



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 8, 2024 – 12:13 PM JST

PDB ID : 8YT2  
Title : Crystal structure of ACMSD mutant W194A  
Authors : Yang, Y.; Liu, A.  
Deposited on : 2024-03-24  
Resolution : 2.02 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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>.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

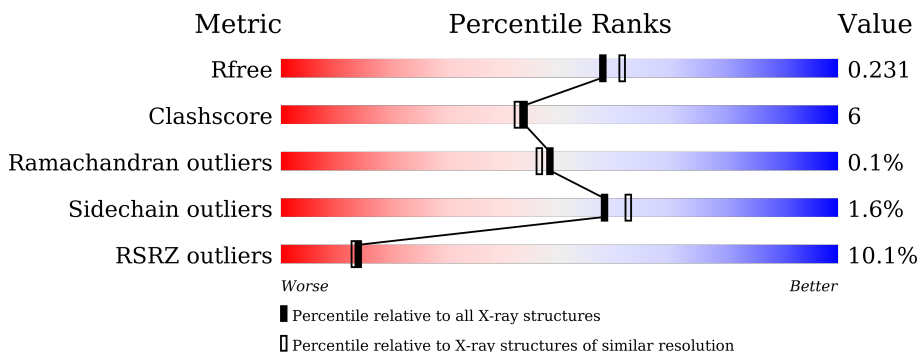
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.02 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))
$R_{free}$	164625	12358 (2.04-2.00)
Clashscore	180529	13897 (2.04-2.00)
Ramachandran outliers	177936	13770 (2.04-2.00)
Sidechain outliers	177891	13769 (2.04-2.00)
RSRZ outliers	164620	12358 (2.04-2.00)

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  $\geq 3$ , 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	334	 3% 87% 11% ..
1	B	334	 9% 90% 8% .
1	C	334	 17% 76% 20% ..

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8356 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 2-amino-3-carboxymuconate 6-semialdehyde decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	329	2574	1640	447	469	18	0	5	0
1	B	330	2576	1641	447	470	18	3	4	0
1	C	325	2544	1622	441	463	18	0	4	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	194	ALA	TRP	engineered mutation	UNP Q83V25
B	194	ALA	TRP	engineered mutation	UNP Q83V25
C	194	ALA	TRP	engineered mutation	UNP Q83V25

- 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	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	280	Total 280	O 280	0	0
3	B	229	Total 229	O 229	0	0

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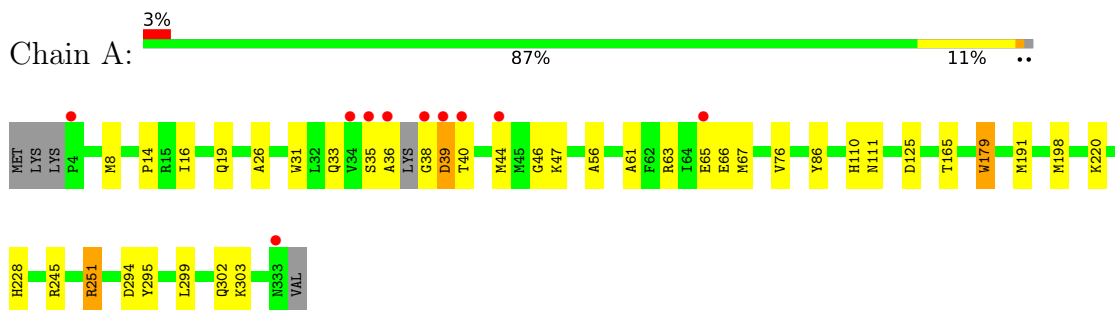
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	C	150	Total 150	O 150	0	0

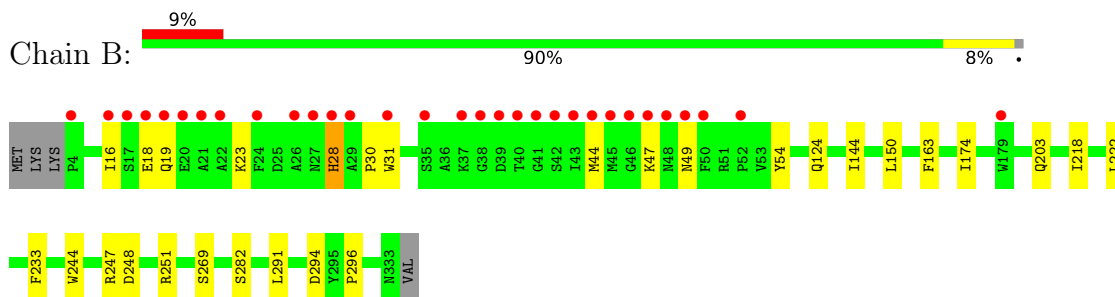
### 3 Residue-property plots [i](#)

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.

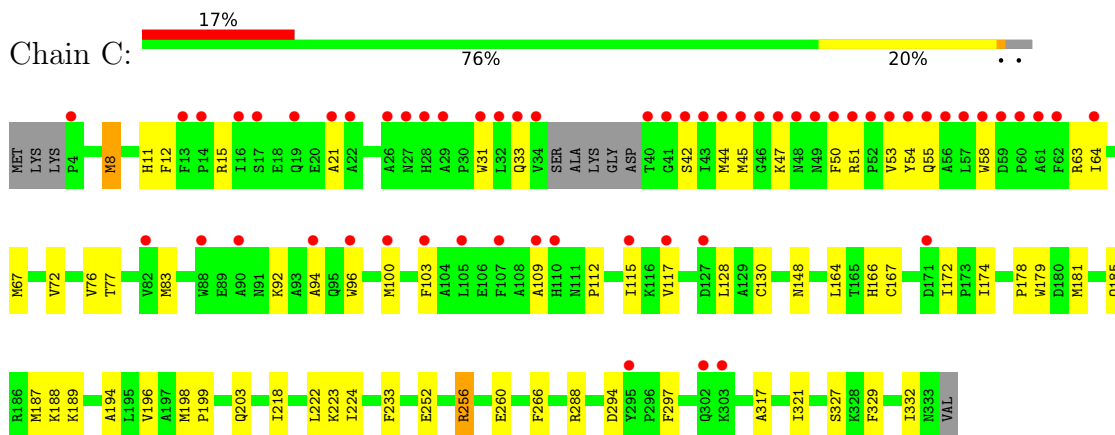
- Molecule 1: 2-amino-3-carboxymuconate 6-semialdehyde decarboxylase



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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.00Å 151.65Å 154.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.10 – 2.02 43.10 – 2.02	Depositor EDS
% Data completeness (in resolution range)	99.7 (43.10-2.02) 93.6 (43.10-2.02)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.58 (at 2.01Å)	Xtrriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, $R_{free}$	0.194 , 0.231 0.194 , 0.231	Depositor DCC
$R_{free}$ test set	77783 reflections (2.54%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.2	Xtrriage
Anisotropy	0.456	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 43.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8356	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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:  
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	0.43	0/2665	0.61	2/3610 (0.1%)
1	B	0.39	0/2664	0.54	0/3609
1	C	0.37	0/2629	0.54	0/3561
All	All	0.40	0/7958	0.57	2/10780 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	251	ARG	NE-CZ-NH2	-8.04	116.28	120.30
1	A	294	ASP	CB-CG-OD1	-6.13	112.78	118.30

There are no chirality outliers.

There are no planarity outliers.

### 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	2574	0	2512	30	1
1	B	2576	0	2519	18	0
1	C	2544	0	2486	44	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	280	0	0	10	6
3	B	229	0	0	1	2
3	C	150	0	0	5	3
All	All	8356	0	7517	92	8

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 6.

All (92) 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:C:64:ILE:HD11	1:C:115:ILE:HD11	1.44	1.00
1:C:83:MET:SD	3:C:501:HOH:O	2.23	0.94
1:A:38:GLY:N	3:A:501:HOH:O	2.04	0.90
1:C:12:PHE:O	3:C:501:HOH:O	1.97	0.81
1:B:44:MET:HE1	1:B:49:ASN:HA	1.67	0.76
1:C:63:ARG:HH12	1:C:77:THR:HG21	1.49	0.75
1:A:110[A]:HIS:NE2	3:A:506:HOH:O	2.24	0.69
1:C:252:GLU:OE2	3:C:502:HOH:O	2.10	0.69
1:A:302:GLN:HG3	1:A:303:LYS:HD3	1.75	0.67
1:B:247:ARG:NH1	3:B:501:HOH:O	2.24	0.67
1:B:144[B]:ILE:HD11	1:B:174:ILE:HG12	1.75	0.66
1:C:53:VAL:HG12	1:C:54:TYR:H	1.63	0.64
1:C:189:LYS:NZ	3:C:509:HOH:O	2.31	0.64
1:C:47:LYS:NZ	3:C:507:HOH:O	2.29	0.63
1:C:185:GLN:O	1:C:188:LYS:HE3	2.00	0.62
1:A:33:GLN:NE2	3:A:508:HOH:O	2.24	0.61
1:A:220:LYS:NZ	3:A:512:HOH:O	2.34	0.60
1:C:45:MET:O	1:C:45:MET:HG3	2.01	0.60
1:C:53:VAL:HG12	1:C:54:TYR:N	2.16	0.60
1:A:191:MET:HE1	1:A:299:LEU:HD11	1.84	0.59
1:A:19:GLN:NE2	3:A:513:HOH:O	2.36	0.59
1:A:14:PRO:HG2	1:A:16:ILE:HD11	1.84	0.59
1:A:36:ALA:HB2	1:A:40:THR:HG22	1.85	0.58
1:A:165[B]:THR:HG21	3:A:518:HOH:O	2.04	0.58
1:A:66:GLU:OE2	3:A:502:HOH:O	2.17	0.56
1:A:26:ALA:O	1:A:46:GLY:HA2	2.06	0.56
1:C:94:ALA:HB2	1:C:128:LEU:HD13	1.87	0.56
1:A:35:SER:O	1:A:38:GLY:HA2	2.06	0.55
1:C:63:ARG:NH1	1:C:77:THR:HG21	2.19	0.55
1:A:31:TRP:CZ2	1:A:44:MET:HG2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:MET:HA	1:A:76:VAL:HB	1.90	0.53
1:C:11:HIS:HB2	1:C:297:PHE:HE2	1.73	0.53
1:C:67[B]:MET:HE2	1:C:72:VAL:HG12	1.91	0.53
1:C:55:GLN:HA	1:C:58:TRP:CH2	2.45	0.52
1:B:28:HIS:O	1:B:28:HIS:ND1	2.42	0.52
1:C:187:MET:HE1	1:C:196:VAL:HB	1.92	0.52
1:B:244:TRP:O	1:B:251:ARG:HG3	2.11	0.51
1:C:181:MET:SD	1:C:198:MET:HG2	2.50	0.51
1:C:130:CYS:HB3	1:C:166:HIS:CD2	2.46	0.51
1:C:42:SER:HA	1:C:53:VAL:HG23	1.94	0.50
1:A:86:TYR:CD2	1:A:179:TRP:CZ2	3.00	0.49
1:C:187:MET:CE	1:C:196:VAL:HB	2.43	0.49
1:C:96:TRP:O	1:C:100:MET:HG2	2.12	0.49
1:B:144[B]:ILE:HD13	1:B:163:PHE:CZ	2.48	0.48
1:B:54:TYR:CE2	1:B:296:PRO:HB2	2.49	0.48
1:C:194:ALA:HA	1:C:198:MET:HG3	1.97	0.47
1:C:317:ALA:O	1:C:321:ILE:HG12	2.14	0.47
1:B:218:ILE:HG21	1:B:222:LEU:HD22	1.96	0.47
1:A:39:ASP:OD1	1:A:39:ASP:N	2.48	0.47
1:A:111:ASN:ND2	3:A:511:HOH:O	2.33	0.47
1:C:31:TRP:CZ3	1:C:33:GLN:HB2	2.50	0.47
1:A:63:ARG:HG2	1:A:67[A]:MET:CE	2.45	0.46
1:A:245:ARG:C	1:A:251:ARG:HH21	2.19	0.46
1:A:251:ARG:HD2	3:A:725:HOH:O	2.15	0.46
1:C:109:ALA:HA	1:C:112:PRO:HG3	1.98	0.46
1:A:125:ASP:OD1	3:A:503:HOH:O	2.20	0.45
1:B:16:ILE:O	1:B:31:TRP:HB2	2.17	0.45
1:C:55:GLN:HA	1:C:58:TRP:CZ3	2.52	0.45
1:B:124:GLN:HA	1:B:150:LEU:HD21	1.99	0.45
1:C:266:PHE:CD2	1:C:288:ARG:HA	2.52	0.44
1:A:36:ALA:CB	1:A:40:THR:HG22	2.47	0.44
1:C:31:TRP:CZ2	1:C:44:MET:HG2	2.53	0.44
1:A:14:PRO:HG2	1:A:16:ILE:CD1	2.46	0.44
1:C:21:ALA:HB2	1:C:31:TRP:HB3	2.00	0.44
1:C:327:SER:HB2	1:C:332:ILE:O	2.17	0.44
1:B:203:GLN:HG3	1:B:233:PHE:HA	2.00	0.43
1:A:61:ALA:HB2	1:A:110[A]:HIS:CE1	2.53	0.43
1:B:248:ASP:N	1:B:248:ASP:OD1	2.51	0.43
1:C:223:LYS:HE2	1:C:329:PHE:HA	2.01	0.43
1:C:198:MET:HB2	1:C:199:PRO:HD3	2.01	0.43
1:B:247:ARG:HA	1:B:247:ARG:HD2	1.68	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:CYS:HB3	1:C:172:ILE:O	2.19	0.43
1:A:198:MET:CE	1:A:228:HIS:CE1	3.02	0.43
1:C:164:LEU:HD11	1:C:224:ILE:HD12	2.00	0.42
1:A:245:ARG:O	1:A:251:ARG:NH2	2.51	0.42
1:A:63:ARG:HG2	1:A:67[A]:MET:HE3	2.01	0.42
1:B:269:SER:OG	1:B:291:LEU:HA	2.20	0.42
1:B:30:PRO:HA	1:B:44:MET:O	2.19	0.42
1:B:18:GLU:HB3	1:B:31:TRP:CZ2	2.55	0.41
1:B:31:TRP:CD1	1:B:44:MET:HB2	2.54	0.41
1:C:50:PHE:HD1	1:C:51:ARG:HG3	1.85	0.41
1:C:164:LEU:HD13	1:C:174:ILE:HD12	2.02	0.41
1:C:8:MET:HA	1:C:76:VAL:HB	2.02	0.41
1:C:51:ARG:HE	1:C:51:ARG:HB3	1.70	0.41
1:C:203:GLN:HG3	1:C:233:PHE:HA	2.02	0.41
1:C:218:ILE:HG21	1:C:222:LEU:HD22	2.03	0.41
1:A:35:SER:HB2	1:A:36:ALA:H	1.62	0.41
1:B:19:GLN:O	1:B:23:LYS:HG3	2.22	0.40
1:A:56:ALA:HB1	1:A:295:TYR:OH	2.22	0.40
1:C:256:ARG:NH2	1:C:260:GLU:OE1	2.48	0.40
1:C:77:THR:O	1:C:117:VAL:HA	2.22	0.40
1:C:148:ASN:OD1	1:C:178:PRO:HA	2.21	0.40

All (8) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:671:HOH:O	3:C:597:HOH:O[6_345]	1.87	0.33
3:A:511:HOH:O	3:A:742:HOH:O[3_454]	1.99	0.21
3:A:770:HOH:O	3:C:639:HOH:O[5_555]	2.00	0.20
3:A:538:HOH:O	3:A:727:HOH:O[3_454]	2.01	0.19
3:A:748:HOH:O	3:C:587:HOH:O[8_545]	2.05	0.15
3:A:506:HOH:O	3:A:513:HOH:O[3_454]	2.07	0.13
3:A:608:HOH:O	3:B:668:HOH:O[8_545]	2.16	0.04
1:A:19:GLN:NE2	1:A:65:GLU:OE2[3_454]	2.17	0.03

## 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	330/334 (99%)	324 (98%)	6 (2%)	0	100	100
1	B	332/334 (99%)	322 (97%)	10 (3%)	0	100	100
1	C	325/334 (97%)	315 (97%)	9 (3%)	1 (0%)	37	34
All	All	987/1002 (98%)	961 (97%)	25 (2%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	15	ARG

### 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	273/273 (100%)	270 (99%)	3 (1%)	70	75
1	B	273/273 (100%)	269 (98%)	4 (2%)	60	65
1	C	270/273 (99%)	264 (98%)	6 (2%)	47	49
All	All	816/819 (100%)	803 (98%)	13 (2%)	58	62

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ASP
1	A	47	LYS

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Mol	Chain	Res	Type
1	A	179	TRP
1	B	28	HIS
1	B	47	LYS
1	B	282	SER
1	B	294	ASP
1	C	8	MET
1	C	92	LYS
1	C	103	PHE
1	C	179	TRP
1	C	256	ARG
1	C	294	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	228	HIS
1	A	302	GLN
1	C	95	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	329/334 (98%)	-0.02	10 (3%) 52 51	16, 28, 53, 66	5 (1%)
1	B	330/334 (98%)	0.27	31 (9%) 15 15	17, 32, 68, 82	4 (1%)
1	C	325/334 (97%)	0.97	58 (17%) 4 4	21, 43, 73, 81	4 (1%)
All	All	984/1002 (98%)	0.40	99 (10%) 14 13	16, 33, 68, 82	13 (1%)

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	43	ILE	6.0
1	C	58	TRP	5.9
1	A	36	ALA	5.4
1	C	46	GLY	4.8
1	C	40	THR	4.7
1	C	34	VAL	4.7
1	C	54	TYR	4.6
1	B	29	ALA	4.5
1	C	53	VAL	4.5
1	A	35	SER	4.2
1	B	26	ALA	4.1
1	C	26	ALA	4.1
1	C	4	PRO	4.0
1	C	50	PHE	4.0
1	C	28	HIS	4.0
1	C	103	PHE	3.9
1	C	41	GLY	3.7
1	B	38	GLY	3.7
1	B	28	HIS	3.7
1	C	32	LEU	3.7
1	B	50	PHE	3.7
1	B	19	GLN	3.6
1	C	49	ASN	3.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	16	ILE	3.5
1	C	45	MET	3.5
1	C	62	PHE	3.5
1	B	35	SER	3.4
1	C	55	GLN	3.4
1	B	46	GLY	3.4
1	C	115	ILE	3.3
1	C	56	ALA	3.3
1	B	179	TRP	3.3
1	C	16	ILE	3.3
1	A	34	VAL	3.3
1	C	100	MET	3.3
1	C	42	SER	3.3
1	C	31	TRP	3.2
1	C	27	ASN	3.2
1	C	33	GLN	3.1
1	B	4	PRO	3.1
1	B	31	TRP	3.1
1	B	37	LYS	3.1
1	C	64	ILE	3.0
1	C	52	PRO	3.0
1	C	19	GLN	3.0
1	A	38	GLY	2.9
1	B	39	ASP	2.9
1	C	127	ASP	2.9
1	C	17	SER	2.8
1	C	22	ALA	2.7
1	C	107	PHE	2.7
1	B	42	SER	2.7
1	C	59	ASP	2.7
1	C	105	LEU	2.7
1	B	40	THR	2.7
1	A	4	PRO	2.7
1	B	18	GLU	2.6
1	A	333	ASN	2.6
1	B	48	ASN	2.6
1	C	48	ASN	2.6
1	B	45	MET	2.6
1	C	14	PRO	2.6
1	B	41	GLY	2.5
1	B	44	MET	2.5
1	C	47	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	44	MET	2.5
1	B	52	PRO	2.4
1	C	90	ALA	2.4
1	C	82	VAL	2.4
1	C	117	VAL	2.4
1	B	43	ILE	2.4
1	B	24	PHE	2.3
1	B	47	LYS	2.3
1	C	21	ALA	2.3
1	C	13	PHE	2.3
1	C	57	LEU	2.3
1	A	40	THR	2.3
1	A	65	GLU	2.2
1	B	20	GLU	2.2
1	C	295	TYR	2.2
1	C	51	ARG	2.2
1	A	44	MET	2.2
1	C	96	TRP	2.2
1	B	17	SER	2.2
1	B	21	ALA	2.2
1	C	29	ALA	2.2
1	C	61	ALA	2.2
1	A	39	ASP	2.2
1	C	88	TRP	2.1
1	C	109	ALA	2.1
1	C	171	ASP	2.1
1	C	110	HIS	2.1
1	C	60	PRO	2.1
1	C	302	GLN	2.1
1	C	94	ALA	2.0
1	B	27	ASN	2.0
1	B	49	ASN	2.0
1	B	22	ALA	2.0
1	C	303	LYS	2.0

## 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](#)

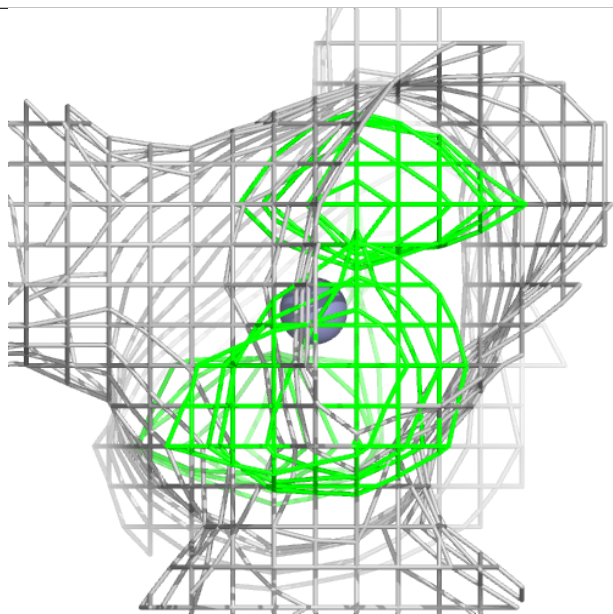
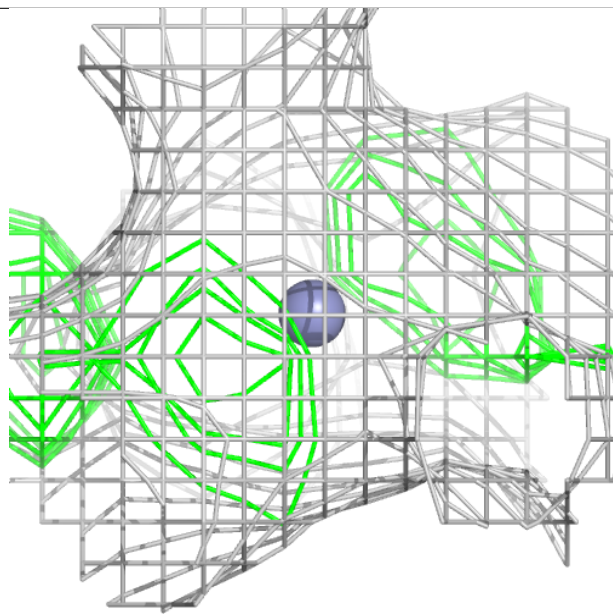
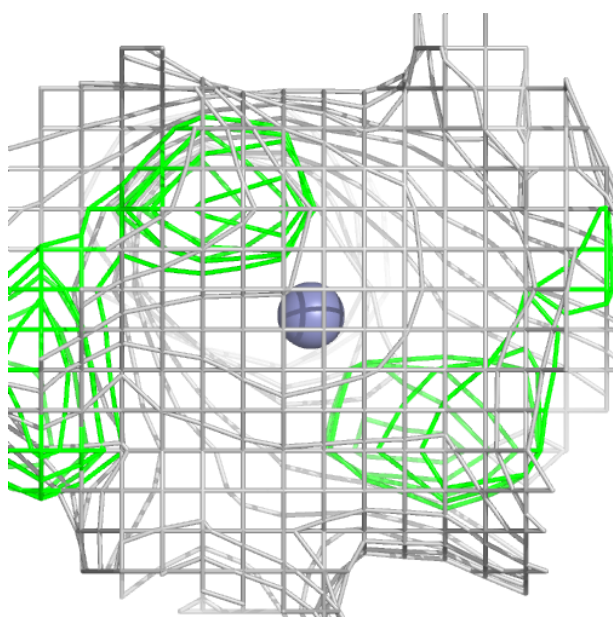
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	ZN	C	401	1/1	0.98	0.05	39,39,39,39	0
2	ZN	B	401	1/1	0.99	0.02	24,24,24,24	0
2	ZN	A	401	1/1	0.99	0.04	22,22,22,22	0

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.

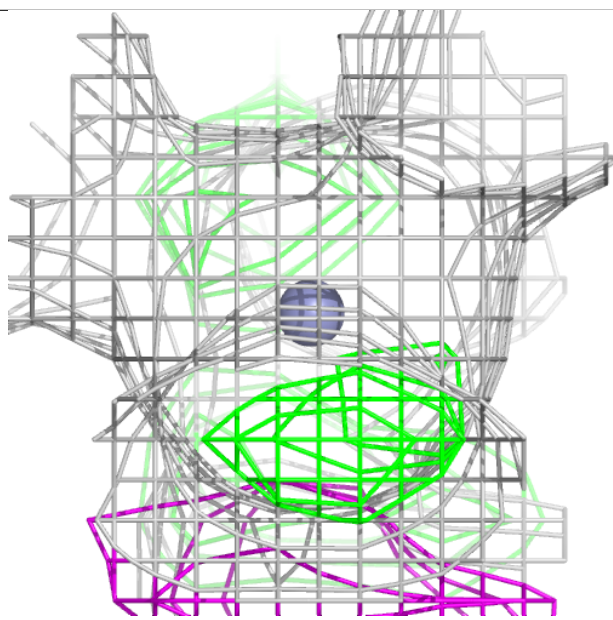
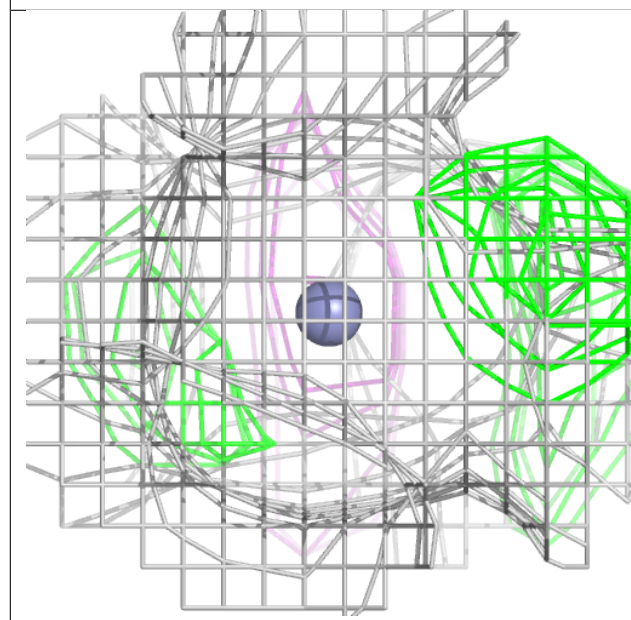
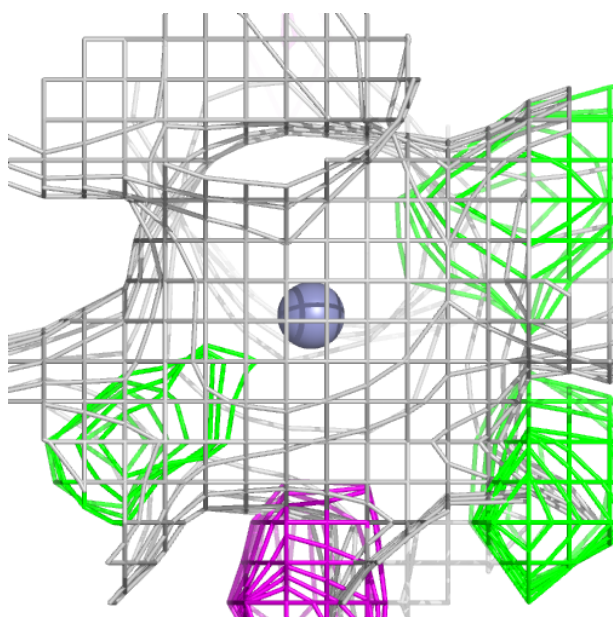
**Electron density around ZN C 401:**

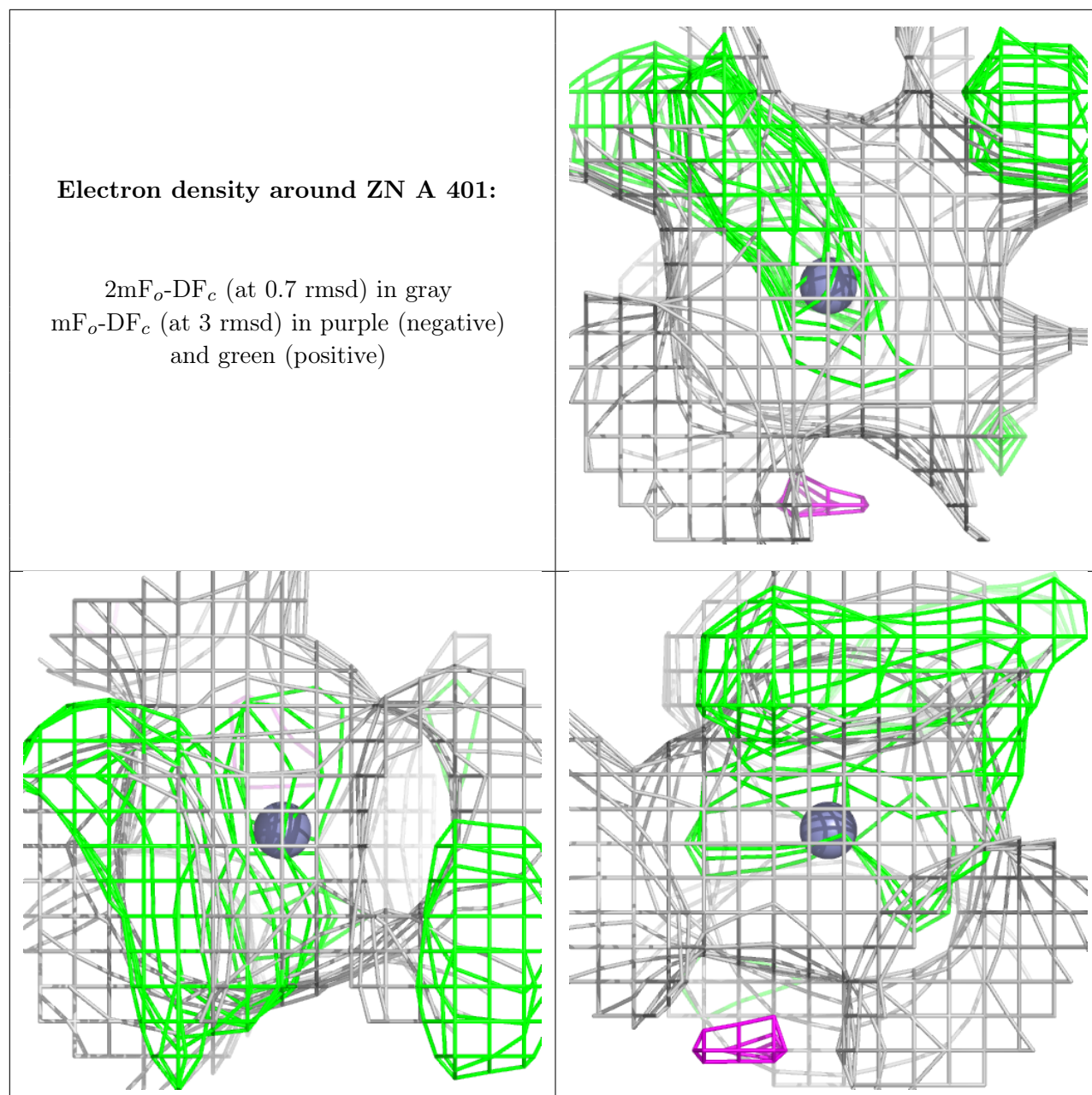
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around ZN B 401:**

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





## 6.5 Other polymers ⓘ

There are no such residues in this entry.