccw_B	1ju2_A	1r6x_A	1wz8_A	2d37_A	2j3x_A	2vg1_B	3ag7_A	3fvh_A	3llb_A
1cf3_A	1jub_B	1r77_B	1wzd_B	2d3d_A	2j5g_A	2vg3_C	3agn_A	3fwa_A	3llu_A
1cg5_A	1juv_A	1r7j_A	1x0c_A	2d3n_A	2j5i_F	2vgp_D	3ah2_A	3fwy_A	3lny_A
1cg5_B	1jvw_A	1r87_A	1x0l_A	2d4n_A	2j5y_A	2vha_B	3ahc_A	3fx4_A	3log_C
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1cka_A	1jyh_A	1r9d_A	1x2t_C	2d5k_C	2j6i_A	2vjv_B	3ai3_C	3fza_A	3lpw_B
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1ctj_A	1k4m_C	1rgx_C	1x91_A	2d81_A	2j8m_A	2vn4_A	3alf_A	3g21_A	3lvf_P
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1d02_B	1k9u_B	1rkq_A	1xg0_B	2de6_F	2jba_B	2vo9_B	3b4u_B	3g7w_A	3ly7_A
1d0d_A	1ka1_A	1rku_A	1xg2_A	2dep_A	2jbv_A	2voc_A	3b4w_A	3g8h_A	3lz5_A
1d2n_A	1kaf_A	1rl0_A	1xg2_B	2dfb_A	2jc4_A	2voz_A	3b51_X	3g98_B	3lzo_B
1d4o_A	1kao_A	1rlh_A	1xg4_A	2dfd_C	2jc5_A	2vpg_A	3b5g_B	3g9m_B	3lzw_A

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1dbw_B	1kew_A	1rqj_A	1xk4_I	2dko_A	2je6_B	2vtc_B	3b64_A	3gbs_A	3m3g_A
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1euh_C	1m0d_C	1t2w_C	1yn8_E	2eky_C	2odf_E	2wf6_A	3c05_D	3h0u_C	3n11_A
1euv_A	1m0s_B	1t3q_A	1yn9_A	2elc_B	2odk_C	2wfc_C	3c0i_A	3h12_B	3n1e_B
1euv_B	1m0u_A	1t3q_B	1ynb_C	2end_A	2oe3_A	2wfh_B	3c1o_A	3h1g_A	3n1f_D
1evh_A	1m15_A	1t3y_A	1ynh_B	2eo4_A	2oeb_A	2wfj_A	3c2u_A	3h1s_B	3n1s_M
1ex2_B	1m1n_E	1t4b_B	1ynp_B	2eq6_B	2ofc_A	2wfo_A	3c3y_B	3h34_A	3n22_A
1ext_A	1m1n_F	1t61_C	1yo3_A	2erf_A	2ofk_A	2wfz_A	3c4s_A	3h3n_X	3n2n_E
1eyh_A	1m1r_A	1t61_E	1yoa_A	2erw_A	2og1_A	2wge_A	3c5a_A	3h4n_A	3n37_A
1eyl_A	1m2d_B	1t6c_A	1yoc_B	2ery_B	2oh5_A	2wgp_B	3c5e_A	3h4x_A	3n3s_A
1eyv_A	1m2h_A	1t6g_D	1yon_A	2esl_A	2ohw_B	2wh7_A	3c5j_A	3h55_B	3n4i_B
1ez3_B	1m2t_B	1t6u_L	1yp1_A	2et1_A	2oif_B	2whg_B	3c5k_A	3h5i_A	3n4j_A
1ezg_B	1m2x_D	1t6v_N	1yph_D	2etb_A	2oiz_B	2wi8_A	3c68_B	3h5j_B	3n5a_A
1ezm_A	1m3u_C	1t7q_B	1yph_E	2etx_A	2oj6_C	2wiy_A	3c6w_A	3h5l_B	3n5b_B
1f08_B	1m40_A	1t7r_A	1yq2_C	2eu7_X	2okl_B	2wj5_A	3c70_A	3h62_B	3n72_B
1f0k_B	1m4i_A	1t8h_A	1yqd_A	2eut_A	2okm_A	2wje_A	3c7f_A	3h6p_B	3n79_A
1f0y_B	1m4j_A	1t8k_A	1yqe_A	2ev1_A	2okq_A	2wjn_C	3c7t_A	3h6p_C	3n98_A
1f1m_C	1m55_A	1t8t_B	1yqw_B	2evb_A	2ol1_B	2wjn_L	3c7x_A	3h78_A	3n9g_H
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1g8k_A	1n7e_A	1u3i_A	1zkc_A	2fn3_A	2p6z_A	2x1b_A	3cu9_A	3huh_A	3o26_A
1g8k_D	1n7s_A	1u53_A	1zke_B	2fn4_A	2p74_A	2x23_B	3cui_A	3hup_B	3o2e_A
1g94_A	1n7s_B	1u55_A	1zkk_B	2fn9_B	2p8b_A	2x2o_A	3cvb_A	3hv2_B	3o3m_C
1g97_A	1n7s_C	1u5d_B	1zkl_A	2fne_A	2p9x_D	2x32_A	3cwn_B	3hvi_A	3o3m_D
1g9g_A	1n7s_D	1u5f_A	1zl0_B	2fnu_A	2pa1_A	2x3h_C	3cwv_A	3hvu_C	3o3u_N
1g9o_A	1n82_B	1u60_B	1zlm_A	2fo3_A	2pa6_B	2x3m_A	3cx5_E	3hvv_A	3o4h_A
1ga6_A	1n83_A	1u6e_A	1zm8_A	2fp1_A	2pa7_B	2x49_A	3cx5_F	3hx9_A	3o4r_B
1gai_A	1n8f_B	1u6r_B	1zn8_A	2fp7_A	2pbc_C	2x4d_A	3cx5_G	3hxa_F	3o4v_B
1gbg_A	1n9l_A	1u6t_A	1zo2_A	2fq3_A	2pbd_P	2x4k_B	3cx5_I	3hxs_B	3o5v_B
1gbs_A	1na0_A	1u6z_B	1zoi_B	2fqw_A	2pbi_C	2x4l_A	3cx5_O	3hxw_A	3o70_A
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1geg_G	1nc5_A	1u9k_A	1zr0_D	2ftx_B	2pcn_A	2x5y_A	3cz1_B	3i1u_A	3o8m_A
1ges_B	1ndd_A	1ua4_A	1zr3_B	2fu0_A	2pdr_B	2x6w_A	3czf_B	3i24_A	3o9z_A
1gk6_A	1ne7_C	1ua6_L	1zr6_A	2fu4_A	2pfz_A	2x7b_A	3czt_X	3i26_D	3oa3_B
1gk7_A	1nep_A	1uai_A	1zs4_D	2fuk_A	2pg0_B	2x7k_A	3czz_B	3i2z_A	3oaj_A
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1gny_A	1nls_A	1ufb_C	1zxt_B	2g30_A	2pkt_A	2xcb_A	3d3b_A	3i4z_B	3oiu_A
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1gwu_A	1nww_A	1umd_D	2a70_A	2gf9_A	2ptt_B	2xkg_A	3dfg_A	3ie4_A	3p1f_A
1gxn_A	1nwz_A	1umk_A	2a7l_B	2gg6_A	2ptz_A	2xkr_A	3dgb_A	3ie5_A	3p1g_A
1gxu_A	1nxc_A	1umz_A	2a8n_A	2gh0_B	2pu3_A	2xla_A	3dgp_A	3iei_C	3p2n_A
1gxy_A	1nxj_A	1uow_A	2a9i_A	2gh0_D	2pu9_A	2xlk_A	3dgp_B	3iev_A	3p2t_A
1gy6_A	1nxm_A	1uoy_A	2a9s_A	2gh9_A	2pu9_B	2xm5_A	3dgt_A	3iez_B	3p3c_A
1gy7_C	1nyk_B	1uqx_A	2aa1_B	2gha_A	2pv2_A	2xmx_A	3dha_A	3ife_A	3p3e_A
1gyh_C	1nyt_C	1uqz_A	2aal_C	2gia_B	2pvb_A	2xn4_A	3dhi_B	3ig9_C	3p3g_A
1gyo_A	1nza_A	1urn_C	2aan_A	2gib_B	2pve_B	2xn6_A	3dhi_C	3igz_B	3p3o_A
1gyv_A	1o04_E	1urr_A	2ab0_A	2giy_A	2pvq_A	2xov_A	3dho_C	3ihw_A	3p48_A
1gyy_B	1o0e_B	1urs_A	2abk_A	2gj3_A	2pwy_A	2xpp_A	3die_A	3ihz_B	3p4t_A
1gzc_A	1o1z_A	1us5_A	2abw_B	2gjd_C	2pxx_A	2xqu_A	3dj9_A	3ii7_A	3p5h_A
1gzw_B	1o26_C	1use_A	2acf_D	2gke_A	2py4_A	2xs4_A	3djh_C	3iij_A	3p73_A
1h03_P	1o4k_A	1usf_B	2ad6_A	2gkm_B	2pyw_A	2xsu_A	3djl_A	3iiu_M	3p73_B
1h0h_B	1o4s_A	1usg_A	2ad6_D	2gkr_I	2pz0_B	2xt2_A	3djo_A	3ij3_A	3p7y_A
1h16_A	1o4t_A	1uso_A	2ae2_A	2gl5_A	2pze_B	2xts_A	3dk9_A	3ijl_A	3p97_C
1h1n_A	1o4v_A	1usq_B	2aen_E	2gmy_E	2pzh_B	2xts_B	3dkc_A	3ik7_D	3p9c_A
1h1y_A	1o4y_A	1uti_A	2aex_A	2gn4_B	2q0l_A	2xtt_B	3dkm_A	3ilo_A	3p9p_A
1h2b_B	1o5u_A	1uu4_A	2ag4_B	2gnc_A	2q20_B	2xu3_A	3dkr_A	3ils_A	3p9x_A
1h2c_A	1o5x_A	1uuq_A	2ag5_B	2gok_A	2q28_A	2xu8_B	3dl0_A	3ilw_A	3pb6_X
1h2e_A	1o7e_B	1uuy_A	2agd_B	2gom_A	2q2a_D	2xvm_B	3dlm_A	3im1_A	3pbf_A
1h2s_A	1o7i_A	1uv4_A	2ahf_A	2gou_A	2q2h_A	2xvs_A	3dm8_A	3im9_A	3pc3_A
1h2s_B	1o7j_C	1uvq_A	2ahn_A	2gpe_B	2q35_A	2xvx_A	3dme_B	3imh_A	3pcv_A
1h4a_X	1o7q_B	1uw4_C	2aib_A	2gqt_A	2q5c_A	2xws_A	3dmg_A	3inz_B	3pd2_B
1h4g_A	1o7z_B	1uw4_D	2akz_B	2gqw_A	2q62_G	2xwt_C	3dmi_A	3iof_A	3pd7_A
1h4p_A	1o82_A	1uwc_A	2anv_A	2grc_A	2q73_C	2xxj_D	3dmo_A	3ioh_A	3pdn_A
1h4r_A	1o8s_A	1uwf_A	2any_A	2grr_B	2q86_B	2xxl_B	3dnf_B	3ioq_A	3pel_B
1h5b_B	1o8x_A	1uwk_B	2ap1_A	2gsd_A	2q87_A	2xy2_A	3dpg_B	3iox_A	3pew_A
1h5q_L	1o91_C	1uwz_A	2apg_A	2gso_B	2q88_A	2xz2_A	3dqg_A	3ip4_A	3pf2_A
1h5v_A	1o98_A	1uxx_X	2aqm_A	2gte_A	2q8n_C	2xzi_A	3dr0_C	3ip8_A	3pfg_A
1h64_Q	1o9i_D	1uxy_A	2aqp_A	2gtr_A	2q8r_G	2y2z_A	3dr4_B	3ipc_A	3pfs_A
1h6f_A	1o9r_E	1uy1_A	2ar1_A	2gu3_A	2q9u_A	2y39_A	3dra_A	3ipf_A	3pg6_C
1h6l_A	1oa2_C	1uyx_A	2arc_B	2gud_B	2qa9_E	2y3q_B	3drf_A	3ipw_A	3pgx_A
1h6u_A	1oa8_A	1uz3_A	2asd_A	2gui_A	2qac_A	2y3v_D	3drw_B	3iq3_A	3phs_A
1h6w_A	1oaa_A	1v05_A	2asu_B	2guv_C	2qap_A	2y3z_A	3drz_B	3iql_A	3phx_B
1h72_C	1oai_A	1v08_B	2at8_X	2guy_A	2qb7_A	2y5p_C	3ds4_B	3irp_X	3pjp_B
1h75_A	1oal_A	1v0z_B	2atb_A	2gw4_D	2qc5_A	2y7b_A	3dsk_A	3irs_A	3pk0_A
1h7e_B	1oao_A	1v2z_A	2atv_A	2gwm_A	2qd6_A	2y88_A	3dso_A	3irv_A	3pkv_A
1h8p_B	1oaq_H	1v30_A	2au7_A	2gxg_A	2qdx_A	2y8m_A	3dt9_A	3is3_A	3plf_D

1h8u_A	1oaq_L	1v33_A	2avd_B	2gyq_B	2qed_A	2yay_A	3dtb_A	3isa_B	3plw_A
1h97_B	1obo_A	1v37_A	2avk_A	2gz1_B	2qee_F	2ygs_A	3dvw_A	3iso_A	3plx_B
1h98_A	1oc2_B	1v4p_C	2axq_A	2gz4_A	2qev_A	2yqu_B	3dwg_A	3isq_A	3pmc_B
1h9m_A	1oc8_A	1v4x_B	2axw_B	2gze_A	2qf4_B	2yrr_B	3dwg_C	3it4_B	3pmd_A
1h9s_B	1ock_A	1v54_A	2ayd_A	2gze_B	2qfa_A	2ysk_A	3dwv_B	3it4_C	3pms_A
1hbn_C	1ocy_A	1v54_J	2b0a_A	2gzg_B	2qfa_B	2yva_B	3dxt_A	3iu5_A	3pmt_A
1hbn_E	1odm_A	1v54_V	2b0t_A	2h17_A	2qfa_C	2yve_A	3dy0_A	3iu7_A	3pna_A
1hc9_B	1odt_H	1v55_D	2b1k_A	2h1c_A	2qfe_A	2yvi_A	3dzw_A	3iux_A	3po0_A
1hd2_A	1oe2_A	1v55_L	2b3f_D	2h1v_A	2qg1_A	2yvo_A	3e05_B	3iwt_A	3po8_A
1hdo_A	1off_A	1v58_B	2b3h_A	2h2b_A	2qgy_B	2yvt_A	3e0i_A	3ix3_B	3pqa_B
1hfe_L	1ofl_A	1v5d_A	2b49_A	2h2r_B	2qhl_B	2yw2_A	3e13_X	3ixq_D	3pr9_A
1hfe_T	1ofs_C	1v5f_A	2b4z_A	2h2z_A	2qho_B	2yw3_A	3e17_B	3jpz_B	3prp_A
1hfo_E	1ofs_D	1v5i_B	2b5a_A	2h3h_A	2qhs_A	2ywd_A	3e2d_A	3jqj_C	3psm_A
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1hh8_A	1ofz_A	1v70_A	2b5w_A	2h54_B	2qif_A	2ywk_A	3e4g_A	3jqu_A	3pvi_B
1hj8_A	1ogd_D	1v7p_C	2b6n_A	2h62_A	2qih_B	2yxm_A	3e4w_B	3jqy_C	3pxl_A
1hjs_B	1ogm_X	1v7r_A	2b7r_A	2h64_B	2qim_A	2yxn_A	3e55_A	3jr0_B	3q0h_A
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1hzo_A	1osy_B	1vg8_C	2bjf_A	2he0_A	2qud_A	2z66_B	3ef6_A	3k3c_D	3qgz_A
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1i0l_A	1ou8_B	1vht_B	2bjq_A	2he4_A	2quo_A	2z6o_A	3eg4_A	3k3v_A	3qhz_M
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1i0v_A	1ov3_A	1vi6_B	2bka_A	2heu_B	2qv5_A	2z6w_A	3ego_B	3k6f_A	3qki_B
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1i27_A	1ox0_A	1vjk_A	2bkm_B	2hfn_H	2qvu_B	2z7f_E	3ehw_B	3k6y_A	3qqi_B
1i2t_A	1oxj_A	1vjw_A	2bko_A	2hgx_B	2qwc_A	2z7f_I	3ei9_B	3k7f_B	3qry_A
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1i7h_A	1ozn_A	1vki_A	2bky_Y	2hke_B	2qxi_A	2z8q_A	3eja_A	3k8d_A	3qy1_B
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1i8f_F	1p1j_A	1vl7_A	2bl8_B	2hls_A	2qzt_B	2z9v_B	3eju_A	3k9o_A	3r0p_B
1i8k_B	1p1m_A	1vlc_A	2blf_A	2hlv_A	2r0b_A	2za0_A	3eki_A	3k9w_A	3r1i_A
1i8o_A	1p1x_B	1vlj_A	2blf_B	2hmq_D	2r0h_C	2zbo_A	3elw_A	3kbf_A	3r1w_C
1i9c_A	1p28_B	1vm9_A	2bme_B	2hor_A	2r16_A	2zbt_B	3elx_A	3kcc_A	3r3r_A
1iap_A	1p3c_A	1vmb_A	2bmo_A	2hos_B	2r1j_R	2zc8_A	3em1_A	3kcg_H	3r3s_C
1iby_B	1p6o_B	1vmf_C	2bmo_B	2hq6_A	2r2y_A	2zd1_A	3emi_A	3kci_A	3r6f_A
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1ig3_A	1p99_A	1vp2_A	2bo1_A	2hqs_H	2r37_A	2zdo_B	3enb_A	3kda_A	4ubp_A
1igq_A	1pa2_A	1vp6_C	2bo4_F	2hqy_A	2r5o_B	2zdr_A	3enk_B	3ke4_A	4ubp_B

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