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Analysis of the quality of crystallographic data and the limitations of structural models

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Crystal structures provide visual models of biological macromolecules, which are widely used to interpret data from functional studies and generate new mechanistic hypotheses. Because the quality of the collected x-ray diffraction data directly affects the reliability of the structural model, it is essential that the limitations of the models are carefully taken into account when making interpretations. Here we use the available crystal structures of members of the glutamate transporter family to illustrate the importance of inspecting the data that underlie the structural models. Crystal structures of glutamate transporters in multiple different conformations have been solved, but most structures were determined at relatively low resolution, with deposited models based on crystallographic data of moderate quality. We use these examples to demonstrate the extent to which mechanistic interpretations can be made safely.

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Abbreviations used: EAAT, excitatory amino acid transporter; EPR, electron paramagnetic resonance; IFC, inward-facing conformation; iOFC, intermediate outward-facing conformation; OFC, outward-facing conformation; TBOA, 0.1-3-benzoyloxyaspartate; TMS, transmembrane helical segment.

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Viewpoint

Introduction

X-ray crystallography is an experimental technique that is used to determine three-dimensional structures of (biological) macromolecules crystallized in an orderly manner. As crystal structures provide visual models, which are typically used to interpret experimental data and generate new mechanistic hypotheses, it is essential that the limitations of crystal structures be carefully taken into account when making interpretations. The quality of the collected x-ray diffraction data are crucial for building a correct structural model. Without evaluation of the underlying crystallographic data, the use of deposited models could lead to erroneous conclusions of mechanistic features of the proteins.

Here we focus on the progress in crystallographic studies of the glutamate transporter family to illustrate to what extent mechanistic features can be reliably extracted from the crystallographic models. Glutamate transporters are an important family of secondary active transporters. In mammals, they play a crucial role in preventing neurotoxicity, by effects of uptake of the neurotransmitter glutamate from the synaptic cleft. More than 20 structures of glutamate transporters in different conformational states have been determined, most of which have been obtained at medium resolution, producing models of rather moderate quality, with the inherent risk of over-interpretation. In this viewpoint, we inspect the crystallographic data and show that the use of the derived models could lead to erroneous conclusions of mechanistic features of the proteins. We underscore the importance of obtaining high-resolution and high-quality crystal structures for understanding the transport mechanism in detail.

Glutamate transporters

Glutamate transporters belong to a large family of secondary active transporters that catalyze uptake of acidic amino acids, neutral amino acids, or dicarboxylic acids in prokaryotes and eukaryotes (Slotboom et al., 1999; Vandenberg and Ryan, 2013; Grewe et al., 2014). Mammalian glutamate transporters, also called excitatory amino acid transporters (EAATs), play a key role in neuronal signaling by clearing excess neurotransmitter glutamate from the presynaptic cleft. EAATs couple glutamate uptake to symport of three sodium ions and one proton and to antiport of one potassium ion (Zerangue and Kavanaugh, 1996; Fig. 1). In Bacteria and Archaea, glutamate transporter homologues catalyze uptake glutamate and aspartate as nutrients. These proteins are either proton- or sodium ion–dependent transporters and do not require potassium ions for transport (Tolner et al., 1995; Gaillard et al., 1996; Slotboom et al., 1999; Ryan et al., 2009).

Until recently, crystal structures were available only for glutamate transporter homologues from the Archaea Pyrococcus horikoshii (GltPh) and Thermococcus kodakarensis (GltTk; Table 1; Yernool et al., 2004; Boudker et al., 2007; Reyes et al., 2009, 2013; Verdon and Boudker, 2012; Jensen et al., 2013; Verdon et al., 2014; Akyuz et al., 2015; Guskov et al., 2016). Both GltPh and GltTk cotransport aspartate with three sodium ions and, in contrast to human EAATs, use neither proton nor potassium gradients (Boudker et al., 2007; Groeneveld...
and Slotboom, 2010; Guskov et al., 2016). GltPh and GltTk share high sequence identity with each other (77%) and with EAATs (∼36%), with even higher conservation of amino acid residues involved in substrate binding (Boudker et al., 2007; Jensen et al., 2013; Silverstein et al., 2015). Structural studies of the archaeal GltPh and GltTk proteins have provided major insight into the transport mechanism of glutamate transporters. Recently, crystal structures of human EAAT1 have also been solved, revealing the architecture of the eukaryotic homologue (Canul-Tec et al., 2017).

Crystal structures overview
Glutamate transporters are homotrimeric proteins (Yernool et al., 2003, 2004; Gendreau et al., 2004; Canul-Tec et al., 2017), which had already been established for several family members before the first crystal structure was solved. Each subunit of the trimer has a complex topology of eight transmembrane helical segments (TMS1–8) and two helical hairpins (HP1 and HP2) that form two domains: a scaffold domain (TMS1, TMS2, TMS4abc, and TMS5), which is involved in trimerization, and a transport domain (TMS3, TMS6, HP1, TMS7ab, HP2, and TMS8), which contains the substrate and cation-binding sites (Fig. 2). Structural differences between the archaeal transporters and the human EAAT1 include deletions and insertions, as well as division of TMS1 into two and TMS8 into three separate helices, TMS1ab and TMS8abc, respectively.

Derivation of a mechanistic model of transport of the archaeal transporters has greatly benefited from crystal structures in different states, such as apo, substrate-bound, occluded binding site, and exposed binding site. Alternative access of the substrate-binding site to either side of the membrane is achieved via an elevator mechanism (for a review see Drew and Boudker, 2016; Ji et al., 2016; Ryan and Vandenberg, 2016), in which the transport domains move up and down relative to the trimerization domains, which are anchored in the membrane. The GltPh transporter has been crystallized with the transport domain in the outward-facing conformation (OFC) and the inward-facing conformation (IFC), with the substrate-binding site located close to the extracellular or cytoplasmic space, respectively (Table 1 and Fig. 2, D and E; Yernool et al., 2004; Boudker et al., 2007; Reyes et al., 2009, 2013; Verdon and Boudker, 2012; Verdon et al., 2014; Akyuz et al., 2015). Comparison of the GltPh structures in the OFC and IFC showed that both scaffold and transport domains are relatively rigid bodies that stay largely unchanged during the elevator-like movement (Reyes et al., 2009). Transfer of the transport domain is made possible by hinge movements in the short loops 2–3 and 5–6. As a result, the transport domain undergoes a transition of 16–18 Å toward the cytoplasm, accompanied by a rotation of ∼37°.

Amino acid residues implicated in substrate and ion binding are highly conserved among glutamate transporters (Fig. 2 C; Boudker et al., 2007; Jensen et al., 2013). The substrate-binding site is formed by tips of HP1 and HP2, the unwound part of TMS7, and the central part of TMS8. In the OFC, helical hairpin HP2 occludes the bound substrate from the solvent in GltPh, GltTk, and EAAT1. The IFC structures of GltPh showed a highly similar occluded conformation of the substrate-binding site. In this occluded state, the tips of structurally related HP1 and HP2 seal off the binding site.
| Glu/EAA T1a | Ligand | Ions | X-link | State | PDB ID | Resolution | Space group | Completeness | Clash score | $R_{work}$/ $R_{free}$ | Comments, new features | Mutations | Reference |
|-------------|--------|------|--------|-------|--------|------------|-------------|--------------|--------------|---------------|--------------------------|-----------|-----------|
| Ph          | Not assigned | OFC | occluded | 1XFH | 3.5  | P 61 | 97.1 (n.r.) | 21  | 29.0/50.9 | Homotramer, bowl shape, overall fold | 7H mutations: D37H, K40H, K125H, K128H, K223H, K264H, E368H | Yernool et al., 2004 |
| Ph          | 1-Asp | OFC | occluded | 2NWL | 2.96 | P 61 | 69.5 (8.8)  | 5  | 23.6/26.5 | Substrate-binding site | 7H mutations | Bondler et al., 2007 |
| Ph          | 1-Asp | T11, T12 | OFC | occluded | 2NWX | 3.29 | P 61 | 69.2 (12.1) | 15 | 26.3/28.6 | Na1 and Na2 binding sites | 7H mutations | Bondler et al., 2007 |
| Ph          | TBOA | OFC | open | 2NWW | 3.2  | P 61 | 74.8 (15.5) | 8  | 24.1/26.0 | Open conformation of HP2; modeling of TBOA binding | 7H mutations | Bondler et al., 2007 |
| Ph          | 1-Asp | Na1, Na2, Hg | IFC | occluded | 3KBC | 3.51 | C2 2 2 | 97.2 (84.5) | 10 | 26.7/27.0 | IFC, elevator mechanism | 7H mutations, K55C, C321A, A364C | Reyes et al., 2009 |
| Ph          | 1-Asp | Na1, Na2, Hg | IFC | occluded | 3V8F | 3.8 | C1 2 1 | 99.5 (97.6) | 26 | 24.5/25.5 | IFC, different mutant | 7H mutations, V216C, C321A, M385C | Verdon and Bondler, 2012 |
| Ph          | 1-Asp | Na1, Na2, Hg | iOFC | occluded | 3V8G | 4.66 | C1 2 1 | 73.1 (11.2) | 14 | 25.5/29.4 | Intermediate OFC | 7H mutations, V198C, C321A, A380C | Verdon and Bondler, 2012 |
| Ph          | 1-Asp | Na1, Na2, Hg | OFC | occluded | 4IZM | 4.5  | P 61 | 99.7 (99.1) | 12 | 25.0/29.9 |  | 7H mutations, L66C, S300C, C321A | Verdon et al., 2014 |
| Ph          | Tk | ORC | occluded | 4KY0 | 3.0  | P 3 2 1 | 99.8 (99.8) | 13 | 21.2/26.6 | OFC apo protein without Na | 7H mutations, K55C, C321A, A364C, E418T | Jensen et al., 2013 |
| Ph          | Tk | ORC | occluded | 4P6H | 4.08 | C2 2 2 | 67.4 (64.4) | 39 | 25.8/29.6 | IFC apo protein with Ti | 7H mutations, K55C, C321A, A364C, E418T | Verdon et al., 2014 |
| Ph          | Tk | ORC | occluded | 4P1A | 3.75 | C2 2 2 | 99.7 (99.7) | 24 | 23.0/25.7 | New cation site | 7H mutations, K55C, C321A, A364C | Verdon et al., 2014 |
| Ph          | Tk | ORC | occluded | 4P19 | 3.25 | C2 2 2 | 99.1 (91.9) | 23 | 22.2/25.8 | IFC apo protein without Na | 7H mutations, K55C, C321A, A364C | Verdon et al., 2014 |
| Ph          | Tk | ORC | occluded | 4P3 | 3.5  | C2 2 2 | 95.5 (93.2) | 12 | 26.3/27.8 |  | 7H mutations, K55C, C321A, A364C | Verdon et al., 2014 |
| Ph          | Tk | ORC | occluded | 4YE | 4.0  | P 1 2 1 | 70.3 (9.3)  | 13 | 24.9/26.6 |  | 7H mutations, R397A | Verdon et al., 2014 |
| Ph          | Tk | ORC | occluded, tip open | 4OYF | 3.41 | P 3 1 | 88.7 (12.2) | 26 | 28.4/29.3 | OFC apo protein with Na | 7H mutations, R397A | Verdon et al., 2014 |
| Ph          | Tk | ORC | occluded | 4OYG/5CFY | 3.5 | P 3 1 | 97.1 (93.7) | 24 | 24.9/29.4 |  | 7H mutations, R397A | Verdon et al., 2014 |
| Ph          | Tk | ORC | occluded | 4X2S | 4.21 | P 6 2 2 | 83.2 (18.3) | 10 | 27.8/31.4 | IFC occluded, locked and unlocked | 7H mutations, R276S, C321A, M395R, E418T | Akyuz et al., 2015 |
| Tk          | Tk | ORC | occluded | 5DWY | 2.7  | P 3 2 1 | 79.0 (17.9) | 5  | 19.8/23.7 | Improved 4KY0 | 7H mutations, L66C, S300C, C321A | Guskov et al., 2016 |
Table 1. Summary of the available crystal structures of the glutamate transporter homologues (Continued)

| Glt/EAAT1 | Ligand | Ions | X-link | State | PDB ID | Resolution | Space group | Completeness | Clash score | Rwork/Rfree | Comments, new features | Mutations | Reference |
|-----------|--------|------|--------|-------|--------|------------|-------------|--------------|-------------|-------------|-----------------------|-----------|-----------|
| Hs        | L-Asp, UCPh101 | Na2 | OFC occluded | 5LM   | 3.25   | P 63       | 80.2 (39.1) | 4            | 21.9/24.0   | Glu uptake, fold, allosteric inhibition by UCPh101 | 73 mutations: R23S, Y44F, F46R, F50L, V51L, T62V, Y63N, T67L, R72P, M73L, V75I, S82A, Q93K, V96I, I101V, V105I, M108L, A110S, S113A, K118R, M119L, T129S, I137L, I141L, H143L, I155T, S157C, N204T, A223L, C229V, V236A, R237L, N239K, K241G, A261L, R249V, E280D, D282N, I258F, R260K, V264I, V271L, M287L, G288E, I290L, A295G, T298M, L306V, A309G, V310L, L316L, V320I, W326F, G330A, L332I, V566I, L580V, F599Y, N492D, S437A, F454L, L458F, T461M, T462V, S463A, H480K, K483E, N484K, R485Q, V487A, M489L | Canul-Tec et al., 2017 |
| Hs        | L-Asp, UCPh101 | Na2 | OFC occluded | 5LM4  | 3.10   | P 63       | 75.9 (31.7) | 4            | 21.7/25.9   | Nearly identical to 5LLM | 73 mutations, K149A, M231I, F235I | Canul-Tec et al., 2017 |
| Hs        | L-Asp, UCPh101 | Na2 | OFC occluded | 5LU   | 3.32   | P 63       | 80.4 (40.1) | 5            | 20.9/25.3   | No inhibitors bound | 73 mutations, M231H, F235I | Canul-Tec et al., 2017 |
| Hs        | UCPh101, TBOATFB | OFC open | 5MJU    | 3.71   | P 63       | 80.3 (40.5) | 3            | 22.7/25.4   | Similar to 5LLM but with HP2 tip open, TBOATFB binding | 73 mutations | Canul-Tec et al., 2017 |

Indicators of low structure quality and uncertain features are shown in bold italic style.

1Ph, Pyrococcus horikoshii (GltPh); Tk, Thermococcus kodakarenensis (GltTk); Hs, Homo sapiens (EAAT1).
2Na1, Na2, Na3, Tl1, Tl2, sodium or thallium ions included in the model in the corresponding sodium site; Tl3, thallium ion in the proposed cation-binding site.
3Overall completeness and completeness for the highest-resolution shell (in parentheses) as given in PDB data refinement statistics, n.r., not reported.
4Clash score value is given according to a global validation metrics of the PDB entry. It is calculated from the pairs of atoms in the model that are unusually close to each other (Chen et al., 2010) and expressed as a number of serious clashes (>0.4 Å) per thousand atoms. Values >20 are considered problematic.
5Rfree is typically ~4–7% higher than Rwork. The extremely small Rwork – Rfree difference might indicate a compromised test data set (Wlodawer et al., 2008; Wlodawer, 2017).
Crystallization of GltPh in the OFC with the competitive inhibitor TBOA (1,1-threo-β-benzylxyloaspartate) revealed an open conformation of hairpin HP2, which had shifted ∼10 Å in the direction of the 3–4 loop from its position in aspartate-bound GltPh (Boudker et al., 2007). The HP2 opening was explained by steric clashes with the benzyl group of the inhibitor modeled to the structure. Although this explanation is reasonable, it is important to note that the GltPh-TBOA structure did not reveal electron density for the benzyl group of the inhibitor (see section TBOA binding and Fig. 6).

It was initially proposed for GltPh that HP2 would be mainly open in the apo state and that aspartate binding causes its closure. However, the first structure of the substrate-free transporter solved for the homologue GltTk revealed an OFC with occluded binding site and closed HP2 (Jensen et al., 2013). A structure of the substrate-free GltPh mutant R397A in OFC in the absence of sodium ions also showed an occluded conformation with HP2 in the closed state. The use of the R397A mutant was necessary to determine the structure of GltPh in apo form, because it has lower affinity for L-aspartate (6.6 µM vs. 27 nM for wild type; Verdon et al., 2014). The occluded apo state is probably required to reorient the transport domain from the IFC to the OFC during the transport cycle.

The structure of GltPh mutant R397A crystallized in the presence of sodium, but absence of aspartate was similar to the structure of aspartate-bound GltPh, except that the HP2 tip was slightly open (Verdon et al., 2014), with a proposed displacement of ∼3 Å. However, the low resolution of the structure and absence of electron density for sodium ions (see section Cation-binding sites and Fig. 4) make it difficult to draw solid conclusions.

A structure of the GltTk homologue revealed the positions of all three sodium-binding sites (Guskov et al., 2016). The sites of two of the sodium ions (Na1 and Na2) correspond to the sites found earlier in the structure of GltPh crystallized with thallium ions (Boudker et al., 2007). The assignment of the third sodium ion allowed further insight into the mechanism of sodium and aspartate coupling during the transport (Guskov et al., 2016). It should be noted that the presence of a bound sodium ion usually cannot be established unequivocally based on the electron density alone because the number of electrons of a sodium ion is identical to that of a water molecule. Therefore, additional indicators such as geometry of the site, distances and angles, or alternative experiments are required for the assign-
ment. The GltBF structures also allowed description of the long extracellular loop between TMS3 and TMS4 (Guskov et al., 2016) that plays an important role in the transport process (Compton et al., 2010). This loop was shown to cover the outer face of the transport domain in such a way that it might restrict movements of HP2 within the substrate-binding pocket.

Recent crystal structures of human EAAT1 provided the first insight into the structure of the eukaryotic glutamate transporters (Canul-Tec et al., 2017). EAAT1 was crystallized in the OFC in complex with ω-aspartate, and in the presence of allosteric and competitive inhibitors. The noncompetitive EAAT1-selective inhibitor UCPH101 (2-amino-4-(4-methoxyphenyl)-7-(naphthalen-1-yl)-5-oxo-5,6,7,8-tetrahydro-4H-chromene-3-carbonitrile) was bound at the interface of transport and scaffold domains in a hydrophobic pocket between TMS3, TMS7, and TMS4c, more than 15 Å away from the substrate/sodium-binding pocket (Canul-Tec et al., 2017). Crystallization of EAAT1 with the TBOA derivative TBOA_TFB (4-(trifluoromethyl)benzoylamino[benzyl-\text{glycine}]) showed a similar open conformation of HP2 as found in the GltPh_TBOA model, but some care needs to be taken in interpretation of the electron density (see section TBOA binding).

Structural data quality indicators

The quality of crystal structures directly depends on the quality of the x-ray diffraction data that were used for their determination. Several articles and reviews describe valuable tools for evaluation of raw experimental data and solved macromolecular structures (Kleywegt, 2000; Wlodawer et al., 2008; Chen et al., 2010; Gore et al., 2012; Adams et al., 2016; Wlodawer, 2017).

Two general indicators for the quality of diffraction data are resolution and data completeness. Resolution defines the level of detail that can be seen in electron-density maps. Generally, resolutions of ~4 Å allow only backbone tracing and visualizing secondary structure elements (α-helices are often much better defined than β-strands). The assignment of side chains at low resolution is usually not possible, and the conformations of side chains in deposited models should be treated with caution. In structures solved at resolutions between 3 and 4 Å, the fold is typically described correctly, even though there is a considerable probability of erroneous assignments and wrong conformations of many side chains. Electron densities at 2.5–3 Å resolution usually allow for unambiguous assignment of the main chain and side chains for the rigid parts of a protein; however, in more flexible parts of a molecule, the probability of incorrectly placed side chains is still high. Ligands that fully occupy their binding sites usually are possible to visualize at this resolution, as well as highly ordered water molecules. At higher resolutions of 2–2.5 Å, auto-building procedures (Cowtan, 2006; Terwilliger et al., 2008) and experienced crystallographers are capable of building a (nearly) complete model and including most of the ordered solvent molecules and ligands in the correct conformations (Blow, 2002).

Most of the GltPh structures were determined using crystals that diffracted to a moderate resolution of 3–4 Å (Table 1). Both structures of GltPh, with protrimers containing transport domains in intermediate positions (Protein Data Bank [PDB] codes 3V8G and 4X2S), as well as GltPh structures in OFC (4IZM and 4OYE) and IFC (4P6H), have resolution lower than or equal to 4 Å.

It is important to note that judging a crystal structure by resolution only is not good practice and could be misleading. Apart from the checking additional quality indicators (see below in this section), the electron-density maps should always be manually inspected. Often, moderate- and low-resolution structures provide electron-density maps of adequate quality to provide reliable insight in the general architecture, as well as some details of the macromolecule (still depending on the resolution). Conversely, models solved from data collected at high (atomic) resolution can have serious errors caused, for example, by insufficient completeness of data or inappropriate refinement protocols (Afonine et al., 2012).

Completeness of data can be defined by the number of collected crystallographic reflections in comparison to the number of theoretically possible reflections unique for the given crystal symmetry. For reliable refinement and model building, the overall completeness should be desirably higher than 90%, and values less than 80% (McCreadie, 1993) are considered poor. Because all reflections contribute to calculation of the electron-density map, the quality of maps calculated from incomplete data will be poor (Wlodawer et al., 2008). Table 1 shows structures that were solved from incomplete datasets (PDB codes 2NWL, 2NWX, 2NWW, 3V8G, 4P6H, 4OYE, 5DWY, and 5LM4).

Again, careful inspection of the electron-density maps is highly recommended to estimate the quality of the structural model. As an example, we compared the quality of the electron-density maps of two GltPh structures in which the transport domain is in neither the OFC nor the IFC, but in an intermediate state (PDB codes 3V8G and 4X2S, with resolutions of 4.21 and 4.66 Å, respectively) with that of GltT (2.70-Å resolution). Fig. 3 shows electron densities for the highly conserved NMDG+ motif, which is located in the unbound region of TMS7 and involved in formation of the substrate-binding and sodium ion–binding sites. The poor electron densities for both GltPh structures in the intermediate states indicate a high chance of misinterpretation. Additionally, the low overall completeness (73.1% for the intermediate OFC) of the structural data affects the reliability of the model. It should be noted that the conclusion from these structures that the transport do-
main is in an intermediate state is probably not affected by the data quality, but the details of the models should be treated with care.

The collected diffraction data (intensities of reflections) and the indirectly derived phases (see Glossary) are used to generate an electron-density map, which is used to build an initial protein model. Further crystallographic refinement includes multiple corrections of the model and improving phases to obtain the best agreement between the reflection amplitudes observed in experiment \( (F_o) \) and calculated from the model \( (F_c) \).

This agreement is monitored with the so-called R-factor (or \( R_{work} \)), calculated using \( \frac{\Sigma |F_o - F_c|}{\Sigma F_o} \). As cross-validation, an additional R-factor (\( R_{free} \)) is calculated using \( \sim 5\text{–}10\% \) of the reflections randomly chosen from the dataset and never included in the refinement process (Brünger, 1992). A low value of \( R_{free} \) is the most common indicator of successful refinement (the lower the value, the better the fit between the experimental data and the model). Comparing the values of \( R_{work} \) and \( R_{free} \) makes it possible to assess potential overfitting. There is a quasilinear relation between the difference between \( R_{free} \) and \( R_{work} \) resolution. \( R_{free} - R_{work} \) differences for structures determined at 3–4-Å resolution should be \( \sim 5\% \), and differences of less than 2% correspond to structures solved at resolution higher than 1 Å (Urzhumtsev et al., 2009).

The final structural model must conform to physical and chemical rules: the model must have reasonable crystal packing of molecules, contacts, and solvent content; correct stereochemistry; and correct bond lengths and angles. Furthermore, a model should have reasonable values for the crystallographic validation criteria: R-factors, B-factors (or displacement parameters which are commonly referred to as temperature factors), clash score (atomic overlaps), and Ramachandran outliers (torsion angles that fall into disallowed areas of a Ramachandran plot; Ramachandran et al., 1963), and it should have a best fit to an electron-density map. Altogether, these parameters are used to analyze the structure quality. While analyzing structural statistics of glutamate transporter homologue structures, we observed that the PDB entries 1XFH, 2NWW, 3KBC, 3V8F, 4P3J, 4OYE, and 4OYF show a very small difference between \( R_{work} \) and \( R_{free} \) factors, which might indicate that the data that were set aside for \( R_{free} \) calculation were used at some stage of refinement (Wlodawer et al., 2008; Wlodawer, 2017), and thus could indicate possible overfitting.

Analysis and validation of structures

Appreciation of the limitations of these structural models will help prevent the generation of hypotheses and follow-up experiments for which there is no solid basis. Next, we discuss Gltkn structures in which sodium/potassium binding sites are interpreted (PDB codes 2NWX, 4P1A, and 4OYF), the TBOA-bound structure (PDB code 2NWW) and structures in which the transport domain is in neither the OFC nor the IFC, but in an intermediate state (PDB codes 3V8G and 4X2S; Table 1). The quality of the crystallographic data for these structures might have affected mechanistic interpretations.

Cation-binding sites. Difficulties in obtaining high-resolution Gltkn structures prevent visualization of sodium ions involved in transport. To model the positions of sodium-binding sites in Gltkn, thallium, which provides a strong anomalous signal, was used in crystallization experiments (Boudker et al., 2007; Verdon et al., 2014). This approach allowed for identification of the locations of sodium-binding sites Na1 and Na2, that were later observed in other crystal structures (Table 1), molecular simulations, and electrostatic calculation studies (Huang and Tajkhorshid, 2008; Gu et al., 2009; Holley and Kavanaugh, 2009; Larsson et al., 2010; Scopelliti et al., 2014), whereas for the Na2 site, other positions were also suggested (Gu et al., 2009; Heinzelmann and Kuyucak, 2014; Venkatesan et al., 2015).
In the crystal structure of the GltPβ mutant R397A (PDB code 4OYF), sodium ions were placed in the Na1 site. However, the absence of electron density in the map indicates that the sodium ion might have been placed incorrectly (Fig. 4). Moreover, in the substrate/sodium-binding site, the model does not fit properly in the density map. Assignment of water molecules at resolution 3.41 Å also seems inappropriate. In addition, the structural statistics of these data show an extremely small difference between R-factors (0.9%).

All in all, the moderate data quality does not seem to provide a solid basis for the interesting suggestion that opening of the HP2 tip after sodium binding can be a mechanism preventing uncoupled uptake of sodium ions (Verdon et al., 2014). Furthermore, such a small movement of the HP2 loop (∼3 Å) in the medium-resolution structure could also be an over-interpretation, especially taking into account the significant coordinate error at this resolution.

Almost identical conformations of the GltPβ OFC structures in the apo state and in the presence of sodium ions suggest minor conformational changes upon sodium binding to the apo protein. This result contrasts with electron paramagnetic resonance (EPR) and fluorescence data showing that sodium binding to the aspartate-free GltPβ is followed by large conformational changes (Hänelt et al., 1997; Zarbiv et al., 1998; Zhang et al., 1998; Bendahan et al., 2000; Rosenthal et al., 2006, 2011; Holley and Kavanaug, 2009; Tao et al., 2010; Mwaura et al., 2012; Heinzelmann and Kuyucak, 2014), but the crystal structures of EAAT1 did not reveal potassium-binding sites (Camul-Tec et al., 2017). Although GltPβ does not transport potassium ions (Raunser et al., 2006; Ryan et al., 2009), it was used for studies of countertransport because of structural similarity with EAATs. Soaking of the IFC apo-GltPβ crystals with thallium ions revealed a new possible cation-binding site that overlaps with the aspartate-binding site (Verdon et al., 2014). Fig. 5 represents electron density in the suggested potassium-binding site (PDB code 4P1A, 3.75-Å resolution). For all three protomers, the difference map at 3σ shows negative density, indicating inappropriate refinement of occupancies or B-factors and/or severe radiation damage. Cartoon representation; thallium ions are shown as brown spheres. Coincident of relatively small conformational changes in the substrate-binding site.

Countertransport of a potassium ion is required for relocation of eukaryotic glutamate transporters to the outward-facing state. The position of the potassium-binding site was studied by mutational and computational studies (Kavanagh et al., 1997; Zarbiv et al., 1998; Zhang et al., 1998; Bendahan et al., 2000; Rosenthal et al., 2006, 2011; Holley and Kavanaug, 2009; Tao et al., 2010; Mwaura et al., 2012; Heinzelmann and Kuyucak, 2014), but the crystal structures of EAAT1 did not reveal potassium-binding sites (Camul-Tec et al., 2017). Although GltPβ does not transport potassium ions (Raunser et al., 2006; Ryan et al., 2009), it was used for studies of countertransport because of structural similarity with EAATs. Soaking of the IFC apo-GltPβ crystals with thallium ions revealed a new possible cation-binding site that overlaps with the aspartate-binding site (Verdon et al., 2014). Fig. 5 represents electron density in the suggested potassium-binding site (PDB code 4P1A, 3.75-Å resolution). For all three protomers, the difference map at 3σ shows negative density, indicating inappropriate refinement of occupancies or B-factors and/or severe radiation damage. Cartoon representation; thallium ions are shown as brown spheres.
TBOA binding. TBOA is a competitive blocker of eukaryotic glutamate transporters (Shimamoto et al., 1998), and the structure of archaeal Glt\textsubscript{ph} with TBOA revealed a movement of HP2 hairpin, providing a possible explanation of the inhibition mechanism (Boudker et al., 2007). Modeling of the inhibitor was based on the anomalous difference map calculated from diffraction data of the Glt\textsubscript{ph} complex with 3-Br-TBOA, which reveals the position of the bromine atom. However, direct evidence based on electron density of the orientation of the full TBOA molecule in this structure is absent. Analysis of the Glt\textsubscript{ph} TBOA structure (PDB code 2NWW) showed peaks of negative electron density for the bulky benzyl group of the inhibitor (Fig. 6). We calculated an electron-density omit map for the model and showed that the benzyl group of the blocker does not fit in the electron density. Instead, there might be an alternative possible orientation of the bound TBOA (Fig. 6) that could also cause displacement of HP2. Similar to Glt\textsubscript{ph}, an opening of HP2 was observed in the structure of human EAAT1 with TBOA\textsubscript{FB} (PDB code 5MJU), where the position of the bound TBOA derivative also requires additional experimental confirmation.

Intermediate-state structures. We analyzed the electron densities of Glt\textsubscript{ph} structures in intermediate states (PDB codes 3V8G and 4X2S). The structure of the Glt\textsubscript{ph} V198C/A380C mutant showed an intermediate OFC (iOFC), where the transport domain of one of the protomers was shifted ∼3.5 Å toward the cytoplasm and rotated ∼15°, suggesting that during the inward movement, rotation of the transport domain precedes its inward translation (Verdon and Boudker, 2012). The structure of Glt\textsubscript{ph} mutant R276S/M395R showed another asymmetric arrangement of protomers. The transport domain of one of the protomers was shifted 2 Å further inward and rotated by 7° (IFC locked configuration) in comparison with the original structure of Glt\textsubscript{ph} in the IFC (mutant K55C/A364C), whereas the transport domains of the other two protomers moved from the scaffold domain by ∼12° (IFC unlocked configuration) compared with the locked protomer (Akyuz et al., 2015).

The difficulties in obtaining crystal structures in intermediate states and the moderate quality of the available Glt\textsubscript{ph} structures most likely are caused by high heterogeneity of the transporter conformations together with short lifetimes of the intermediates. The crystal lattice might be a factor that limits the number of observed conformations of the transporter. The presence of almost identical structures of Glt\textsubscript{ph} for the two extreme states solved from crystals with different crystal packing (six space groups for outward-facing conformation P 1 2 1, C 1 2 1, P 3 1, P 3 2 1, P 6 1, and P 6 2, and two space groups for inward-facing conformation C 1 2 1 and C 2 2 2) gives credibility to the functional relevance of these conformations. In addition, the existence of these states is consistent with a plethora of other data (Akyuz et al., 2013, 2015; Erkens et al., 2013; Georgieva et al., 2013; Hänelt et al., 2013; Ruan et al., 2017). However, the two structures of Glt\textsubscript{ph} in different intermediate states (in space groups C 1 2 1 [iOFC] and P 6 5 2 2 [IFC locked and unlocked protomers]) may be affected by crystal packing. The crystals of Glt\textsubscript{ph} in the iOFC state (Verdon and Boudker, 2012) show contacts of the transport domain with symmetry molecules. Crystal contacts could also contribute to the stabilized (or forced formation) of the observed unlocked IFC state (PDB code 4X2S). The unlocked protomers (chains B and C) seem to have different crystal-packing environments than the single locked protomer (Fig. 7). Because of steric clashes between loop 4c-5 (chain B) and helix HP1b (chain C\textsubscript{syn}) the 4c-5 hairpin is shifted in comparison with the locked chain. Therefore, the unlocked protomers from symmetry molecules could stabilize each other in the crystal lattice.

Conclusion and outlook

Intensive structural studies of glutamate transporter homologues have provided fundamental insight into protein architecture and transport mechanisms. Many interpretations of the determined structures are ex-
Chains B and C are symmetry mates, where the molecule that forms an interface with chain B is shown in blue. mologue proteins (GltPh, GltTk, EAAT1), with crystals of for different crystallization conditions of different ho-
tremely valuable and have greatly expanded our insight into membrane protein conformational changes. None-
Figure 7. Contacts between GltPh asymmetric IFS protomers related by noncrystallographic symmetry (PDB code 4X2S). Superposition of unlocked protomers B (green) and C (gray) and a locked protomer A (yellow). Chain Csym of a symmetry molecule that forms an interface with chain B is shown in blue. Chains B and Csym are symmetry mates, where steric clashes between the loop 4c-5 (chain B) and helix HP1b (chain Csym) may have caused the shift of 4c-5 hairpin (shown with a dashed arrow), creating an "unlocked" conformation. Cartoon representation; amino acid residues that could cause steric clashes are shown as sticks.

tremendously valuable and have greatly expanded our insight into membrane protein conformational changes. None-
theless, some conclusions based on moderate-quality structures hampers the determination of positions of water molecules in the binding site, which is important for performing molecular simulations and understanding the influence of solvent on substrate/sodium coupling. Obtaining high-resolution structures of glutamate transporter homologues in different states and the combination of x-ray crystallography with molecular simulations and such techniques as single-molecule fluorescence resonance energy transfer (smFRET) and atomic force microscopy (AFM) should reveal gating events of transport cycle that still remain unclear.

The critical evaluation performed in this viewpoint is aimed to emphasize that care should be taken when using medium-quality structures as an input for further experiments, such as molecular dynamic simulations, EPR studies, and drug design. When using the structures of GltPh, in intermediate states, it is necessary to remember that crystal contacts could stabilize these conformations, and transport domains do not obligatorily pass these states while traversing the membrane. Similarly, metal cations that were placed in the deposited structural models solely on the basis that they theoretically should have been there, but for which experimental evidence such as electron density was lacking, should be treated with the utmost caution. The exact positions of the TBOA ligand and its derivative were not entirely determined based on electron density, which, for instance, will affect structure-based design of new inhibitors.

It is also important to realize that many of the solved crystal structures were not of the wild-type protein but of mutants that behaved better in expression, purification, and crystallization. The highest-resolution structures of the glutamate transporter homologues are reported for the GltPh wild-type protein (Jensen et al., 2013; Guskov et al., 2016; although even in this case, the protein has an extra His-tag). Because crystallization of the wild-type GltPh did not succeed, all GltPh structures were obtained for the mutant proteins, with at least seven point substitutions of nonconserved amino acid residues. These mutants had a higher expression level and crystallized more successfully than the wild-type GltPh (Yernool et al., 2004). Because of difficulties in purification of the wild-type EAAT1, thermostabilized versions of the protein were used for crystallization that share an overall sequence identity of ∼75% with the wild type and up to ∼90% identity at the substrate- and sodium-binding sites. In total, 73–76 mutations were introduced to increase protein stability and obtain functionally active protein (Canul-Tec et al., 2017). Although the function of the mutants appears to be largely unaffected compared with the wild-type protein, there may be yet-undetected functional differences.

Finally, as with any other structure deposited into the PDB database, one should remember that a structure is always a user interpretation of experimental data, and...
it is prone to contain (some) errors. Therefore, the model should not be taken for granted, but the underlying data (including the electron-density map) should be explored and checked before planning new experiments to test hypotheses, or when using the models for explanations of biological functions.

**Glossary**

**Reflections** are defined as regularly spaced spots with varying intensities recorded on a detector as a result of x-rays scattering by a crystal. To generate an electron-density map, not only the amplitudes but also the phases are needed. **Phases** cannot be recorded during experiment, which is known as the **phase problem**. Phases can be obtained either via single (or multiple) isomorphous replacement (SIR/MIR), when a heavy atom is introduced into a crystal and then diffraction from a derivative crystal is compared with the one of a native crystal, and using direct methods to determine the positions of heavy atoms, which in turn helps to estimate phases; or by using anomalous x-ray scattering (single-wavelength anomalous diffraction [SAD] or multi-wavelength anomalous dispersion [MAD]) when an introduction of a heavy atom causes a phase shift (anomalous dispersion) used to estimate phases; or by using initial phases from a structurally similar protein (molecular replacement). The **electron-density map** is the direct result of a crystallographic experiment and is a three-dimensional description of the electron density of the molecules in a crystal. A structural model of the molecules is built to fit the electron density.

After generating the initial electron-density map and building a starting model, structural **refinement** takes place, which aims to improve the phases and find the best agreement between the measured data and the constructed model. **Resolution** (in crystallography) is a measure of details that can be distinguished in an electron-density map; measured in angstroms (1 Å = 0.1 nm).

**Difference electron-density maps** are used to check the fit of the model to the diffraction data. The **2Fo-Fc map** is a composite map that is commonly used as a working map against which the model is checked. The **Fo-Fc map** is a tool to visualize possible misfits and errors. **Omit maps** are used to minimize the model bias and are particularly useful to verify assignment of ligands in binding sites. Maps are typically countered at different levels of **sigma** (σ), which is referred to as the standard deviation. The typical sigma value for a 2Fo-Fc map is 1σ, and for a Fo-Fc map, 3σ.

**R-factor**, or **R_work**, is a measure of the agreement between the collected diffraction data and the model. **B-factor**, or atomic displacement parameter (ADP), measures the displacement of an atom caused by thermal fluctuations, conformational disorder, and crystal lattice disorder. It is useful to detect the mobile portions of a model.

**Occupancy** of a given atom shows the fraction of molecules (from 0 to 1.00) in the crystal in which this particular atom actually occupies the position specified in the model.

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