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# X-ray Structure of the Magnesium(II)•ADP•Vanadate Complex of the *Dictyostelium discoideum* Myosin Motor Domain to 1.9 Å Resolution<sup>†,‡</sup>

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**ABSTRACT:** The structure of the vanadate-trapped ADP complex of a truncated head of *Dictyostelium* myosin II consisting of residues Asp 2–Asn 762 has been determined by molecular replacement at 1.9 Å resolution and refined to a crystallographic *R*-factor of 19.4%. The crystals belong to the orthorhombic space group *C*222<sub>1</sub> where *a* = 84.50 Å, *b* = 145.4 Å, and *c* = 152.8 Å. The conformation of the protein is similar to that of MgADP•AlF<sub>4</sub>•S1Dc [Fisher, A. J., et al. (1995) *Biochemistry* 34, 8960–8972]. The nucleotide binding site contains a complex between MgADP and vanadate where MgADP exhibits a very similar conformation to that seen in previous complexes. The vanadate ion adopts a trigonal bipyramidal coordination. The three equatorial oxygen ligands are fairly short, average 1.7 Å, relative to a single bond distance of ~1.8 Å and are coordinated to the magnesium ion, Nζ of Lys 185, and five other protein ligands. The apical coordination to the vanadate ion is filled by a terminal oxygen on the β-phosphate of ADP and a water molecule at bond distances of 2.1 and 2.3 Å, respectively. The long length of the apical bonds suggests that the bond order is considerably less than unity. This structure confirms the earlier suggestion that vanadate is a model for the transition state of ATP hydrolysis and thus provides insight into those factors that are responsible for catalysis. In particular, it shows that the protein ligands and water structure surrounding the γ-phosphate pocket are oriented to stabilize a water molecule in an appropriate position for in-line nucleophilic attack on the γ-phosphorus of ATP. This structure reveals also an orientation of the COOH-terminal region beyond Thr 688 which is very different from that observed in either MgADP•BeF<sub>3</sub>•S1Dc or chicken skeletal myosin subfragment 1. This is consistent with the COOH-terminal region of the molecule playing an important role in the transduction of chemical energy of hydrolysis of ATP into mechanical movement.

The orthovanadate ion is a potent inhibitor of many enzymes that catalyze phosphoryl transfer (Gresser & Tracey, 1990). It is an effective inhibitor in part because it has very similar size and charge to inorganic phosphate but also because it readily increases its coordination sphere to five and exhibits considerable plasticity in its bond distances (Holloway & Melnick, 1986). These features allow this ion to adopt a trigonal bipyramidal coordination that has been proposed to mimic the conformation of the phosphate group at the transition state expected for phosphoryl transfer (Lindquist et al., 1973; Westheimer, 1987) and has been observed in the complex of ribonuclease with uridine vanadate (Wlodawer et al., 1983). As a consequence of these properties vanadate has proved to be a valuable tool for studying enzyme mechanism. This is particularly true for myosin, the major ATPase of muscle, that is inhibited strongly by vanadate both in solution and in muscle fibers (Goodno, 1979; Dantzig & Goldman, 1985).

In myosin, ATP hydrolysis is not coincident with the force-generating step (Lymn & Taylor, 1971; Goldman, 1987).

Instead, ATP binding initially reduces the affinity of myosin for actin, after which hydrolysis of ATP occurs rapidly and results in a metastable ternary complex between myosin, ADP, and inorganic phosphate. In this state the equilibrium complex between ATP and ADP•P<sub>i</sub> is between 1 and 10 for skeletal muscle depending on the temperature and ionic strength (Bagshaw & Trentham, 1973, 1974; Taylor, 1977). Release of the hydrolysis products is catalyzed by rebinding to actin which is accompanied by the energy transduction step. Vanadate inhibits the myosin ATPase activity by forming, in the absence of actin, a long-lived complex with MgADP that is believed to mimic either the transition state for hydrolysis or the ADP•P<sub>i</sub> state (Goodno, 1979; Goodno & Taylor, 1982). The half-life for dissociation of this complex at 0 °C is ~4 days (Goodno, 1979, 1982; Werber et al., 1992). Interestingly, the rate of inhibition is considerably less than the diffusion limit for binding. Thus, formation of the inhibitory ternary complex was interpreted as a multistep process, in which there was initial formation of an equilibrium complex, followed by slow isomerization to form the inhibited state. Furthermore, ADP•Vi<sup>1</sup> reduces

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<sup>‡</sup> The X-ray coordinates have been deposited in the Brookhaven Protein Data Bank (file name 1VOM).

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<sup>1</sup> Abbreviations: myosin S1, myosin subfragment 1; S1Dc, *Dictyostelium discoideum* myosin motor domain; PMSF, phenylmethane-sulfonic acid; BTP, bis-Tris-propane; MgPP<sub>i</sub>•S1Dc, magnesium pyrophosphate complex of truncated *D. discoideum* myosin motor domain; EG, ethylene glycol; MgADP•BeF<sub>3</sub>•S1Dc, the beryllium fluoride–ADP complex of *D. discoideum* myosin motor domain; MgADP•AlF<sub>4</sub>•S1Dc, the aluminum fluoride–ADP complex of *D. discoideum* myosin motor domain; MgADP•VO<sub>4</sub>•S1Dc, the vanadate–ADP complex of *D. discoideum* myosin head; S1, subfragment-1; Vi, vanadate (VO<sub>4</sub><sup>3-</sup>).

the binding affinity of myosin for actin ( $1.5 \times 10^{-3} \text{ M}^{-1}$ ), although less than that induced by the  $\text{ADP}, \text{P}_i$  state under the same conditions. Actin also increases the rate of release of vanadate by  $10^5$  compared to that of myosin $\cdot\text{ADP}\cdot\text{Vi}$  alone, although the release of vanadate is still slow. The actin-activated ATPase activity of myosin is about 90% inhibited by  $\text{ADP}\cdot\text{Vi}$  at high vanadate concentrations (Goodno & Taylor, 1982); however, there is some indication that this is due in part to the formation of polymeric vanadate ions (Smith & Eisenberg, 1990). Spectroscopic studies of spin-labeled myosin subfragment 1 have also shown that the  $\text{ADP}\cdot\text{Vi}$  complex exhibits many of the structural properties of the  $\text{ADP}, \text{P}_i$  state (Wells & Bagshaw, 1984). Consequently, the  $\text{ADP}\cdot\text{Vi}$  complex is often considered to be close to the conformation of myosin at the start of the power stroke.

Formation of the metastable, yet dynamic,  $\text{ADP}, \text{P}_i$  state is an unusual feature for an enzyme. The  $\text{MgADP}\cdot\text{Vi}$  complex provides an opportunity to arrest the contractile cycle at a critical point and provides a chance to study this important state. A detailed study of the mechanical properties of muscle fibers revealed that tension and stiffness in actively contracting fibers are suppressed by vanadate and that this is due to the formation of a long-lived  $\text{MgADP}\cdot\text{Vi}$  complex analogous to that observed with myosin alone (Dantzig & Goldman, 1985). This allowed the role of a specific state in the contractile cycle to be characterized under differing physiological conditions (Dantzig & Goldman, 1985; Chase et al., 1993; Wilson et al., 1995).

Vanadate has also proved to be a valuable tool for mapping the active site of myosin due to the stability of divalent metal  $\text{ADP}\cdot\text{Vi}$  complexes. This stability allowed complexes of myosin with photoreactive ADP analogs to be separated from excess reagent prior to irradiation, which dramatically improved the specificity of labeling (Yount et al., 1992). As a consequence a significant number of residues in the active site were unequivocally identified. The vanadate ion itself is also photoreactive. Illumination of the myosin $\cdot\text{ADP}\cdot\text{Vi}$  complex with UV light above 300 nm causes modification of a specific serine in the active site of skeletal muscle myosin and release of vanadate (Cremo et al., 1988, 1989; Grammer et al., 1988). Subsequent rebinding of  $\text{MgADP}\cdot\text{Vi}$  and further illumination results in peptide bond cleavage, as in other systems (Gibbons et al., 1987; Grammer et al., 1988). These reactions served to identify a critically important serine residue in the coordination of the  $\gamma$ -phosphate. Together, these chemical studies played an important role in the development of a structural mechanism for the myosin ATPase activity (Rayment et al., 1993a,b; Fisher et al., 1995a,b).

It is thus evident that considerable biochemical and biophysical effort has been expended on the  $\text{MgADP}\cdot\text{Vi}$  complex of myosin as part of the greater goal of understanding the molecular basis of muscle contraction. We report here the structure of the  $\text{MgADP}\cdot\text{VO}_4$  complex of the truncated head of *Dictyostelium discoideum* at 1.9 Å resolution. This study complements earlier structures of the truncated myosin head of *Dictyostelium* myosin complexed with  $\text{MgADP}\cdot\text{BeF}_3^-$  and  $\text{MgADP}\cdot\text{AlF}_4^-$  which mimic the

ATP and transition-state states, respectively (Fisher et al., 1995a,b). The vanadate complex represents a more realistic analog of the transition state than the structure of  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$  that was reported only at 2.6 Å resolution. As such, it indicates the structural features that are important for catalysis. Furthermore, the present model reveals the orientation of the COOH-terminal domain and the loops that connect the major tryptic fragments which were missing in the structure of  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$ .

## EXPERIMENTAL PROCEDURES

**Protein Purification and Crystallization.** Truncated myosin subfragment 1, residues Asp 2 to Asn 762, from *D. discoideum* (S1Dc) was purified as described previously (Fisher et al., 1995b). Prior to crystallization,  $\text{MgADP}$  was trapped in the active site by the addition of stock solutions to a final concentration of 2 mM ADP, 3 mM sodium vanadate, and 1 mM  $\text{MgCl}_2$ . A stock solution of 400 mM vanadate at pH 10.0 was prepared as described by Goodno (1982). Crystals of the vanadate-trapped ADP complex of myosin S1 ( $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ ) were grown by microbatch from 8.5% PEG 8000, 25 mM Hepes, pH 7.0, 250 mM NaCl, 2 mM DTT, and 3% 2-methyl-2,4-pentanediol. The protein concentration in the final droplet was about 5 mg/mL. The protein/precipitant solutions were microseeded from preliminary hanging-drop experiments and left at 4 °C. Small crystals generally appeared overnight and typically took from 2 to 3 weeks to reach maximum dimensions of  $0.6 \times 0.4 \times 0.15$  mm.

**Data Collection and Processing.** The  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  crystals are orthorhombic with unit cell dimensions  $a = 88.5$  Å,  $b = 145.4$  Å, and  $c = 152.8$  Å and belong to space group C222<sub>1</sub>. The crystals are isomorphous with those of the aluminum fluoride-trapped ADP complex of myosin S1,  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$ , which has cell dimensions of  $a = 87.9$  Å,  $b = 149.0$  Å, and  $c = 153.8$  Å (Fisher et al., 1995b). High-resolution X-ray data were collected with a MAR detector from one frozen crystal on beamline 7-1 at the Stanford Synchrotron Radiation Laboratory. The crystal was transferred from the crystallization medium into a synthetic mother liquor containing 15% PEG 8000, 300 mM NaCl, 2 mM ADP, 3 mM sodium vanadate, 1 mM  $\text{MgCl}_2$ , and 5% ethylene glycol (EG) in 25 mM Hepes, pH 7.0, for transportation. Prior to freezing, the crystal was transferred gradually into a solution containing 18% PEG 8000, 300 mM NaCl, 2 mM ADP, 3 mM sodium vanadate, 1 mM  $\text{MgCl}_2$ , 30% EG, and 25 mM Hepes, pH 7.0. The crystal was placed into three solutions consisting of 1:3, 2:2, and 3:1 18% PEG buffered as above:cryoprotectant mother liquor, 5 min per step, and then finally into the cryoprotectant mother liquor for a final 5 min. A droplet of this solution containing the crystal was picked up in a loop of surgical suture and rapidly frozen in a stream of nitrogen at -160 °C (Teng, 1990; Rodgers, 1994).

X-ray data were collected with the oscillation method (Arndt & Wonacott, 1977) on a 30 cm MAR detector at a wavelength of 1.08 Å. An oscillation range of 1° was used, and 95 frames were recorded with a crystal-to-image distance of 120 mm. The images were processed with the program DENZO (Otwinowski, 1986) and scaled and merged using ROTAVATA and AGROVATA from the CCP4 suite of programs (CCP4, 1994). Partially recorded reflections

<sup>2</sup> The exact composition of the beryllium fluoride species is unknown (Henry et al., 1993) whereas the aluminum fluoride complex has been shown to contain four equivalent fluorine atoms (Maruta et al., 1993). Consequently, these complexes will be designated as  $\text{BeF}_3^-$  and  $\text{AlF}_4^-$ .

Table 1: X-ray Data Processing

no. of crystals used	1
maximum resolution ( $d_{\min}$ , Å)	1.90
total reflections measured to $d_{\min}$	393986
independent reflections to $d_{\min}$	75066
$R_{\text{merge}}$ (%) <sup>a</sup>	2.8
theoretical no. of reflections to $d_{\min}$	77683
cumulative % completeness	97
% completeness in highest resolution shell <sup>b</sup>	92
unit cell parameters	
$a$ (Å)	88.5
$b$ (Å)	145.4
$c$ (Å)	152.8

<sup>a</sup>  $R = \Sigma |I - \bar{I}| / \Sigma I \times 100$ . <sup>b</sup> 1.97–1.9 Å.

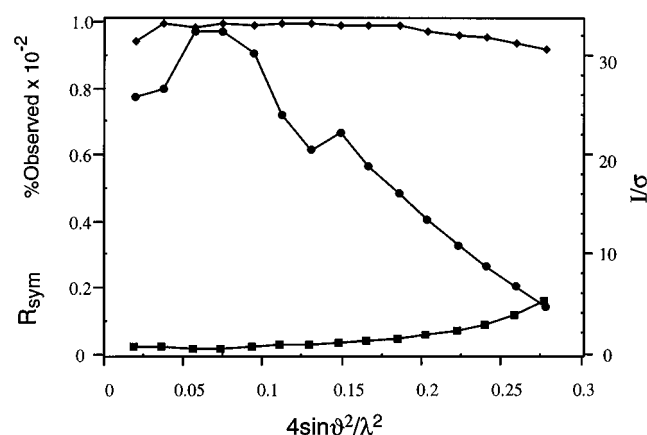


FIGURE 1: Percentage of the theoretical number of reflections (◆), the average  $I/\sigma$  (●) as a function of  $4 \sin^2 \theta / \lambda^2$ , and  $R_{\text{merge}}$  (■) as a function of  $4 \sin^2 \theta / \lambda^2$  for the final  $\text{MgADP} \cdot \text{VO}_4 \cdot \text{S1Dc}$  data set.

recorded on adjacent images were added to give full reflections, while the intensities of partials with no match on adjacent images and with calculated partialities greater than 0.7 were scaled by the inverse of their partiality. Of the 393 986 measured reflections, 138 354 were fully recorded and 88 639 were partially recorded. A final unique, non-zero data set of 75 066 reflections was obtained with an  $R_{\text{merge}}$  of 0.028 on intensities ( $R_{\text{merge}} = \Sigma |I - \bar{I}| / \Sigma I$ ). The data set was 97% complete to 1.9 Å resolution (Table 1). Figure 1 shows the variation of the completeness of the data and  $R_{\text{merge}}$  as a function of resolution. In the highest resolution shell, between 1.97 and 1.9 Å, the data are 92% complete, with an average  $I/\sigma$  of 4.9.

**Structure Determination and Refinement.** Although the  $\text{MgADP} \cdot \text{VO}_4 \cdot \text{S1Dc}$  crystals were essentially isomorphous with those of  $\text{MgADP} \cdot \text{AlF}_4 \cdot \text{S1Dc}$ , an initial crystallographic  $R$ -factor calculated between the  $\text{MgADP} \cdot \text{AlF}_4 \cdot \text{S1Dc}$  model refined at 2.6 Å (Fisher et al., 1995b) and the  $\text{MgADP} \cdot \text{VO}_4 \cdot \text{S1Dc}$  data was 48.5%. This was possibly due to the changes in the cell parameters between the two crystals. Consequently, the molecular replacement program AMORE (Navaza, 1993) was used to place the model of  $\text{MgADP} \cdot \text{AlF}_4 \cdot \text{S1Dc}$  in the cell. This revealed that there was a rotation and translation of 1° and 0.75 Å between the coordinates in these two cells.

Prior to refinement of the  $\text{MgADP} \cdot \text{AlF}_4 \cdot \text{S1Dc}$ -derived model against the X-ray data, the solvent molecules, the  $\text{Mg}^{2+}$ -ADP, and the  $\text{AlF}_4^-$  were removed, along with 10 residues at the COOH terminus. The model consisted of 5500 protein atoms (650 residues) comprising residues Asn 2–Gln 19, Thr 28–Val 65, Gly 68–Gly 201, Ser 208–Phe

487, Asp 509–Arg 620, and Asn 626–Gly 680. The structure was refined with 20 cycles of conjugate gradient refinement with the program TNT (Tronrud et al., 1987) while increasing the resolution from 3.0 to 2.3 Å, resulting in a drop in the crystallographic  $R$ -factor from 0.415 to 0.343. A  $2F_o - F_c$  electron density map displayed on an Evans and Sutherland PS390 with the molecular graphics program FRODO (Jones, 1978, 1985) showed continuous density for all the atoms in the initial model, along with density for some of the missing residues. In addition, electron density in the vicinity of the active site could be clearly identified as an ADP moiety. Contouring an  $F_o - F_c$  electron density map at  $6\sigma$  showed a peak between the side chains of Thr 186 and Ser 237, ligands of the magnesium ion in  $\text{MgADP} \cdot \text{BeF}_x \cdot \text{S1Dc}$ ,  $\text{MgADP} \cdot \text{AlF}_4 \cdot \text{S1Dc}$  (Fisher et al., 1995b), and  $\text{MgPP}_i \cdot \text{S1Dc}$  (Smith & Rayment, 1995). An  $\text{Mg}^{2+}$  ion was built into this density together with two solvent molecules that were clearly interacting with the  $\text{Mg}^{2+}$ . The density for the vanadate group at a height of  $>20\sigma$  could be seen in both maps adjacent to the  $\beta$ -phosphate of the ADP and connected to the  $\text{Mg}^{2+}$  density. This was not built in at this stage, since the orientation of the atoms surrounding the vanadium atom could not be unambiguously determined.

Over the course of 20 more stages of TNT refinement and manual model rebuilding, the resolution limits were extended to 20.0–1.9 Å and several pieces of missing structure were added. The electron density adjacent to the ADP and  $\text{Mg}^{2+}$  ion was clearly trigonal planar in shape, with a small lobe of density perpendicular to the plane. A trigonal planar  $\text{VO}_3$  group was added to the model with a fourth oxygen atom occupying a small lobe of density in an apical position relative to the  $\text{VO}_3$  plane and directly opposite one of the oxygen atoms on the  $\beta$ -phosphate, the fifth vanadium ligand. The  $\text{NH}_2$ -terminal section of the polypeptide chain was completed. This region is folded somewhat differently from the corresponding area in  $\text{MgADP} \cdot \text{BeF}_x \cdot \text{S1Dc}$ , due primarily to the close contact of a symmetry-related molecule. The helix between Lys 488 and Asn 500, which could not be readily traced in the  $\text{MgADP} \cdot \text{AlF}_4 \cdot \text{S1Dc}$  structure, was also added to the model. This helix adopts a different conformation from the corresponding helix in  $\text{MgADP} \cdot \text{BeF}_x \cdot \text{S1Dc}$ , in that the helix is markedly bent at Lys 488. The polypeptide chain from Asn 500 to Asp 509, missing in the three previous S1Dc structures determined to date, was located after refinement of the newly located helix between Lys 488 and Asn 500. Finally, residues Arg 620 to Asn 626, a flexible loop region at the junction between the central 50 kDa and the COOH-terminal 20 kDa sections of the heavy chain, were built into weak but continuous electron density.

The position of the helix between Gln 480 and Asn 500 led to the location of parts of the missing COOH-terminal section. Superposition of the COOH-terminal domain from  $\text{MgADP} \cdot \text{BeF}_x \cdot \text{S1Dc}$ , based on the position of this helix, revealed several parts of the missing domain corresponding to three strands (Lys 690–Tyr 698, Glu 735–Phe 739, and Thr 742–Arg 747) which were subsequently built into the density as polyalanine. Residues Lys 690–Glu 759 from  $\text{MgADP} \cdot \text{BeF}_x \cdot \text{S1Dc}$  were superimposed upon the newly located COOH terminus of  $\text{MgADP} \cdot \text{VO}_4 \cdot \text{S1Dc}$  on the basis of these three strands, and these rotated coordinates were appended to model for  $\text{MgADP} \cdot \text{VO}_4 \cdot \text{S1Dc}$ . Simulated annealing refinement with the program X-PLOR (Brünger et al., 1987; Brünger, 1990), followed by positional refine-

Table 2: Refinement Statistics<sup>a</sup>

resolution limits (Å)	20.0–1.9
initial <i>R</i> -factor <sup>b</sup>	41.5
final <i>R</i> -factor	19.4
no. of reflections used	73626
no. of protein atoms	5766
no. of solvent molecules	705
other molecules, ions	1 $\text{Mg}^{2+}$ , 1 ADP, 1 $\text{VO}_4^{3-}$
av <i>B</i> -value, protein atoms (Å <sup>2</sup> )	33.1
av <i>B</i> -value, solvent atoms (Å <sup>2</sup> )	43.3
weighted rms deviations from ideality	
bond length (Å)	0.012
bond angles (deg)	2.656
planarity (trigonal) (Å)	0.004
planarity (others) (Å)	0.010
torsional angle (deg) <sup>c</sup>	17.320

<sup>a</sup> TNT refinement. <sup>b</sup>  $R = \sum ||F_o| - k|F_c|| / \sum |F_o|$ . <sup>c</sup> No restraints were placed on torsional angles during refinement.

ment with TNT, gave an *R*-factor of 0.250. This region of the structure was further improved with omit maps calculated with SIGMAA coefficients (Read, 1986) to minimize model bias.

During the refinement and model building, a close contact was observed between the sulfhydryl group of Cys 442 and the 2-fold-related side chain in an adjacent molecule. The electron density reveals that there is an intermolecular disulfide bond between these side chains. This cysteine residue is located on the same side of the molecule as the actin binding surface but is a considerable distance from the nucleotide binding site, the actin binding site, and the COOH-terminal domain, such that it is unlikely that it influences the conformation of the molecule. This linkage was also observed in  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$  but not in  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$ . It appears that the crystal packing in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  favors the formation of this linkage, though it is unknown if dimerization is necessary for crystal growth.

A systematic search for solvent molecules was undertaken with the programs PEAKMAX and WATPEAKS (CCP4, 1994). An  $F_o - F_c$  electron density map was searched for the highest peaks above  $4\sigma$ , and these peaks were then tested against the atomic coordinates of the protein to see whether they fell within a specified distance of a potential hydrogen bond donor or acceptor (between 2.4 and 3.5 Å). The location and geometry of these water molecules were checked manually on a Silicon Graphics Indigo 2 with the program O (Jones et al., 1991). A total of 705 water molecules were added to the structure during the course of the refinement.

At the completion of the refinement and model building, the final *R*-factor was 0.194 for all data (73 626 reflections) between 20.0 and 1.9 Å resolution, with rms deviations from standard bond lengths and angles of 0.012 and 2.66°, respectively. Relevant refinement statistics are given in Table 2. The average error in the model was estimated from a Luzzati plot (Luzzati, 1952) (data not shown) to be between 0.175 and 0.20 Å. A Ramachandran plot (Ramakrishnan & Ramachandran, 1965) of the main chain conformational angles (Figure 2) indicates that most of the non-glycine and non-proline residues lie within or very close to the allowed regions of conformational space. A plot of the main chain temperature factors and correlation coefficients is shown in Figure 3. A representative section of electron density is shown in Figure 4.

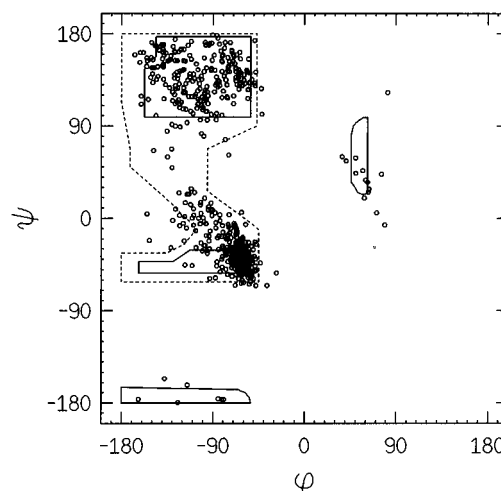


FIGURE 2: Plot of the main chain conformational torsion angles  $\phi$  and  $\psi$  for the non-glycyl residues in the final model for  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ .

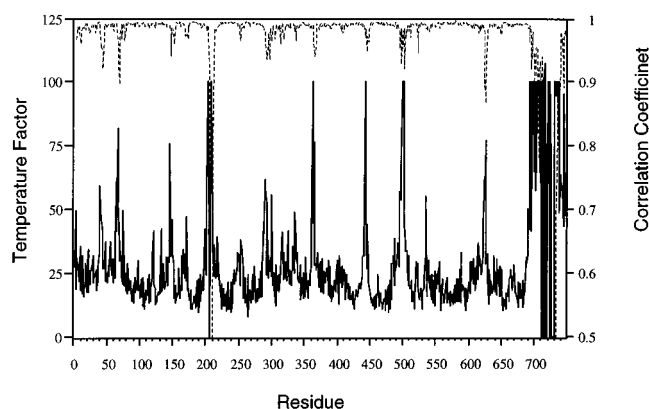


FIGURE 3: Plot of the variation of the average main chain temperature factors (solid lines) and the main chain correlation coefficients (dashed lines) with residue number. The correlation coefficients were calculated with the program OVERLAPMAP (CCP4, 1994).

## RESULTS AND DISCUSSION

**The Final Model.** The refined  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  model consists of 5766 protein atoms, 705 solvent molecules, 1 adenosine diphosphate molecule, 1  $\text{Mg}^{2+}$  ion, and 1  $\text{VO}_4$  moiety. The polypeptide chain runs from Asn 2–Gln 204, Gly 209–Pro 710, Val 712–Asp 715, Gln 720–Thr 723, and Asn 731–Arg 747. The COOH-terminal region is rather fragmented, and although three strands and parts of two helices are in the same relative orientation as the corresponding region in  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$ , there is no electron density for the loops connecting the secondary structure elements and their location cannot be identified even after superposition of the COOH terminus of  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  onto the current model. However, the three strands all have very well-defined electron density associated with them and have good density for their side chains. This section of the  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  model is clearly not as well-defined as the remainder of the structure, as can be seen in a plot of the average main chain *B*-factor as a function of residue number (Figure 3). The average main chain *B*-value for the residues from Lys 690 to Arg 747 is 81.8 Å<sup>2</sup>, while for the remainder of the model, the average *B*-value is 24.8 Å<sup>2</sup>. Real space correlation coefficients (Figure 3) calculated with the

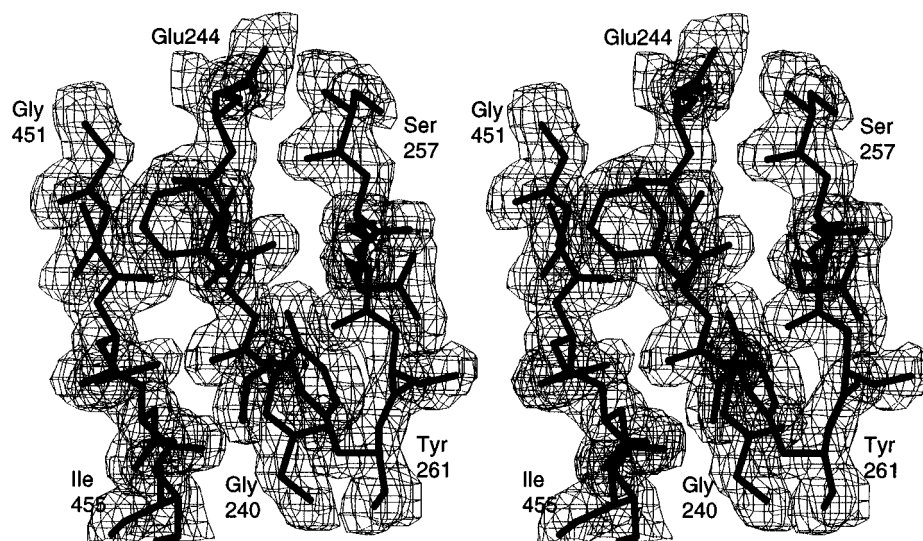


FIGURE 4: Stereoview of a piece of representative  $2F_o - F_c$  electron density in the central  $\beta$ -sheet that forms the platform for the nucleotide binding site. This figure and Figure 8 were prepared with the programs FRODO and MOLVIEW (Jones, 1985; Smith, 1993).

program OVERLAPMAP (CCP4, 1994) also show lower than normal values for the latter part of the COOH terminus. The discussion of the structure will focus first on the overall conformation of the protein and then on the contents of the active site.

**Protein Conformation.** The overall conformation of residues Asn 2–Thr 688, which includes the  $\text{NH}_2$ -terminal 25 kDa, the central 50 kDa, and approximately 70 amino acid residues of the COOH-terminal 20 kDa section, is essentially identical to that of the  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$  (Fisher et al., 1995a,b). This is not unexpected since the  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  and  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$  complexes crystallize in the same space group and unit cell. The rms difference between the 643 common residues between Asn 2 and Thr 688 is 0.67 Å, where the reduction in the number of residues arises because the structure of  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$  was incomplete.

The conformation of  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  is significantly different from that of the  $\text{MgADP}\cdot\text{BeF}_3\cdot\text{S1Dc}$ , as was noted previously for the  $\text{MgADP}\cdot\text{AlF}_4$  complex (Fisher et al., 1995a,b). As before, the narrow cleft that splits the central 50 kDa section of the heavy chain is partially closed in the  $\text{MgADP}\cdot\text{VO}_4$  complex relative to that seen in  $\text{MgADP}\cdot\text{BeF}_3\cdot\text{S1Dc}$ . The conformational changes in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  associated with Gly 457 are essentially identical to those seen in  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$ . Likewise, the hydrogen-bonding pattern at the back of the cleft is very similar even though the contents of the  $\gamma$ -phosphate pocket are different. However, since the  $\text{MgADP}\cdot\text{VO}_4$  complex was determined at higher resolution and is more complete, several sections of the molecule, including parts of the COOH-terminal domain that were previously disordered, can now be seen (Figure 5). Many of these show conformational changes relative to  $\text{MgADP}\cdot\text{BeF}_3\cdot\text{S1Dc}$  as discussed below.

**Trp 501–Gly 507.** One section missing in both  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$  and  $\text{MgADP}\cdot\text{BeF}_3\cdot\text{S1Dc}$  (though present in chicken skeletal S1) extends from Trp 501 to Gly 507 and contains the tryptophan residue that is believed to be responsible for the fluorescence enhancement observed during ATP hydrolysis (Hiratsuka, 1992). Tryptophan fluorescence has proved to be invaluable for following the conformational state of the myosin head during ATP hy-

drolysis and has provided an experimental probe for following the kinetic behavior of the contractile cycle (Morita, 1967; Werber et al., 1972; Trentham et al., 1976). This provided the evidence that ATP binding is a multistep process that consists of several distinct conformational states (Lymn & Taylor, 1971; Trybus & Taylor, 1982). It has been suggested that only one or two tryptophan residues experience an altered environment (Werber et al., 1972; Papp & Highsmith, 1993) and that these are located in the 50 kDa tryptic fragment (Werber et al., 1987). Even so, it has proved difficult to identify exactly which tryptophan(s) and hence component(s) of the protein is (are) responsible for these phenomena. It has been proposed that Trp 510 in skeletal muscle myosin (Trp 501 in S1Dc) is responsible for the fluorescence changes based on fluorescence energy transfer measurements, proximity arguments from cross-linking between SH1 and SH2 to cysteines in the 50 kDa section of the heavy chain, and sequence conservation (Warrick & Spudich, 1987; Johnson et al., 1991; Hiratsuka, 1992; Rayment et al., 1996). *Dictyostelium* myosin II exhibits a fluorescence enhancement though at a reduced level compared to that of skeletal myosin (Ritchie et al., 1993).

The section of random coil containing Trp 501 in S1Dc exhibits different conformations in the beryllium and vanadate complexes (Figure 6). Trp 501 lies under the pocket that contains the reactive cysteine residue in skeletal myosin (Thr 688 in S1Dc) and is surrounded by the hydrophobic residues Tyr 494, Phe 503, Phe 692, and a highly conserved Gly 691. These residues are conserved in chicken skeletal myosin. Trp 501 is buried in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  whereas in chicken skeletal myosin S1 it is exposed to solvent on one edge. The exact reason for the fluorescence enhancement cannot be explained by the present structures since it is likely that the exact nature of the conformational change that occurs around Trp 501 is influenced by the essential light chain which is missing from the structures of S1Dc. It has been suggested that the fluorescence enhancement might be due to an interaction between an ionizable side chain and the indole ring (Bivin et al., 1993). The use of the  $\text{ADP}\cdot\text{Vi}$  complex to account for the fluorescence enhancement must also be qualified by the observation that in rabbit skeletal muscle myosin the  $\text{ADP}\cdot\text{Vi}$  complex shows a lower level of

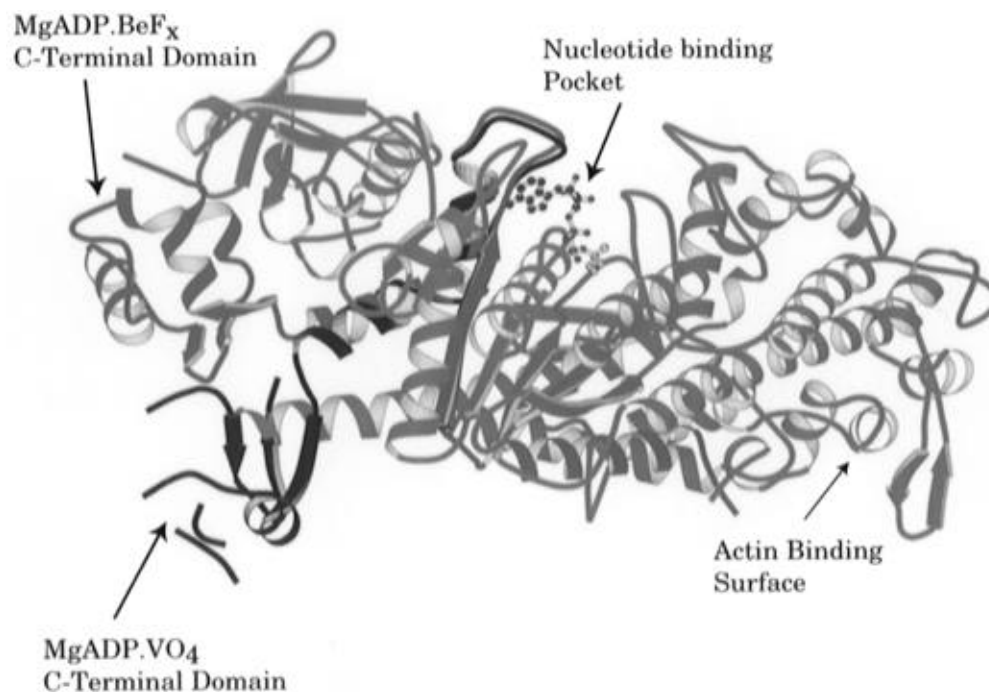


FIGURE 5: Ribbon drawing of the entire  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  structure and residues Thr 649–Gly 749 of  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  viewed approximately parallel to the actin binding surface and looking along the nucleotide binding pocket. The structures were aligned by matching the upper domain of the central 50 kDa sections of the polypeptide chains (residues Asn 2–Gly 457) with the program LSQKAB implemented in the CCP4 program package (Kabsch, 1976; CCP4, 1994). The  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  structure is shown in green, red, and blue to distinguish the  $\text{NH}_2$ -terminal, central, and  $\text{COOH}$ -terminal sections of the myosin heavy chain. The structure of  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  is shown in black. This reveals the dislocation of the  $\text{COOH}$ -terminal domain in  $\text{S1Dc}\cdot\text{VO}_4\cdot\text{MgADP}$ . This figure and Figures 6, 7, 9 and 12 were prepared with the molecular graphics program MOLSCRIPT (Kraulis, 1991).

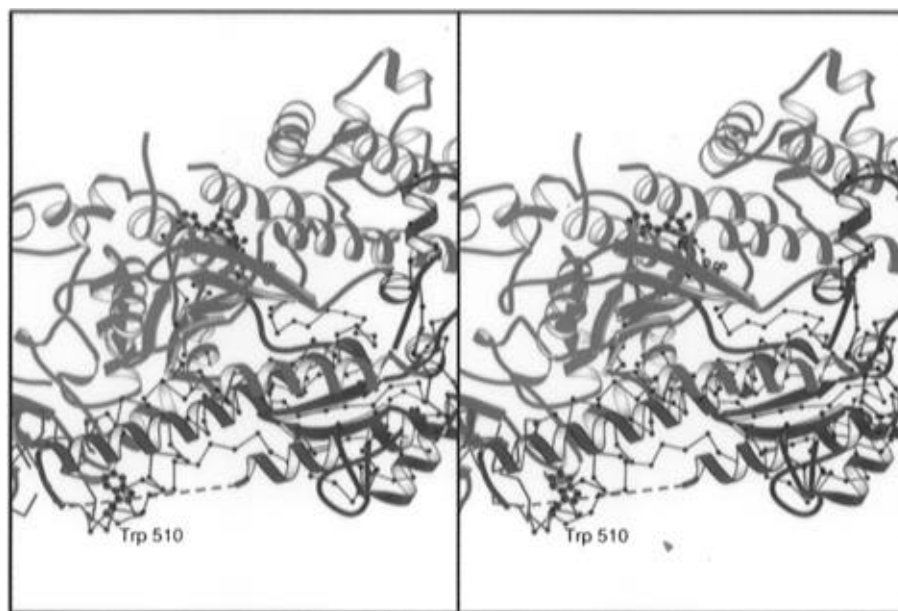


FIGURE 6: Stereoview of the changes surrounding Trp 501 in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  relative to  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  where the structure of the beryllium fluoride complex is shown in ribbon representation with a color scheme for the heavy chain similar to that in Figure 5 with the exception that residues 454–518 are depicted in dark brown and the remainder of the lower domain of the central 50 kDa section of the heavy chain is shaded in darker red and residues Asp 518–Arg 747 in the vanadate complex are shown in  $\alpha$ -carbon representation. Although residues Trp 501–Gly 507 are disordered in the beryllium fluoride complex, it is clear that the helix that supersedes Trp 501 has rotated approximately  $24^\circ$ .

fluorescence enhancement than ATP ( $\text{ADP}, \text{P}_i$ ) though the latter is a mixture of states.

**Conformational Changes in the 25 kDa  $\text{COOH}$ -Terminal Section.** The superposition of the  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  onto  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ , based on the least squares fit of the upper domains of the central 50 kDa section of the heavy chain (Figure 5), reveals that residues Thr 688–Gly 749 in

the  $\text{COOH}$ -terminal section of the heavy chain adopt very different conformations in these structures. Indeed, relative to the position in  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  the  $\text{COOH}$ -terminal domain in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  has translated by more than  $23 \text{ \AA}$  and rotated by approximately  $70^\circ$ . This change is prompted by movement of the lower domain of the 50 kDa section that in turn affects movement of the  $\text{COOH}$ -terminal

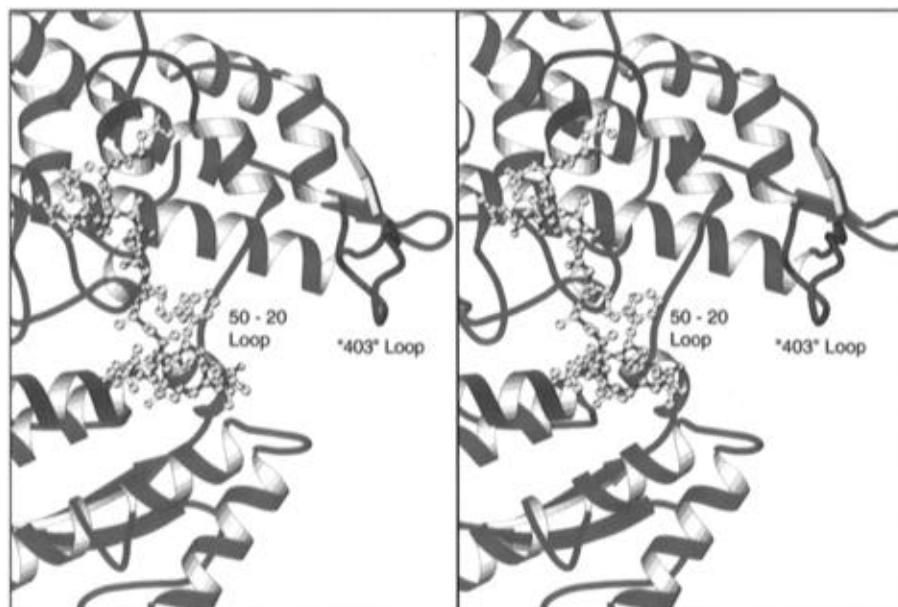


FIGURE 7: Stereoview of the junction between the 50 and 20 kDa sections of the heavy chain. All of the atoms of the variable loop are shown whereas the 50 and 20 kDa sections are depicted as ribbon representations in red and blue, respectively. The loop that contains the most common mutation in familial hypertrophic cardiomyopathy and the site of phosphorylation in some nonmuscle myosin are depicted in dark brown.

part of the molecule via the helix that connects the helix containing the reactive cysteines (Cys 697 and Cys 707) in skeletal muscle. The currently observed disposition of the COOH terminus is probably of limited biological significance due to the absence of the essential light chain. It is anticipated that this part of the molecule moves during the formation of the metastable state but that its movement is influenced by the adjacent essential light chain (Fisher et al., 1995a). This conclusion is demanded by the extensive biochemical evidence that shows that the equivalent region in skeletal muscle that encompasses the reactive cysteine residues can undergo a large conformational change when nucleotide binds (Reisler et al., 1974; Wells & Yount, 1980; Chalovich et al., 1983; Huston et al., 1988). It is well established that Cys 697 and Cys 707 can form a disulfide bond in the presence of nucleotide (Huston et al., 1988), which requires these two residues to be in close proximity. In the present structure the helix equivalent to that which separates the reactive cysteines in nucleotide-free chicken skeletal S1 is still present, which suggests that a different conformational change occurs when the essential light chain is present.

**25–50 and 50–20 Loop.** In all of the previous structures of myosin the loops that connect the major tryptic fragments were disordered. In the present structure weak density for the loop between the 25 and 50 kDa sections of the heavy chain could be seen but was not modeled. However, it was possible to build a single conformation for the loop that connects the central 50 kDa and COOH-terminal 20 kDa sections. This loop lies in fairly close proximity to the body of the protein and extends away from the surface only at the end close to the start of the first helix of the 20 kDa section (Figure 7). This loop has been implicated in actin binding from biochemical and model building studies (Mornet et al., 1979; Rayment et al., 1993a). The temperature factors for the loop are high and are indicative of considerable flexibility (Figure 3). It is likely that this loop adopts a

different conformation when the myosin head is bound to actin. The sequence of the loop that connects the 50 and 20 kDa sections of the heavy chain is highly variable across the myosin superfamily (Warrick & Spudich, 1987; Spudich, 1994). In most cases the loops are considerably larger than observed in *Dictyostelium* myosin. There is evidence from mutagenesis of *Dictyostelium* myosin that the nature of this loop influences the kinetic parameters and motility of myosin (Uyeda et al., 1994). The present structure imposes constraints on the location of these insertions, since all myosins must recognize and bind to actin with similar binding constants.

Figure 7 also shows the orientation of the adjacent loop ("403" loop) that carries the site of phosphorylation in nonmuscle myosins (Pollard et al., 1991) and the most common mutation in familial hypertrophic cardiomyopathy (Rayment et al., 1995). This loop is believed to interact with actin (Rayment et al., 1993a). Here, the loop extends away from the surface of the protein as a short two-stranded antiparallel sheet and does not form any intermolecular contacts with symmetry-related molecules. This is in contrast to both chicken S1 and MgADP•BeF<sub>3</sub>•S1Dc where the conformation of this loop is stabilized and influenced by interactions with neighboring molecules.

**Conformation of MgADP•VO<sub>4</sub>.** The electron density for the MgADP•VO<sub>4</sub> is shown in Figure 8A, and the overall location of the nucleotide complex relative to the major secondary structural elements is shown in Figure 9. The conformation of ADP, the magnesium ion, and its associated water molecules is unambiguous and very similar to that seen in MgADP•BeF<sub>3</sub>•S1Dc and MgADP•AlF<sub>4</sub>•S1Dc. The density associated with the vanadium atom (Figure 8B) is clearly trigonal bipyramidal where three oxygen atoms lie in a plane and the axial positions are occupied by a bridging oxygen from the  $\beta$ -phosphate and an additional oxygen atom. The geometry of the vanadate moiety is shown in Figure 10A. The presence of a single vanadium moiety in the active site, when ADP is present, is consistent with the <sup>51</sup>V NMR studies



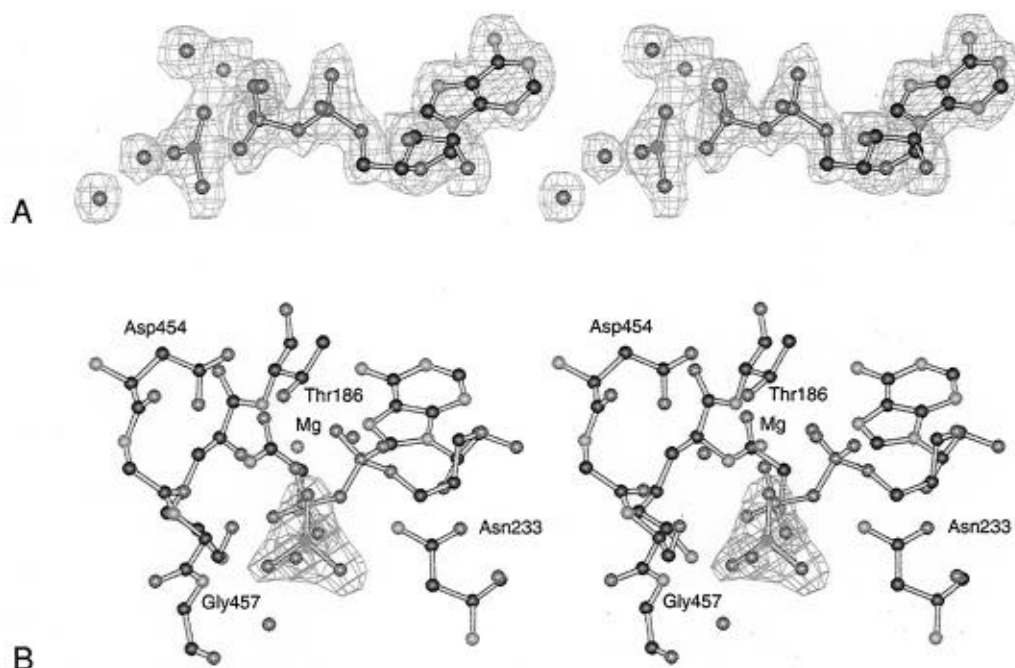


FIGURE 8: Stereoview of the electron density associated with the nucleotide binding site. (A)  $2F_o - F_c$  electron density when the  $\text{MgADP}\cdot\text{vanadate}$  complex was included in the phase calculation. (B)  $F_o - F_c$  electron density when the vanadate moiety and the bridging oxygen of the  $\beta$ -phosphate were excluded from the refinement and phase calculation.

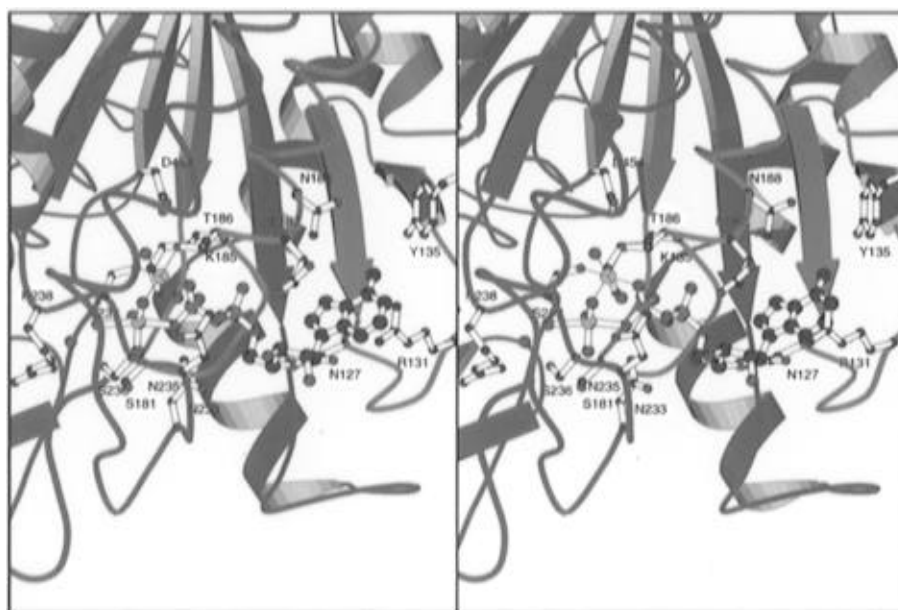


FIGURE 9: Stereo ribbon representation of the  $\gamma$ -phosphate pocket of  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ . The heavy chain is displayed in green, red, and blue to delineate the  $\text{NH}_2$ -terminal, central, and  $\text{COOH}$ -terminal sections that extend from residues Asp 2 to Gln 205, Gly 209 to Ala 621, and Lys 622 to Gly 749, respectively.

of the interaction between ADP, vanadate, and myosin (Ringel et al., 1990).

The vanadate moiety was refined with restraints of  $90^\circ$  on the apical–equatorial bond angles and with target values of 2.2 and 1.7 Å for the apical and equatorial bond distances, respectively. It is clear that the refined model fits the unrestrained electron density well. The final refined bond distances reveal that the two apical bond V–O distances are 2.3 and 2.1 Å, respectively, whereas the equatorial V–O bond distances are 1.7, 1.6, and 1.7 Å respectively. The numbering of the oxygen ligands is given in Figure 12 and Table 3. The bond distances clearly fall into two classes. Although the overall coordinate error is estimated to be  $\sim 0.2$  Å, it is anticipated that the error in the active site will be

less, since this is one of the better defined regions of the molecule. Thus the difference in bond length between the apical and equatorial groups is probably significant, although no distinction can be made about the bond lengths within each group. Vanadium exhibits a wide range of bond distances to oxygen ligands, where a single bond and double bond are typically 1.79 Å and typically 1.57 Å, respectively (Brown & Wu, 1976). These values suggest that the apical bonds to the vanadium ion in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  have a valency that is considerably less than unity, whereas the equatorial bonds as a whole are greater than unity (Brown & Wu, 1976). The resolution of the X-ray data is not high enough to distinguish between a planar  $\text{VO}_3^-$  moiety with two short bonds and one long bond and a delocalized system

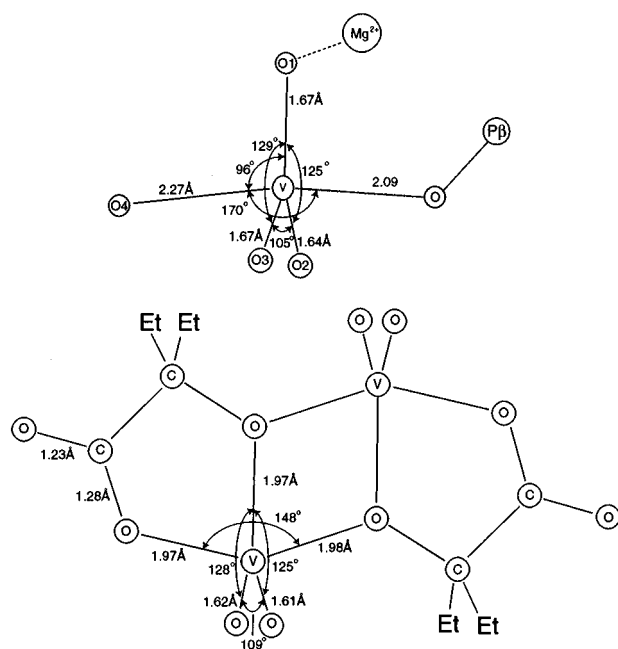


FIGURE 10: Geometry of the vanadate moiety in (A, top) the  $\gamma$ -phosphate binding pocket of  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  and (B, bottom) the trigonal bipyramidal vanadium complex found in  $(\text{NH}_4)_2[\text{VOC}(\text{CH}_2\text{CH}_3)_2\text{COO}](\text{O})_2]_2$  (Hambley et al., 1992).

Table 3

atom 1 <sup>a</sup>	atom 2 <sup>a</sup>	bond distances (Å)	
		$\text{MgADP}\cdot\text{VO}_4$	$\text{MgADP}\cdot\text{BeF}_x^b$
Thr 186 O $\gamma$	$\text{Mg}^{2+}$	2.0	2.1
Ser 237 O $\gamma$	$\text{Mg}^{2+}$	2.1	2.3
OW1	$\text{Mg}^{2+}$	2.0	2.1
OW2	$\text{Mg}^{2+}$	2.1	2.1
P $\beta$ O1	$\text{Mg}^{2+}$	2.2	2.1
OV1, F1	$\text{Mg}^{++}$	1.9	2.1
Ser 237 N	OV1, F1	2.9	2.9 (3.0)
Ser 181 O $\gamma$	OV2, F2	2.6	2.6 (2.9)
Ser 236 O $\gamma$	OV2, F2	2.8	2.9 (2.8)
Asn 233 N $\delta$	OV2, F2	3.1	3.1 (2.9)
Lys 185 N $\zeta$	OV3, F3	2.7	2.8 (2.9)
Gly 457 N	OV3, F3	2.8	6.9 (2.9)
Ser 236 O $\gamma$	OV4, H $_2$ O <sup>c</sup>	3.0	4.2
Ser 237 O	OV4, H $_2$ O <sup>c</sup>	2.7	3.0
OW3	OV4	2.6	
OW3	Gly 457 O	2.6	
OW3	Glu 459 O $\epsilon$ 2	2.7	

<sup>a</sup> Where there are two atoms listed, the first corresponds to an atom in  $\text{MgADP}\cdot\text{VO}_4$  whereas the second is the equivalent atom in  $\text{MgADP}\cdot\text{BeF}_x$ . <sup>b</sup> The second entry in this column gives the distance between an atom in  $\text{MgADP}\cdot\text{BeF}_x$  and an atom in the  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  complex after the nucleotide complex was transferred into the  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  coordinate frame. The rotation and translation matrices were derived by aligning Leu 175 to Val 187 and Asn 234 to Arg 238, the protein ligands that coordinate the nucleotides, with the program LSQKAB implemented in the CCP4 program package (Kabsch, 1976; CCP4, 1994). The nucleotides were excluded from the calculation. <sup>c</sup> This refers to the water molecule that is equivalent to OV4 that is coordinated to F3 in  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$ .

with three equally short bonds. However, the conformation observed in the model compounds, discussed below, favors an asymmetric arrangement.

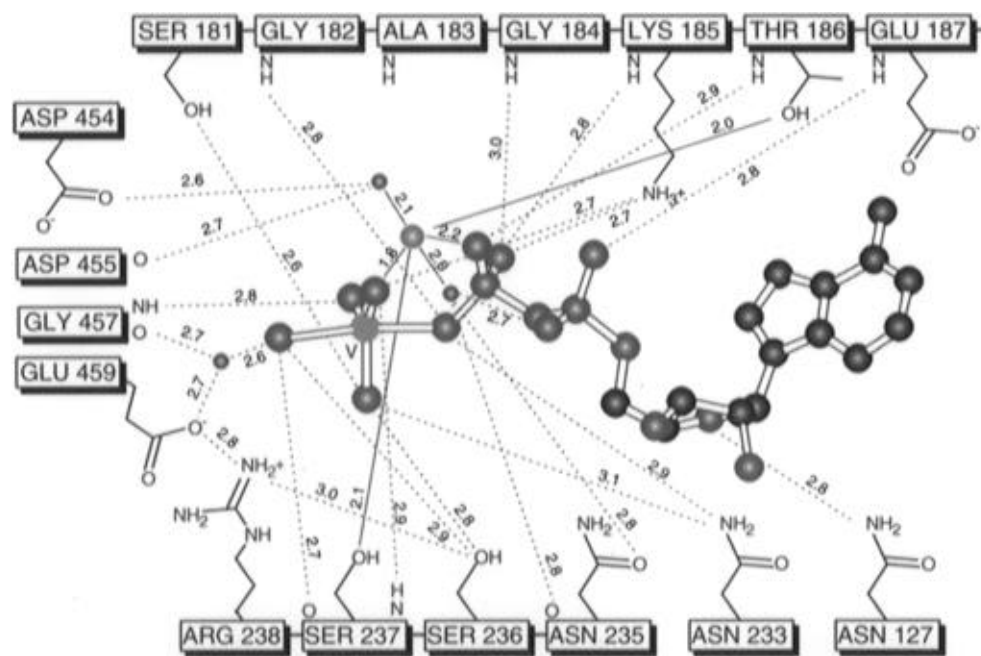
Vanadium(V) adopts a variety of coordinations (Holloway & Melnick, 1986). The most common is a distorted octahedral coordination that contains a nonlinear  $\text{VO}_2^+$  entity with two fairly short VO bonds ( $\sim 1.64$  Å) and four other ligands which show substantially longer bond distances in

the range 1.9– $\sim 2.3$  Å (Scheidt et al., 1971). Trigonal bipyramidal coordination with oxygen ligands is less common but has been shown to occur in solution in dimeric complexes between vanadium and 1,2-diols (Gresser & Tracey, 1986; Ray et al., 1995). The crystal structures of several model compounds including complexes with a 1,2-diol and a 2-hydroxy acid ligand have been reported (Crans et al., 1991; Hambley et al., 1992). The geometry of the latter compound,  $(\text{NH}_4)_2[\text{VOC}(\text{CH}_2\text{CH}_3)_2\text{COO}](\text{O})_2]_2$ , is shown in Figure 10B. In this complex the ligands bound to the vanadium adopt a distorted trigonal bipyramidal arrangement. The apical distances are fairly long (average 1.98 Å) whereas two of the equatorial distances are short (1.605 and 1.617 Å) and the third long (1.97 Å). Similar arrangements of ligands and bond distances have been observed in other trigonal bipyramidal complexes of vanadium(V).

Trigonal bipyramidal geometry for vanadium(V) has been observed in the active site of an enzyme in the complex of ribonuclease with uridine vanadate (Wlodawer et al., 1983) and more recently in transition-state analog complexes of rat acid phosphatase (Lindqvist et al., 1994). The latter study was at fairly low resolution such that no conclusions could be drawn about the geometry of its vanadium moiety. The structure of uridine vanadate in ribonuclease is distorted trigonal bipyramidal and similar to that seen in the model compounds (Crans et al., 1991) and in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  even though the environment and ligands are quite different.

The protonation state of the vanadate ion in the active site when complexed with  $\text{MgADP}$  is unknown. At pH 7.0 the major monomeric species in solution is  $\text{H}_2\text{VO}_4^-$  (Pope & Dale, 1968; Wells & Bagshaw, 1984). Examination of the hydrogen-bonding pattern surrounding  $\text{MgADP}\cdot\text{VO}_4$  (Figures 11 and 12B and Table 3) suggests that the equatorial oxygen atoms coordinated to the magnesium ion (OV1) and Lys 185 (OV2) are not protonated. The third equatorial oxygen atom (OV3) is coordinated to O $\gamma$  of Ser 181, N $\delta$ 2 of Asn 233, and O $\gamma$  of Ser 236 where it appears that Ser 181 and Asn 233 both function as hydrogen donors. O $\gamma$  of Ser 236 is within hydrogen-bonding distance of both the terminal oxygen of the vanadate moiety (OV4) and the third equatorial oxygen such that its proton could be directed toward either of these atoms. Indeed, it is possible that the proton on O $\gamma$  of Ser 236 is shared by OV4 and OV2 since the angle subtended at O $\gamma$  by OV4 and OV2 is 55°. The V–O bond distance (2.3 Å) to the terminal oxygen implies this is a very weak bond and requires that this ligand is either  $\text{HO}^-$  or  $\text{H}_2\text{O}$ . Examination of the hydrogen bond network around the apical oxygen strongly suggests that OV4 is a water molecule for the following reasons. OV4 forms short hydrogen bonds to the carbonyl oxygen of Ser 237, the O $\gamma$  of Ser 236, and an additional water molecule (OW3). These ligands and vanadium ion are arranged tetrahedrally around OV4. OW3 forms additional short hydrogen bonds with good geometry to the carbonyl oxygen of Gly 457 and O $\epsilon$ 2 of Glu 459. This requires that the two protons on OW3 are directed toward these latter two ligands and therefore requires a proton to reside on OV4 and be directed toward OW3. The water structure around OV4 probably plays a critical role in stabilizing the structure necessary for catalysis as discussed below.

**Mechanistic Implications.** It is well established that hydrolysis of ATP occurs by attack of a water molecule on the  $\gamma$ -phosphorus (Sleep et al., 1980; Webb & Trentham,



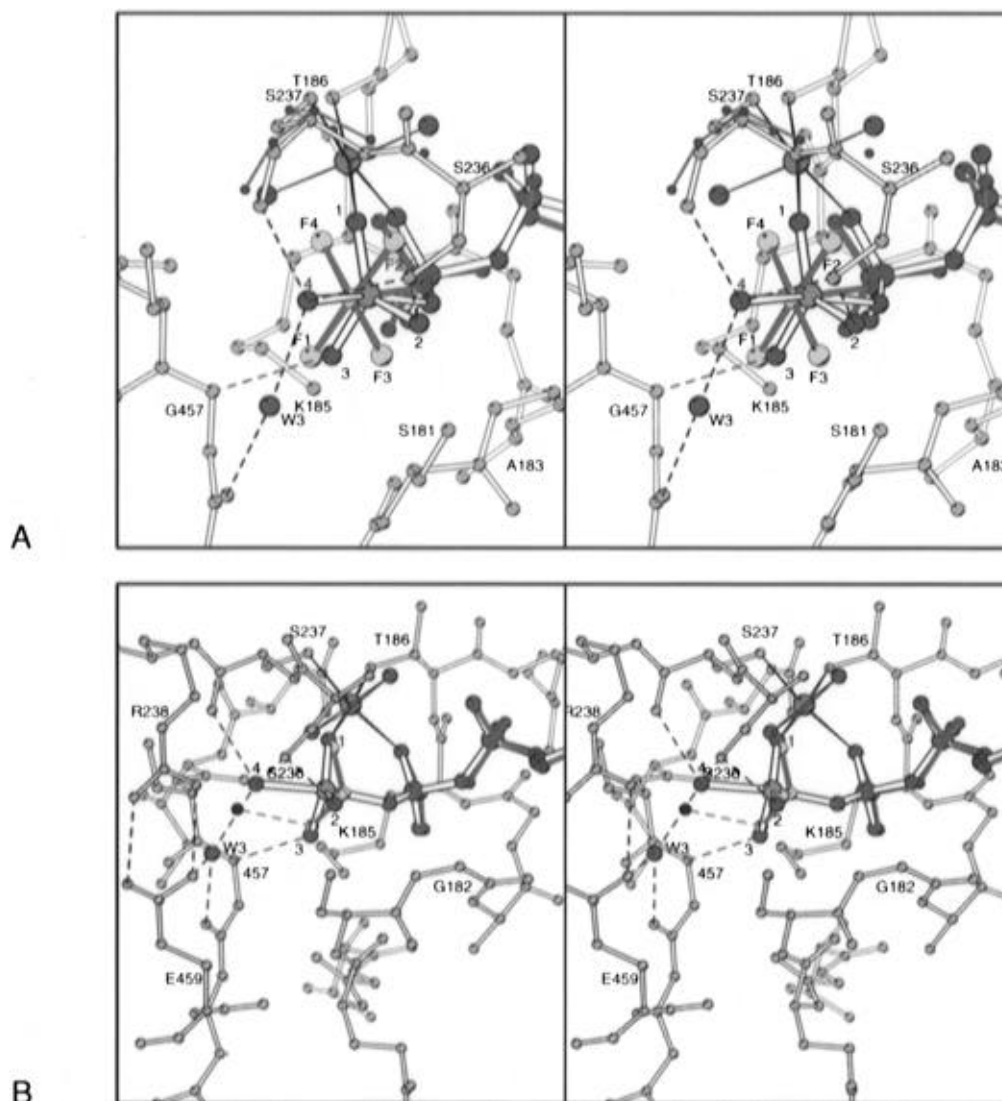


FIGURE 12: A close-up stereoview of the  $\gamma$ -phosphate binding pocket of  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  onto which (A)  $\text{ADP}\cdot\text{AlF}_4$  and b)  $\text{ADP}\cdot\text{BeF}_3$  have been superimposed. The rotation and translation matrices were derived by aligning the protein ligands that coordinate the nucleotide (Leu 175–Val 187, Asn 234–Arg 238, and Asp 454–Asp 459 for  $\text{MgADP}\cdot\text{AlF}_4$  and Leu 175–Val 187 and Asn 234–Arg 238 for  $\text{Mg}\cdot\text{ADP}\cdot\text{BeF}_3$ ) with the program LSQKAB implemented in the CCP4 program package (Kabsch, 1976; CCP4, 1994) (rms differences of 0.37 and 0.38 Å, respectively). The nucleotides were excluded from the calculations. The magnesium ion, its associated water molecules, and the protein atoms are shown for  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ . Ser 236 and one of the water molecules bound to the magnesium ion in  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$  are also shown in dark gray. For clarity, the other atoms in  $\text{MgADP}\cdot\text{AlF}_4\cdot\text{S1Dc}$  and  $\text{MgADP}\cdot\text{BeF}_3\cdot\text{S1Dc}$  are not shown since their positions are not significantly different from those of the vanadate complex.

structure are given in Table 3. This suggests that the leaving group,  $\text{MgADP}$ , does not change significantly as the transition state is approached (at least within the experimental error of these structures). The overlap also shows that the three fluorine ligands of  $\text{BeF}_3$  and three equatorial ligands on vanadate lie close to the same plane. Furthermore, the rotational orientation of each set of three atoms is very similar in both complexes. This suggests (if  $\text{BeF}_3$  and  $\text{VO}_4$  are assumed to be models of the ground and transition states) that in going from the ATP ground state to the transition state the oxygen atoms remain close to the observed position of the fluorines and vanadium oxygens while the phosphorus to oxygen distance increases. This fits into the expected picture for phosphate hydrolysis. However, Figure 12B poses an interesting question of why the  $\text{BeF}_3$  adduct does not adopt the conformation observed in the vanadate complex? On the basis of the earlier structure of the aluminum fluoride complex it was suggested that the transition-state conformation was attained because the longer

Al–O bond distance allowed the formation of the additional hydrogen bond to the amide hydrogen of Gly 457 (Fisher et al., 1995b). However, a fluorine atom of  $\text{BeF}_3$  is only 2.9 Å from the amide nitrogen of Gly 457 when transferred to the vanadate active site. This is not significantly different from the observed hydrogen bond distance of 2.8 Å between OV3 and this amide nitrogen in the vanadate complex. If the hydrogen bond distances alone are indicative of strength, why does the polypeptide chain in the  $\text{MgADP}\cdot\text{BeF}_3\cdot\text{S1Dc}$  complex adopt a different conformation from that seen in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ ? The alternative question is what are the factors that stabilize the conformation of the  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  complex? These are difficult questions to answer. One possible difference between these two arrangements lies in the orientation of the hydrogen bond acceptor atoms of the vanadate and  $\text{BeF}_3$  and the orientation of the amide hydrogen. The  $\text{V}-\hat{\text{O}}-\text{N}$  and  $\text{Be}-\hat{\text{F}}-\text{N}$  bond angles are  $131^\circ$  and  $160^\circ$ , respectively, whereas the amide hydrogen is estimated to be in direct line with the vanadate oxygen.

However, there is little relationship between the length (and strength) and the angle at the acceptor group, although angles for most hydrogen bonds cluster about  $129^\circ$  in proteins where the hydrogen bond is not restricted by secondary structural constraints (Baker & Hubbard, 1984). A more likely reason for differences in conformation adopted by the  $\text{BeF}_x$  and vanadate complexes is the differences in the water structure surrounding these moieties in the  $\gamma$ -phosphate pocket.

There is an extensive hydrogen bond network surrounding the apical oxygen (or water) of the vanadate moiety with an approximately tetrahedral distribution of ligands. This suggests that the axial approach of the nucleophilic water molecule on the  $\gamma$ -phosphorus of ATP would be stabilized by these interactions. The constellation of interactions that stabilizes the location of the water molecule in the vanadate complex is not available in the beryllium fluoride complex. The equivalent water molecule in  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  is hydrogen bonded to F3 and the carbonyl oxygen of Ser 237, where the protons on the water molecule are oriented toward these two hydrogen bond acceptors (Figure 12B). It lies approximately  $1.1 \text{ \AA}$  from the location of the apical water (OV4) on the vanadate moiety in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ . In order for the protein to adopt the conformation observed in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ , the water molecule associated with F3 must move; otherwise, it will experience a bad contact with the  $\alpha$ -carbon of Ser 456. Likewise, if this water is to undergo nucleophilic attack on the terminal phosphorus, it must move to an in-line position, similar to that occupied by OV4 in the vanadate moiety. However, movement of the water molecule to an in-line location, in the absence of a conformational change in the protein, would be unfavorable for two reasons. It would lack the conformational stability provided by OW3 (whose location is also a consequence of the conformational change) and also lose its earlier hydrogen bond to F3. Furthermore, once in the in-line position the water molecule could not form reasonable hydrogen bonds with any of the other fluorine atoms. The latter arises not only from geometric considerations but also because movement into the in-line position requires that the protons on the attacking water be directed away from the fluorine atoms to form hydrogen bonds with  $\text{O}_\gamma$  of Ser 236 and OW3. Thus it would appear that the conformation observed in  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  is optimized to orient a water molecule for nucleophilic attack on the  $\gamma$ -phosphorus atom. Conversely, this suggests that premature hydrolysis of ATP and loss of hydrolysis products when the apex of the  $\gamma$ -phosphate pocket is open is prevented by the stereochemically restricted environment of the active site.

There has been considerable discussion over the nature of the transition state for phosphoryl transfer in enzymes and in solution (Westheimer, 1987). In reactions with model compounds in aqueous solution there is compelling evidence for a metaphosphate-like transition state which is essentially dissociative without the formation of metaphosphate itself [see Herschlag and Jencks (1989) and references cited therein]. The situation is less clear for enzymatically catalyzed reactions, many of which involve participation of a divalent cation in the nucleotide binding (Hollfelder & Herschlag, 1995). It has been shown in solution that divalent cations such as  $\text{Mg}^{2+}$  do not increase the associative character of the transition state (Herschlag & Jencks, 1987). However, the experiments on model compounds have not necessarily emulated the environment of the active site of an enzyme.

In particular, it is difficult to simulate the restricted stereochemistry and ionic configuration provided by a nucleotide binding site. The structure of  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  provides a glimpse of the environment that is likely to surround a metaphosphate-like intermediate at the transition state. Unfortunately, in the absence of additional spectral studies, it is impossible to correlate the structure of the vanadium in the active site with the bond order at the transition state for myosin. Such a study has been carried out and described in great detail for muscle phosphoglucomutase by Ray and co-workers (Ray et al., 1990; Ray & Post, 1990; Deng et al., 1993; Ray et al., 1993) from which it was concluded that there is significant bond order to the attacking and leaving groups in the transition state for phosphoryl transfer in this enzyme. For myosin it would appear that there is no difference in the environment or structure of the ligands that coordinate ADP in either  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  and  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$ . This suggests that the leaving group (ADP) experiences a very similar environment in the ground and transition states. Rather it seems that hydrolysis requires a conformational change in the protein that orients the nucleophilic water for attack on the  $\gamma$ -phosphate. This structure appears to be more consistent with greater bond order to the attacking and leaving groups in the transition state for hydrolysis than anticipated for a purely dissociative mechanism.

Finally, it is of interest that formation of the ternary complex between vanadate, MgADP, and myosin is many orders of magnitude slower than would be expected from a diffusion-limited reaction. This was previously interpreted as evidence for a slow conformational change in the protein following the initial binding of vanadate (Goodno, 1979). The structural change observed between  $\text{MgADP}\cdot\text{BeF}_x\cdot\text{S1Dc}$  and  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  could be viewed as consistent with those observations. However, the onset of inhibition by beryllium fluoride is also slow, even though this complex exhibits the same conformation as that seen in  $\text{MgPP}_i\cdot\text{S1Dc}$  (Smith & Rayment, 1995). Thus it seems likely that the slow inhibition is a more complex process associated with formation of a ternary chemical species in the active site.

## CONCLUSION

In recent years vanadate has been often replaced by aluminum and beryllium fluoride as a phosphate analog in biochemical studies (Chabre, 1990) on account of vanadate's tendency to polymerize at physiological hydrogen ion concentrations (Pope & Dale, 1968) and because it is photoreactive (Gibbons et al., 1987; Grammer et al., 1988). Indeed, aluminum and beryllium fluoride bind and affect the properties of a wide range of enzymes that includes the G-proteins (Sternweis & Gilman, 1982; Bigay et al., 1985, 1987), actin and tubulin (Combeau & Carlier, 1988, 1989), and myosin (Phan & Reisler, 1992; Werber et al., 1992; Maruta et al., 1993; Phan et al., 1993). However, neither of these metallofluorides functions as a true analog of the transition state for phosphate ester bond cleavage. In myosin, the beryllium fluoride moiety observed in the active site is tetrahedral such that the complex with ADP mimics ATP and is more representative of the ground state prior to hydrolysis (Fisher et al., 1995b). Conversely, aluminum fluoride forms a complex with the corresponding nucleotide diphosphate in both the G-proteins and myosin where the coordination of the aluminum is approximately square

bipyramidal (Coleman et al., 1994; Sondek et al., 1994; Fisher et al., 1995b). The aluminum fluoride complex is believed to mimic the transition state for hydrolysis, at least insofar as the biological properties of the protein are concerned; however, the extra fluorine ligand prevents it from being a true analog. The structure of  $\text{MgADP}\cdot\text{VO}_4\cdot\text{S1Dc}$  described here shows how the extra fluorine ligand is accommodated in myosin's active site and demonstrates again that vanadate is a good structural analog of the transition state for phosphoryl transfer.

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