

Allosteric Communication in Dihydrofolate Reductase: Signaling Network and Pathways for Closed to Occluded Transition and Back

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Escherichia coli dihydrofolate reductase (DHFR) catalyzes the reduction of dihydrofolate to tetrahydrofolate. During the catalytic cycle, DHFR undergoes conformational transitions between the closed (CS) and occluded (OS) states that, respectively, describe whether the active site is closed or occluded by the Met20 loop. The CS→OS and the reverse transition may be viewed as allosteric transitions. Using a sequence-based approach, we identify a network of residues that represents the allostery wiring diagram. Many of the residues in the allostery wiring diagram, which are dispersed throughout the adenosine-binding domain as well as the loop domain, are not conserved. Several of the residues in the network have been previously shown by NMR experiments, mutational studies, and molecular dynamics simulations to be linked to equilibration conformational fluctuations of DHFR. To further probe the nature of events that occur during conformational fluctuations, we use a self-organized polymer model to monitor the kinetics of the CS→OS and the reverse transitions. During the CS→OS transition, coordinated changes in a number of residues in the loop domain enable the Met20 loop to slide along the α -helix in the adenosine-binding domain. Sliding is triggered by pulling of the Met20 loop by the β G– β H loop and the pushing action of the β G– β H loop. The residues that facilitate the Met20 loop motion are part of the network of residues that transmit allosteric signals during the CS→OS transition. Replacement of M16 and G121, whose C $^{\alpha}$ atoms are about 4.3 Å in the CS, by a disulfide cross-link impedes that CS→OS transition. The order of events in the OS→CS transition is not the reverse of the forward transition. The contact Glu18–Ser49 in the OS persists until the sliding of the Met20 loop is nearly complete. The ensemble of structures in the transition state in both the allosteric transitions is heterogeneous. The most probable transition-state structure resembles the OS (CS) in the CS→OS (OS→CS) transition, which is in accord with the Hammond postulate. Structures resembling the OS (CS) are present as minor (~1–3%) components in equilibrated CS (OS) structures.

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Abbreviations used: DHFR, dihydrofolate reductase; MD, molecular dynamics; CS, closed state; OS, occluded state; DHF, 7,8 dihydrofolate; THF, 5,6,7,8 tetrahydrofolate; NADPH, nicotinamide adenine dinucleotide phosphate; SCA, statistical coupling analysis; SOP, self-organized polymer; TSE, transition-state ensemble; MSA, multiple sequence alignment; WT, wild type.

Introduction

Conformational fluctuations of proteins have been argued to play a central role in enzyme catalysis.^{1–4} Such a concept is appealing because the energy landscape of enzymes even in the folded state is rugged,⁵ and hence thermal energy might be sufficient to access several conformational substates during a typical reaction cycle.² In recent years, results from a number of studies have been used to

propose that dynamic motions in a network of residues that promote catalytically relevant structural transitions may be encoded in the protein structure.^{6–16} While it is difficult to unambiguously demonstrate whether collective dynamics involving a network of residues facilitates catalysis,¹⁷ it is clear that enzymes sample a number of distinct states during a reaction cycle. In the best studied example of *Escherichia coli* dihydrofolate reductase (DHFR) the role of the conformational motions in the enzyme in facilitating the hydride transfer has been linked using mutational studies,^{10,18,19} NMR relaxation dispersion measurements^{20–22} that probe the dynamics on microsecond to millisecond time scale, molecular dynamics (MD) simulations,^{6,7,13} and sequence analysis.⁶

The emphasis on correlated motions on enzyme catalysis has been repeatedly questioned by Olsson *et al.*,¹⁷ who have shown that catalytic rates are largely affected by changes in the free energy barriers (Δg^\ddagger) in the chemical reaction step.^{23–26} Thus, mutational effects or other constraints simply alter Δg^\ddagger and, hence, the catalytic rates. Complex enzyme motion in a multidimensional free energy landscape is to a large extent orthogonal to the dynamics along the optimized reaction coordinate. Regardless of the rate of correlated dynamical motions on the rates of hydride transfer in DHFR, it is known that the enzyme cycles through a number of states during the catalytic cycle. The dynamics of transition between such states (referred to as allosteric states) is the topic of interest in this study. Whether the time scales in such conformational transitions occur are linked to catalysis is unclear.¹⁷

DHFR catalyzes the reduction of 7,8 dihydrofolate (DHF) to 5,6,7,8 tetrahydrofolate (THF).¹ By binding the cofactor, nicotinamide adenine dinucleotide phosphate (NADPH), hydride transfer from NADPH to protonated DHF leads to production of NADP⁺ and THF.²⁷ DHFR, which is required for normal folate metabolism in prokaryotes and eukaryotes, plays an important role in cell growth and proliferation in prokaryotes and eukaryotes.²⁸ As the result of its obvious clinical importance, it has been studied extensively using a wide range of experimental and theoretical methods.¹

High-resolution crystal structures show that the *E. coli* DHFR enzyme has eight β -strands and four α -helices interspersed with flexible loops that connect the secondary structural elements.^{29,30} The structure of DHFR can be partitioned into adenosine-binding and loop subdomains.³⁰ In the catalytic cycle, Met20 loop changes conformation between closed (CS) and occluded (OS) states (Fig. 1). Interactions through a hydrogen bond network with the β F– β G loop (residues 117–131) stabilize the CS.³¹

The crystal structures of *E. coli* DHFR complexes in the catalytic cycle have given a detailed map of the structural changes that occur in the enzyme.³⁰ In addition, the conformational changes in *E. coli* DHFR in response to binding have been inferred using various experimental techniques, including X-ray crystallography, fluorescence, and NMR.^{21,29,30}

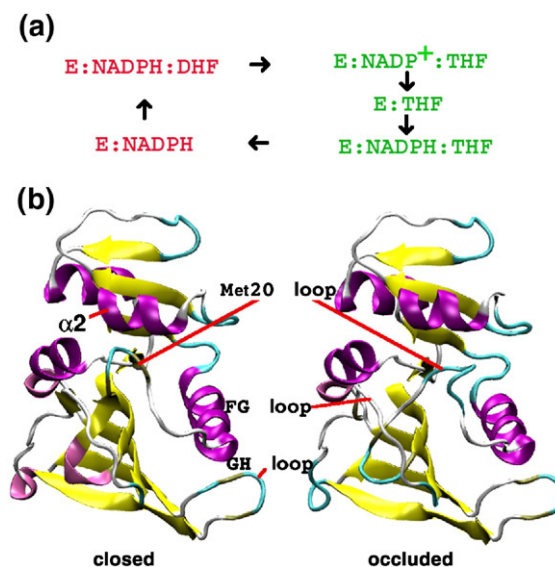


Fig. 1. Catalytic cycle and structures of closed and occluded states. (a) Scheme of catalytic cycle of DHFR that shows the two key conformations adopted by the enzyme. The Met20 loop closes the active loop in the E–NADPH–DHF complex, while it is occluded in the E–NADP⁺–THF complex. (b) Structure of the closed state (CS) (PDB code 1RX2) is on the left and that of the occluded state (OS) (PDB code 1RX7) is on the right. For clarity, we have explicitly labeled the structural elements that facilitate the allosteric transitions. The major changes are localized in the Met20 loop.

Comparison of the CS and OS structures shows that the conformations of the Met20 loop undergoes the largest change during the reaction cycle. As a result, the states of DHFR are classified using the conformations of the Met20 loop. The active site is either closed or occluded depending on the conformation of the Met20 loop (Fig. 1). Thus, the motion of the Met20 loop coordinates the dynamical changes in DHFR during the different stages of the catalytic cycle.

Although the structures of the CS and OS are known, the dynamic pathways connecting the two allosteric states have not been characterized.^{1,2} In this paper, we address the following questions: (1) Can the evolutionary footprints in the DHFR family of sequences be used to obtain a network of residues in DHFR that is linked to the CS→OS and the reverse transition in the enzyme? If so, what role do these residues play in the kinetics of CS→OS and the reverse transitions? (b) What are the pathways and the nature of the kinetics associated with transition from OS to CS and back? (c) What are the structures of the transition-state ensemble (TSE) in the OS→CS transition and in the reverse reaction? We use a combination of bioinformatics methods^{32,33} and Brownian dynamics simulations of coarse-grained models of DHFR to address these questions. It should be emphasized that our study focuses only on the kinetics of CS→OS and OS→CS transitions, and not on whether the motions that drive these transitions affect hydride transfer reactions. The pre-

cise linkage between equilibrium or dynamics motions of proteins and catalysis continues to be a topic of debate.^{4,17}

In order to determine the network of residues in DHFR that regulates the allosteric transitions we adopt a sequence-based method,³³ which is based on statistical coupling analysis (SCA).^{34–37} The SCA identifies many residues that are dispersed between the two subdomains as being relevant in the function of DHFR. Although several of these residues are not strongly conserved, they are predicted to covary across the DHFR family. In order to probe allostery in DHFR, we carried out simulations using a coarse-grained self-organized polymer (SOP) model.³⁸ The Brownian dynamics simulations reveal the dynamical changes that occur during the CS→OS and OS→CS transitions. The conformational changes in the Met20 loop, which occur by a sliding motion along a helix in the adenosine-binding domain, is preceded by coordinated rupture of interactions between Met20 and β F– β G loops and the formation of contacts between Met20 and β G– β H loops. Simulations in which Met16 and Gly121 are cross-linked by a disulfide bond show that the CS→OS transition is dramatically affected. In accord with recent NMR experiments,^{2,39} we find a small component (~1–3%) of OS (CS) structures are populated by thermal fluctuations when DHFR is in the CS (OS) state. The structures of the TSE are broad both in the forward and in the reverse direction. The presence of a broad TSE and small barrier separating the CS and OS supports the conformational selection model that posits that due to the heterogeneous nature of fluctuations, conformations resembling the OS are present in the CS and *vice versa*.

Results and Discussion

Allostery wiring diagram shows that key residues are dispersed throughout the structure

We obtained 526 sequences for the DHFR family from Pfam⁴⁰ (entry 00186), and realigned them using the Clustalw package.⁴¹ We manually deleted certain sequences and generated a multiple sequence alignment (MSA) that contained 462 sequences. Each of the 462 sequences has 323 residues including gaps. With the fraction of the sequences in the subalignment set to $f=0.35$ (see Methods) in the SCA, there are 74 allowed perturbations ($S_j=0$ for $j=1, 2, 3, \dots, 74$) at the various positions in the DHFR family. We used the clustering protocol to identify the set of covarying residues.^{42,43} After rescaling the $\Delta\Delta G_{ij}$ matrix (Eq. (5) in Methods) ($i=1, 2, 3, \dots, 158$ and $j=1, 2, 3, \dots, 74$) and using the Euclidean similarity measure in the coupled two-way clustering algorithm,³³ we obtained a cluster of 21 residues and a cluster of 19 perturbations. As in our previous work,³³ we propose that the residues that are clustered both in positions and perturbations constitute the minimal robust network of residues that signal the kinetics of

the CS→OS transition and back. The relevant network of spatially separated residues constitutes an allostery wiring diagram (Fig. 2a) and may encode for the promoting motions.

To determine if the residues in the network predicted by SCA merely reflect sequence conservation we calculated the sequence entropy $S_i = -\sum_{x=1}^{20} p_i^x \ln(p_i^x)$. For a perfectly conserved residue, $S_i=0$. If we assume that a residue is strongly conserved if $S_i \leq 0.1$, then there are very few residues with high sequence conservation. These are G15, P21, W22, T35, G43, L54, R57, G95, and G96 (Fig. 2b). Sequence entropy is too restrictive in assessing the nature of mutations that are tolerated at a given position. The allowed variations in the amino acid substitution is better captured using the chemical sequence entropy,⁴⁴ $S_{\text{CSE}} = -\sum_{x=1}^4 p_i^x \ln(p_i^x)$, where the 20 amino acids are divided into four classes, namely, hydrophobic (H), polar (P), positively charged (+), and negatively charged (-).⁴⁴ Using chemical sequence entropy, residues, namely, I14, G15, M20, P21, W22, D27, F31, T35, V40, I41, M42, G43, T46, W47, S49, I50, G51, L54, R57, I60, I61, L62, S63, I91, M92, V93, G95, G96, V99, Y100, L110, T113, I115, and F125, are strongly ($S_{\text{CSE}} \leq 0.1$) conserved.

It is not surprising that many of the residues identified in the allostery wiring diagram (Fig. 2) are also strongly conserved as they are associated directly with the binding surface that stabilizes the closed conformation. The SCA also identifies residues N18, L28, K38, V72, S77, A84, G97, and Q108 that are neither highly conserved nor adjacent to conserved residues. It appears that many of the residues in the network are relevant for executing dynamical motions that drive the allosteric transitions in DHFR or for cofactor binding. For example, N18 forms contact with H124 in the CS. Similarly, during the OS→CS transition, L28 comes close to I50 upon binding of various ligands, which results in the closure of the active-site cleft.⁴⁵ Residue K38, which is in the hinge region, facilitates rotation of the adenosine-binding domain towards the loop domain (residues M1–D37 and A107–R159).¹

The key residues in the allostery wiring diagram have been shown in previous theoretical and experimental studies to be important either in catalysis or in binding of cofactors. Cameron and Benkovic¹⁸ and Wang *et al.*⁴⁶ showed that mutations of residues (M42 and G121) that are far from the active site affect the hydride transfer rates. Based on equilibrium covariance matrix fluctuations of the C $^{\alpha}$ atoms obtained from all-atom MD simulations, Rod *et al.* showed that interactions of M42 with other residues (H45, D28, S49) would also be involved in the CS→OS conformational transition.¹³ Mutations of positions M42 and/or G121, which lead to anti-correlated motions between the two subdomains, are found to be part of the predicted allostery wiring diagram. Agarwal *et al.* used sequence conservation of a small data set of DHFR sequences to identify a network of residues whose coordinated motion is apparently linked to catalysis.^{6,7} Among them, I14 is found to be in the allostery wiring diagram that we

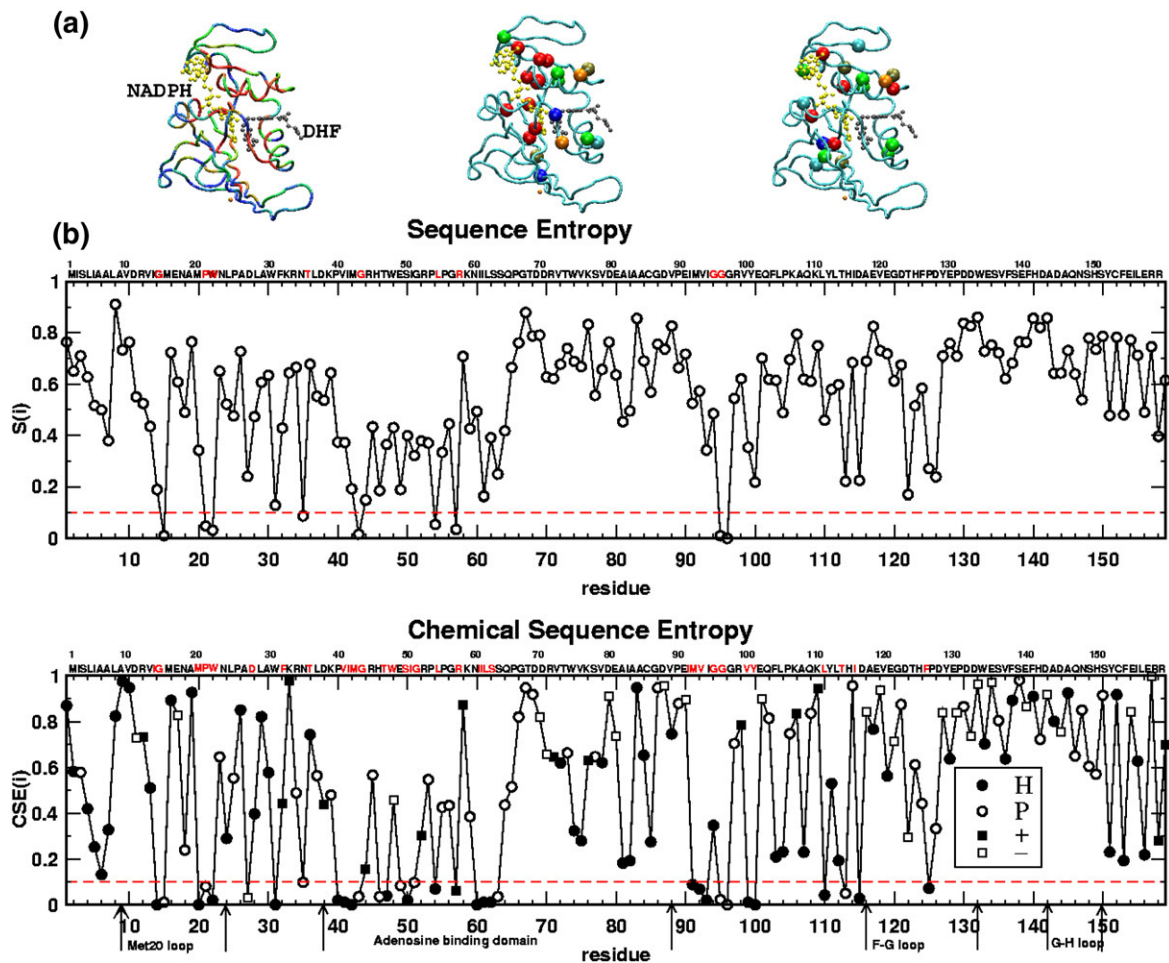


Fig. 2. Sequence conservation with respect to the structure of the CS. (a) In the CS structure on the left we have color coded the backbone to reflect the extent of sequence conservation. Red color represents strong conservation ($S(i) < 0.1$) and nonconserved residues are in blue. The residues that are clustered in the position in the SCA (V13, I14, N18, M20, D27, L28, K38, V40, I41, M42, W47, I50, G51, N59, I60, L62, Q65, I94, V99, Y111, and T113) are shown in the middle structure. The colors of the residues indicate the values of the $S_{CSE}(i)$ with red representing strong conservation of the chemical identity. The right structure shows the network of residues that appear as perturbation in the SCA (D11, R12, V13, D27, A29, K38, V40, W47, I50, G51, P53, L62, V72, S77, A84, G97, V99, Q108, and Y111). In the three structures, the cofactors (NADPH and DHF) are shown using all-atom representation. (b) The top panel shows position-dependent sequence entropy ($S(i)$) obtained by aligning the *E. coli* DHFR against the rest of the 426 sequences. Strong conservation ($S(i) < 0.1$) is observed only for a small fraction of residues. The chemical sequence entropy, $S_{CSE}(i)$ in the bottom panel, shows that for a substantial fraction of residues only the chemical identity changes. These residues are dispersed throughout the structure.

have identified using SCA. It was also found that motions of residues W22, D27, M42, I60, L62, and T113 that form a hydrogen bond network with DHF in the active site might also be involved in coupled promoting motions.^{6,7} Taken together, the present and previous studies show that the allosteric wiring diagram, which represents the network of signaling residues in DHFR, is spread throughout the structure (Fig. 2). More importantly, many nonconserved residues are part of the network.

Motions between the two subdomains in the CS and OS are anti-correlated

The root-mean-square deviation (RMSD) between the closed and occluded crystal structures of *E. coli*

DHFR is only 1.18 Å. However, the RMSD of the active Met20 loop (residues A9–L24) between the two end point structures is almost three times larger (≈ 3.35 Å). In order to assess the differences in the structures of the two states at finite temperature, we equilibrated the OS and CS conformations at 300 K. Comparison of the thermally averaged contact maps shows that the closed state differs from the occluded conformation mainly in the Met20 loop and the secondary structural elements that are affected by the motions (see below) of the Met20 loop (data not shown). The largest changes occur in the β F– β G (D116–D132) and β G– β H (D142–S150) loops and the α -helix H2 of the adenosine-binding domain (residues R44–I50). The crystal structures and the thermally equilibrated CS and OS also show that in

the CS→OS transition the conformational fluctuations in the Met20 loop have to be accompanied by the following changes: (1) Contacts between the Met20 and β F- β G loops should be ruptured. (2) Interactions between helix 2 and the Met20 loop should be disrupted, and reform in a different location. (3) Stabilizing contacts between Met20 and

β G- β H loops should form. If these processes are disrupted then it is likely that the catalytic efficiency of DHFR may be compromised. Indeed, experimental findings of the importance of mutating M42, G121, S148, or any two of these residues on the hydride transfer rates can be rationalized based solely on a static picture.¹³

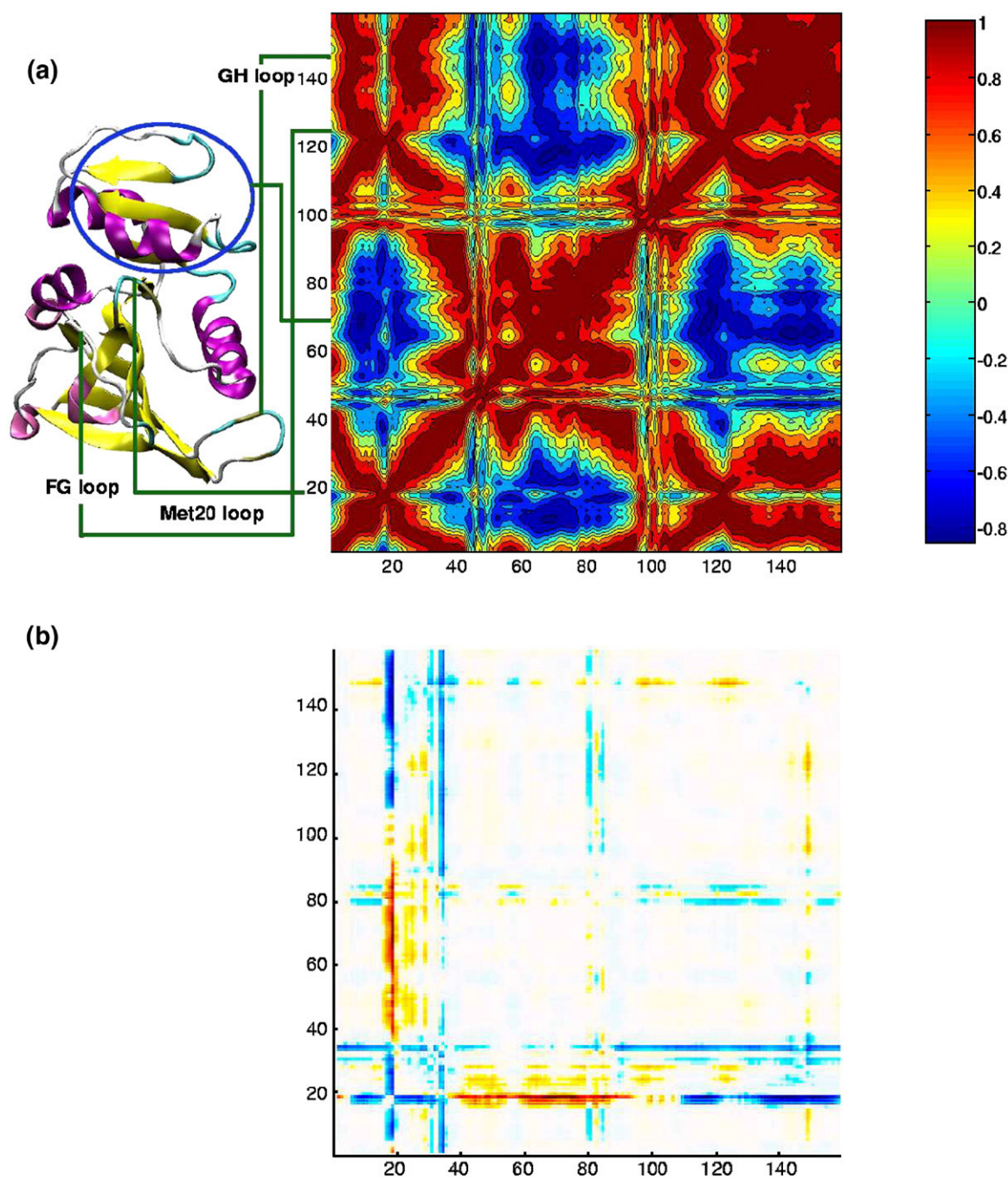


Fig. 3. Correlated and anti-correlated motions in DHFR. Covariance matrix of equilibrium fluctuations of the unit vectors constructed from the coordinates of the C^α atoms (Eq. (1)) of the WT DHFR in the CS. The residues associated with the structural elements are shown on the left. The scale on the right measures the extent of correlation. In the bottom panel we show $|C_{ij}^{CS} - C_{ij}^{OS}|$ using the same scale. For clarity, we highlight only those regions that are different in the two allosteric states. The simplicity of the SOP model has allowed us to probe the equilibrium fluctuations for about 1 msec.

The correlated motions in DHFR are computed using time average covariance matrix defined as,

$$\langle C_{ij}(X) \rangle = \frac{1}{T_{\text{obs}}} \int_0^{T_{\text{obs}}} \Delta \hat{r}_i(t) \cdot \Delta \hat{r}_j(t) dt \quad (1)$$

where $\Delta \hat{r}_i(t) = (\vec{r}_i(t) - \vec{r}_i^{wt}) / |\vec{r}_i(t) - \vec{r}_i^{wt}|$ is the unit vector of the displacement of the i th C α atom with respect to its initial value, and X is either CS or OS. The direction of motion of the i th residue is given by $\Delta \hat{r}_i$. If $\langle C_{ij} \rangle$ is positive then the motion of the two residues i and j are correlated while negative values correspond to anti-correlation. For perfectly correlated (anti-correlated) residues, $\langle C_{ij} \rangle$ is +1 (−1). The covariance map for the CS shows anti-correlated motion between the Met20 loop and the adenosine-binding domain, as well as between the β F– β G and β G– β H loops (see the dark blue regions in Fig. 3). Thus, the adenosine-binding domain and the loop domains move in an anti-correlated manner. Similar conclusions were obtained using all-atom simulations of the wild-type (WT) DHFR.¹³ The present simulations and previous MD studies^{6–9,13,15} point to the importance of correlated motions between regions that are spatially well separated. The cross correlations in the interdomain motions shown in Fig. 3 are obtained by averaging the structural fluctuations over 1 ms, and may well be relevant in facilitating cofactor binding and solvent rearrangement needed for catalysis.²⁶ The static picture alone is not sufficient to describe the kinetics of transitions between the CS and OS. Only by probing the kinetics of conformational fluctuations in the CS→OS (and the backward) transitions can we predict the order of events that results in the conformational changes in the all-important Met20 loop.

The bottom panel in Fig. 3 shows the differences in the covariance matrices $\Delta C_{ij} = \langle C_{ij}(\text{CS}) \rangle - \langle C_{ij}(\text{OS}) \rangle$ in regions that are significantly different between the two allosteric states. The red region between the Met20 loop and the adenosine-binding domain indicates more anti-correlated motions in OS than in the CS. The blue region between the Met20 loop and the other two loops shows less anti-correlated motions and more correlated motions in OS than in CS.

Kinetics of CS→OS transition involves deformation of the Met20 loop

In order to dissect the kinetics of structural changes in the Met20 loop during the forward (CS→OS) and the backward (OS→CS) directions we have performed a number of simulations using the procedures described in the Methods section. Although it is clear that the Met20 loop plays an essential role in this transition, the order of events that drives its conformational change is not known.^{1,2} We monitor the Met20 loop kinetics using two surrogate reaction coordinates. One is the global RMSD, Δ_G , which is obtained by aligning the instantaneous conformation of DHFR at time t with either the CS or the OS

structure. During the CS→OS transition, Δ_G should increase with respect to the CS and decrease with respect to the OS. From the time-dependent variations in Δ_G we can infer the changes in the Met20 loop with respect to the entire structure. To determine the changes that are localized in the Met20 loop we calculated a local RMSD, Δ_L , which uses only the coordinates of the active loop. From the time-dependent changes in Δ_L , which is computed by aligning the Met20 loop and computing its RMSD (with respect to the starting conformation) during the two transitions, we can explicitly identify the dominant motions (translation, rotation, or twist) of the loop. The kinetics expressed in terms of the local coordinate Δ_L yields the conformational changes of only the Met20 loop.

The time-dependent changes in the global RMSD, $\Delta_G(t)$, with respect to the CS show considerable dynamical heterogeneity (Fig. 4). The bottom panel in Fig. 4, for one trajectory, shows that there are multiple recrossings across the transition region, which is suggestive of a rather broad transition region (see below). Prior to the CS→OS transition ($t < 80 \mu\text{s}$ in Fig. 4) $\Delta_G(t)$ undergoes substantial fluctuations, which suggests that high-energy states are being sampled while DHFR is in the CS. More importantly, such fluctuations can lead to infrequent

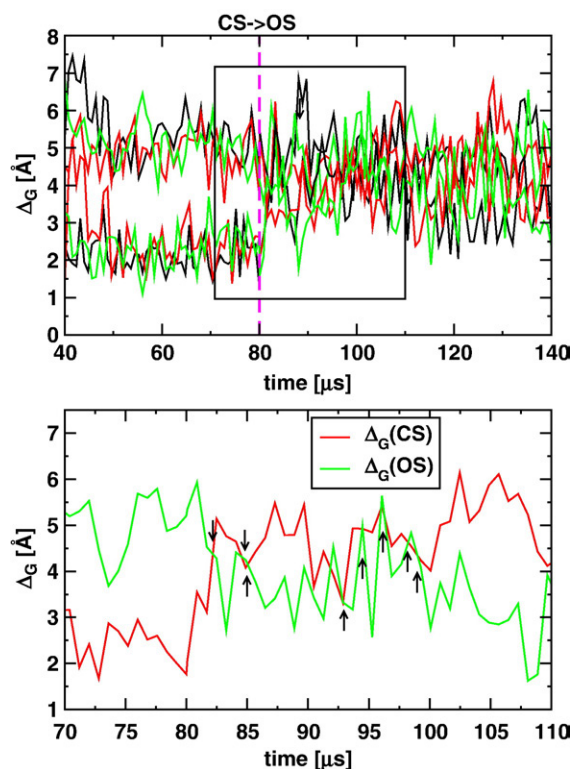


Fig. 4. RMSD as a function of time during the CS→OS transition. Time-dependent changes in the global RMSD ($\Delta_G(t)$) for a few representative trajectories as a function of t are given in the top panel. The dynamical changes in $\Delta_G(t)$ for one of the trajectories for the time interval enclosed by the box are shown below. The arrows show that frequent recrossings between CS and OS states occur prior to the completion of CS→OS transition.

visits to conformations that are similar to the OS (see below). The broad distribution of transition times and multiple recrossings attests to the plasticity of the enzyme during the conformational transition.

Although there is great diversity in the dynamics of the individual trajectories, $\langle \Delta_G(t) \rangle$ and $\langle \Delta_L(t) \rangle$, obtained by averaging over an ensemble of initial conformations, can be approximately described using a two-state model (Fig. 5a). Comparison of $\Delta_G(t)$ and $\Delta_L(t)$ shows (Fig. 5a) that deformations of the Met20 loop occurs after the global motions in the CS \rightarrow OS transition. Because the long time values of $\langle \Delta_L \rangle$ are less than $\langle \Delta_G \rangle$ values, we surmise that the structural changes in the Met20 loop involve translation and rotational motion towards the OS structure.

Sliding of the Met20 loop across $\alpha 2$ is the rate-limiting step in the CS \rightarrow OS transition

In order to understand the mechanism of the communication during the CS \rightarrow OS transition we monitored the local movements of the Met20 loop and the helix $\alpha 2$ in the adenosine-binding domain. Rupture of the contacts in the CS (Asn18-His45, Asn18-Ser49, and Ala19-Ser49) and formation of Glu17-Ser49 during the CS \rightarrow OS transition facilitates the sliding of Met20 along $\alpha 2$ (Fig. 6a). The relative

sliding motion between $\alpha 2$ and the Met20 loop enables NADPH to move closer to DHF.

In the loop subdomain, the flexible Met20 loop interacts simultaneously with both the βF - βG and βG - βH loops (Fig. 1). In order to dissect the order of events that occurs in the CS \rightarrow OS transition, we have computed the kinetics of breakage and formation of a number of contacts involving the two loops (Fig. 6a-c). By fitting the time-dependent changes in the formation and rupture of contacts to single exponential kinetics we find that the rupture of contacts between the Met20 loop and βF - βG loop in CS and formation of contacts between residues in the Met20 loop and βG - βH loop occur nearly simultaneously (on the microsecond time scale) (see Fig. 6a-c). Only subsequently (on a time scale of about 2 μ s), the interaction between Glu17 (in the Met20 loop) and Ser49 (in $\alpha 2$) that exists only in the CS, takes place. Thus, the sliding of the Met20 loop on $\alpha 2$ requires coordinated motion of a number of residues in the loop domain.

We can further dissect the nature of the sliding motion of the Met20 loop along $\alpha 2$ by simultaneously measuring the changes in the angles and the distances between selected residues. We have computed the time-dependent changes in the distances between Asn18-His45 (R_1), Ala19-Ser49 (R_2), Asn18-Met42 (R_3), and Glu17-Ser49 (R_4), respectively. The

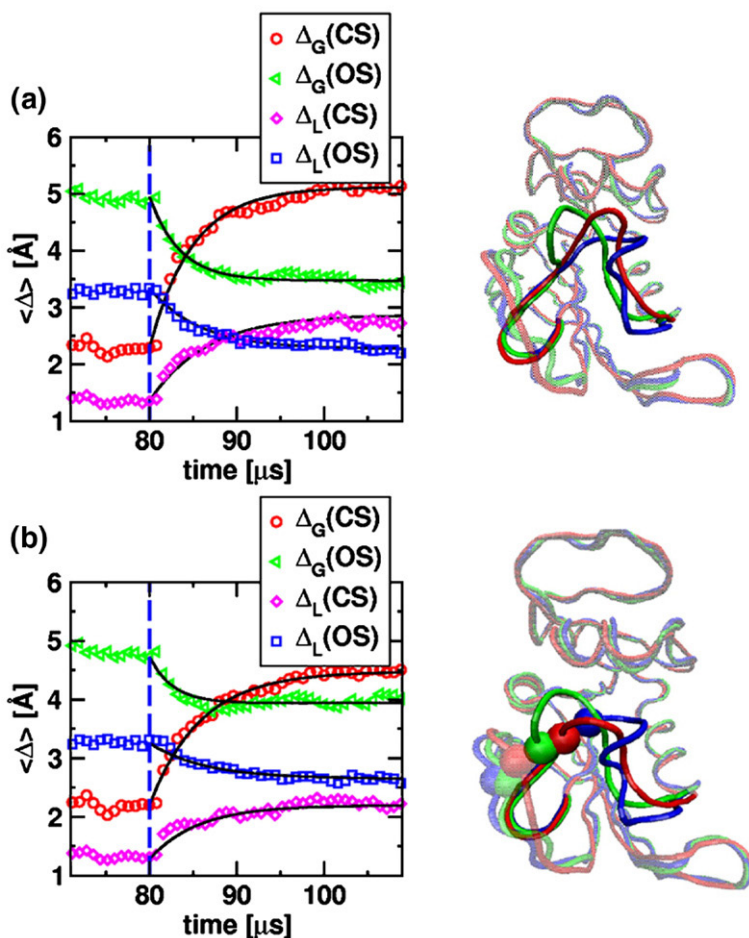


Fig. 5. Kinetics of allosteric transitions probed using RMSD. Time dependent changes in the global, $\langle \Delta_G(t) \rangle$, and the local, $\langle \Delta_L(t) \rangle$, RMSD of the Met20 loop averaged over 50 trajectories. The meaning of the symbols are given in the insets. The RMSDs are measured with respect to the starting and ending states. For example, $\langle \Delta_G(\text{CS}) \rangle$ means that the global RMSD is computed with respect to the CS. The changes in $\langle \Delta_G(t) \rangle$ and $\langle \Delta_L(t) \rangle$ for the WT CS \rightarrow OS are shown in (a), and the results for the CL are shown in (b). The structures on the right in both (a) and (b) represent superposition of the CS, OS, and the average TS conformations. Conformation of the Met20 loop in the CS (green), OS (blue), and TS (red) are highlighted. The cross-link between 16 and 121 is explicitly shown in (b).

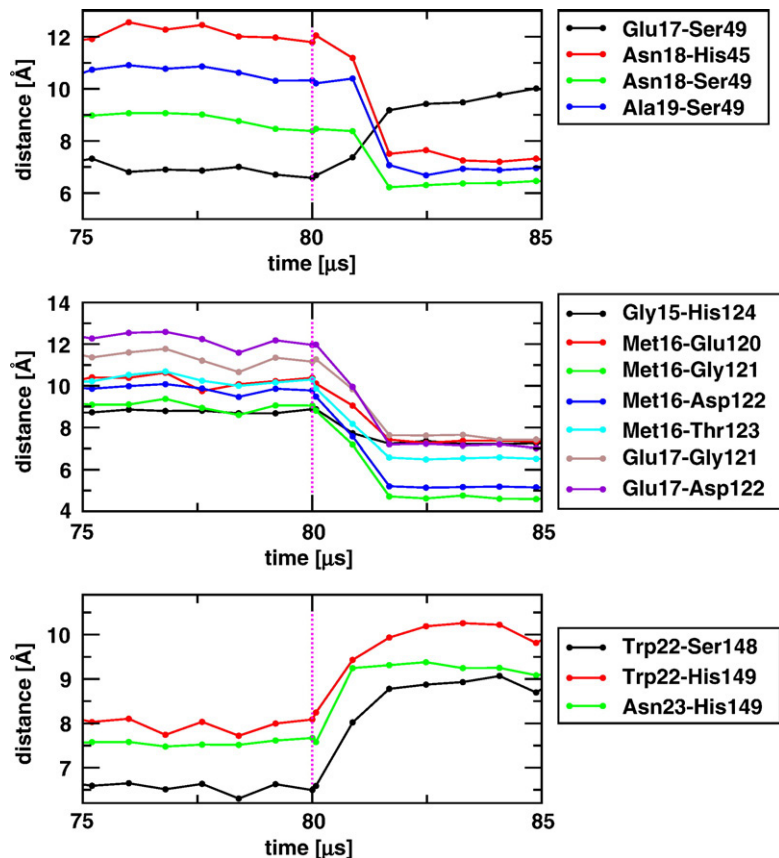


Fig. 6. Kinetics of rupture of individual contacts between residues in the various substructures of DHFR during the CS→OS transition. (a) This panel shows the changes in the distance between the residues in the Met20 loop and $\alpha 2$ that rupture and form. (b) Same as (a) except the residues represent interactions between the Met20 loop and the βF - βG loop. (c) Kinetics describing the formation of interactions between the Met20 loop and the βG - βH loop. In all cases, the identities of the residues are shown on the right.

sliding motion is vividly illustrated using the changes in the angles that the vectors \vec{R}_1 , \vec{R}_2 , \vec{R}_3 , and \vec{R}_4 make with the axis of $\alpha 2$. Angles are defined as $\alpha_i = \cos^{-1}(\vec{R}_i \cdot \vec{U}_{H2})$, $i=1, 2, 3, 4$, and \vec{U}_{H2} is the unit vector of the $\alpha 2$ helix axis. The two-dimensional projection of (R_i, α_i) ($i=1, 2, 3, 4$), which represents the values of (R_i, α_i) that are sampled in the kinetic trajectories, shows that α_i values decrease monotonically during the CS→OS transition. The averages over all the trajectories for α_i also show a monotonic decrease. The averages also show that the α_i values are either clustered around the CS or the OS. In other words, there is very little backtracking in the sliding movement of the Met20 loop along H2. The histogram of the angles and distances sampled during the transition in Fig. 7 also shows the fluctuations in α_i ($i=1, 2, 3, 4$) are centered around the OS values, which suggests that (in terms of these microscopic variables) the transition occurs when the conformation is close to the OS. This result is also in accord with the results in Fig. 6a which shows that Glu17-Ser49 only forms when the interactions in the CS are ruptured, a process that occurs closer to the completion of the CS→OS transition. The structural changes that accompany the sliding motion of the Met20 loop involve concerted motion of a number of residues (see the diagram on the left in Fig. 8). The figures summarize the collective motions of residues in both the subdomains that facilitate the structural deformations in the Met20 loop.

Cysteine cross-link inhibits CS→OS transition

The kinetics in both the forward and the backward (see below) transitions show that the coordinated motion in the loop subdomain plays an important role in enabling the Met20 loop communicate with the adenosine-binding domain. In the crystal structure of CS, the distance between the C^α atoms of Met16 and Gly121 is about 4.3 Å. It is possible to mutate these residues to Cys to establish a disulfide cross-link. We have simulated the kinetics of the CS→OS transition in the cross-link mutant (referred to as CL) to assess the extent to which the motion of the Met20 loop is inhibited. Previously, it has been argued that constraining even residues that are 28 Å apart can affect hydride transfer rates.⁴⁷ Our purpose in studying the CL mutant is to see how the strain in the loop domain would affect the communication between the two domains. Since the disulfide bond constrains the distance between Met16 and Gly121 to 4.3 Å, the anti-correlated motion between the Met20 and βF - βG loops should be impeded. The time dependencies of $\langle \Delta_L(\text{CS} | t) \rangle$ and $\langle \Delta_L(\text{OS} | t) \rangle$ show that the Met20 loop does not fully adopt its conformation in the OS (compare Fig. 5a and b). Similarly, the long time values of $\langle \Delta_G(\text{CS}) \rangle$ and $\langle \Delta_G(\text{OS}) \rangle$ in the mutant are different from those in the WT (see Fig. 5b). In the WT, βG - βH loops are involved in the coordinated motion between two domains. Surprisingly, the cross-link has little effect on the relative

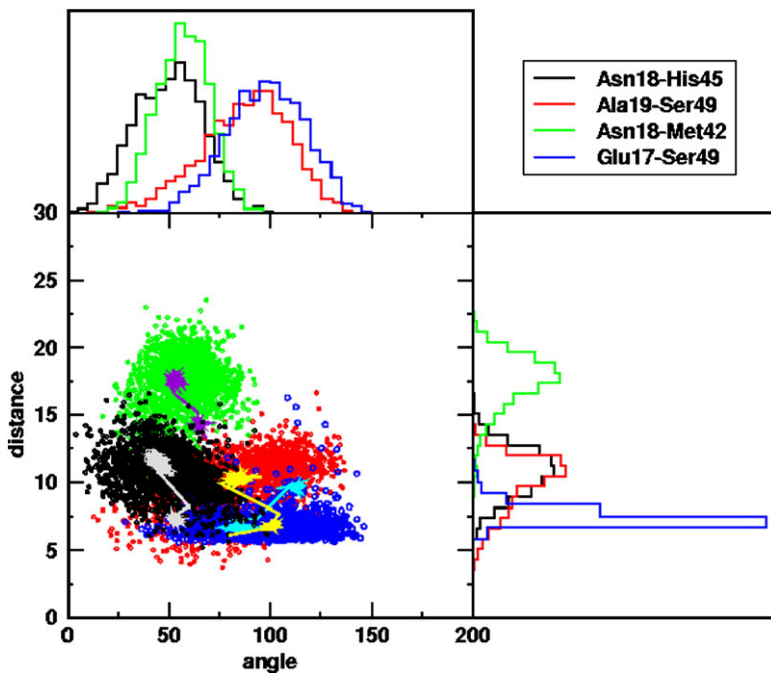


Fig. 7. Illustration of the sliding of the Met20 loop along α_2 . Two-dimensional projection of the distance (R_i) and angle (α_i) that are kinetically sampled in the 50 trajectories during the CS \rightarrow OS transition. The units are angstrom and degree for distances and angles, respectively. The angles α_i are defined in the text. The monitored residues are identified in the upper right corner. The colors gray, yellow, purple, and cyan represent ensemble averages. The monotonic decrease in all the angles shows sliding of the Met20 loop along α_2 . Histograms of the distance and the angles for the residue pairs are displayed on the right and the top, respectively.

motion between the β_G - β_H loop and the Met20 loop. The time-dependent changes that monitor the formation of contacts between Trp22-His149 and Asn23-His149 are similar in the WT and the cross-link mutant. Because the interactions between the Met20 loop and β_G - β_H loop are not fully inhibited in the CL, the sliding motion across α_2 with the formation of Glu17-Ser49 can occur (Fig. 10a), albeit less efficiently. We predict that due to the incomplete CS \rightarrow OS transition the cross-link will dramatically affect the rate of the forward hydride transition. Experiments using CL can shed further light on the

importance of enzyme motion in catalysis, which remains controversial.^{6,7,17}

Deformation of the Met20 loop drives the global motion during the OS \rightarrow CS transition

The time constant for the local kinetics of the Met20 loop in the OS \rightarrow CS transition obtained from $\langle \Delta_L(t) \rangle$ (Fig. 9) is greater than the time scale in which $\langle \Delta_G(t) \rangle$ changes. This implies that the deformation of the Met20 loop is the first event in the OS \rightarrow CS transition. In contrast, during the

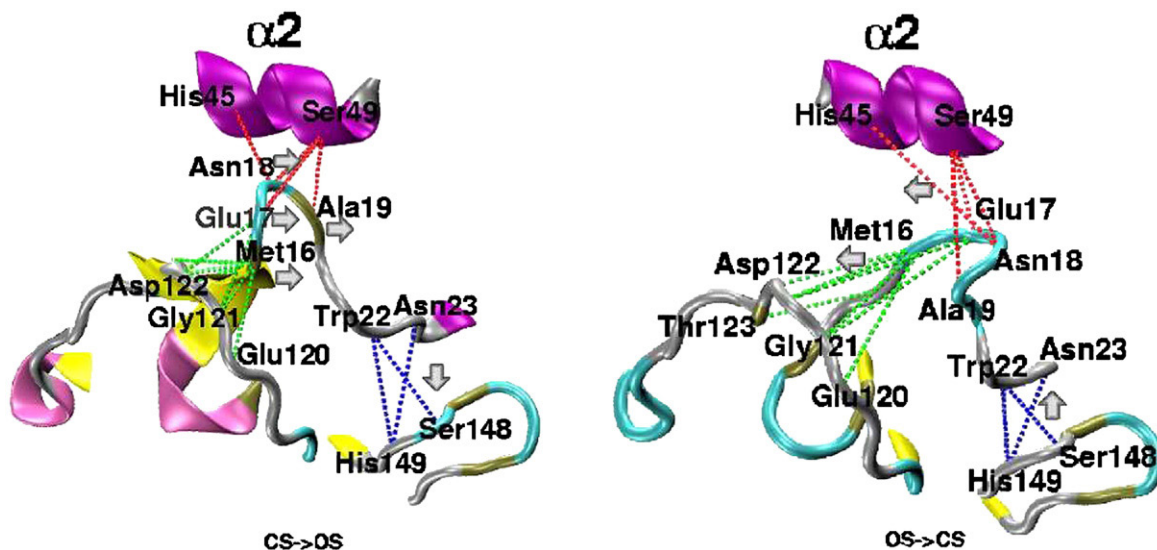


Fig. 8. Structural representation of the coordinated changes in the distances of residues that accompany the sliding motion in the CS \rightarrow OS (left side) and OS \rightarrow CS (right side) transition. The arrows indicate the direction in which the structural changes occur. The displayed structural changes were inferred from the kinetics shown in (Figs. 6, 7, and 10). In the forward transition the Met20 loop is pulled by the β_G - β_H loop, which results in it being pushed away from the β_F - β_G loop. The push-pull process results in the sliding of the Met20 loop. The mechanism is approximately reserved in the OS \rightarrow CS transition.

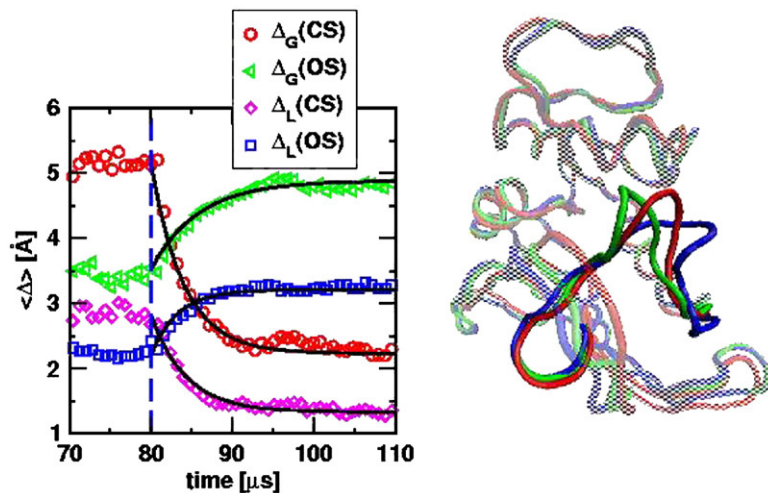


Fig. 9. Changes in $\Delta_G(t)$ and $\Delta_L(t)$ for the OS→CS transitions. Same as Fig. 5 except that the transition is from OS→CS. The conformation of the Met20 loop in the TS (red) is different from that in Fig. 5.

CS→OS transition, only in the final stages does the Met20 loop occlude the active site.

Although the initial change in the OS→CS transition involves the deformation of the Met20 loop (Fig. 9), the microscopic events that drive this transition are distinct from those seen in the CS→OS transition. Remarkably, the rupture of Glu17-Ser49 occurs only after the formation of the contact between the Met20 loop and $\alpha 2$. The time-dependent changes in the contacts present only in the CS (Asn18-His45, Asn18-Ser49, and Ala19-Ser49) occur while Glu17-Ser49 (in the OS) contact still persists (Fig. 10b). We suggest that binding of NADPH, which is required for THF to be released, assists in the formation of contacts between the Met20 loop and βF - βG , and between the Met20 loop and $\alpha 2$. Only after these contacts are established does the contact between Glu17-Ser49 rupture (Fig. 10b). Upon rupture of the Glu17-Ser49 contact, the Met20 loop slides back to its closed conformation, and THF is released.

The simulations also show coordinated motions among the three loops in the loop subdomain during the OS→CS transition (see the right side of Fig. 8). From the analysis of the time-dependent changes in the distances between a number of residues, we conclude that the βF - βG loop stretches the Met20 loop by forming a number of contacts (Gly15-His124, Met16-Glu120, Met16-Gly121, Met16-Asp122, Met16-Thr123, Glu17-Gly121, and Glu17-Asp122) with the Met20 loop. In concert with these events, the strain imposed on the Met20 loop by the βG - βH loop is released by rupture of contacts (Trp22-Ser148, Trp22-His149, and Asn23-His149) with the Met20 loop. The pull (by the βF - βG loop) and push (by the βG - βH loop) action on the Met20 loop must take place before the Met20 loop slides back to its conformation on the CS (Fig. 6b). These results show that the pathways in the OS→CS transition are not the reverse of what transpires during the CS→OS transition. The structural changes in the

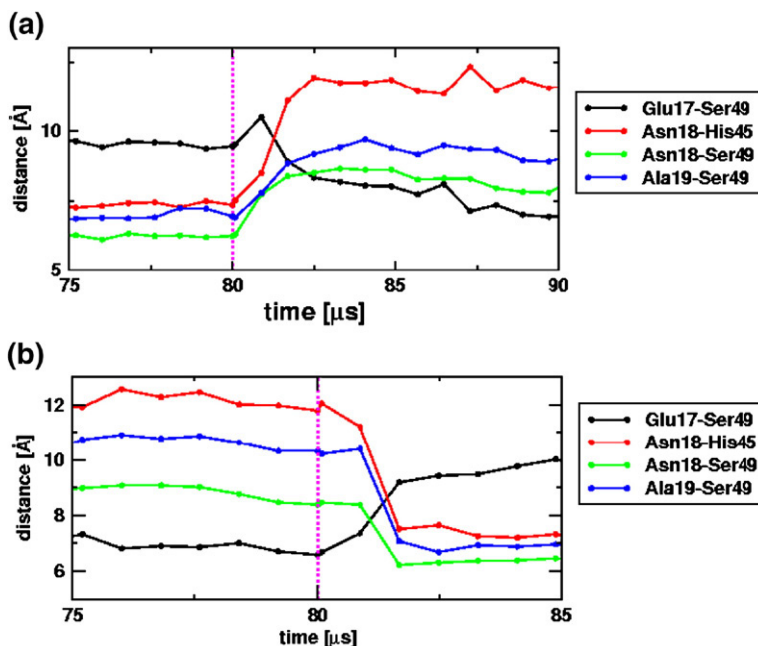


Fig. 10. Dissection of the local changes in the kinetics in CL (CS→OS) and WT (OS→CS). (a) Time-dependent changes in the distances between select residues from the Met20 loop and $\alpha 2$ for the CS→OS transition in the CL. The transition is from CS→OS. (b) Same as (a) except these represent changes that occur during the OS→CS transition for the WT.

Met20 loop and the concerted motions of a number of residues that drive these changes are shown on the right side of Fig. 8.

Residues in the allostery wiring diagram code for ligand binding and dynamics

The SCA predicts a number of residues that are expected to be relevant either in the motion of DHFR or in the function (Fig. 2a). Some of the residues in the network are related to cofactor binding and interaction with the active site, while others are directly involved in accommodating the motion of the Met20 loop during the CS→OS transition. For example, SCA identified Leu28, Ala29, and Ser63 (Fig. 2), all of which are involved in ligand binding or binding-involved dynamics. The amino acid at location 29, which in *E. coli* DHFR is Ala, is in contact with His28, showing isomerization between two isoforms of the apoenzyme.¹ In *Lactobacillus casei* enzyme, the conversion between the isoforms occurs only for the folate-bound complex, while in human DHFR there appears to be only conformation in the methotrexate–DHFR complex.¹ The importance of Ser63 in maintaining a hydrogen bond with NADPH was noted in the MD simulations.^{6,7} Similarly, Asp27 is involved in a hydrogen network with DHF in the active site.⁴⁵ The network predicted by SCA also contains Ile60 and Leu62, both of which have been recognized to be dynamically involved in interactions with the Met20 loop. SCA also suggests that Ile94 and Gly97 should play a role in the function of DHFR. Because SCA cannot assess the importance of absolutely conserved residues, it is likely that neighboring residues Gly95 and Gly96 may be relevant in the reaction cycle of DHFR.^{6,7} It is noteworthy that the SCA identified a network of residues in the helical region $\alpha 2$ in the adenosine-binding domain as being important. The present simulations show that the critical sliding motion of the Met20 loop along $\alpha 2$ completes the allosteric transitions. Mutations in the region (Ile41–His45), that is, far from the active site, have great influence on the forward hydride transfer reaction without affecting cofactor binding.^{8,9} It appears that the predictions of the SCA can be rationalized in light of a number of experimental and theoretical studies that have identified the importance of concerted motions among a sparse network of residues on the reaction cycle of DHFR. The sequence-based approach fails to identify key residues (Gly121 being the most important) that apparently play a role in catalysis.¹⁸

The average TS structure resembles OS (CS) in the CS→OS (OS→CS) transition

We have used the global RMSD (Δ_G) as a surrogate reaction coordinate to determine the structures of the TSE. We assume that the transition state (TS) for a molecule is reached for the first time at t_{TS} , if $|\Delta_G^C(t_{TS}) - \Delta_G^O(t_{TS})| < \epsilon$ ($\epsilon = 0.5 \text{ \AA}$) is satisfied. Our criterion places the TS equidistant (in terms of the

global RMSD) from the CS and OS. Comparison of the contact maps (data not shown) for the TSE, CS, and OS shows that both the transitions exhibit major changes more with respect to the starting than the ending state. The largest changes between the CS and OS, which take place in the Met20 and βF – βG loops, occur before the TS is reached.

The heterogeneity observed in the dynamics of the CS→OS transition is also reflected in the distribution $P(t_{TS})$ of the transition time t_{TS} (Fig. 11a). Surprisingly, $P(t_{TS})$ is approximately uniform in the CS→OS transition (Fig. 11a). As a result, the TSE structures are much less heterogeneous in the forward than in the backward direction (Fig. 11c). However, the spread in t_{TS} is broader in the forward direction compared to the backward direction. From the TSE we can compute a Tanford β -like parameter, q^\ddagger ($0 \leq q^\ddagger \leq 1$), using

$$q^\ddagger = \frac{\max(\Delta^\ddagger) - \Delta^\ddagger}{\max(\Delta^\ddagger) - \min(\Delta^\ddagger)} \quad (2)$$

where $\Delta^\ddagger = (\Delta_G^C(t_{TS}) + \Delta_G^O(t_{TS}))/2$ and $\max(\Delta^\ddagger)$ and $\min(\Delta^\ddagger)$ are the maximum and minimum values of Δ^\ddagger , respectively. If q^\ddagger is close to 0 (1) then the most probable TS is starting (ending) allosteric state. For the CS→OS transition the average value of q^\ddagger is 0.66 (Fig. 11b), which implies that the TSE structures are more OS-like (see the average TS structures in Figs. 5 and 9). Although the distribution $P(q^\ddagger)$ for the OS→CS is very broad (Fig. 11d), the most probable q^\ddagger is closer to the CS than to the OS. Thus, in both the transitions the average TSE structures resemble the high-energy allosteric states. This observation supports the recent inferences drawn from the NMR relaxation time measurements² that the high-energy conformation is populated (in the preequilibrium sense) in both the allosteric states. From the Hammond postulate, it follows that the TSE structures should resemble the high free energy states in accord with the present simulation results. Surprisingly, we further predict that the TSE structures for the OS→CS transition are conformationally much more heterogeneous than in the forward direction (compare Fig. 11b and d).

A small fraction of OS (CS) is present under equilibrium conditions in the CS (OS) state

Although the dominant basin of attraction corresponds to a unique native, folded state enzymes can sample other conformations, albeit not frequently, through thermal fluctuations. Some of the conformations that are sampled in the ensemble of the equilibrated CS can correspond to the structures in the OS.² Allosteric mechanism based on the pre-existing equilibrium⁴⁸ is qualitatively different from the induced-fit model,⁴⁹ which posits that the conformational transitions in the CS occur only after the ligand binds. Indeed, several experiments, including the recent reports on DHFR,² suggest that a small population of OS conformations are in equilibrium with the CS structures. Similarly, we

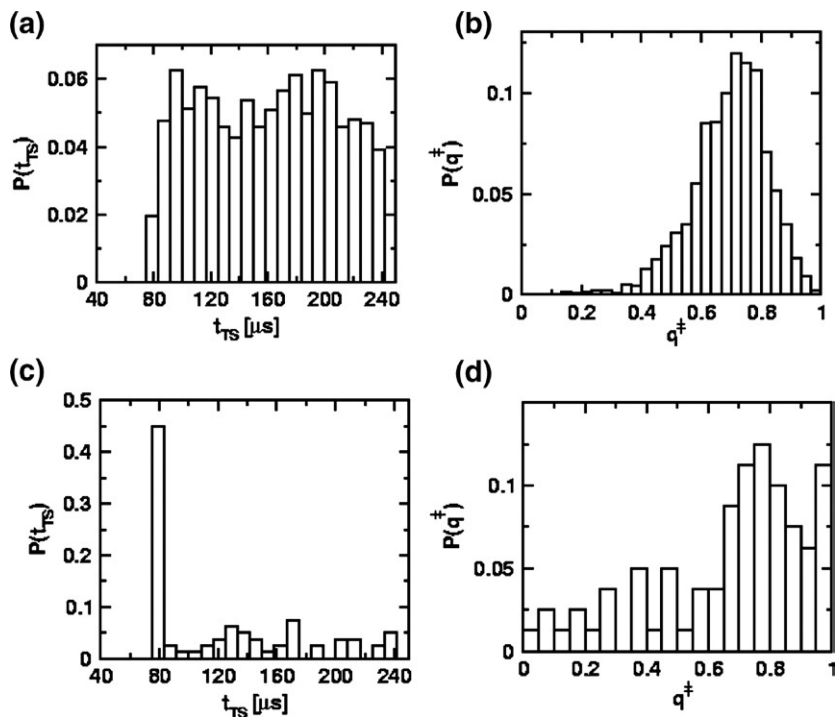


Fig. 11. Characteristics of the TSE. (a) and (c) show the distribution of transition times $P(t_{TS})$ for the forward and reverse transition, respectively. (b) and (d) represent the distributions $P(q^\ddagger)$ of q^\ddagger (see Eq. (2)) for the CS \rightarrow OS and OS \rightarrow CS transitions, respectively. In both cases, the TSE is broad. However, the width of the TSE (inferred from $P(q^\ddagger)$) in the reverse direction is larger. The fluctuation $(\langle q^{\ddagger 2} \rangle - \langle q^\ddagger \rangle^2) / \langle q^{\ddagger 2} \rangle$ is 0.2 for CS \rightarrow OS and 0.6 for OS \rightarrow CS.

expect that CS structures should be accessible when the molecule is predominantly in the OS.

In order to probe the validity of the conformational selection model⁴⁸ we calculated the distribution $P(\Delta\Delta_G)$, where

$$\Delta\Delta_G = \Delta_G^{OS} - \Delta_G^{CS} \quad (3)$$

where Δ_G^{OS} is the equilibrium RMSD of conformations in the CS with respect to the OS structure, and Δ_G^{CS} is the corresponding RMSD with respect to the CS structure. If DHFR is in the CS without ever sampling the OS-like structures then we expect that $\Delta_G^{CS} \approx 0$. As a result, $P(\Delta\Delta_G)$ should be identically zero whenever $\Delta\Delta_G < 0$. Thus, the observation of negative values of $\Delta\Delta_G$ is an indication of preexisting OS-like structures even under equilibrium conditions that favor CS (Fig. 12a). Fig. 12a (Fig. 12b) shows that $P(\Delta\Delta_G)$ is nonzero for a small range of negative (positive) $\Delta\Delta_G$ in the ensemble of CS (OS). The population of the microspecies CS (OS) in the OS (CS) basin is $\sim 3\%$ ($\sim 1\%$). Surprisingly, these estimates are similar to the values reported by Boehr *et al.*² The presence of higher energy species also suggests, in accord with the Hammond postulate, that the TS structure should be OS-like in the CS \rightarrow OS transition. This inference, which follows from the conformational selection model is in accord with our simulations. We predict that mutations that destabilize either the CS or the OS will affect the kinetics of the allosteric transitions.

Concluding Remarks

From the perspective of allostery, it is not surprising that communication between residues that

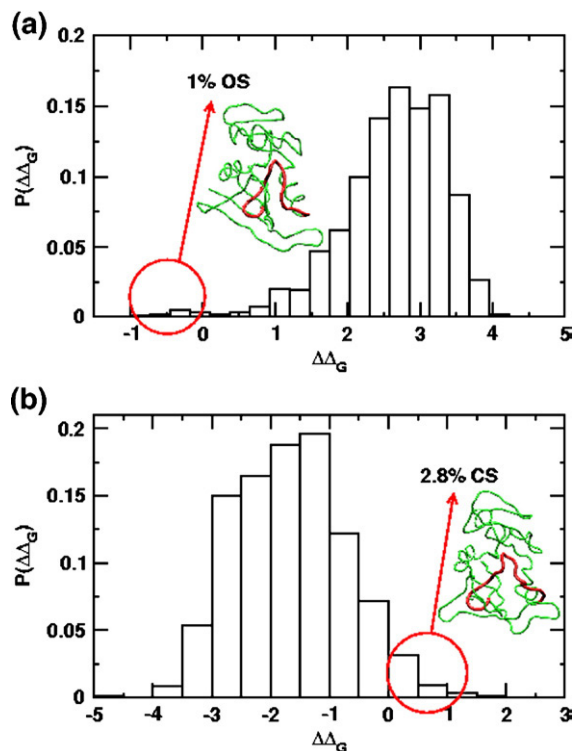


Fig. 12. Sampling of OS (CS) in the CS (OS) state. (a) Distribution of $P(\Delta\Delta_G)$, calculated using an ensemble of equilibrated conformations in the CS, as a function of $\Delta\Delta_G$ (Eq. (3)). The negative regions represent sampling of conformations that resemble the OS. (b) Same as (a) except $P(\Delta\Delta_G)$ is obtained from an ensemble of equilibrated structures in the OS state. Under equilibrium conditions, a minor population (~ 1 – 3%) of the product-like structures is present. The displayed structure in (a) is OS-like, while the one in (b) is CS-like.

are spatially well separated facilitates the CS→OS transition.⁵⁰ We have used a sequence-based method to identify a network of mechanically important residues that could control the kinetics of conformational transitions. The residues in the network are dispersed both in the adenosine binding and in the loop domains. Coordinated motions among these residues and others control the structural transitions and perhaps the forward and backward hydride transfer reaction. Surprisingly, several of these residues are not strongly conserved, although their chemical character is often preserved across the various species. Hydride transfer experiments on the WT DHFR and its mutants^{4,10} have already pointed out the importance of many of the residues in the network. In addition, all-atom MD simulations^{6,13} and NMR experiments^{1,2} have implicated the key role of the network residues in the dynamics of DHFR. Although it is difficult to unambiguously establish a direct link between the DHFR motions (equilibrium or dynamic) and hydride transfer reaction,¹⁷ the perturbation of these residues will affect magnetic resonance relaxation dispersion.

The kinetics of the allosteric transitions in the forward (CS→OS) and the reverse (OS→CS) directions, using the SOP model, reveal in great detail the order of events that results in the movement of the Met20 loop. In the forward direction, several contacts in the CS rupture and new ones form in the OS. The concerted kinetics associated with these contacts, most of which are associated with the Met20, β F- β G, and β G- β H loops facilitate the sliding motion of the Met20 loop so that it occludes the active site (Fig. 1). Surprisingly, the pathways in the OS→CS transition are not the reverse of the forward reaction. In particular, the interactions between Glu17-Ser49, whose rupture facilitates the sliding of the Met20 back to its CS position, persist till late in the OS→CS transition. In the forward direction, Glu17-Ser49 contact occurs late for the sliding motion of Met20 along α 2 to take place. The broad transition-state region, both in the forward and backward directions, attests to the inherent plasticity of enzymes in general and DHFR in particular. These results support the notion that mutations that inhibit the equilibrium fluctuations leading to the population of the minor species can adversely affect the rates of hydride transfer reactions. Indeed, the observed decrease in the hydride transfer rate in G121V has been rationalized using this picture.¹⁸

Of particular importance is the link between the present studies and the recent NMR relaxation measurements reported by Boehr *et al.*,² which showed that at equilibrium, there is a small percentage of OS structures in the ensemble of CS conformations. Similarly, when DHFR is in the OS dynamical fluctuations populate a small component (~1–3%) of CS structures. Our simulation results are in accord with the NMR experiments.² These results support the emerging notion that, in enzymes, conformations resembling the cofactor-bound struc-

ture is already present in the apoenzyme. The cofactors dynamically funnel the minor populations so that the equilibrium shifts to the holoenzyme. The present simulations show that such conformational fluctuations occur on a microsecond time scale. Because of the simplicity of the SOP model, the estimated time scale should be taken as a lower bound. The ability to access the higher free energy states on the (microsecond to millisecond) time scale is a consequence of the conformational heterogeneity of the enzyme, which leads to low barriers separating the relevant kinetic states. In DHFR, this is reflected in the broad TSE with heterogeneous structures that result in a broad distribution of crossing times between the allosteric states.

We also obtained the temperature (T) dependence of the rates of the forward and reverse transitions for the WT and the forward transition for the CL. The rates were computed by fitting the time dependence of $\langle \Delta_G(t) \rangle$ for T in the range 285 K $< T <$ 315 K. The averaging is performed using 20 trajectories. We find that the three rates follow the Arrhenius behavior. Because the SOP is a coarse-grained model, the activation barrier is severely underestimated. Nevertheless, the results show that the rates of the allosteric transitions are enhanced as T increases. Needless to say, altering T might also change the reorganization free energies of the solvent, which could be a dominant factor in determining the catalytic rates.^{17,26,51}

The predicted temperature dependence of the CS→OS transition might provide a way to test the extent to which correlated enzyme dynamics is important in catalysis. If the rates of conformational fluctuations are drastically different from the rate of the chemical step then it is unlikely that the correlated motions of the enzyme is crucial to catalysis. On the other hand, if the two states are comparable then the conformational changes during the CS→OS transition might be coupled to hydride transfer. In general, it is important to formulate a method that couples the dynamics of the CS→OS transition (including the cofactors) and the chemical step. Such a formalism must account for both the kinetics of transitions along the lines described here and the hydride transfer processes described by others.^{6,26}

The SOP model, which was introduced to carry out simulations of large systems,^{52,53} does not include a number of relevant interactions. Most notably, the lack of an explicit model for hydrogen bonds prevents us from examining their role in the allosteric transitions. The role the network of hydrogen bonds of DHFR plays in affecting the CS→OS transition can only be vicariously gleaned using the SOP model. On the other hand, the major advantage of the SOP model is that long-time simulations for a large number of trajectories can be carried out. Indeed, the nontrivial prediction that the coordinated motions of specific residues throughout the structure trigger the movement of the Met20 loop is amenable to experimental tests. The nonconserved residues identified in this work

can form the basis of future mutagenesis experiments. We believe that a combination of computational methods (sequence-based technique, coarse-grained and all-atom MD simulations) and NMR, single molecule, and biochemical experiments are needed to fully dissect the interplay between enzyme motion and catalysis.

Methods

Statistical coupling analysis

In order to identify the residues that are involved in transmitting allosteric signals, we use our formulation³³ of the sequence-based SCA introduced by Suel *et al.*,³⁴ Hatley *et al.*,³⁵ and Jain and Ranganathan.³⁶ A statistical free energy-like function at each position, i , in a multiple sequence alignment is defined as

$$\frac{\Delta G_i}{k_B T^*} = \sqrt{\frac{1}{C_i} \sum_{x=1}^{20} \left[p_i^x \ln \left(\frac{p_i^x}{p_x} \right) \right]^2} \quad (4)$$

where, $k_B T^*$ is an arbitrary energy unit, C_i is the number of types of amino acid that appears at position i , p_x is the mean frequency of amino acid x in the MSA. In Eq. (1), $p_i^x = \frac{n_i^x}{N_i}$, where n_i^x is the number of times amino acid x appears at position i in the MSA, and $N_i = \sum_{x=1}^{20} n_i^x$.

The basic hypothesis of the SCA is that correlation or covariation between two positions i and j may be inferred by comparing the statistical properties of the MSA and a subalignment of sequences (derived from the MSA) in which a given amino acid is conserved ($S_j=0$) at j . The restriction that $S_j=0$ in the subalignment is referred to as sequence perturbation at position j . The effect of perturbation is assessed using

$$\frac{\Delta \Delta G_{ij}}{k T^*} = \sqrt{\frac{1}{C_i} \sum_{x=1}^{20} \left[p_{i,R}^x \ln \left(\frac{p_{i,R}^x}{p_x} \right) - p_i^x \ln \left(\frac{p_i^x}{p_x} \right) \right]^2} \quad (5)$$

where $p_{i,R}^x = n_{i,R}^x / N_{i,R}$, $n_{i,R}^x$ and $N_{i,R}$ are the number of sequences in the subalignment in which x appears in the i th position, and $N_{i,R} = \sum_{x=1}^{20} n_{i,R}^x$.

In order to obtain statistically meaningful results using the SCA, it is crucial to choose the subalignments appropriately. Let $f = p / N_{\text{MSA}}$ where p is the number of sequences in the subalignment and N_{MSA} is the total number of sequences in the MSA. We choose $f (=0.35$ for the DHFR family) to satisfy the central limit theorem³³ so that the statistical properties from the subalignments coincide with the full MSA. Using $f=0.35$, we calculated the matrix elements $\Delta \Delta G_{ij}$ that estimate the response of position i in the MSA to all allowed perturbations at j ($S_j=0$). The rows (labeled i) in $\Delta \Delta G_{ij}$ correspond to positions in the MSA. We determined the network of covarying residues using the elements $\Delta \Delta G_{ij}$ in conjunction with a coupled two-way clustering algorithm.⁵⁴ The extent to which the rows $\Delta \Delta G_{ij}$ and $\Delta \Delta G_{kj}$ are similar is assessed using the Euclidean measure.³³ Because $\Delta \Delta G_{ij}=0$ for perfectly conserved positions and for sites where the amino acids are found at their mean frequencies in the MSA ($p_i^x = p_x$), the SCA cannot predict the role these residues play in the function or dynamics of the enzyme.

Self-organized polymer model for closed and occluded states

We have carried out Brownian dynamics simulations to obtain the kinetics of transitions between the allosteric states. Because of long time scales involved in these transitions, we use a coarse-grained SOP model for DHFR in the CS and OS. The validity of the SOP model has been established in the context of mechanical unfolding of RNA and proteins,³⁸ allostery in GroEL,⁵³ and conformational changes in kinesin.⁵⁵ In the SOP model, the structure of a protein is represented using only the C^α coordinates. Because we are interested in the kinetics of CS→OS and OS→CS transitions, the energy functions are state dependent. The state-dependent energy function in the SOP representation of protein structures in terms of the C^α coordinates r_i ($i=1, 2, \dots, N$, with N being the number of amino acids), is

$$\begin{aligned} V\{r_i|X\} = & V_{\text{FENE}} + V_{\text{NB}}^A + V_{\text{NB}}^R \\ = & - \sum_{i=1}^{N-1} \frac{k}{2} R_0^2 \log \left(1 - \frac{(r_{i,i+1} - r_{i,i+1}^0(X))^2}{R_0^2} \right) \\ & + \sum_{i=1}^{N-3} \sum_{j=i+3}^N \epsilon_h \left[\left(\frac{r_{ij}^0(X)}{r_{ij}} \right)^{12} - 2 \left(\frac{r_{ij}^0(X)}{r_{ij}} \right)^6 \right] \Delta_{ij} \\ & + \sum_{i=1}^{N-2} \epsilon_l \left(\frac{r_{i,i+2}^0}{r_{i,i+2}} \right)^6 + \sum_{i < j} \epsilon_l \left(\frac{\sigma}{r_{ij}} \right)^6 (1 - \Delta_{ij}), \end{aligned} \quad (6)$$

where the label X refers to the allosteric state CS or OS. In Eq. (6), $r_{i,i+1}$ is the distance between two consecutive C^α atoms, r_{ij} is the distance between the i th and j th C^α atoms, and the superscript 0 denotes their values in the crystal structure of the allosteric state X . The first term in Eq. (6), the finite extensible nonlinear elastic (FENE) potential, accounts for chain connectivity. The stability of the state X is described by the nonbonded interactions (second term in Eq. (6)) that assign attractions between residues that are in contact in X . Nonbonded interactions between residues that are not in contact in X are taken to be purely repulsive (third term in Eq. (6)). The value of $\Delta_{i,j}$ is 1 if i and j are in native contact and is zero otherwise.

In the SOP model, there are only two independent parameters. The results are insensitive to the precise values of k , R_0 , and ϵ_l . The two key parameters are ϵ_h , a single-energy scale that describes the stability of state X , and the cutoff distance R_C for native contacts. Because R_C is, to a large extent, determined by the contact map, there is very little freedom in its choice. We assume that native contact exists if the distance between the i th and j th C^α atoms is less than 8 Å. The spring constant k in the FENE potential (first term in Eq. (6)) for stretching the covalent bond is 20 kcal/(mol Å²), $\epsilon_h = 2$ kcal/mol, and the value of R_0 , which gives the allowed extension of the covalent bond, is 2 Å.

Brownian dynamics simulations of allosteric transitions

The kinetics of forward and backward transitions between CS and OS are probed using a method that was recently used to study allosteric transitions in GroEL.⁵³ The basic assumption of the method is that the local strain that DHFR experiences (due to a ligand or cofactor binding) propagates faster across the structure than the conformational transitions that lead to the CS→OS and

vice versa. In other words, the global structural relaxation is the slow step in the allosteric transition.

Using the SOP model, we simulated the transition between the CS (PDB code 1RX2) and OS (PDB code 1RX7) by assuming that the dynamics of the protein can be adequately described by the Langevin equation in the overdamped limit. Transitions from one allosteric state (CS) to another (OS) are induced by starting from a conformation corresponding to the CS. The transition is induced by using the forces computed from the OS, i.e., from $H\{r_i|\text{OS}\}$. The explicit equations of motion for CS→OS are

$$\zeta \frac{\partial r_i}{\partial t} = -\frac{\partial H(r_i|\text{OS})}{\partial r_i} + F(t) \quad (7)$$

where $H(r_i|\text{OS})$ is the Hamiltonian of the OS, ζ is the friction coefficient, $F(t)$ is the random force, and r_i is the position of the i th residue at time t . The initial ($t=0$) value of r_i is taken from the Boltzmann distribution at temperature T corresponding to the CS,

$$P(r_i(0)) \sim e^{-\beta H(r_i|\text{CS})} \quad (8)$$

where $\beta = 1/(k_B T)$ and k_B is the Boltzmann constant. The random force, $F(t)$, satisfies

$$\langle F(t) \rangle = 0 \quad (9)$$

and

$$\langle F(t)F(t') \rangle = 2k_B T \zeta \delta(t - t') \quad (10)$$

where the averages are over the trajectories. As long as potential conditions are satisfied,⁵⁶ our method for inducing transitions ensures that, at long times, DHFR will explore the conformations corresponding to the OS. At long times, the ensemble of conformations obeys the Boltzmann distribution corresponding to the OS so that $P(r_i|\text{OS}) \sim e^{-\beta H(r_i|\text{OS})}$. Thus, on general theoretical grounds, our procedure guarantees that CS→OS transition can be realized and that the dynamics represents the microscopic events that drive the transition of interest. To monitor the reverse reaction, we begin with an initial equilibrated ensemble of structures corresponding to the OS and integrate the equations of motion (Eq. (7)) with the forces arising from the CS.

The procedure used to induce the allosteric transition hinges on the physically reasonable assumption that the time scales involved in the conformational changes in the enzymes are much longer than the time needed for locally induced strain (due to cofactor binding, for example) to propagate through the structure. In order to test this assumption, we varied the rate at which the CS→OS transition is allowed to take place by allowing $r_{ij}^o(\text{CS} \rightarrow \text{OS})$ to evolve slowly on a relatively long time scale. We accomplish the slower evolution using,

$$r_{ij}^o(\text{CS} \rightarrow \text{OS}) = \frac{(K - k)r_{ij}^o(\text{CS}) + kr_{ij}^o(\text{OS})}{K} \quad (11)$$

The majority of the results were obtained using $K = k = 1$. To vary the strain propagation time we also performed simulations using $K = 100$ and increased k in steps. The CS→OS conformational switch was made smoothly over a range of times, namely, 0.12, 0.16, 0.2, and 0.24 μs . The kinetics of $\langle \Delta_G(t) \rangle$ for the CS→OS transition, which reports on the time dependence of the global RMSD changes, for the four cases coincide with the results in Figs. 5 and 9 (data not shown). These additional simulations justify the assumption

underlying our procedure for inducing the conformational transition.

Time scales and simulation details

In order to decipher the events that drive the conformational changes in the Met20 loop during the catalytic cycle, we performed three different simulations. We first simulated the kinetics of CS→OS transitions to determine the order of events during the forward reaction. In order to assess the roles of the residues G121 and M16 (the C $^\alpha$ distance between the two is about 4.3 Å in the CS), in the CS→OS transition we mutated M16–G121 interaction by a disulfide bond. Such a cross-link, referred to as CL, can be made by mutating these two residues to cysteines. The disulfide bond is simulated by adding a FENE potential between M16 and G121 (see Eq. (6)). The CL mutant allows us to assess the coupling between two distal residues, one in the Met20 loop and the other in the βF – βG loop, on the CS→OS transition. Experiments by Hammes-Schiffer and Benkovic have established that mutation of G121 can affect the hydride transfer reaction.⁴ Finally, we also simulated the OS→CS transition that occurs during the release of THF.

We used Brownian dynamics algorithm using an integration time step $\Delta\tau_H = \tau_L \frac{\zeta \epsilon_i h}{k_B T}$. A typical value for τ_L for proteins is 3 ps.⁵⁷ The simulations were performed with $\zeta = 50\tau_L^{-1}$, which approximately corresponds to water viscosity. The typical value of the integration step size is $h = 0.16\tau_L$. During the transition from one allosteric state to another, we reduced h 10-fold to maintain numerical stability. We first equilibrate DHFR in the CS at $T = 300$ K for 80 μs . Subsequently, the forces are computed using the OS Hamiltonian. The equations of motion are integrated for long times (typically exceeding 700 μs) so that the transition to the OS is complete. A similar procedure is used for the reverse reaction and the cysteine cross-link mutants. We generated 50 trajectories for each conformational transition so that the reported results for the kinetics are statistically significant.

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