Structural Insights into the Catalytic Mechanism of Bacterial Guanosine-diphosphate-D-mannose Pyrophosphorylase and Its Regulation by Divalent Ions

Marie-Cécile Pelissier, Scott A. Lesley, Peter Kuhn, and Yves Bourne

From the *Architecture et Fonction des Macromolécules Biologiques, UMR-6098, CNRS, Université Aix-Marseille, F-13288 Marseille, France, the ‡Genomics Institute of the Novartis Research Foundation, San Diego, California 92121, and the ¶Scripps Research Institute, La Jolla, California 92037

GMP catalyzes the formation of GDP-Man, a fundamental precursor for protein glycosylation and bacterial cell wall and capsular polysaccharide biosynthesis. Crystal structures of GMP from the thermophilic bacterium Thermotoga maritima in the apo form, in complex with the substrates mannose-1-phosphate or GTP and bound with the end product GDP-Man in the presence of the essential divalent cation Mg²⁺, were solved in the 2.1–2.8 Å resolution range. The T. maritima GMP molecule is organized in two separate domains: a N-terminal Rossman fold-like domain and a C-terminal left-handed β-helix domain. Two molecules associate into a dimer through a tail-to-tail arrangement of the C-terminal domains. Comparative analysis of the structures along with characterization of enzymatic parameters reveals the bases of substrate specificity of this class of sugar nucleotidyltransferases. In particular, substrate and product binding are associated with significant changes in the conformation of loop regions lining the active center and in the relative orientation of the two domains. Involvement of both the N- and C-terminal domains, coupled to the catalytic role of a bivalent metal ion, highlights the catalytic features of bacterial GMPs compared with other members of the pyrophosphorylase superfamily.

Nucleoside-5′-diphosphosugars (NDP-sugars), referred to as sugar nucleotides, represent the most common form of activated donor substrates used by glycosyltransferases in various biosynthetic pathways. GDP-Man, the activated form of Man, is required for mannosylation processes within the cell and is central for protein glycosylation and glyrophospholipid anchor synthesis in eukaryotes. In bacteria, GDP-Man is an essential precursor of Man-containing polysaccharides found in capsular and other cell wall components. In this context, the genomes of thermophilic anaerobes are particularly rich in carbohydrate-active enzymes to produce exopolysaccharides to confer various cell surface-associated functions.

In addition to its direct utilization for synthetic purposes, GDP-Man can be enzymatically converted to other GDP-sugars, such as GDP-L-fucose, GDP-D-mannuronate, and GDP-D-rhamnose, which in turn are incorporated into various glycoconjugates. GDP-Man is synthesized from the glycolytic intermediate fructose-6-phosphate and GTP in three steps. A phosphomannose isomerase (PMI) first converts fructose-6-phosphate to mannose-6-phosphate, which is then converted to mannose-1-phosphate (Man1P) by a phosphomannomutase. Finally, the GMP/Man1P guanylyltransferase catalyzes the condensation of GTP and Man1P to GDP-Man. The GMP enzyme, also referred to as PMI (EC 2.7.7.13) and first characterized in Arthrobacter sp. (2), has been described in several species. In some bacterial species, such as Pseudomonas aeruginosa, the noncontiguous GMP and PMI activities reside on separate domains of a bifunctional enzyme (3). Although the sequences from mono- and bifunctional PMIs, classified as PMI of type I and II, respectively, lack significant overall homology, the sequence associated to GMP activity has been conserved during the course of evolution (4). Indeed, at the sequence level, monofunctional GMPs and the GMP domain of bifunctional PMIs share the consensus sequence GXGYRX₂K, which is the signature motif of pyrophosphorylases (PPases). Both groups carry also a F(V)EKP motif described as part of the GMP active site (4, 5). All of the characterized GMPs require a bivalent cation for catalysis. In addition to these overall features, the oligomeric state and substrate specificity of GMPs can differ. Bacterial GMP enzymes appear to be mostly dimeric, whereas the eukaryotic enzymes can adopt various oligomeric forms, as exemplified by the active hexameric form of the Leishmania major GMP (6). Oligomerization could affect substrate specificity depending on another regulatory subunit (7).

As a representative of bacterial GMPs, Thermotoga maritima GMP (TmGMP) shows high sequence identity (~35%) only with eukaryotic GMPs from amoebae, sea anemone, fungi, and
the plant *Ricinus communis*, yet mammalian GMP enzymes consist of α (43 kDa) and β subunits (37 kDa) that share only ~18% sequence identity with TmGMP, including the conservation of the two signature motifs.

In most cases, GMPs display maximal activity on the physiological substrates, Man1P and GTP. However, puzzling results were obtained with the bifunctional GMPs from *Escherichia coli* (8) and *Pyrococcus furiosus* (9), both of which exhibit rather wide substrate tolerance. The *P. furiosus* GMP-PMI enzyme is unusually promiscuous in that it is able to synthesize with good efficiency up to 17 different NDP-sugars, including various GDP-sugar and NDP-Man products. Similarly, the GMP from *Leptospira interrogans*, responsible for the infectious disease leptospirosis, shows atypical broad substrate specificity (10). Purified pig liver GMP can accept either Man1P or Glc1P as a sugar moieity, whereas the recombinant β subunit shows high activity for GDP-Man (11).

Although crystal structures of several members of the NDP-sugar pyrophosphorylase superfamily have documented the diversity in combinations of nucleotides and sugar substrates, the molecular determinants responsible for guanosine and mannose specificities have yet to be identified. Here we report the crystal structures, solved in the 2.8–2.1 Å resolution range, of the putative monofunctional GMP from the thermophilic bacterium *T. maritima* in the absence and presence of bound Man1P, GTP, and GDP-Man ligands. This first characterization of the TM1033 gene product reveals the overall architecture and oligomeric assembly of a GMP member and provides us with a comprehensive view of ligand-free and ligand-bound GMP in the presence of the catalytically important Mg2+.

Together with a detailed biochemical characterization of the catalytic activity, structural comparison with other members of the pyrophosphorylase superfamily permits a detailed description of the active site region along with the conformational changes associated with ligand binding. The structural similarities between TmGMP and other homologues from the monofunctional class of GMP and the GMP domain of bifunctional GMPs document the structural determinants responsible for broad substrate specificity and the molecular evolution of monofunctional versus bifunctional GMPs in bacteria.

**EXPERIMENTAL PROCEDURES**

**Cloning, Expression, and Purification—**TmGMP, TM1033 (GDP-mannose pyrophosphorylase/mannose-1-phosphate guanylyltransferase; UniProt Q9X0C3) was amplified by PCR from *T. maritima*, strain MSB8, genomic DNA using *Pfu* Turbo (Stratagene) and primer pairs encoding the predicted 5′- and 3′-ends of TmGMP. The PCR product was cloned into the *E. coli* strain Origami (DE3) pLysS cells were grown at 37 °C in Luria-Bertani broth supplemented with 100 μg/ml ampicillin and 34 μg/ml chloramphenicol until A600 reached 0.6. Expression was induced with 0.15% (w/v) arabinose, and the cells were maintained for 6 h at 42 °C. The cells were harvested, and the pellet was resuspended in lysis buffer consisting of 50 mM Tris-HCl, pH 8.0, 300 mM NaCl, 10 mM imidazole, 0.25 mg/ml lysozyme, and 1 mM PMSF and stored at −80 °C. Bacterial pellet suspension was thawed and incubated for 30 min at 4 °C with 10 μg/ml DNase I and 20 mM MgSO4. After sonication, soluble extract recovered by centrifugation was applied onto a 5-ml Ni2+ chelating column (GE Healthcare) pre-equilibrated in 50 mM Tris-HCl, pH 8.0, 300 mM NaCl, 10 mM imidazole. TmGMP was eluted with an imidazole gradient, concentrated by ultrafiltration, and purified by size exclusion chromatography on a Superdex-200 (26/60 column; GE Healthcare) in 10 mM Tris, pH 8.0, and 150 mM NaCl. Purified TmGMP was concentrated by ultrafiltration. Protein purity and integrity were analyzed by SDS-PAGE and MALDI-TOF mass spectrometry.

**Size Exclusion Chromatography-Multi-angle Laser Light Scattering Characterization—**Size exclusion chromatography experiments were carried out on an Alliance 2695 HPLC system (Waters) using a silica gel KW804 column (Shodex). TmGMP was loaded at 3 mg/ml (in 100, 300, or 500 mM NaCl) and 10 mg/ml (in 100 mM NaCl) and eluted with 10 mM Hepes, pH 7.3, and 100, 300, or 500 mM NaCl (flow rate, 0.5 ml/min). Detection was achieved by a triple-angle light scattering detector (MiniDAWN™ TREOS; Wyatt Technology), a quasi-elastic light scattering instrument (Dynapro; Wyatt Technology), and a differential refractometer (Optilab rEX; Wyatt Technology). Molecular weight and hydrodynamic radius were determined with the ASTRA V software (Wyatt Technology), using a differential index of refraction, dn/dc with a value of 0.175 ml/g.

**Crystallization and Data Collection—**Small crystals of apo TmGMP were obtained at 20 °C by screening the PACT premier (Molecular Dimensions Ltd.) and MPD suite (Qiagen) crystallization kits using a nanoliter sitting drop setup with automated crystallization Freedom (Tecan) and Honeybee (Cartesian) robots. Larger crystals were grown in hanging drops by mixing equal volumes of protein (20 mg/ml in 10 mM Tris, pH 8.0, 150 mM NaCl) and reservoir (35% (v/v) MPD, 0.1 M phosphate citrate, pH 7.5) solutions. The three TmGMP complexes were formed by incubating the enzyme (12.5 or 25 mg/ml in 10 mM Hepes, pH 7.5, 100 mM NaCl, 10 mM MgCl2) with a 16:1 (Man1P) or 8:1 (GTP and GDP-Man) molar excess of ligand for 30 min at room temperature. Crystallization of the TmGMP-Man1P complex was achieved in sitting drops using a protein to well solution ratio of 3:1 and 35% MPD as the well solution. For the TmGMP-GDP-Man complex, sitting drops were set up by mixing equal volumes of the protein solution and well solution made of 30% MPD, 0.1 M sodium acetate, pH 4.6, 20 mM MgCl2. Crystals of the TmGMP GTP complex were obtained in hanging drops with a protein to well solution ratio of 2:1 and 30% MPD, 0.1 M sodium acetate, pH 5.0, 20 mM MgCl2 as the well solution. The crystals were flash-cooled in liquid nitrogen. The data were collected on ESRF (Grenoble, France) and SOLEIL (Saint-Aubin, France) beamlines, processed with MOSFLM (13) or XDS (14), and scaled and merged with SCALA (15).

**Structure Determination and Refinement—**The structure of apo TmGMP was solved by molecular replacement using
**TABLE 1**

Data collection and refinement statistics

<table>
<thead>
<tr>
<th></th>
<th>apo</th>
<th>Man1P</th>
<th>GTP</th>
<th>GDP-Man</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Data collection</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Beamsline</td>
<td>ID29 (ESRF)</td>
<td>Proximal (SOLEIL)</td>
<td>ID14-EH2 (ESRF)</td>
<td>ID14-EH4 (ESRF)</td>
</tr>
<tr>
<td>Resolution (Å)</td>
<td>65.37–2.35 (2.48–2.35)</td>
<td>65.21–2.10 (2.21–2.10)</td>
<td>67.57–2.80 (2.95–2.80)</td>
<td>50.0–2.70 (2.85–2.70)</td>
</tr>
<tr>
<td>Space group</td>
<td>P2₁</td>
<td>P2₁</td>
<td>P2₁</td>
<td>C22₂</td>
</tr>
<tr>
<td>Cell dimension</td>
<td>64.01, 92.00, 69.69</td>
<td>63.93, 91.74, 69.73</td>
<td>65.93, 79.57, 70.95</td>
<td>84.23, 96.04, 217.12</td>
</tr>
<tr>
<td>β (°)</td>
<td>110.25</td>
<td>110.75</td>
<td>107.75</td>
<td>111.25</td>
</tr>
<tr>
<td>Unique reflections</td>
<td>31,744</td>
<td>43,388</td>
<td>17,147</td>
<td>27,340</td>
</tr>
<tr>
<td>Completeness (%)</td>
<td>99.2 (96.9)</td>
<td>98.7 (98.8)</td>
<td>98.9 (99.1)</td>
<td>99.8 (99.9)</td>
</tr>
<tr>
<td>Redundancy</td>
<td>6.0 (5.4)</td>
<td>3.1 (3.1)</td>
<td>3.1 (3.1)</td>
<td>5.7 (5.8)</td>
</tr>
<tr>
<td>&lt;i&gt;Δ&lt;/i&gt;/&lt;&lt;i&gt;o&lt;/i&gt;</td>
<td>23.5 (2.5)</td>
<td>17.3 (2.5)</td>
<td>16.2 (2.6)</td>
<td>24.4 (4.2)</td>
</tr>
<tr>
<td>&lt;i&gt;R&lt;/i&gt;merge (%)</td>
<td>5.5 (47)</td>
<td>4.3 (47.1)</td>
<td>6.1 (48)</td>
<td>5.3 (43.7)</td>
</tr>
<tr>
<td><strong>Refinement</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No molecules (arbitrary units)</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td><strong>R</strong>&lt;sub&gt;crys&lt;/sub&gt; (%)</td>
<td>22.4 (36.8)</td>
<td>18.70 (28.70)</td>
<td>21.60 (32.10)</td>
<td>19.11 (24.80)</td>
</tr>
<tr>
<td><strong>R</strong>&lt;sub&gt;free&lt;/sub&gt; (%)</td>
<td>27.3 (39.2)</td>
<td>23.01 (31.70)</td>
<td>26.97 (40.10)</td>
<td>24.41 (29.80)</td>
</tr>
<tr>
<td>RMSD&lt;sup&gt;e&lt;/sup&gt; (Å)</td>
<td>1.154</td>
<td>1.335</td>
<td>1.218</td>
<td>1.457</td>
</tr>
<tr>
<td>Number of atoms</td>
<td>5365/5416</td>
<td>5456/5454</td>
<td>5420/5404</td>
<td>5421/5420</td>
</tr>
<tr>
<td>Protein</td>
<td>48/—</td>
<td>162/7</td>
<td>20/2</td>
<td>38/1</td>
</tr>
<tr>
<td>Ligands</td>
<td>32</td>
<td>64</td>
<td>78</td>
<td>78</td>
</tr>
<tr>
<td>Average B-factor (Å²)</td>
<td>76.03</td>
<td>50.53</td>
<td>75.18</td>
<td>64.08</td>
</tr>
<tr>
<td>Water/ions</td>
<td>47.16/—</td>
<td>38.32/44.45</td>
<td>30.61/41.42</td>
<td>30.95/26.55</td>
</tr>
<tr>
<td>Ligand</td>
<td>49.6</td>
<td>56.25</td>
<td>42.95</td>
<td>42.95</td>
</tr>
<tr>
<td>Ramachandran analysis</td>
<td>97</td>
<td>97.6</td>
<td>95</td>
<td>97.3</td>
</tr>
<tr>
<td>Favored (%)</td>
<td>0.2</td>
<td>0.2</td>
<td>0.2</td>
<td>0</td>
</tr>
<tr>
<td>Outliers (%)</td>
<td>0</td>
<td>95</td>
<td>95</td>
<td>95</td>
</tr>
<tr>
<td><strong>Protein Data Bank accession code</strong></td>
<td>2XSS</td>
<td>2X65</td>
<td>2X60</td>
<td>2XSZ</td>
</tr>
</tbody>
</table>

<sup>a</sup> <i>R</i>merge = Σ||<i>F</i>obs−<i>F</i>calc||2/Σ||<i>F</i>calc||2.

<sup>b</sup> <i>R</i>crys = Σ||<i>F</i>obs||2−||<i>F</i>calc||2/Σ||<i>F</i>calc||2.

<sup>c</sup> <i>R</i>free is calculated for randomly selected reflections excluded from refinement.

<sup>d</sup> RMSD, root mean square deviation from ideal geometry.

<sup>e</sup> For each subunit in the dimer.

——

PHASER (16) and the N- and C-terminal domains of *Thermus thermophilus* GMP (TtGMP; Protein Data Bank accession code 2CU2) separately as search models. A partially refined model was then used as a template to solve the structure of each of the three complexes. The model was manually corrected, and water molecules and ligand(s) were generated with SKETCHER (17) and added with COOT (18). Random sets of reflections were set aside for cross-validaton purposes. The models were refined with REFMAC5 (19) using Translation/Libration/Screw (TLS) refinement (three TLS groups) based on group definition proposed by the TLS Motion Determination (TLSMD) server (20). Non-crystallographic symmetry (NCS) restraints were applied for refinement of the four structures. The data collection and refinement statistics are reported in Table 1. All of the structures encompass residues 1–333. The C-terminal region 334–363 is disordered and could not be modeled, except for the Man1P complex where residue 334 could be inserted. Peaks above 6 σ in the residual electron density maps were attributed to a bound Mg<sup>2+</sup> near each of the three ligands. The stereochemistry of each structure was analyzed with MolProbity (21). The atomic coordinates and structure factors of apo TmGMP and the complexes with Man1P, GTP, and GDP-Man have been deposited with the Protein Data Bank (22) (see Table 1 for accession codes). Figs. 1–4 were generated with PyMOL (23).

Overall View of the Structures—The apo-, Man1P-, GTP-, and GDP-Man-TmGMP structures, refined in the 2.1–2.8 Å resolution range (“Experimental Procedures” and Table 1), show well defined electron densities for most of the protein regions and bound ligands. A TmGMP monomer is made of two separate domains and has overall dimensions of ~45 × ~40 × ~60 Å (Fig. 1). The large N-terminal domain (residues 1–263) folds into a αβα sandwich reminiscent of the dinucle-
Crystal Structure of a GDP-mannose Pyrophosphorylase

![Crystal Structure Diagram](image)

**FIGURE 1. Overall view of a TmGMP subunit and the TmGMP dimer.** A, ribbon diagrams of a TmGMP monomer in the apo (left panel) and GDP-Man-bound (right panel) forms viewed down the active site and colored as a rainbow gradient from blue (N-terminal) to red (C-terminal). The nucleotide-binding (NBS) and sugar-binding (SBS) sites are indicated. B, the TmGMP dimer, viewed in two orientations rotated by 90°, is shown with the N- and C-terminal domains colored green/blue and orange/yellow, respectively, for each of the two domains within a subunit. GDP-Man is bound at each active site and is shown through a transparent surface. The GDP-Man is shown with orange carbon, red oxygen, blue nitrogen, and magenta phosphorus atoms.

Crystallization of GDP-Man-bound TmGMP reveals that the dimer interface is formed by a parallel tail-to-tail arrangement of the left-handed β-helices from each monomer, as previously observed for the ADP-Glc PPase from potato tuber (7) and *Agrobacterium tumefaciens* (26). This tight arrangement results in an elongated and continuous β-helix structure central to the dimeric assembly. A total surface of ~2700 Å² is buried to a 1.4-Å probe radius at the interface. In addition to contacts mediated by the β-helix complementation, the dimeric assembly is stabilized through numerous hydrophobic contacts involving residues from the

---

Contribution to the stabilization of the relative orientation of the two domains.

**Dimeric Assembly—** Size exclusion chromatography shows that TmGMP behaves predominantly as a dimer in solution, consistent with the oligomeric assembly observed for most bacterial GMPs. Further analysis was performed at various ionic strengths using multi-angle light scattering with a refractive index detector. In all cases, multi-angle light scattering measurement yielded a molecular mass of 80 kDa (5% experimental error) for TmGMP, with a polydispersity of 1.01, in agreement with a dimeric assembly, stable even at high salt concentrations (data not shown).

Each of the four structures shows two molecules tightly packed as a dimer within the asymmetric unit (Fig. 1). The dimer interface is formed by a parallel tail-to-tail arrangement of the left-handed β-helices from each monomer, as previously observed for the ADP-Glc PPase from potato tuber (7) and *Agrobacterium tumefaciens* (26). This tight arrangement results in an elongated and continuous β-helix structure central to the dimeric assembly. A total surface of ~2700 Å² is buried to a 1.4-Å probe radius at the interface. In addition to contacts mediated by the β-helix complementation, the dimeric assembly is stabilized through numerous hydrophobic contacts involving residues from the

---

...
Crystal Structure of a GDP-mannose Pyrophosphorylase

FIGURE 2. Active site region of TmGMP with bound substrates and product. A, molecular surface of TmGMP, oriented as in Fig. 1, surrounding the active site region with bound GDP-Man and Mg\(^{2+}\) ion (gray sphere) colored as in Fig. 1. The signature motif is shown in purple. B, close-up views of TmGMP with bound GTP, Man1P, and GDP-Man (left panel, top to bottom). The side chains in the nucleotide-binding site and signature motif are shown in orange, those in the sugar-binding site are in yellow, and those in the C-terminal domain are in gray. The two Asp side chains that coordinate Mg\(^{2+}\) are shown in cyan, and the water molecules are red spheres. The corresponding \(F_o - F_c\) omit electron density maps (right panel, top to bottom) are contoured at 3.0 \(\sigma\) (cyan) and 5.0 \(\sigma\) (black).

Active sites of the dimer are located on opposite faces and are \(~55\) Å apart.

Comparative analysis of the structures of TmGMP bound to each of the two substrates, GTP and Man1P, and the end product GDP-Man reveals that the structure of the GDP-Man complex illustrates most interactions responsible for substrate binding, especially at the nucleotide- and sugar-binding sites. The guanidine moiety is sandwiched between loop \(\beta 1-\alpha 1\), which contains the canonical signature motif GGXGXR(L)XPLX\(_2\)PK of GMPs (5), and loop \(\beta 3-\alpha 3\) (Fig. 2).

Selective recognition of the guanidine purine ring is achieved by interactions of the exocyclic amino group with the main chain carbonyl group of Val\(^{16}\) and the carboxyl moiety of Glu\(^{80}\) and by interactions of the guanidine carbonyl with the main chain nitrogen atoms of Lys\(^{84}\) and Asn\(^{85}\). The O2, O3, and O4 hydroxyls of the sugar moiety interact with residues that emerge from the \(B_\text{III}--\alpha 10\) sheet and helix \(\alpha 9\) and are strictly conserved within bacterial GMPs. The O6 hydroxyl is coordinated by the conserved His\(^{110}\) and Asp\(^{260}\) (Fig. 2). Polar contacts involved in the anchoring of GTP, Man1P, and GDP-Man are summarized in supplemental Table SI.

Major differences occur in the mode of binding of the phosphate backbone between the GTP- and GDP-Man complexes. In the GDP-Man complex, the phosphate groups span the active site, where they interact with the two conserved Asp\(^{109}\) and Asp\(^{260}\) side chains through a Mg\(^{2+}\). Two water molecules complete the octahedral coordination geometry characteristic of Mg\(^{2+}\) (Fig. 2). In the GTP complex the phosphate groups point away from the sugar-binding site, and the \(\beta\) and \(\gamma\)-phosphates, which constitute the leaving pyrophosphate entity, are anchored within a groove where they interact with the main chain nitrogen atoms of residues Gly\(^{12}\), Glu\(^{13}\), and Arg\(^{14}\) of the signature motif (Fig. 2). The solvent-exposed \(\alpha\)-phosphate is in contact with the invariant Arg\(^{14}\) and Lys\(^{25}\).

Insights into Substrate Binding and Catalysis—The PPase activity is characterized by a sequential order of binding of substrates and relies on accurate positioning and direct reactivity between the two substrates more than on strictly catalytic residues (27). Indeed, PPase activity was shown to depend critically on the presence of a divalent cation, mostly Mg\(^{2+}\), that counterbalances the negative charges of the phosphate groups in the active site and provides bridging interactions between these two polar moieties of opposite charges (27). In most characterized PPases, the reaction proceeds via a sequential ordered bi-bi mechanism with NTP binding prior to sugar-1P binding (28). Once both substrates are bound, the phosphate group of the sugar attacks on one side of the \(\alpha\)-phosphate of NTP to form a NDP-sugar, with the concomitant breaking of the phosphodiester bond on the opposite face to release pyrophosphate (Fig. 3). The reaction can also proceed via a ping-pong mechanism that requires formation of a covalent NMP-enzyme intermediate, so far described only for Salmonella dTDP-Glc PPase (29).

Comparative analysis of the structures of apo TmGMP and its GTP complex reveals that GTP binding is associated with large conformational changes of loop regions surrounding the active site, along with side chain reorientations (Fig. 1). In the nucleotide-binding site, the \(\beta 1-\alpha 1\) loop is displaced by \(1.5\) Å to favor interactions with the \(\beta\) and \(\gamma\)-phosphates of GTP. The C-terminal domain rotates by \(\sim 10°\) toward the N-terminal domain as to push helix \(\alpha 8\) toward the nucleotide-binding site. This event allows Arg\(^{326}\) in helix \(\alpha 8\) to establish long range interaction with the distal \(\gamma\)-phosphate (Fig. 2). A di-acid bridge is formed between the conserved Asp\(^{109}\) and Asp\(^{260}\) side chains, the latter residue being located in the hinge region between the N- and C-terminal
The side chain of the conserved Lys171 in the sugar-binding site and restraint active site accessibility (Fig. 2). 10° toward Man1P, which results in the global closure of Ser190, thus rigidifying the sugar-binding site.

Although the exact mechanism used by TmGMP to catalyze GDP-Man formation is still unknown, our structural study suggests that TmGMP follows a sequential mechanism. Neither GTP nor GDP-Man are involved in a covalent NMP-enzyme intermediate in the respective complex structures, as would be expected in the case of a ping-pong mechanism. Moreover, searches for structural homologues using the DALI server (35) revealed that the structures most closely related to TmGMP are those of the Helicobacter pylori (Protein Data Bank accession code 2QH5) and T. thermophilus GMPs (Protein Data Bank accession code 2CU2), that belong to the class of bifunctional PMI-GMPs and monofunctional GMPs, respectively. In these enzymes, the C-terminal domain holds a second enzymatic activity in addition to the nucleotidytranferase activity, as seen for some bifunctional GMPs (PMI) and UDP-GlcNAc PPsases, which exhibit phosphomannose isomerase and acetyltransferase activity, respectively (33, 34). The C-terminal domain can also regulate the PPase activity by mediating enzyme oligomerization (6) and/or by binding allosteric regulators (7).

Sequences for structural homologues using the DALI server (35) revealed that the structures most closely related to TmGMP are those of the Helicobacter pylori (Protein Data Bank accession code 2QH5) and T. thermophilus GMPs (Protein Data Bank accession code 2CU2), that belong to the class of bifunctional PMI-GMPs and monofunctional GMPs, respectively. In these enzymes, the C-terminal domain holds a second enzymatic activity in addition to the nucleotidytranferase activity, as seen for some bifunctional GMPs (PMI) and UDP-GlcNAc PPsases, which exhibit phosphomannose isomerase and acetyltransferase activity, respectively (33, 34). The C-terminal domain can also regulate the PPase activity by mediating enzyme oligomerization (6) and/or by binding allosteric regulators (7).
could not be deciphered from the HpGMP structure solved from a variant lacking the C-terminal domain.

Beside the structures of GMP members, the structure most closely related to that of TmGMP is that of UDPGlc PPase from Corynebacterium glutamicum (CgUGP) (36, 37). Most of the structural elements of CgUGP are similar to those of TmGMP, except that the CgUGP structure lacks TmGMP helices α7 and α8 and comprises two additional helices inserted in the α2-β3 loop. The C-terminal domain of CgUGP is made of a helix-loop-helix motif that, conjointly with the two additional helices, is responsible for dimer formation (Fig. 4). Comparative analysis of the CgUGP and TmGMP active sites reveals major differences related to the specific anchoring of their respective substrates, even if the global architecture is conserved. The nucleotide-binding site of CgUGP selectively filters pyrimidine bases by steric constraints that prevent accommodation of purine bases. Specific recognition of a glucose moiety by the CgUGP active site is achieved through with the presence of the small Thr242 side chain (equivalent to TmGMP Asp239). Moreover, the side chain conformation of Leu140 and Tyr218 imposes steric constraints incompatible with the binding of a mannose moiety with an O2 hydroxyl in axial configuration. In GMPs, these two residues correspond to a Pro or Ala (Pro107 in TmGMP) and a conserved Phe (Phe193 in TmGMP), respectively.

**Structural Basis of the GMP Activity in Bifunctional Enzymes—** The kinetic parameters of T. maritima and H. pylori GMP versus Man1P and GDP substrates are very similar, consistent with the structural conservation of residues involved in substrate binding and catalysis (Table 2). This suggests that the GMP-catalyzed reaction requires a specific active site architecture and proceeds similarly for mono- and bifunctional GMPs. Moreover, the two separate catalytic domains of bifunctional PMI/GMP can communicate to modulate their catalytic activities, as exemplified by the H. pylori enzyme, where GDP-Man binding to the GMP domain decreases the PMI domain affinity for Fru6P. Conversely, Man6P binding to the PMI domain seems to affect GDP-Man binding to the GMP domain (38). Furthermore, the bifunctional GMP/PMI P. furiosus PsIB, harboring inactive mutations for PMI activity, conserves an unaltered GMP activity (39). Most importantly, a truncated form of the P. furiosus bifunctional PMI/GMP lacking the PMI domain has very weak GMP activity, whereas its affinity for Man1P is unaltered. Compared with full-length P. furiosus PMI/GMP, the truncated enzyme no longer displays broad substrate tolerance (9). This is consistent with our findings showing the implication of the TmGMP C-terminal domain in substrate coordination. Indeed, the conserved Arg326 in monofunctional GMPs participates in GTP γ-phosphate coordination and corresponds to a conserved Lys residue in bifunctional PMI/GMP that could play a similar role.

**The PMI and GMP activities of the bifunctional P. aeruginosa enzyme were strongly reduced upon mutation of Ser12** (equivalent to Glu13 in TmGMP) to Ala, whereas affinities for the two Man1P and GTP substrates were not affected (3). In TmGMP, Glu13 belongs to the signature motif, and its side chain participates in the active site interface, whereas the main chain amino group coordinates the GTP γ-phosphate. Mutation of this residue is not expected to affect GTP binding, but

---

**TABLE 2**

<table>
<thead>
<tr>
<th>Bacterial Source</th>
<th>Man1P</th>
<th>GDP</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Arthrobacter</em> (3)*b</td>
<td>35</td>
<td>130</td>
</tr>
<tr>
<td><em>P. aeruginosa</em> (3)</td>
<td>8.2</td>
<td>41</td>
</tr>
<tr>
<td><em>S. enterica</em> (41)</td>
<td>15</td>
<td>40</td>
</tr>
<tr>
<td><em>M. smegmatis</em> (42)</td>
<td>168</td>
<td>113</td>
</tr>
<tr>
<td><em>H. pylori</em> (38)</td>
<td>22</td>
<td>ND*</td>
</tr>
<tr>
<td><em>P. furiosus</em> (9)</td>
<td>72</td>
<td>ND</td>
</tr>
<tr>
<td><em>L. interrogans</em> (10)</td>
<td>63</td>
<td>256</td>
</tr>
<tr>
<td><em>T. maritima</em></td>
<td>12.8</td>
<td>63.7</td>
</tr>
</tbody>
</table>

*a* The numbers in parentheses are reference numbers.

*b* This study.

* cND, not determined.

---

**FIGURE 4. Structural comparison.** A, schematic diagram of the molecular organization of nonfunctional GMP versus bifunctional GMP/PMI. The positions of the three signature motifs are indicated as vertical bars. B–D, ribbon diagrams of TtGMP (8), the GMP domain of bifunctional PMI-GMP from *H. pylori* (HpGMP) (C), and UDP-Glc PPase from *C. glutamicum*, oriented as in Fig. 1 (D, left panel). The GMP domain is colored as in Fig. 2. Close-up overlay (right panel in D) of the active site regions of TmGMP and UDP-Glc PPase with bound ligands. GDP-Man is shown with cyan and orange carbon for the nucleotide and sugar moieties, respectively. UDP-Glc is shown with white carbon. Conservation of the active site topology and near perfect overlap of bound GDP-Man, UDP-Glc, and Mg2+ are evident. C-ter, C-terminal; N-ter, N-terminal.
glycosyltransferases, PPases can be employed to generate NDP-sugar libraries for synthesis of a large variety of glycosylated compounds using a chemoenzymatic strategy called natural product glycorandomization (40).

In summary, the structures of TmGMP in the apo form and as three complexes with Man1P, GTP, and GDP-Man provide a comprehensive view of the monofunctional class of bacterial GMPs and document the key catalytic role of the Mg$^{2+}$ cofactor and the requirement of both domains for catalysis. Comparison with other PPases reveals subtle structural adaptations within the Rossman-like domain for recognition of GTP and Man1P. This study provides a novel template to understand the basis of nucleotide and sugar substrate selectivity among the monoverse bifunctional classes of GMPs, as a premise for the design of novel PPase inhibitors.

Acknowledgments—We thank Abraham Saliba for contribution to initial experiments, Gerlind Salzenbacher for helpful discussion, Giuliano Sciara and Stephanie Blangy for size exclusion chromatography-multi-angle light scattering experiments, Maria Luz Cardenas and Athel Cornish-Bowden for advice in enzyme kinetics, and Bruno Coutard and Pascale Marchot for critical reading of the manuscript. We acknowledge the European Synchrotron Radiation Facility and the Synchrotron Soleil for provision of beam time, and we thank ESRF and Soleil staff for assistance in using the beamlines.

REFERENCES

Crystal Structure of a GDP-mannose Pyrophosphorylase