

PRL3 pseudophosphatase activity is necessary and sufficient to promote metastatic growth

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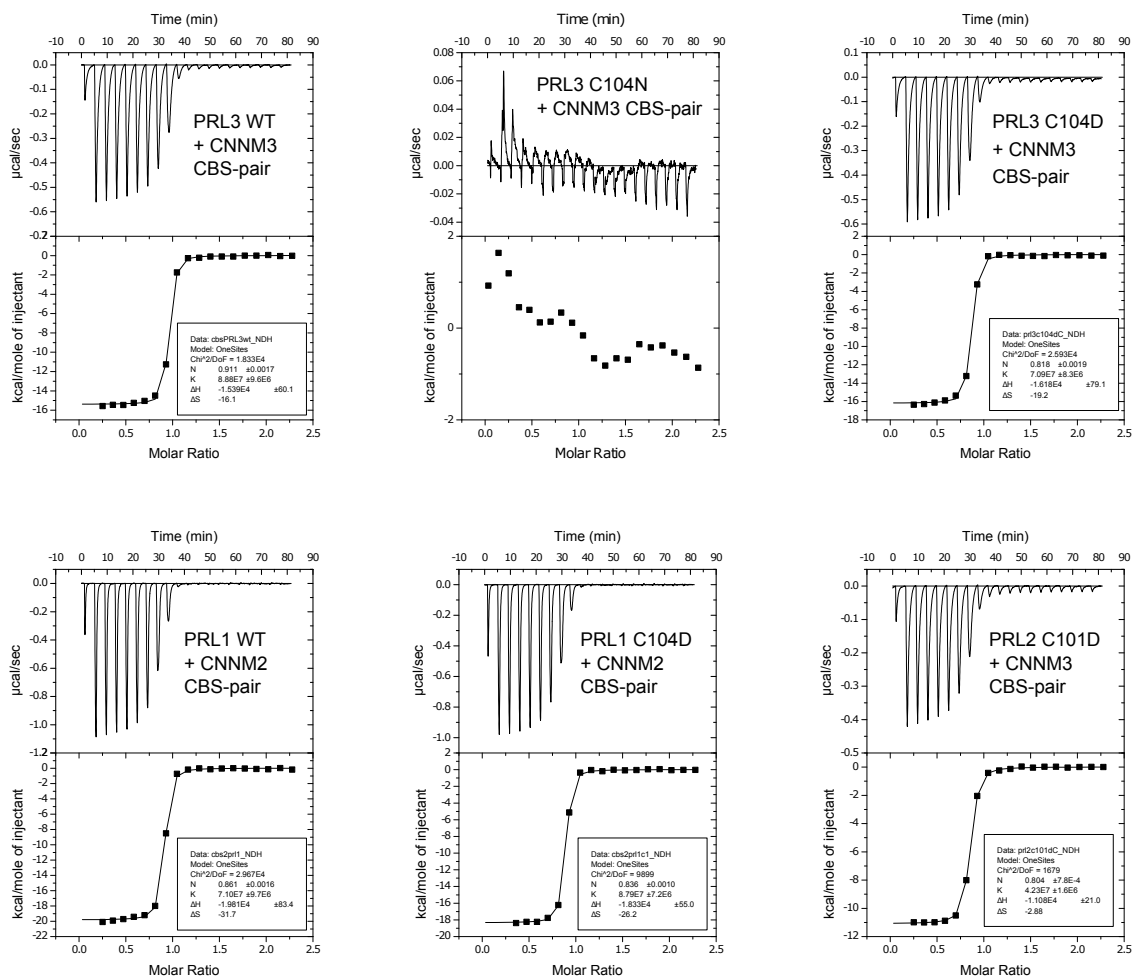
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Table S1: Data Collection and Refinement Statistics

	PRL2 C101D/CBS	PRL1 C104D/CBS
Data collection		
Space group	I222	I222
Cell dimensions		
<i>a</i> , <i>b</i> , <i>c</i> (Å)	56.86, 124.54, 153.41	52.14, 127.94, 152.16
Resolution (Å)	50-2.90 (2.95-2.90)	50-2.75 (2.80-2.75)
<i>R</i> _{sym}	0.074 (0.592)	0.069 (0.549)
<i>I</i> / σ <i>I</i>	13.0 (1.2)	24.6 (1.6)
Completeness (%)	93.7 (93.2)	99.8 (99.1)
Redundancy	2.9 (2.9)	5.0 (5.1)
Refinement		
Resolution (Å)	24.2 - 2.88	41.1 - 2.76
No. reflections	11721	12756
<i>R</i> _{work} / <i>R</i> _{free}	0.238/0.295	0.240/0.281
No. atoms		
Protein	2237	2306
Water	4	9
Nucleotide		
<i>B</i> -factors		
Protein	106.6	88.7
Water	79.4	73.0
Nucleotide		
R.m.s deviations		
Bond lengths (Å)	0.005	0.006
Bond angles (°)	0.75	0.82
Ramachandran statistics (%)		
Most favored regions	92.7	96.3
Additional allowed regions	7.3	3.4
Disallowed regions	0.0	0.3

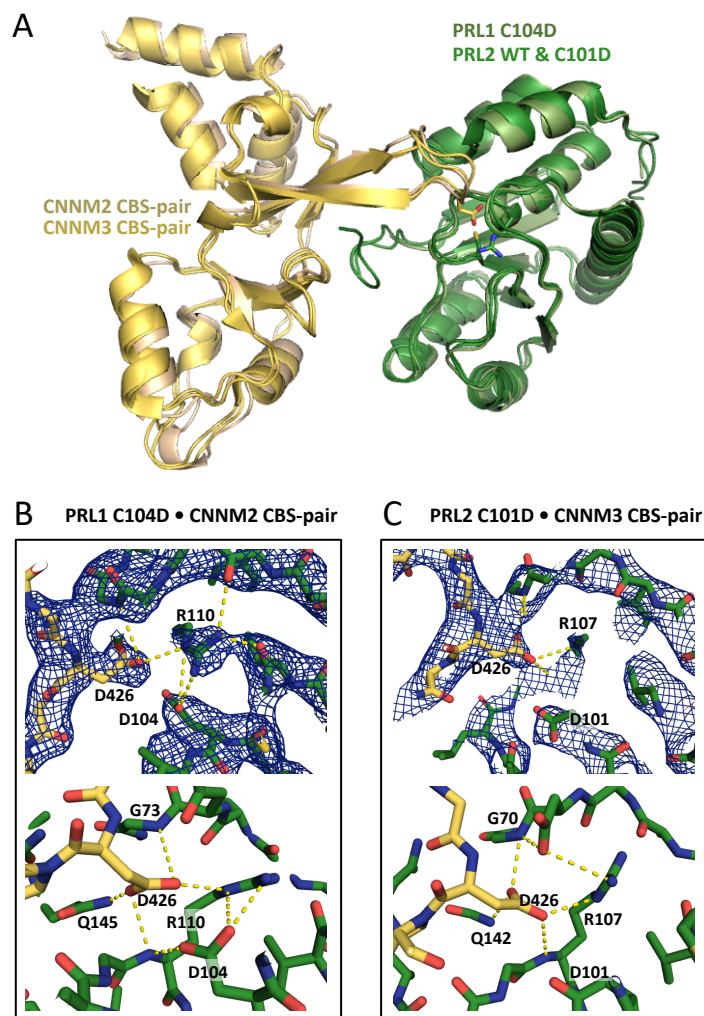
¹Highest resolution shell is shown in parentheses.

Supplemental Material



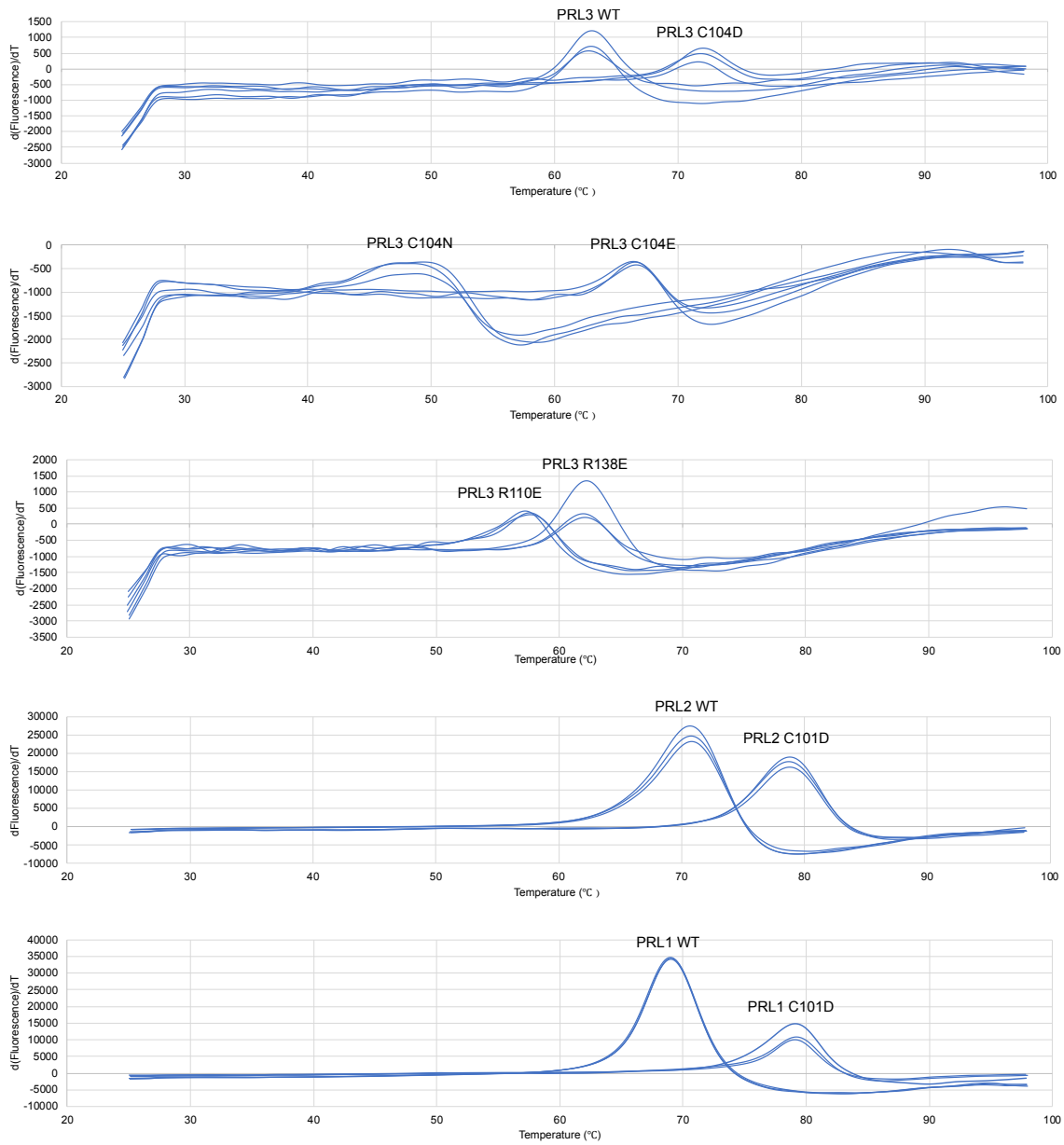
Supplemental Figure S1. Isothermal titration curves.

ITC thermograms of PRL binding to CNNM CBS-pair GST fusion proteins.



Supplemental Figure S2. Comparison of mutant and wild-type structures. (A) Overlay of three crystal structures: PRL1 C104D with CNNM2 CBS-pair domain, PRL2 C101D with CNNM3 CBS-pair domain, and wild-type PRL2 with CNNM3 CBS-pair domain. Key residues for the interaction, CNNM aspartic acid 426, PRL2 cysteine 101 and arginine 107, are shown in stick form. (B & C) Electron density maps (top) and polar contacts (bottom) in the PRL1 C104D and PRL2 C104D complexes.

Supplemental Material



Supplemental Figure S3. Differential scanning fluorimetry measurements of PRL stability.