Supporting Information

Double boron atoms doped Graphdiyne as efficient metal-free electrocatalysts for nitrogen reduction into ammonia: A First-Principles Study

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1. Table S1. The cohesive energies of pristine-GDY and double boron atoms doped GDY-2B configurations.

2. Scheme. S1. Schematic depiction of the distal pathway and alternating pathway for NRR on configuration GDY-2B via end-on N₂ adsorption mode.

3. Fig. S1. Optimized structures (top-view and side-view) for (a) pristine-GDY, (b) GDY-2B(S_1S_1'), (c) GDY-2B(S_2S_2'), (d) GDY-2B(S_2S_3'), (e) GDY-2B(S_3S_3'), (f) GDY-2B(A_1A_1'), (g) GDY-2B(A_1A_2), (h) GDY-2B(A_1A_3), (i) GDY-2B(S_1A_1), (j) GDY-2B(S_2A_1), (k) GDY-2B(S_3A_1), (l) GDY-2B(S_4A_1). Brown and pink balls stand for carbon and boron atoms respectively.

4. Fig. S2. Optimized structures with bond length (Å) labeled for (a) $GDY-2B(S_1S_1')$, (b) $GDY-2B(S_2S_2')$, (c) $GDY-2B(S_2S_3')$, (d) $GDY-2B(A_1A_1')$, (e) $GDY-2B(A_1A_2)$, (f) $GDY-2B(S_4A_1)$.

5. Fig. S3. The Bader charge values on (a) pristine-GDY and GDY-2B configurations (b) GDY-2B(S_1S_1'), (c) GDY-2B(S_2S_2'), (d) GDY-2B(S_2S_3'), (e) GDY-2B(A_1A_1'), (f) GDY-2B(A_1A_2), (g) GDY-2B(S_4A_1).

6. Fig. S4. Total density of states (TDOS) and partial density of states (PDOS) of (a) $GDY-2B(S_1S_1')$, (b) $GDY-2B(S_2S_2')$, (c) $GDY-2B(S_2S_3')$, (d) $GDY-2B(A_1A_1')$, (e) $GDY-2B(A_1A_2)$ and (f) $GDY-2B(S_4A_1)$. The Fermi level is set to zero, as shown by the black dashed line.

7. Fig. S5. Potential energy surfaces for NRR on GDY-2B(S_4A_1) configuration through (a) consecutive, (b) enzymatic mechanisms as the hydrogenation beginning at the S_4 -site B atom at different applied potentials, together with free energy and (c) the relative geometric structures for each elementary step.

8. Fig. S6. Potential energy surfaces for NRR on GDY-2B(A_1A_1') configuration through (a) consecutive, (b) enzymatic, (c)distal and (d)alternating mechanisms at different applied potentials, together with free energy and the relative geometric structures for each elementary step of (e) consecutive and enzymatic mechanisms, and (f) distal and alternating mechanisms.

9. Fig. S7. Potential energy surfaces for NRR on GDY-2B(A_1A_2) configuration through (a) consecutive, (b) enzymatic mechanisms as the hydrogenation beginning at the A_1 -site B atom at different applied potentials, together with free energy and (c) the relative geometric structures for each elementary step.

10. Fig. S8. Potential energy surfaces for NRR on GDY- $2B(A_1A_2)$ configuration through (a) consecutive, (b) enzymatic mechanisms as the hydrogenation beginning at the A₂-site B atom at different applied potentials, together

with free energy and (c) the relative geometric structures for each elementary step.

11. Fig. S9. (a) Free energy diagram for the HER on GDY- $2B(S_2S_2')$ and (b) the corresponding structures of GDY- $2B(S_2S_2')$ with H atom adsorbed after optimization.

12. Fig. S10. The calculated band structure of (a) pristine-GDY and (b) $GDY-2B(S_4A_1)$. The Fermi level is set to zero.

13. Fig. S11. The Bader charge values on N_2 adsorbed GDY-2B configurations via side-on mode on (a) GDY-2B(S_2S_2'), (b) GDY-2B(A_1A_1'), (c) GDY-2B-(A_1A_2), (d) GDY-2B-(S_4A_1), and via end-on mode on (e) GDY-2B(A_1A_1'), respectively.

14. Fig. S12. (a) The electron density difference of N_2 molecule adsorbed on GDY-2B(S₄A₁) with the isosurface level set to be 0.002 e/Å³. Yellow and blue regions represent electron accumulation and depletion, respectively. (b) Partial density of states (PDOS) of N_2 molecule adsorbed on GDY-2B(S₄A₁) and the Fermi level is set to zero, as shown by the black dashed line.

15. Fig. S13. (a) Definition of three moieties of N_xH_y adsorbed on GDY-2B(S₄A₁) by using *N-*NH as the model.
(b) Charge variation of three moieties along the preferable enzymatic mechanism on GDY-2B(S₄A₁).

16. Fig. S14. Variations of temperature and energy against the time for AIMD simulations of GDY-2B(S_2S_2'), and inserts are top and side views of the snapshot of the atomic configuration. The simulation is run under 500 K for 10 ps with a time step of 1 fs.

17. Fig. S15. The corresponding structures of N_2 adsorption on pristine GDY (a)before and (b)after optimization in top-view and side-view.

Configuration	$E_{\rm coh}({\rm eV})$
pristine-GDY	-7.205
$GDY-2B(S_1S_1')$	-7.144
$GDY-2B(S_2S_2')$	-7.139
$GDY-2B(S_2S_3')$	-7.138
GDY-2B(S ₃ S ₃ ')	-7.137
$GDY-2B(A_1A_1')$	-7.143
$GDY-2B(A_1A_2)$	-7.130
$GDY-2B(A_1A_3)$	-7.101
$GDY-2B(S_1A_1)$	-7.174
$GDY-2B(S_2A_1)$	-7.169
$GDY-2B(S_3A_1)$	-7.149
$GDY-2B(S_4A_1)$	-7.156

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Fig. S2. Optimized structures with bond length (Å) labeled for (a) GDY-2B(S_1S_1'), (b) GDY-2B(S_2S_2'), (c) GDY-2B(S_2S_3'), (d) GDY-2B(A_1A_1'), (e) GDY-2B(A_1A_2), (f) GDY-2B(S_4A_1).



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Fig. S5. Potential energy surfaces for NRR on GDY-2B(S_4A_1) configuration through (a) consecutive, (b) enzymatic mechanisms as the hydrogenation beginning at the S_4 -site B atom at different applied potentials, together with free energy and (c) the relative geometric structures for each elementary step.



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Fig. S7. Potential energy surfaces for NRR on GDY-2B(A_1A_2) configuration through (a) consecutive, (b) enzymatic mechanisms as the hydrogenation beginning at the A_1 -site B atom at different applied potentials, together with free energy and (c) the relative geometric structures for each elementary step.



Fig. S8. Potential energy surfaces for NRR on GDY-2B(A_1A_2) configuration through (a) consecutive, (b) enzymatic mechanisms as the hydrogenation beginning at the A_2 -site B atom at different applied potentials, together with free energy and (c) the relative geometric structures for each elementary step.



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Ab initio molecular dynamics (AIMD) simulations are performed in the canonical ensemble (NVT), with the temperature controlled by the Nosé–Hoover thermostat approach (J. Chem. Phys. 1984, 81, 511–518/ Phys. Rev. A 1985, 31, 1695–1697). And the simulations are run for a time period of 10.0 ps with a typical time interval of 1 fs under 500 K.



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