Chemical control of structure and guest uptake by a conformationally mobile porous material

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A porous material that can rearrange its own skeleton — not just open and close a gate, but actually choose between multiple distinct shapes — depending on what molecule you pour into it. Let that sit for one moment. Most porous materials are rigid scaffolds. This one behaves more like a protein.

That's the core of what Katsoulidis and colleagues at Liverpool built and characterized: a zinc-based metal-organic framework threaded with a tripeptide linker that navigates a genuine conformational energy landscape, selecting between structural forms in response to chemistry. The paper isn't just about a clever material. It's about importing a biological principle — the idea that shape-shifting is a feature, not a flaw — into synthetic porous solids.

To understand why that matters, start with the alternatives. Zeolites and classic rigid metal-organic frameworks have fixed pore geometries. Their single stable structure is exactly what makes them predictable and useful for separations and catalysis. But that rigidity is also a ceiling. A framework locked into one shape can't reconfigure its internal surface to recognize different molecules the way an enzyme can. Flexible metal-organic frameworks exist — some slide, some hinge — but they tend to produce only limited rearrangements, a small number of accessible states. What Katsoulidis and colleagues demonstrate is something more ambitious: a framework with a full conformational energy landscape, meaning multiple distinct minima, each corresponding to a real crystal structure with different pore geometry and different function.

The material is called ZnGGH. The name tells you what it's made of: zinc ions coordinated to glycyl-glycyl-L-histidine, a tripeptide. When the C-terminal carboxylate and the histidine imidazole are deprotonated, GGH becomes a four-point ligand that links zinc into a three-dimensional chiral porous network. The as-made material, ZnGGH-1, forms when you heat zinc acetate with the peptide in a mixture of dimethylformamide and water at ninety degrees Celsius for forty-eight hours, and it comes out in seventy-five percent yield. Its one-dimensional pores contain one dimethylformamide molecule and roughly zero point eighty-five water molecules per formula unit.

What makes this framework special is the Gly-Gly segment of the linker. Peptide backbones can rotate about single bonds, and that rotation is the engine of conformational diversity here. The key bond is the N-C alpha bond of the central glycine — its torsion angle, called phi-1, spans one hundred fifty-six degrees across the nine distinct crystal structures the team experimentally observed. That's not a subtle wiggle. At phi-1 equal to two hundred sixty-eight degrees, you get a twisted structure. At one hundred thirty-three degrees, a straight one. At one hundred eighty degrees, an intermediate. Each rotation physically relocates the N-terminal glycine, changing the size, shape, and hydrogen-bonding environment of the pore.

Those differences are measurable. The dimethylsulfoxide solvated form, ZnGGH-2, adopts the twisted conformation. The Gly-Gly amide points into the pore and hydrogen-bonds with dimethylsulfoxide, producing the smallest pore window in the series: four point five angstroms. The dimethylformamide stabilized form, ZnGGH-3, adopts the straight conformation, where linkers align into an antiparallel beta-sheet-like hydrogen-bond network, and the pore window opens to five point four angstroms — the largest observed. That's a roughly twenty percent difference in window size driven entirely by which solvent occupies the pore.

And that difference in window size is the switch that controls guest uptake. ZnGGH-2 sitting in dimethylsulfoxide won't adsorb larger guests like dioxane or cyclopentanol. The twisted conformation locks them out. But exchange dimethylsulfoxide for dimethylformamide, and the framework transforms to ZnGGH-1 or ZnGGH-3 — the straight-linker forms — and those guests enter. The team measured the pore composition directly by proton nuclear magnetic resonance after one such exchange experiment: adding dimethylformamide to a dioxane suspension of ZnGGH-2 converted the material to ZnGGH-1, with a final pore composition of dioxane to dimethylformamide to dimethylsulfoxide to peptide of zero point forty-seven to zero point twenty-six to zero point eleven to one. Powder X-ray diffraction confirmed a direct structural transformation with no intermediate phases. More

broadly, dioxane, cyclopentanol, furfural, and furfuryl alcohol are adsorbed by ZnGGH in the presence of any pore solvent except dimethylsulfoxide. Dimethylsulfoxide is the off switch.

Katsoulidis and colleagues frame this in language borrowed from protein chemistry. Conformational selection is when a small molecule stabilizes a higher-energy structural form that already exists in the framework's repertoire — the scaffold had that shape available, and the guest reaches in and locks it. Induced fit is when the guest imposes a structure the framework wouldn't adopt on its own. Most of the nine observed ZnGGH structures fall into the conformational selection category. One exception is ZnGGH-4, the water- or methanol-solvated form, which is unstable as an empty host but stabilized by a single solvent molecule forming two hydrogen bonds. That's induced fit — a guest reaching in and creating a valley that wasn't there before.

To map this landscape precisely, the team ran density functional theory — DFT — calculations and nudged elastic band simulations on a periodic model of ZnGGH. DFT calculates the electronic energy of the framework in different configurations, while the nudged elastic band method traces the minimum-energy path between two structural minima, giving you the barrier height between them. Using the PBE functional with van der Waals corrections, they optimized the empty framework and found three minima: S-ZnGGH (straight), T-ZnGGH (twisted), and F-ZnGGH (folded). All six experimentally observed straight-linker structures relax to the same empty straight minimum. The barriers between minima are twelve point four kilojoules per mole to fold from straight, and nineteen point five kilojoules per mole to twist. Those values are comparable to barriers in fast-folding proteins. The landscape is accessible at room temperature — the valleys are real, the barriers are crossable.

What computation revealed that experiment alone couldn't is the relative depths of those valleys and how guests reshape them. The dimethylsulfoxide solvated twisted form ZnGGH-2 corresponds to T-ZnGGH, which is inactive for dioxane. When dimethylformamide displaces dimethylsulfoxide, the energy ranking shifts, S-ZnGGH becomes the occupied minimum, and dioxane uptake turns on. This is not a passive structural response. The chemistry of the pore content deterministically selects which valley the framework sits in.

Bring it all together and you get a concrete picture of what chemical control means here. The conformational switch is the peptide backbone. The knob that turns the switch is pore chemistry — which solvent is present. The output is a measurable change in pore window size, from four point five to five point four angstroms, that

governs whether a given guest can enter. Three energy minima, two barrier heights, nine observed structures, one underlying tripeptide scaffold.

The protein analogy that opens this story isn't decorative. Enzymes achieve selectivity by presenting the right surface geometry to the right substrate, and that geometry is itself regulated by small molecules. ZnGGH does the same thing, but in a crystalline solid you can synthesize in seventy-five percent yield from commercially available components. The conformational energy landscape isn't a side effect of using a flexible linker. It's the designed feature. Katsoulidis and colleagues demonstrate that you can read out which minimum the framework occupies by looking at pore composition, you can predict it computationally, and you can drive it chemically.

The near-term implications follow directly from the mechanism. If solvent identity selects the structural form, and structural form controls which guests enter, then you have a chemically programmable sorbent — one you could in principle tune for selective separations, triggered capture, or sensing. The deeper contribution is conceptual: this paper shows that the conformational energy landscape is a designable parameter of a porous material. Not just how open or closed a pore is, but how many shapes it can take, what the barriers between them are, and which chemistry reaches in to choose. That's a different kind of control than anything a rigid zeolite offers.

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