



Full wwPDB X-ray Structure Validation Report ⓘ

May 20, 2024 – 06:25 PM EDT

PDB ID : 8UW6
Title : Acetylnithine deacetylase from Escherichia coli, di-zinc form.
Authors : Osipiuk, J.; Endres, M.; Kelley, E.; Becker, D.P.; Joachimiak, A.; Center for Structural Biology of Infectious Diseases (CSBID)
Deposited on : 2023-11-06
Resolution : 1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

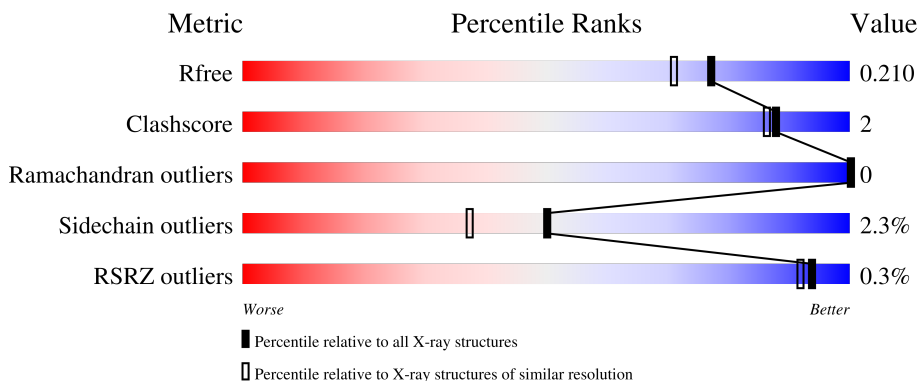
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

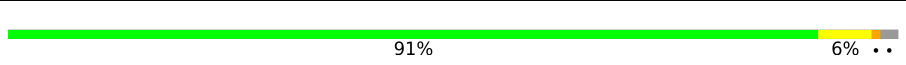
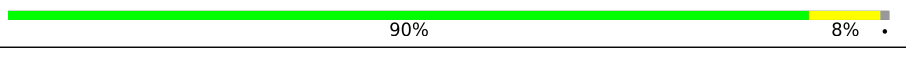
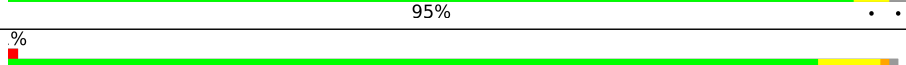

The reported resolution of this entry is 1.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	386	 91% 6% ..
1	B	386	 90% 8% .
1	C	386	 95% . .
1	D	386	 91% 7% ..

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13422 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Acetylornithine deacetylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	380	3033	1933	520	567	13	0	12	0
1	B	381	3083	1967	533	570	13	0	17	0
1	C	380	2985	1898	517	557	13	0	4	0
1	D	381	3020	1922	521	564	13	0	9	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	cloning artifact	UNP Q8X742
A	-1	ASN	-	cloning artifact	UNP Q8X742
A	0	ALA	-	cloning artifact	UNP Q8X742
B	-2	SER	-	cloning artifact	UNP Q8X742
B	-1	ASN	-	cloning artifact	UNP Q8X742
B	0	ALA	-	cloning artifact	UNP Q8X742
C	-2	SER	-	cloning artifact	UNP Q8X742
C	-1	ASN	-	cloning artifact	UNP Q8X742
C	0	ALA	-	cloning artifact	UNP Q8X742
D	-2	SER	-	cloning artifact	UNP Q8X742
D	-1	ASN	-	cloning artifact	UNP Q8X742
D	0	ALA	-	cloning artifact	UNP Q8X742

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

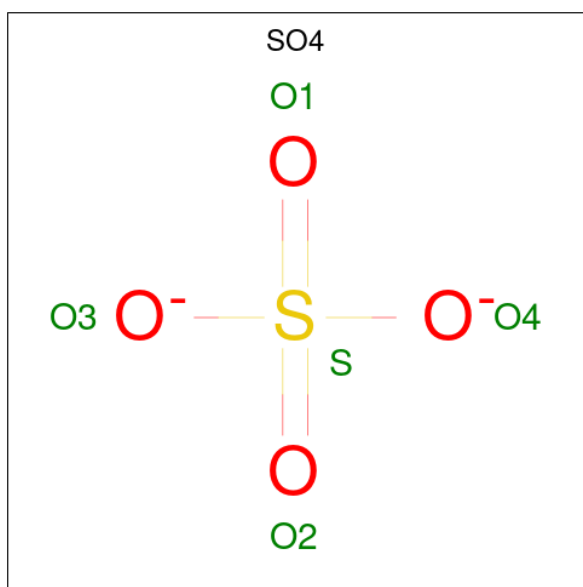
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Zn	0	0
			3	3		
2	C	2	Total	Zn	0	0
			2	2		
2	D	3	Total	Zn	0	0
			3	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		
4	B	1	Total	C	N	O	0	0
			8	4	1	3		
4	B	1	Total	C	N	O	0	0
			8	4	1	3		
4	C	1	Total	C	N	O	0	0
			8	4	1	3		
4	D	1	Total	C	N	O	0	0
			8	4	1	3		
4	D	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	C	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

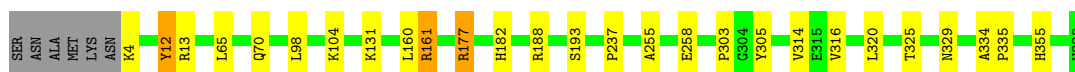
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	374	Total O 374 374	0	0
6	B	269	Total O 269 269	0	3
6	C	348	Total O 348 348	0	0
6	D	219	Total O 219 219	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

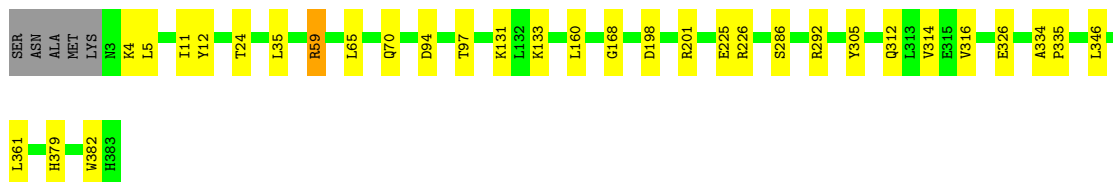
- Molecule 1: Acetylnithine deacetylase

Chain A:  91% 6% ..



- Molecule 1: Acetylnithine deacetylase

Chain B:  90% 8% .

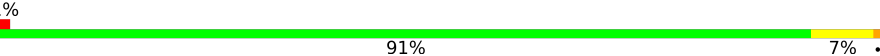


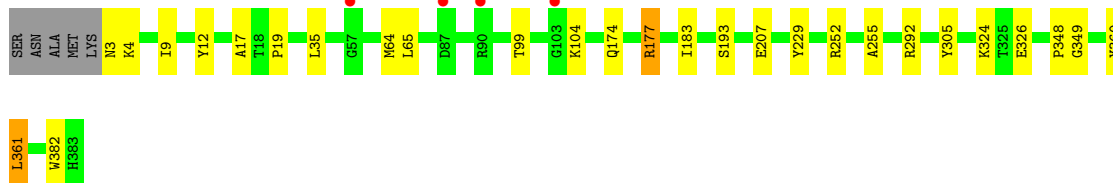
- Molecule 1: Acetylnithine deacetylase

Chain C:  95% ..



- Molecule 1: Acetylnithine deacetylase

Chain D:  91% 7% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.40Å 126.32Å 123.41Å 90.00° 90.88° 90.00°	Depositor
Resolution (Å)	48.54 – 1.80 48.49 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.5 (48.54-1.80) 97.5 (48.49-1.80)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.163 , 0.203 0.173 , 0.210	Depositor DCC
R_{free} test set	7260 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for -h,-l,-k 0.000 for -h,l,k 0.036 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13422	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, SO4, EDO, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.51	0/3147	0.78	4/4288 (0.1%)
1	B	0.45	0/3216	0.75	1/4380 (0.0%)
1	C	0.49	0/3075	0.76	0/4193
1	D	0.45	0/3125	0.75	2/4262 (0.0%)
All	All	0.48	0/12563	0.76	7/17123 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	1
1	D	0	1
All	All	0	6

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	177	ARG	NE-CZ-NH2	8.39	124.50	120.30
1	A	177	ARG	NE-CZ-NH1	-7.32	116.64	120.30
1	B	292	ARG	NE-CZ-NH2	-6.24	117.18	120.30
1	A	161	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	D	292	ARG	NE-CZ-NH2	-5.59	117.51	120.30
1	A	12	TYR	CB-CG-CD1	5.09	124.05	121.00
1	D	177	ARG	NE-CZ-NH2	-5.09	117.76	120.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	161	ARG	Sidechain
1	A	177	ARG	Sidechain
1	B	59[A]	ARG	Sidechain
1	B	59[B]	ARG	Sidechain
1	C	177	ARG	Sidechain
1	D	177	ARG	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3033	0	3006	15	0
1	B	3083	0	3077	14	0
1	C	2985	0	2940	8	0
1	D	3020	0	2986	11	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0
2	D	3	0	0	0	0
3	A	15	0	0	1	0
3	C	10	0	0	0	0
4	A	8	0	10	0	0
4	B	16	0	22	0	0
4	C	8	0	10	0	0
4	D	16	0	22	0	0
5	A	4	0	6	1	0
5	C	4	0	6	0	0
6	A	374	0	0	6	0
6	B	269	0	0	3	0
6	C	348	0	0	5	0
6	D	219	0	0	2	0
All	All	13422	0	12085	49	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (49) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:GLN:NE2	6:A:605:HOH:O	2.31	0.62
1:A:329:ASN:HB3	6:A:853:HOH:O	2.06	0.56
1:D:348:PRO:HB2	1:D:361:LEU:HD11	1.89	0.53
1:D:349:GLY:CA	1:D:361:LEU:HD12	2.39	0.52
1:D:349:GLY:HA3	1:D:361:LEU:HD12	1.92	0.52
1:A:70:GLN:HG2	6:A:639:HOH:O	2.10	0.50
1:D:104:LYS:HD3	1:D:360:TYR:CE1	2.46	0.50
1:B:65[A]:LEU:HD21	1:B:160:LEU:HD11	1.94	0.50
1:A:104:LYS:HD2	6:A:610:HOH:O	2.11	0.50
1:A:13[B]:ARG:HG3	1:A:98:LEU:HD23	1.95	0.49
1:C:206:ILE:HG13	1:C:254:CYS:SG	2.53	0.49
1:B:133[B]:LYS:HE2	1:B:382:TRP:O	2.14	0.48
3:A:507:SO4:O4	6:A:601:HOH:O	2.18	0.48
1:D:193:SER:HB2	1:D:255:ALA:HB2	1.96	0.47
1:C:283:ALA:HB3	1:C:284:PRO:HD3	1.97	0.47
1:B:24:THR:O	1:B:59[A]:ARG:NH2	2.41	0.47
1:B:133[B]:LYS:CE	1:B:382:TRP:O	2.62	0.47
1:A:320[A]:LEU:HG	6:A:740:HOH:O	2.14	0.46
1:C:93:ARG:HA	6:C:661:HOH:O	2.15	0.46
1:C:334:ALA:N	1:C:335:PRO:CD	2.79	0.46
1:D:17:ALA:O	1:D:19:PRO:HD3	2.16	0.45
1:D:324:LYS:HE2	1:D:326:GLU:OE2	2.16	0.45
1:D:252:ARG:HD3	6:D:781:HOH:O	2.16	0.45
1:B:326[B]:GLU:OE1	6:B:601:HOH:O	2.21	0.44
1:A:193:SER:HB2	1:A:255:ALA:HB2	1.99	0.44
1:A:188:ARG:HE	1:A:258[B]:GLU:CD	2.21	0.44
1:C:158:THR:O	6:C:601:HOH:O	2.21	0.44
1:B:334:ALA:N	1:B:335:PRO:CD	2.81	0.43
1:B:168:GLY:HA2	1:B:346:LEU:O	2.18	0.43
1:B:225[A]:GLU:HG3	1:B:226:ARG:HG3	1.99	0.43
1:B:131:LYS:HE3	6:B:837:HOH:O	2.19	0.43
1:A:314:VAL:HG13	1:A:325:THR:CG2	2.49	0.43
1:A:355:HIS:CD2	1:A:355:HIS:N	2.88	0.42
1:C:70:GLN:HA	6:C:678:HOH:O	2.19	0.42
1:A:65:LEU:HD21	1:A:160:LEU:HD11	2.01	0.42
1:B:5:LEU:HG	1:B:11:ILE:HD11	2.00	0.42
1:A:182:HIS:ND1	5:A:506:EDO:H21	2.34	0.42
1:B:314:VAL:HG21	6:B:746:HOH:O	2.20	0.42
1:D:9:ILE:HD12	1:D:9:ILE:HA	1.93	0.42
1:D:64:MET:HG2	1:D:65:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:207:GLU:OE1	6:D:601:HOH:O	2.22	0.41
1:B:94:ASP:OD2	1:B:97:THR:OG1	2.38	0.41
1:B:198:ASP:OD2	1:B:201[B]:ARG:HD2	2.21	0.41
1:A:316:VAL:O	1:A:320[A]:LEU:HG	2.20	0.40
1:A:334:ALA:N	1:A:335:PRO:CD	2.84	0.40
1:C:93:ARG:CA	6:C:661:HOH:O	2.68	0.40
1:C:93:ARG:HB3	6:C:661:HOH:O	2.20	0.40
1:B:316:VAL:HG21	1:B:379[B]:HIS:CD2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	390/386 (101%)	385 (99%)	5 (1%)	0	100	100
1	B	397/386 (103%)	392 (99%)	5 (1%)	0	100	100
1	C	382/386 (99%)	375 (98%)	7 (2%)	0	100	100
1	D	388/386 (100%)	379 (98%)	9 (2%)	0	100	100
All	All	1557/1544 (101%)	1531 (98%)	26 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	331/324 (102%)	326 (98%)	5 (2%)	65	56
1	B	338/324 (104%)	329 (97%)	9 (3%)	44	31
1	C	323/324 (100%)	317 (98%)	6 (2%)	57	46
1	D	329/324 (102%)	317 (96%)	12 (4%)	35	20
All	All	1321/1296 (102%)	1289 (98%)	32 (2%)	50	36

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	12	TYR
1	A	237	PRO
1	A	303	PRO
1	A	305	TYR
1	B	4	LYS
1	B	12	TYR
1	B	35	LEU
1	B	70	GLN
1	B	286	SER
1	B	305	TYR
1	B	312[A]	GLN
1	B	312[B]	GLN
1	B	361	LEU
1	C	12	TYR
1	C	201	ARG
1	C	256	TRP
1	C	286[A]	SER
1	C	286[B]	SER
1	C	305	TYR
1	D	3	ASN
1	D	4	LYS
1	D	12	TYR
1	D	35	LEU
1	D	99	THR
1	D	174[A]	GLN
1	D	174[B]	GLN
1	D	183	ILE
1	D	229	TYR
1	D	305	TYR
1	D	361	LEU
1	D	382	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	245	HIS
1	B	70	GLN
1	B	245	HIS
1	B	272	ASN
1	C	192	GLN
1	D	190	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 10 are monoatomic - leaving 13 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	EDO	C	505	-	3,3,3	0.22	0	2,2,2	0.28	0
4	TRS	B	505	-	7,7,7	0.13	0	9,9,9	0.39	0
3	SO4	C	503	-	4,4,4	0.40	0	6,6,6	0.21	0
3	SO4	C	506	-	4,4,4	0.40	0	6,6,6	0.17	0
3	SO4	A	504	-	4,4,4	0.39	0	6,6,6	0.08	0
3	SO4	A	503	-	4,4,4	0.47	0	6,6,6	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	TRS	A	505	2	7,7,7	0.25	0	9,9,9	0.27	0
4	TRS	C	504	2	7,7,7	0.35	0	9,9,9	0.33	0
4	TRS	D	504	2	7,7,7	0.20	0	9,9,9	0.40	0
4	TRS	B	504	2	7,7,7	0.20	0	9,9,9	0.25	0
5	EDO	A	506	-	3,3,3	0.12	0	2,2,2	0.49	0
3	SO4	A	507	-	4,4,4	0.40	0	6,6,6	0.12	0
4	TRS	D	505	-	7,7,7	0.10	0	9,9,9	0.29	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	C	505	-	-	0/1/1/1	-
4	TRS	B	505	-	-	6/9/9/9	-
4	TRS	C	504	2	-	0/9/9/9	-
4	TRS	A	505	2	-	0/9/9/9	-
4	TRS	B	504	2	-	0/9/9/9	-
4	TRS	D	504	2	-	2/9/9/9	-
5	EDO	A	506	-	-	1/1/1/1	-
4	TRS	D	505	-	-	7/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	506	EDO	O1-C1-C2-O2
4	B	505	TRS	N-C-C1-O1
4	B	505	TRS	N-C-C3-O3
4	D	504	TRS	N-C-C3-O3
4	D	505	TRS	C2-C-C1-O1
4	D	505	TRS	N-C-C1-O1
4	D	505	TRS	C1-C-C3-O3
4	D	505	TRS	N-C-C3-O3
4	B	505	TRS	C2-C-C1-O1
4	B	505	TRS	C3-C-C1-O1
4	B	505	TRS	C1-C-C3-O3

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Mol	Chain	Res	Type	Atoms
4	B	505	TRS	C2-C-C3-O3
4	D	505	TRS	C3-C-C1-O1
4	D	505	TRS	C3-C-C2-O2
4	D	505	TRS	C2-C-C3-O3
4	D	504	TRS	C1-C-C3-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	506	EDO	1	0
3	A	507	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	380/386 (98%)	-0.39	0 100 100	11, 20, 39, 54	0
1	B	381/386 (98%)	-0.46	0 100 100	16, 24, 41, 63	0
1	C	380/386 (98%)	-0.36	1 (0%) 94 92	12, 22, 42, 64	0
1	D	381/386 (98%)	-0.24	4 (1%) 82 80	17, 30, 57, 78	0
All	All	1522/1544 (98%)	-0.36	5 (0%) 94 92	11, 24, 47, 78	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	103	GLY	3.4
1	D	57	GLY	2.5
1	D	90	ARG	2.2
1	C	126	ASP	2.1
1	D	87	ASP	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

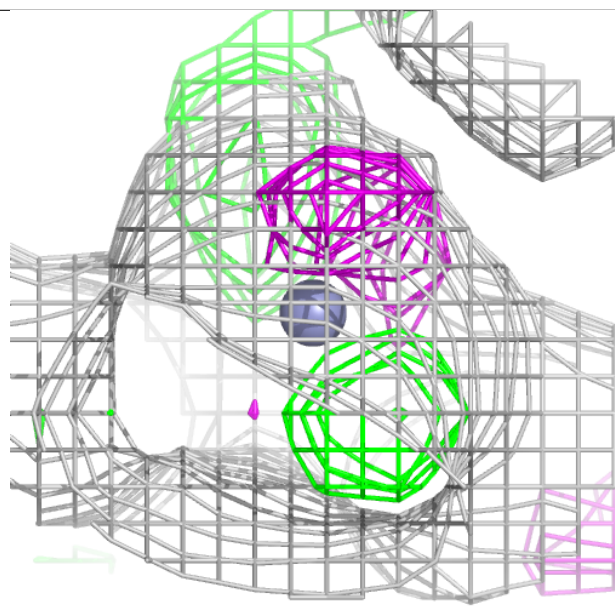
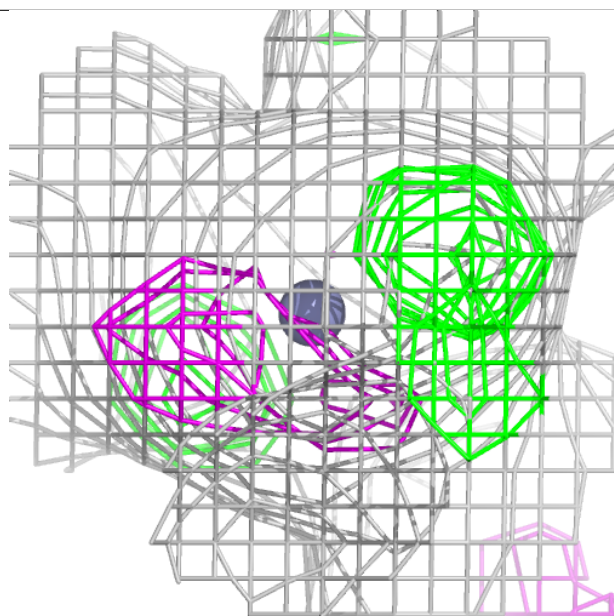
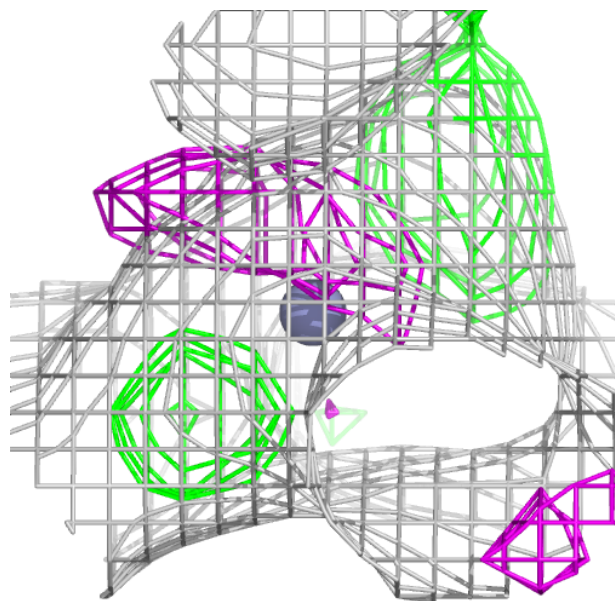
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	A	506	4/4	0.86	0.13	44,44,48,53	0
5	EDO	C	505	4/4	0.86	0.11	37,42,44,51	0
4	TRS	D	505	8/8	0.88	0.16	23,26,29,29	8
2	ZN	D	503	1/1	0.90	0.06	43,43,43,43	0
4	TRS	B	505	8/8	0.91	0.11	25,32,35,35	0
4	TRS	B	504	8/8	0.93	0.11	17,24,25,27	8
4	TRS	A	505	8/8	0.93	0.12	12,16,18,18	8
4	TRS	C	504	8/8	0.93	0.13	12,19,22,24	0
3	SO4	C	503	5/5	0.95	0.09	35,37,38,38	5
4	TRS	D	504	8/8	0.97	0.10	26,31,32,36	0
3	SO4	A	504	5/5	0.97	0.17	44,46,49,50	5
3	SO4	C	506	5/5	0.97	0.11	40,43,44,49	5
3	SO4	A	507	5/5	0.97	0.11	37,46,47,49	0
3	SO4	A	503	5/5	0.98	0.07	25,28,30,31	5
2	ZN	D	501	1/1	0.99	0.06	25,25,25,25	0
2	ZN	D	502	1/1	0.99	0.06	26,26,26,26	1
2	ZN	B	501	1/1	1.00	0.08	18,18,18,18	0
2	ZN	B	502	1/1	1.00	0.05	22,22,22,22	1
2	ZN	B	503	1/1	1.00	0.06	21,21,21,21	0
2	ZN	C	501	1/1	1.00	0.09	14,14,14,14	0
2	ZN	C	502	1/1	1.00	0.06	19,19,19,19	1
2	ZN	A	501	1/1	1.00	0.09	13,13,13,13	0
2	ZN	A	502	1/1	1.00	0.07	17,17,17,17	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

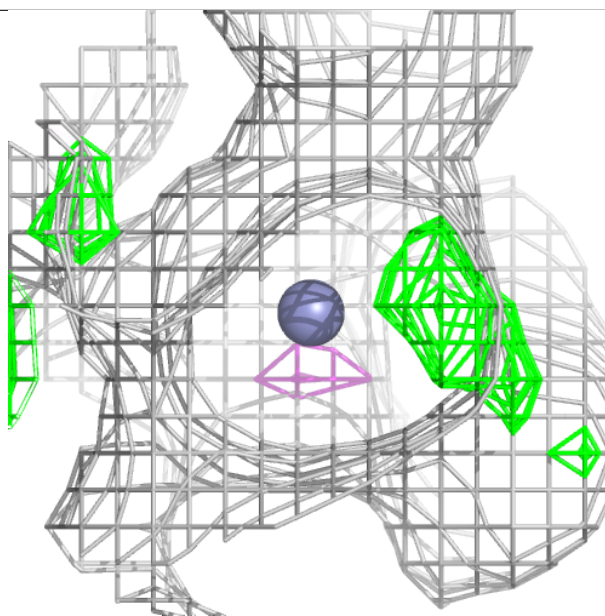
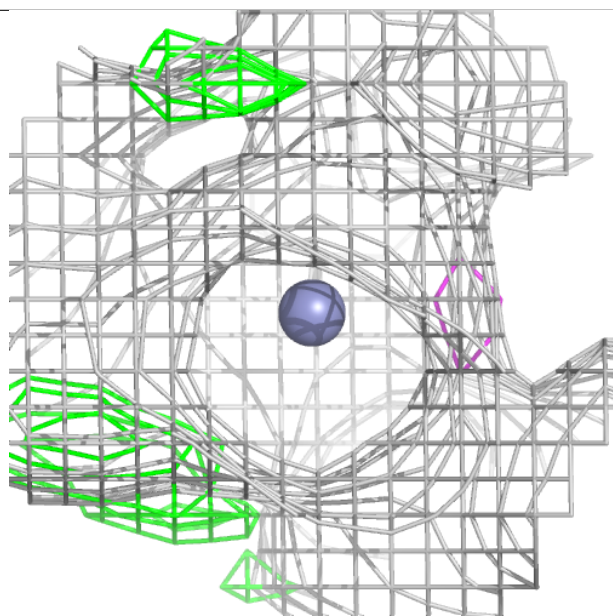
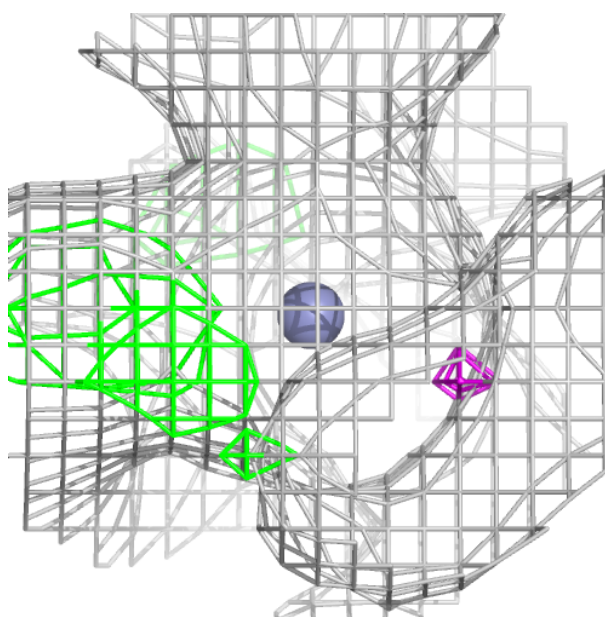
Electron density around ZN D 503:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



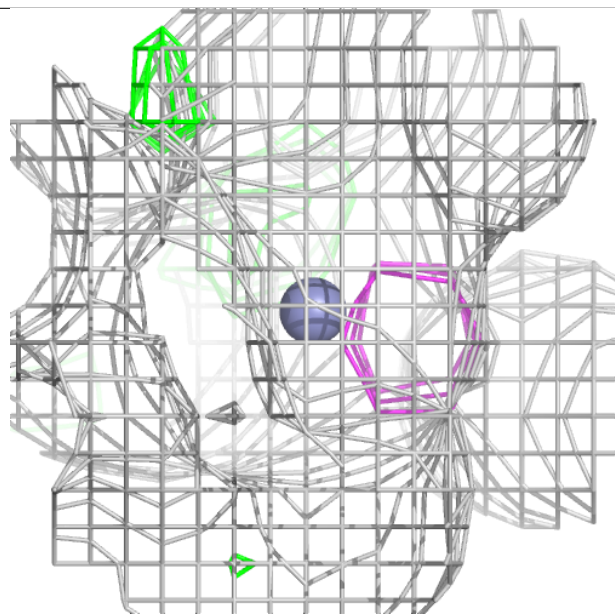
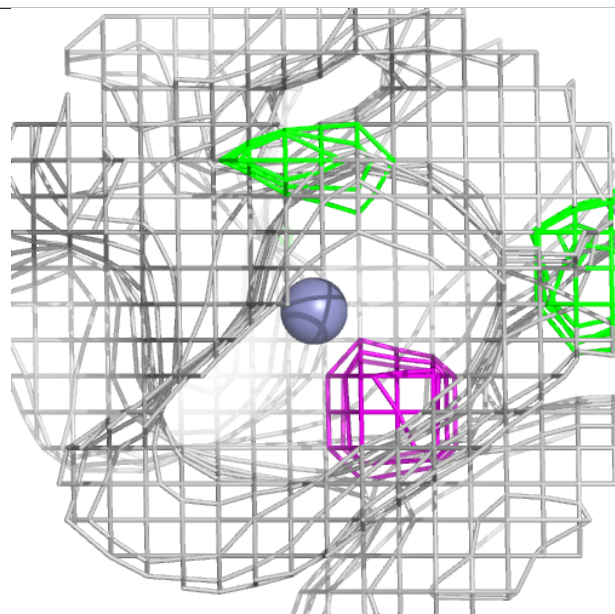
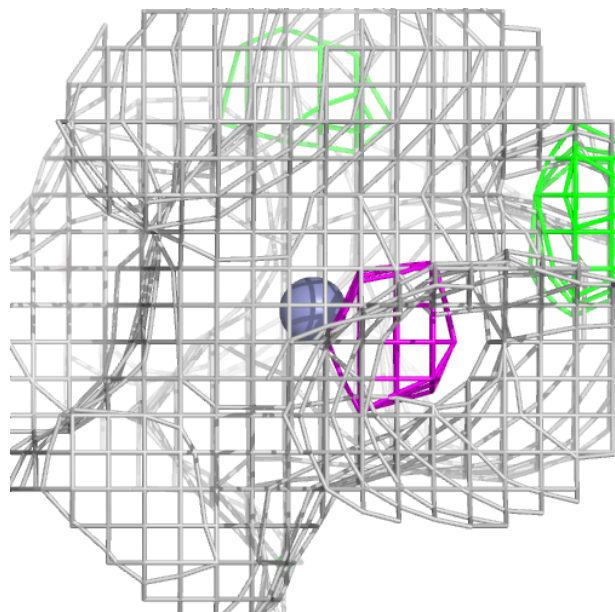
Electron density around ZN D 501:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



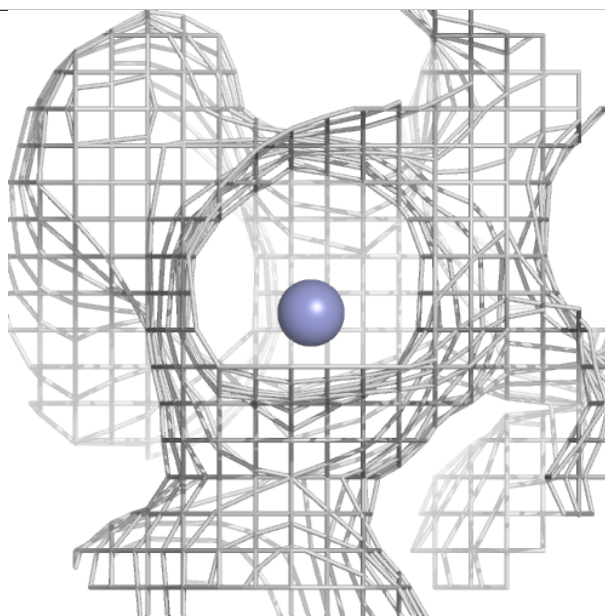
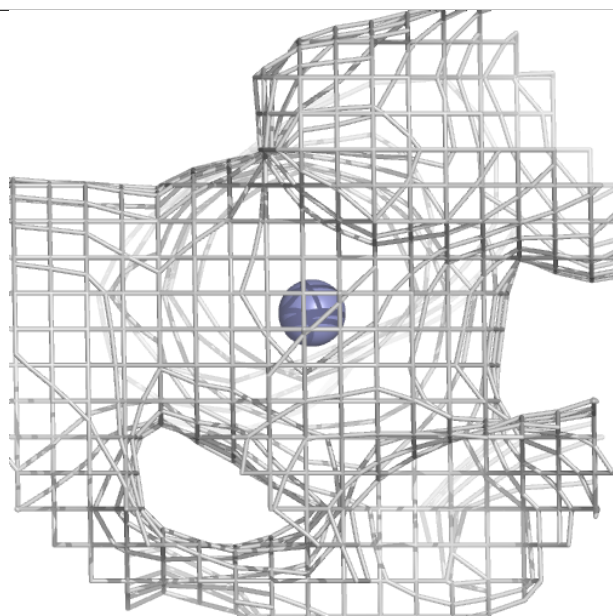
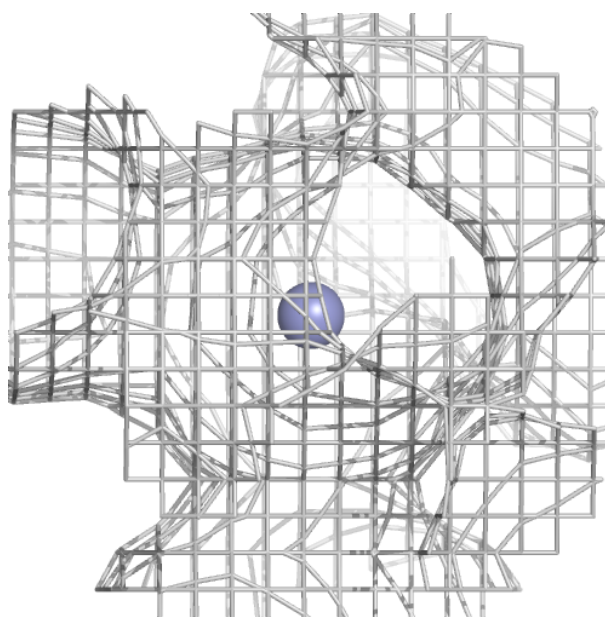
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and green (positive)



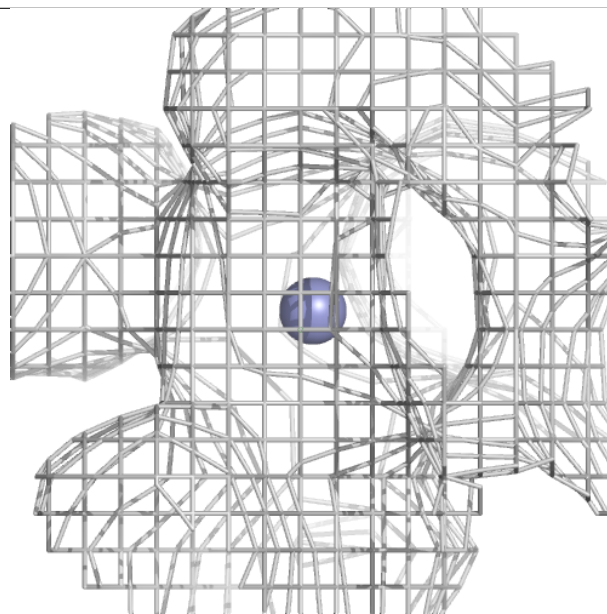
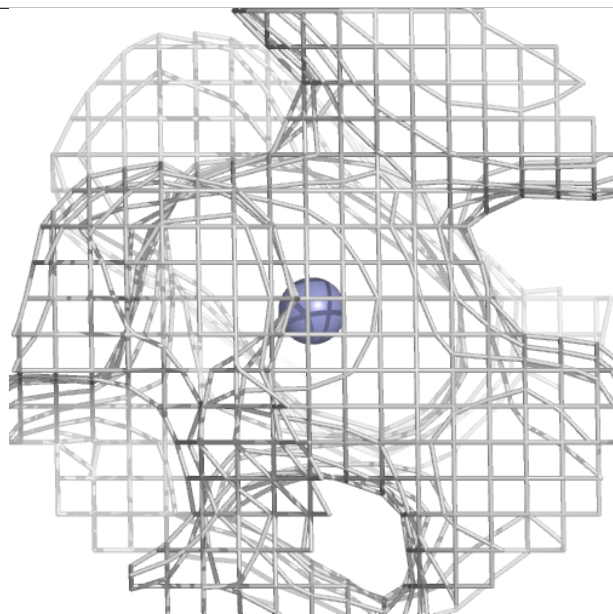
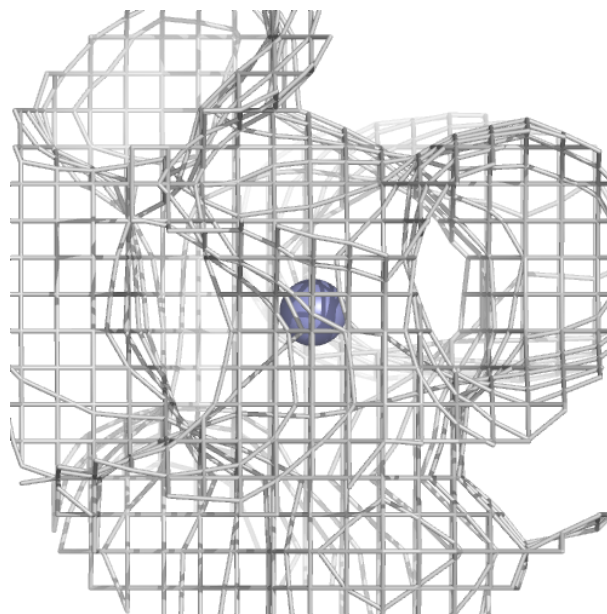
Electron density around ZN B 501:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



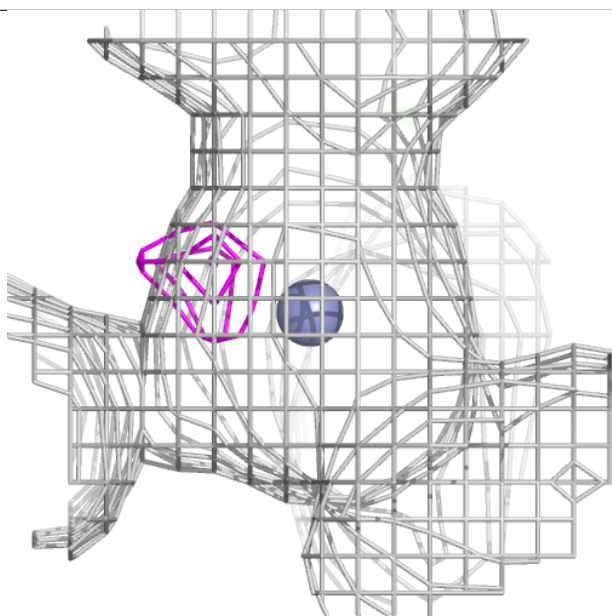
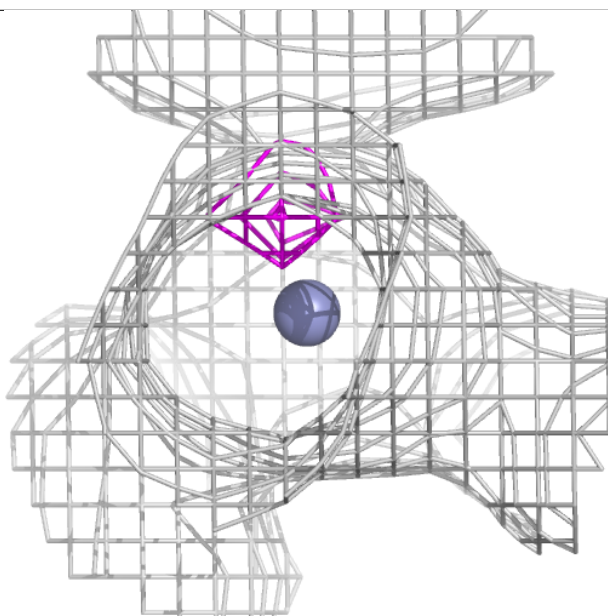
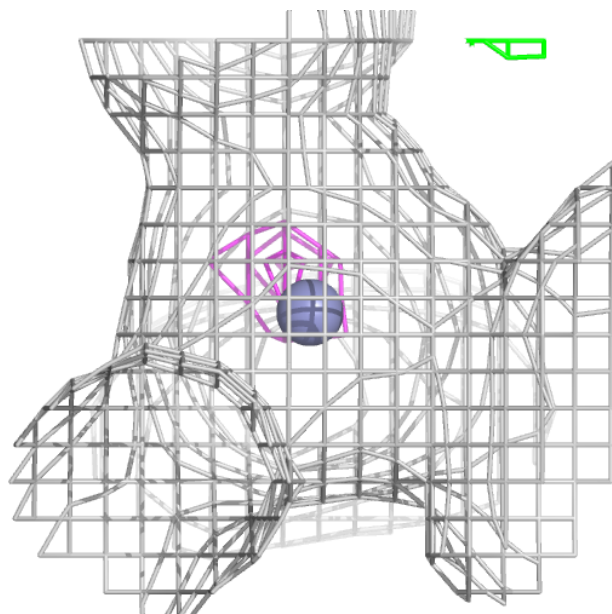
Electron density around ZN B 502:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



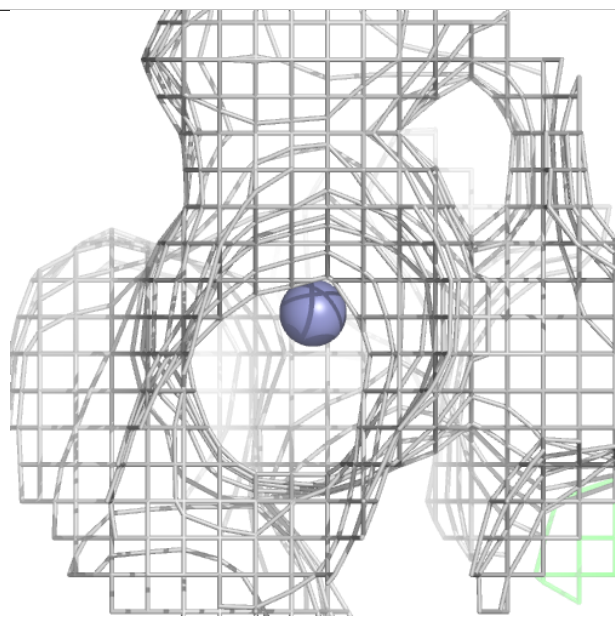
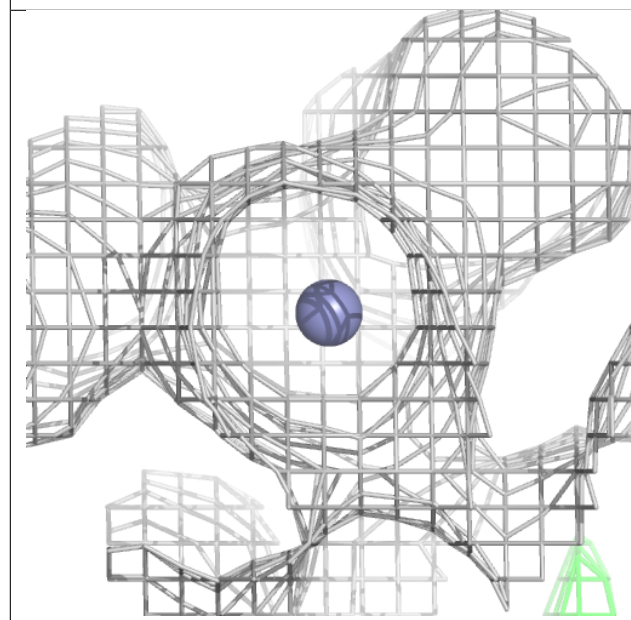
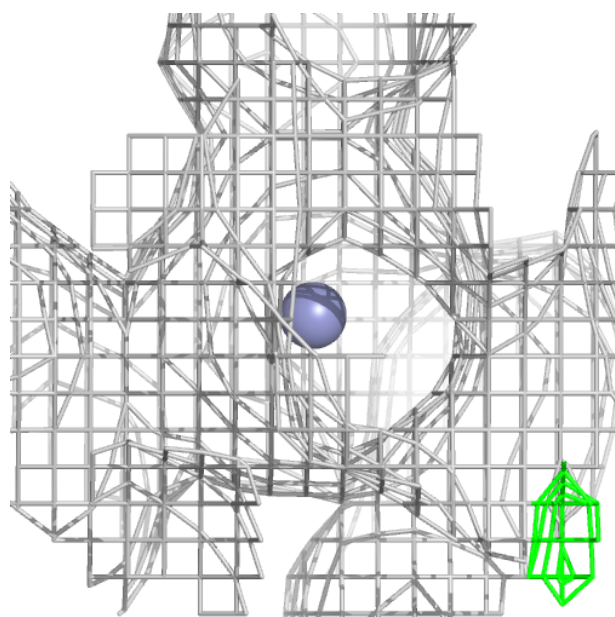
Electron density around ZN B 503:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



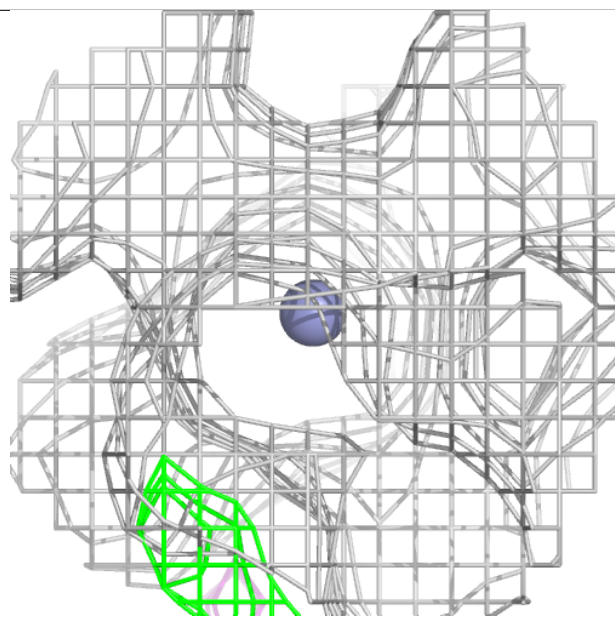
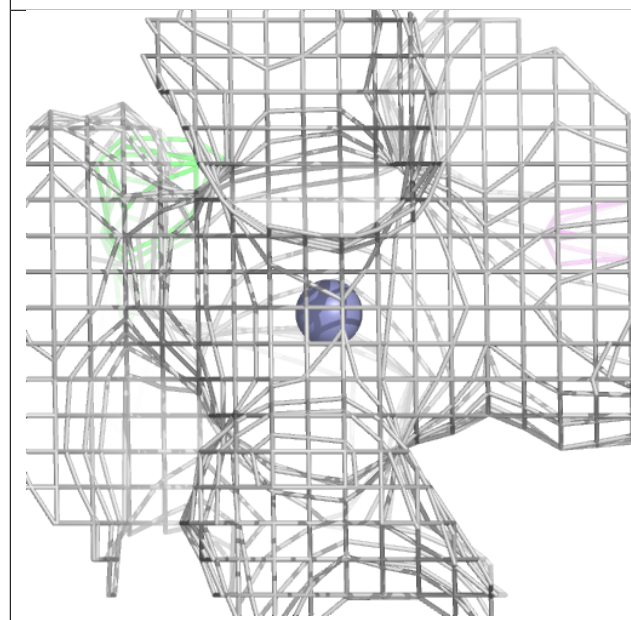
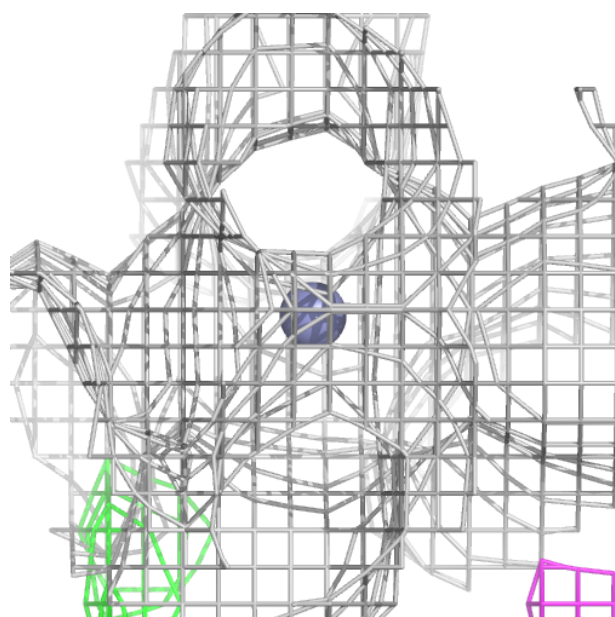
Electron density around ZN C 501:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



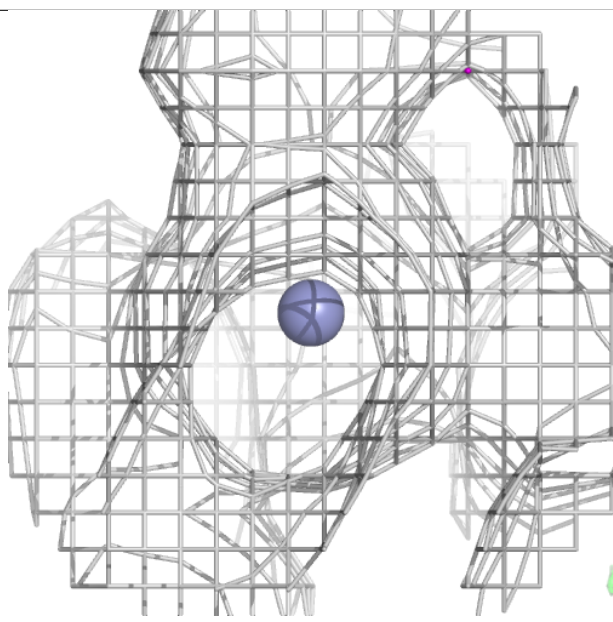
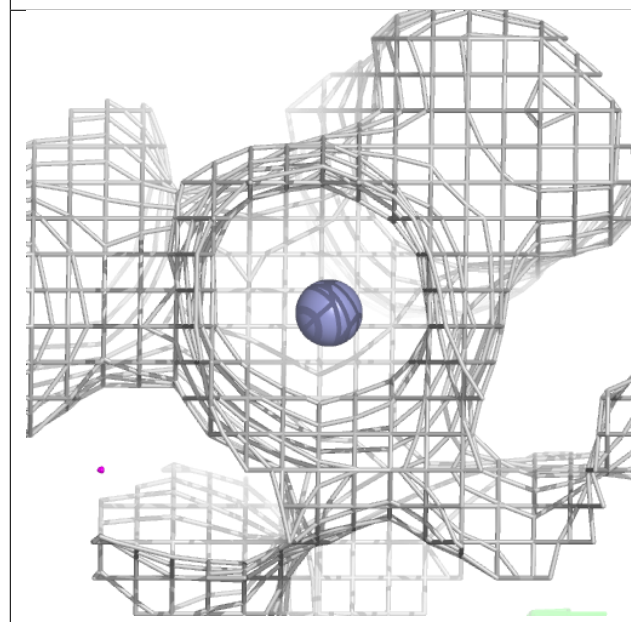
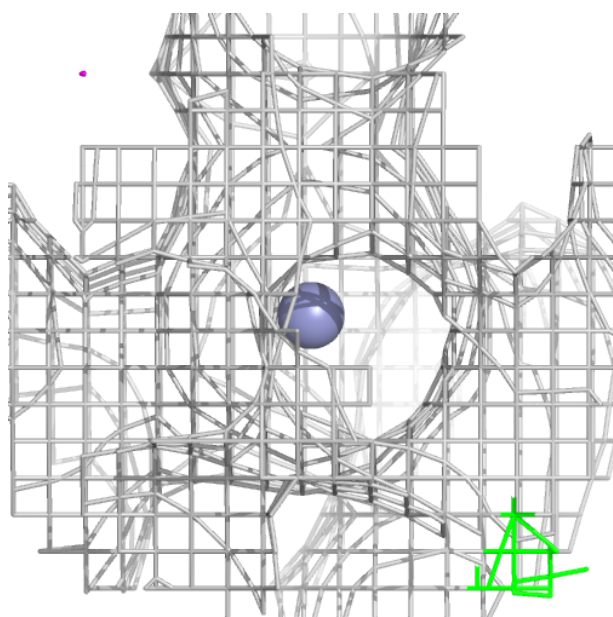
Electron density around ZN C 502:

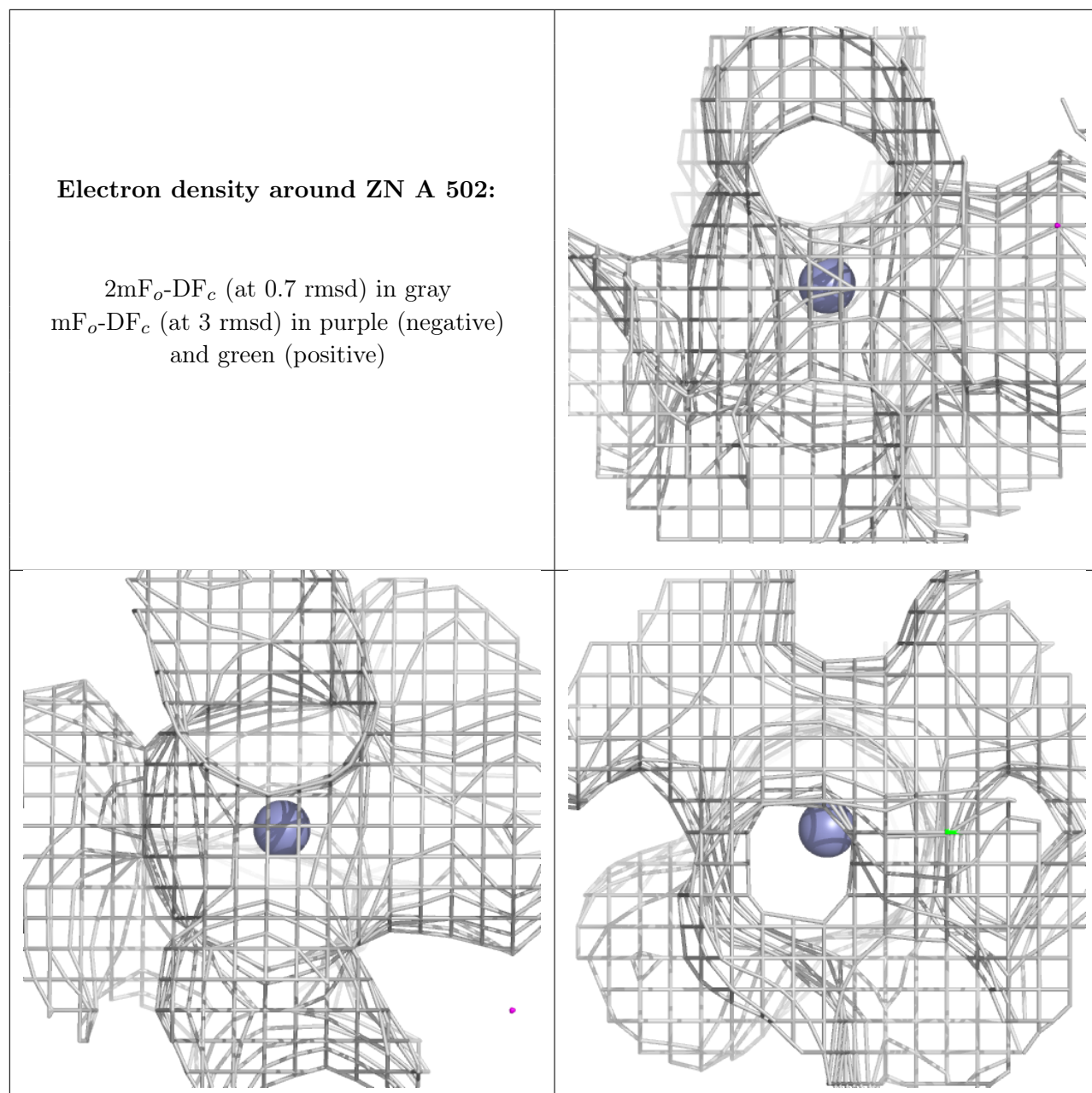
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN A 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.