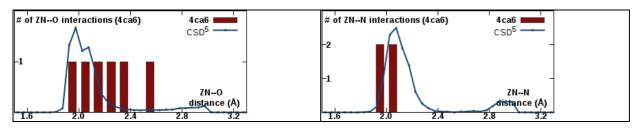
## **CheckMyMetal(CMM)** report for PDB code: 4ca6

PDB title: Human angiotensin converting enzyme n-domain in complex with a phosphinic tripeptide fi (1.9Å)

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:1001	ZN	Zn	1	18 (18.2)	$O_3N_2$	2	<u>0.11</u>	<u>Trigonal</u> <u>Bipyramidal</u>	13°	0	0	
A:1002	CL	Cl	1	19.3 (19.5)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
B:1001	ZN	Zn		16.6 (16.7)	O <sub>3</sub> N <sub>2</sub>	2.3	<u>0.11</u>	<u>Trigonal</u> <u>Bipyramidal</u>	13.4°	0	( )	Mn, Zn, Fe
B:1003	CL	Cl		24.5 (27.9)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
	Le	gend:	Not applicable	utlier <u>Bo</u>	<i>rderline</i> A	cceptable						

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 pdb4ca6.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
- Maintained by: Heping Zheng < dust@iwonka.med.virginia.edu >

## 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.