CheckMyMetal(CMM) report for PDB code: 6f9r

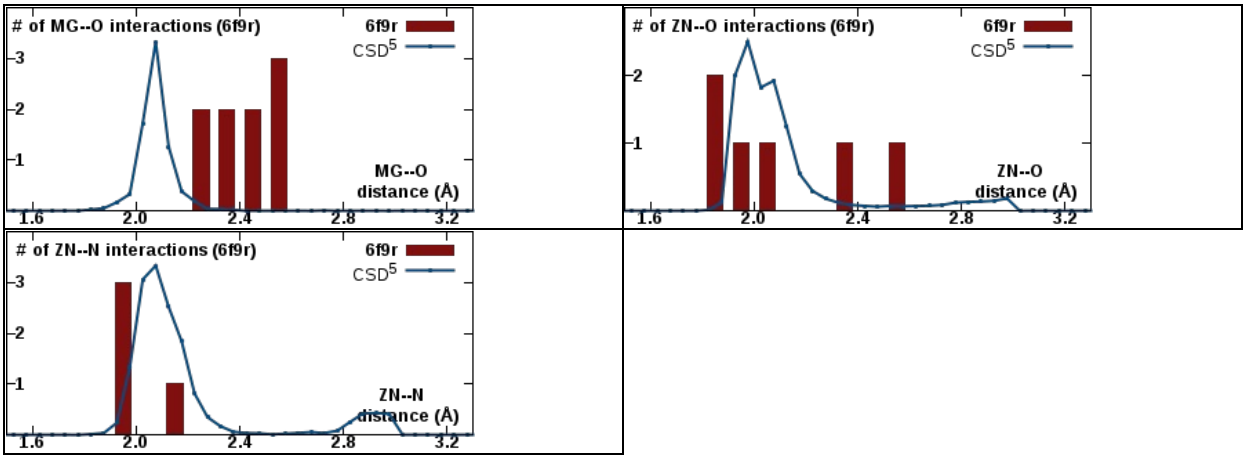
PDB title: Crystal structure of human angiotensin-1 converting enzyme n-domain in complex with sampatrilat-asp. (1.9Å)

ID	Res.	Metal	*Occupancy*	*B factor (env.)*[1]	*Ligands*	*Valence*[2]	*nVECSUM*[3]	*Geometry*[1,4]	*gRMSD*(°)[1]	*Vacancy*[1]	Bidentate	Alt. metal
A:709	ZN	Zn	1	21.6 (24.5)	O_3N_2	*2.4*	*0.14*	*Trigonal Bipyramidal*	*15°*	0	0	Mn, Fe, Zn
A:711	CL	Cl	1	26.7 (29.5)		N/A	N/A	**Free**	N/A	N/A	N/A	
A:714	MG	Mg	1	*26.1 (33.7)*	O_4	**0.6**	**0.4**	Octahedral	12.4°	**33%**	0	Na
B:710	ZN	Zn	1	28.2 (29.5)	O_3N_2	2.2	0.079	*Trigonal Bipyramidal*	*15.1°*	0	0	
B:712	CL	Cl	1	24.1 (22.8)		N/A	N/A	**Free**	N/A	N/A	N/A	
B:715	MG	Mg	1	*45.6 (38.9)*	O_4N_1	**0.8**	**0.3**	Octahedral	**22.4°**	*16%*	0	
B:716	MG	Mg	1	*44 (34.7)*	O_1	**0.08**	**1**	**Poorly Coordinated**	N/A	N/A	0	

Legend: Not applicable | **Outlier** | *Borderline* | Acceptable

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. *Valence* 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 pdb6f9r.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.