

**Publication****Alternating-access mechanism in conformationally asymmetric trimers of the betaine transporter BetP****JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 3893687**Author(s)** Perez, Camilo; Koshy, Caroline; Yildiz, Ozkan; Ziegler, Christine**Author(s) at UniBasel** [Perez, Camilo](#) ;**Year** 2012**Title** Alternating-access mechanism in conformationally asymmetric trimers of the betaine transporter BetP**Journal** Nature**Volume** 490**Number** 7418**Pages / Article-Number** 126-30**Mesh terms** Apoproteins, metabolism; Bacterial Proteins, metabolism; Betaine, metabolism; Binding Sites; Biological Transport; Carrier Proteins, metabolism; Corynebacterium glutamicum, chemistry; Crystallography, X-Ray; Cytoplasm, metabolism; GABA Plasma Membrane Transport Proteins; Models, Molecular; Periplasm, metabolism; Plasma Membrane Neurotransmitter Transport Proteins, chemistry; Protein Conformation; Protein Folding; Protein Multimerization; Sodium, metabolism; Structure-Activity Relationship; Symporters

Betaine and Na(+) symport has been extensively studied in the osmotically regulated transporter BetP from *Corynebacterium glutamicum*, a member of the betaine/choline/carnitine transporter family, which shares the conserved LeuT-like fold of two inverted structural repeats. BetP adjusts its transport activity by sensing the cytoplasmic K(+) concentration as a measure for hyperosmotic stress via the osmosensing carboxy-terminal domain. BetP needs to be in a trimeric state for communication between individual protomers through several intratrimeric interaction sites. Recently, crystal structures of inward-facing BetP trimers have contributed to our understanding of activity regulation on a molecular level. Here we report new crystal structures, which reveal two conformationally asymmetric BetP trimers, capturing among them three distinct transport states. We observe a total of four new conformations at once: an outward-open apo and an outward-occluded apo state, and two closed transition states—one in complex with betaine and one substrate-free. On the basis of these new structures, we identified local and global conformational changes in BetP that underlie the molecular transport mechanism, which partially resemble structural changes observed in other sodium-coupled LeuT-like fold transporters, but show differences we attribute to the osmolytic nature of betaine, the exclusive substrate specificity and the regulatory properties of BetP.

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