SUPPORTING INFORMATION

SUPPORTING METHODS

S1. Determination of cystathionine γ - and β -lyase activities of XometC

Cystathionine is degraded to cysteine and to homocysteine by γ - and β -elimination activities, respectively. Both cysteine and homocysteine were detected in the enzyme reaction with purified XometC through a method that measured DTNB-derivatized (*vide infra*) products (Bruinenberg *et al.*, 1997). The separation of the DTNB-derivatized products was conducted by reverse phase HPLC using an Agilent 1260 infinity liquid chromatography system with a TSK-GEL® ODS-80Ts 5- μ m C₁₈ Column (4.6 mm × 250 mm) (TOSOH). HPLC solvent A consisted of water and 0.2%(v/v) acetic acid, whereas solvent B consisted of water, 50%(v/v) acetonitrile, and 0.2%(v/v) acetic acid. The gradient program used 100% solvent A for 5 min after sample injection, a linear gradient of 0–100% solvent B over 35 min, and an isocratic step in 100% solvent B for 10 min and solvent A for 7 min. The flow rate was 0.8 ml.min⁻¹.

S2. Lyase activities of XometC for diverse substrates including 1-serine dehydratase activity

The lyase activity including L-serine dehydratase activity was measured for diverse substrates. The lyase activity for L-cystathionine was determined by measuring the formation of free thiol groups in products (Uren, 1987). The lyase activity for L-o-succinyl homoserine, homoserine, and L-serine was measured by the production of keto acids (Esaki & Soda, 1987). The lyase activity for L-serine cleaves off the OH group from the Cβ carbon in serine, which is also called as L-serine dehydratase activity. The assay for the formation of thiol groups was performed in reaction buffer (100 μl) containing 0.1 *M* Tris pH 8.0, 0.2 m*M* 5,5′-dithiobis-(2-nitrobenzoic acid) (DTNB, Ellman's reagent), 0.01 m*M* PLP, various concentrations of substrates, and XometC (1 ug), and the reactions were conducted at 30°C

for 30 min. The quantity of thiol groups was measured by the absorbance at 412 nm. L-Cysteine was used as a standard. The assays for the production of keto acids were conducted in a solution (200 μ l) containing 0.1 M Tris pH 8.0, 0.01 mM PLP, various concentrations of substrate, and XometC (1 ug). For L-serine substrate, 10 ug of XometC was used. The mixtures were incubated for 30 min at 30°C, and the reaction was stopped by adding 50% trichloroacetic acid (32.5 μ l). The precipitated protein was removed by centrifugation. The supernatant (100 μ l) was mixed with 0.5 M sodium acetate buffer (200 μ l, pH 5.0) and 0.1% 3-methyl-2-benzothiazolinone hydrazone hydrochloride (80 μ l) and incubated at 50°C for 30 min. The mixture was then cooled to room temperature, and the absorbance at A₃₂₀ was measured. Pyruvic acid and 2- α -butyric acid were used as standards. Enzyme kinetic parameters were calculated using the assays indicated above and a Lineweaver-Burk plot. All

S3. UV-Vis spectroscopy study

measurements were performed in triplicate.

UV-visible spectra were measured at room temperature with the XometC protein (6 mg.ml⁻¹) using a SpectraMax® 190 spectrophotometer (Molecular Devices, USA).

Supporting References

Bruinenberg, P. G., De Roo, G. & Limsowtin, G. (1997). Appl Environ Microbiol 63, 561-566.

Esaki, N. & Soda, K. (1987). Methods Enzymol 143, 459-465.

Uren, J. R. (1987). Methods Enzymol 143, 483-486.

Supporting Table S1. Kinetic parameters of lyase activity of Xomet for substrates

Substrates	Kinetic parameters			
Substrates	Km (mM)	kcat (min ⁻¹)	kcat/Km (min ⁻¹ . mM ⁻¹)	
L-cystathionine	0.27±0.08	73.0±0.7	270	
L-o-succinyl homoserine	1.30±0.06	102.0±0.8	79	
L-homoserine	6.80±0.28	84.3±1.0	12	
L-serine	5.10±0.38	8.5±0.4	2	

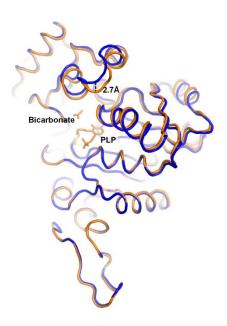
Supporting Table S2. Dihedral angles between pyridine ring and Schiff base linkage of PLP and of the terminal four atoms of Lys210 side-chain in different intermediates

Average dihedral angle (°)		Dihedral angle (°) of each monomer			
PLP (pyridine ring and Schiff base linkage)	Lys210 sidechain (terminal four atoms)	Crystal name	Monomer ID	PLP (pyridine ring and Schiff base linkage)	Lys210 sidechain (terminal four atoms)
Native 34	44	Native	A	40	10
			В	24	77
			С	38	63
			D	33	25
52	5	PGD_EAA_IAI	D	52	5
			В	34	n/a
EAS 25	n/a	EAS_EAA	С	18	n/a
			D	24	n/a
EAA 22	n/a	EAS_EAA	A	22	n/a
		PGD_EAA_IAI	A	21	n/a
46	18	PGD_EAA_IAI	В	43	16
IAI 46	10	PGD_EAA_IAI	С	48	20
	PLP (pyridine ring and Schiff base linkage) 34 52	PLP (pyridine ring and Schiff base linkage) 34 44 52 5 25 n/a 22 n/a	Lys210 Sidechain (terminal four atoms) Crystal name 34	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	PLP Sidechain (pyridine ring and Schiff base linkage)

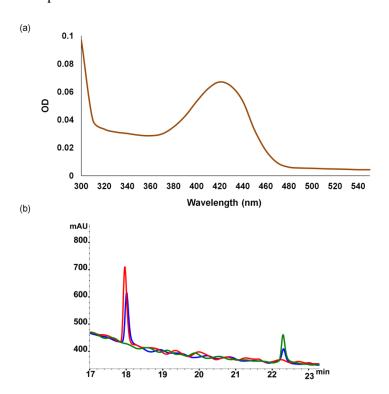
Supporting Table S3. RMSD between 12 protomers in XometC crystals

			Aligned length	21.622
Crystal	Moving molecule A	Fixed molecule B	(a.a)	RMSD
	A (381)		381	0.601
Native	B (381)		381	0.000
(AIXZ)	C (378)		378	0.312
	D (378)		378	0.320
	A (EAA, 383)		381	0.611
EAS_EAA	B (EAS, 383)	Native	381	0.612
(4IY7)	C (EAS, 383)	(monomer B, 381)	381	0.574
	D (EAS, 385)		381	0.606
	A (EAA, 383)		381	0.602
PGD_EAA_IAI	B (IAI, 382)		381	0.588
(4IYO)	C (IAI, 382)		381	0.513
	D (PGD, 386)		381	0.591
Crystal	Moving molecule A	Fixed molecule B		
Crystal	Moving molecule A	Fixed molecule B	Aligned length	RMSD
Crystal	Moving molecule A	Fixed molecule B	Aligned length (a.a)	RMSD
Crystal	Moving molecule A A (381)	Fixed molecule B		RMSD 0.219
Crystal	-	Fixed molecule B	(a.a)	
	A (381)	Fixed molecule B	(a.a)	0.219
Native	A (381) B (381)	Fixed molecule B	(a.a) 381 381	0.219
Native	A (381) B (381) C (378)	Fixed molecule B	(a.a) 381 381 378	0.219 0.611 0.528
Native	A (381) B (381) C (378) D (378)	Fixed molecule B EAS_EAA	(a.a) 381 381 378 378	0.219 0.611 0.528 0.541
Native (AIXZ)	A (381) B (381) C (378) D (378) A (EAA, 383)		(a.a) 381 381 378 378 381	0.219 0.611 0.528 0.541 0.000
Native (AIXZ) EAS_EAA	A (381) B (381) C (378) D (378) A (EAA, 383) B (EAS, 383)	EAS_EAA	(a.a) 381 381 378 378 381 381	0.219 0.611 0.528 0.541 0.000 0.168
Native (AIXZ) EAS_EAA	A (381) B (381) C (378) D (378) A (EAA, 383) B (EAS, 383) C (EAS, 383)	EAS_EAA	(a.a) 381 381 378 378 381 381 381	0.219 0.611 0.528 0.541 0.000 0.168 0.163
Native (AIXZ) EAS_EAA	A (381) B (381) C (378) D (378) A (EAA, 383) B (EAS, 383) C (EAS, 383) D (EAS, 385)	EAS_EAA	(a.a) 381 381 378 378 381 381 381 381	0.219 0.611 0.528 0.541 0.000 0.168 0.163 0.138
Native (AIXZ) EAS_EAA (4IY7)	A (381) B (381) C (378) D (378) A (EAA, 383) B (EAS, 383) C (EAS, 383) D (EAS, 385) A (EAA, 383)	EAS_EAA	(a.a) 381 381 378 378 381 381 381 381	0.219 0.611 0.528 0.541 0.000 0.168 0.163 0.138 0.066
Native (AIXZ) EAS_EAA (4IY7) PGD_EAA_IAI	A (381) B (381) C (378) D (378) A (EAA, 383) B (EAS, 383) C (EAS, 383) D (EAS, 385) A (EAA, 383) B (IAI, 382)	EAS_EAA	(a.a) 381 381 378 378 381 381 381 381	0.219 0.611 0.528 0.541 0.000 0.168 0.163 0.138 0.066 0.180

Numbers in parentheses show the number of amino acids.

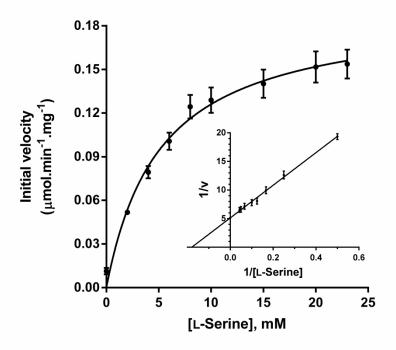


Supporting Figure S1. Superimposed structures of bicarbonate-bound (orange) and unliganded (blue) protomers in native XometC crystals. Bound bicarbonate and PLP-linked lysine residue are shown as stick presentation.

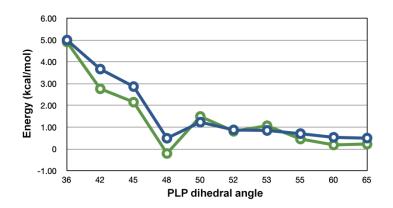


Supporting Figure S2. UV-Vis absorbance spectrum of native XometC and the measurement of CGL and CBL activity for CTT. (a) The absorption spectrum of native XometC showed a major peak centered at 423 nm of the internal aldimine structure. Absorption spectra were measured in the solution containing 6 mg.ml⁻¹ of XometC, 25 mM Tris pH 7.5, and 3 mM β -mercaptoethanol. (b)

Separation of DTNB-derivatives of reaction products of CTT by XometC in reverse-phase HPLC. Red and green lines show the standard equal molar amounts of Cys-TNB and HomoCys-TNB, respectively. Blue line shows DTNB-derivatives of reaction products of CTT. The molar ratio of Cys-TNB (γ -elimination reaction product) to HomoCys-TNB (β -elimination reaction product) is 1.4.



Supporting Figure S3. The initial velocity of L-serine dehydratase activity of XometC for L-serine substrate.



Supporting Figure S4. The calculated activation energy (Ea) and reaction energy (Er) from IA to GD at various fixed dihedral angles. Ea is shown as blue line and Er is shown as green line.

Supporting Figure S5. The chemical structure of cystathionine which is a pseudo-symmetric substrate is shown with a red oval at its pseudo-symmetric center. Two serine molecules are also shown that mimic the half molecule of the pseudo-symmetric cystathionine.