Supplementary Table 1 Summary of sigma-scaled anomalous peak heights from methionine sulfur atoms and assigned iodine signals after refinement

Spy:Im7 E12I (cryst	al 1)	Spy:Im7 E12I (cryst	al 2)	Spy:Im7 A13I			
Median Methionine S	3.9	Median Methionine S	3.35	Median Methionine S	4		
lodine(s)	4.8	lodine(s)	3.8	lodine(s)	4.1		
			3.7		4.1		
Spy:Im7 E14I		Spy:Im7 Q17I		Spy:Im7 L19I (crystal 1)		Spy:Im7 L19I (crystal 2)	
Median Methionine S	3.5	Median Methionine S	3.15	Median Methionine S	3.5	Median Methionine S	3.1
lodine(s)	3.3	lodine(s)	3.5	lodine(s)	3.3	lodine(s)	3.0
	4.7		3.4		6.1		3.4
	3.4		3.3		3.5		3.4
	4.4						3.0
	3.5						4.6
							3.8
Spy:Im7 E21I (cryst	al 1)	Spy:Im7 E21I (cryst	al 2)	Spy:Im7 V27I		Spy:Im7 A28I	
Median Methionine S	3.95	Median Methionine S	3.6	Median Methionine S	3.7	Median Methionine S	3.5
lodine(s)	4.4	lodine(s)	3.9	lodine(s)	4.4	lodine(s)	3.1
	3.8						4.4
	3.7						3.6
							3.3
							3.2
							4.1
							3.5

Supplementary Table 2 Additional crystallography statistics

	Spy:Im7 A28I	Spy:Im7 A28I	Spy:Im7 V27I	Spy:Im7 V27I
Data collection				
Wavelength (Å)	1.90749	0.88554	1.90749	0.88553
Space group	P4122	P4122	P4122	P4122
Cell dimensions				
a, b, c (Å)	43.08, 43,08, 259.8	43.2, 43.2, 260.6	42.6, 42.6, 257.1	42.6, 42.6, 256.8
α,β,γ (°)	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90
Resolution (Å)	52.97-2.70(2.83-2.70)	30.62-2.31(2.39-2.31)	42.60-2.91(3.08-2.91)	28.53-2.59(2.71-2.59)
R_{merge} (%)	16.8(29.7)	11.8(23.1)	5.1(17.3)	5.0(14)
$I/\sigma(I)$	10.0(8.7)	14.7(9.0)	15.9(6.8)	22.6(10.5)
Completeness (%)	100(100)	100(100)	97.7(94.9)	95.2(87.2)
Redundancy	11.7(11.8)	13.4(13.2)	4.9(4.7)	7.4(7.7)

	Spy:Im7 E12I (crystal 2)	Spy:Im7 E12I (crystal 2)
Data collection		
Wavelength (Å)	1.90749	0.88553
Space group	P4122	P4122
Cell dimensions		
a, b, c (Å)	42.8, 42.8 257.9	42.9, 42.9, 258.8
α,β,γ (°)	90, 90, 90	90, 90, 90
Resolution (Å)	64.48-2.91(3.08-2.91)	29.53-2.59(2.71-2.59)
R_{merge} (%)	6.1(17)	5.5(19.6)
<i>Ι</i> /σ(<i>I</i>)	20.0(10.4)	17.8(6.9)
Completeness (%)	99.8(99.6)	99.7(99.3)
Redundancy	8.2(8.1)	6.0(5.5)

	Spy:Im7 A13I	Spy:Im7 A13I	Spy:Im7 E14I	Spy:Im7 E14I
Data collection				
Wavelength (Å)	1.90748	0.88554	1.90749	0.88553
Space group	P4122	P4122	P4122	P4122
Cell dimensions				
a, b, c (Å)	43.1, 43.1, 259.9	43.1, 43.1, 259.8	42.8, 42.8, 256.7	42.9, 42.9, 257.5
α,β,γ (°)	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90
Resolution (Å)	51.97-2.80(2.95-2.80)	32.47-2.82(2.97-2.82)	64.19-2.91(3.08-2.91)	28.61-2.59(2.71-2.59)
R_{merge} (%)	5.3(11.5)	5.1(11.2)	6.4(26.8)	7.0(40.1)
$I/\sigma(I)$	30.6(18.5)	30.6(18.7)	18.7(6.6)	16.1(4.6)
Completeness (%)	99.9(100)	99.5(98.9)	95.2(89.6)	94.8(88.7)
Redundancy	12.6(12.6)	11.9(11.8)	8.0(8.4)	7.7(8.0)

	Spy:Im7 E12I (crystal 1)	Spy:Im7 E12I (crystal 1)	Spy:Im7 Q17I	Spy:Im7 Q17I
Data collection				
Wavelength (Å)	1.90749	0.88553	1.90748	0.88553
Space group	P4122	P4122	P4122	P4122
Cell dimensions				
a, b, c (Å)	42.7, 42.7, 257.5	42.7, 42.7, 257.8	42.7, 42.7, 257.3	42.7, 42.7, 257.6
α,β,γ (°)	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90
Resolution (Å)	42.71-2.91(3.08-2.91)	29.41-2.59(2.71-2.59)	64.32-2.91(3.08-2.91)	28.47-2.59(2.71-2.59)
R_{merge} (%)	5.1(11.3)	6.2(16.5)	6.7(22.3)	5.7(38.4)
$I/\sigma(I)$	24.2(14.8)	18.8(10.2)	21.0(8.3)	14.4(3.6)
Completeness (%)	90.0(92.7)	88.7(90.6)	94.7(87.7)	93.4(87.0)
Redundancy	7.3(6.8)	7.7(7.1)	8.0(8.6)	5.3(5.4)

Spy:Im7 L19I (crystal 1)	Spy:Im7 L19I (crystal 1)	Spy:Im7 L19I (crystal 2)	Spy:Im7 L19I (crystal 2)
1.90749	0.88553	1.90749	0.88553
P4122	P4122	P4122	P4122
42.9, 42.9, 257.3	42.9, 42.9, 257.9	42.9, 42.9, 257.3	42.9, 42.9, 257.9
90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90
64.32-2.91(3.08-2.91)	28.62-2.59(2.71-2.59)	64.32-2.91(3.08-2.91)	30.38-2.59(2.71-2.59)
7.0(16.9)	7.4(31.0)	7.7(26.1)	10.0(71.8)
19.1(10.2)	17.1(6.2)	16.7(7.1)	12.3(2.7)
100(100)	95.6(96.8)	100(100)	99.9(100)
8.5(8.5)	9.2(8.8)	8.4(8.6)	8.0(8.2)
	Spy:Im7 L191 (crystal 1) 1.90749 P4 ₁ 22 42.9, 42.9, 257.3 90, 90, 90 64.32-2.91(3.08-2.91) 7.0(16.9) 19.1(10.2) 100(100) 8.5(8.5)	Spy:Im7 L191 (crystal 1) Spy:Im7 L191 (crystal 1) 1.90749 0.88553 P4122 P4122 42.9, 42.9, 257.3 42.9, 42.9, 257.9 90, 90, 90 90, 90, 90 64.32-2.91(3.08-2.91) 28.62-2.59(2.71-2.59) 7.0(16.9) 7.4(31.0) 19.1(10.2) 17.1(6.2) 100(100) 95.6(96.8) 8.5(8.5) 9.2(8.8)	Spy:Im7 L191 (crystal 1) Spy:Im7 L191 (crystal 2) 1.90749 0.88553 1.90749 P4122 P4122 P4122 42.9, 42.9, 257.3 42.9, 42.9, 257.9 42.9, 42.9, 257.3 90, 90, 90 90, 90, 90 90, 90, 90 64.32-2.91(3.08-2.91) 28.62-2.59(2.71-2.59) 64.32-2.91(3.08-2.91) 7.0(16.9) 7.4(31.0) 7.7(26.1) 19.1(10.2) 17.1(6.2) 16.7(7.1) 100(100) 95.6(96.8) 1000(100) 8.5(8.5) 9.2(8.8) 8.4(8.6)

	Spy:Im7 E21I (crystal 1)	Spy:Im7 E21I (crystal 1)	Spy:Im7 E21I (crystal 2)	Spy:Im7 E21I (crystal 2)
Data collection				
Wavelength (Å)	1.90749	0.88553	1.90749	0.88553
Space group	P4122	P4122	P4122	P4122
Cell dimensions				
a, b, c (Å)	42.7, 42.7, 256.8	42.7, 42.7, 257.6	42.8, 42.8, 257.6	42.8, 42.8, 258.2
α,β,γ (°)	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90
Resolution (Å)	42.19-2.91(3.08-2.91)	30.28-2.59(2.71-2.59)	64.39-2.91(3.08-2.91)	32.27-2.59(2.71-2.59)
R_{merge} (%)	4.8(7.9)	4.7(15.2)	6.3(13.6)	6.6(15.9)
$I/\sigma(I)$	28.9(19.6)	25.6(12.6)	20.3(11.0)	19.4(10.1)
Completeness (%)	100(100)	99.9(100)	99.8(99.3)	99.9(100)
Redundancy	8.6(8.7)	8.8(8.9)	8.1(7.9)	8.6(8.5)

Supplementary Table 3 Strains and plasmids

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Strain	Genotype or relevant characteristics	Source
SQ765	MG1655 ($F^{-}\lambda^{-}$ ilv G^{-} rfb-50 rph-1), Δ hsdR	19
SQ1805	SQ765, pCDFTrc-ssIm7L53AI54A, pTrc-spy	19
SQ1809	SQ765, pCDFTrc-ssIm7L53AI54A	19
SQ2049	SQ765, pCDFTrc-ssIm7L53AI54A, pTrc-spy 33-130	This study
SQ2050	SQ765, pCDFTrc-ssIm7L53AI54A, pTrc-spy 30-130	This study
SQ2051	SQ765, pCDFTrc-ssIm7L53AI54A, pTrc-spy 27-130	This study
SQ2052	SQ765, pCDFTrc-ssIm7L53AI54A, pTrc-spy 24-130	This study
SQ2053	SQ765, pCDFTrc-ssIm7L53AI54A, pTrc-spy 21-130	This study

Plasmid	Relevant characteristics	Source
pTrc-spy	Spy cloned into pTrc99a derived vector pssTrx	19
pTrc-spy 33-130	Spy fragment (33-130) with native signal sequence cloned into pssTrx	This study
pTrc-spy 30-130	Spy fragment (30-130) with native signal sequence cloned into pssTrx	This study
pTrc-spy 27-130	Spy fragment (27-130) with native signal sequence cloned into pssTrx	This study
pTrc-spy 24-130	Spy fragment (24-130) with native signal sequence cloned into pssTrx	This study
pTrc-spy 21-130	Spy fragment (21-130) with native signal sequence cloned into pssTrx	This study