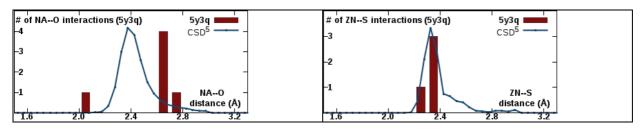
CheckMyMetal(CMM) report for PDB code: 5y3q

PDB title: Crystal structure of sars coronavirus papain-like protease conjugated with beta-mercaptoethanol (1.6Å)

ID	Res.	Metal	Occupancy	B factor (env.) ¹	Ligands	Valence ²	nVECSUM ³	Geometry ^{1,4}	gRMSD(°) ¹	Vacancy ¹	Bidentate	Alt. metal
A:401	ZN	Zn		21.6 (22.2)	S_4	2.1	0.04	Tetrahedral	2.8°	0	0	
A:403	NA	Na	1	<u>19.5</u> (12.9)	Ο ₃	0.3	0.26	<u>Tetrahedral</u>	5.1°	<u>25%</u>	0	
A:404	NA	Na	1	26.2 (13.4)	O_2N_1	0.8	0.66	<u>Square</u> <u>Planar</u>	32.4°	<u>25%</u>	0	
A:405	NA	Na	1	16 (13.9)	<u>O</u> 1	0.09	1	Poorly Coordinated	N/A	N/A	0	
A:406	NA	Na	1	27.4 (22.1)		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
A:407	NA	Na	1	<u>17 (9.2)</u>		N/A	N/A	<u>Free</u>	N/A	N/A	N/A	
Legend:			Not applicable	utlier Bo	<u>rderline</u> A	cceptable						

Column	Description								
Occupancy	Occupancy of ion under consideration								
B factor (env.) ¹	Metal ion B factor, with valence-weighted environmental average B factor in parenthesis								
Ligands	Elemental composition of the coordination sphere								
Valence ²	Summation of bond valence values for an ion binding site. <i>Valence</i> accounts for metal-ligand distances								
nVECSUM ³	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 ^{1,4}	Arrangement of ligands around the ion, as defined by the NEIGHBORHOOD algorithm								
gRMSD(°) ¹	R.M.S. Deviation of observed geometry angles (L-M-L angles) compared to ideal geometry, in degrees								
Vacancy ¹	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 pdb5y3q.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.