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Crystal Structures of Complexes with Cobalt-Reconstituted Human Arginase I

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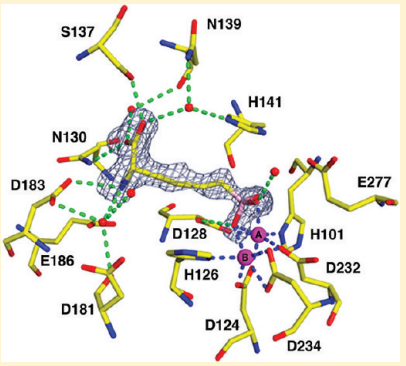
ABSTRACT: The binuclear manganese metalloenzyme human arginase I (HAI) is a potential protein drug for cancer chemotherapy, in that it is capable of depleting extracellular L-Arg levels in the microenvironment of tumor cells that require this nutrient to thrive. Substitution of the native Mn^{2+}_2 cluster with a Co^{2+}_2 cluster in the active site yields an enzyme with enhanced catalytic activity at physiological pH (~7.4) that could serve as an improved protein drug for L-Arg depletion therapy [Stone, E. M., Glazer, E. S., Chantranupong, L., Cherukuri, P., Breece, R. M., Tierney, D. L., Curley, S. A., Iverson, B. L., and Georgiou, G. (2010) *ACS Chem. Biol.* 5, 333−342]. A different catalytic mechanism is proposed for Co^{2+}_2-HAI compared with that of Mn^{2+}_2-HAI, including an unusual Nε−Co^{2+} coordination mode, to rationalize the lower K_M value of L-Arg and the lower K_i value of L-Orn. However, we now report that no unusual metal coordination modes are observed in the cobalt-reconstituted enzyme. The X-ray crystal structures of unliganded Co^{2+}_2-HAI determined at 2.10 Å resolution (pH 7.0) and 1.97 Å resolution (pH 8.5), as well as the structures of Co^{2+}_2-HAI complexed with the reactive substrate analogue 2(*S*)-amino-6-boronohexanoic acid (ABH, pH 7.0) and the catalytic product L-Orn (pH 7.0) determined at 1.85 and 1.50 Å resolution, respectively, are essentially identical to the corresponding structures of Mn^{2+}_2-HAI. Therefore, in the absence of significant structural differences between Co^{2+}_2-HAI and Mn^{2+}_2-HAI, we suggest that a higher concentration of metal-bridging hydroxide ion at physiological pH for Co^{2+}_2-HAI, a consequence of the lower pK_a of a Co^{2+}-bound water molecule compared with a Mn^{2+}-bound water molecule, strengthens electrostatic interactions with cationic amino acids and accounts for enhanced affinity as reflected in the lower K_M value of L-Arg and the lower K_i value of L-Orn.



Arginase is a binuclear manganese metalloenzyme that catalyzes the hydrolysis of L-arginine (L-Arg) to form L-ornithine (L-Orn) and urea.[1−5] This metalloenzyme is becoming increasingly prominent in the exploration and development of new approaches to cancer chemotherapy. For example, arginase activity is upregulated in certain human colon cancer and breast cancer cell lines, resulting in decreased L-Arg levels and increased L-Orn levels; because L-Orn is a biosynthetic precursor of polyamines that facilitate tumor cell growth and proliferation, arginase inhibition decreases L-Orn levels and disrupts the L-Orn supply for polyamine biosynthesis, thereby inhibiting cell proliferation.[6−9] Conversely, some cancer cells are auxotrophic for L-Arg and depend on extracellular L-Arg to thrive; such cancer cells can be targeted with L-Arg depletion therapy.[10,11] For example, hepatocellular carcinoma cells[12] and prostate carcinoma cells[10,13] require extracellular L-Arg to thrive, in the absence of which they undergo apoptosis.[14] Accordingly, arginase is a potential protein drug for cancer chemotherapy insofar that it can efficiently deplete extracellular L-Arg levels in the tumor microenvironment. To this end, the substitution of the native Mn^{2+}_2 cluster with a Co^{2+}_2 cluster in the active site of human arginase I (HAI) yields an enzyme with enhanced catalytic activity at physiological pH (~7.4) that can potentially serve as an even more effective agent for L-Arg depletion therapy.[14]

The catalytic mechanism of Mn^{2+}_2-HAI is believed to be initiated by the nucleophilic attack of a metal-bridging hydroxide ion at the guanidinium carbon of L-Arg to form a neutral tetrahedral intermediate, which subsequently collapses to form products L-Orn and urea (Figure 1a).[5,15,16] A key feature of this mechanistic proposal is a non-metal binding site for the guanidinium group of L-Arg in the precatalytic enzyme−substrate complex. This hypothesis is consistent with structure−activity relationships established for rat arginase I mutants in which the metal binding sites are perturbed by substitution of the metal ligands.[17] These mutants exhibit nearly invariant K_M values regardless of whether Mn^{2+}_A or Mn^{2+}_B binding is perturbed; a more significant effect on K_M would be expected if an inner-sphere substrate−metal coordination interaction occurred in the precatalytic enzyme−substrate complex. This hypothesis is also consistent with the X-ray crystal structures of HAI as well as rat arginase I complexed with boronic acid substrate analogue inhibitors.[16,18] Specifically, the trigonal planar boronic acid moieties of substrate analogues 2(*S*)-amino-6-boronohexanoic acid (ABH)[19] and *S*-(2-boronoethyl)-L-cysteine[20] undergo nucleophilic attack to form negatively charged tetrahedral boronate

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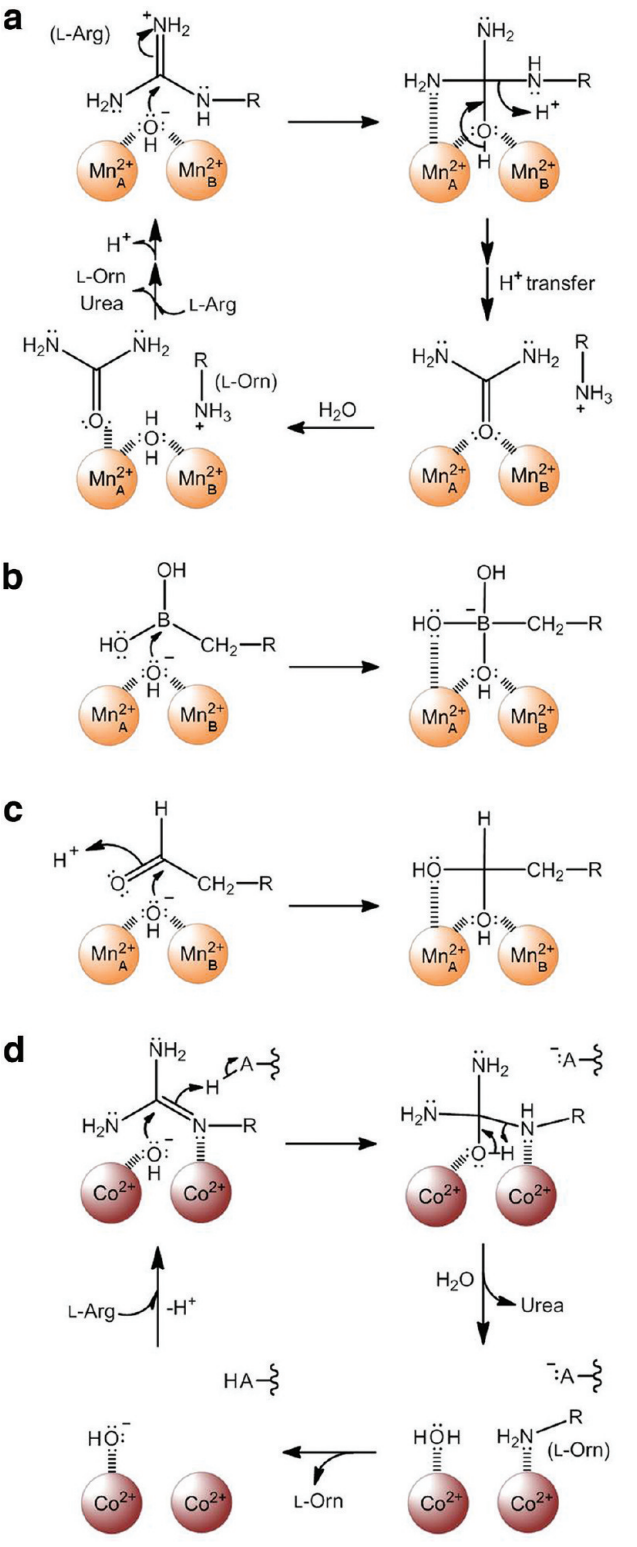

Figure 1. (a) Proposed mechanism of Mn^{2+}_2-HAI.[5] (b) Binding of a boronic acid inhibitor as the tetrahedral boronate anion mimics the tetrahedral intermediate and its flanking transition states in catalysis.[16,18,20] (c) Binding of an aldehyde inhibitor as the tetrahedral gem-diol mimics the tetrahedral intermediate and its flanking transition states in catalysis.[21] (d) Proposed mechanism of Co^{2+}_2-HAI.[14]

anions. Each tetrahedral boronate anion coordinates to the Mn^{2+}_2 cluster in the HAI active site in much the same manner expected for the tetrahedral intermediate in catalysis (Figure 1b); a similar binding mode is also observed for 2(*S*)-amino-7-oxoheptanoic acid, an aldehyde amino acid analogue of L-Arg, which binds as the tetrahedral gem-diol (Figure 1c).[21] The geometry required for the binding of such boronic acid or aldehyde hydrates as analogues of the tetrahedral intermediate is not readily compatible with a substrate–metal coordination interaction in the precatalytic enzyme–substrate complex. However, coordination of the Nη2 atom of L-Arg to Mn^{2+}_A can occur during nucleophilic attack: formation of the C–O bond breaks the Y-shaped guanidinium π system and localizes a lone electron pair on the Nη2 atom, which can then coordinate to Mn^{2+}_A (Figure 1a).[5]

Curiously, Co^{2+}_2-HAI is proposed to catalyze L-Arg hydrolysis through a mechanism significantly different from that of Mn^{2+}_2-HAI.[14] Specifically, the Nε atom of L-Arg is proposed to coordinate directly to an unspecified Co^{2+} ion in the precatalytic enzyme–substrate complex, after which the Co^{2+}-bound guanidinium group undergoes nucleophilic attack by a hydroxide ion bound to the adjacent Co^{2+} ion to form the tetrahedral intermediate; this intermediate is stabilized by coordination of the Nε and Oη atoms to the Co^{2+} ions and ultimately collapses to yield L-Orn and urea (Figure 1d). This proposal emanates from two observations. First, the K_M of L-Arg at pH 8.5 with Co^{2+}_2-HAI is 11-fold lower than that measured with Mn^{2+}_2-HAI, which implicates the Co^{2+}_2 cluster in a stronger substrate binding interaction. Second, the inhibition constant (K_i) of L-Orn is 26-fold lower than that of L-leucine against Co^{2+}_2-HAI at pH 8.5, whereas the corresponding K_i values are relatively unchanged versus those of Mn^{2+}_2-HAI at pH 8.5. These data are interpreted to suggest that the side chain Nε atom of L-Orn coordinates directly to a Co^{2+} ion.[14]

To improve our understanding of structure–mechanism relationships in the cobalt-reconstituted enzyme, we now report the X-ray crystal structures of Co^{2+}_2-HAI and its complexes with a boronic acid substrate analogue as well as the catalytic product. Specifically, we describe the structures of metal-free HAI at 1.64 Å resolution, unliganded Co^{2+}_2-HAI at pH 7.0 (2.10 Å resolution) and pH 8.5 (1.97 Å resolution), Co^{2+}_2-HAI complexed with ABH at 1.85 Å resolution, and Co^{2+}_2-HAI complexed with L-Orn at 1.50 Å resolution. These structures show that Co^{2+} substitution does not trigger any significant structural changes in the active site of HAI. Moreover, these structures do not provide any evidence of different enzyme–substrate, enzyme–intermediate, or enzyme–product binding modes compared with the corresponding structures of Mn^{2+}_2-HAI.

EXPERIMENTAL PROCEDURES

Preparation of Crystalline Co^{2+}_2-HAI and Its Complexes. Recombinant HAI was expressed in *Escherichia coli* and purified as described previously[16] and crystallized in the unliganded state according to published procedures.[22] Metal-free HAI crystals were prepared by soaking Mn^{2+}_2-HAI crystals for 7 days in 15 mM EDTA, 15 mM dipicolinic acid, 100 mM HEPES (pH 7.0), and 30% (v/v) Jeffamine ED-2001. Essentially complete metal removal was confirmed by X-ray crystal structure determination, which revealed the absence of both metal ions in the active site. Crystals of metal-free HAI were reconstituted with Co^{2+} at pH 7.0 by soaking in a buffer solution containing 20 mM $CoCl_2$, 100 mM HEPES (pH 7.0), and 30% (v/v) Jeffamine ED-2001 for 25 h. Metal-free HAI crystals were reconstituted with Co^{2+} at pH 8.5 by soaking in

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20 mM $CoCl_2$, 100 mM Bicine (pH 8.5), and 32% (v/v) Jeffamine ED-2001 for 21 h. The $Co^{2+}{}_2$-HAI−ABH complex was prepared by soaking a $Co^{2+}{}_2$-HAI crystal in 20 mM ABH, 5 mM $CoCl_2$, 100 mM HEPES (pH 7.0), and 30% (v/v) Jeffamine ED-2001 for 39 h. The $Co^{2+}{}_2$-HAI−L-Orn complex was prepared by soaking a $Co^{2+}{}_2$-HAI crystal in 20 mM L-Orn, 5 mM $CoCl_2$, 0.1 M HEPES (pH 7.0), and 30% (v/v) Jeffamine ED-2001 for 24 h. All crystals were flash-cooled in liquid nitrogen with their corresponding mother liquor solutions serving as cryoprotectants.

X-ray Crystal Structure Determinations. X-ray diffraction data from single crystals of metal-free HAI, $Co^{2+}{}_2$-HAI, the $Co^{2+}{}_2$-HAI−ABH complex, and the $Co^{2+}{}_2$-HAI−L-Orn complex were collected on beamline X29 (λ = 0.9795 Å) of the National Synchrotron Light Source at Brookhaven National Laboratory (Upton, NY). Diffraction data were indexed, integrated, and scaled using the *HKL-2000* suite.[23] These twinned arginase crystals belonged to apparent space group *P*3, as reported for the $Mn^{2+}{}_2$-HAI−ABH complex,[16] and their unit cell dimensions were very similar (Table 1).

Structures were determined by molecular replacement using Phaser[24] as implemented in CCP4,[25] with the chain A structure of the $Mn^{2+}{}_2$-HAI−ABH complex (PDB entry 2AEB)[16] less inhibitor, Mn^{2+} ions, and solvent atoms used as the search probe for rotation and translation function calculations. Each refinement was performed with CNS (version 1.2),[26] and model building was performed with Coot (version 0.6.1).[27] Hemihedral twinning operation parameters used in the refinement were $-h$, $-k$, and l, while the twinning fraction depended on the data set (Table 1).

Crystallographic refinement of each structure against twinned intensity data was performed as previously described.[16] Water molecules were included in the later stages of each refinement. For the $Co^{2+}{}_2$-HAI−ABH and $Co^{2+}{}_2$-HAI−L-Orn complexes, gradient omit maps clearly showed ligands bound to the active site of each monomer in the asymmetric unit, and ligand atoms were added and refined with full occupancy. Thermal *B* factors for ligands were consistent with the average *B* factor calculated for the entire protein (Table 1). Disordered segments M1−S5 and P320−K322 at the N- and C-termini,

Table 1. Data Collection and Refinement Statistics

		$Co^{2+}{}_2$-HAI			
	metal-free HAI	pH 7.0	pH 8.5	$Co^{2+}{}_2$-HAI−ABH	$Co^{2+}{}_2$-HAI−L-Orn
		Data Collection			
resolution limits (Å)	50.0−1.64	50.0−2.10	50.0−1.97	50.0−1.85	50.0−1.50
total no./no. of unique reflections measured	837181/78451	174332/37395	179056/40321	247148/53857	558194/102235
unit cell dimensions					
a, *b*, *c* (Å)	90.86, 90.86, 69.88	90.41, 90.41, 69.74	87.42, 87.42, 67.25	90.43, 90.43, 69.43	90.49, 90.49, 69.69
α, β, γ (deg)	90, 90, 120	90, 90, 120	90, 90, 120	90, 90, 120	90, 90, 120
R_{merge} [a,b]	0.080 (0.430)	0.126 (0.417)	0.097 (0.608)	0.078 (0.586)	0.109 (0.550)
$I/\sigma(I)$ [a]	35.18 (5.46)	12.25 (4.18)	14.98 (2.20)	19.55 (2.32)	14.63 (2.89)
completeness (%) [a]	99.3 (95.4)	100 (100)	98.9 (96.3)	99.3 (98.4)	99.9 (100)
		Refinement			
no. of reflections used in refinement/test set	70907/6432	34308/1833	36032/1913	46410/5045	94996/4852
twinning fraction	0.50	0.45	0.30	0.50	0.45
R_{twin} [c]	0.155	0.147	0.144	0.195	0.148
$R_{twin/free}$ [c]	0.197	0.209	0.193	0.239	0.178
no. of solvent molecules [d]	207	127	223	233	277
no. of ligand molecules [d]	0	0	2	2	3
no. of Co^{2+} ions [d]	0	4	4	4	4
Root-mean-square deviation [e]					
bonds (Å)	0.008	0.008	0.007	0.007	0.007
angles (deg)	1.5	1.5	1.5	1.5	1.6
Average B factor (Å^2) [f]					
main chain	24	24	24	27	20
side chain	26	25	26	28	21
solvent	26	24	28	28	23
ligand	−	−	36	22	23
Co^{2+} ions	−	20	25	20	15
Ramachandran plot (%) [e]					
allowed	89.2	85.7	88.4	86.9	90.4
additionally allowed	10.2	13.9	11.2	12.7	9.2
generously allowed	0.6	0.0	0.4	0.2	0.2
disallowed	0.0	0.4	0.0	0.2	0.2
PDB entry	3TF3	3TH7	3THE	3THH	3THJ

[a]Values in parentheses are for the highest-resolution shell. [b]$R_{merge} = \sum|I - \langle I\rangle|/\sum I$, where I is the observed intensity and $\langle I\rangle$ is the average intensity calculated from replicate data. [c]$R_{twin} = \sum||(|F_{calc/A}|^2 + |F_{calc/B}|^2)^{1/2} - |F_{obs}||/\sum|F_{obs}|$ for reflections contained in the working set. $|F_{obs}|$ is the observed structure factor amplitude, and $|F_{calc/A}|$ and $|F_{calc/B}|$ are the structure factor amplitudes calculated for twin domains A and B, respectively. R_{twin} underestimates the residual error in the model over the two twin-related reflections by a factor of approximately 0.7. The same expression describes $R_{twin/free}$, calculated for test set reflections excluded from refinement. [d]Per asymmetric unit. [e]Calculated using PROCHECK.[35] [f]Calculated using MOLEMAN.[36]

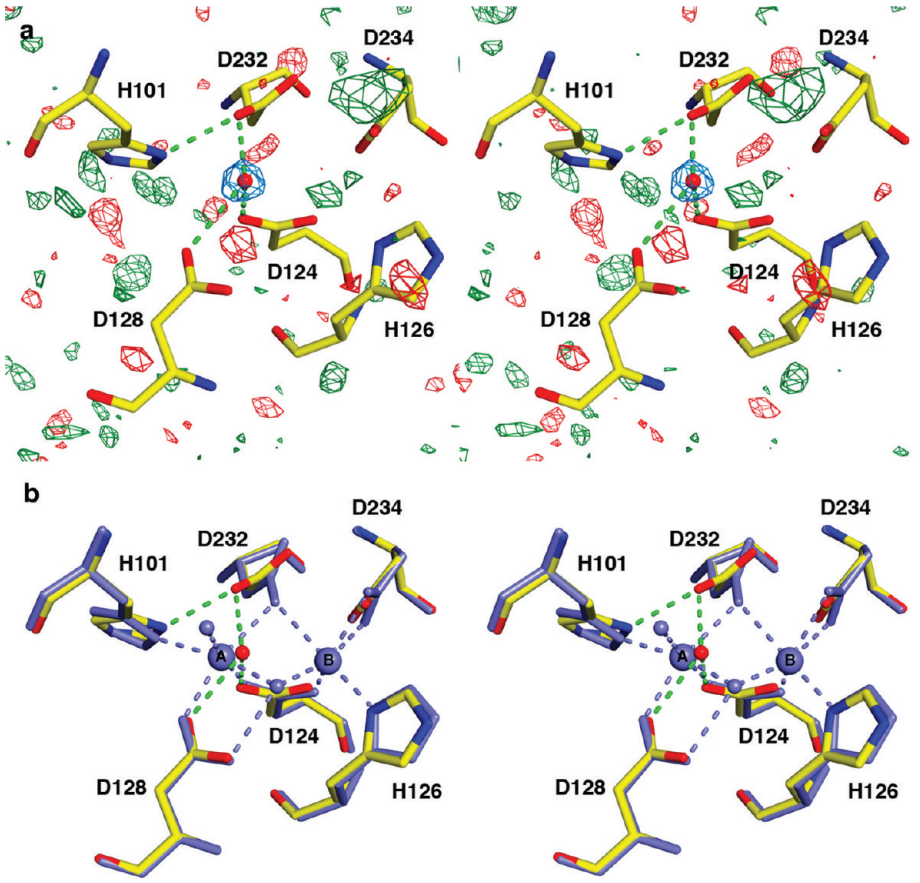

Figure 2. (a) Final $|F_o| - |F_c|$ map of metal-free HAI contoured at 3.0σ (green) and −3.0σ (red). Only spurious noise peaks are observed, and none correspond to residual metal ions. A water molecule (red sphere), confirmed in a simulated annealing omit map contoured at 3.0σ (blue), is hydrogen bonded (green dashed lines) to D124, D128, and D232. Atoms are color-coded as follows: yellow for C, blue for N, and red for O. (b) Superposition of A chains for metal-free HAI (pH 7.0, color-coded as in panel a) and Mn^{2+}_2-HAI (pH 7.5) (PDB entry 2PHA, all atoms and interactions colored light blue). Apart from small conformational changes of D232 and H101, protein residues in the apoenzyme are nearly preformed for ideal metal coordination interactions.

respectively, were excluded from all final models. Ramachandran plots revealed Q65 with a disallowed conformation in certain structures. For Co^{2+}_2-HAI (pH 7.0), this included monomers A and B; in the Co^{2+}_2-HAI−ABH and Co^{2+}_2-HAI−L-Orn complexes, this included only monomer A. In general, Q65 was characterized by well-defined electron density in these structures, so its conformation was not ambiguous. Moreover, this residue adopted a similar conformation in Mn^{2+}_2-HAI (PDB entry 2PHA),[22] so its unfavorable conformation was not likely to be an artifact. Data collection and refinement statistics for all structure determinations are listed in Table 1.

RESULTS

Metal-Free HAI. The structure of metal-free HAI is the first structure of any arginase in which both active site metal ions are absent (Figure 2a). The overall structure is comparable to that of unliganded wild-type HAI (Mn^{2+}_2-HAI, PDB entry 2PHA[22]) with a root-mean-square deviation (rmsd) of 0.24 Å for 313 Cα atoms. Metal binding residues D128, D124, H126, D232, D234, and H101 remain fully ordered despite the loss of Mn^{2+}_A and Mn^{2+}_B; however, H101 and D232 undergo slight conformational changes to form a hydrogen bond upon metal dissociation (Figure 2b). Thus, the metal binding site is nearly preformed with optimal geometry for metal binding; i.e., minimal conformational changes are necessary for binding the two metal ions required for catalysis.

Co^{2+}_2-HAI. The overall fold of unliganded Co^{2+}_2-HAI at pH 7.0 and 8.5 is essentially identical to that of unliganded Mn^{2+}_2-HAI at pH 7.5 (PDB entry 2PHA[22]), with an rmsd of 0.26 Å for 313 Cα atoms or 0.47 Å for 313 Cα atoms, respectively. Interestingly, no metal-bound solvent molecules are observed at pH 7.0, except for a single solvent molecule bound to the Co^{2+}_A ion of chain A (Figure 3a), which could imply weaker coordination or disorder. However, metal-bound solvent molecules are fully visible in the structure of Co^{2+}_2-HAI determined at pH 8.5 (Figure 3b) and are identical to those observed in the structure of unliganded Mn^{2+}_2-HAI[22] (Figure 3c). Parenthetically, we note that a bicine buffer molecule is observed to bind at the mouth of the Co^{2+}_2-HAI active site at pH 8.5 (data not shown).

Co^{2+}_2-HAI−ABH Complex. The structure of the Co^{2+}_2-HAI−ABH complex at pH 7.0 is essentially identical to the structure of the Mn^{2+}_2-HAI−ABH complex (PDB entry 2AEB)[16] in both the overall fold (rmsd = 0.25 Å for 313 Cα atoms) and the intermolecular interactions of ABH in the active site. A simulated annealing omit map is shown in Figure 4a along with a superposition of the Mn^{2+}_2-HAI−ABH complex. The boronic acid side chain of ABH undergoes nucleophilic attack, probably by the metal-bridging hydroxide ion, to yield a tetrahedral boronate anion that coordinates to the Co^{2+}_A and Co^{2+}_B ions. The α-carboxylate of ABH accepts hydrogen bonds from N130, S137, and two water molecules, and the α-amino group donates hydrogen bonds to D183 and two water molecules.

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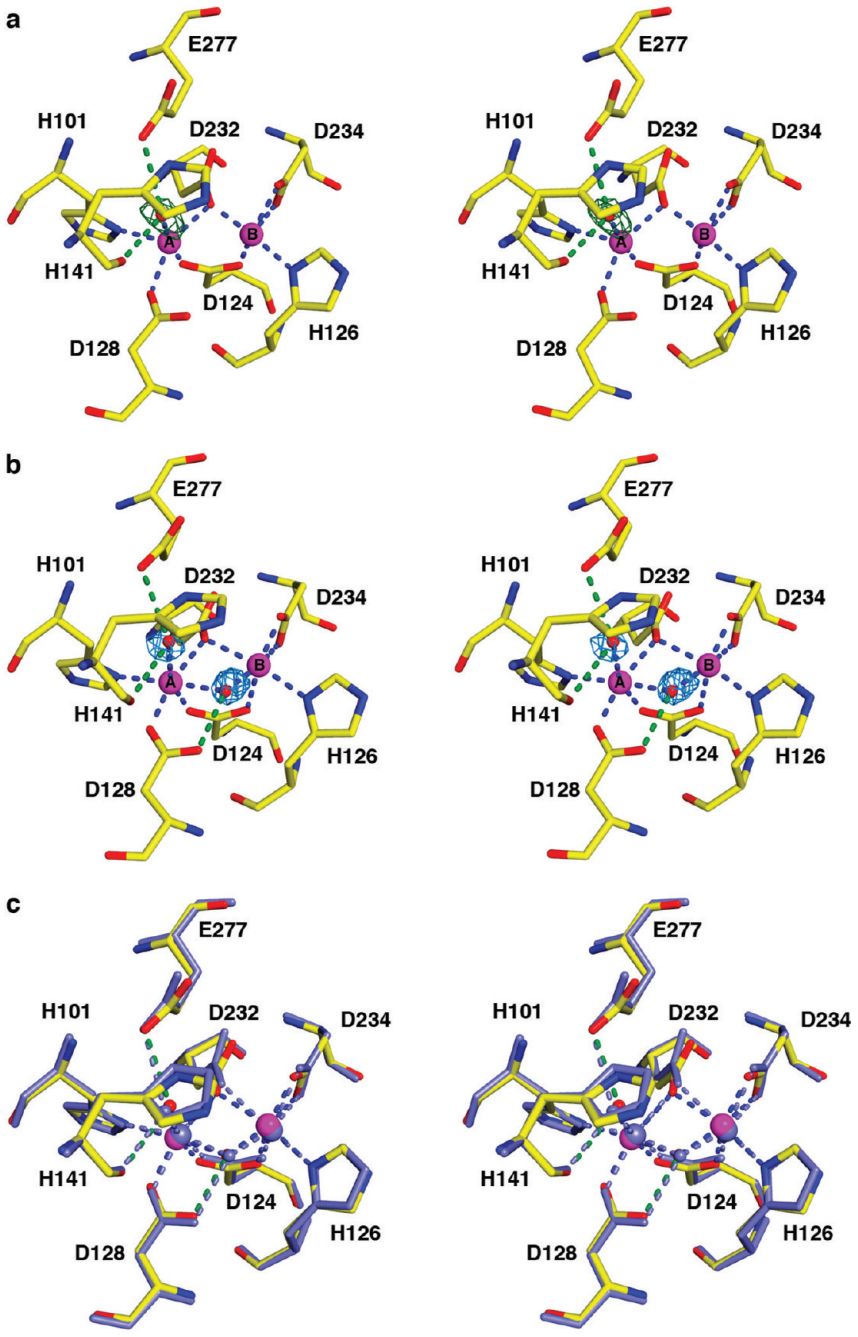

Figure 3. (a) Simulated annealing omit map (green) of the Co^{2+}_A-bound solvent molecule in chain A of Co^{2+}_2-HAI at pH 7.0, contoured at 3.5σ. Atoms are color-coded as follows: yellow for C, blue for N, red for O, magenta spheres for Co^{2+}, and red spheres for solvent. Metal coordination and hydrogen bond interactions are represented as blue and green dashed lines, respectively. (b) Simulated annealing omit map (blue) of the Co^{2+}-bound solvent molecules in Co^{2+}_2-HAI at pH 8.5, contoured at 4.2σ. Atoms and intermolecular interactions are color-coded as in panel a. (c) Superposition of A chains for Co^{2+}_2-HAI (pH 8.5) (color-coded as in panel b) and Mn^{2+}_2-HAI (pH 7.5) (PDB entry 2PHA, all atoms colored light blue).

Water molecules hydrogen bonded with the α-carboxylate and the α-amino groups also hydrogen bond with active site protein residues as summarized in Figure 4b.

Co^{2+}-HAI–L-Orn Complex. The structure of the Co^{2+}_2-HAI–L-Orn complex determined at pH 7.0 has an overall fold similar to that of the Mn^{2+}_2-HAI–L-Orn complex determined at pH 6.5,[28] and the rmsd for 314 Cα atoms is 0.17 Å. A simulated annealing omit map is shown in Figure 5. The terminal amino group of L-Orn donates hydrogen bonds to D128, the backbone carbonyl of H141, and two solvent molecules, one of which is the metal-bridging hydroxide ion. The α-amino and α-carboxylate groups of L-Orn make interactions similar to those observed for ABH in the Co^{2+}_2-HAI–ABH complex (Figure 4) and the Mn^{2+}_2-HAI–ABH complex.[16] Parenthetically, we note that in the Co^{2+}_2-HAI–L-Orn complex, an additional L-Orn molecule binds to the surface of monomer A in the asymmetric unit, where the backbone carbonyl groups of T134 and T135 accept hydrogen bonds from the α-amino group and the ε-amino group of L-Orn, respectively (data not shown). This second L-Orn molecule is characterized by weak electron density consistent with reduced

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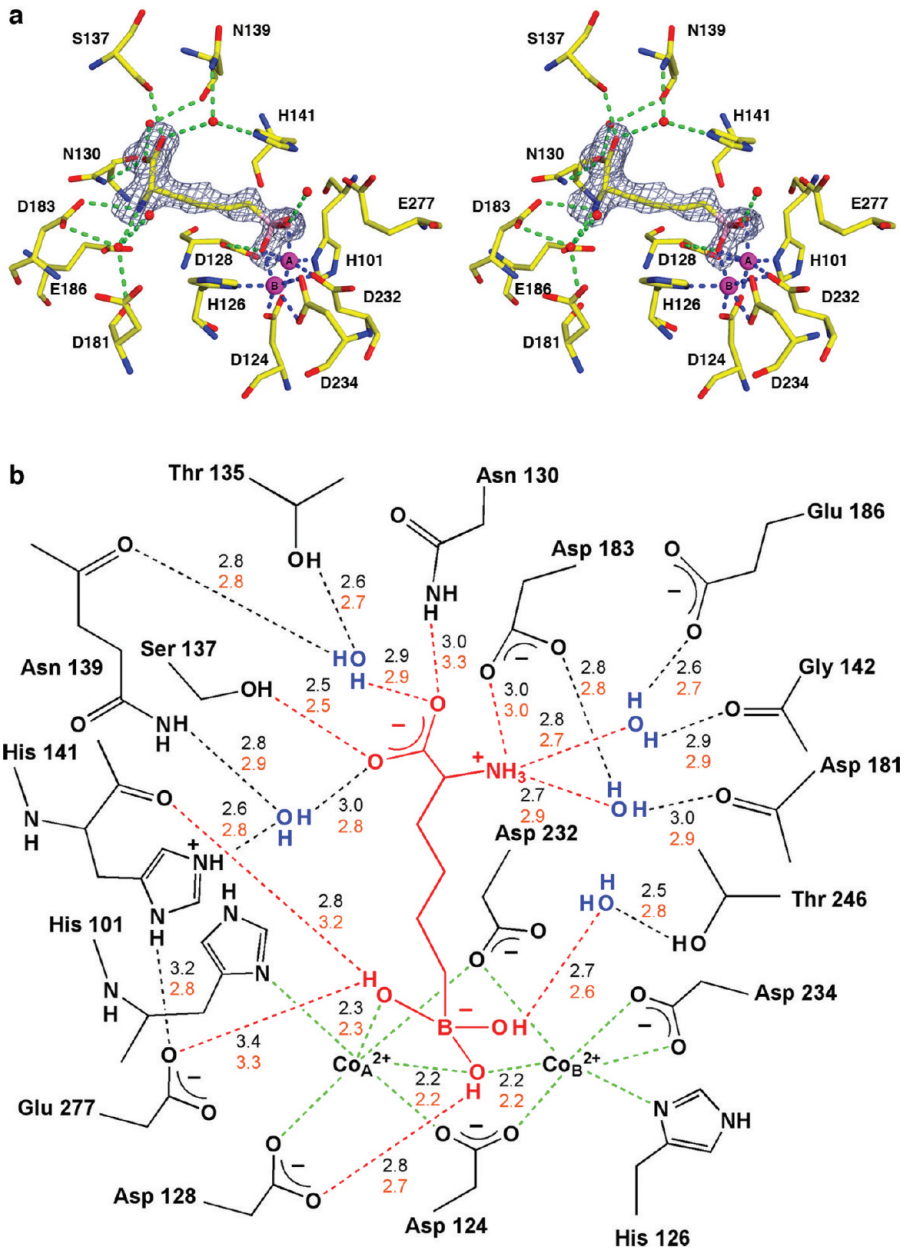

Figure 4. (a) Simulated annealing omit map (gray) of the inhibitor ABH bound in the active site of Co^{2+}_2-HAI, contoured at 4.0σ. The boronic acid moiety of ABH binds as a tetrahedral boronate anion that mimics the tetrahedral intermediate and its flanking transition states in the reaction catalyzed by Co^{2+}_2-HAI. Atoms are color-coded as follows: yellow for C, blue for N, red for O, pink for B, magenta spheres for Co^{2+}, and red spheres for solvent. Metal coordination and hydrogen bond interactions are represented by blue and green dashed lines, respectively. (b) Scheme illustrating average distances (angstroms) of intermolecular interactions in the Co^{2+}_2-HAI–ABH complex (black numbers) and Mn^{2+}_2-HAI–ABH complex (PDB entry 2AEB) (orange numbers).

occupancy; because Stone and colleagues do not report any nonlinearity in product inhibition,[14] L-Orn binding to this second site does not appear to significantly affect catalysis.

DISCUSSION

The first successful preparation of a crystalline metal-free arginase described in this work allows for the substitution of metal ions other than the native Mn^{2+} ions in the active site. Previous studies with rat arginase I show that only one Mn^{2+} ion is readily extracted from the Mn^{2+}_2 cluster,[29] so the human enzyme offers a distinct advantage for the preparation of the metal-free apoenzyme. Significantly, Co^{2+}_2-HAI is said to have ideal functional properties for use in the treatment of L-Arg auxotrophic tumors, e.g., as assayed against human melanoma and hepatocellular carcinoma cell lines: a decreased pK_a for metal-bound water, a decreased K_M for substrate L-Arg, and a decreased K_i for product L-Orn.[14]

Functional studies of Co^{2+}_2-HAI[14] are interpreted to reflect the proposed mechanism in Figure 1d, which includes the following chemical steps: (1) deprotonation of L-Arg, (2) tautomerization of the neutral guanidinium group and coordination of the Nε atom to a Co^{2+} ion, (3) nucleophilic attack at the guanidinium carbon by a Co^{2+}-bound hydroxide ion, (4) formation of the tetrahedral intermediate in which the Oη and Nε atoms are coordinated to separate Co^{2+} ions, (5) collapse of the tetrahedral intermediate to yield product L-Orn with its Nε

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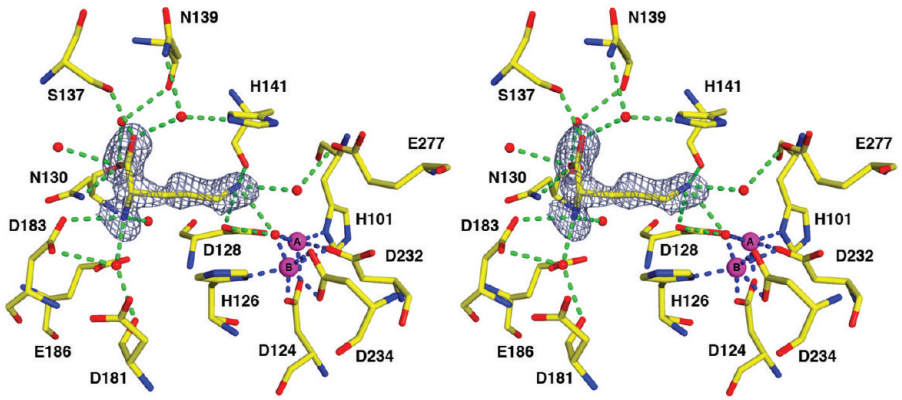

Figure 5. Simulated annealing omit map (gray) of the catalytic product L-Orn bound in the active site of Co^{2+}_2-HAI at pH 7.0, contoured at 3.0σ. Atoms are color-coded as follows: yellow for C, blue for N, red for O, magenta spheres for Co^{2+}, and red spheres for solvent. Metal coordination and hydrogen bond interactions are represented by blue and green dashed lines, respectively.

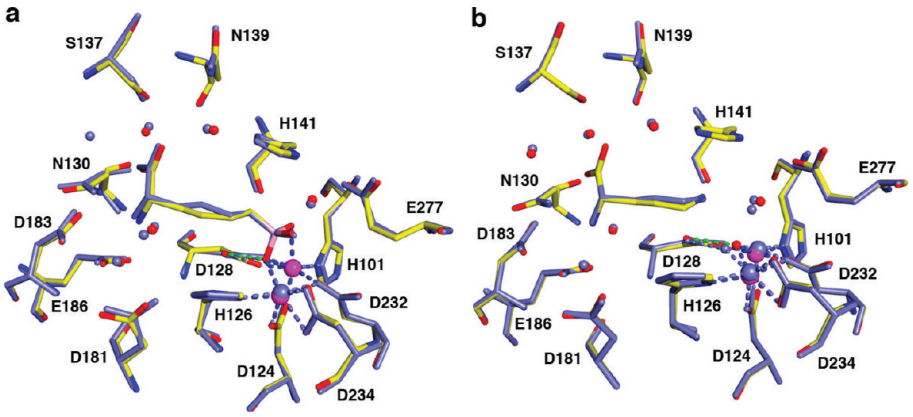

Figure 6. (a) Superposition of the Co^{2+}_2-HAI–ABH complex (color-coded as in Figure 4a) and the Mn^{2+}_2-HAI–ABH complex at pH 7.5 (PDB entry 2AEB, all atoms and metal coordination interactions colored light blue). Apart from a 0.5 Å shift of the side chain Cγ atom of ABH, the structures of these complexes are essentially identical. (b) Superposition of the Co^{2+}_2-HAI–L-Orn complex (color-coded as in Figure 5) and the Mn^{2+}_2-HAI–L-Orn complex (PDB entry 3GMZ, all atoms and interactions colored light blue).

atom coordinated to one Co^{2+} ion, and a water molecule that displaces urea to coordinate to the other Co^{2+} ion, and (6) ionization of Co^{2+}-bound water to regenerate the nucleophilic Co^{2+}-bound hydroxide ion.

X-ray crystal structures of Co^{2+}_2-HAI allow us to evaluate certain aspects of this mechanistic proposal. First, it is intriguing to consider the possibility that the Nε atom of L-Arg or L-Orn coordinates to an active site metal ion. While it is unusual to consider the inner-sphere coordination of the guanidinium Nε or Nη atom of L-Arg to a metal ion, such interactions are occasionally observed.[30] However, because the Nε atom of L-Orn does not coordinate to metal ions in the active site of Co^{2+}_2-HAI (Figure 5) or Mn^{2+}_2-HAI,[28] the observed binding mode is at odds with the Nε–Co^{2+} coordination mode proposed for L-Orn, and by inference the Nε–Co^{2+} coordination mode proposed for L-Arg, in Figure 1d.[14] Because L-Orn adopts an identical binding mode in the active sites of Mn^{2+}_2-HAI and Co^{2+}_2-HAI (Figure 6), the lower K_i value of L-Orn for binding to Co^{2+}_2-HAI must therefore arise from an indirect effect of the metal ions, e.g., the hydrogen bond between the L-Orn side chain and the metal-bridging solvent molecule (Figure 5). The concentration of metal-bridging hydroxide ion is greater for Co^{2+}_2 than for Mn^{2+}_2 at physiological pH,[14] which in turn would strengthen its hydrogen bond and electrostatic interactions with the positively charged side chain of L-Orn.

The binding of ABH as the tetrahedral boronate anion likely mimics the binding of the tetrahedral intermediate and its flanking transition states in catalysis by Mn^{2+}_2-rat arginase I,[18] Mn^{2+}_2-HAI,[16] Co^{2+}_2-HAI (this work), and Mn^{2+}_2-arginase from *Plasmodium falciparum*.[31] The binding conformation of ABH to these enzymes is essentially identical (as illustrated in Figure 6 for Co^{2+}_2-HAI and Mn^{2+}_2-HAI), such that the amino acid side chain is extended into the active site with all C–C bonds adopting trans or nearly trans conformations. Identical binding modes of ABH to these enzymes suggest identical binding modes for the corresponding tetrahedral intermediate and its flanking transition states, i.e., identical catalytic mechanisms.

Further analysis of the binding mode of ABH to Co^{2+}_2-HAI suggests that the boronate anion hydroxyl groups O2 and O3 correspond to the two hydroxyl groups of the native boronic acid, whereas boronate anion hydroxyl group O1 corresponds to the metal-bridging hydroxide ion of the native enzyme. This binding mode is most consistent with a mechanism in which the trigonal planar boronic acid moiety of ABH (or the trigonal planar guanidinium group of the substrate) enters the active site of Co^{2+}_2-HAI and subsequently undergoes nucleophilic attack by a metal-bridging hydroxide ion to yield the tetrahedral boronate anion (or tetrahedral intermediate), with a metal-bridging hydroxyl group (i.e., the former metal-bridging hydroxide ion) and the terminal O2 hydroxyl group (or Nη2

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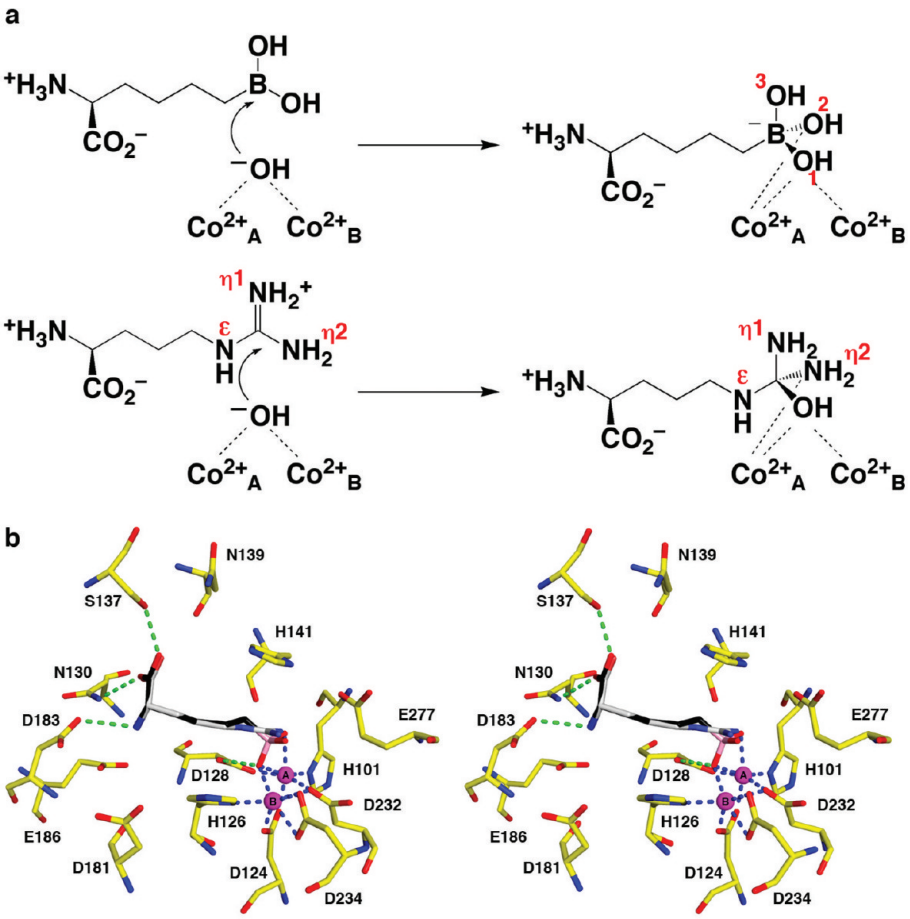

Figure 7. (a) Attack of the nucleophilic metal-bridging hydroxide ion at the boronic acid moiety of the inhibitor ABH results in the formation of a tetrahedral boronate anion that mimics the formation of the tetrahedral intermediate in catalysis. While this chemistry is illustrated for Co^{2+}_2-HAI, it is identical to that of Mn^{2+}_2-HAI. Selected atoms discussed in the text are indicated with red labels. (b) Model of L-Arg superimposed on the experimentally determined structure of ABH bound in the active site of Co^{2+}_2-HAI, which mimics the binding of the tetrahedral intermediate and its flanking transition states in catalysis. Atoms are color-coded as follows: yellow (protein), black (ABH), or gray (L-Arg) for C; blue for N; red for O; and magenta spheres for Co^{2+}. Solvent molecules were omitted for the sake of clarity; metal coordination and hydrogen bond interactions for ABH are represented as blue and green dashed lines, respectively. The side chain Nη1 and Nη2 atoms of L-Arg correspond to the boronate O3 and O2 atoms (atom labels are shown in panel a). Nucleophilic attack of a metal-bridging hydroxide ion (which would correspond to the position of the boronate O1 atom) at the planar guanidinium group of L-Arg satisfies the principle of least nuclear motion and simply requires the pyramidalization of the guanidinium carbon (or the boron atom of the boronic acid) as it undergoes the transition from sp^2 to sp^3 hybridization. This conclusion is valid for both Co^{2+}_2-HAI and Mn^{2+}_2-HAI.

amino group) coordinated to Co^{2+}_A (Figure 7a). This mechanistic model is identical to that outlined for Mn^{2+}_2-HAI[5] and is derived from that initially proposed by Kanyo and colleagues for Mn^{2+}_2-rat arginase I,[15] which satisfies the principle of least nuclear motion (Figure 7b).[32] Alternative mechanistic models, such as that initially proposed for Co^{2+}_2-HAI,[14] involve additional chemical or conformational steps that would add seemingly unnecessary nuclear motions to the mechanistic sequence.

The observed binding mode of the tetrahedral boronate anion form of ABH to Co^{2+}_2-HAI is not consistent with the proposed binding mode of the tetrahedral intermediate that involves metal coordination by the Nε atom of L-Arg (Figure 1d).[14] A key structural feature that prevents a closer approach of the Nε atom of L-Arg or L-Orn to the binuclear metal cluster is the extensive array of hydrogen bond interactions that anchor the α-amino and α-carboxylate groups of amino acids bound in the arginase active site (e.g., see the scheme summarizing the binding mode of ABH in Figure 4b). This hydrogen bond array ensures the precise molecular recognition of L-amino acids in the arginase active site. Modification or deletion of these enzyme−substrate hydrogen bonds significantly compromises catalysis, either by mutagenesis in the enzyme active site[33] or by modification of substrate structure or stereochemistry.[34]

Finally, while the proposed mechanism of Co^{2+}_2-HAI summarized in Figure 1d[14] is inconsistent with the X-ray crystal structures of Co^{2+}_2-HAI reported herein, the fact remains that functional studies clearly indicate a decreased K_M value for substrate L-Arg and a decreased K_i value for product L-Orn.[14] If functional differences between Co^{2+}_2-HAI and Mn^{2+}_2-HAI do not arise from structural differences in the binding of substrate, tetrahedral intermediate, and product, from what do they arise? Given that the metal-bridging solvent molecule exhibits a lower pK_a in Co^{2+}_2-HAI, there would be a higher concentration of the negatively charged metal-bridging hydroxide ion at physiological pH in comparison with that in Mn^{2+}_2-HAI.[14] As previously mentioned, this would enhance the hydrogen bond and electrostatic interactions with the positively charged side chain of L-Orn and thereby enhance affinity, which would account for the lower K_i value measured against Co^{2+}_2-HAI.

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Similarly, we suggest that the lower K_M value measured for L-Arg with Co^{2+}_2-HAI results from an enhanced electrostatic interaction (but not a hydrogen bond interaction) between the positively charged guanidinium side chain of L-Arg and the negatively charged metal-bound hydroxide ion in the precatalytic Michaelis complex. Thus, in the absence of significant structural differences between Mn^{2+}_2-HAI and Co^{2+}_2-HAI complexes, we suggest that a simple electrostatic interaction dependent upon the predominant ionization state of a metal-bound water molecule, not a direct metal coordination interaction, could explain the functional differences between Co^{2+}_2-HAI and Mn^{2+}_2-HAI.

■ ASSOCIATED CONTENT

Accession Codes

The atomic coordinates and structure factors of metal-free human arginase I, Co^{2+}_2-human arginase I at pH 7.0 and pH 8.5, and Co^{2+}_2-human arginase I complexed with 2(*S*)-amino-6-boronohexanoic acid and L-ornithine have been deposited in the Protein Data Bank as entries 3TF3, 3TH7, 3THE, 3THH, and 3THJ, respectively.

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■ ABBREVIATIONS

Mn^{2+}_2-HAI, native human arginase I; Co^{2+}_2-HAI, cobalt-reconstituted human arginase I; L-Arg, L-arginine; L-Orn, L-ornithine; ABH, 2(*S*)-amino-6-boronohexanoic acid; HEPES, *N*-(2-hydroxyethyl)piperazine-*N*′-2-ethanesulfonic acid; PDB, Protein Data Bank.

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