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Supporting information for article:

Similarities in the structure of the transcriptional repressor AmtR in two different space groups suggest a model for the interaction with GlnK

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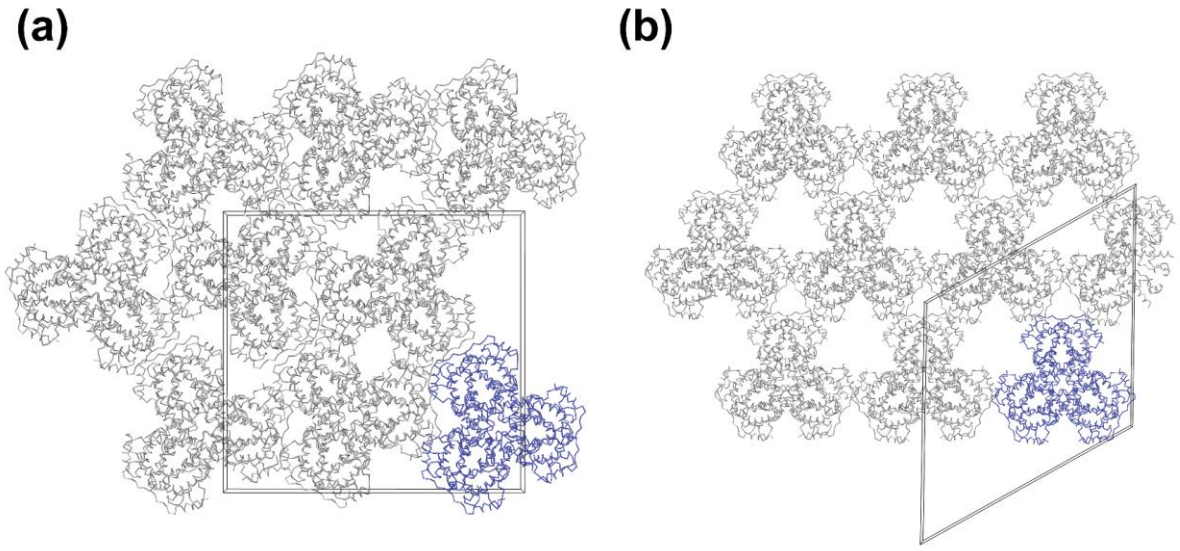

Figure S1 Crystal packing in (a) $AmtR_{orth}$ (solvent content 41.2 %) and (b) $AmtR_{tri}$ (solvent content 49.1 %). In both cases,the packing is viewed in direction of the *c*-axis (hexagonal setting in $AmtR_{tri}$). In this direction, three AmtR dimers assemble such that either a non-crystallographic ($AmtR_{orth}$) or a crystallographic ($AmtR_{tri}$) contiguous 3_1 screw axis symmetry is formed. A prototypical trimer of AmtR dimers is highlighted in blue in both panels.

Table S1 Unit cell and asymmetric unit in $AmtR_{orth}$ and 5DY1 ($AmtR_{tri}$)

	Space group	*a* (Å)	*b* (Å)	*c* (Å)	α (°)	β (°)	γ (°)	Solvent (%)	Z_{asu}
$AmtR_{orth}$	$P2_12_12$	149.8	160.6	51.4	90	90	90	41.2	6
$AmtR_{tri}$	H3	160.5	160.5	52.4	90	90	120	49.1	2