Model of Aquaporin-4 Supramolecular Assembly in Orthogonal Arrays Based on Heterotetrameric Association of M1-M23 Isoforms

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Supporting Material

Matrix multiplication approach to compute AQP4 tetramer-OAP association

The association model is based on AQP4 N-terminus M23-M23 intermolecular interactions as the dominant interaction driving AQP4 OAP association. M23 AQP4 (red, Fig. S1) with its N-terminus (green) has association valency, which is represented by the number 1. M1 (white) has zero association valency.

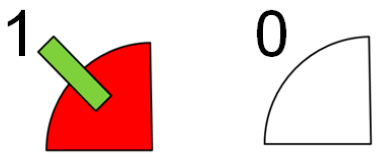

Figure S1. Association valencies of M23 and M1 AQP4.

There are six independent configurations of each tetramer, which are represented by 2-by-2 matrices according to their association valency values, as shown in Fig. S2. Each potential OAP binding site is also represented by a 2-by-2 matrix, as shown in Fig. S3.

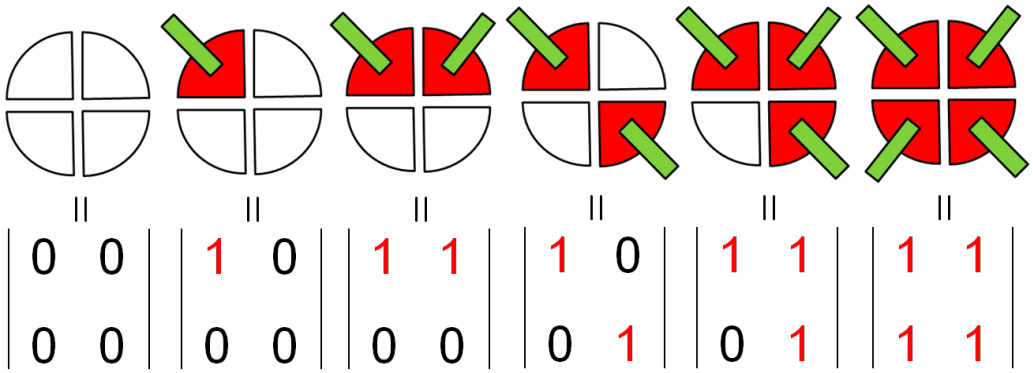

Figure S2. Six independent tetramer configurations and their corresponding matrices.

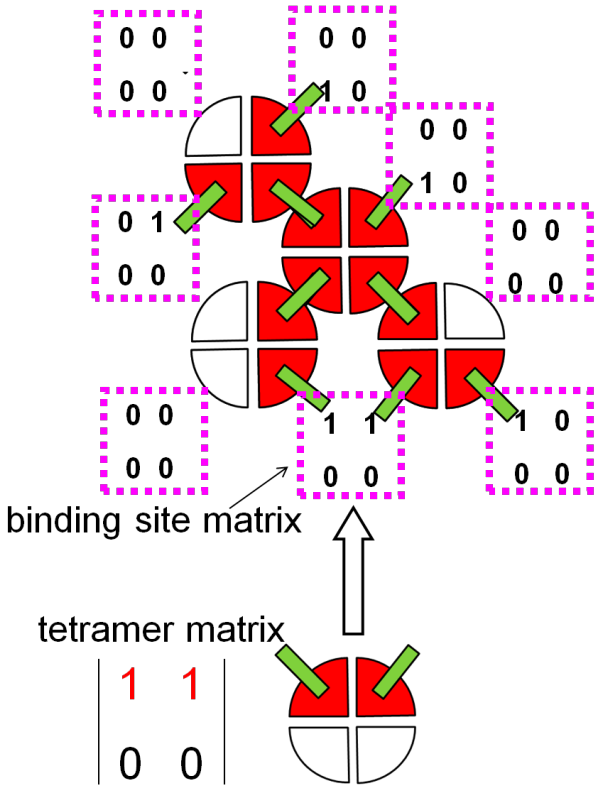

Figure S3. Matrices corresponding to potential sites of tetramer binding to an OAP.

Each tetramer can bind at each potential OAP binding site in four possible rotational configurations (rotamers), in which the 2-by-2 matrix is rotated using rotation function: rot90(**T**, k), where **T** is tetramer matrix and k=0, 1, 2 and 3, respectively, for 0, 90, 180 and 270 degree rotations (Fig. S4).

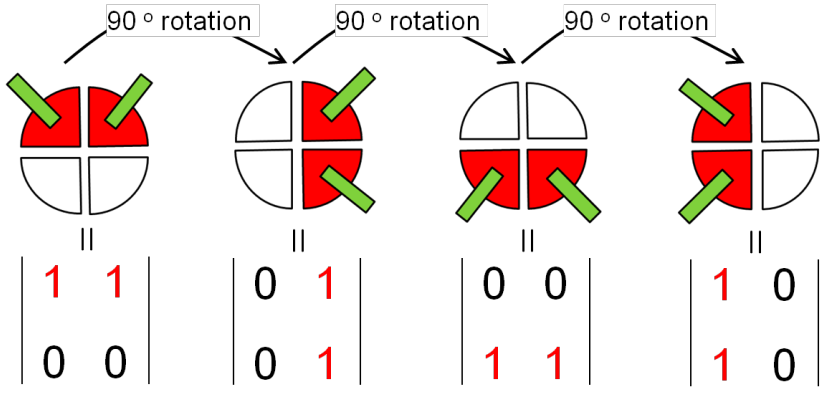

Figure S4. Schematic showing matrices for tetramer rotamers.

Association scores are calculated at each binding site by multiplication of the binding site matrix by the tetramer matrix (association score = **B** x **T**), as shown in Fig. S5. There are four possible association scores at the each binding site corresponding to each rotamer.

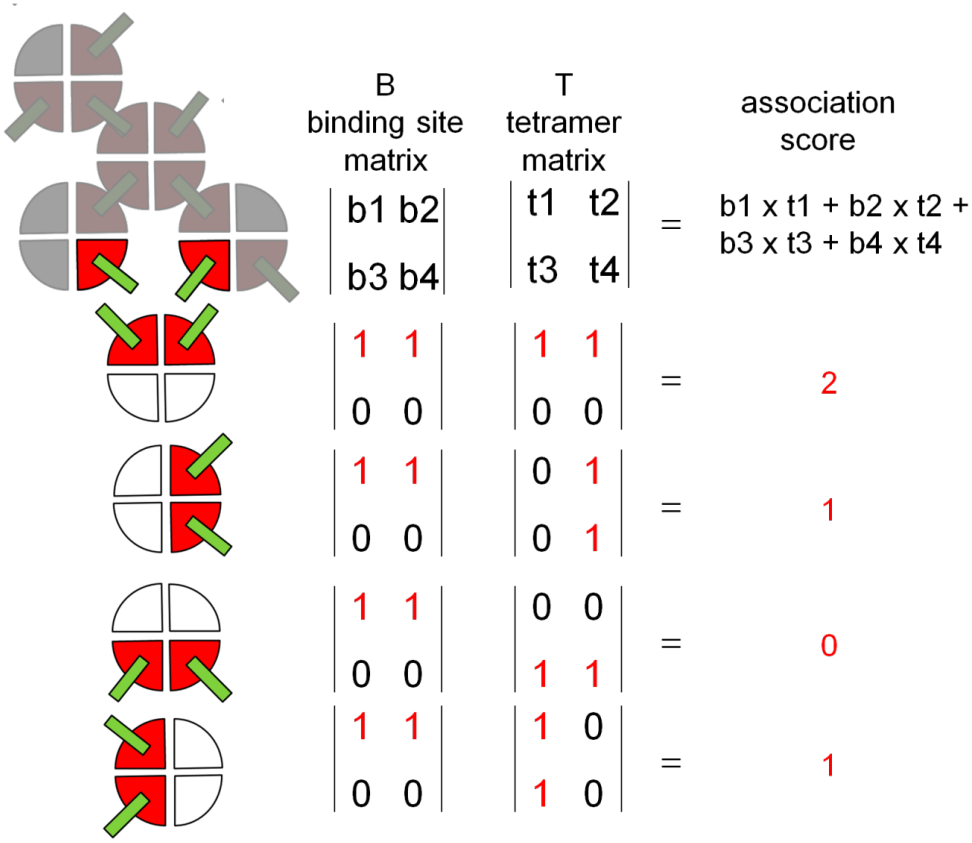

Figure S5. Determination of association score by multiplication of binding site matrix and tetramer matrix.

The association scores are then used to specify OAP binding site per association rules of the model.