Efficient preparation of two-dimensional defect-free atom arrays with near-fewest sorting-atom moves

Cheng Sheng¹,^{*} Jiayi Hou,^{1,2} Xiaodong He^{1,*}, Peng Xu,¹ Kunpeng Wang,¹ Jun Zhuang,^{1,2} Xiao Li,¹ Min Liu¹,[†] Jin Wang,¹ and Mingsheng Zhan^{1,†}

¹State Key Laboratory of Magnetic Resonance and Atomic and Molecular Physics, Wuhan Institute of Physics and Mathematics, APM, Chinese Academy of Sciences, Wuhan 430071, China

²School of Physical Sciences, University of Chinese Academy of Sciences, Beijing 100049, China

(Received 17 December 2020; revised 4 March 2021; accepted 15 March 2021; published 2 April 2021)

Sorting atoms stochastically loaded in optical tweezer arrays via an auxiliary mobile tweezer is an efficient approach to preparing intermediate-scale defect-free atom arrays in arbitrary geometries. However, the high filling fraction of atom-by-atom assemblers is impeded by redundant sorting moves with imperfect atom transport, especially for scaling the system size to larger atom numbers. Here we propose a sorting algorithm [the heuristic cluster algorithm (HCA)] which provides the near-fewest number of moves $N_m \approx N$ (N is the number of defect sites to be filled) and experimentally demonstrate a 5×6 defect-free atom array with 98.4(7)% filling fraction for one rearrangement cycle. Furthermore, we compare the HCA with two other algorithms by simulating results and find that the HCA is well suited for large-scale atom assemblers. Our method is essential to scale hundreds of assembled atoms for bottom-up quantum computation, quantum simulation, and precision measurement.

DOI: [10.1103/PhysRevResearch.3.023008](https://doi.org/10.1103/PhysRevResearch.3.023008)

I. INTRODUCTION

Bottom-up-built single-atom arrays have rapidly developed into a versatile platform for quantum many-body simulation [1–4], quantum metrology [5,6], and quantum computation [7–12]. This is mainly owing to several crucial advantages in addition to configurable defect-free atom arrays via atom rearrangement [13–18], long coherence times of quantum bits (qubits) well isolated from the environment [5,19–21], and controllable long-range interactions using Rydberg atoms [22–25]. A great amount of quantum science and technology based on assembled-atom platforms will strongly benefit from scaling the system size to larger atom numbers, such as building a fault-tolerant information processor with sufficient logic qubits to solve classical intractable tasks [26,27]. Currently, the preparation of hundreds of atoms with full control over spatial geometries is important but still a challenge.

In recent years, atom-by-atom assemblers have been scaled from one dimension to three dimensions [28,29], while the array size has been increased to about 200 atoms [30]. An effective and conventional approach to achieving defect-free atom arrays in arbitrary geometries is sorting randomly distributed atoms to target sites via an auxiliary mobile tweezer

(MT) [15,18]. Generally, a rearrangement for one atom contains the actions of extracting the atom by the MT with a deeper trap depth, moving the atom in the MT along a certain path, and releasing it onto a target site. The filling fractions of the final atom arrays are closely related to the success rate of transporting single atoms to target sites (defined as transfer efficiency) because the failure to extract atoms by a MT makes the atoms stay *in situ* and may cause collisional loss in the next transfer process. Moreover, the atom loss in the MT and the imperfect release of atoms into target sites lead to defects in final atom arrays. To increase the filling fraction, an optimal sorting path with the number of moves N_m as small as possible can minimize the influence of the imperfection during the atom rearrangement. Therefore, finding an atom-sorting algorithm well suited for large-scale defect-free atom assemblers is essential.

A sorting algorithm called the heuristic path-finding algorithm (HPFA) has been proposed to prepare a 7×7 atom array with a filling fraction of 96% for a 5×5 atom array [15]. A similar heuristic shortest-move algorithm has been applied to rearrange 111 atoms and the cumulative success rate of a 4×4 atom array is less than 20% for one rearrangement cycle mainly limited by a 75% transfer efficiency (might be induced by the short lifetime in the MT) [18]. However, these sorting algorithms are not optimal for large-scale atom arrays due to a number of redundant moves involved. Although finding the sorting path with the smallest N_m is a difficult computational task (likely to be an NP-complete problem), here we propose a heuristic cluster algorithm (HCA) which significantly reduces the N_m for sorting atoms and demonstrate it experimentally by preparing a 5×6 atom array with 98.4(7)% filling fraction for one rearrangement cycle.

*hexd@wipm.ac.cn

†mszhan@wipm.ac.cn

Published by the American Physical Society under the terms of the Creative Commons Attribution 4.0 International license. Further distribution of this work must maintain attribution to the author(s) and the published article's title, journal citation, and DOI.

FIG. 1. Images of two-dimensional defect-free atom arrays. (a) Loading rate histogram of 64 tweezers. The average loading rate of 64 tweezers is 53% measured by repeating the loading process 200 times. (b) Fluorescence count distribution for 64 tweezers during 80 ms of exposure after repeating the loading process 200 times. The region of interest for each tweezer is 2×2 pixels. (c) Schematic of the experimental setup. (d) Preparation of a filled tweezer at target sites via transporting a single atom (blue disk) from another filled tweezer with the MT. This process represents one move. (e) Defect-free atom arrays in the specific patterns of capital letters via atom rearrangement. The unused extra atoms are discarded by moving them to positions far away from the field of view. The distance between neighboring atoms is $5 \mu\text{m}$.

We begin in Sec. II by introducing an 8×8 tweezer array setup. In Sec. III we improve the atom lifetime in the MT and prove that the atom loss has no obvious relation to the move distance. In this case, a sorting algorithm that provides the fewest moves is preferred. In Sec. IV three sorting algorithms are briefly described and compared. In Sec. V we experimentally measure the filling fraction of atom arrays utilizing these algorithms with two different transfer efficiencies and give the results of large-scale atom array simulations.

II. EXPERIMENTAL PREPARATION OF ATOM ASSEMBLERS

The 8×8 optical tweezer array is generated by an 808-nm laser beam deflected in two orthogonal directions by a dual-axis acousto-optic deflector (AOD). The dual-axis AOD is driven respectively by two radio-frequency (rf) signals with eight tones (the central frequency is 96 MHz and the frequency gap between the neighboring tones is 2 MHz), which are produced by an arbitrary waveform generator (AWG) (Keysight M3202A). The optical homogeneity of the trap array is less than 10% after optimization. The 830-nm MT is also created by an AOD driven by a voltage controlled oscillator (VCO) (Mini-circuits ZOS-150+) with the frequency tuned by a DC voltage. The Gaussian waist of the tweezer in the array and of the MT are both about $1.0 \mu\text{m}$. Our experimental setup is shown schematically in Fig. 1(c).

Single ^{87}Rb atoms are stochastically loaded from a magneto-optical trap into optical tweezer arrays with a trap depth of $U_0/k_B \approx 0.8 \text{ mK}$ for each tweezer in 950 ms, where k_B is the Boltzmann constant. Images of atom fluorescence are taken by an electron multiplying charge-coupled device camera (Princeton Instruments ProEM+:1024B). The photoelectron count threshold and the regions of interest for every tweezer are periodically calibrated by a computer program

via automatically analyzing a series of atom array images. Figures 1(a) and 1(b) illustrate the loading rates and the average threshold of 64 sites, respectively. Next, atoms in reservoir tweezers are transferred to the target sites using a MT in a real-time sorting path calculated by a sorting algorithm. The sorting path is composed of three waveforms to control the intensity and the X and Y positions of the MT. For the rearrangement process as depicted in Fig. 1(d), we spend 1 ms adiabatically increasing the trap depth of the MT to 2.3 mK after the MT overlaps a filled reservoir tweezer. Then the MT extracts the atom and moves at a speed of $5 \mu\text{m/ms}$ across the void tweezers to the target site. After the atom in the MT is released into the target site in 1 ms, the next rearrangement cycles for other target sites are carried out. Finally, we acquire a new image to reveal the new positions of the atoms in the array as shown in Fig. 1(e). The total rearrangement time is less than 80 ms for a 5×6 atom assembler. The tweezer array generated by our scheme can be scaled to 32×32 sites as shown in Fig. 1(c), but the size of atom assemblers is limited by the optical power of the 808-nm laser beam for reliable atom loading. To achieve a large-scale atom assembler with high filling fraction in the future, sufficient laser power would be required.

III. ATOM LIFETIMES IN A MOBILE TWEEZER

In order to optimize the filling fraction of defect-free atom arrays, we first improve the atom lifetime in a MT because transported atom loss directly leads to the defects in the final atom arrays. As described above, the position of the MT is controlled by the frequency of rf signals which are sent into the AOD. We experimentally find that the atom lifetime is affected by the beam-pointing fluctuations of the MT [31]. The beam-pointing noise observed by the sideband of the rf signal frequency spectra as depicted in Fig. 2(a) causes a

FIG. 2. Atom lifetimes in a MT. (a) Frequency spectra of the rf signals. Orange, red, and purple curves show respectively the results from the three approaches. The sidebands are induced by the noise of the DC voltage to control the rf in the mode of frequency modulation. (b) Atom survival probability as a function of the frequency of the sinusoidal signal modulated onto the driving rf signal of the AOD. The modulating time is 30 ms and the fluctuation distance is ± 25 nm. The purple curve is fitted to the Gaussian function. (c) Atom survival probability in a static MT. The solid curves are fitted to Eq. (1). The values of position stability are $2.3 \times 10^{-5} \mu\text{m}/\text{Hz}^{1/2}$ (orange circles), $8.2 \times 10^{-6} \mu\text{m}/\text{Hz}^{1/2}$ (red squares), and $2.4 \times 10^{-6} \mu\text{m}/\text{Hz}^{1/2}$ (purple diamonds) and the position fluctuation heating rates are 23, 2.9, and 0.24 mK/s. (d) Atom survival probability in a MT after transferring across several void tweezers in the array. The black squares, blue triangles, red circles represent the results with MT depths of 2.27, 0.82, and 0.77 mK, respectively; the trap depth of void tweezers is 0.8 mK. The length of one grid is the distance between two neighboring sites.

heating effect when the noise frequency is about 93.4(4) kHz (equal to the atom oscillation frequency in the harmonic trap), as shown in Fig. 2(b). Since the heating rate is constant, the survival probability of an atom in the MT as a function of time can be expressed as [32]

$$P_s(t) = 1 - \left[1 + \nu(t) + \frac{1}{2}\nu^2(t)\right]e^{-\nu(t)}, \quad (1)$$

where $\nu(t) = U_0/k_B(T_0 + rt)$, with t the atom hold time in the MT, $T_0 = 20 \mu\text{K}$ the initial atom temperature, and r the heating rate. We measure the atom lifetime in a static MT with a rf signal of different frequency spectra generated by three approaches. The first manner (orange circles) is that the rf signals come from a signal generator (Agilent E4433B, with a deviation of frequency modulation of 5 MHz/V) with frequency modulated by a DC voltage sent from an analog output (National Instruments PXI-6733). In the second manner (red squares), a purer DC voltage is generated by an AWG (Keysight 33522A) instead of the analog output. For the third one (purple diamonds), the VCO produces the rf signals tuned by the DC voltage output from the AWG. We conclude that the lifetime depends on the amplitude of the sidebands (about

93-kHz detuning from the carrier), as depicted in Fig. 2(c). The lifetime is further increased to 13.3 s when we apply continuous laser cooling (turning on repumped light resonant with $|5s_{1/2}, f=1\rangle \rightarrow |5p_{1/2}, f=1\rangle$ and cooling light red detuned by 24–54 MHz from $|5s_{1/2}, f=2\rangle \rightarrow |5p_{3/2}, f=3\rangle$ simultaneously). Additionally, we should note that another heating effect due to the light interference between neighboring tweezers in the array reduces the atom lifetime to 2.1 s, but this heating effect can also be suppressed by the continuous laser cooling (the atom lifetime in tweezer arrays can be extended to a vacuum-limited lifetime of 16.9 s). The cooling process, however, will destroy the internal state if the atoms are encoded into qubits; thus our work to improve the atom lifetime in a MT without cooling is still necessary.

Furthermore, the atom survival probability in the MT is measured after the MT moves across several void tweezers as shown in Fig. 2(d). We observe that it decreases as the number of void tweezers is increased when the MT depth is less than or approximately equal to the depth of each void tweezer. In contrast, atoms are preserved well when the MT depth is sufficiently deep. Therefore, we tend to choose a sorting algorithm with a smaller N_m in our tailored atom assembler platform and the move distance is not taken into main consideration.

IV. SORTING-ATOM ALGORITHMS

Now we introduce the sorting-atom process of the HCA, the A* searching algorithm (ASA), and the HPFA, respectively, as sketched in Fig. 3. The HCA, aiming at decreasing N_m as small as possible, is proposed to find an optimized sorting path to fill empty target sites with source atoms in reservoir traps. We refer to all the reservoir tweezers as the outside region and all target sites as the inside region. Three blue sections adjacent to the outside region and two orange sections isolated from the outside region are defined as open regions and closed regions, respectively. The number of defect target sites $N = N_1 + N_2$, where N_1 and N_2 represent the number of filled target sites in open regions and closed regions, respectively. The total number of moves $N_m = N_o + N_c$, where N_o and N_c represent the number of moves to fill the open regions and closed regions, respectively. In addition, $N_o = N_1$, because the open regions can be directly filled with source atoms in the outside region and N_o is the smallest number to fill target sites. Further, $N_c > N_2$, since we need to carry out extra moves to transport the obstacle atoms which block the move path. The core ideal of the HCA is to convert the closed regions to open regions. Thus the first step of the HCA is to identify the open regions and closed regions. Then obstacle atoms (in dashed circles) that block the connection between the closed regions and the open regions are moved to the closed regions to open them. The obstacle atoms are sought around the open regions site by site (sometimes, more than one atom should be moved to open up the closed regions). After that, all regions are open and filled with the source atoms in order (the site with the longest distance from the outside region filled first).

The ASA is another sorting-atom algorithm developed by us that fills the empty target sites from the center to the edge in two main steps. The first step is to find the center location of the atom array and classify the layers (the section in the blue,

FIG. 3. Schematic diagrams and flowcharts of the HCA, ASA and HPFA. The sorting process is from left to right.

orange, and red dotted line square) in inside-out order. The second is to fill the trap, one layer after the other. Tweezers of target sites adjacent to the reservoir tweezers are defined as the first layer. The second layer contains the sites in the inside region adjacent to the first layer. The classifying layer process continues until no new layer can be found. The last one is the center of the atom array. Usually, since filling from the center significantly reduce the sorting moves, this is the reason why we classify the layers. In the second step, the ASA fills the layer one by one in the reverse order of layers. The search source atom process is similar to the A* searching algorithm (finding the nearest atom and moving it by passing the obstacles to the target site in the shortest path).

Compared with the HPFA in Ref. [15], our HPFA does a certain amount of optimization to reduce the complexity of the calculation and N_m . The upgraded HPFA does not calculate all the distances between each atom and each target tweezer. Instead, we define a parameter named the search length, which is set to one at the beginning. We check all the empty tweezers whether there are atoms in the reservoir tweezers satisfied with the search length. If there are multiple choices, we will select the one which has the fewest obstacle atoms in the sorting path to achieve as few moves as possible. If there is an obstacle atom blocking the sorting path, we move this atom to the target site and replace the obstacle by a source atom.

FIG. 4. Finding the shortest route to connect all regions. (a) Route composed of only region-region connections with 14 obstacle atoms (in dash line regions). (b) Route composed of region-region and region-junction connections with 11 obstacle atoms.

The search length is continuously increasing until all the target tweezers are settled.

To further explore the smallest N_m , we need to determine how to connect all the closed regions and open regions with the shortest route, as illustrated in Fig. 4(a). Because the shortest connecting route means that the fewest obstacle atoms should be transported to the closed regions. This task is akin to the traveling salesman problem (TSP), which various heuristic algorithms have tried to solve. A region in the atom array can be simplified as a site in the TSP, and the goal of searching for the shortest traveling distance also represents finding the shortest connecting route to open the closed regions. In fact, the connecting route shown in Fig. 4(b) is shorter than the route in Fig. 4(a). Although this indicates that finding the smallest N_m is a more complicated mathematic problem than the TSP, using heuristic algorithms to solve the TSP applied to upgrade the HCA is still a promising way to further minimize N_m , especially for thousands of assembled atoms with high initial loading rate.

V. NUMBER OF MOVES AND FILLING FRACTIONS

All three sorting algorithms seem feasible and effective to prepare two-dimensional defect-free atom arrays of small size; however, their costs of transfer moves and distance are different, especially when the atom size is increased. Simulation results show that the HPFA provides the shortest transfer distance [see Fig. 5(a)] but costs the most N_m [see Fig. 5(b)]. In contrast, we adopt the HCA with the smallest N_m at the expense of the longest transfer distance since the transfer distance has no obvious relation to the filling fraction of the final atom arrays. The HCA will be a better sorting algorithm for near-term intermediate-scale atom arrays with 196 atoms compared to the HPFA and ASA due to a significantly reduced N_m , as seen in Fig. 5(c). That the simulating number of moves is almost equal to the experimental result is verified by preparing a 5×6 atom array. We prepare a 5×6 atom array with a measured filling fraction of 98.4(7)% for one rearrangement cycle (after correcting the 4% atom loss during the probing atom process and the background gas collisions) as illustrated in Fig. 5(d).

FIG. 5. Number of moves of the HCA, ASA, and HPFA and filling fractions of the defect-free atom array as the number of filled sites increased. (a) Results of the simulation of the transfer moves as a function of the number of filled sites. (b) Results of the simulation of the transfer distances as a function of the number of filled sites. The error bars are caused by the randomly distributed initial atom arrays with 50% loading rate. The target sites are all squares. (c) Histogram of the number of moves to prepare a 14×14 square array for 10 000 initial random loading instances. (d) Experimental filling fraction of an atom array after the atom rearrangement by the ASA, HCA, and HPFA. The solid and dashed lines represent the experimental results from 97.7% and 88.0% transfer efficiency, respectively (the average values for 64 sites). The lower transfer efficiency is obtained by the position displacement between the MT and each site in the tweezer array. (e) Simulation of the filling fraction of a large-scale atom array using the ASA, HCA, and HPFA. The solid and dashed lines represent the simulating results from 99% and 90% transfer efficiency, respectively. The filling fraction $F_{ASA} < F_{HPFA} < F_{HCA}$ for $N \leq 64$, while $F_{HPFA} < F_{ASA} < F_{HCA}$ for $N > 64$, where N (also in Fig. 5) is the number of target sites, not the number of defect sites, to be filled. (f) Simulation of the cumulative success rate ($R_c = \eta^N$) of the final atom array as the number of filled sites with 99% transfer efficiency.

Furthermore, we experimentally measure [see Fig. 5(d)] and simulate [see Fig. 5(e)] the filling fractions η of defect-free atom arrays using these three sorting algorithms as a function of the target array size N . The η is given by $\eta = 1 - n(1 - \zeta)$, where ζ is the transfer efficiency and n represents the number of moves per one filled target site. As the experimental and simulating results show, although the distinction of the filling fractions using different algorithms is small when the transfer efficiency is high and the array size is not large, the sorting algorithm with smaller n demonstrates an obvious advantage as the transfer efficiency is decreased or the array size is enlarged. The experimental filling fraction decays as the number of filled sites increases mainly induced by the nonuniform transfer efficiency of 64 sites (the efficiency of transporting atoms to the edge sites in the atom array is lower than the transfer efficiency to the center sites due to imperfect overlaps between the MT and the edge sites in tweezer arrays). Additionally, we find that the simulating filling fractions with the HCA and ASA are approximately constant as the number of filled sites increases, while the HPFA shows a rapid decline, which means the HPFA is not appropriate for large-scale atom arrays even with a high transfer efficiency. Additionally, since

the cumulative success rate of the final atom assembler is greatly affected by sorting algorithms as shown in Fig. 5(f), selecting the best one is crucial.

Additionally, we note that the total rearrangement time also could also be a factor that affects the filling fraction because the atom survival probability in a tweezer array after the rearrangement is limited by the atom lifetime. For example, if we prepare a 30×30 atom array (the details of the transfer process have been described above), the ASA, HCA, and HPFA take 6.7, 8.2, and 9.6 s, respectively. This indicates that the ASA may be the best choice when rearrangement time dominates the filling fraction. However, a much faster transfer speed of 100 nm/ μ s reported in [15] can significantly reduce rearrangement time. Although our time-dependent transfer process is not optimal, the total rearrangement time for intermediate-scale atom arrays is still short enough compared with the atom lifetime in tweezer arrays. Hence, currently, we do not take the rearrangement time into account when selecting a sorting algorithm. By precise control of the time-dependent move path and the trap depth of the MT, a fast and adiabatic transport approach could further reduce the time cost without heating atoms [33,34].

VI. CONCLUSION

To improve the filling fraction of defect-free atom array, we have proposed a sorting algorithm (the HCA) which significantly reduces the sorting moves to near N . We have experimentally demonstrated the advantage of high filling fraction with the HCA over other sorting algorithms and simulated the feature of the HCA that it can maintain a high and uniform filling fraction as the size of the atom assembler increased. This property indicates that our approach is promising for simulations of quantum dynamics [35] and gauge theories [36], error-corrected quantum computations [37,38], preparation of single-molecule arrays [39–41], and quantum metrologies based on large-scale reconfigurable atom arrays.

Note added. Recently, we became aware of related work preparing an enhanced atom-by-atom assembly [42].

ACKNOWLEDGMENTS

This work was supported by the National Key Research and Development Program of China under Grants No. 2017YFA0304501, No. 2016YFA0302800, and No. 2016YFA0302002; the National Natural Science Foundation of China under Grants No. 11774389 and No. 12004395; the Strategic Priority Research Program of the Chinese Academy of Sciences under Grant No. XDB21010100; and the Youth Innovation Promotion Association of CAS under Grants No. 2019325 and No. 2017378.

C.S. and J.H. contributed equally to this work.

-
- [1] H. Bernien, S. Schwartz, A. Keesling, H. Levine, A. Omran, H. Pichler, S. Choi, A. S. Zibrov, M. Endres, M. Greiner, V. Vuletić, and M. D. Lukin, Probing many-body dynamics on a 51-atom quantum simulator, *Nature (London)* **551**, 579 (2017).
 - [2] A. Keesling, A. Omran, H. Levine, H. Bernien, H. Pichler, S. Choi, R. Samajdar, S. Schwartz, P. Silvi, S. Sachdev, P. Zoller, M. Endres, M. Greiner, V. Vuletić, and M. D. Lukin, Quantum Kibble-Zurek mechanism and critical dynamics on a programmable Rydberg simulator, *Nature (London)* **568**, 207 (2019).
 - [3] S. de Léséleuc, V. Lienhard, P. Scholl, D. Barredo, S. Weber, N. Lang, H. P. Büchler, T. Lahaye, and A. Browaeys, Observation of a symmetry-protected topological phase of interacting bosons with Rydberg atoms, *Science* **365**, 775 (2018).
 - [4] A. Browaeys and T. Lahaye, Many-body physics with individually controlled Rydberg atoms, *Nat. Phys.* **16**, 132 (2020).
 - [5] M. A. Norcia, A. W. Young, W. J. Eckner, E. Oelker, J. Ye, and A. M. Kaufman, Seconds-scale coherence on an optical clock transition in a tweezer array, *Science* **366**, 93 (2019).
 - [6] I. S. Madjarov, A. Cooper, A. L. Shaw, J. P. Covey, V. Schkolnik, T. H. Yoon, J. R. Williams, and M. Endres, An Atomic-Array Optical Clock with Single-Atom Readout, *Phys. Rev. X* **9**, 041052 (2019).
 - [7] T. Xia, M. Lichtman, K. Maller, A. W. Carr, M. J. Piotrowicz, L. Isenhowe, and M. Saffman, Randomized Benchmarking of Single-Qubit Gates in a 2D Array of Neutral-Atom Qubits, *Phys. Rev. Lett.* **114**, 100503 (2015).
 - [8] Y. Wang, A. Kumar, T. Wu, and D. S. Weiss, Single-qubit gates based on targeted phase shifts in a 3D neutral atom array, *Science* **352**, 1562 (2017).
 - [9] C. Sheng, X. He, P. Xu, R. Guo, K. Wang, Z. Xiong, M. Liu, J. Wang, and M. Zhan, High Fidelity Single-Qubit Gates on Neutral Atoms in a Two Dimensional Magic-Intensity Optical Dipole Trap Array, *Phys. Rev. Lett.* **121**, 240501 (2018).
 - [10] H. Levine, A. Keesling, G. Semeghini, A. Omran, T. T. Wang, S. Ebadi, H. Bernien, M. Greiner, V. Vuletić, H. Pichler, and M. D. Lukin, Parallel Implementation of High Fidelity Multi-qubit Gates with Neutral Atoms, *Phys. Rev. Lett.* **123**, 170503 (2019).
 - [11] T. M. Graham, M. Kwon, B. Grinkemeyer, Z. Marra, X. Jiang, M. T. Lichtman, Y. Sun, M. Ebert, and M. Saffman, Rydberg-Mediated Entanglement in a Two-Dimensional Neutral Atom Qubit Array, *Phys. Rev. Lett.* **123**, 230501 (2019).
 - [12] I. S. Madjarov, J. P. Covey, A. L. Shaw, J. Choi, A. Kale, A. Cooper, H. Pichler, and V. Schkolnik, J. R. Williams and M. Endres, High-fidelity entanglement and detection of alkaline-earth Rydberg atoms, *Nat. Phys.* **16**, 857 (2020).
 - [13] H. Kim, W. Lee, H.-g. Lee, H. Jo, Y. Song, and J. Ahn, *In situ* single-atom array synthesis using dynamic holographic optical tweezers, *Nat. Commun.* **7**, 13317 (2016).
 - [14] M. Endres, H. Bernien, A. Keesling, H. Levine, E. R. Anschuetz, A. Krajenbrink, C. Senko, V. Vuletic, M. Greiner, and M. D. Lukin, Atom-by-atom assembly of defect-free one-dimensional cold atom arrays, *Science* **354**, 1024 (2016).
 - [15] D. Barredo, S. Léséleuc, V. Lienhard, T. Lahaye, and A. Browaeys, An atom-by-atom assembler of defect-free arbitrary two-dimensional atomic arrays, *Science* **354**, 1021 (2016).
 - [16] W. Lee, H. Kim, and J. Ahn, Defect-free atomic array formation using the Hungarian matching algorithm, *Phys. Rev. A* **95**, 053424 (2017).
 - [17] M. O. Brown, T. Thiele, C. Kiehl, T.-W. Hsu, and C. A. Regal, Gray-Molasses Optical-Tweezer Loading: Controlling Collisions for Scaling Atom-Array Assembly, *Phys. Rev. X* **9**, 011057 (2019).
 - [18] D. O. de Mello, D. Schäffner, J. Werkmann, T. Preuschoff, L. Kohfahl, M. Schlosser, and G. Birkel, Defect-Free Assembly of 2D Clusters of More Than 100 Single-Atom Quantum Systems, *Phys. Rev. Lett.* **122**, 203601 (2019).
 - [19] J. Yang, X. He, R. Guo, P. Xu, K. Wang, C. Sheng, M. Liu, J. Wang, A. Derevianko, and M. Zhan, Coherence Preservation of a Single Neutral Atom Qubit Transferred between Magic-Intensity Optical Traps, *Phys. Rev. Lett.* **117**, 123201 (2016).
 - [20] R. Guo, X. He, C. Sheng, J. Yang, P. Xu, K. Wang, J. Zhong, M. Liu, J. Wang, and M. Zhan, Balanced Coherence Times of Atomic Qubits of Different Species in a Dual 3×3 Magic-Intensity Optical Dipole Trap Array, *Phys. Rev. Lett.* **124**, 153201 (2020).
 - [21] G. Li, Y. Tian, W. Wu, S. Li, X. Li, Y. Liu, P. Zhang, and T. Zhang, Triply Magic Conditions for Microwave Transition of Optically Trapped Alkali-Metal Atoms, *Phys. Rev. Lett.* **123**, 253602 (2019).

- [22] E. Urban, T. A. Johnson, T. Henage, L. Isenhower, D. D. Yavuz, T. G. Walker, and M. Saffman, Observation of Rydberg blockade between two atoms, *Nat. Phys.* **5**, 110 (2009).
- [23] M. Saffman, T. G. Walker, and K. Mölmer, Quantum information with Rydberg atoms, *Rev. Mod. Phys.* **82**, 2313 (2010).
- [24] T. Wilk, A. Gaetan, C. Evellin, J. Wolters, Y. Miroshnychenko, P. Grangier, and A. Browaeys, Entanglement of Two Individual Neutral Atoms Using Rydberg Blockade, *Phys. Rev. Lett.* **104**, 010502 (2010).
- [25] Y. Zeng, P. Xu, X. He, Y. Liu, M. Liu, J. Wang, D. J. Papoular, G. V. Shlyapnikov, and M. Zhan, Entangling Two Individual Atoms of Different Isotopes via Rydberg Blockade, *Phys. Rev. Lett.* **119**, 160502 (2017).
- [26] D. S. Weiss and M. Saffman, Quantum computing with neutral atoms, *Phys. Today* **70**(7), 44 (2017).
- [27] M. Saffman, Quantum computing with atomic qubits and Rydberg interactions: Progress and challenges, *J. Phys. B* **49**, 202001 (2016).
- [28] D. Barredo, V. Lienhard, S. de Léséleuc, T. Lahaye, and A. Browaeys, Synthetic three-dimensional atomic structures assembled atom by atom, *Nature (London)* **561**, 79 (2018).
- [29] A. Kumar, T. Wu, F. Giraldo, and D. S. Weiss, Sorting ultracold atoms in a three-dimensional optical lattice in a realization of Maxwell's demon, *Nature (London)* **561**, 83 (2018).
- [30] Y. B. Wang, S. Shevate, T. M. Wintermantel, M. Morgado, G. Lochead, and S. Whitlock, Preparation of hundreds of microscopic atomic ensembles in optical tweezer arrays, *npj Quantum Inf.* **6**, 54 (2020).
- [31] T. A. Savard, K. M. O'Hara, and J. E. Thomas, Laser-noise induced heating in far-off resonance optical traps, *Phys. Rev. A* **56**, R1095(R) (1997).
- [32] C. Tuchendler, A. M. Lance, A. Browaeys, Y. R. P. Sortais, and P. Grangier, Energy distribution and cooling of a single atom in an optical tweezer, *Phys. Rev. A* **78**, 033425 (2008).
- [33] X. Chen, E. Torrontegui, D. Stefanatos, J.-S. Li, and J. G. Muga, Optimal trajectories for efficient atomic transport without final excitation, *Phys. Rev. A* **84**, 043415 (2011).
- [34] G. T. Hickman and M. Saffman, Speed, retention loss, and motional heating of atoms in an optical conveyor belt, *Phys. Rev. A* **101**, 063411 (2020).
- [35] S. Choi, C. J. Turner, H. Pichler, W. W. Ho, A. A. Michailidis, Z. Papić, M. Serbyn, M. D. Lukin, and D. A. Abanin, Emergent SU(2) Dynamics and Perfect Quantum Many-Body Scars, *Phys. Rev. Lett.* **122**, 220603 (2019).
- [36] A. Celi, B. Vermersch, O. Viyuela, H. Pichler, M. D. Lukin, and P. Zoller, Emerging Two-Dimensional Gauge Theories in Rydberg Configurable Arrays, *Phys. Rev. X* **10**, 021057 (2020).
- [37] A. G. Fowler, J. M. Auger, S. Bergamini, and D. E. Browne, Surface codes: Towards practical large-scale quantum computation, *Phys. Rev. A* **86**, 032324 (2012).
- [38] J. M. Auger, S. Bergamini, and D. E. Browne, Blueprint for fault-tolerant quantum computation with Rydberg atoms, *Phys. Rev. A* **96**, 052320 (2017).
- [39] L. Anderegg, L. W. Cheuk, Y. C. Bao, S. Burchesky, W. Ketterle, K.-K. Ni, and J. M. Doyle, An optical tweezer array of ultracold molecules, *Science* **365**, 1156 (2019).
- [40] J. T. Zhang, Y. Yu, W. B. Cairncross, K. Wang, L. R. B. Picard, J. D. Hood, Y.-W. Lin, J. M. Hutson, and K.-K. Ni, Forming a Single Molecule by Magnetoassociation in an Optical Tweezer, *Phys. Rev. Lett.* **124**, 253401 (2020).
- [41] X. He, K. Wang, J. Zhuang, P. Xu, X. Gao, R. Guo, C. Sheng, M. Liu, J. Wang, J. Li, G. V. Shlyapnikov, and M. Zhan, Coherently forming a single molecule in an optical trap, *Science* **370**, 331 (2020).
- [42] K.-N. Schymik, V. Lienhard, D. Barredo, P. Scholl, H. Williams, A. Browaeys, and T. Lahaye, Enhanced atom-by-atom assembly of arbitrary tweezers arrays, *Phys. Rev. A* **102**, 063107 (2020).