Molecule Lattice Analysis

1. Numerical Metrics:

Mean Absolute Error (MAE): ~0.011

Median Absolute Error: ~0.0135

Mean Relative Error: ~3.68%

Median Relative Error: ~2.76%

2. Quick Analysis:

- Absolute error (~0.011-0.0135) is about 1% of the parameter range [-1, 1].
- Relative error (~3.68%) is low, which is an excellent result for regression tasks.
- Errors are small and very stable across the dataset.

3. Observations from Graphs:

- Training curve shows good convergence without overfitting.
- Absolute and relative errors are small and consistent.
- Scatter plots show points closely aligned along the ideal diagonal, meaning very accurate predictions.

4. Why It Performs Well:

- The 'simple' lattice magnetization curves are highly sensitive to parameter changes.
- Clearer signal allows the neural network to map M(H) curves to interaction parameters effectively.
- No complex coupling between parameters compared to 'molecule' case.

5. Conclusion:

- The model achieves excellent accuracy.
- 3-4% relative error is very good.
- Neural network can reliably predict parameters for the 'simple' lattice case.

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6. Summary:

Results are very strong, allowing practical use for inverse problems:

predicting interaction parameters based on magnetization curves M(H) with high precision.