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Dissecting conformational contributions to glycosidase catalysis and inhibition
Gaetano Speciale¹, Andrew J Thompson², Gideon J Davies² and Spencer J Williams¹

Glycoside hydrolases (GHs) are classified into >100 sequence-based families. These enzymes process a wide variety of complex carbohydrates with varying stereochemistry at the anomeric and other ring positions. The shapes that these sugars adopt upon binding to their cognate GHs, and the conformational changes that occur along the catalysis reaction coordinate is termed the conformational itinerary. Efforts to define the conformational itineraries of GHs have focussed upon the critical points of the reaction: substrate-bound (Michaelis), transition state, intermediate (if relevant) and product-bound. Recent approaches to defining conformational itineraries that marry X-ray crystallography of enzymes bound to ligands that mimic the critical points, along with advanced computational methods and kinetic isotope effects are discussed.

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Glycoside hydrolases catalyze the hydrolytic cleavage of the glycosidic bond. They are enzymes of enduring interest owing to the ubiquity of carbohydrates in nature and their importance in human health and disease, the food, detergent, oil & gas and biotechnology industries. Glycoside hydrolases generally, but not quite exclusively, perform catalysis with a net retention or inversion of anomeric stereochemistry. The gross mechanisms of glycosidases were postulated by Koshland in 1953 [1⁹], and his prescient insights remain largely true to this day. The glycoside hydrolases are an immensely varied group of enzymes and are usefully classified on the basis of sequence according to the CAZy system (www.cazy.org; see also Cazypedia: www.cazypedia.org), which reveals a growing and formidable diversity of proteins (133 families as of 2014) [2]. What continues to occupy the attention of mechanistic enzymologists is a complete description of the fine details of the overall reaction coordinate. The free energy profile of catalysis is a composite of terms including: bond-making and breaking; the establishment and disbandment of stereochemical effects; and conformational effects. Conformational interactions include substrate-based: vicinal (e.g. eclipsing, gauche, Δ2), 1,3-diaxial, and 1,4-bridgehead; and enzyme-based: local and global conformational changes of the enzyme that occur on the time-scale of catalysis [3].

Two major areas of inquiry are active in the area of conformation and glycoside hydrolases:

1. What are the conformational changes that occur during catalysis upon substrate binding, at the transition state(s), intermediates (if relevant), and product? Aside from the elemental interest in this question, there is the potential for utilizing this information to develop glycosidase inhibitors that take advantage of the considerable amounts of energy used to selectively bind the transition state (for a glycosidase with a catalytic rate enhancement of 10¹⁷, the calculated transition state affinity is 10⁻²² M [4]), with the enticing possibility that differences in transition state conformation may allow the development of glycosidase-selective inhibitors.

2. Once transition-state structural information is acquired and used to inspire inhibitor development, do the resulting inhibitors actually bind by utilizing the same interactions that are used to stabilize the transition state — that is, are they genuine transition state mimics? The answers to this question speak to our abilities to realize this unique form of rational inhibitor design.

In this review we cover recent developments in the understanding of conformational reaction coordinates and how such information is acquired; and what constitutes good transition state mimicry by inhibitors. This work extends two recent comprehensive reviews [5,6⁵].

Conrotions along the reaction coordinate
Substantial evidence has accrued that retaining and inverting glycoside hydrolases perform catalysis through an oxocarbenium ion-like transition state with significant bond breakage to the departing group and limited bond formation to the attacking nucleophile (Figure 1a) [7]. On
the basis of the four idealized half-chair and boat conformations expected for the transition state (see Side Panel A), four ‘classical’ conformational itineraries may be identified (Figure 1b). In these simplified presentations, it is apparent that C1 scribes an arc along the conformational reaction coordinate as it undergoes an electrophilic migration from the leaving group to a nucleophile. However, other ring atoms also change positions, in particular O5 and C2. The subtle change in the position of O5 has little mechanistic consequence other than to allow development of the partial double bond. Interactions at C2 are usually (but not always, see: [8]) significant and for the β-glucosidase Abg from Agrobacterium sp. or for α-glucosidase of Saccharomyces cerevisiae [9] have been shown to contribute 18–22 kJ mol\(^{-1}\) to transition state stabilization [10], highlighting that the repositioning of C2 and its substituent and other electronic changes accompanying formation of the oxocarbenium

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**Side panel A Theoretical considerations of the transition state conformation**

It is a stereoelectronic requirement that the development of a partial double bond between O5 and C1 results in flattening of the system C2–C1–O5–C5, with the remaining pyranose C3 and C4 atoms having freedom to move [11]. The possible idealized transition state structures that satisfy these requirements are \(3^3H_4, 4^4H_3\) and \(B_{2,5}\) (and the closely related but usually higher energy \(^4E, ^2E, E_4\) and \(E_3\)). As the oxocarbenium ion-like transition states of glycosidases are ‘central’ transition states it is appropriate to invoke the principle of least nuclear motion, which states that elementary reactions that involve the least change in atomic position and electronic configuration will be favoured [12,13]. Accordingly, the conformational reaction coordinate will most likely involve ground state conformations (corresponding to Michaelis, intermediate and product complexes) that are close neighbors to the transition state conformations. The conformational relationships of pyranose rings [14] may be conveniently summarized using a Cremer-Pople sphere [15] or its equivalent Mercator and polar projections (Figure 1).

---

**Figure 1**

(a) Possible flattened transition state conformations

(a) Half-chair transition states

\[
\begin{align*}
&\text{(a) Half-chair transition states} \\
&\text{(b) Boat transition states} \\
&\text{(b) Main conformations of a pyranose ring on the Cremer-Pople sphere and the Mercator projection}
\end{align*}
\]

---

(a) Classical glycosidase mechanisms

Inverting β-glycoside hydrolases

(i) Classical glycosidase mechanisms

Retaining β-glycoside hydrolases:

(ii)

(iii)

(b) Classical conformational itineraries

(i) Classical conformational itineraries

(ii)

(iii)

(iv)

(c) Strategies to study species along the reaction coordinate

(i) Non-hydrolyzable substrate mimics that allow study of the Michaelis complex:

(ii) Reagents that kinetically trap glycosyl enzyme intermediates:

(iii) Sugar-shaped heterocycles as possible transition state or intermediate mimics:

NAGthiazoline
mannoimidazole
isofagomine
neuromycin
zanamivir
oseltamivir
kifunensine
acarbose

(a) Mechanisms of classical (i) inverting and retaining glycosidases that utilize (ii) an enzymic nucleophile or (iii) substrate-assisted catalysis.
(b) Classical conformational itineraries around planar, oxocarbenium ion-like transition states in (i,ii) half-chair (H) or (iii,iv) boat (B) conformations.
(c) Strategies and reagents used to study key species along the reaction coordinate.
ion-like transition state can provide substantial amounts of stabilization energy. The ground state conformations and those of intermediates and transition states need not sit squarely on the graticules of the major meridians and latitudes but may be located within the conformational space nearby (see Side Panel A).

Powerful computing resources allow the calculation of the energy of every possible conformation of individual sugars providing a so-called free energy landscape (FEL). Each carbohydrate stereoisomer possesses a unique FEL, owing to the presence of various substituents, the resulting hydrogen-bonding interactions, local steric interactions, and the contribution of the anomic effect. This computational approach was first applied to β-glucopyranose and 9 energetic minima were identified [16]. Aside from the global minimum of 4C1, the remaining 8 local minima were approximate B and S conformations; however these differed from the canonical B and S conformations owing to the lack of rigidity of the ring, and the presence of attractive (hydrogen bonding) and repulsive (eclipsing and 1,3-diaxial) interactions. Several of these conformations were identified as pre-activated for catalysis, with pseudo-axial C1–O1 bonds leading to a lengthening of the C1–O1 bond and a shortening of the O5–C1 bond owing to the developing anomic effect, and partial charge at C1 (see Side Panel B). Enticingly, the pre-activated conformations are those that are most frequently observed in so-called Michaelis complexes (representing E.S complexes) studied by X-ray crystallography for Gs that process β-glucosides. FEL analysis has been extended to include α-glucopyranose, β-xylpyranose, β-mannopyranose, and β-N-acetylglucopyranosamine [17], and α-mannopyranose [18*], with the data supporting the conclusion that for these sugars the catalytically relevant conformations are frequently the energetically predisposed distorted structures. These observations are harmonious with the suggestion of Wolfenden that the fact that many enzymes achieve rates approaching the diffusion limit suggests that they have evolved to recognize species that are reasonably populous in solution [19].

Defining the conformational coordinate: Is seeing believing?

X-ray crystallography is a powerful technique that provides a detailed molecular description of the catalytic machinery of an enzyme. While unliganded (apo) structures provide some information that can be used to help understand mechanism, the acquisition of complexes, with substrates (or substrate analogues), sugar-shaped inhibitors, mechanism-based inhibitors, or products have the potential to reveal intricate details of the amino acid residues involved in catalysis and the conformations of enzyme-bound species (Figure 1c). Three main strategies for the acquisition of Michaelis (E.S)-like complexes of retaining and inverting glycosidases are: firstly, co-crystallization of non-hydroxyable substrate mimics with wild-type enzyme (Figure 1c(i)) [22], or secondly, co-crystallization of substrate with catalytically inactive mutant enzymes, or thirdly, co-crystallization of substrate and wildtype enzyme at a pH at which it is inactive. Occasionally, Michaelis complexes have been obtained serendipitously at pH values under which the enzyme is active; the reason for lack of hydrolysis in these cases is unclear [23,24].

For retaining glycoside hydrolases that proceed through a glycosyl enzyme intermediate, fairly effective methods have been developed to allow the trapping of kinetically competent intermediates [25]; the general principle is to rapidly access the glycosyl enzyme intermediate using a good leaving group, but to modify the sugar such that its turnover to product is slowed, allowing its accumulation and study. The initial work by Legler involved addition to glycals to generate 2-deoxyglycosyl enzymes [26] or use of aryl 2-deoxyglycosides [27], and was elegantly extended by Withers to 2-deoxy-2-fluoro-, 2-deoxy-2,2-difluoro- and 5-fluoro glycosyl fluorides (and closely related 2,4-dinitrophenyl, and other activated glycosides) [25] (Figure 1c(ii)). For reasons that are not entirely clear, for α-glycosidases the use of C5-inverted 5-fluoro-glycosyl fluorides for the corresponding enzymes usually yield better trapping results than for the stereochemically-matched alternative. For retaining enzymes that proceed by anchimeric assistance from a 2-acylamido group, sulfur mimics of the proposed oxazoline (or oxazolinium ion) intermediate, most notably NAGthiazoline [28,29], have proved effective as inhibitors and informative as mechanistic probes for crystallographically studying the intermediate (Figure 1c(iii)).
It is important to recognize that all X-ray structures of protein–ligand complexes are by their very nature not catalytically competent and thus care must be taken in how to interpret the important clues they provide in the proposal of a credible conformational itinerary. Kinetically trapped species recapitulate the major bond-forming and breaking events but the structural modifications made to allow kinetic trapping may perturb substrate interactions that are important for defining the conformational reaction coordinate. Occasionally, crystallization efforts at non-optimal pH have led to the acquisition of apparently bonafide Michaelis complexes; however even these constitute complexes with catalytically-incompetent enzymes and the interpretation of these structures must recognize that these do not lie on the reaction coordinate. Complexes with substrate and enzyme may be ‘pre-Michaelis’ complexes that represent enzyme-bound species that precede the formation of the true Michaelis complex, or may be catalytically irrelevant species that are actively misleading. Product bound to enzyme may have relaxed from its first formed conformation as the lack of a sizeable anomic substituent prevents the enzyme from utilizing +1 subsite interactions to stabilize its conformation. Nonetheless, with some exceptions, most pseudo-Michaelis, glycosyl enzyme intermediate or thiazoline intermediate, and product complexes are sufficiently akin to hypothetical bonafide species on the reaction coordinate to allow cautious but probably reasonable insights into mechanism.

Caution must also be exercised when studying complexes with sugar-shaped heterocycles that function as competitive inhibitors (Figure 1c(iii)). While superficially these compounds resemble aspects of the proposed transition state, there are intrinsic limitations of what can be mimicked in a chemically stable compound, including hybridization changes, partial charge development, and fractional bond orders. A study of the FELs of two inhibitors that display superficial transition state mimicry: isofagomine and mannoimidazolide revealed dramatic differences (Figure 2a) [30**]. Isofagomine is strongly biased toward a $^4C_1$ conformation, with potential transition state mimicking $^4H_3$ and $B_{2.5}$ conformations lying 12 and 8 kcal mol$^{-1}$ higher, respectively, and importantly with a significant barrier to attaining those conformations. On the other hand while mannoimidazolide prefers $^4H_3$ and $^3H_4$ conformations (with a 1 kcal mol$^{-1}$ preference for the latter), the $B_{2.5}$ conformation is also energetically accessible. Overlaying the observed conformations of isofagomine-type and mannoimidazolide-type inhibitors from X-ray structures with manno-processing enzymes of various GH families reveals all isofagomine complexes adopt a $^4C_1$ conformation, whereas for mannoimidazolide the $B_{2.5}$ conformation is observed on enzymes of families GH2, 26, 38, 92 and 113, implying a $^1S_5$→$B_{2.5}$→$^3S_2$ conformational itinerary. One interesting footnote is that non-ground state conformations of isofagomine-type inhibitors have been observed on family GH6 cellulases in either $^2S_0$ or $^2S_1$ conformations [31,32]. The energetic difficulties in attaining such conformations highlight their special significance when seen and in these cases they reflect the proposed $^2S_0$→$^2S_1$ itinerary.

While the FEL of an isolated carbohydrate is often biased toward those conformations pre-activated for catalysis, further substrate distortion presumably occurs upon binding to enzyme. Quantum mechanics/molecular mechanics calculations of α-mannopyranose revealed that a FEL determined within the constraints of a GH47 α-mannosidase is moulded by the enzyme to dramatically limit the conformations accessible by the substrate to a previously inaccessible region of the FEL for the substrate off-enzyme (Figure 2b) [18**]. In support of the theoretical predictions, X-ray analysis of ‘snapshot’ complexes of the enzyme with a substrate analogue, transition state, and product mimics supported a $^3S_1$→$^4H_4$→$C_4$ conformational itinerary predicted on the basis of the FEL remodelling.

### Sugars getting into shape: News dispatches from the families

Table 1 summarizes well-defined conformational itineraries for a range of GH enzymes (see Supporting Information for a more detailed listing). We present a few highlights from the last two years that are not covered in detail elsewhere.

β-Hexosaminidases of family GH3 perform catalysis through a two step mechanism with the initial substitution step occurring by an enzymatic nucleophile to afford a glycosyl enzyme intermediate (Figure 1a(ii)). Insight into the reaction coordinate has been obtained through trapping a glycosyl enzyme intermediate in a $^3C_1$ conformation using the mechanism based inhibitor 5F-GlcNacF, suggesting a $^3S_1$→$^4H_3$→$C_1$ itinerary [33*]. Interestingly, a complex with an inactive mutant with substrate, and of wild-type with product, also revealed $^3C_1$ conformations. In this case there is strong evidence that the complex with substrate is not a bonafide Michaelis complex as a loop containing the putative histidine general acid/base undergoes a dramatic movement. In the product complex it appears that the sugar has relaxed to a more stable conformation.

Family GH39 α-L-iduronidase (IDUA) is a retaining lysosomal enzyme that assists in the stepwise degradation of heparin sulfate and dermatan sulfate, and which is of interest for enzyme replacement therapy of the associated lysosomal storage disorder (LSD) mucopolysaccharidosis type I [34*]. Michaelis complexes with iduronate analogues in $^3S_2$ conformations, and the trapping of a glycosyl enzyme on IDUA in a $^3S_1$$^z$$^2B$ conformation using 2-deoxy-2-fluoro-α-L-idopyranosyluronic
(a) Assigning the conformational itinerary of a family GH26 retaining β-mannanase
(i) Mannomimidazole, but not isofagomine, faithfully reports transition state conformation
(ii) X-ray ‘snapshots’ along the reaction coordinate
(iii) Proposed conformational itinerary

(b) Assigning the conformational itinerary of a family GH47 inverting α-mannosidase
(i) Free energy landscape of methyl α-D-mannopyranoside
(ii) X-ray ‘snapshots’ along the reaction coordinate
(iii) Proposed conformational itinerary

Computational studies, in concert with X-ray crystallography and inhibitor design and synthesis, assist in assigning conformational itineraries. (a) Assigning the conformational itinerary of Cellvibrio japonicas GH26 β-mannanase Man26C. (i) Free energy landscapes reveal mannomimidazole, unlike isofagomine, is able to attain the conformations relevant to glycosidase catalysis; (ii) X-ray structures of a Michaelis complex (1GVY), glycosyl enzyme intermediate (1GW1), and transition state mimicking β-mannosyl-1,4-mannoimidazole complex (4CD5); (iii) proposed conformational itinerary. (b) Assigning the conformational itinerary of Caulobacter strain K31 GH47 α-mannosidase. (i) Free energy landscapes highlight substrate preactivation off-enzyme, and reshaping of the available conformations on-enzyme; (ii) X-ray structures of Michaelis complex (4AYP), transition state mimicking mannomimidazol complex (4AYQ), and product mimicking noeuromycin complex (4AYR); (iii) proposed conformational itinerary.
Table 1

<table>
<thead>
<tr>
<th>Transition state conformation</th>
<th>GH families</th>
<th>Configuration of substrate</th>
<th>Enzymatic activities</th>
</tr>
</thead>
<tbody>
<tr>
<td>$^3H_2$ (1H$^2$ for sialidases)</td>
<td>29, 33, 34, 47</td>
<td>$\alpha$-fucos (1-2-galacto) sialic acid, $\alpha$-Gluco-4-xi</td>
<td>$\alpha$-Fucosidase, $\alpha$-Mannosidase</td>
</tr>
<tr>
<td>$^4H_2$</td>
<td>1, 2, 3, 5, 7, 10, 12, 16, 20, 22, 26, 27, 30, 84</td>
<td>$\alpha$-galacto, $\alpha$-rhamno $\beta$-Glucosidase/cellulose/lichenases/3- $\beta$-mannosidase</td>
<td></td>
</tr>
<tr>
<td>$^5B_1$</td>
<td>6, 8, 11</td>
<td>$\alpha$-galacto, $\alpha$-gluco $\beta$-Glucosidase, $\beta$-Hexosaminidase</td>
<td></td>
</tr>
<tr>
<td>$^5B_1$</td>
<td>2, 26, 38, 92, 113</td>
<td>$\alpha$-manno, $\alpha$-gluco, $\alpha$-xilo Xylanase</td>
<td></td>
</tr>
<tr>
<td>$^4E$</td>
<td>117</td>
<td>3,6-anhydro-L-galacto $\alpha$-Fucosidase, $\alpha$-Mannosidase</td>
<td></td>
</tr>
</tbody>
</table>

acid fluoride, imply a $^{2,5}S_0$→$^{2,5}B_1$→$^5S_1$ conformational itinerary (Figure 3a) [35**].

Family GH59 $\beta$-galactocerebrosidase (GALC) degrades glycosphingolipids and its deficiency leads to another LSD, Krabbe disease. X-ray ‘snapshots’ of a Michaelis complex (using 4-nitrophenyl $\beta$-D-galactopyranoside), a 2-deoxy glycosyl enzyme (from galactal addition), and product (with galactose) showed the sugar ring in a $^4C_1$ conformation in all structures [36*]. This surprising result, reminiscent of that seen with the GH2 $\beta$-galactosidase LacZ [37], was interpreted as suggesting that no distortion of the ring occurs along the reaction coordinate. Interestingly, the acid/base residue in the substrate complex is incorrectly positioned suggesting that this is not a Michaelis complex; additionally, the product complex may have relaxed from its first-formed conformation.

Family GH117 $\alpha$-1,3-L-neoagarobiase has been described as a keystone enzyme owing to its role in agarose degradation, which provides the capability for the human gut microbiota to degrade seaweed diets [38**]. These interesting (probably inverting) enzymes act on 3,6-anhydro-$\alpha$-L-galactosides (Figure 3b). The 3,6-anhydro bridge imparts significant rigidity on the sugar to prefer $^4C_1$ and $^1A^B$ conformations. A Michaelis complex of an inactive mutant with neoagarobiase highlighted a histidine residue as a potential catalytic general acid and revealed a $^1A^B$ conformation, suggestive of a $^1A^B$→$^4E$→$^4C_1$ conformational itinerary.

GH11 xylanases are an as yet unresolved case. Early structures of intermediate complexes trapped with 2-fluoro sugars were interpreted as $^{2,5}B_1$ conformations [39,40], suggesting a possible $^{2,5}S_0$→$^{2,5}B_1$→$^5S_1$ itinerary. Very recently a long sought apparent Michaelis complex of xylohexaose bound to the xylanase XynII from Tricho-derma reesi revealed a slightly distorted $^4C_1$ conformation [41]. Confounding this issue, product complexes with GH11 enzymes reveal a range of different conformations that are inconsistent with the proposed itinerary.

On the importance of being mannose

The majority of common, naturally occurring sugars in their ground-state chair conformation either have an equatorial hydroxyl at C2 (galactosides, glucosides, xylosides, fucosides), or no substituent (sialosides, formally C3). Mannosides and rhamnosides, bearing axial 2-hydroxyls in the ground state conformations, provide exceptions that have interesting and significant consequences for reactivity that lies at the heart of what has been described the recalcitrant chemistry of mannose. For $\alpha$-mannosides in a $^4C_1$ conformation, in addition to the existence of the stabilizing anomeric effect that dissuades substrate distortion, the presence of the strongly electron-withdrawing OH at C2 results in opposing dipoles at C1 and C2 that provide additional ground state stabilization. For $\beta$-mannosides in a $^4C_1$ conformation, the anomeric effect provides little stabilization. In addition, other destabilizing effects are operative. Collectively, these can be described as a $\Delta \Sigma$ effect, a term first coined by Reeves [42]. The $\Delta \Sigma$ effect describes the destabilizing effect of an oxygen on one carbon that bisects two oxygens substituted on an adjacent carbon, aligning dipoles and causing gauche-gauche interactions between the vicinal oxygens. Nucleophilic substitutions at Cl of $\alpha$-mannosides have to contend with a developing $\Delta \Sigma$ effect. Reflecting these complexities, nature has devised some remarkable strategies for enzymes to solve these problems.

$\alpha$-Mannosidases of families GH38, 47 and 92 are metal dependent, with crystallographic evidence for the divalent metal cation (Zn$^{2+}$ or Ca$^{2+}$) binding O2 and O3. This interesting observation may provide a means to overcome the high stability of the unreactive $^4C_1$ conformation of $\alpha$-mannosides, and encourage contraction of the ground state O2–C2–C3–O3 torsion angle within the $^4C_1$ conformation.
of 60° toward the 0–15° angle expected at the \( B_{2,5} \) transition state [43]. In addition the flexible coordination number and geometry of calcium may allow coordination and delivery of the nucleophilic water, thereby providing a way to overcome a developing \( \Delta 2 \) effect [43]. A computational study of a GH38 \( \alpha \)-mannosidase suggested that \( Zn^{2+} \) coordination may stabilize charge that develops on O2 at the oxocarbenium ion like transition state [44].

Remarkably, this calculation revealed that the charge on zinc varies reciprocally with the charge developing on the oxocarbenium ion-like TS.

There is now compelling evidence that family GH2, 26 and 113 retaining \( \beta \)-mannosidases, and GH38 retaining and GH92 inverting \( \alpha \)-mannosidases, utilize \( B_{2,5} \) transition states with Michaelis complexes in a \( 1S_5 \) (for \( \beta \cdot \)) or
neuraminidases (for α-), and thus operate through $^{1}S_{5} \rightarrow B_{2.5} \rightarrow ^{0}S_{2}$
conformational itineraries [30**]. The Michaelis complex
conformation provides a pseudo axial arrangement of the
anomeric leaving group and permits inline attack of the
nuclophile; and importantly the $^{1}S_{5}$ conformation
relieves the Δ2 effect. One question that logically arises
from studies of transition state conformation is whether
all enzymes within a family operate with the same con-
formational itinerary? Family GH26 contains enzymes that
act on β-mannosides, β-glucosides and β-xylidoses:
lichenases (which hydrolyse the mixed linkage β-1,3-; β-
1,4-glucan lichenan), β-mannanase and β-1,3-xylanases.
Studies of Michaelis complexes and trapped glycosyl
enzymes provides good evidence for an alternative
$^{1}S_{3} \rightarrow ^{4}H_{1} \rightarrow ^{2}C_{1}$ itinerary for lichenases [45] and β-1,3-
xylanases [46*]. The different conformations of the
transition state of the β-glucos/xylo and β-mann
configured substrates result in the substrates at C2 being pseudo-
equatorial in both cases and lying at essentially the same
place in space, explaining how the conserved catalytic
machinery of different GH26 family members can toler-
ate differently configured sugars, with the specificity
arising from a large difference in the positions of the
C3 substituents [45], a relationship which is highlighted
by the common inhibition of β-mannosidases and β-
glucoisidases by isoagomine lactam [47].

Uncertainty surrounds the conformational itineraries of α-
mannosidases of families GH76, 99 and 125. No complexes
are available for GH76 that could provide any insight into
a possible itinerary. For GH99, which contains retaining
endo-acting α-mannosidases, the only complexes available
are with isoagomine and deoxymannojirimycin-derived
inhibitors, and these bind in $^{4}C_{1}$ conformations which
match the ground state of the inhibitors, so it is not clear
whether these complexes represent enzyme-induced or
substrate-biased conformations. However, on the basis of
an inability to identify a catalytic nucleophile in the com-
plex with α-glucosyl-1,3-isoagomine, a neighboring group
participation mechanism for GH99 was suggested that
proceeded through a 1,2-anhydro sugar [48*]. This proposal
implies the intermediate adopts a $^{4}H_{5}$ conformation, and
least nuclear motion would predict a $^{4}G_{1} \rightarrow ^{4}E \rightarrow ^{4}H_{5}$ itin-
ery (Figure 3c). For the inverting GH125 α-mannosi-
dases, a pseudo Michaelis complex is available which has the
−1 sugar in an undistorted $^{4}C_{4}$ conformation, which
matches that observed with a complex with deoxymanno-
jirimycin [49]. The lack of distortion for enzyme bound to
the non-hydrolyzable substrate is surprising.

**Neuraminidases: of conformational itineraries and transition state mimicry by inhibitors**

Neuraminidases (sialidases) are glycosidases that cleave
sialic acid residues, with the family GH34 viral surface,
retaining neuraminidases being significant as the epon-
ymous enzymes in the HNXN classification system of
influenza viruses. Influenza virus neuraminidases play
key roles in the infection of cells by the virus and the
ability of progeny virions to detach from an infected cell
and infect new cells. In two related studies, Withers and
co-workers [50**] and Gao and co-workers [51] designed
a series of neuraminidase inhibitors that combine features of
deoxylfluorosugar inhibitors modified to incorporate
structural features of the clinically-approved drugs zana-
mivir (Relenza) and oseltamivir (Tamiflu). X-ray struc-
tures of an elusive tyrosyl enzyme intermediate revealed a
$^{3}C_{2}$ conformation (Figure 4a). While a $^{1}S_{3} \rightarrow ^{2}H_{5} \rightarrow ^{2}C_{5}$
(equivalent to a $^{3}S_{1} \rightarrow ^{2}H_{4} \rightarrow ^{1}C_{4}$ for a hexopyranose) is
consistent with this data and was proposed for neurami-
idases of GH33 [52], Bennet reported kinetic isotope
effect analysis of the GH33 *Micromonaspora viridifaciens*

tialase that implied a Michaelis complex in a $^{6}S_{0}$ ($^{1}S_{1}$ for
aldose) conformation [53], a conformation also seen in the
Michaelis complex of a GH33 transialidase from *Trypa-

**Glycosidase conformational itineraries** Speciale et al. 9

*Zanamivir and oseltamivir are potent competitive inhibi-
tors of viral neuraminidases and bear some similarity to
the proposed transition state of neuraminidase, yet it is
clear whether either compound achieves its potency
through transition state mimicry. As espoused by Wol-
fenden [54] and Thompson [55] and elegantly summar-
ized by Bartlett [56], critical analysis of transition-state
mimicry can be achieved by comparing the effects of
equivalent structural perturbations on the affinity of the
true transition state (via effects on substrate $k_{cat}/K_{M}$)
and on the affinity of the transition state analogue (via $K_{I}$
values), plotted as a linear free energy relationship. Two
approaches may be used to introduce perturbations:
firstly, modifications to the inhibitor and the correspond-
ing substrate and measurement of kinetic parameters
with the wild-type enzyme, or secondly, mutation of
enzymatic active site residues to afford mutant enzymes,
which are studied with the same inhibitor and substrate.
A limitation of the former method is the effort that needs to
be expended on synthesis of derivatives, but which allow
atomic level modifications to be made limited only by the
imagination and synthetic chemistry. Limitations of the
latter include the rather blunt tool of site-directed muta-
genesis which is restricted to the genetically encoded
natural amino acids, and the possibility that mutational
perturbations may affect the fundamental reaction mecha-
nism of the enzyme.

Zanamivir was designed to improve the known sialidase
inhibitor neuraminic acid glycal (Neu5Ac2en) by the
rational inclusion of an enzyme-specific guanidine group
targeting a negatively charged pocket near the active site
[57]. Neu5Ac2en bears some similarity to the transition
state by virtue of $sp^{2}$ hybridization at C2. It can be argued
that a transition state mimicking inhibitor has the poten-
tial to provide potent inhibitors that should be resistant to

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mutations within the active site, as mutations that affect the ability of the inhibitor to bind should also affect the catalytic proficiency of the enzyme to similar degrees, resulting in loss of fitness for the virus. By making alterations in the structure of zanamivir at the 4-position and relating the effects of these changes upon inhibitor $K_I$ values to the equivalent changes to the substrate and their effect upon $k_{cat}/K_M$ or $K_M$ Bennett and co-workers showed that zanamivir is not a transition state analogue and is better considered a ground state analogue [58*]. Notably, this is consonant with the observation that influenza strains resistant to zanamivir possess reduced binding avidity for this drug but still possess catalytic competence. With impressive foresight, this possibility was suggested in the earliest publication describing the invention of zanamivir [57]. The failure of zanamivir in this Bartlett analysis is perhaps not overly surprising. Zanamivir has a double bond between C2–C3, and cannot adopt the $^4H_5$ conformation predicted for the transition state of GH33 sialidases; indeed an $E_3$ conformation is observed for zanamivir in complexes (Figure 4b). On the other hand oseltamivir (Tamiflu) is a carbocycle with a double bond located at the appropriate position to mimic the partial C2–O5 double bond at the transition state, and is observed to bind to sialidases in a $^4H_5$ conformation matching that of the transition state [59]. It will be interesting to see if Bartlett analysis applied to oseltamivir provides evidence of transition state mimicry. This situation is worth comparing with the powerful α-glucosidase inhibitor acarbose, which has a double bond C5=C6 (using pyranose numbering) and cannot adopt a planar conformation matching that expected for a glycosidase transition state; Bartlett analysis of acarbose with a GH14 cyclodextrin glycosyltransferase gives good correlation of log $K_I$ with log $k_{cat}/K_M$, but also good correlation with log $K_M$ suggesting both substrate and transition state mimicry [60].

**Conclusions**

A sophisticated view of glycoside hydrolase catalysis is now evident in which conformational changes occur that predispose substrates to react through oxocarbonium ion like transition states that are in accord with stereoelectronic and least nuclear motion principles. The challenges of these studies include the fact that X-ray crystal structures in complex with ligands by their very nature result in perturbation of the system for species nominally on or near the reaction coordinate, and for species off the
reaction coordinate, great care needs to be taken to ensure that ground state conformational preferences do not bias interpretations. Kinetic isotope effect measurements and computational analysis can provide much needed help in assigning conformational itineraries. Compelling data is now available to assign conformational itineraries for a large number of GH families, yet as highlighted above, there are examples in which crystallographic data alone do not allow proposal of conformational itineraries. In these cases application of KIE analyses and theoretical approaches may help reveal a likely itinerary.

There is a growing need for glycosidase inhibitors that exhibit selectivity against specific glycosidas, both to enable chemical biology approaches in glycobiology such as unravelling the roles of specific glycoside hydrolases in complex biochemical pathways [61], and in translational applications, for example, as folding chaperones for treatment of lysosomal storage disorders [62], and as enzyme inhibitors targeting aberrant glycosylation [63]. One of the long-term goals of conformational analysis of the glycosidase reaction coordinate is the hope that such information can inform the design of potent inhibitors, and in addition that these may be specific for particular conformational itineraries. While using such information in the design of inhibitors is not the primary focus of this review it is probably fair to say that as a general rule while the destination is now clear, the path to achieve this is not. Some success has been achieved with inhibitors that have particular conformational biases such as the selectivity of kifunensine for GH47 α-mannosidas. However, the crude attempts to achieve unusual conformations by structural means such as the introduction of bridges across the molecule are typically not tolerated by glycosidase active sites, although the 3,6-anhydro sugars processed by the GH117 α-1,6-neogarabiose might constitute a logical target for applying such an approach. More generally, smarter, less intrusive ways are needed to control the conformation of inhibitors through the application of stereoelectronic principles and hybridization. A better understanding of the intrinsic conformational preferences of existing glycosidase inhibitors would greatly assist in directing these efforts.

Conflicts of interest
None declared.

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Appendix A. Supplementary data
Supplementary material related to this article can be found, in the online version, at http://dx.doi.org/10.1016/j.sbi.2014.06.003.

References and recommended reading
Papers of particular interest, published within the period of review, have been highlighted as:

● of special interest
●● of outstanding interest

This timeless review demands close reading by beginning and advanced students of glycosidase mechanism.


A recent, comprehensive review of the assignment of conformational itineraries to glycoside hydrolases.


A comprehensive study combining theory, inhibitor design and X-ray crystallography to assign the conformational itinerary of a GH47 α-mannosidase. Atomic resolution structures of a Michaelis complex, transition state mimicking mannoimidazole and product mimic show how the enzyme distorts the substrate and transition state. QM/MM
calculations reveal how the free energy landscape of isolated α-1,5-mannose is molded on enzyme to only allow one energetically accessible conformational itinerary.


Glycosidase inhibitors are often used to assign conformations to species along the reaction coordinate but it is not obvious whether it is appropriate to do so. Computational studies reveal that mannosidase is energetically poised to report faithfully on half-chair and boat conformations relevant to the transition state of glycosidases, whereas for iso-fagomine the equivalent conformations are difficult to achieve. A complex with a β-mannosyl-1,4-mannosidase revealed a B2,5 conformation for β-mannanases of GH26 and GH113.


This study reports a series of GH3 retaining β-hexosaminidase X-ray structures in complex with substrate, a glycosyl enzyme and product. Remarkably all structures possess the same 1C0 conformation. A large protein loop containing the putative histidine acid base residue is dislocated in the complex with substrate suggesting that this is not a bonafide Michaelis complex.


This and the next study provide a comprehensive structural view of the lysosomal storage disorder-associated human family GH39 iduronidase (IDUA). Structures of a Michaelis complex and glycosyl enzyme reveal important conformations allowing assignment of a conformational itinerary. A remarkable feature of IDUA is that an N-glycan comprises part of the active site, explaining the requirement for correct glycosylation to maintain enzymatic activity.


See annotation to Ref. [34].


A detailed structural picture of GH59 human β-galactocerebrosidase, associated with a lysosomal storage disorder.


This landmark paper describes a structural study of a fascinating GH117 enzyme that plays a keystone role in the ability of the human microbiota to degrade the seaweed polysaccharide agarose. Owing to the structural constraint imposed by the 3,6-anhydro-α-1,4-galactose bridge, this enzyme appears to go via a rare 2E transition state conformation.


This paper describes a structural study of a GH26 1,3-xylanase, including the trapping of a 2-fluoroglycosyl enzyme, identification of the catalytic nucleophile and the proposal of a conformational itinerary.

47. Vincent F, Gloorer TM, Macdonald J, Morland C, Stick RV, Dias FMV et al.: Common inhibition of both β-glucosidases and β-mannosidases by isofagomine lactam reflects different


This work describes the first structural study of a bacterial GH99 enzyme as a model for the mammalian endo--mannosidase that cleaves glucose-substituted mannose residues in N-linked glycans. On the basis of an inability to identify a candidate nucleophile in a complex with an isoagomine derived inhibitor, a mechanism involving neighboring group participation and a 1,2-anhydro sugar intermediate is proposed.


In this and Ref. [51*], a series of 3-fluoro sialic acid inhibitors are developed that act as specific, mechanism based anti-influenza drugs, by accumulating a covalent intermediate on the GH34 influenza neuraminidase. X-ray structures reveal the conformation of the covalent glycosyl tyrosine allowing the assignment of a conformational itinerary. These compounds are active in cell-based assays and in animal models, with efficacies comparable to that of the neuraminidase inhibitor zanamivir and with broad-spectrum activity against drug-resistant strains.


See annotation to Ref. [50*].


In this paper the authors apply the Bartlett linear free energy approach to test whether the anti-influenza drug Relenza achieves inhibition of neuraminidase by transition state analogy. The negative result has implications for the acquisition of drug resistance by mutations that reduce inhibitor binding but maintain catalytic activity.


