Supplementary Information

Table S1: Crystallographic data statistics for the 3-wavelength Se-methionine MinDΔ10-D40A-MgATP complex.

Data Statistics	Inflection	Peak	High energy remote
Wavelength (Å)	0.97937	0.97879	0.91837
Space group	$P2_12_12_1$	$P2_12_12_1$	$P2_12_12_1$
Unit cell	a = 83.9Å	a = 84.0Å	a = 83.9Å
	b = 86.5 Å	b = 86.5 Å	b = 86.4 Å
	c = 111.4 Å	c = 111.4 Å	c = 111.3 Å
	α = β = γ = 90.0°	α = β = γ = 90.0°	α = β = γ = 90.0°
Resolution Limits, Å	100-2.5	100-2.6	100-2.5
No. of unique reflections	28505	25301	28310
Completeness, % (all data)	98.6 (96.4)	98.8 (97.0)	98.5 (96.4)
Redundancy	6.9 (5.8)	7.0 (6.3)	7.0 (6.4)
$I/\sigma_{(I)}$	13.9 (1.6)	13.8 (2.0)	14.9 (1.9)
R_{merge}	0.07 (0.67)	0.08 (0.60)	0.07 (0.61)

Table S2. Summary of the analysis of MinD Mutations

Residue	MinC Activation[1]	Rescue by MinE[2]	Interaction with MinE (B2H)[3]	Self-Dimerization (B2H[4]
G42D	0	N/A	0	++
L43D	0	N/A	0	++
R44G	0	N/A	+++++	ND
D47R	0	N/A	0	+
L48K	+++++	+	0	
G51D	+++++	+++++		
C52A	+++++	+++++		
C52R	+++++	+++++		
E53A	+++++	0	ND	
E53K	+++++	0	0	
R54E	+++++	+++++		
R55E	+++++	+++	+++++	
V56E	+	N/A	0	+++++
V57E	+	N/A	+++++	
Y58D	+	N/A	+	+++++
D59R	0	N/A	0	0
V61E	+	N/A	0	+++++
N62K	++	N/A	+	+++++
Q65R	+++++	+++	+++++	
D67R	+++++	++	++	
Q72R	+++++	+++++		
I75D	+++++	+++++		
K76D	+++++	+++++		
K78A	+++++	++++		
R79D	+++++	+++++		
Q90A	++	N/A	+++++	
T91K	0	N/A	+++++	
R92A	0	N/A	+++++	
D93R	+++++	+++++		
K94D	0	N/A	++	+++++
D95R	+++++	+++++		
T98D	+++++	++++		
R99D	+++++	+++++		
E100K	+++++	+++++		
K104E	+++++	++++		
E146K	0	N/A	0	0/+
V147E	+++++	0	0	
S148E	0	N/A	0	+++
V150E	0	N/A	0	0

R151A	+	N/A	+++++	
D154A	+	N/A	+	+++++
R155E	+	N/A	0	+++
L157D	+	N/A	0	+
G158R	+	N/A	+++++	
I159D	++++	+++++		
A161R	++	N/A	+++++	
S162K	+++++	++++	++++	
K163D	+++++	+++++	+++++	
A167K	+++++	++++		
E168A	+++++	++++		
N169R	+++++	+++		
G170R	+++++	+++++		
E172K	+++++	+++++		
P173R	0	N/A	+++++	
K175D	+++++	+++++		
E176K	+++++	+++++		
R187A	+++++	+++++		
V188E	+++	N/A	0	0
R190A	+++++	+++++		
G191E	+++++	+++++		
G191R	+++++	+++++		
D192Y	+++++	0	0	
M193L	+++++	+	+	
L194D	+++++	+	0	
S195R	+++++	+++++		
E197K	+++++	+++++		
D198R	+++++	0	+	
E201A	+++++	+++++		
I202D	+++++	0	0	
R204A	+++++	+++++		
K206E	+++++	+++++		
D214A	+++++	+++++		
Q215E	+++++	+++		
L218E	++++	++	0	
R219A	+++++	+++++		
S221A	+++++	+++++		
S221R	+++++	+	0	
N222A	+++++	0	0	
N222E	+++++	+		
N222R	+++++	+		
G224C	+++++	0	0	
E225K	+++++	+++++		
L229K	+++++	+++++		

N232A	+++++	++++		
I246D	+++++	+++++		
F253D	+++++	+++++		

Note

For all assays the tests were scored qualitatively. N/A, not applicable.

[1] MinC activation was scored as follows: 0 = no activation, cells grow fine; +++++ = no growth; in cases where there was some growth it is indicated by + to ++++

[2] Rescue from MinC/MinD killing. 0 = no rescue; +++++ = complete rescue; partial rescue was scored from + to ++++.

[3] Interaction between MinD and MinE assayed by growth with X-gal. 0 = no color development; +++++ = dark blue; lighter colors were scored from + to ++++.

[4] MinD self-interaction assayed by growth with X-gal. 0 = no color development; +++++ = dark blue; lighter colors were scored from + to ++++.

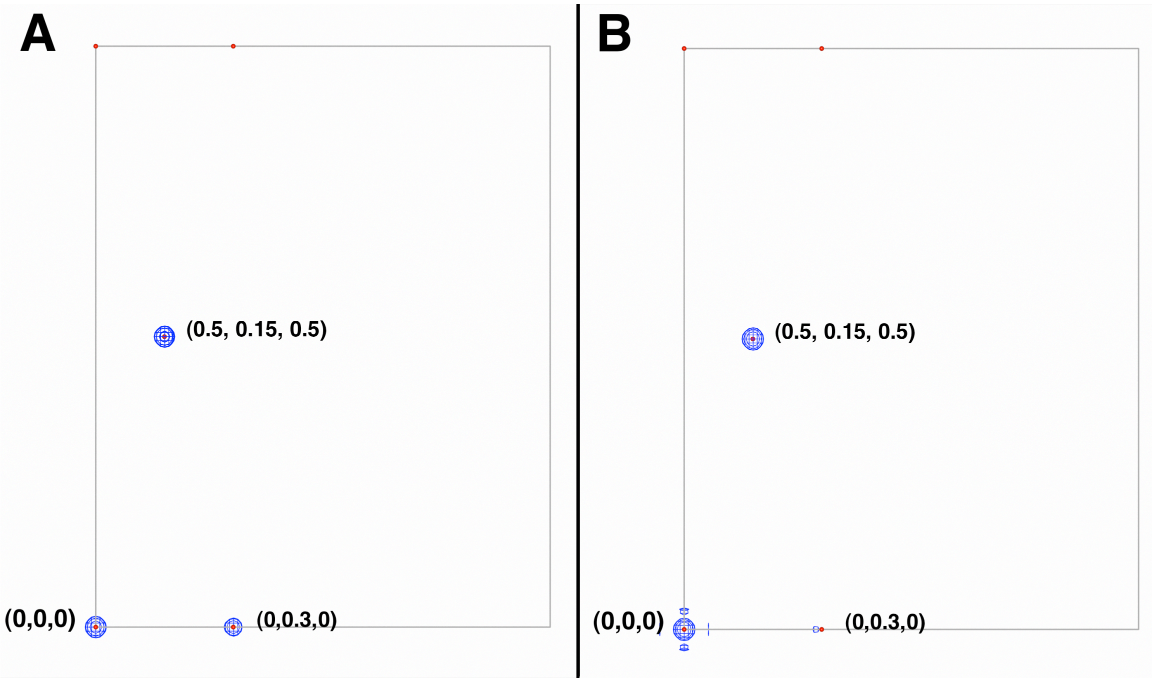

Figure S1: Patterson map oriented along the b-c face. A) Uncorrected data rendered at 10 σ demonstrating the translational symmetry peaks at (0.5, 0.15, 0.5) for the NCS related molecule and at (0, 0.3, 0) due to the LTD translated molecule. B) Patterson map rendered at 5 σ after correction of the data indicating the absence of the LTD peak at (0,0.3,0). The figure was generated using CCP4MG.

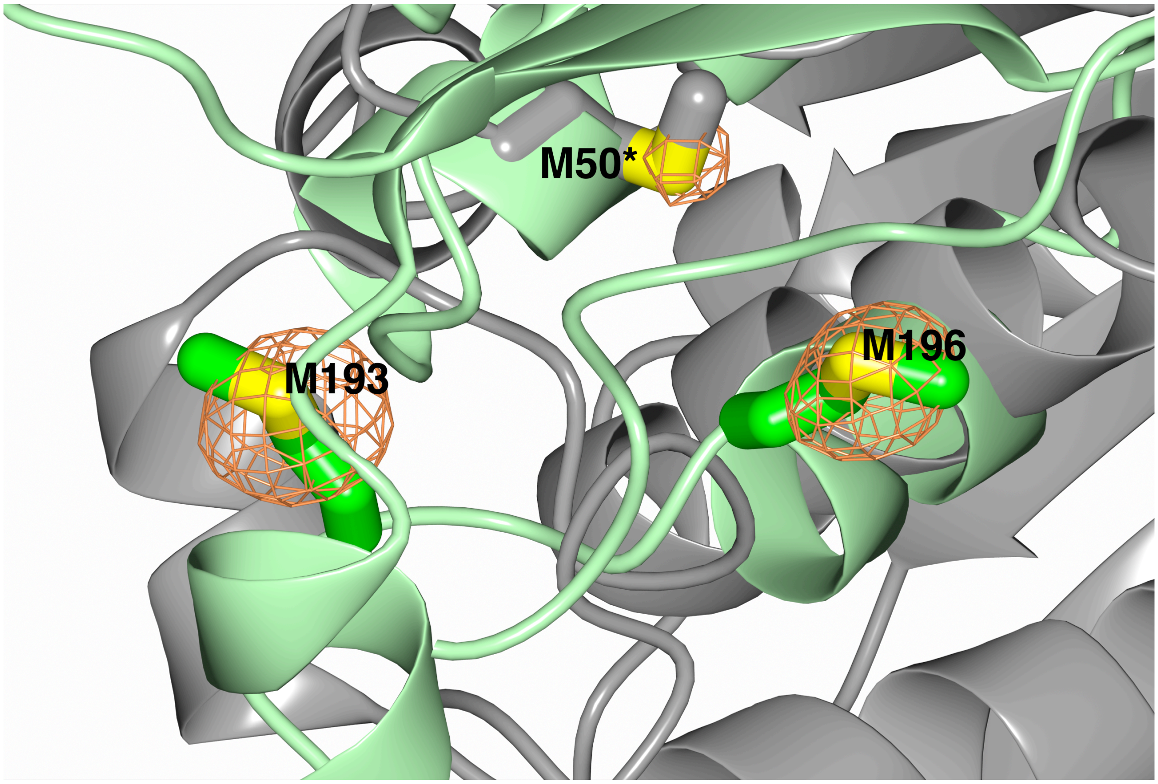

Figure S2: Anomalous peaks for selenium atoms illustrate the presence of lattice translation defect (LTD) in the uncorrected data for the Se-methionine labeled MinDΔ10-D40A -Mg-ATP complex. The anomalous map is rendered at 5 σ. Methionine residues 193 and 196 in the final structure are labeled and rendered in green, while methionine 50 from the opposite monomer of the LTD translated dimmer is labeled as M50* and rendered in grey. The anomalous peak height for M50* is consistent with the reduced occupancy of the LTD dimmer.

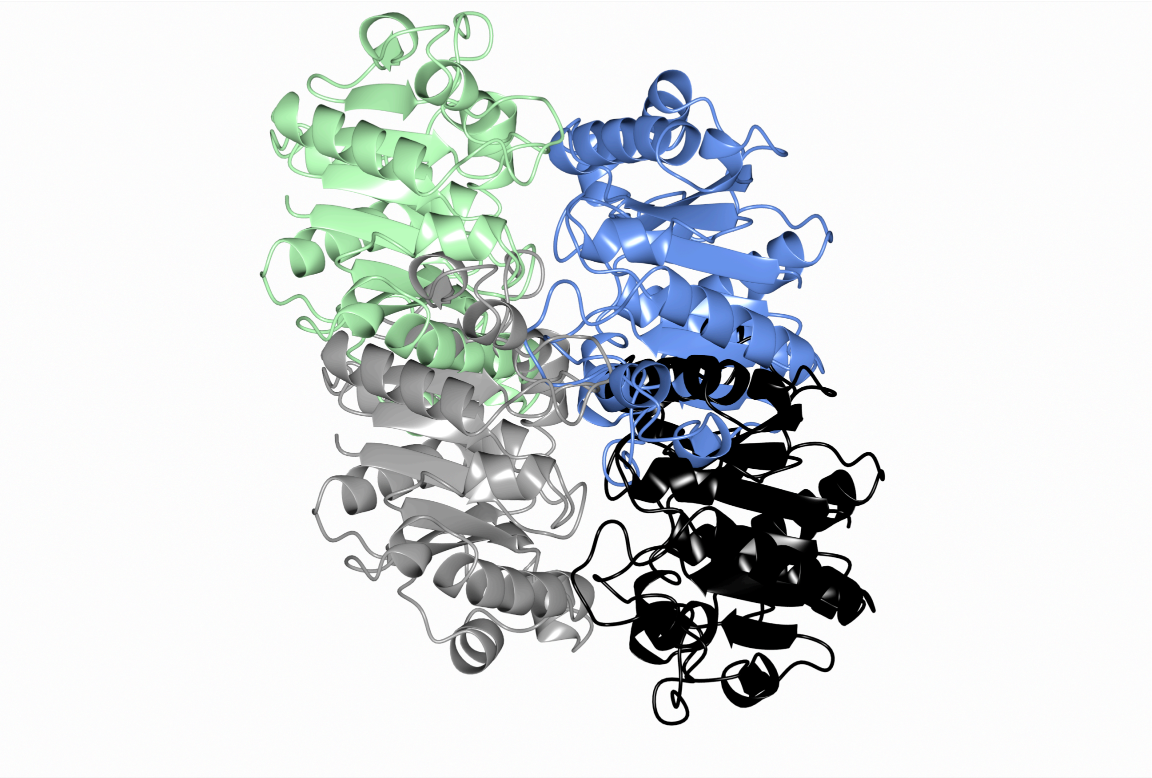

Figure S3: Relationship of the LTD related molecules in the ASU. The two minD dimers, related by a translation along b of 26 Å are illustrated. The molecules of the translated dimmer are rendered in grey and black, respectively, while the corresponding molecules in the final structure are rendered in green and blue.