

Supplementary information, Table S1. Data collection and refinement statistics (molecular replacement)

	NAMPT-NAT
Data collection	
Space group	P212121
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	86.2, 93.6, 242.6
α , β , γ (°)	90, 90, 90
Resolution (Å)	49.6-2.20 (2.28-2.20)
<i>R</i> _{sym} or <i>R</i> _{merge} (%)	14.2 (116.4)
<i>I</i> / σ <i>I</i>	19.8 (2.6)
Completeness (%)	88.6 (78.6)
Redundancy	10.2 (8.4)
Refinement	
Resolution (Å)	49.6-2.20
No. reflections	88,420
<i>R</i> _{work} / <i>R</i> _{free} (%)	17.7 / 23.5
No. atoms	15,522
Protein	14,808
Ligand/ion	118
Water	596
<i>B</i> -factors	34.7
Protein	34.6
Ligand/ion	47.9
Water	34.0
R.m.s. deviations	
Bond lengths (Å)	0.003
Bond angles (°)	0.60

Values in parentheses are for the highest-resolution shell