Table S1

Comparison of the kinetic parameters obtained for alternative mechanisms from fits of the data for H_2S generation from cysteine by yCBS[a]

	Ping-pong	**Random-sequential**	**Ordered-sequential**
V_{max1}, U/mg	3.7 ± 1.1	3.73 ± 1.35	3.57 ± 1.0
K_{M1}, mM	3.6 ± 1.7	3.6 ± 1.8	3.4 ± 1.7
V_{max2}, U/mg	9.0 ± 1.3	9.3 ± 1.4	9.1 ± 1.5
K_{M2}, mM	33.0 ± 3.8	32.2 ± 4.4	33.1 ± 4.2
K_d, mM	---	----	$2.3\times 10^{-9} \pm 3.6$
n	2.4 ± 0.5	2.2 ± 0.5	2.4 ± 0.6
R^2	0.995	0.995	0.995

[a] The fits are for the experimental data (open circles) shown in Fig. 3A and the values are reported as mean ±SD.

Table S2

Kinetic parameters obtained for H_2S generation from cysteine and homocysteine for hCBS and yCBS[a]

	hCBS	**yCBS**
V_{max3}, U/mg	18.7 ± 2.6	60 ± 2.4
K_{M3}, mM	3.2 ± 1.3	0.13 ± 0.02
n	0.74 ± 0.1	0.9 ± 0.1
R^2	0.992	0.985

[a] The fits are for the experimental data (open circles) shown in Figs. 3B and 4C for yCBS and hCBS respectively. The values are reported as mean ± SD. For both hCBS and yCBS, reasonable fits were only obtained for the ping-pong mechanism but not sequential (random or ordered binding) mechanism. The values of V_{max1}, V_{max2}, K_{m1}, K_{m2} from Table 1 were used as an input parameters.

Table S3

Comparison of the kinetic parameters obtained for alternative mechanisms for fitting the data for H_2S generation by hCBS from cysteine[a]

	Ping-Pong	**Random-Sequential**	**Ordered-Sequential**
V_{max1}, U/mg	0.46 ± 0.08	0.52 ± 0.04	0.48 ± 0.52
K_{M1}, mM	[b]6.8 ± 1.7	[b]6.8 ± 1.7	[b]6.8 ± 1.7
V_{max2}, U/mg	0.82 ± 0.08	0.88 ± 0.10	0.82 ± 0.14
K_{M2}, mM	27.3 ± 3.73	29.6 ± 10.2	27.9 ± 16.8
K_i	K_{M2}	K_{M2}	K_{M2}
K_d, mM	-	-	0.51 ±14.41
n	1.33 ± 0.25	1.09± 0.18	1.33 ± 0.27
R^2	0.9992	0.9992	0.9996

[a] The fits are for the experimental data (open circle) shown in Fig. 4B and the values are reported as mean ±SD. [b]The value for K_{M1} was used as an input parameter from the HPLC analysis (Table 1).