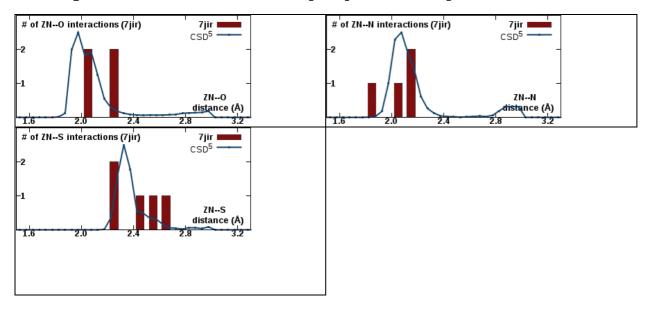
## **CheckMyMetal(CMM)** report for PDB code: 7jir

PDB title: The crystal structure of papain-like protease of sars cov-2, c111s mutant, in complex with plp\_snyder457 (2.1Å)

Warr	Warning: Valence and nVECSUM parameters should be interpreted with great care due to the presence of multi-nuclear metal clusters around A:504											
	Warning: Coordinating ligands by symmetry operation are labeled with prefix 'sym-'											
	War	ning:	Partial occu	pancy of	the meta	al is not a	djusted upon symmetry operation					
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:502	ZN	Zn	1	134.1 (128.4)	$S_3$	<u>1.1</u>	0.43	Tetrahedral	<u>19.7°</u>	<u>25%</u>	0	
A:503	ZN	Zn	1	<u>100</u> (81.1)	<u>O<sub>1</sub>N<sub>1</sub></u>	<u>1.1</u>	0.67	Linear	<u>30.5°</u>	0	0	Hg
A:504	ZN	Zn	<u>0.6</u>	<u>43.9</u> (57.2)	$O_1N_1S_1$	1.7	<u>0.17</u>	Tetrahedral	<u>14.7°</u>	<u>25%</u>	0	Cu, Zn, Co
A:504	ZN	Zn	0.4	55.1 (59.3)	O <sub>1</sub> N <sub>1</sub> S <sub>1</sub>	<u>1.5</u>	0.25	Tetrahedral	13°	<u>25%</u>	0	Cu, Co
A:505	ZN	Zn	1	54.3 (55.7)	<u>O<sub>1</sub>N<sub>1</sub></u>	1.9	0.096	<u>Trigonal</u> <u>Planar</u>	2.6°	33%	0	Cu
A:506	CL	Cl	1	<u>98.1</u> (62.7)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
A:507	CL	Cl	1	<u>55 (64.6)</u>		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
A:508	CL	Cl	1	56.1 (60)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
A:509	CL	Cl	1	<u>68.1</u> (56.9)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
	Le	gend:	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 pdb7jir.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.