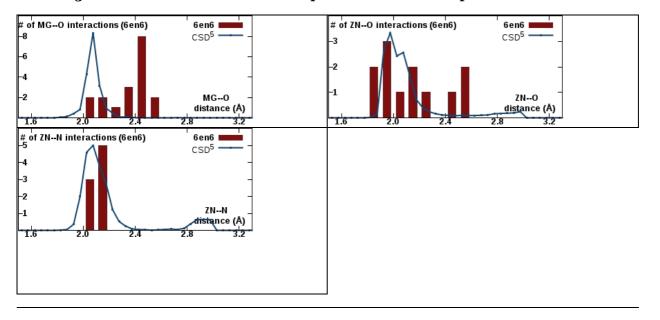
## **CheckMyMetal(CMM)** report for PDB code: 6en6

PDB title: Crystal structure b of the angiotensin-1 converting enzyme n-domain in complex with a diprolyl inhibitor. (1.8Å)

ID	Res.	Metal	Occupancy	B factor (env.) <sup>1</sup>	Ligands	Valence <sup>2</sup>	nVECSUM <sup>3</sup>	Geometry <sup>1,4</sup>	gRMSD(°) <sup>1</sup>	Vacancy <sup>1</sup>	Bidentate	Alt. metal
A:710	ZN	Zn	1	16.7 (15.5)	O <sub>3</sub> N <sub>2</sub>	1.8	<u>0.16</u>	<u>Trigonal</u> <u>Bipyramidal</u>	<u>14.5°</u>	0	0	Co, Zn
A:712	CL	Cl	1	17.8 (19.3)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
A:713	MG	Mg	1	<u>23.7</u> (29.3)	$O_4$	<u>0.8</u>	<u>0.35</u>	Octahedral	11.2°	<u>33%</u>	0	Na, Ca
B:709	ZN	Zn	1	17.4 (18.2)	O <sub>3</sub> N <sub>2</sub>	1.9	<u>0.14</u>	<u>Trigonal</u> <u>Bipyramidal</u>	<u>15.2°</u>	0	0	Co, Zn
B:711	CL	Cl	1	19.3 (18.8)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
B:712	MG	Mg	1	<u>24.2</u> (30.1)	O <sub>5</sub>	<u>0.9</u>	0.32	Octahedral	7.4°	<u>16%</u>	0	Ca
C:708	ZN	Zn	1	18.6 (18.6)	$O_3N_2$	1.7	0.04	<u>Trigonal</u> <u>Bipyramidal</u>	13.2°	0	0	
C:710	CL	Cl	1	20.8 (23)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
C:711	MG	Mg	1	<u>25 (31.3)</u>	<u>O<sub>4</sub>N<sub>1</sub></u>	1	<u>0.36</u>	Octahedral	7.5°	<u>16%</u>	0	
D:709	ZN	Zn	1	17.7 (18.6)	O <sub>3</sub> N <sub>2</sub>	1.8	<u>0.15</u>	<u>Trigonal</u> <u>Bipyramidal</u>	<u>15.6°</u>	0	0	Co, Zn
D:711	CL	Cl	1	18.3 (18)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
D:712	MG	Mg	1	<u>13.8</u> (21.4)	<u>O<sub>5</sub>N<sub>1</sub></u>	<u>0.8</u>	0.099	Octahedral	8.1°	0	0	
	Legend: Not applicable Outlier Borderline Acceptable											

Column	Description							
Occupancy	Occupancy of ion under consideration							
B factor (env.) <sup>1</sup>	Metal ion B factor, with valence-weighted environmental average B factor in parenthesis							
Ligands	Elemental composition of the coordination sphere							
Valence <sup>2</sup>	Summation of bond valence values for an ion binding site. <i>Valence</i> accounts for metal-ligand distances							
nVECSUM <sup>3</sup>	Summation of ligand vectors, weighted by bond valence values and normalized by overall valence. Increase when the coordination sphere is not symmetrical due to incompleteness.							
Geometry <sup>1,4</sup>	Arrangement of ligands around the ion, as defined by the NEIGHBORHOOD algorithm							
gRMSD(°) <sup>1</sup>	R.M.S. Deviation of observed geometry angles (L-M-L angles) compared to ideal geometry, in degrees							
Vacancy <sup>1</sup>	Percentage of unoccupied sites in the coordination sphere for the given geometry							
Bidentate	Number of residues that form a bidentate interaction instead of being considered as multiple ligands							
Alt. metal	A list of alternative metal(s) is proposed in descending order of confidency, assuming metal environment is accurately determined. This feature is still experimental. It requires user discrimination and cannot be blindly accepted							

## Metal-ligand distance distributions for pdb6en6.ent in comparison with CSD



(1) Zheng H, Chordia MD, Cooper DR, Chruszcz M, Müller P, Sheldrick GM, Minor W (2014) Nature Protocols, 9(1), 156-70.

(2) Brown ID (2009) *Chem. Rev., 109,* 6858-6919.
(3) Müller P, Köpke S, Sheldrick GM (2003) *Acta Crystallogr. D Biol. Crystallogr., 59,* 32-37.
(4) Kuppuraj G, Dudev M, Lim C (2009) *J. Phys. Chem. B, 113,* 2952-2960.

(5) CSD: Cambridge Structural Database

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## Citing CheckMyMetal (CMM):

Validation of metal-binding sites in macromolecular structures with the CheckMyMetal web server. Zheng, H., Chordia, M.D., Cooper, D.R., Chruszcz, M., Müller, P., Sheldrick, G.M., Minor, W. (2014) Nature Protocols, 9(1), 156-70.