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2 **Supplementary Information for**

3 **Eigenvector Centrality for Characterization of Protein Allosteric Pathways**

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10 **This PDF file includes:**

- 11 Supplementary text
- 12 Figs. S1 to S2
- 13 References for SI reference citations

14 Supporting Information Text

15 1. Relationship between modularity and eigenvector centrality

16 It is possible to define an eigenvector centrality-based modularity matrix that could offer a clear connection between the
17 community structure and the plots of the centrality. Lets consider a weighted graph $\tilde{G} = (V, E)$ with nodes in V edges in E
18 where the weights w_{ij} between nodes i and j are given by the elements of the adjacency matrix, this is $w_{ij} = A_{ij}$. Following
19 the definition of modularity matrix B of reference (1) we have:

$$20 \quad B_{ij} = A_{ij} - \frac{g_i g_j}{2m} \quad [1]$$

21 Where $m = 1/2 \sum_l g_l = 1/2 \sum_{lk} A_{lk}$ is the total number of edges and $g_{i/j}$ is the node degree (total connection) for node
22 i/j . From the definition of the eigenvector centrality, we know that:

$$23 \quad \sum_l c_l^2 = 1 \Leftrightarrow \sum_l 2m c_l^2 = 2m = \sum_l g_l \quad [2]$$

24 Where c_l is the eigenvector centrality value for node l .

25 With this new definition of the node degree as a scaled node centrality, we can rewrite the modularity matrix of reference
26 (1) as follows:

$$27 \quad B_{ij} = A_{ij} - 2m c_i^2 c_j^2 \quad [3]$$

$$28 \quad \tilde{B}_{ij} = \frac{A_{ij}}{2m} - c_i^2 c_j^2 \quad [4]$$

29 The two terms of equation 4 can be interpreted as a sort of probability of signal flow. The first term can be viewed as the
30 probability of a signal flowing from i to j or vice-versa through a direct connection whereas the second term can be interpreted
31 as the probability of flowing from i to j or vice-versa through an indirect connection. This stems from the fact that the square
32 of the centrality value has the property of a probability measure since $\sum_i c_i^2 = 1$ and $0 \leq c_i^2 \leq 1 \forall i$.

33 Let us now have a vector of labels \mathbf{s} such that $s_i = -1$ or $+1$ depending if node i belongs to one or another community. To
34 get the optimal community partitioning we want $\max_{\mathbf{s}}(Q(\mathbf{s})) = \max_{\mathbf{s}}(\mathbf{s}^t \tilde{B} \mathbf{s})$ and the ij cotribution to the argument of the
35 “min” function will be:

$$36 \quad s_i \frac{A_{ij}}{2m} s_j - s_i c_i^2 c_j^2 s_j \quad [5]$$

37 From the probability interpretation we note that if nodes i and j have a strong indirect connection but with $A_{ij} \simeq 0$ then
38 we need to classify them as belonging to different communities ($s_i s_j = -1$) in order to maximize Q . In the opposite case, if
39 $A_{ij} \gg 0$ and the indirect connection is low, we need to classify them as belonging to the same communities ($s_i s_j = 1$) in order
40 to maximize Q . The situations in between will be decided by the balance between the first and second term of equation 4.

41 2. Renormalization of centrality values for plotting purposes

42 We have performed a plot of the centrality values with a color scale that can be added in temperature factor field (beta) (2) of
43 a PDB file. In order to do this, the following transformation is applied to the centrality values:

$$44 \quad c_i \leftarrow 2 \frac{c_i - c_{min}}{(c_{max} - c_{min})} - 1 \quad [6]$$

45 With this transformation we ensure that if $c_i = c_{min} \Rightarrow c_i \leftarrow -1$ and if $c_i = c_{max} \Rightarrow c_i \leftarrow 1$

46 3. Correlation matrix as a function of the damping

47 Figure S1 shows the correlation matrices plotted for different values of λ . We can see a clear transition to a diagonal dominant
48 matrix when $\lambda = 1.66$.

49 4. Centrality-Degree comparisson

50 The EC (Eq. 3) measure is also intimately related to the degree centrality (DC) (Eq. 1). However, in Section 3 it is shown
51 that the difference between these two measurements encodes very fundamental aspects of the system’s behavior. In order to
52 gauge this difference, the upper panel of Figure S2 represents the normalized PRFAR - *apo* values of EC plotted against the
53 corresponding DC distribution. As expected, the two measurements are very similar. Interestingly, the decrease of the locality
54 factor λ enhances the difference between EC and DC. This shows that the nature of the EC - DC difference is manifested
55 mainly in the local component of the correlations, which is fully consistent with the interpretation of the distribution defined in
56 eq. 11 as a *neighborhood centrality*.

57 The lower panel of Figure S2 shows the *neighborhood centrality* values for $\lambda = 5 \text{ \AA}$ as defined by Eq. 11 (red line).
58 Alternatively, the EC/DC ratio yields qualitatively similar results, and hence, in principle this is an alternative way of defining

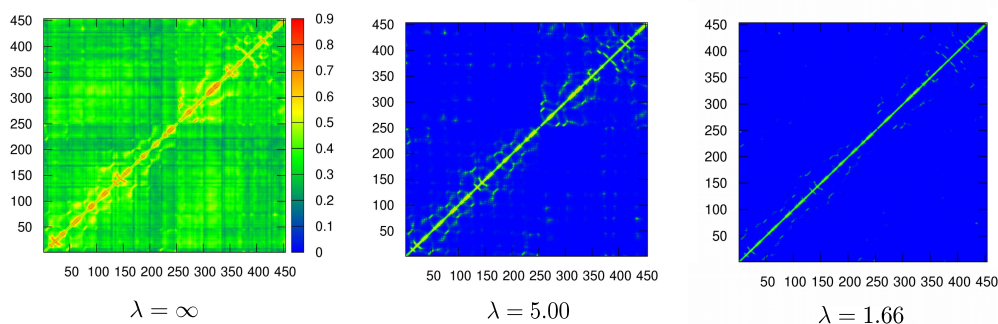


Fig. S1. Correlation matrix plots for APO for different values of λ . For $\lambda = 1.66$ the correlation matrix becomes almost diagonal.

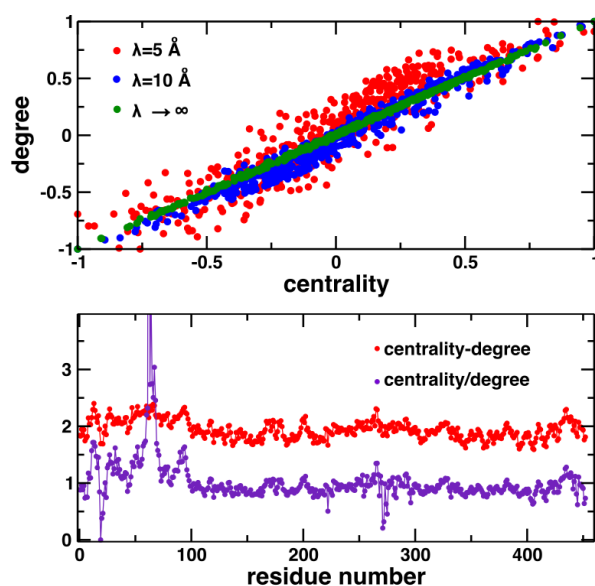


Fig. S2. (Upper panel) Normalized PRFAR - *apo* EC vs DC plots at $\lambda = 5 \text{ \AA}$, 10 \AA and $\lambda \rightarrow \infty$. (Lower Panel) EC - DC (red) and EC/DC (purple) PRFAR - *apo* distributions. In order to avoid dividing by nearly zero values all the DC and EC values were shifted up by one.

59 the *neighborhood centrality*. However, one drawback associated to the EC/DC ratio is that the distribution presents locally
 60 large amplitude fluctuations that mask the global features of the system, hindering the clear interpretation of the colored
 61 representations presented in Figures 3, 5, 6, 7 and 8.

62 5. NMR Relaxation Dispersion Experiments and Data Processing

63 Multiple-quantum CPMG experiments probing ILV methyl groups ($^1\text{CH}_3$) were performed on 14.1 T Varian Inova and 18.8 T
 64 Agilent NMR spectrometers at 30 °C. A constant relaxation delay period of 30 ms was used in the CPMG pulse sequence,
 65 with τ_{cp} delays of 0.0, 0.4167, 0.50, 0.625, 0.7682, 1.0, 1.4286, 2.0, 2.5, 3.333, 5.0, and 10.0 ms, and a recycle delay of 2.0 s.
 66 NMR spectra were processed with NMRPipe and analyzed in SPARKY. Transverse relaxation rates (R_2) were determined by
 67 measuring peak intensities of each ILV methyl resonance at multiple τ_{cp} delay points with a Perl-based exponential curve-fitting
 68 script. Relaxation dispersion curves were generated by plotting R_2 versus $1/\tau_{cp}$ using in-house scripts. Relaxation dispersion
 69 data obtained at two static magnetic fields were fit simultaneously using the fast CPMG equation and uncertainty values were
 70 obtained from replicate spectra.

71 6. Protein Expression and Purification

72 The HisH and HisF proteins were expressed separately at 37 °C in M9 minimal medium containing CaCl_2 , MgSO_4 , and MEM
 73 vitamins. The HisF subunit was grown in 100% D_2O supplemented with $^1\text{NH}_4\text{Cl}$ and $^2\text{C}_6\text{H}_{12}\text{O}_6$ and isotopic labeling of
 74 isoleucine, leucine, and valine ($^1\text{CH}_3$ -ILV) methyl groups was achieved with 60 mg/L of alpha-ketobutyric acid [methyl- ^{13}C ;

75 3,3-D2] and 100 mg/L of alpha-ketoisovaleric acid [3-methyl-13C; 3,4,4,4-D4] added 30min prior to induction. HisH was grown
76 in deuterated M9 with naturally abundant nitrogen and carbon isotopes. Following induction at 37 °C with 1 mM IPTG, cells
77 were harvested by centrifugation, resuspended in 10mM Tris, 10mM CAPS, 300mM NaCl, and 1 mM b-mercaptoethanol at pH
78 7.5 and co-lysed by ultrasonication. Cell debris was removed by centrifugation and the IGPS complex was purified by Ni-NTA
79 affinity chromatography.

80 **References**

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- 82 2. PDB (2017) Pdb file format.