Finding high-quality metal ion-centric regions across the worldwide Protein Data Bank

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Abstract: As the number of macromolecular structures in the worldwide Protein Data Bank (wwPDB) continues to grow rapidly, more attention is being paid to the quality of its data, especially for use in aggregated structural and dynamics analyses. In this study, we systematically analyzed 3.5 Å regions around all metal ions across all PDB entries with supporting electron density maps available from the PDB in Europe. All resulting metal ion-centric regions were evaluated with respect to four quality-control criteria involving electron density resolution, atom occupancy, symmetry atom exclusion, and regional electron density discrepancy. The resulting list of metal binding sites passing all four criteria possess high regional structural quality and should be beneficial to a wide variety of downstream analyses. This study demonstrates an approach for the pan-PDB evaluation of metal binding site structural quality with respect to underlying x-ray crystallographic experimental data represented in available electron density maps of proteins. For non-crystallographers in particular, we hope to change the focus and discussion of structural quality from a global evaluation to a regional evaluation, since all structural entries in the wwPDB appear to have both regions of high and low structural quality.

Keywords: metalloprotein; electron density analysis; pdb-eda; metal binding site; regional protein structure analysis

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1. Introduction

Metal ions are important components in biological processes, especially at the biochemical and cellular levels. An estimated 30 to 40 percent of proteins across the combined proteome of the biosphere binds at least one metal ion [1,2]. Protein metal binding is part of many biochemical mechanisms including signal transduction, enzyme catalysis, and protein structural integrity [3-5]. The local protein structure environment around bound metal ions can provide clues to the biochemical and cellular function of the binding [6-8] and how sequence-based structural changes modulates metal binding [9,10]. However, the quality of 3D protein structural data around metal binding sites can vary dramatically from structure to structure, and especially from region to region [8,11]. Therefore, when analyzing metal binding site structure and dynamics, the quality of utilized worldwide Protein Data Bank (wwPDB) [12] entries should be evaluated, especially in the metal binding site region [2,8,13]. The potential impact of crystallization artifacts on ligand binding affinities has already been demonstrated [14]. Also, current methods and tools for this regional evaluation around metal ions, focused only on the PDB structural entry itself, have proven useful for weeding out some metal binding sites with poor regional structural quality [13]. However, comparison to the raw electron density itself represents a gold standard of evaluation against experimental data that can demonstrate the reliability and usability of a given metal binding site region [8,15]. These comparisons of metal binding site structure to the underlying electron density

data has been facilitated by structure factor deposition requirements of the wwPDB since 2008 and electron density maps made available previously by the Uppsala Electron Density Server [16] and now by the PDB in Europe (PDBe) [17]. But this electron density evaluation of regional structural quality has been a tedious process done by manual visual inspection, without objective metrics of quality. To alleviate these shortcomings in electron density evaluation, we have developed new analysis and evaluation methods in a Python package called pdb-eda [18] that facilitate the systematic quality control of protein structural regions of interest across large numbers of wwPDB entries and their corresponding electron density maps. In this study, we apply pdb-eda to a systematic electron density analysis of all metal binding sites containing a bound metal ion. This analysis provides an evaluation of the quantity of metal binding sites in the wwPDB based on metrics of regional structural quality with respect to the underlying electron density data used to derive the metal binding site structure. Our goal is to provide a set of metal binding sites that are of high regional quality for a wide variety of downstream structural, dynamic, and functional analyses.

2. Methods

Structural data from wwPDB listed on Jul 3, 2018 was used for the analysis. Their electron density data, if available, was acquired from the PDBe website. We used version 1.0 of the pdb-eda Python package [18] to analyze all downloaded PDB entries and matching electron density maps. Metal ions were detected across these PDB entries and filtered against four major quality control criteria:

1) electron density resolution less than or equal to 2.5 Å.

2) atom occupancy greater than or equal to 0.9.

3) no symmetry atoms within 3.5 Å.

4) sum of electrons of discrepancy within a 3.5 Å region surrounding the metal ion point position is less than a data-derived cutoff.

The resolution and occupancy information were retrieved directly from the PDB structure entry file in PDB Molecular Format (ent) format. We considered a resolution less than or equal to 2.5 Å and an occupancy greater than or equal to 0.9 as meeting an acceptable level of quality for most downstream structural and dynamic studies, since water and small ligands are typically visible below this resolution. Symmetry related atoms were calculated from the REMARK SMTRY records in the PDB structure data, as we took into account nearby asymmetric units. Atom-atom distance between a metal ion and all symmetry related atom were computed and metal ions were filtered out if any symmetry atom point positions were present within 3.5 Å of the metal ion point position. Electron density maps were analyzed using the self-developed Python package, pdb-eda. This package provides methods for converting the electron density discrepancies in Fo-Fc density maps into numbers of electrons of discrepancy, when a significant protein component exists in the entry. A sum of the absolute value of both positive and negative electron discrepancies was computed for all significant discrepancies within 3.5 Å of the metal. Significant discrepancies were decided by a 1.5 standard deviation cutoff based on each individual electron density map, which is the commonly accepted cutoff for visualizing significant electron density map discrepancies. After filtering by criteria 1 and 2, we derived the distribution of all metal ion electron discrepancies sums and filtered out outliers by a 2 standard deviation cutoff. With the resulting filtered distribution, we set a max electron discrepancy sum cutoff to 1 standard deviation of this distribution. The electron density overlay graphs were prepared using the LiteMol Viewer [19]. All results and code used to generate the results for this study are available on FigShare: https://doi.org/10.6084/m9.figshare.8044451.

3. Results

We started with a list of 141,616 usable PDB entries, and 53,146 of them contains at least one metal ion. It is about 38 percent, which agrees very well with other studies and predictions [1,2]. In this study, we considered four major criteria in filtering "high-quality" metal ions, usable for downstream structural and dynamic analyses: resolution, occupancy, presence of symmetry atoms,

and significant discrepancies in terms of numbers of electrons. Figure 1 shows both high- and low-quality examples based on these four criteria, as illustrated in an overlay of the electron density map over the structural model.

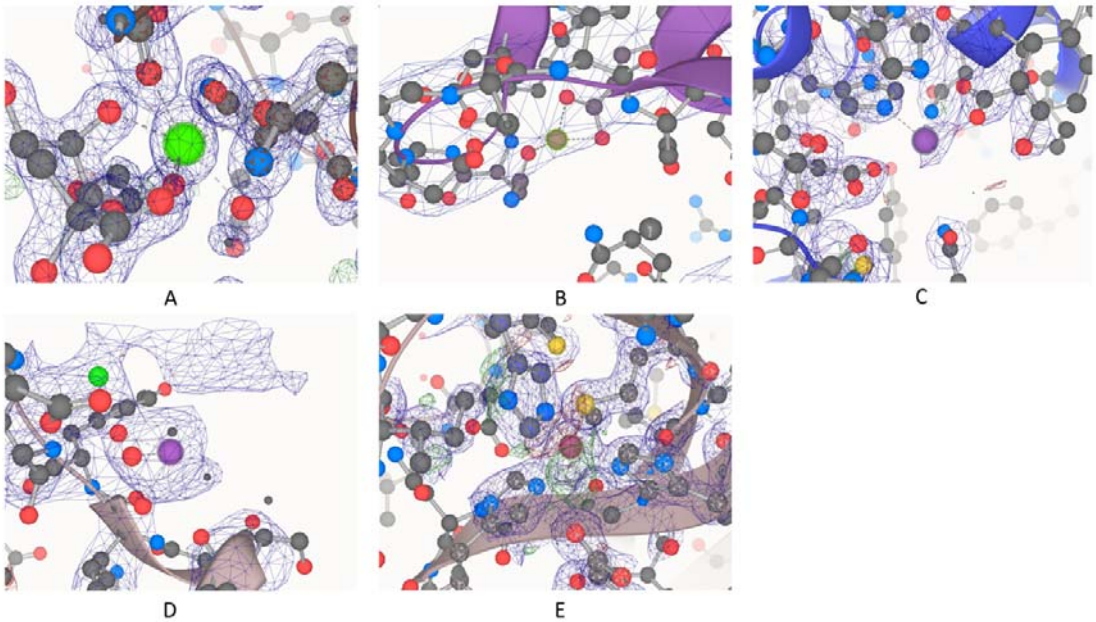

Figure 1. High and low quality examples for all four criteria: (A) PDB ID: 5FVN.F.405.CA, representative of high-quality by passing all four criteria; (B) PDB ID: 1YV0.C.163.MG, resolution: 7 Å; (C) PDB ID: 3CIA.B.701.ZN, occupancy: 0.7; (D) PDB ID: 5ER8.A.706.MN, symmetry atoms nearby; (E) PDB ID: 3LZQ.A.200.CU, high discrepancy between calculated and observed electron density maps.

Table 1 shows a tabulation of 56 different elemental types of metal ions observed in the wwPDB, with respect to four quality-control criteria. Zinc is present in the highest number of PDB entries, while magnesium has the highest number of metal sites. This is probably due to the presence of large numbers of magnesium ions in certain PDB entries like those of the ribosome [20]. Overall, 9 metals had over 1000 examples across the PDB that passed the four criteria. An additional 8 metals had over 100 examples that passed all four criteria. For the rest of this study, we will look at each of the four criteria in more detail, with respect to five of the most important and common metal ions in biochemistry: zinc, calcium, iron, manganese, and copper.

Table 1. Tabulation of different elemental types of metal ions observed in the wwPDB with respect to four quality-control criteria.

Metal	Number of PDB entries	Number of total metal ion sites	Number with < 2.5 Å resolution	Number with high occupancy	Number with no nearby symmetry atoms	Number with no significant discrepancy densities	Number that passes all criterion
Zn	13497	67405	56176	62550	62967	23883	13230
Mg	13225	85080	30537	81528	81463	48708	18305
Ca	10138	44538	36193	41929	41176	23836	15787
Fe	8054	41898	32283	39207	41499	20881	14427
Na	7516	23697	16645	22523	21072	18295	10700
Mn	3177	14347	9037	12089	13630	8755	4275
K	2390	8819	5671	7498	7678	5541	2973

Ni	1533	3578	2803	2752	2943	2093	986
Cu	1469	6918	5913	5548	6474	3676	2111
Co	1146	3601	2897	2920	3288	1687	976
Cd	926	6535	5351	4708	4863	2334	624
Hg	640	2302	1525	808	2223	528	11
U	507	6032	5522	4553	5196	2351	1693
Pt	242	869	564	212	802	249	4
Mo	209	785	685	505	692	323	147
Al	189	399	187	390	399	217	112
Be	187	510	273	461	504	318	175
Ba	166	900	399	558	733	186	6
Ru	162	341	288	163	318	113	8
Sr	151	3972	1394	3764	3869	2846	745
V	143	488	285	399	462	219	130
Cs	115	666	402	251	526	226	14
W	96	1743	396	1218	1639	280	15
Yb	91	247	189	136	127	60	6
Au	90	437	275	120	373	136	2
Li	73	124	110	116	109	96	72
Gd	65	444	408	268	409	134	22
Pb	62	229	113	87	187	63	5
Y	58	218	168	154	108	77	16
Tl	54	400	143	119	383	82	1
Ir	51	333	132	138	317	44	0
Rb	49	229	139	73	174	83	4
Sm	45	205	106	132	142	42	11
Ag	34	381	329	361	365	67	25
Pr	31	77	56	46	40	23	4
Eu	24	71	64	14	60	23	3
Pd	24	108	108	55	79	19	2
Os	23	101	34	77	97	20	3
Re	21	71	71	27	68	13	3
Rh	20	68	68	25	62	18	1
Tb	18	168	139	134	157	20	3
Ta	18	529	106	42	503	199	0
Lu	15	62	46	31	54	19	0
Ho	13	55	47	43	44	7	0
La	11	115	107	106	112	1	1
Cr	10	53	43	49	52	8	5
Ga	10	80	80	80	80	5	5
Sn	9	16	16	6	16	2	0
Sb	5	10	4	6	10	7	3
Ce	4	70	70	66	70	0	0
Er	3	18	0	17	0	1	0
Zr	3	31	28	30	0	0	0
In	2	3	1	3	0	1	0
Bi	2	2	2	0	2	0	0
Hf	2	44	44	43	0	10	9
Dy	1	26	26	0	0	18	0
Total	66819	330448	218698	299138	308616	168843	87660

3.1. Resolution

The electron density resolution represents an overall metric of structural quality for an x-ray crystallographic structure. Structural entries with a resolution below 2.5 Å are generally considered usable for many structural and dynamics analyses. Figure 2 illustrates the distribution of resolution for the top five most essential metals in biology. In general, the overall and individual metal ions

have similar distributions. The distribution for manganese has several spikes, which is mainly due to the over-representation of replicate values from structural entries with large numbers of manganese ions.

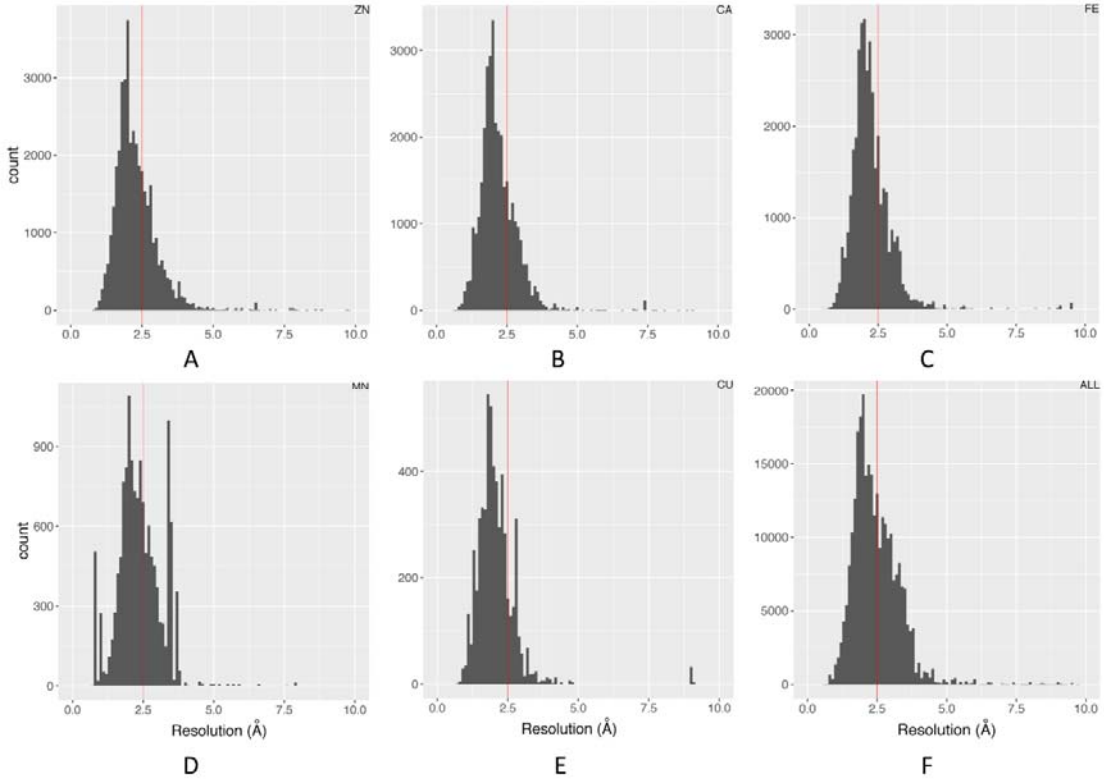

Figure 2. Distribution and 2.5 Å cutoff of structure resolutions: (A) Zn; (B) Ca; (C) Fe; (D) Mn; (E) Cu; (F) All metal ions.

3.2. Occupancy and Symmetry related atoms

The majority of metal ions have an occupancy of 1. However, there are two general cases where low occupancy occurs. In the first general case, when there is more than one conformation available during the structure determination, multiple conformations (typically two) are often kept in the data and are often marked as "ALT". Thus, different conformations will only possess the metal ions with partial occupancy. Typically for two conformations, the occupancy will be 0.5 for each conformation. For the second general case, only a fraction of the repeating unit cells in the protein crystal has the observed metal ion, and the occupancy will represent the percentage of the crystal structure with the metal ion bound. In either case, low occupancy sites can be considered low-quality for aggregated analyses, since only a fraction of the experimental data supports the given model of the metal ion position. A filter of 0.9 occupancy removes about 10% of all metal ions and is consistent for most of individual metal ions. Therefore, this criterion only removes a minority of metal ion sites.

Crystal contacts can pose as an artifact, affecting the binding of the metal ion, especially on the surface of a protein structure. It may represent a false binding that does not biologically exist, i.e. when the crystal packing environment is no longer available. Also, crystal contacts can affect protein-ligand binding [14]. Our study demonstrates that only about 7% of metal ion sites are filtered out by a 3.5 Å symmetry atom exclusion criterion.

3.3. Discrepancy between calculated and observed electron density maps

Figure 1 demonstrates why electron density maps can be extremely useful for validating high-quality regions within protein structures. As described in the methods, we used our pdb-eda Python package to compare every metal binding site to its Fo-Fc electron density map. Figure 3 shows the distributions of the sum of absolute electron disagreement within a 3.5 Å radius of each metal ion. Overall and individual metal ions demonstrate very similar distributions, justifying the calculation of a single data driven cutoff from the overall distribution. The final data-driven cutoff for the sum of absolute electron discrepancy is approximately 19.3 electrons and is based on one standard deviation of the Figure 3F distribution with outliers removed. This is a purposely conservation quality control criterion, representing roughly two water molecules worth of electron discrepancy. However, only 24.8% of metal ion sites are filtered out by this criterion.

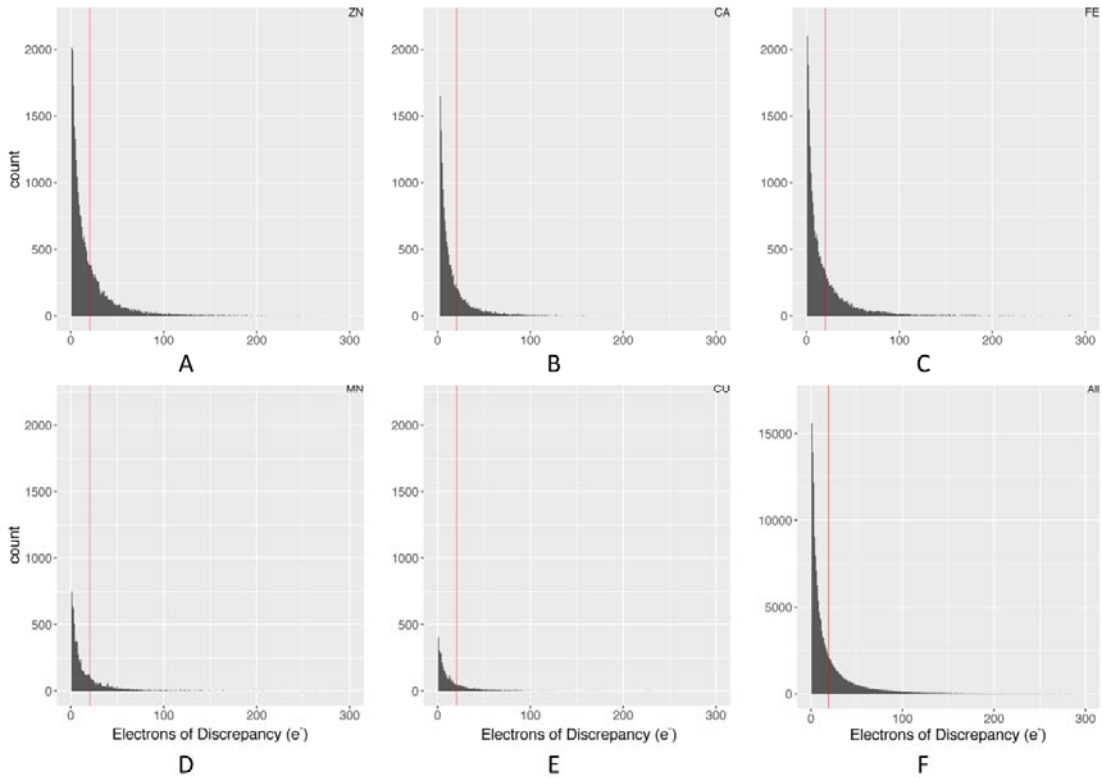

Figure 3. Distribution of electron discrepancy within 3.5 Å of the metal ion: (A) Zn; (B) Ca; (C) Fe; (D) Mn; (E) Cu; (F) All metal ions. The red line represents a 1 standard deviation cutoff calculated from the distribution in graph F with outliers removed.

4. Discussion

As illustrated by previous studies, regional structural quality affects the usability of bound ligand structure, including bound metal ions, for accurately interpreting structural, dynamic, and chemical properties of ligand binding sites [14,21,22]. Therefore, steps should be taken to ensure the quality of metal binding sites for various downstream structural and dynamics analyses. As the number of structures available in PDB continues to grow dramatically every year, more attention is being paid to ensuring that only high-quality datasets are used in these studies. Toward this goal, we have developed new methods in the open-source pdb-eda Python package that enable the evaluation of regional structural quality with respect to underlying experimental data.

In this study, we demonstrate the use of electron density maps for a systematic evaluation of regional structural quality around all metal binding sites in the PDB with matching electron density maps provided by the PDBe. This is one of 4 criteria used for evaluating the structural quality of metal binding sites for the purpose of generating large high-quality datasets for downstream analyses. The other criteria include electron density resolution, exclusion of nearby symmetry atoms,

and the occupancy of the metal ion. For commonly-bound metal ions, additional criteria can be used for quality control [13], including the evaluation of bond lengths between ligating atoms (using the coordination chemistry definition of ligand) and the metal ion and coordination shell considerations [8,23,24]. However, several of these evaluations require the accurate identification of ligating atoms and is complicated by the wide variation in coordination geometries. Moreover, these additional criteria cannot be practically applied to all 56 elemental types of metals analyzed in this study, given the current examples available in the PDB. Therefore, we limited to four criteria that could be straight-forwardly applied to all elemental types of metal ions currently present in the PDB.

A full list of metal binding sites that pass all four criteria utilized in this study can be found in Table S1 (in FigShare repository), along with the values used for criterion evaluation. In addition, all code used to generate this table is available in a FigShare repository along with all metals binding sites evaluated in this study. Therefore, metal binding sites can be re-evaluated against modified criteria that match the quality-control requirements of a given downstream analysis. Also with this code, future versions of the PDB can be analyzed in a similar manner to regenerate an updated list of metal binding sites.

In conclusion, we have demonstrated an approach for the pan-PDB evaluation of metal binding site structural quality with respect to underlying x-ray crystallographic experimental data represented in available electron density maps of proteins. Especially for non-crystallographers, we hope to change the focus and discussion of structural quality from a global evaluation to a regional evaluation, since all structural entries in the wwPDB appear to have both regions of high and low structural quality.

Supplementary Materials: All results and code used to generate the results for this study are available on FigShare: https://doi.org/10.6084/m9.figshare.8044451.

Author Contributions: S.Y. and H.M. conceptualized the study; S.Y. conducted the data analysis and visualization; S.Y. and H.M. validated the results, wrote the original draft, and edited and reviewed the manuscript.

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Conflicts of Interest: The authors declare no conflict of interest.

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