



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 3, 2025 – 04:19 PM EDT

PDB ID : 9N1F / pdb\_00009n1f  
Title : Crystal Structure of the Ark2C-Ubc13 Ub-Mms2 complex  
Authors : Paluda, A.; Middleton, A.J.; Day, C.L.  
Deposited on : 2025-01-26  
Resolution : 2.10 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 : 4-5-2 with Phenix2.0rc1  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

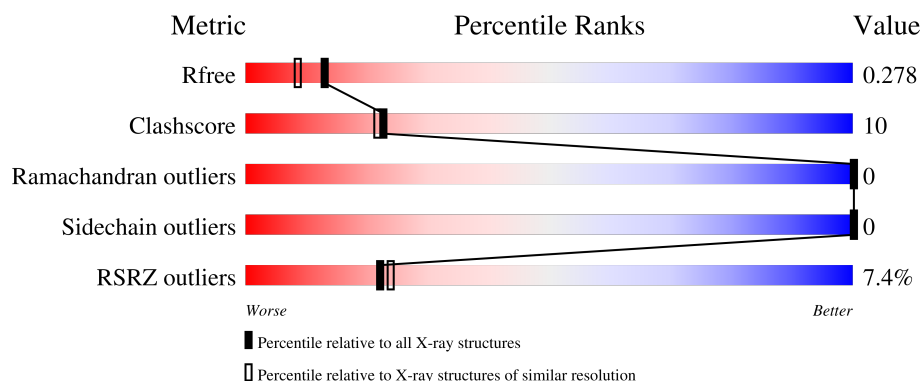
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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	87	 7% 72% 9% 17%
2	B	157	 0% 83% 12% 5%
3	C	145	 3% 83% 11% 6%
4	D	76	 26% 72% 26% 0%

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3541 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 E3 ubiquitin-protein ligase ARK2C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	72	Total	C	N	O	S	0	0	0
			590	370	102	109	9			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	250	GLY	-	expression tag	UNP Q6ZSG1
A	251	PRO	-	expression tag	UNP Q6ZSG1
A	252	LEU	-	expression tag	UNP Q6ZSG1
A	253	GLY	-	expression tag	UNP Q6ZSG1
A	254	SER	-	expression tag	UNP Q6ZSG1
A	?	-	ARG	deletion	UNP Q6ZSG1
A	?	-	ARG	deletion	UNP Q6ZSG1
A	?	-	PRO	deletion	UNP Q6ZSG1
A	?	-	GLN	deletion	UNP Q6ZSG1
A	?	-	ASP	deletion	UNP Q6ZSG1
A	?	-	GLY	deletion	UNP Q6ZSG1
A	?	-	LYS	deletion	UNP Q6ZSG1
A	?	-	GLY	deletion	UNP Q6ZSG1
A	?	-	LYS	deletion	UNP Q6ZSG1
A	?	-	LYS	deletion	UNP Q6ZSG1

- Molecule 2 is a protein called Ubiquitin-conjugating enzyme E2 N.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	149	Total	C	N	O	S	0	0	0
			1187	761	205	218	3			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLY	-	expression tag	UNP P61088

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	PRO	-	expression tag	UNP P61088
B	-2	LEU	-	expression tag	UNP P61088
B	-1	GLY	-	expression tag	UNP P61088
B	0	SER	-	expression tag	UNP P61088
B	87	LYS	CYS	engineered mutation	UNP P61088
B	92	THR	LYS	engineered mutation	UNP P61088
B	94	GLN	LYS	engineered mutation	UNP P61088

- Molecule 3 is a protein called Ubiquitin-conjugating enzyme E2 variant 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	137	Total	C	N	O	S	0	1	0
			1097	689	192	208	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	32	ALA	SER	engineered mutation	UNP Q15819

- Molecule 4 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	76	Total	C	N	O	S	0	0	0
			601	378	105	117	1			

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

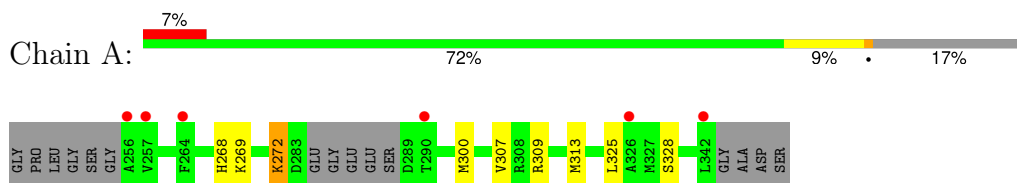
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	5	Total	O	0	0
			5	5		
6	B	33	Total	O	0	0
			33	33		
6	C	26	Total	O	0	0
			26	26		

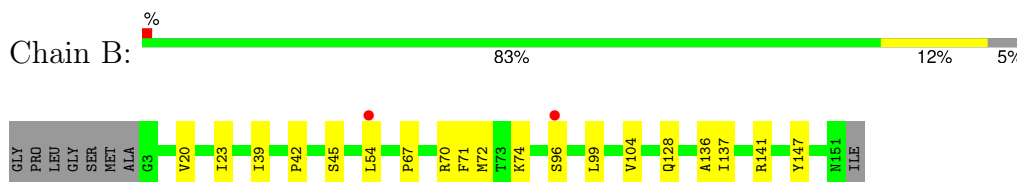
### 3 Residue-property plots [i](#)

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.

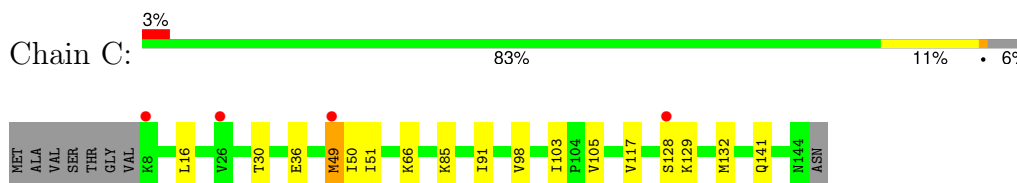
- Molecule 1: E3 ubiquitin-protein ligase ARK2C



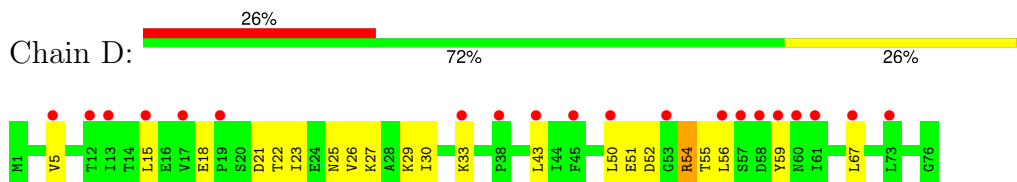
- Molecule 2: Ubiquitin-conjugating enzyme E2 N



- Molecule 3: Ubiquitin-conjugating enzyme E2 variant 2



- Molecule 4: Ubiquitin



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.73Å 100.42Å 142.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.00 – 2.10 41.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (41.00-2.10) 99.9 (41.00-2.10)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.13	Depositor
R, $R_{free}$	0.229 , 0.279 0.228 , 0.278	Depositor DCC
$R_{free}$ test set	1514 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.8	Xtriage
Anisotropy	0.420	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 40.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3541	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.92% 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	0.91	0/600	1.01	1/806 (0.1%)
2	B	1.07	0/1217	1.03	0/1659
3	C	1.10	1/1120 (0.1%)	1.03	0/1515
4	D	0.84	0/607	0.96	1/816 (0.1%)
All	All	1.02	1/3544 (0.0%)	1.02	2/4796 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	49	MET	CG-SD	-7.02	1.63	1.80

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	LYS	N-CA-C	6.19	118.55	108.76
4	D	54	ARG	N-CA-C	5.68	117.66	110.33

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	590	0	578	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1187	0	1191	22	0
3	C	1097	0	1097	17	0
4	D	601	0	629	27	0
5	A	2	0	0	0	0
6	A	5	0	0	1	0
6	B	33	0	0	1	0
6	C	26	0	0	0	0
All	All	3541	0	3495	72	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 10.

All (72) 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)
4:D:23:ILE:HD12	4:D:51:GLU:O	1.44	1.17
3:C:91:ILE:CD1	3:C:98:VAL:HG22	1.93	0.98
2:B:54:LEU:HD21	2:B:71:PHE:CD1	1.99	0.97
4:D:21:ASP:O	4:D:56:LEU:HG	1.66	0.96
2:B:54:LEU:HD23	2:B:71:PHE:HA	1.46	0.94
4:D:21:ASP:HB2	4:D:56:LEU:CD1	2.00	0.89
4:D:21:ASP:HB2	4:D:56:LEU:HD11	1.55	0.89
4:D:18:GLU:O	4:D:56:LEU:HD12	1.74	0.88
4:D:54:ARG:HD2	4:D:59:TYR:OH	1.76	0.85
1:A:272:LYS:HZ1	1:A:300:MET:HE3	1.45	0.81
4:D:23:ILE:CD1	4:D:51:GLU:O	2.26	0.81
4:D:15:LEU:HA	4:D:33:LYS:NZ	2.02	0.74
2:B:72:MET:HE1	6:B:211:HOH:O	1.88	0.74
2:B:54:LEU:HD21	2:B:71:PHE:CE1	2.24	0.72
1:A:272:LYS:NZ	1:A:300:MET:HE3	2.06	0.69
2:B:54:LEU:HD21	2:B:71:PHE:CG	2.27	0.68
4:D:21:ASP:HB2	4:D:56:LEU:HD12	1.76	0.67
2:B:96:SER:OG	2:B:99:LEU:HG	1.98	0.64
1:A:272:LYS:NZ	1:A:300:MET:CE	2.62	0.62
4:D:26:VAL:O	4:D:29:LYS:N	2.33	0.62
2:B:70:ARG:HD3	3:C:16:LEU:HD11	1.81	0.62
3:C:30:THR:HA	3:C:51:ILE:HD12	1.83	0.60
3:C:91:ILE:HD13	3:C:98:VAL:HG22	1.83	0.59
4:D:18:GLU:O	4:D:56:LEU:CD1	2.48	0.58
2:B:54:LEU:CD2	2:B:71:PHE:CD1	2.82	0.57
4:D:5:VAL:HG22	4:D:67:LEU:HB2	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:54:LEU:CD2	2:B:71:PHE:CG	2.87	0.57
3:C:91:ILE:HD12	3:C:98:VAL:HG22	1.82	0.56
2:B:70:ARG:CD	3:C:16:LEU:HD11	2.36	0.56
3:C:49:MET:HG2	3:C:50:ILE:N	2.20	0.56
2:B:39:ILE:HG13	2:B:54:LEU:HD12	1.89	0.54
3:C:49:MET:CG	3:C:50:ILE:N	2.71	0.53
3:C:85:LYS:HE3	3:C:141:GLN:HG2	1.91	0.52
1:A:325:LEU:HA	1:A:328:SER:O	2.09	0.52
3:C:105:VAL:HG21	3:C:117:VAL:HG12	1.90	0.52
2:B:39:ILE:HD12	2:B:54:LEU:CD1	2.41	0.51
2:B:20:VAL:HG11	2:B:23:ILE:HD12	1.92	0.51
4:D:23:ILE:HD13	4:D:50:LEU:C	2.36	0.51
3:C:129:LYS:HA	3:C:132:MET:HE3	1.92	0.51
2:B:42:PRO:O	2:B:45:SER:OG	2.27	0.51
1:A:272:LYS:HZ1	1:A:300:MET:CE	2.18	0.50
2:B:128:GLN:HG3	2:B:136:ALA:HB2	1.93	0.50
4:D:22:THR:HA	4:D:55:THR:HA	1.93	0.50
4:D:18:GLU:N	4:D:21:ASP:OD2	2.44	0.49
4:D:54:ARG:HD2	4:D:59:TYR:HH	1.75	0.48
4:D:15:LEU:HD23	4:D:33:LYS:HZ3	1.77	0.48
3:C:129:LYS:HA	3:C:132:MET:CE	2.43	0.48
2:B:39:ILE:HD12	2:B:54:LEU:HD11	1.96	0.47
4:D:25:ASN:O	4:D:29:LYS:HG2	2.13	0.47
3:C:85:LYS:NZ	3:C:141:GLN:NE2	2.62	0.47
4:D:67:LEU:N	4:D:67:LEU:HD12	2.29	0.47
3:C:128[B]:SER:O	3:C:132:MET:HB2	2.14	0.46
4:D:27:LYS:NZ	4:D:52:ASP:OD1	2.41	0.45
3:C:36:GLU:OE2	3:C:66:LYS:HE3	2.16	0.45
2:B:54:LEU:HD23	2:B:71:PHE:CA	2.32	0.45
3:C:91:ILE:HD11	3:C:98:VAL:HG22	1.90	0.45
4:D:15:LEU:CD2	4:D:33:LYS:NZ	2.80	0.44
1:A:309:ARG:HD3	1:A:313:MET:HE3	1.98	0.44
2:B:74:LYS:HD3	2:B:147:TYR:CE2	2.52	0.44
2:B:39:ILE:CD1	2:B:54:LEU:CD1	2.96	0.44
2:B:20:VAL:CG1	2:B:23:ILE:HD12	2.48	0.44
4:D:15:LEU:HD23	4:D:33:LYS:NZ	2.32	0.44
1:A:268:HIS:CE1	1:A:307:VAL:HG23	2.53	0.43
1:A:269:LYS:NZ	6:A:501:HOH:O	2.51	0.43
4:D:50:LEU:HD22	4:D:59:TYR:CD2	2.53	0.43
4:D:22:THR:HG22	4:D:55:THR:HG22	1.99	0.43
3:C:103:ILE:HG22	3:C:105:VAL:HG12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:26:VAL:O	4:D:27:LYS:C	2.61	0.41
2:B:137:ILE:O	2:B:141:ARG:HG3	2.20	0.41
4:D:54:ARG:HD2	4:D:59:TYR:CZ	2.52	0.41
2:B:67:PRO:HG2	2:B:104:VAL:HG21	2.03	0.41
4:D:30:ILE:CD1	4:D:43:LEU:HD21	2.51	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	68/87 (78%)	65 (96%)	3 (4%)	0	100	100
2	B	147/157 (94%)	142 (97%)	5 (3%)	0	100	100
3	C	136/145 (94%)	134 (98%)	2 (2%)	0	100	100
4	D	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
All	All	425/465 (91%)	409 (96%)	16 (4%)	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	69/78 (88%)	69 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	127/132 (96%)	127 (100%)	0	100	100
3	C	123/128 (96%)	123 (100%)	0	100	100
4	D	68/68 (100%)	68 (100%)	0	100	100
All	All	387/406 (95%)	387 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	323	GLN
2	B	43	GLN
2	B	123	ASN
2	B	135	GLN
3	C	93	ASN
3	C	141	GLN
4	D	68	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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(Å²)	Q<0.9
1	A	72/87 (82%)	0.79	6 (8%)	19	20	44, 67, 98, 128	0
2	B	149/157 (94%)	0.34	2 (1%)	74	76	34, 51, 77, 92	0
3	C	137/145 (94%)	0.31	4 (2%)	54	55	23, 50, 75, 104	1 (0%)
4	D	76/76 (100%)	1.56	20 (26%)	2	2	64, 100, 126, 147	0
All	All	434/465 (93%)	0.62	32 (7%)	22	24	23, 56, 113, 147	1 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	256	ALA	6.0
4	D	56	LEU	5.1
4	D	73	LEU	4.2
4	D	50	LEU	4.0
4	D	61	ILE	4.0
1	A	342	LEU	3.8
4	D	15	LEU	3.2
4	D	17	VAL	3.1
4	D	67	LEU	2.9
4	D	57	SER	2.9
1	A	257	VAL	2.9
4	D	5	VAL	2.8
1	A	290	THR	2.8
4	D	53	GLY	2.7
3	C	128[A]	SER	2.6
4	D	59	TYR	2.6
2	B	96	SER	2.6
4	D	19	PRO	2.4
4	D	33	LYS	2.4
3	C	26	VAL	2.4
4	D	38	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
3	C	8	LYS	2.3
4	D	45	PHE	2.3
4	D	13	ILE	2.3
4	D	43	LEU	2.3
1	A	326	ALA	2.2
1	A	264	PHE	2.1
2	B	54	LEU	2.1
3	C	49	MET	2.1
4	D	12	THR	2.0
4	D	60	ASN	2.0
4	D	58	ASP	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](#)

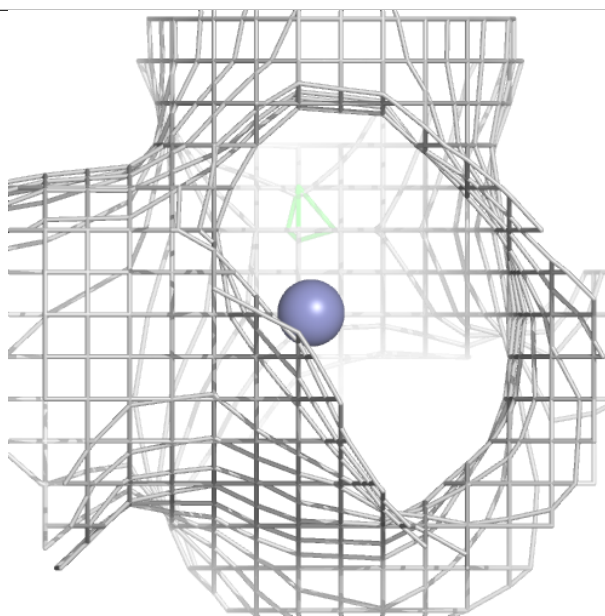
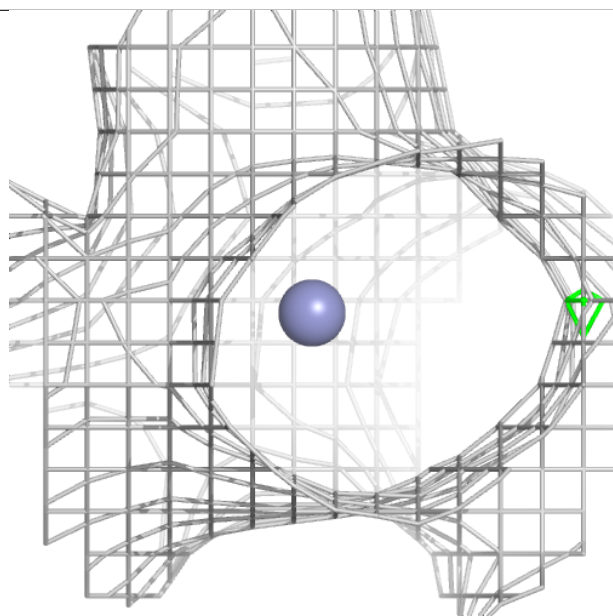
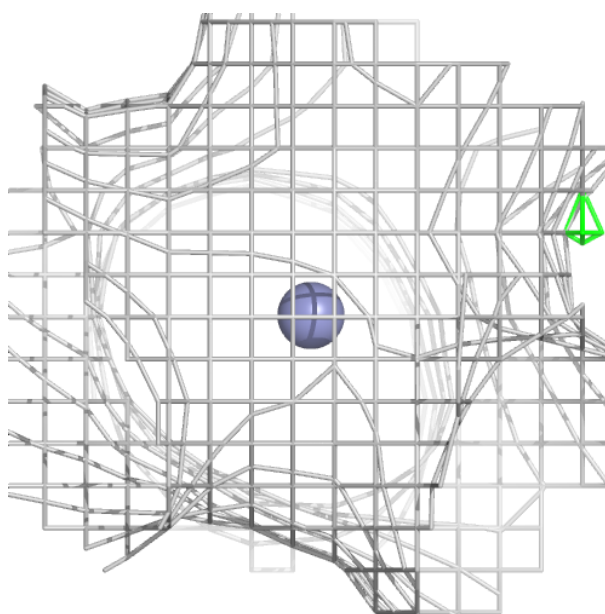
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	ZN	A	401	1/1	0.99	0.02	49,49,49,49	0
5	ZN	A	402	1/1	1.00	0.02	55,55,55,55	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.

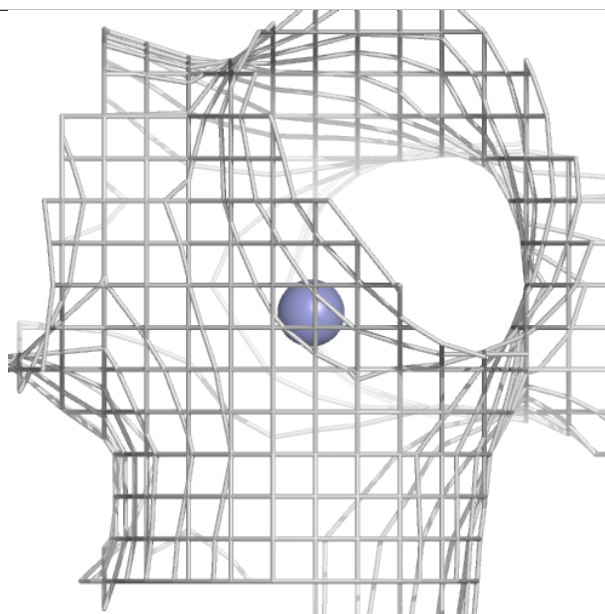
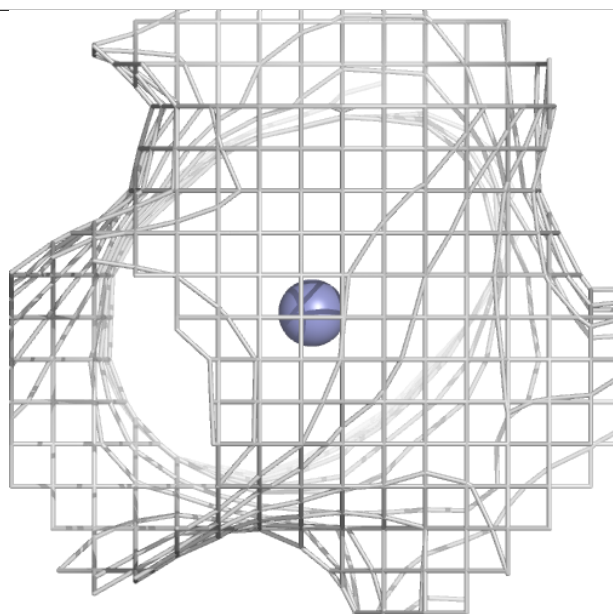
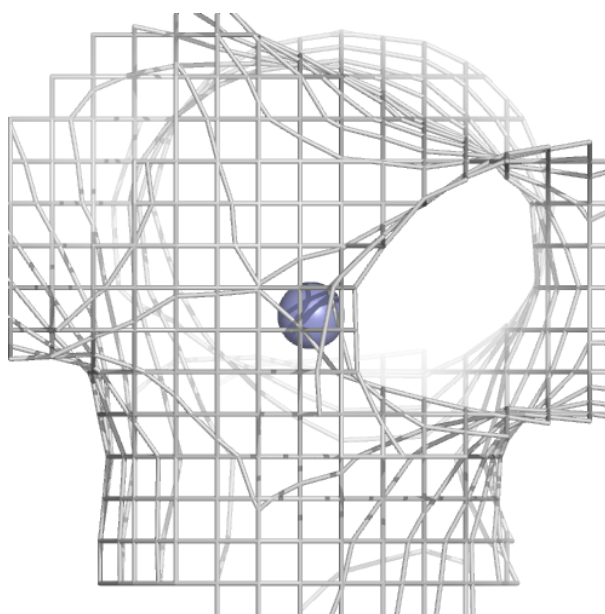
**Electron density around ZN A 401:**

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



**Electron density around ZN A 402:**

$2mF_o-DF_c$  (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.