Table S1: UNC119 crystallographic data and refinement statistics

Data		
Crystal	HR3066a[a]	Au10pe
Space Group	$P2_12_12_1$	$P2_12_12_1$
Unit Cell Dimensions	a=77.89, b= 79.56, c=189.72	a=78.55, b=79.71 , c=189.59
Resolution (Å)	50.0 – 1.95	30.0 – 2.00
Resolution (Å) (high-resolution shell)	(2.02 – 1.95)	(2.07 – 2.00)
# Reflections measured	1,169,802	1,252,665
# Unique reflections	166,290[a]	82,342
Redundancy	7.0	15.2
Completeness (%)	99.6 (100)	100 (100)
$<I/\sigma(I)>$	26 (2.9)	11 (2.5)
Mosaicity (^{o})	0.37	1.1
Rsym[b]	0.088 (0.537)	0.116 (0.701)
Refinement		
Resolution (Å)	40.51 – 1.95	29.37 – 1.99
Resolution (Å) – (high-resolution shell)	(1.97 – 1.95)	(2.04 – 1.99)
# Reflections used for refinement	165,606[a]	78,089
# Reflections in Rfree set (%)	8,332 (5.0)	4,139 (5.3)
R[c]	0.191 (0.247)	0.200 (0.226)
Rfree[d]	0.214 (0.251)	0.250 (0.276)
RMSD: bonds (Å) / angles (°)	0.005 / 1.3	0.012 / 1.304
<B> (Å^2): Tα peptide residues/ # atoms	N/A	41 / 268
<B> (Å^2): UNC119 only / # atoms	33 / 8,265	29 / 8,299
<B> (Å^2): water molecules / # water	41 / 803	39 / 793
ϕ/ψ most favored (%)	99	97

Values in parenthesis refer to data in the high resolution shell.

[a] Friedel pairs were used in phasing and refining HR3066a.

[b] Rsym = $\Sigma|I-<I>|/\Sigma I$ where I is the intensity of an individual measurement and <I> is the corresponding mean value.

[c] R = $\Sigma||Fo|-|Fc||/\Sigma|Fo|$, where $|Fo|$ is the observed and $|Fc|$ the calculated structure factor amplitude.

[d] Rfree is the same as R calculated with a randomly selected test set of 5% (HR3066a[a]) or 5.3% (Au10pe) reflections that were never used in refinement calculations.