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 $t_0=0^\circ$) 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): $\eta \sim 0.4$, $\Delta/R \sim 1.16$, and $t_{\min} \sim 302^\circ$.

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 $\mu=180^\circ$. 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 $\mu=180^\circ$. 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 $\eta \sim 0.4$ and $\Delta/R \sim 1.16$, 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 $t_0=0^\circ$) 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 $\epsilon_0 \sim 99.8^\circ$ (the ratio of the distance to the tube diameter is found to be $1.00\dots$ and both the angles are $90.0\dots^\circ$ 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 $3.81\text{\AA}$, the tube radius is found to be $\Delta \sim 2.63\text{\AA}$. 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 $2\Delta \sim 5.26\text{\AA}$ (see Figure 3d-e and Table 1).

It is important to note that, for both helices and sheets, the side-chains do not clash sterically unlike in a well-packed compact arrangement of parallel strands in a hexagonal array. 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 ($49.7 \pm 3.9^\circ$) are a bit lower than the theoretical prediction of 52.4° because the distance between a hydrogen-bonded donor and acceptor ($\text{N-H}\cdots\text{O}=\text{C}$) 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 ($N_i-H\cdots O_{i-4}$ and $O_i\cdots H-N_{i+4}$) at each residue. Antiparallel strand pairs were identified by three inter-pair hydrogen bonds at (i,j) , $(i+2,j-2)$, and $(i-2,j+2)$, $i \in \text{strand1}$, $j \in \text{strand2}$. 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 $(i-2,j-1)$, $i \in \text{strand1}$, $j \in \text{strand2}$, 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.

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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 $\eta=(P/2\pi R)\sim 0.4$ and a local radius of curvature of the helix, $R_{\text{local}}=R(1+\eta^2)\sim 1.16R$. The tube radii Δ in the two cases are different: $\Delta/R_{\text{local}}=1/2$ 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 $\Delta=R_{\text{local}}$, 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 $\sim 1.16R$. (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 $(\Delta/R) \sim 1.16$ 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 $2\Delta \sim 5.26\text{\AA}$ 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 $2\Delta \sim 5.26\text{\AA}$. 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 $\sim 180^\circ$ 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 $\mu = 180^\circ$. 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 $3.81\text{\AA}$ 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 $2.6\text{\AA}$, 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 $2\Delta=5.26\ldots \text{\AA}$		
Quantity	Theory	PDB data
HELIX		
Rotation angle ε [$^\circ$]	99.8	99.1 ± 3.4
Number of residues per turn	3.61	3.63 ± 0.13
Helix radius R [$\text{\AA}$]	2.27	2.30 ± 0.07
Rise per residue p [$\text{\AA}$]	1.58	1.51 ± 0.08
Helix pitch P [$\text{\AA}$]	5.69	5.47 ± 0.49
Pitch to radius ratio $\eta = P/(2\pi R)$	0.400	0.377 ± 0.046
$\angle (\pi(i-1, i, i+3), \pi(i, i+3, i+4))$ [$^\circ$]	69.1	70.0 ± 4.4
Local radius of curvature [$\text{\AA}$]	2.74	2.73 ± 0.05
θ [$^\circ$]	91.8	91.3 ± 2.2
μ [$^\circ$]	52.4	49.7 ± 3.9
SHEET		
Type I β-sheet: parallel		
θ [$^\circ$]	flexible	121 ± 10
μ [$^\circ$]	~ 180	191 ± 17
$d(i, M_j)$ [$\text{\AA}$]	$2\Delta=5.26$	5.26 ± 0.16
Type II β-sheet: antiparallel		
θ [$^\circ$]	flexible	127 ± 10
μ [$^\circ$]	~ 180	186 ± 20
$d(i, j)$ [$\text{\AA}$]	$2\Delta=5.26$	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 $3.81 \pm 0.02 \text{\AA}$. The chain is defined by discrete points denoted by $1, 2, 3, \dots, i, \dots$ $d(i, j)$ 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	liqc_C	lpnc_A	1w0p_A	2buw_B	2hwn_D	2rc3_A	2zk9_X	3euf_D	3kl0_B
1ali_A	liqq_A	lpnd_A	1w0u_A	2bv2_B	2hxm_A	2rc8_B	2zkd_B	3eul_A	3kl6_B
1a2p_B	liqz_A	lpp0_C	1wlh_C	2bv4_A	2hxp_A	2rci_A	2zl6_B	3eun_A	3klq_A
1a2y_A	lirq_A	lpsr_A	1w2c_A	2bw0_A	2hxs_A	2rcq_A	2znd_A	3eup_B	3klr_A
1a2y_B	lisp_A	lptq_A	1w2i_B	2bw8_A	2hxt_A	2rcv_E	2znr_A	3evf_A	3kmt_C
1a2z_C	lisu_A	lpuc_A	1w3i_A	2bwf_A	2hy5_A	2rcz_B	2zoo_A	3evk_D	3kmv_D
1a34_A	lit2_B	lpuf_B	1w3w_A	2bwl_A	2hy5_B	2rdh_C	2zpd_A	3evy_B	3knb_B
1a3a_A	litw_D	lpvm_A	1w3y_A	2bwr_B	2hy7_A	2rdq_A	2zpo_A	3ew0_A	3knv_A
1a4i_B	litx_A	lpvx_A	1w4s_A	2c0c_A	2hyk_A	2rdu_A	2zpu_A	3ew1_D	3kp8_A
1a73_A	liu8_B	lpxv_B	1w4t_A	2c0h_A	2hyv_A	2rdz_A	2zqe_A	3ewi_A	3kpb_D
1a7d_A	liue_B	lpyo_B	1w4v_B	2c0r_B	2hzi_B	2ree_A	2zqm_A	3exe_D	3kq0_A
1a7t_B	liuz_A	lpzs_A	1w4x_A	2c0z_A	2hzy_B	2reg_A	2zqn_B	3exr_A	3kqi_A
1a88_A	liv3_D	lq08_B	1w53_A	2c1d_D	2i0q_A	2rem_B	2zs0_A	3ey6_A	3kqr_A
1a8q_A	liv9_A	lq0q_A	1w5r_B	2c1s_A	2i1n_A	2rer_A	2zs0_D	3eye_A	3kre_A
1a8s_A	liwd_A	lq0r_A	1w66_A	2c1v_B	2i24_N	2rfg_A	2zsl_B	3eyi_A	3krs_A
1a92_C	lix1_B	lq1r_B	1w6s_C	2c29_F	2i2q_A	2rfm_B	2zsl_C	3eyp_B	3kru_A
1ab1_A	lixg_A	lq1u_A	1w6s_D	2c2n_A	2i3f_A	2rh2_A	2zsi_A	3ezi_B	3kse_D
1aba_A	liy8_C	lq2h_A	1w70_A	2c2p_A	2i49_A	2rh3_A	2ztl_C	3f0y_C	3ksh_A
1afb_3	liyb_A	lq4u_B	1w8o_A	2c2u_A	2i4a_A	2rhi_A	2zu1_B	3f17_A	3ksv_A
1ag9_B	liye_C	lq5m_B	1w8u_A	2c3n_C	2i5r_B	2rhk_C	2zu2_A	3f1l_A	3ksx_A
1agy_A	liyn_A	lq5z_A	1w99_A	2c41_F	2i5v_O	2ri0_B	2zux_B	3f1p_A	3kt9_A
1ah7_A	lizc_A	lq6o_A	1w9p_A	2c42_B	2i61_A	2ri7_A	2zuy_A	3f1p_B	3ktz_A
1aho_A	lize_A	lq7l_A	1w9s_A	2c4e_A	2i62_D	2ri9_A	2zw2_A	3f2e_A	3kuz_B
1aii_A	lj05_B	lq7l_B	1wa3_A	2c4f_T	2i6v_A	2rik_A	2zwd_A	3f2u_A	3kus_B
1ako_A	lj0h_B	lq8f_A	1wb0_A	2c4j_D	2i7c_C	2riq_A	2zww_A	3f3q_A	3kuv_A
1aky_A	lj0p_A	lqau_A	1wb6_B	2c4n_A	2i7d_A	2rji_A	2zwn_A	3f3x_A	3kwe_A
1aoh_B	lj1y_A	lqav_A	1wba_A	2c53_A	2i7f_B	2rjw_A	2zww_A	3f47_A	3kxt_A
1aoz_A	lj24_A	lqaz_A	1wbe_A	2c6q_B	2i8t_B	2rk3_A	2zx2_A	3f4m_A	3kyj_A
1arb_A	lj27_A	lqb5_E	1wbh_B	2c6u_A	2i9a_D	2rk5_A	2zxx_B	3f4s_A	3kz5_A
1ast_A	lj2j_B	lqb7_A	1wbi_H	2c6z_A	2i9i_A	2rk1_A	2zxy_A	3f52_A	3kz7_A
1atg_A	lj2r_A	lqba_A	1wbj_A	2c78_A	2iax_A	2rkq_A	2zya_B	3f51_B	3kzj_A
1atl_B	lj30_B	lqcx_A	1wbj_B	2c7p_A	2ib8_A	2rku_A	2zyh_B	3f5o_G	3kzu_B
1atz_B	lj34_A	lqd1_B	1wc2_A	2c81_A	2ibj_A	2rky_C	2zyo_A	3f6o_A	3l07_B
1aun_A	lj34_B	lqd2_A	1wc9_A	2c82_B	2ibl_A	2sak_A	2zzd_E	3f6q_A	3l0f_A
1avb_A	lj3w_C	lqd9_C	1wcf_A	2c8h_D	2ibp_B	2sec_I	2zzd_J	3f6q_B	3l0l_B
1awd_A	lj48_A	lqdd_A	1wcf_B	2c92_D	2ic6_A	2sga_A	2zzj_A	3f6y_A	3l18_A
1aye_A	lj71_A	lqfv_B	1wck_A	2c95_B	2ic7_B	2sn3_A	2zzr_A	3f74_B	3l1e_A
1b0b_A	lj75_A	lqgi_A	1wd3_A	2c9q_A	2idl_B	2tnf_B	2zzs_O	3f75_A	3l2c_A
1b16_A	lj77_A	lqgj_A	1wdd_S	2cal_A	2if6_A	2uuy_B	2zzv_B	3f75_P	3l32_A
1b1c_A	lj7d_A	lqgu_D	1wdy_A	2car_B	2ifc_C	2uv4_A	3a02_A	3f7l_A	3l39_A
1b2s_F	lj7g_A	lqh5_B	1wf3_A	2cb5_A	2ig8_A	2uvj_A	3a03_A	3f7q_A	3l3u_A
1b37_B	lj8e_A	lqhf_A	1whi_A	2cb8_A	2igi_A	2uvo_B	3a04_A	3f8m_B	3l41_A
1b3a_B	lj8u_A	lqho_A	1wka_A	2cbz_A	2igp_A	2uw1_A	3a07_A	3f97_A	3l42_A
1b4f_B	lj9l_A	lqhq_A	1wko_A	2cc6_A	2igv_A	2uwa_A	3a09_A	3f9b_A	3l46_A
1b5e_A	lja9_A	lqhv_A	1wkq_B	2cch_B	2igx_A	2uyt_A	3a0y_B	3f9r_A	3l4p_A
1b63_A	ljae_A	lqj5_B	1wkr_A	2ccq_A	2ih5_A	2uyw_A	3a16_C	3fas_B	3l4r_A
1b66_A	ljak_A	lqjc_B	1wku_B	2ccw_A	2ihd_A	2uyz_A	3a1c_A	3fb9_A	3l5l_A
1b67_A	ljat_A	lqjw_B	1wkx_A	2cdn_A	2i12_A	2uyz_B	3a21_A	3fbg_A	3l6g_A
1b8a_B	ljay_B	lqkk_A	1wld_A	2cf7_C	2i1d_A	2uz1_D	3a2q_A	3fbl_A	3l6n_A
1b8d_K	ljcd_A	lql0_B	1wlg_B	2cfe_A	2ijh_A	2uzc_C	3a2v_I	3fd7_B	3l77_A
1b8p_A	ljev_A	lql3_B	1wlz_C	2cg7_A	2ijq_A	2v09_A	3a2z_A	3fde_B	3l7h_B
1b93_A	ljd0_B	lqlw_A	1wm2_A	2cgq_A	2ijx_D	2v0h_A	3a39_A	3fdl_A	3l7t_B
1bas_A	ljd1_C	lqmy_C	1wma_A	2chc_B	2imf_A	2v0s_A	3a3d_B	3fdq_A	3l8e_B
1baz_A	ljd5_A	lqnj_A	1wmd_A	2cia_A	2imi_B	2v0u_A	3a3v_A	3fdr_A	3l8w_A
1bdo_A	ljd8_B	lqnn_C	1wmh_A	2ciu_A	2imq_X	2v1o_B	3a40_X	3fe0_A	3l91_A
1beh_A	ljd1_A	lqnp_A	1wmw_A	2ciw_A	2in8_A	2v1q_A	3a4r_A	3fe7_A	3l91_B
1bf6_A	ljek_A	lqnx_A	1wmz_D	2cj3_A	2inc_A	2v1w_B	3a4u_A	3fev_A	3l9a_X
1bgf_A	ljev_A	lqoz_B	1wn2_A	2cj4_A	2inc_B	2v25_A	3a4w_B	3ff5_B	3l9f_D
1bgp_A	ljf8_A	lqre_A	1wny_A	2cjj_A	2ior_A	2v27_A	3a57_A	3ff7_C	3l9s_A

1bhp_A	1jfl_B	1qrp_E	1wo8_D	2cjl_B	2ioy_B	2v2g_C	3a5p_D	3ff9_B	319u_A
1bj7_A	1jfr_A	1qsl_A	1wod_A	2cjp_A	2ip2_B	2v33_B	3a5r_A	3fg0_F	319y_B
1bkp_A	1jfu_A	1qsa_A	1wog_E	2cjs_C	2ip6_A	2v36_D	3a6r_B	3fgd_A	3las_B
1bn8_A	1jfx_A	1qsg_A	1woq_B	2ckf_D	2ipr_B	2v3g_A	3a72_A	3fh2_A	3lat_A
1bq8_A	1jgl_A	1qt9_A	1wor_A	2ckk_A	2iq7_A	2v3s_A	3a7l_A	3fhg_A	3lbe_D
1bqb_A	1jhd_A	1qtn_A	1wpa_A	2cks_A	2iqj_A	2v4n_A	3a7n_A	3fid_A	3lbf_C
1bqk_A	1jhf_A	1qtw_A	1wpn_B	2cm4_A	2iru_B	2v4v_A	3a8g_B	3fil_B	3lbl_A
1brt_A	1jhg_A	1qu1_D	1wpu_A	2cmj_B	2is8_A	2v5i_A	3a8u_X	3fiq_A	3lbm_B
1bs3_B	1jhj_A	1qve_B	1wq8_A	2cmt_A	2is9_A	2v5j_A	3a9b_A	3fju_B	3lcc_A
1bs9_A	1jhs_A	1qw9_B	1wqj_B	2cn3_B	2it1_A	2v5z_A	3a9f_A	3fkb_E	3lcm_A
1bsg_A	1ji1_A	1qwd_A	1wqj_I	2cnz_A	2iu5_A	2v6a_O	3a9j_A	3fkc_A	3ld3_A
1bue_A	1jid_A	1qwg_A	1wr8_B	2cov_I	2ium_A	2v6k_B	3a9l_B	3fke_A	3ldd_A
1bx4_A	1jif_A	1qwk_A	1wrdr_A	2cs7_A	2ivf_A	2v6u_A	3a9q_N	3flg_A	3le0_A
1bx7_A	1jke_C	1qwm_B	1wri_A	2cu5_A	2ivf_B	2v7w_C	3a9s_B	3flv_A	3le3_A
1bxu_A	1jkg_A	1qwz_A	1wrm_A	2cvd_D	2ivn_A	2v84_A	3aa0_A	3fn5_A	3le4_A
1bxy_A	1jkx_A	1qxy_A	1ws8_A	2cve_A	2ivx_A	2v89_A	3aa6_B	3fp5_A	3let_A
1byi_A	1jll_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	2cwg_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	3lfg_C
1c1k_A	1jlt_B	1r17_A	1wtj_A	2cws_A	2iwk_A	2v9v_A	3aba_A	3fpu_B	3lg5_A
1c1l_A	1jml_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	1jrr_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	2vfg_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	3lmy_A
1cg5_B	1jvw_A	1r87_A	1x0l_A	2d4n_A	2j5y_A	2vha_B	3ahc_A	3fx4_A	3log_C
1chd_A	1jwq_A	1r88_B	1x1i_A	2d4p_A	2j5z_C	2vi8_A	3ahn_A	3fx7_A	3lp6_C
1cip_A	1jy2_N	1r89_A	1x1n_A	2d4v_C	2j6a_A	2vig_A	3ahx_D	3fyl_B	3lpc_A
1cjc_A	1jy2_R	1r8h_D	1x1o_B	2d5b_A	2j6b_A	2vj0_A	3ahy_A	3fy3_A	3lpe_B
1cju_A	1jy3_P	1r8s_A	1x2i_A	2d5c_A	2j6f_A	2vjp_B	3ahz_A	3fym_A	3lpe_G
1cka_A	1jyh_A	1r9d_A	1x2t_C	2d5k_C	2j6i_A	2vjv_B	3ai3_C	3fza_A	3lpw_B
1clc_A	1jyo_B	1r9h_A	1x38_A	2d5w_B	2j6l_F	2vk8_C	3aia_A	3fzy_B	3lqw_A
1cnv_A	1k07_A	1r9l_A	1x3o_A	2d5z_B	2j73_B	2vkj_A	3aj7_A	3g00_A	3lr4_A
1cnz_B	1k0i_A	1ra0_A	1x3x_B	2d68_B	2j7j_A	2vkl_A	3ajo_A	3g0e_A	3lrt_A
1coj_A	1k0m_A	1rc9_A	1x46_A	2d69_A	2j7z_A	2vkv_A	3ajx_C	3g0m_A	3ls0_A
1cpq_A	1k1e_K	1rdo_2	1x54_A	2d6m_A	2j8b_A	2vla_A	3ak2_B	3g1l_A	3ls9_A
1cqm_B	1k20_A	1rfs_A	1x6i_A	2d73_A	2j8g_A	2vlf_B	3ak8_H	3g1p_B	3ltj_A
1cru_B	1k2e_A	1rfy_B	1x6x_X	2d7t_H	2j8h_A	2vlu_A	3akb_A	3g1v_A	3luc_A
1cs6_A	1k4i_A	1rg8_B	1x8d_C	2d7t_L	2j8k_A	2vmc_A	3akh_A	3g20_B	3lum_D
1ctj_A	1k4m_C	1rgx_C	1x91_A	2d81_A	2j8m_A	2vn4_A	3alf_A	3g21_A	3lvf_P
1cuo_A	1k5c_A	1rgz_A	1x9i_A	2d8d_B	2j8w_A	2vn6_A	3alu_A	3g2b_A	3lw6_A
1cxy_A	1k5n_A	1rh6_B	1x9u_A	2dc1_B	2j9c_B	2vn6_B	3amn_B	3g2s_B	3lwg_B
1cyd_D	1k66_B	1rh9_A	1xcr_A	2dc3_A	2j9o_B	2vng_A	3ans_B	3g46_B	3lwz_A
1cyo_A	1k6a_A	1rhc_A	1xd3_C	2dc4_B	2j9w_A	2vnk_C	3ap9_A	3g48_A	3lx3_A
1cz9_A	1k6d_B	1rie_A	1xdw_A	2ddb_C	2ja2_A	2vnl_A	3apa_A	3g5k_D	3lxx_A
1cza_N	1k7c_A	1rjd_A	1xeo_A	2ddx_A	2jab_C	2vnz_X	3apr_E	3g5w_C	3lxx_F
1czf_A	1k7i_A	1rkd_A	1xes_B	2de3_A	2jaf_A	2vo4_A	3b34_A	3g6m_A	3lxy_A
1czn_A	1k94_A	1rki_A	1xfk_A	2de6_A	2jb0_A	2vo8_A	3b42_A	3g7n_B	3ly0_B
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

1d4t_A	1kap_P	1rlk_A	1xg7_B	2dgl_C	2jcb_A	2vpj_A	3b5l_B	3g9x_A	3m07_A
1d5l_B	1kaz_A	1rm6_A	1xgs_A	2dga_A	2jqc_A	2vq4_A	3b5m_B	3ga3_A	3m0f_A
1d5t_A	1kdg_B	1rm6_B	1xiw_A	2dge_B	2jda_A	2vqg_D	3b5n_A	3ga4_A	3m0j_A
1d7o_A	1kdj_A	1rm6_C	1xiw_C	2dgk_A	2jdd_A	2vri_A	3b5n_B	3gad_F	3m0m_B
1daa_B	1kdo_B	1roc_A	1xiw_H	2dho_A	2jdf_A	2vrs_C	3b5n_D	3gah_A	3m1h_B
1dbf_A	1keq_B	1rp0_B	1xk4_H	2dkj_A	2jdk_D	2vsv_A	3b5n_K	3gbe_A	3m2l_D
1dbw_B	1kew_A	1rqj_A	1xk4_I	2dko_A	2je6_B	2vtc_B	3b64_A	3gbs_A	3m3g_A
1dci_C	1kfw_A	1rro_A	1xky_B	2dm9_B	2je8_B	2vuj_A	3b6i_A	3gc6_A	3m4d_A
1deu_A	1kg2_A	1rtq_A	1xkz_B	2dp6_A	2jek_A	2vun_B	3b76_A	3gc7_A	3m5l_A
1dfu_P	1kgc_D	1rtt_A	1xlq_C	2dp9_A	2jep_B	2vuo_A	3b7e_A	3gd6_A	3m5q_A
1dgf_A	1khi_A	1ru0_B	1xm8_A	2dpf_D	2jft_A	2vv6_D	3b7s_A	3gd8_A	3m66_A
1dhn_A	1khq_A	1ru4_A	1xmk_A	2dqa_A	2jg6_A	2vve_A	3b84_A	3gdc_A	3m6b_A
1dj0_B	1kid_A	1rv9_A	1xmp_B	2dql_A	2jh1_A	2vvp_B	3b8f_C	3gdl_B	3m6z_A
1djr_G	1kjb_A	1rwh_A	1xmt_A	2dr1_B	2jhf_B	2vvt_B	3b8i_E	3ge3_A	3m73_A
1dk8_A	1klx_A	1rwj_A	1xng_B	2dri_A	2jhg_A	2vvw_A	3b8z_B	3ge3_E	3m7o_A
1dl5_B	1km9_A	1rwr_A	1xnk_A	2drm_B	2ji7_A	2vw8_A	3b9c_C	3gfu_A	3m7q_B
1dlf_H	1kms_A	1rwy_B	1xo7_B	2ds2_D	2jik_A	2vwf_A	3b9d_A	3gg7_A	3m8j_A
1dlf_L	1kmt_A	1rwz_A	1xoc_A	2ds5_A	2jjc_A	2vwr_A	3b9w_A	3gg9_B	3m8o_H
1dlj_A	1kng_A	1rx0_C	1xov_A	2dsj_B	2jff_A	2vws_C	3ba1_A	3ggw_C	3m8o_L
1dlw_A	1knt_A	1ry9_C	1xph_A	2dsn_B	2jjn_A	2vx5_A	3baa_A	3ggy_A	3m8t_B
1dly_A	1koe_A	1ryi_B	1xpp_C	2dsx_A	2jjs_C	2vxn_A	3bal_B	3gh6_A	3m8u_A
1dm1_A	1kol_B	1ryo_A	1xqo_A	2dt4_A	2jk9_A	2vxq_A	3bbb_D	3gha_A	3m9l_C
1doi_A	1kop_A	1ryp_I	1xre_A	2dtj_A	2jkb_A	2vxt_I	3bc1_B	3gip_A	3m9q_B
1dok_A	1kp6_A	1ryp_J	1xrk_B	2dtx_A	2jkg_A	2vxt_L	3bc9_A	3gir_A	3mab_A
1dp7_P	1kpt_A	1ryp_K	1xs5_A	2dur_A	2jkh_A	2vxy_A	3bd1_A	3gk7_B	3mao_A
1dpj_A	1kpu_B	1ryp_Z	1xso_B	2dvm_B	2jl1_A	2vyo_A	3bd2_A	3gkb_C	3maz_A
1dpt_A	1kq1_B	1rzh_H	1xs7_A	2dvx_B	2jlp_A	2vyq_A	3bec_A	3gkj_A	3mb4_B
1dqg_A	1kq3_A	1rzh_L	1xt5_A	2dwu_A	2jlq_A	2vyw_A	3beo_A	3gkm_A	3mb5_A
1dqj_A	1kqj_A	1rzh_M	1xtt_C	2dxe_B	2lis_A	2vyx_C	3ber_A	3gkr_A	3mbg_B
1dqp_A	1kqr_A	1s1d_B	1xty_B	2dy0_A	2mnr_A	2vzc_A	3bex_A	3gkt_A	3mbk_B
1dqz_A	1krh_A	1s2o_A	1xul_D	2dy1_A	2nml_A	2vzm_A	3bf7_B	3gkv_B	3mbx_H
1ds1_A	1krn_A	1s3c_A	1xul_T	2dyj_B	2nmx_A	2w0p_B	3bfb_B	3gl0_A	3mcb_B
1dsx_C	1ks8_A	1s57_B	1xvg_C	2dyr_K	2nn8_A	2w15_A	3bfo_B	3glr_A	3mdl_A
1dsz_A	1ku1_A	1s5m_A	1xvg_E	2dyu_A	2nnr_A	2w1j_B	3bfq_G	3glv_B	3md7_A
1dtd_B	1kug_A	1s5u_D	1xvo_A	2dze_A	2nnu_A	2w1p_A	3bfv_A	3gmf_A	3md9_A
1duv_H	1kvd_C	1s69_A	1xvx_A	2e0q_A	2no4_A	2w1r_A	3bg8_A	3gmg_A	3mdm_A
1dxe_B	1kve_D	1s9r_A	1xw6_A	2e0t_A	2npt_D	2w1v_A	3bgo_P	3gmi_A	3mds_B
1dxj_A	1kw6_B	1sa3_A	1xwt_A	2e1l_B	2nql_B	2w20_A	3bh4_A	3gms_A	3mdu_A
1dxy_A	1kwf_A	1sat_A	1xwv_A	2e1n_B	2nsl_B	2w2b_B	3bh7_A	3gmv_X	3meb_B
1dys_B	1kwg_A	1sau_A	1xww_A	2e1z_A	2nsf_A	2w2j_A	3bh7_B	3gmxB	3mf7_A
1dzk_A	1kzq_A	1sbp_A	1xx1_C	2e27_L	2nsz_A	2w2k_A	3bj1_C	3gn9_C	3mgn_B
1e0w_A	1l2p_A	1sd5_A	1xxq_D	2e2o_A	2nt4_A	2w31_B	3bje_A	3gne_A	3mh9_A
1e25_A	1l2t_B	1sdi_A	1xyz_A	2e3a_A	2ntp_A	2w39_A	3bkj_A	3gnr_A	3mhs_B
1e29_A	1l3p_A	1sds_A	1y0h_A	2e3z_B	2nug_B	2w3g_A	3bkj_H	3go2_A	3mhy_C
1e2w_B	1l5o_A	1seg_A	1y0m_A	2e42_A	2nuh_A	2w3j_A	3bkr_A	3go6_A	3mi4_A
1e3d_B	1l5w_B	1sen_A	1y1p_A	2e4t_A	2nuk_A	2w3p_B	3bkt_A	3goc_B	3mil_A
1e4c_P	1l6r_A	1sf9_A	1y1x_A	2e5f_A	2nuw_A	2w3v_A	3bl6_A	3goe_A	3mjo_B
1e4m_M	1l6w_B	1sff_C	1y20_A	2e5y_B	2nw2_B	2w3x_A	3bmb_B	3gon_A	3mjv_B
1e4v_A	1l7l_A	1sfs_A	1y2t_B	2e6f_A	2nx0_A	2w40_A	3bmw_A	3gox_B	3mkh_B
1e59_A	1l9l_A	1sg4_C	1y37_A	2e6u_X	2nx4_C	2w43_A	3bmx_B	3gp3_D	3mlb_A
1e5k_A	1l9x_A	1sgw_A	1y43_B	2e7u_A	2nxb_B	2w47_A	3bn6_A	3gp4_B	3mm5_B
1e5m_A	1l6b_A	1sh7_B	1y4j_B	2e7z_A	2nyb_A	2w4c_A	3bnj_A	3gpg_B	3mm6_A
1e6i_A	1lc3_A	1sh8_B	1y4w_A	2e85_A	2nz7_A	2w4f_A	3bo6_B	3gqh_A	3mmg_A
1e6y_B	1lc5_A	1shu_X	1y51_A	2e8e_A	2nzh_A	2w4i_F	3bod_A	3gqj_A	3mmh_B
1e7l_B	1lcl_A	1skz_A	1y5i_B	2e9m_A	2o07_B	2w50_B	3boe_A	3grh_A	3mmw_D
1e7s_A	1lcp_A	1smo_A	1y60_E	2e9y_B	2o0b_A	2w5q_A	3boi_A	3grn_A	3mn1_C
1e9g_A	1le6_A	1sn2_B	1y66_C	2ea3_A	2o1c_B	2w70_A	3bom_C	3gru_A	3mos_A
1eaj_B	1lgt_A	1snn_A	1y6i_A	2eab_A	2o1k_B	2w7n_A	3bom_D	3gsh_A	3moy_A
1eao_A	1lj5_A	1stm_B	1y7p_B	2ebb_A	2o20_F	2w7w_B	3bov_A	3gt5_A	3mpc_A
1ear_A	1lj9_B	1svb_A	1y7t_B	2ebo_C	2o28_A	2w83_C	3bp5_A	3gv6_A	3mpz_B
1eb6_A	1ljo_A	1svd_M	1y7w_A	2ecs_A	2o2c_C	2w86_A	3bpj_B	3gvf_A	3mq2_B
1eco_A	1lk5_B	1svf_B	1y80_A	2ecu_A	2o2p_D	2w8x_A	3bpv_A	3vgv_B	3mqd_A

ledg_A	llkp_A	lsw5_B	ly8a_A	2eao_B	2o36_A	2w8y_B	3bpw_A	3gvo_A	3mqh_D
ledq_A	lllf_B	lswy_A	ly9l_A	2eey_A	2o37_A	2w9l_A	3bpz_D	3gw9_C	3ms5_A
leej_B	lllm_C	lsxq_B	ly9w_B	2efr_B	2o4a_A	2w98_B	3bqp_B	3gwa_A	3msu_B
legw_B	llo6_A	lsxr_A	ly9z_B	2efv_A	2o4t_A	2w9h_A	3br8_A	3gwc_D	3msx_B
leis_A	llq9_A	lsy7_B	lyac_B	2egd_B	2o4v_B	2w9r_A	3bs1_A	3gwh_B	3mte_A
lej0_A	llqa_A	lsyy_A	lyar_D	2egj_A	2o5f_B	2wa2_B	3bs2_A	3gwi_A	3mtr_B
lej2_A	llqv_A	lszh_A	lyar_N	2egv_A	2o5g_A	2waa_A	3bs9_B	3gwk_E	3mu7_A
lejb_A	llqx_A	lszn_A	lyb0_B	2eh6_A	2o5u_A	2wb6_A	3bsy_B	3gwm_A	3muj_B
lekj_C	llr7_A	lszo_K	lyb5_A	2ehg_A	2o6f_A	2wbf_X	3buu_B	3gwn_A	3muz_3
lekx_A	llrh_A	lt00_A	lybi_B	2ehq_A	2o6p_A	2wbs_A	3bv6_D	3gx8_A	3mwc_A
lelk_A	lls6_A	lt06_A	lybk_D	2eht_A	2o6s_A	2wc8_B	3bvk_F	3gxb_A	3mwf_A
lelr_A	lls9_A	lt0b_D	lybz_A	2ehz_A	2o74_F	2wci_A	3bwh_A	3gxr_B	3mwj_A
lelu_A	llst_A	lt0f_B	lyd3_A	2ei5_B	2o7i_A	2wcj_A	3bwu_D	3gzg_A	3mx6_B
lelw_A	llt1_H	lt0f_C	lydy_A	2eiq_B	2o90_A	2wco_A	3bx4_B	3gzh_A	3mxn_A
lenf_A	llua_C	lt0p_B	lyfn_C	2eix_A	2o9c_A	2wcr_A	3bx4_B	3gzk_A	3mxn_B
leo6_B	llvw_B	lt0t_X	lyfu_A	2eiy_B	2o9s_A	2wcu_A	3bx6_B	3gzx_A	3mxu_A
lep0_A	llw6_E	lt1g_A	lyif_A	2eja_B	2oaa_B	2wdc_A	3by4_A	3gzx_B	3myb_A
leq9_B	llw6_I	lt1j_B	lyii_A	2ejn_B	2obi_A	2wds_A	3byb_B	3h01_A	3mzv_B
les5_A	llwb_A	lt1v_B	lykd_A	2ejw_A	2obl_A	2wdu_B	3byp_A	3h04_A	3n08_A
lesw_A	llwd_B	lt2d_A	lyki_B	2ejx_A	2ocg_A	2we5_C	3bzz_B	3h09_B	3n0i_B
leu3_A	lly2_A	lt2h_B	lyn3_B	2ekp_A	2ode_D	2wei_A	3c05_A	3h0o_A	3n10_B
leuh_C	lm0d_C	lt2w_C	lyn8_E	2eky_C	2odf_E	2wf6_A	3c05_D	3h0u_C	3n11_A
leuv_A	lm0s_B	lt3q_A	lyn9_A	2elc_B	2odk_C	2wfc_C	3c0i_A	3h12_B	3n1e_B
leuv_B	lm0u_A	lt3q_B	lynb_C	2end_A	2oe3_A	2wfh_B	3c1o_A	3h1g_A	3n1f_D
levh_A	lm15_A	lt3y_A	lynh_B	2eo4_A	2oeb_A	2wfi_A	3c2u_A	3h1s_B	3n1s_M
lex2_B	lm1n_E	lt4b_B	lynp_B	2eq6_B	2ofc_A	2wfo_A	3c3y_B	3h34_A	3n22_A
lext_A	lm1n_F	lt61_C	lyo3_A	2erf_A	2ofk_A	2wfi_A	3c4s_A	3h3n_X	3n2n_E
leyh_A	lm1r_A	lt61_E	lyoa_A	2erw_A	2ogl_A	2wge_A	3c5a_A	3h4n_A	3n37_A
leyl_A	lm2d_B	lt6c_A	lyoc_B	2ery_B	2oh5_A	2wgp_B	3c5e_A	3h4x_A	3n3s_A
leyv_A	lm2h_A	lt6g_D	lyon_A	2esl_A	2ohw_B	2wh7_A	3c5j_A	3h55_B	3n4i_B
lez3_B	lm2t_B	lt6u_L	lyp1_A	2et1_A	2oif_B	2whg_B	3c5k_A	3h5i_A	3n4j_A
lezz_B	lm2x_D	lt6v_N	lyph_D	2etb_A	2oiz_B	2wi8_A	3c68_B	3h5j_B	3n5a_A
lezm_A	lm3u_C	lt7q_B	lyph_E	2etx_A	2oj6_C	2wiy_A	3c6w_A	3h5l_B	3n5b_B
lf08_B	lm40_A	lt7r_A	lyq2_C	2eu7_X	2okl_B	2wj5_A	3c70_A	3h62_B	3n72_B
lf0k_B	lm4i_A	lt8h_A	lyqd_A	2eut_A	2okm_A	2wje_A	3c7f_A	3h6p_B	3n79_A
lf0y_B	lm4j_A	lt8k_A	lyqe_A	2ev1_A	2okq_A	2wjn_C	3c7t_A	3h6p_C	3n98_A
lf1m_C	lm55_A	lt8t_B	lyqw_B	2evb_A	2oll_B	2wjn_L	3c7x_A	3h78_A	3n9g_H
lf1u_A	lm5t_A	lt8z_C	lyqw_Q	2ewh_A	2olm_A	2wjn_M	3c8e_A	3h7h_A	3n9i_B
lf39_A	lm6j_B	lt92_B	lyqz_A	2ewt_A	2oln_A	2wk0_A	3c8i_A	3h7h_B	3n9u_B
lf3u_G	lm70_D	lt9i_B	lyrk_A	2ex0_B	2olp_A	2wkk_C	3c8o_A	3h7i_A	3n9u_C
lf46_B	lm7a_B	lt9a_A	lysl_X	2ex2_A	2olr_A	2wkx_A	3c8p_A	3h7r_A	3nbk_A
lf4p_A	lm7g_A	lt9b_B	lysl_B	2exh_D	2omy_B	2wl1_A	3c97_A	3h7u_A	3ncl_A
lf5j_A	lm7j_A	lt99_B	lyt3_A	2exv_A	2omz_A	2wm3_A	3c9a_B	3h81_C	3ncl_A
lf5v_A	lm7s_D	lt9g_A	lytq_A	2ez9_A	2on5_A	2wm8_A	3c9h_B	3h87_B	3ndh_B
lf60_A	lm8s_A	ltaw_B	lyu0_A	2f0c_A	2oo1_B	2wmf_A	3c9u_B	3h87_D	3ndj_A
lf60_B	lm93_B	ltbf_A	lyuz_B	2f23_B	2op3_A	2wn3_C	3c9x_A	3h8g_C	3ndo_A
lf71_A	lm9z_A	ltc5_B	lyw5_A	2f2b_A	2op6_A	2wnp_F	3c9z_A	3h8t_A	3nfw_A
lf8m_C	lmb4_A	ltca_A	lywm_A	2f51_A	2opc_A	2wns_A	3ca7_A	3h8x_A	3nfw_B
lf94_A	lmc2_A	ltcn_A	lyxy_A	2f5g_B	2opg_B	2wnv_F	3cai_A	3h91_A	3ng7_X
lf9f_D	lmd6_A	ltez_B	lyya_A	2f5t_X	2oqb_A	2wnx_A	3cb0_D	3h9c_A	3ngf_A
lfcz_A	lme4_A	ltf1_A	lyzf_A	2f5v_A	2or7_A	2wny_B	3cb6_A	3h9e_O	3ngh_A
lfd3_A	lmex_L	ltf4_A	lyzl_A	2f60_K	2os5_A	2woe_C	3cbq_A	3ha9_A	3ngj_A
lfe0_B	lmfa_H	ltg0_A	lyzm_A	2f6e_A	2os9_B	2wol_A	3cbx_A	3hc4_L	3ngp_A
lfec_B	lmg4_A	ltg7_A	lyzq_A	2f6u_A	2osa_A	2wot_A	3ccd_B	3hcj_A	3ni0_A
lfeh_A	lmgq_C	ltgr_A	lyzx_A	2f7b_A	2otu_E	2wp7_A	3ce6_A	3hcn_B	3ni2_A
lfj2_B	lmgr_A	ltgx_B	lyz0_A	2f91_A	2oui_A	2wpq_C	3ce7_A	3hd4_A	3nis_B
lfk5_A	lmgt_A	lt7_H	lyz0_C	2f99_C	2ous_A	2wpv_D	3cfe_H	3hdf_B	3nj2_A
lfj_A	lmhn_A	lthg_A	lyz0j_A	2f9i_D	2ov0_A	2wpv_E	3cfz_A	3hdl_A	3nje_B
lfm0_D	lmhx_A	lthm_A	lyz0j_B	2f9n_B	2ow9_B	2wqi_D	3cgl_A	3he5_C	3njd_C
lfm4_A	lmi3_B	lthx_A	lyz0s_C	2fao_B	2ows_A	2wqk_A	3cgi_C	3he5_D	3nn1_A
lfm9_A	lmix_A	lthz_A	lyz1s_A	2fb5_A	2ox0_A	2wqr_A	3chj_A	3he8_B	3no0_A
lfob_A	lmj5_A	ltjy_A	lyz2a_A	2fba_A	2ox4_H	2wsb_C	3chm_A	3hef_B	3no7_A

1fp2_A	1mk0_A	1tke_A	1z2n_X	2fbd_A	2ox6_B	2wt1_A	3ci7_A	3hf5_C	3noj_A
1fpo_B	1mkk_A	1tn4_A	1z2u_A	2fbn_A	2oxc_A	2wta_A	3cij_A	3hfo_A	3nok_A
1fmt_B	1mla_A	1to4_A	1z3e_A	2fbq_A	2oxg_A	2wtg_A	3cin_A	3hfw_A	3nol_A
1fr3_A	1mlw_A	1toa_B	1z3e_B	2fc3_A	2oxg_Y	2wtm_C	3cip_G	3hg3_B	3noo_B
1frb_A	1mn8_B	1tov_A	1z3q_A	2feb_A	2oxn_A	2wto_A	3civ_A	3hgb_A	3nqx_A
1fsg_A	1mo0_B	1tp5_A	1z47_A	2fer_A	2oy2_F	2wu9_A	3cjp_B	3hgm_A	3nr1_A
1ftr_A	1mo9_A	1tp6_A	1z4j_A	2fcw_A	2oy7_A	2wue_A	3cjs_B	3hgu_A	3ns2_A
1fus_A	1mof_A	1tp9_B	1z4r_A	2fcw_B	2oya_B	2wuh_A	3ckf_A	3hh7_A	3ns6_B
1fw4_A	1moq_A	1tqh_A	1z6n_A	2fd5_A	2oynd_A	2wuk_A	3cl5_A	3hh8_A	3nsl_F
1fx4_A	1mpg_B	1tr0_J	1z6o_D	2fdn_A	2oynd_A	2wut_A	3cla_A	3hhi_B	3nsx_B
1fxl_A	1mpl_A	1tsf_A	1z6o_M	2fdv_A	2ozf_A	2wv3_A	3cls_D	3hht_B	3nsz_A
1fxo_G	1mug_A	1tt2_A	1z76_B	2fdx_A	2ozl_A	2wvf_A	3cm0_A	3his_A	3nt1_B
1fzl_A	1mv8_C	1tt8_A	1z7x_W	2fe3_A	2ozn_A	2wvg_F	3cmj_A	3hjb_A	3ntk_A
1g01_A	1mvf_A	1tu1_B	1z8o_A	2fe5_A	2ozn_B	2wvv_A	3cmj_A	3hje_A	3nua_A
1g0o_C	1mvf_D	1tu7_B	1z96_A	2fe8_A	2p02_A	2ww2_B	3cnk_B	3hjr_A	3nv1_A
1gl2_A	1mvo_A	1tu9_A	1zbf_A	2ff4_A	2p09_A	2ww5_A	3cnm_A	3hjs_A	3nvs_A
1gl5_B	1mxg_A	1tua_A	1zch_A	2ffu_A	2p0f_A	2wwe_A	3cnu_A	3hl5_B	3nvw_J
1gl1_A	1mxr_A	1tuh_A	1zcz_A	2ffu_B	2p1g_B	2wwf_C	3cou_A	3hlx_A	3nwo_A
1g29_C	1my5_A	1tuk_A	1zdz_A	2fgo_A	2p1m_B	2wwk_T	3cp5_A	3hm5_A	3nxb_B
1g2o_C	1my6_B	1tvn_B	1zdz_A	2fgr_A	2p39_A	2wwx_A	3cp7_B	3hmc_A	3ny3_A
1g2q_A	1mz4_A	1txg_B	1zdy_A	2fhf_A	2p3h_A	2wwx_B	3cpq_B	3hms_A	3ny7_A
1g2r_A	1mz9_A	1ty9_A	1zem_A	2fhz_A	2p49_B	2wx9_A	3cpt_A	3hnb_M	3nye_A
1g3k_B	1mzy_A	1tzw_A	1zgd_B	2fhz_B	2p4e_P	2wy3_B	3cq5_B	3hnx_A	3nyk_A
1g4i_A	1n08_B	1tzy_C	1zhh_A	2fi1_A	2p4k_A	2wy4_A	3cql_A	3hol_A	3nyt_A
1g5a_A	1n0q_B	1tzy_F	1zhq_A	2fi9_A	2p51_A	2wy7_Q	3cqt_A	3hpc_X	3nzn_B
1g61_A	1n13_G	1u07_A	1zhv_A	2fj8_A	2p54_A	2wy8_A	3cry_A	3hr0_A	3o07_A
1g6a_A	1n1j_A	1u09_A	1zhx_A	2fl4_A	2p57_A	2wya_A	3csk_A	3hra_A	3o0a_B
1g6c_B	1n1j_B	1u11_A	1zi9_A	2flh_B	2p5k_A	2wyq_A	3ct1_A	3hrx_A	3o0d_C
1g6g_A	1n3y_A	1u1w_B	1zja_A	2fli_A	2p5y_A	2wz9_A	3ctg_A	3hs3_A	3o0g_D
1g6h_A	1n5w_D	1u2b_A	1zjc_A	2fm6_A	2p65_A	2wzm_A	3ctk_A	3hsh_A	3o1g_A
1g6u_B	1n63_C	1u2h_A	1zjj_B	2fma_A	2p68_A	2wzx_A	3ctp_B	3hss_B	3o1k_B
1g8a_A	1n63_E	1u2p_A	1zk4_A	2fmm_C	2p6h_B	2x0k_A	3ctz_A	3ht1_A	3o1n_A
1g8i_B	1n71_C	1u2w_B	1zk7_A	2fmp_A	2p6w_A	2x18_E	3cu4_A	3ht5_A	3o1p_A
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	3hxx_A	3o70_A
1gci_A	1na5_A	1u84_A	1zos_C	2fr2_A	2pbi_D	2x5c_B	3cxk_A	3hz2_A	3o79_A
1gcq_C	1nb9_A	1u8f_Q	1zps_B	2fr5_C	2pbp_A	2x5f_B	3cxz_A	3hzb_E	3o7b_A
1gde_B	1nbc_B	1u8v_C	1zpw_X	2frg_P	2pc8_A	2x5h_B	3cy4_A	3i0w_A	3o83_B
1gee_E	1nbu_D	1u8y_B	1zq9_B	2ft0_A	2pcj_B	2x5x_A	3cyi_A	3ila_A	3o85_B
1geg_G	1nc5_A	1u9k_A	1zr0_D	2ftx_B	2pcn_A	2x5y_A	3cz1_B	3ilu_A	3o8m_A
1ges_B	1nnd_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	3o9z_B
1gk7_A	1nep_A	1uai_A	1zs4_D	2fuk_A	2pg0_B	2x7k_A	3czz_B	3i2z_A	3oaj_A
1gk9_A	1nf8_A	1uas_A	1zsw_A	2fvh_A	2pgo_A	2x7m_A	3d03_B	3i31_A	3oam_A
1gk9_B	1nff_B	1ub3_A	1zsx_A	2fvv_A	2ph3_A	2x8h_A	3d0n_A	3i33_A	3obu_A
1gl2_A	1nfv_N	1uc4_A	1zt5_A	2fvy_A	2phn_A	2x8r_A	3d0o_A	3i35_A	3ocu_A
1gl2_B	1ng6_A	1uc4_G	1zu3_A	2fwh_A	2pi6_A	2x8s_A	3d1b_C	3i36_A	3od9_A
1gl2_C	1nh2_A	1uca_A	1zuo_A	2fyg_A	2pie_A	2x8x_X	3d1g_A	3i3f_B	3odg_A
1gl2_D	1nh2_B	1ucr_B	1zuu_A	2fyx_A	2piy_B	2x96_A	3d1k_A	3i3g_C	3ofk_C
1gmu_C	1nhc_E	1ucs_A	1zuy_A	2fzp_A	2pjz_A	2xb4_A	3d2q_A	3i45_A	3og9_B
1gmy_A	1nhk_L	1udc_A	1zv1_A	2fzv_B	2pk3_A	2xbk_A	3d2w_A	3i47_A	3ogn_B
1gn0_A	1nki_B	1ueb_A	1zwh_A	2fzw_B	2pk8_A	2xbl_A	3d30_A	3i48_B	3ogr_A
1gnl_A	1nkp_D	1uek_A	1zwz_A	2g2n_C	2pkf_A	2xbp_A	3d32_A	3i4o_B	3oid_C
1gnt_A	1nln_A	1uf5_A	1zx6_A	2g2s_A	2pko_A	2xc2_A	3d34_A	3i4s_A	3oig_A

lgny_A	lnls_A	lufb_C	lzxt_B	2g30_A	2pkt_A	2xcb_A	3d3b_A	3i4z_B	3oiu_A
lgo3_N	lnnf_A	lufi_B	lzxz_A	2g45_D	2plt_A	2xce_F	3d3z_A	3i57_B	3oj7_A
lgoi_B	lnnh_A	lufy_A	lzz0_A	2g5x_A	2pmk_A	2xcj_A	3d43_B	3i5c_B	3ojs_A
lgp6_A	lnns_A	lug6_A	lzzg_B	2g64_A	2pmr_A	2xcz_A	3d47_A	3i5r_A	3ol0_A
lgpe_A	lnnw_B	lugi_E	lzzk_A	2g6f_X	2pn6_A	2xda_A	3d4i_A	3i5x_A	3ol3_A
lgni_A	lnoa_A	lugp_B	lzzo_A	2g76_A	2pn8_B	2xde_A	3d4u_B	3i6c_A	3omc_B
lgpu_A	lnof_A	lugx_A	lzzw_A	2g7o_A	2pnd_A	2xdg_A	3d6r_A	3i6t_B	3omt_A
lgq1_A	lnog_A	luha_A	256b_B	2g84_A	2pnx_A	2xdj_F	3d79_A	3i7u_B	3onr_I
lgq8_A	lnox_A	luhe_A	2a07_K	2g8o_B	2pny_A	2xdp_A	3d7a_B	3i8s_C	3oo8_A
lgql_B	lnpy_B	luhk_B	2a0n_A	2g9f_A	2poi_A	2xdw_A	3d8t_A	3i94_A	3ooi_A
lgqv_A	lnq6_A	lui0_A	2a14_A	2ga4_D	2pok_B	2xe4_A	3d95_B	3i96_A	3op8_A
lgtf_I	lnq7_A	luiw_C	2a15_A	2gag_A	2por_A	2xed_A	3d9t_A	3i98_E	3opk_A
lgtv_A	lnqu_B	luj0_A	2a26_C	2gag_B	2pos_D	2xet_B	3d9x_C	3i9q_A	3oq2_A
lgtz_D	lnr0_A	luj2_A	2a28_A	2gag_C	2ppp_A	2xeu_A	3d9y_A	3ia2_F	3oqy_B
lgu2_A	lnr4_G	luj8_A	2a2n_C	2gas_A	2ppt_B	2xev_A	3da0_C	3ia4_D	3orh_C
lgu7_B	lnsc_B	luk7_A	2a2r_B	2gb4_B	2pqm_B	2xf2_A	3dac_A	3ian_A	3orv_B
lgud_A	lnth_A	lukf_A	2a40_E	2gbt_A	2pqr_B	2xfd_A	3dai_A	3iar_A	3orv_D
lgug_D	lntv_A	lukm_A	2a4v_A	2gbw_E	2pqr_D	2xfv_A	3dan_A	3iav_A	3ose_A
lgui_A	lnty_A	lukm_B	2a4x_A	2gc4_L	2pqx_A	2xh2_C	3daq_A	3ib7_A	3osm_A
lgv5_A	lnvm_C	luku_A	2a53_C	2gdq_B	2pr5_A	2xhi_A	3dau_A	3ich_A	3oti_B
lgvj_A	lnvm_F	lukz_A	2a5d_A	2gdz_A	2psd_A	2xhn_A	3dc5_C	3idl_A	3ouf_B
lgvn_D	lnw2_H	lulk_A	2a61_C	2gec_A	2psp_B	2xi8_A	3dcn_A	3id7_A	3ovp_B
lgwe_A	lnwa_A	lulr_A	2a6s_B	2gey_D	2pst_X	2xij_A	3del_B	3ida_A	3oyy_B
lgwi_B	lnwp_A	lumd_C	2a6x_A	2gf3_B	2pth_A	2xio_A	3deo_A	3idw_A	3p0t_A
lgwu_A	lnww_A	lumd_D	2a70_A	2gf9_A	2ptt_B	2xkg_A	3dfg_A	3ie4_A	3p1f_A
lgxn_A	lnwz_A	lumk_A	2a7l_B	2gg6_A	2ptz_A	2xkr_A	3dgb_A	3ie5_A	3p1g_A
lgxu_A	lnxc_A	lumz_A	2a8n_A	2gh0_B	2pu3_A	2xla_A	3dgp_A	3iei_C	3p2n_A
lgxy_A	lnxj_A	luow_A	2a9i_A	2gh0_D	2pu9_A	2xlk_A	3dgp_B	3iev_A	3p2t_A
lgy6_A	lnxm_A	luoy_A	2a9s_A	2gh9_A	2pu9_B	2xm5_A	3dgt_A	3iez_B	3p3c_A
lgy7_C	lnyk_B	luqx_A	2aa1_B	2gha_A	2pv2_A	2xmx_A	3dha_A	3ife_A	3p3e_A
lgyh_C	lnyt_C	luqz_A	2aal_C	2gia_B	2pvb_A	2xn4_A	3dhi_B	3ig9_C	3p3g_A
lgyo_A	lnza_A	lurn_C	2aan_A	2gib_B	2pve_B	2xn6_A	3dhi_C	3igz_B	3p3o_A
lgyv_A	lo04_E	lurr_A	2ab0_A	2giy_A	2pvq_A	2xov_A	3dho_C	3ihw_A	3p48_A
lgyy_B	lo0e_B	lurs_A	2abk_A	2gj3_A	2pwy_A	2xpp_A	3die_A	3ihz_B	3p4t_A
lgzc_A	lo1z_A	lus5_A	2abw_B	2gid_C	2pxx_A	2xqu_A	3dj9_A	3ii7_A	3p5h_A
lgzw_B	lo26_C	luse_A	2acf_D	2gke_A	2py4_A	2xs4_A	3djh_C	3iij_A	3p73_A
lh03_P	lo4k_A	lusf_B	2ad6_A	2gkm_B	2pyw_A	2xsu_A	3djl_A	3iiu_M	3p73_B
lh0h_B	lo4s_A	lusg_A	2ad6_D	2gkr_I	2pz0_B	2xt2_A	3djo_A	3ij3_A	3p7y_A
lh16_A	lo4t_A	luso_A	2ae2_A	2gl5_A	2pze_B	2xts_A	3dk9_A	3ijl_A	3p97_C
lh1n_A	lo4v_A	lusq_B	2aen_E	2gmy_E	2pzh_B	2xts_B	3dkc_A	3ik7_D	3p9c_A
lh1y_A	lo4y_A	luti_A	2aex_A	2gn4_B	2q0l_A	2xtt_B	3dkm_A	3ilo_A	3p9p_A
lh2b_B	lo5u_A	luu4_A	2ag4_B	2gnc_A	2q20_B	2xu3_A	3dkr_A	3ils_A	3p9x_A
lh2c_A	lo5x_A	luuq_A	2ag5_B	2gok_A	2q28_A	2xu8_B	3dl0_A	3ilw_A	3pb6_X
lh2e_A	lo7e_B	luuy_A	2agd_B	2gom_A	2q2a_D	2xvm_B	3dlm_A	3im1_A	3pbf_A
lh2s_A	lo7i_A	luv4_A	2ahf_A	2gou_A	2q2h_A	2xvs_A	3dm8_A	3im9_A	3pc3_A
lh2s_B	lo7j_C	luvq_A	2ahn_A	2gpe_B	2q35_A	2xvx_A	3dme_B	3imh_A	3pcv_A
lh4a_X	lo7q_B	luw4_C	2aib_A	2gqt_A	2q5c_A	2xws_A	3dmg_A	3inz_B	3pd2_B
lh4g_A	lo7z_B	luw4_D	2akz_B	2gqw_A	2q62_G	2xwt_C	3dmi_A	3iof_A	3pd7_A
lh4p_A	lo82_A	luwc_A	2anv_A	2grc_A	2q73_C	2xxj_D	3dmo_A	3ioh_A	3pdn_A
lh4r_A	lo8s_A	luwf_A	2any_A	2grr_B	2q86_B	2xxl_B	3dnf_B	3ioq_A	3pel_B
lh5b_B	lo8x_A	luwk_B	2ap1_A	2gsd_A	2q87_A	2xy2_A	3dpg_B	3iox_A	3pew_A
lh5q_L	lo91_C	luwz_A	2apg_A	2gso_B	2q88_A	2xz2_A	3dqq_A	3ip4_A	3pf2_A
lh5v_A	lo98_A	luxx_X	2aqm_A	2gte_A	2q8n_C	2xzi_A	3dr0_C	3ip8_A	3pfg_A
lh64_Q	lo9i_D	luxy_A	2aqp_A	2gtr_A	2q8r_G	2y2z_A	3dr4_B	3ipc_A	3pfs_A
lh6f_A	lo9r_E	luy1_A	2ar1_A	2gu3_A	2q9u_A	2y39_A	3dra_A	3ipf_A	3pg6_C
lh6l_A	loa2_C	luyx_A	2arc_B	2gud_B	2qa9_E	2y3q_B	3drf_A	3ipw_A	3pgx_A
lh6u_A	loa8_A	luz3_A	2asd_A	2gui_A	2qac_A	2y3v_D	3drw_B	3iq3_A	3phs_A
lh6w_A	loaa_A	lv05_A	2asu_B	2guv_C	2qap_A	2y3z_A	3drz_B	3iql_A	3phx_B
lh72_C	loai_A	lv08_B	2at8_X	2guy_A	2qb7_A	2y5p_C	3ds4_B	3irp_X	3pjp_B
lh75_A	loal_A	lv0z_B	2atb_A	2gw4_D	2qc5_A	2y7b_A	3dsk_A	3irs_A	3pk0_A
lh7e_B	loao_A	lv2z_A	2atv_A	2gwm_A	2qd6_A	2y88_A	3dso_A	3irv_A	3pkv_A
lh8p_B	loaq_H	lv30_A	2au7_A	2gxx_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	2qgl_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	3jpp_B	3prp_A
1hfo_E	1ofs_D	1v5i_B	2b5a_A	2h3h_A	2qhs_A	2ywd_A	3e2d_A	3jqj_C	3psm_A
1hfs_A	1ofw_A	1v6s_A	2b5h_A	2h31_A	2qia_A	2ywj_A	3e3u_A	3jqj_A	3pna_A
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
1hl7_B	1oh0_A	1v7z_F	2b82_A	2h6f_A	2qkh_A	2yxo_B	3e6j_A	3js4_B	3q12_C
1hle_A	1oh4_A	1v8c_C	2b9w_A	2h6f_B	2qkp_C	2yxx_A	3e6s_F	3js5_A	3q1x_A
1hlq_C	1oh9_A	1v8f_A	2ba2_C	2h6n_A	2qlt_A	2yxx_A	3e6z_X	3js8_A	3q20_B
1hm6_B	1ohp_B	1v8h_A	2bay_E	2h6u_G	2qmc_A	2yyv_B	3e7d_A	3jsl_B	3q23_B
1hml_A	1oi6_B	1v93_A	2bba_A	2h88_A	2qmc_D	2yyy_A	3e7h_A	3jsy_B	3q2e_A
1hmt_A	1ojk_A	1v96_B	2bbe_A	2h88_B	2qmm_A	2yz1_B	3e7r_L	3jte_A	3q3u_A
1hnj_A	1ojq_A	1v98_A	2bcg_G	2h88_D	2qmq_A	2yzc_D	3e8m_B	3jtm_A	3q49_B
1hpl_A	1ojx_C	1v9f_A	2bcg_Y	2h88_P	2qn0_A	2yzh_C	3e8t_A	3jtz_A	3q4t_A
1hpg_A	1ok0_A	1vbi_A	2bcm_B	2h8e_A	2qnw_A	2yzt_A	3e96_B	3ju2_A	3q4u_A
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1ht6_A	1on3_A	1vbw_A	2bd0_D	2h9b_A	2qpn_B	2z0j_E	3ea3_B	3jva_F	3q62_B
1ht9_B	1ong_A	1vc4_B	2bek_D	2h9h_A	2qpww_A	2z0m_A	3ea6_A	3jxo_A	3q6d_B
1hw1_B	1oni_C	1vcd_A	2bem_A	2ha8_B	2qq4_B	2z0t_C	3eaz_A	3jxs_A	3q6l_A
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1hx6_C	1oot_A	1vd6_A	2bf6_A	2hba_A	2qrw_I	2z1c_B	3edf_A	3jzy_A	3qan_C
1hxd_D	1oqj_A	1ve1_A	2bfb_A	2hby_A	2qsa_A	2z2f_A	3edv_A	3k0l_A	3qat_B
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1hz4_A	1orn_A	1vfl_A	2bh8_B	2hc9_A	2qsb_B	2z3g_D	3eeh_A	3k26_A	3qc7_A
1hz6_C	1orr_A	1vfr_B	2bii_B	2hd9_A	2qt7_B	2z3v_A	3ees_A	3k2w_E	3qds_B
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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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1i0r_A	1ouw_C	1vhw_A	2bk9_A	2hek_B	2quy_H	2z6r_A	3egg_D	3k62_A	3qk8_C
1i0v_A	1ov3_A	1vi6_B	2bka_A	2heu_B	2qv5_A	2z6w_A	3ego_B	3k6f_A	3qki_B
1i1n_A	1ow3_A	1vim_A	2bkf_A	2hew_F	2qvb_A	2z72_A	3egw_C	3k6i_A	3qmd_A
1i24_A	1owf_A	1vj2_A	2bkl_B	2hf9_A	2qvo_A	2z79_B	3ehg_A	3k6v_A	3qp4_A
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
1i4u_A	1oxs_C	1vk5_A	2bkr_A	2hhv_A	2qwl_A	2z84_A	3eif_A	3k7i_B	3qu1_B
1i6m_A	1oyg_A	1vkc_A	2bkx_A	2hin_B	2qwo_B	2z8f_A	3ej9_B	3k7p_B	3qug_A
1i77_A	1oz9_A	1vke_F	2bky_B	2hiv_A	2qx8_B	2z8l_A	3ej9_C	3k89_A	3qxc_A
1i7h_A	1ozn_A	1vki_A	2bky_Y	2hke_B	2qxi_A	2z8q_A	3eja_A	3k8d_A	3qy1_B
1i7k_A	1ozw_B	1vkk_A	2bl0_A	2hl7_A	2qy1_B	2z8u_B	3ejf_A	3k8u_A	3qyj_A
1i8a_A	1p0f_B	1vl1_A	2bl0_B	2hlc_A	2qy9_A	2z8x_A	3ejg_A	3k8w_A	3qzb_A
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	3eml_A	3kcg_H	3r3s_C
1iby_B	1p6o_B	1vmf_C	2bmo_B	2hq6_A	2r2y_A	2zdl_A	3emi_A	3kci_A	3r6f_A
1idp_A	1p71_A	1vmj_A	2bnm_B	2hqh_C	2r31_A	2zdh_A	3emw_A	3kcp_A	3sil_A
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

lihj_B	lpam_B	lvph_E	2bo9_C	2hra_A	2r6j_B	2zex_A	3enu_A	3kef_B	4vub_A
liib_B	lpcf_C	lvps_A	2bo9_D	2hrv_B	2r75_1	2zez_B	3eoi_A	3keo_B	5pal_A
lijb_A	lpdo_A	lvq3_B	2boo_A	2hsa_A	2r8e_E	2zfc_B	3epr_A	3kfa_A	6cel_A
lijt_A	lpe9_B	lvqe_A	2bpd_B	2ht9_B	2r8o_A	2zfd_A	3eqn_B	3kff_A	6rxn_A
lijx_C	lpfb_A	lvsr_A	2bpq_A	2hta_A	2r8q_A	2zfd_D	3er6_A	3kg0_C	7fd1_A
lijy_B	lpgv_A	lvvf_A	2bqx_A	2hu9_A	2r99_A	2zgq_A	3era_B	3kgr_A	7rsa_A
likt_A	lpj5_A	lvyo_A	2br9_A	2hur_B	2r9f_A	2zhj_A	3erj_A	3kgz_B	8abp_A
lio0_A	lpk3_B	lvzi_B	2bsj_A	2hv8_A	2ra3_B	2zhn_A	3erx_B	3kh7_A	
liom_A	lpkh_A	lvzy_B	2bt6_A	2hv8_E	2ra4_A	2zhz_C	3esg_B	3kij_C	
lloo_B	lpl3_A	lw0d_A	2bt9_A	2hvm_A	2ra6_B	2zib_A	3esl_B	3kki_A	
liq6_B	lpl8_D	lw0n_A	2buu_A	2hvw_C	2rbk_A	2zjd_C	3eu9_C	3kkq_A	