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# Constrained Diffusion for Accelerated Structure Relaxation of Inorganic Solids with Point Defects

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**Jingyi Cui**

University of Virginia  
cau8rc@virginia.edu

**Jacob K. Christopher**

University of Virginia  
csk4sr@virginia.edu

**Ankita Biswas**

University of Virginia  
ab8ky@virginia.edu

**Prasanna V. Balachandran**

University of Virginia  
pvb5e@virginia.edu

**Ferdinando Fioretto**

University of Virginia  
fioretto@virginia.edu

## Abstract

Point defects affect material properties by altering electronic states and modifying local bonding environments. However, high-throughput first-principles simulations of point defects are costly due to large simulation cells and complex energy landscapes. To this end, we propose a generative framework for simulating point defects, overcoming the limits of costly first-principles simulators. By leveraging a primal-dual algorithm, we introduce a constraint-aware diffusion model which outperforms existing constrained diffusion approaches in this domain. Across six defect configuration settings for  $\text{Bi}_2\text{Te}_3$ , the proposed approach provides state-of-the-art performance generating physically grounded structures.

## 1 Introduction

Point defects play an important role in determining the properties of crystalline materials [1–4]. Recent work on additive manufacturing (AM) of thermoelectric materials reveals a more complex relationship between processing conditions and point defects than in traditional methods [5–7]. They are exploited to tailor the structural, electronic, and thermal properties of advanced materials for technological applications.

Layered chalcogenides, a promising material class, are highly susceptible to point defects due to their mixed bonding with weak interlayer van der Waals interactions and strong intralayer covalent bonds, which critically influence electronic and phononic transport properties [8, 9]. A well-known example is bismuth telluride ( $\text{Bi}_2\text{Te}_3$ ), which has been widely studied for its high thermoelectric efficiency in the low-temperature regime [10–13]. The performance of  $\text{Bi}_2\text{Te}_3$  is strongly governed by defect concentration and configuration, and preliminary AM work has shown that laser processing parameters can change thermoelectric properties to optimize efficiency and carrier transport. [6, 7].

Point defects are hard to probe directly and are typically identified indirectly via combined techniques. Traditionally, density functional theory (DFT) have been used to complement experimental methods for defect identification [14] which is computationally expensive, making high-throughput studies computationally prohibitive. This situation highlights the need for alternative approaches, such as surrogate models, to supplement the DFT calculations. In related domains, deep learning methods have successfully overcome these barriers [15]. Generative models enable digital twins for defect prediction, with diffusion models achieving state-of-the-art material generation and inverse design [16–18]. Yet, these models excel at generating realistic data, struggle with strict physical constraints. Without reliability, designs risk impracticality and may hinder transition to production.

For other scientific applications, these challenges have been addressed through physics-aware generative processes. Simple constraints can be injected into sampling [19–21], but complex ones often

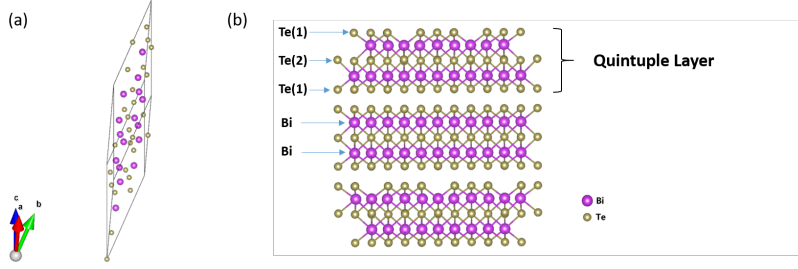


Figure 1: **(a)** A  $2 \times 2 \times 2$  supercell of  $\text{Bi}_2\text{Te}_3$  for DFT simulations. **(b)** Another supercell representation, highlighting quintuple layer, structure  $\text{Te}(1)\text{--Bi--Te}(2)\text{--Bi--Te}(1)$  with vacancy defect.

require integrating costly simulators with high overhead [22, 23]. In this case, runtime demands may limit utility, making rejection sampling more efficient. For physics-informed generation of materials like  $\text{Bi}_2\text{Te}_3$ , first-principle simulators [24] are challenging, as constraints lack closed forms and evaluations scale exponentially with system size.

**Contributions.** To address these existing challenges, this paper makes the following contributions: **(1)** It extends previous constrained generation approaches to handle complex constraints modeled by tractable functions and neural surrogates, leveraging a primal-dual algorithm. **(2)** It provides the first study which explores constrained diffusion to supplement the DFT-based point defect simulation of a thermoelectric material ( $\text{Bi}_2\text{Te}_3$ ). **(3)** Through rigorous evaluation across six defect configurations of interest, we provide state-of-the-art performance for generative modeling of physically realistic predictions of layered chalcogenides.

## 2 Preliminaries

**Score-based Diffusion Models** [25, 26], and equivalently denoising diffusion probabilistic models [27, 28], model data distributions by introducing a forward noising process and training a neural network to approximate its reverse. In the *forward process*, a clean sample  $\mathbf{x}_0 \sim p_{\text{data}}(\mathbf{x}_0)$  is gradually perturbed through a sequence of intermediate distributions  $\{p_t(\mathbf{x}_t)\}_{t=0}^T$ . This is achieved using a Gaussian noise kernel with a predefined variance schedule  $\bar{\alpha}_t$ , which increases with  $t$ . As  $t \rightarrow T$ , the distribution of  $\mathbf{x}_t$  converges to a standard Gaussian, such that  $p_T(\mathbf{x}_T) \approx \mathcal{N}(0, I)$ . This process facilitates the training of a score network  $\mathbf{s}_\theta(\mathbf{x}_t, t)$ , which learns the score function  $\mathbf{s}_\theta(\mathbf{x}_t, t) \approx \nabla_{\mathbf{x}_t} \log p_t(\mathbf{x}_t | \mathbf{x}_0)$  by error in the predicted score estimate:

$$\min_{\theta} \mathbb{E}_{t \sim [T, 1], \mathbf{x}_0 \sim p_{\text{data}}} [\|\mathbf{s}_\theta(\mathbf{x}_t, t) - \nabla_{\mathbf{x}_t} \log p_t(\mathbf{x}_t | \mathbf{x}_0)\|_2^2] \quad (1)$$

The trained score network  $\mathbf{s}_\theta(\mathbf{x}_t, t)$  is then used in the *reverse process* to iteratively reconstruct data samples from the training distribution  $p_{\text{data}}$ . At each timestep  $t$ , the score function is applied to the reverse process, transitioning Gaussian noise  $\mathbf{x}_T \sim \mathcal{N}(0, I)$  to high fidelity samples.

**Projected Diffusion Models** [19] build from Langevin Dynamics employed by score-based diffusion models, interpreting the sampling process as an optimization with respect to a series of intermediate probability density functions (Equation (2a)). In doing so, the formulation enabled a natural extension to constrained sampling problems by enforcing constraint adherence on the sample:

$$\underset{\mathbf{x}_T, \dots, \mathbf{x}_0}{\text{minimize}} \sum_{t=T, \dots, 0} -\log p_t(\mathbf{x}_t | \mathbf{x}_0) \quad (2a)$$

$$\text{s.t.: } \mathbf{x}_T, \dots, \mathbf{x}_0 \in \mathbf{C}. \quad (2b)$$

Constraints can then be enforced by extending the reverse process with Projected Langevin Dynamics, such each update step is projected to the nearest feasible point by  $\mathcal{P}_{\mathbf{C}}(\mathbf{x}) = \arg \min_{\mathbf{y} \in \mathbf{C}} \|\mathbf{y} - \mathbf{x}\|_2^2$ :

$$\mathbf{x}_t^{(i+1)} = \mathcal{P}_{\mathbf{C}}(\mathbf{x}_t^{(i)} + \gamma_t \mathbf{s}_\theta(\mathbf{x}_t^{(i)}, t) + \sqrt{2\gamma_t} \epsilon) \quad (3)$$

where  $\gamma_t$  is the step size decreasing with  $t$ , and  $\epsilon$  is Gaussian noise.

## 3 Constrained Diffusion for Point Defect Generation

Generating relaxed atomic structures with targeted defects in  $\text{Bi}_2\text{Te}_3$  is a challenging problem, as the combinatorial diversity of defect placements creates a vast configuration space where DFT becomes

computationally prohibitive. To address this, we propose a *generative diffusion framework* that samples  $\text{Bi}_2\text{Te}_3$  structures under prescribed stoichiometries. Given target counts of Bi and Te atoms in a supercell, as shown in Figure 1, the model generates diverse arrangements that explore physically meaningful defects while retaining diffusion sampling’s inherent randomness. However, diffusion alone does not ensure physical plausibility, motivating the adoption of three constraint types.

1. *Geometric Constraints.* Ensure physically-meaningful interatomic distances and periodic boundary conditions. Physical validity requires a lower bound on interatomic distances to prevent atomic collapse. For consistency with DFT simulations, generated structures must also satisfy periodic boundary constraints to align with reference distributions. Thus,

$$\|r_i - r_j\| \geq d_{\min}, \quad \forall i \neq j; \quad f_i \in [0, 1]^3, \quad (4)$$

where  $d_{\min}$  is the minimum allowable interatomic distance between arbitrary atoms  $r_i$  and  $r_j$ , and  $f_i$  is the fractional coordinate constrained to  $[0, 1]^3$  to enforce periodic boundary conditions.

2. *Distributional Constraints.* Align radial distributions (within  $5\text{\AA}$ ) with reference data; This reflects structural patterns, such as relative intensities of coordination shells. This yields,

$$D_{[0, R_c]}(p_{\text{gen}}, p_{\text{ref}}) \leq \varepsilon, \quad (5)$$

where  $D_{[0, R_c]}$  measures discrepancy between distributions over distances in  $[0, R_c]$ ,  $p$  denotes the empirical distribution of pairwise distances in generated and reference structures.

3. *Force Minimization.* Stable structures are defined by low total forces, rendering force minimization critical for physical plausibility. As shown in Section 4, stochastic generations often yield high forces. We therefore introduce a *soft* force-minimization constraint, adding a  $\|\text{force}(r)\|^2$  prediction term from a surrogate [29] to the objective (2a), optimized at sampling.

**Terminal Set Constraints.** Projection-based constraint enforcement can be very effective in many applications. Unlike post-processing, these techniques yield higher-fidelity outputs to the learned distribution, as the score function refines samples displaced from high-density regions. Yet, projected diffusion models rely on a stringent assumption: *Constraints can be meaningfully imposed on any  $\mathbf{x}_t \sim p_t(\mathbf{x}_t)$  for an arbitrary  $t$*  [19].

Often, it may be reasonable to assume that constraints can be modeled at intermediate states (e.g., path planning, where even noisy samples form valid trajectories) [30]. However, this assumption does not hold in many scientific applications such as ours, where complex dynamics require surrogates that are unreliable on noisy samples. This challenge, studied in training-free guidance [31–33], can lead to “misaligned gradients,” only matching the true value as  $t \rightarrow 0$ , leading to compounding errors [34, 35]. Alternatively, finetuning on noisy data is often ineffective: **(1)** Labels are not available for our constraints due to simulators requirements [24], which are not only prohibitive due to runtime but also as the DFT process fails on increasingly noisy samples. **(2)** Even when labels are available, gradient inaccuracies remain a concern [36].

Hence, designing a constraint evaluation surrogate robust to high noise levels is prohibitive for complicated constraint sets. A more promising strategy is to relax the intermediate feasibility assumption. To facilitate this, our framework treats the objective in Equation (2) as a *multi-stage optimization problem*. While Equation (2b) enforces  $\mathbf{x}_t \in \mathbf{C}$ , from a multi-stage perspective only the terminal state  $\mathbf{x}_0$  must be feasible. Thus, intermediate constraints serve as a conservative proxy for final feasibility, while earlier states may remain unconstrained if the process yields  $\mathbf{x}_0 \in \mathbf{C}$ .

Hence, we impose the constraints only on the final minimization of  $-\log p_{\text{data}}(\mathbf{x}_0)$ . This can then be interpreted as terminal set constraints drawn from Model Predictive Control theory [37], where feasibility is often only enforced on final decision variables. This removes dependence on intermediate feasibility assumptions as constraints are only imposed on clean samples within  $p_{\text{data}}$ .

**Primal-Dual Projection Algorithm.** As neural surrogates provide differentiable loss functions, it is most reasonable to solve the projection mapping using a gradient-based approach. To facilitate this, we adopt the Augmented Lagrangian representation of the constraint problem following Liang et al., incorporating constraints into the objective through Lagrange multipliers [38], and yielding:

$$\mathcal{L}(\mathbf{y}, \mathbf{x}_0^{(i)}; \lambda, \mu) := \|\mathbf{y} - \mathbf{x}_0^{(i)}\|_2^2 + \sum_j \lambda_j c_j(\mathbf{y}) + \sum_k \frac{\mu_k}{2} c_k(\mathbf{y})^2 \quad (6)$$

where  $\lambda = \{\lambda_1, \dots, \lambda_N\}$  and  $\mu = \{\mu_1, \dots, \mu_N\}$  are dual variables associated with  $N$  constraint violation functions  $c = \{c_1, \dots, c_N\}$  and  $\mathbf{y}$  is the solution optimized. Ensuring the strongest

Method	Config	RMSD ↓	RDF ↓	Force (eV/Å) ↓
Conditional DM	16Bi + 21Te	1.86 ± 0.33	65.85 ± 19.75	1.85 × 10 <sup>9</sup>
	16Bi + 22Te	1.93 ± 0.36	82.11 ± 29.54	3.49 × 10 <sup>9</sup>
Projected DM	16Bi + 21Te	2.54 ± 0.55	1.11 ± 0.77	8.35 × 10 <sup>2</sup>
	16Bi + 22Te	1.41 ± 0.83	0.78 ± 0.55	7.20 × 10 <sup>1</sup>
Post-proc DM	16Bi + 21Te	2.30 ± 0.40	27.25 ± 28.30	8.45 × 10 <sup>6</sup>
	16Bi + 22Te	1.14 ± 0.65	21.82 ± 28.09	9.29 × 10 <sup>6</sup>
<b>Ours</b>	16Bi + 21Te	<b>0.90 ± 0.38</b>	<b>0.30 ± 0.11</b>	<b>7.88 × 10<sup>-2</sup></b>
	16Bi + 22Te	<b>1.02 ± 0.70</b>	<b>0.35 ± 0.18</b>	<b>1.44 × 10<sup>-1</sup></b>

Table 1: Empirical comparison across stoichiometric configurations. Extended table in Appendix C.

relaxation of this projection, the Lagrangian dual is used to optimize the dual variables [39]:

$$\arg \max_{\lambda, \mu} \left( \arg \min_{\mathbf{y}} (\mathcal{L}(\mathbf{y}, \mathbf{x}_0^{(i)}; \lambda, \mu)) \right) \quad (7)$$

This converges to satisfy the distance and distributional constraints while simultaneously minimizing the force and remaining close to the original input. Following Equation (3), we begin applying this as our projection operator at  $t = 0$ . More details are provided in Appendix B.

## 4 Experiments

**Baselines.** We compare our approach against three representative baselines: **(1)** conditional diffusion models [40], where constraints are incorporated during training and sampling to bias the denoising process toward feasible regions. **(2)** post-processing optimization [41], where the final output of an unconstrained diffusion model is projected onto the constraint set in a single step. **(3)** projected diffusion models [19], which enforce constraints at every denoising step. This represents the current state-of-the-art but relies on meaningful constraint evaluation under noisy configurations.

**Evaluation.** We target four categories of defects that frequently occur in Bi<sub>2</sub>Te<sub>3</sub> structure systems: Te vacancies, Bi vacancies, Bi on Te anti-site, and Te on Bi anti-site. Additional details on the problem setup and results are provided in Appendix C. Our evaluation consists of the following metrics:

- **RMSD (Root Mean Square Deviation):** Computes positional deviation between generations and closest reference structures by matching atoms via a Hungarian matching algorithm.
- **RDF (Radial Distribution Function):** Compares radial distributions for all generations within 5Å to assess global geometric consistency. This indicates the accuracy of positions and heights of nearest neighbor shell peaks under a common defect.
- **Force (eV/Å):** Reports the total force as computed by a neural surrogate [29]. Lower force indicates generations closer to stable states and more suitable for downstream simulations.

**Interpretation.** As shown in Table 1, our method achieves substantially lower deviation from reference structures and reduced total forces. Existing approaches observe key limitations: **(1)** conditional diffusion preserves structural characteristics but allows overlapping atoms, undermining physical realism and leading to extremely high total force; **(2)** post-processing, while improving over the conditional model, struggles to impose the highly nonconvex constraints in a single step, as the final output often deviates from the constraint set significantly; **(3)** projected diffusion provides the strongest baseline, but misaligned gradients at higher noise results in higher RDF deviation. In contrast, our method preserves diffusion dynamics while ensuring feasibility. By applying constraints on the final Langevin optimization, gradient inaccuracies are avoided (unlike projected diffusion models), while providing a sufficient number of constrained diffusion steps to ensure feasibility (unlike post-processing schemes). We achieve the lowest RMSD in nearly all settings, the highest RDF similarity (by more than 2x), and lower total forces by several orders of magnitude.

## 5 Conclusion

Motivated by the real-world importance of thermoelectric defect structure modeling, this paper addresses existing barriers by integrating constraints into the sampling process through tractable functions and neural surrogate models. Building upon a primal–dual projection algorithm, this work provides effectively enforces feasibility while addressing challenges with misaligned gradients. Across six representative defect configurations in Bi<sub>2</sub>Te<sub>3</sub>, our approach provides state-of-the-art performance in producing physically realistic structures, highlighting the significance of our framework for complex material systems.

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## A Related Work

**Constraint Conditioning** [40, 42] enables controllable generation by incorporating a conditioning variable to bias the posterior which is sampled. Accomplished either explicitly through the addition of classifier-derived gradient signals or implicitly by training the denoiser with specific conditioning labels, these techniques provide soft guidance towards particular subdistributions. Notably, these methods have been applied to improve constraint adherence in a variety of applications including [fill in references]. Yet, while constraint conditioning can improve feasibility rates in specific cases, it is unreliable when exact satisfaction is required. Particularly when constraint sets are complex, conditioning methods have been shown ineffective in providing viable outputs, a challenge that is demonstrated in our empirical analysis.

**Post-Processing Optimization** [41] provides an alternative approach which injects constraints following the denoising process. These approaches leverage a generative model to produce a starting structure  $\mathbf{x}_0$ , after which domain-specific corrections are applied. For material structure generations, this often consists of running DFT simulators [24] to relax the atomic configurations, ensuring stability as the structure is refined to reach equilibrium. Yet, these approaches are inherently void of distributional information, and the optimization procedure may drive the samples away from the learned distribution. While the original candidate structure will fall within  $p_{\text{data}}$ , without access to the learned score function or likelihood estimates, post-processing can degrade sample quality, resulting in an output distribution that is constrained but no longer resembles the training data.

## B Augmented Lagrangian Method

In our settings, projection is required to ensure a collection of physical constraints. Unlike standard convex projection operators, these constraints are often highly non-convex and some are evaluated through surrogate models, such as pretrained MACE model. This makes exact projection onto feasible set intractable. To overcome this, we rely on the Augmented Lagrangian Method (ALM) [38]. Instead of attempting to solve the constrained problem in a closed form, Lagrangian relaxation converts these into differentiable residuals. By combining linear multipliers  $\lambda$  and quadratic penalties  $\mu$ , ALM provides a mechanism to gradually enforce feasibility.

Let  $\mathbf{x}_0$  denote the current sample produced by the diffusion process, and let  $\mathbf{y}$  be the projected candidate. We aim to find  $\mathbf{y}$  that remains close to  $\mathbf{x}_t$  while reducing constraint violations. The approach introduces a relaxed objective by embedding constraint residuals into the optimization problem:

$$\mathcal{L}(\mathbf{y}, \mathbf{x}_0^{(i)}; \lambda, \mu) := \|\mathbf{y} - \mathbf{x}_0^{(i)}\|_2^2 + w \cdot \|\text{force}(\mathbf{y})\|_2^2 + \sum_j^N \lambda_j c_j(\mathbf{y}) + \sum_k^N \frac{\mu_k}{2} c_k(\mathbf{y})^2 \quad (8)$$

where  $\{c_1, \dots, c_N\}$  denotes a series of differentiable violation residual of constraints. Additionally, we treat the force prediction provided by MACE [29] as a minimization term (scaled by  $w$ ) rather than as a hard constraint, due to runtime considerations and surrogate predictive accuracy. This formulation transforms the constrained projection into a differentiable optimization problem that can be solved iteratively alongside diffusion sampling. Algorithm 1 summarizes the procedure: starting from the diffusion output  $\mathbf{x}_t$ , we iteratively compute constraint residuals, update the augmented objective, take a gradient step, and adjust multipliers and penalties.

In our implementation, the residual vector  $\tilde{\phi}(\mathbf{y})$  collects violations from three major classes of constraints: (i) geometric constraints, including minimum interatomic distances and periodic boundaries; (ii) distributional constraints, capturing radial distribution alignment; and (iii) force minimization, based on surrogate predicted forces.

## C Evaluation Setup

Our model is trained on full DFT relaxation trajectories. The training dataset consists of approximately 13,000 structures from DFT trajectories. Each structure is represented by atom types and corresponding 3D coordinates in Cartesian space. Our generative model starts from Gaussian noise and progressively denoises toward physically relaxed structures under the targeted defect configurations. Each of the six stoichiometric configurations was evaluated with 100 generated samples, resulting in 600 structures per method. These six configurations were chosen because they are the most prevalent in our training trajectories and serve as representative cases of the four major defect categories considered [43]. All methods are evaluated under a shared random seeds to ensure comparability.

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### Algorithm 1: Augmented Lagrangian Projection

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**Input:**  $\mathbf{x}_t$ , Lagrange multiplier:  $\lambda$ , quadratic penalty:  $\mu$ , scaling constant:  $\alpha$ , step size:  $\gamma$ , tolerance:  $\delta$

```

 $\mathbf{y} \leftarrow \mathbf{x}_t$ 
while  $\sum_i c_i(\mathbf{y}) < \delta$  do
    for  $j \leftarrow 1$  to  $\text{max\_inner\_iter}$  do
         $\mathcal{L}_{\text{ALM}} \leftarrow \|\mathbf{x}_t - \mathbf{y}\|_2^2 + \sum_j^N \lambda_j c_j(\mathbf{y}) + \sum_k^N \frac{\mu_k}{2} c_k(\mathbf{y})^2$ 
         $\mathbf{y} \leftarrow \mathbf{y} - \gamma \nabla_{\mathbf{y}} \mathcal{L}_{\text{ALM}}$ 
     $\lambda \leftarrow \lambda + \mu \sum_j^N \lambda_j c_j(\mathbf{y}); \mu \leftarrow \min(\alpha\mu, \mu_{\text{max}})$ 
 $\mathbf{x}_{t-\Delta} \leftarrow \mathbf{y}$ 
return  $\mathbf{x}_{t-\Delta}$ 

```

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**Metric computation** For pairwise RMSD similarity, given a generated structure and the set of relaxed references under the same stoichiometric composition. Before measuring, both structures are centered, and atoms are matched by species. Within each species, we form the pairwise Euclidean distance matrix between generated and reference coordinates and solve an optimal one to one assignment using the Hungarian algorithm[44]. The final RMSD is taken under this assignment and reported at the structure level of the sampling set.

The RDF characterizes the radial number density of neighbors, i.e., the probability density of finding another atom at distance  $r$ [45]. We compute  $g(r)$  for generated structures under a  $5\text{\AA}$  local cutoff. Among relaxed references of the same composition, we then identify the nearest reference in RDF space by minimizing the RMSD between RDF profiles. The result is recorded as the sample’s distributional deviation. This procedure provides a global distribution check that is independent of the previous RMSD assignment.

To assess proximity to locally stable states, we estimate total forces for all generated samples with a pretrained surrogate and summarize each structure by the magnitude of its total forces. Lower values indicate that the generated configuration lies closer to an equilibrium basin and is more suitable as an input to downstream relaxation. We report mean total forces over the sampled set to enable comparison across methods.

Method	Config	RMSD ↓	RDF ↓	Force (eV/Å) ↓
Conditional DM	16Bi + 21Te	$1.86 \pm 0.33$	$65.85 \pm 19.75$	$1.85 \times 10^9$
	16Bi + 22Te	$1.93 \pm 0.36$	$82.11 \pm 29.54$	$3.49 \times 10^9$
	18Bi + 22Te	$2.10 \pm 0.38$	$87.90 \pm 39.29$	$1.64 \times 10^9$
	14Bi + 26Te	$1.22 \pm 0.60$	$40.63 \pm 41.77$	$1.28 \times 10^9$
	14Bi + 24Te	$0.75 \pm 0.81$	$27.41 \pm 44.46$	$5.52 \times 10^8$
	13Bi + 24Te	$0.95 \pm 0.51$	$22.17 \pm 33.53$	$3.90 \times 10^8$
Projected DM	16Bi + 21Te	$2.54 \pm 0.55$	$1.11 \pm 0.77$	$8.35 \times 10^2$
	16Bi + 22Te	$1.41 \pm 0.83$	$0.78 \pm 0.55$	$7.20 \times 10^1$
	18Bi + 22Te	$1.85 \pm 1.17$	$1.45 \pm 1.62$	$5.85 \times 10^3$
	14Bi + 26Te	$1.43 \pm 0.78$	$1.00 \pm 0.67$	$5.04 \times 10^1$
	14Bi + 24Te	$2.35 \pm 0.45$	$0.94 \pm 0.49$	$5.50 \times 10^1$
	13Bi + 24Te	$2.93 \pm 0.39$	$1.44 \pm 0.38$	$1.17 \times 10^2$
Post-proc DM	16Bi + 21Te	$2.30 \pm 0.40$	$27.25 \pm 28.30$	$8.45 \times 10^6$
	16Bi + 22Te	$1.14 \pm 0.65$	$21.82 \pm 28.09$	$9.29 \times 10^6$
	18Bi + 22Te	$1.41 \pm 0.45$	$63.27 \pm 35.58$	$1.69 \times 10^8$
	14Bi + 26Te	$1.16 \pm 0.62$	$50.00 \pm 35.32$	$6.54 \times 10^7$
	14Bi + 24Te	$2.17 \pm 0.38$	$37.37 \pm 28.29$	$1.61 \times 10^7$
	13Bi + 24Te	$2.75 \pm 0.34$	$59.24 \pm 28.05$	$1.76 \times 10^7$
Ours	16Bi + 21Te	$0.90 \pm 0.38$	$0.30 \pm 0.11$	$7.88 \times 10^{-2}$
	16Bi + 22Te	$1.02 \pm 0.70$	$0.35 \pm 0.18$	$1.44 \times 10^{-1}$
	18Bi + 22Te	$1.22 \pm 0.42$	$0.47 \pm 0.22$	$3.00 \times 10^{-1}$
	14Bi + 26Te	$1.00 \pm 0.39$	$0.28 \pm 0.19$	$1.67 \times 10^{-1}$
	14Bi + 24Te	$0.68 \pm 0.56$	$0.30 \pm 0.11$	$1.80 \times 10^{-1}$
	13Bi + 24Te	$0.99 \pm 0.49$	$0.36 \pm 0.06$	$1.93 \times 10^{-1}$

Table 2: Complete experimental results across all six stoichiometric configurations in four defect categories: Te vacancies (16Bi + 22Te, 16Bi + 21Te), Bi vacancies (14Bi + 24Te, 13Bi + 24Te), Bi in Te antisites (18Bi + 22Te), and Te in Bi antisites (14Bi + 26Te).