



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:11 AM UTC

PDB ID : 9EKK / pdb\_00009ekk  
Title : Thomasclavelia ramosa Immunoglobulin A Protease Middle (Protease) Domain with C-terminal Domain #1 (Crystallized as Purified)  
Authors : Tran, N.; Frenette, A.; Holyoak, T.  
Deposited on : 2024-12-02  
Resolution : 1.65 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 Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

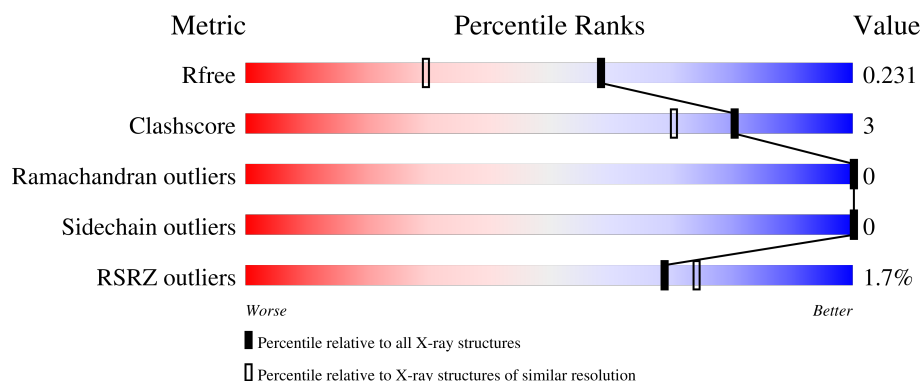
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.65 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))
$R_{free}$	180053	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	548	<div> <div></div> <div>94%</div> <div>6%</div> </div>
1	B	548	<div> <div>2%</div> <div>92%</div> <div>8%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10205 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 IgA protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	547	Total	C	N	O	S	0	15	0
			4480	2846	738	878	18			
1	B	547	Total	C	N	O	S	0	10	0
			4451	2824	736	874	17			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	1
			3	3		
2	B	2	Total	Zn	0	1
			3	3		

- Molecule 3 is PRASEODYMIUM ION (CCD ID: PR) (formula: Pr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Pr	0	1
			2	2		
3	B	1	Total	Pr	0	1
			2	2		

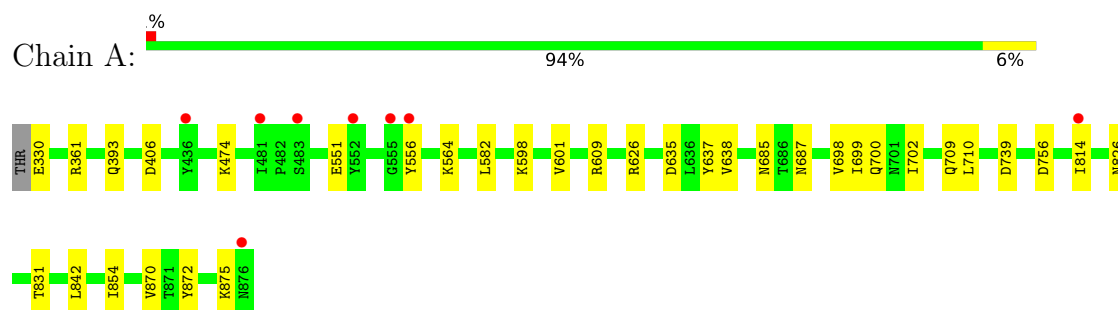
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	658	Total	O	0	0
			658	658		
4	B	606	Total	O	0	0
			606	606		

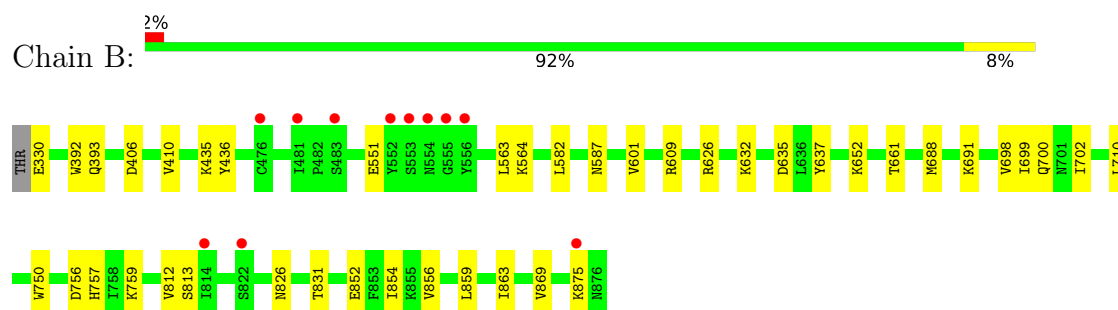
### 3 Residue-property plots

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: IgA protease



#### • Molecule 1: IgA protease



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.69Å 91.27Å 86.86Å 90.00° 91.09° 90.00°	Depositor
Resolution (Å)	55.34 – 1.65 55.34 – 1.65	Depositor EDS
% Data completeness (in resolution range)	91.6 (55.34-1.65) 91.6 (55.34-1.65)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.49 (at 1.65Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, $R_{free}$	0.196 , 0.231 0.196 , 0.231	Depositor DCC
$R_{free}$ test set	6358 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.1	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 36.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for -h,-l,-k 0.000 for -h,l,k 0.116 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10205	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.70% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PR, 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	0.28	0/4635	0.50	0/6282
1	B	0.25	0/4591	0.46	0/6223
All	All	0.27	0/9226	0.48	0/12505

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	4480	0	4324	20	0
1	B	4451	0	4280	26	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	658	0	0	1	1
4	B	606	0	0	4	1
All	All	10205	0	8604	46	1

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 3.

All (46) 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:699[B]:ILE:HD13	1:A:710:LEU:HD12	1.74	0.69
1:A:564:LYS:NZ	1:A:756:ASP:OD2	2.26	0.68
1:A:406:ASP:OD1	4:A:1101:HOH:O	2.13	0.65
1:B:406:ASP:OD1	4:B:1101:HOH:O	2.15	0.63
1:B:852:GLU:HB2	1:B:875[A]:LYS:HE3	1.85	0.58
1:A:814:ILE:HD12	1:A:872:TYR:HE1	1.69	0.57
1:A:635:ASP:HA	1:A:702:ILE:HB	1.87	0.57
1:B:688:MET:HA	1:B:691:LYS:HD2	1.90	0.54
1:B:812:VAL:HG22	1:B:863:ILE:HG21	1.89	0.53
1:B:635:ASP:HA	1:B:702:ILE:HB	1.90	0.52
1:B:435:LYS:HE3	1:B:436:TYR:CZ	2.45	0.51
1:B:564:LYS:HG3	1:B:757:HIS:O	2.11	0.51
1:A:551:GLU:HB2	1:A:609:ARG:HB2	1.93	0.51
1:A:626:ARG:HD3	1:A:626:ARG:C	2.35	0.51
1:B:652:LYS:NZ	4:B:1127:HOH:O	2.43	0.50
1:B:813:SER:HB2	1:B:869:VAL:HG22	1.94	0.50
1:A:582:LEU:HG	1:A:698:VAL:HG11	1.94	0.50
1:B:551:GLU:HB3	1:B:601:VAL:HG11	1.94	0.50
1:B:551:GLU:HB2	1:B:609:ARG:HB2	1.93	0.49
1:B:661[A]:THR:HG23	4:B:1164:HOH:O	2.12	0.48
1:B:393:GLN:HG2	1:B:831:THR:O	2.13	0.48
1:B:563:LEU:HD13	1:B:759:LYS:HG3	1.95	0.47
1:B:582:LEU:HG	1:B:698:VAL:HG11	1.96	0.47
1:B:856:VAL:HG11	1:B:859:LEU:HD12	1.97	0.47
1:A:638:VAL:HG22	1:A:699[A]:ILE:HD12	1.97	0.47
1:B:587[B]:ASN:ND2	4:B:1136:HOH:O	2.47	0.47
1:A:393[A]:GLN:HG2	1:A:831:THR:O	2.16	0.45
1:B:750:TRP:CH2	1:B:756:ASP:HA	2.51	0.45
1:B:626:ARG:C	1:B:626:ARG:HD3	2.41	0.45
1:B:812:VAL:HG21	1:B:863:ILE:HD13	1.99	0.45
1:A:551:GLU:HB3	1:A:601:VAL:HG11	2.00	0.44
1:A:361:ARG:HD3	1:A:842:LEU:HD22	2.00	0.44
1:A:474:LYS:HB2	1:A:474:LYS:HE2	1.86	0.43
1:A:854:ILE:HD11	1:A:875:LYS:HG2	2.00	0.43
1:A:556:TYR:HB2	1:A:598:LYS:HD3	2.01	0.43
1:A:637:TYR:HB3	1:A:700:GLN:HB3	2.01	0.42
1:B:632:LYS:HE2	1:B:632:LYS:HB3	1.78	0.42
1:B:637:TYR:HB3	1:B:700:GLN:HB3	2.02	0.42
1:A:709:GLN:NE2	1:A:739:ASP:OD1	2.53	0.42
1:A:814:ILE:HD13	1:A:870:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:330:GLU:HB2	1:B:826:ASN:OD1	2.20	0.41
1:B:392:TRP:CE2	1:B:410:VAL:HG21	2.55	0.41
1:B:854:ILE:HD11	1:B:875[A]:LYS:HG3	2.02	0.41
1:A:330:GLU:HB2	1:A:826:ASN:OD1	2.21	0.41
1:B:699:ILE:HD13	1:B:710:LEU:HD12	2.03	0.40
1:A:685:ASN:OD1	1:A:687:ASN:HB2	2.21	0.40

All (1) 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)
4:A:1123:HOH:O	4:B:1656:HOH:O[2_545]	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	560/548 (102%)	547 (98%)	13 (2%)	0	100	100
1	B	555/548 (101%)	539 (97%)	16 (3%)	0	100	100
All	All	1115/1096 (102%)	1086 (97%)	29 (3%)	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	504/490 (103%)	504 (100%)	0	100	100
1	B	499/490 (102%)	499 (100%)	0	100	100
All	All	1003/980 (102%)	1003 (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 (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	543	HIS
1	A	679	ASN
1	A	733	GLN
1	B	437	ASN
1	B	449	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 10 ligands modelled in this entry, 10 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 [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, 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	547/548 (99%)	-0.03	8 (1%) 72 77	11, 24, 37, 58	15 (2%)
1	B	547/548 (99%)	0.14	11 (2%) 65 70	13, 27, 40, 58	10 (1%)
All	All	1094/1096 (99%)	0.06	19 (1%) 69 74	11, 25, 39, 58	25 (2%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	814	ILE	3.8
1	B	552	TYR	3.5
1	A	552	TYR	3.1
1	A	483	SER	2.9
1	A	814	ILE	2.8
1	B	822	SER	2.8
1	B	476	CYS	2.8
1	B	483	SER	2.6
1	B	555	GLY	2.6
1	A	436	TYR	2.5
1	B	481	ILE	2.5
1	B	554	ASN	2.4
1	B	556	TYR	2.4
1	A	556	TYR	2.3
1	A	876	ASN	2.2
1	B	553	SER	2.2
1	B	875[A]	LYS	2.1
1	A	481	ILE	2.1
1	A	555	GLY	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 oligosaccharides in this entry.

## 6.4 Ligands [i](#)

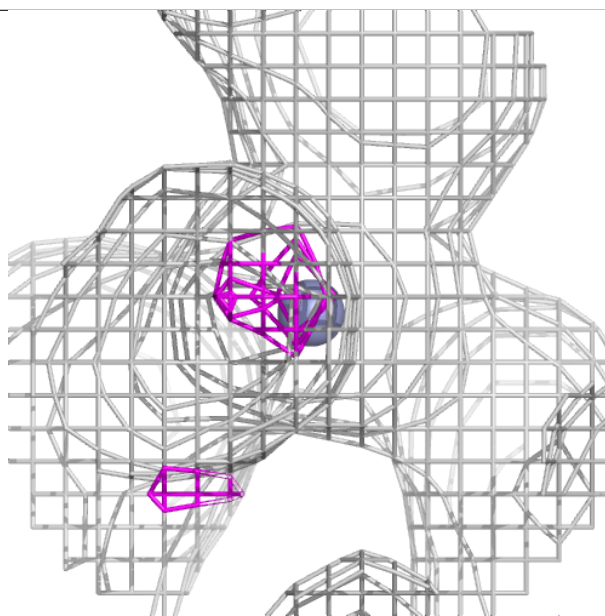
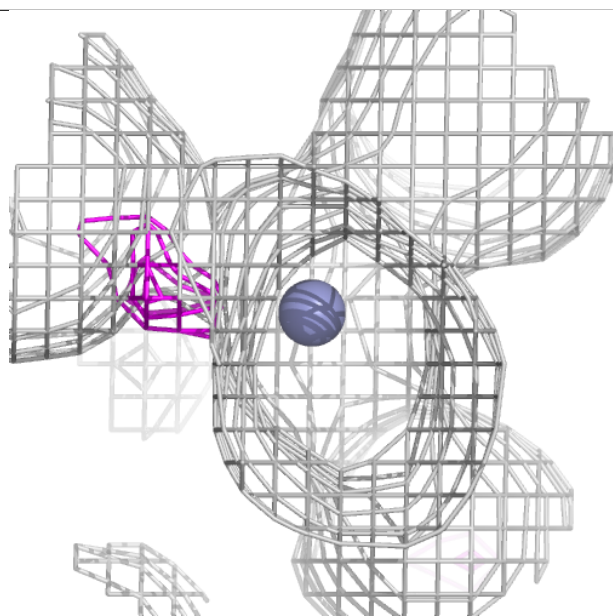
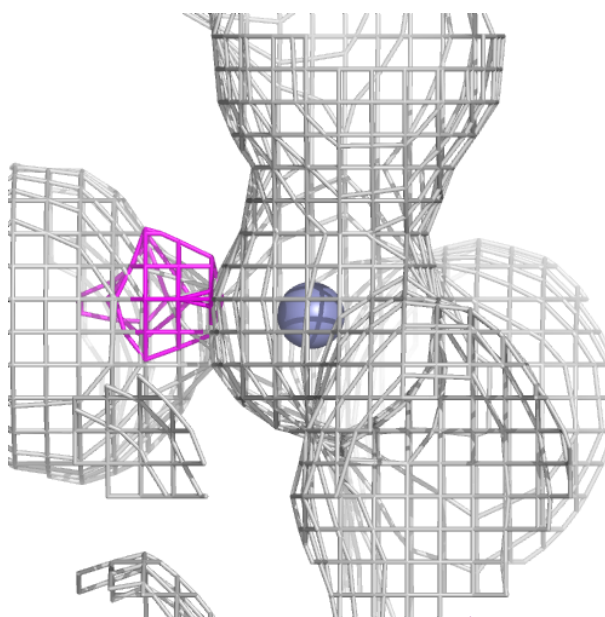
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	B	1001	1/1	0.90	0.07	20,20,20,20	1
2	ZN	A	1001	1/1	0.93	0.07	19,19,19,19	1
2	ZN	B	1002[A]	1/1	0.93	0.08	42,42,42,42	1
2	ZN	B	1002[B]	1/1	0.93	0.08	33,33,33,33	1
2	ZN	A	1002[B]	1/1	0.96	0.05	35,35,35,35	1
2	ZN	A	1002[A]	1/1	0.96	0.05	35,35,35,35	1
3	PR	B	1003[A]	1/1	0.97	0.05	36,36,36,36	1
3	PR	B	1003[B]	1/1	0.97	0.05	81,81,81,81	1
3	PR	A	1003[A]	1/1	0.99	0.03	29,29,29,29	1
3	PR	A	1003[B]	1/1	0.99	0.03	38,38,38,38	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.

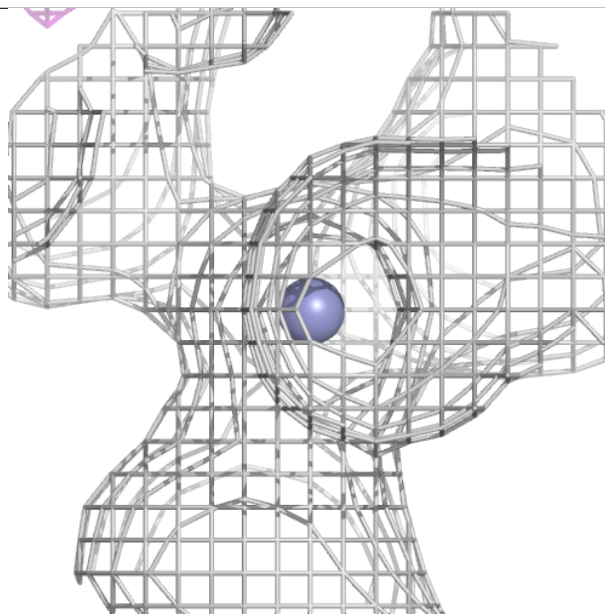
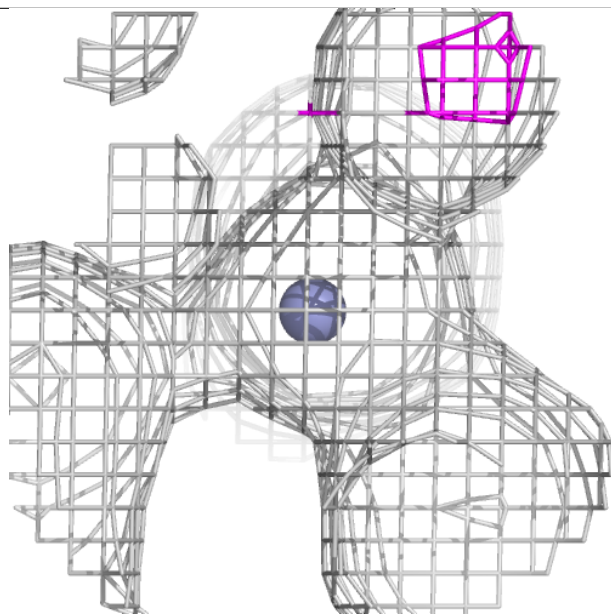
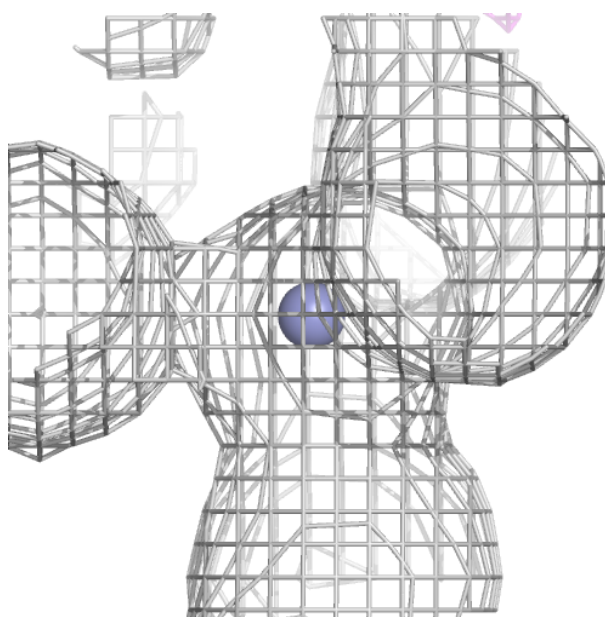
**Electron density around ZN B 1001:**

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



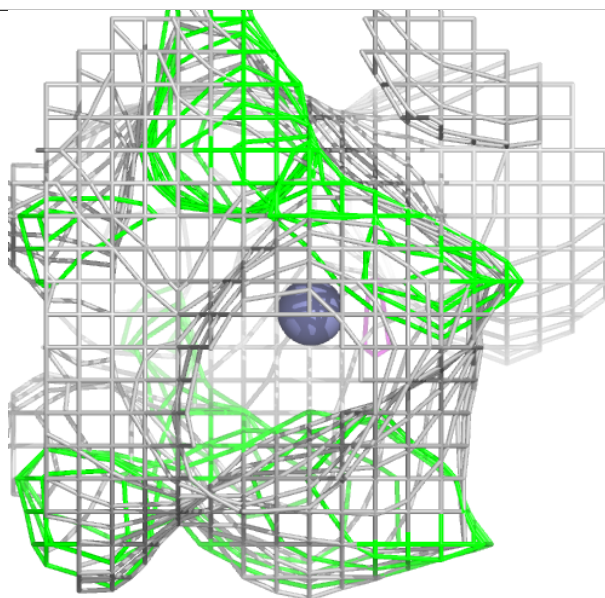
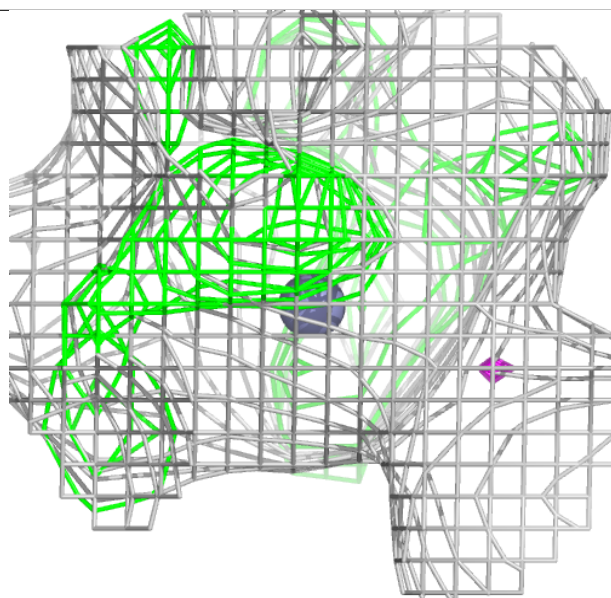
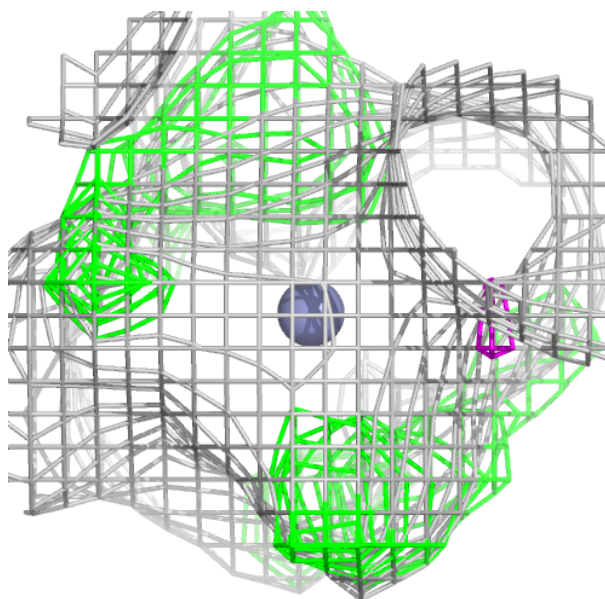
**Electron density around ZN A 1001:**

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



**Electron density around ZN B 1002 (A):**

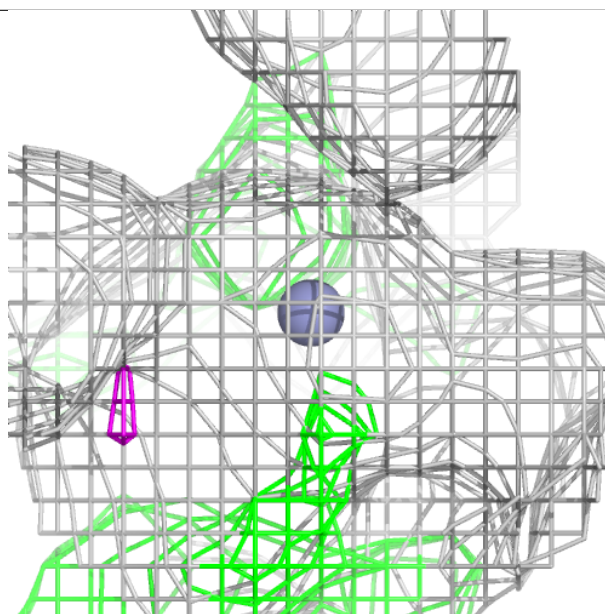
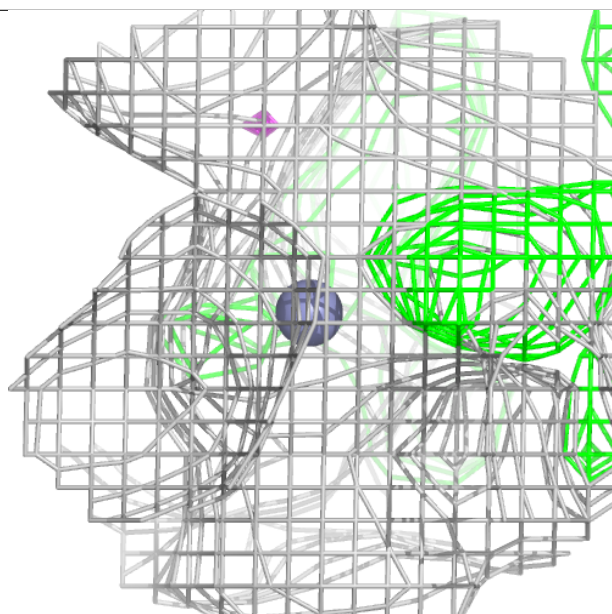
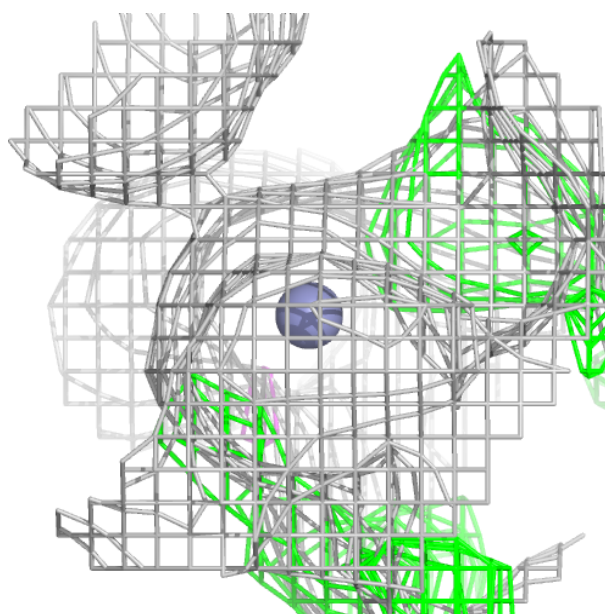
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around ZN B 1002 (B):**

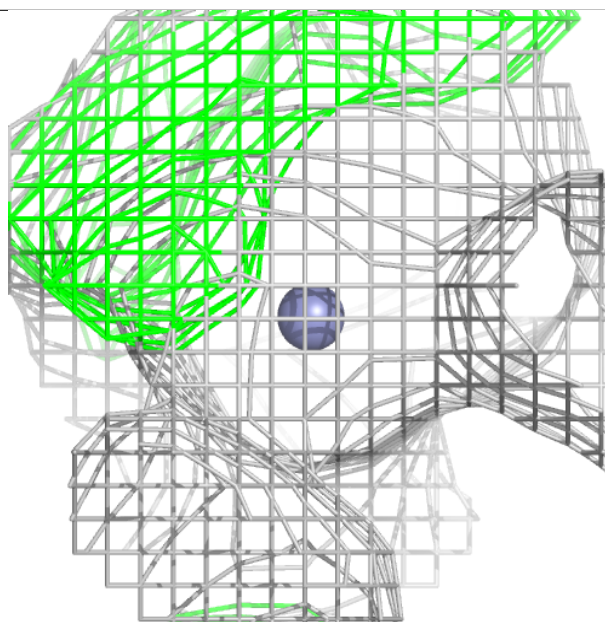
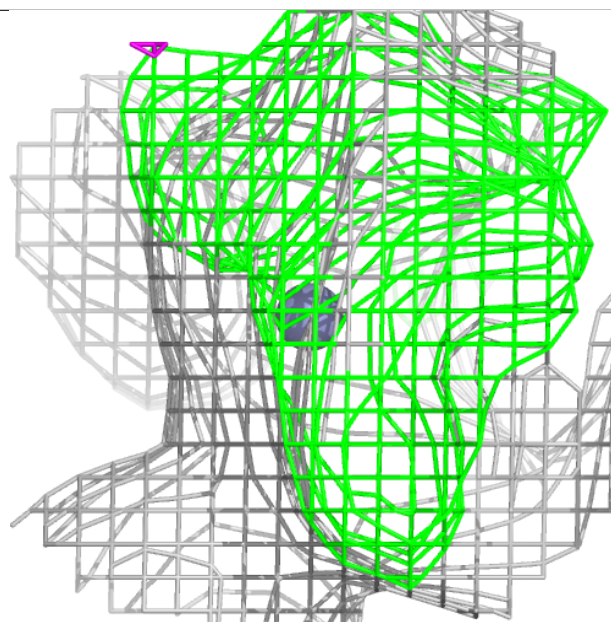
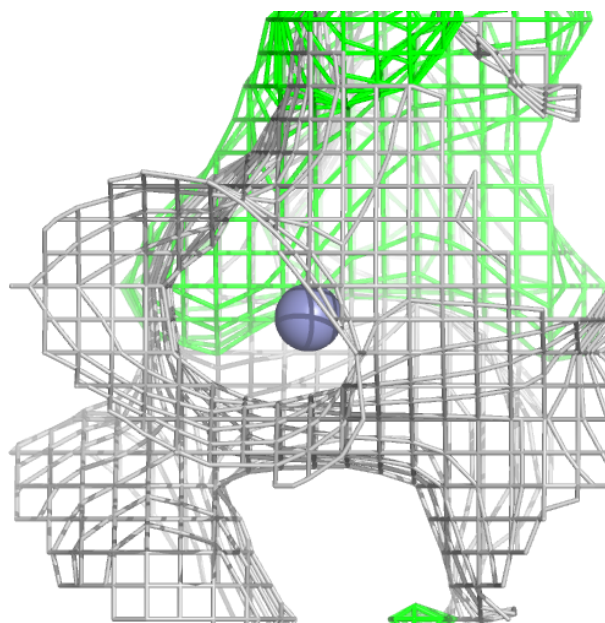
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





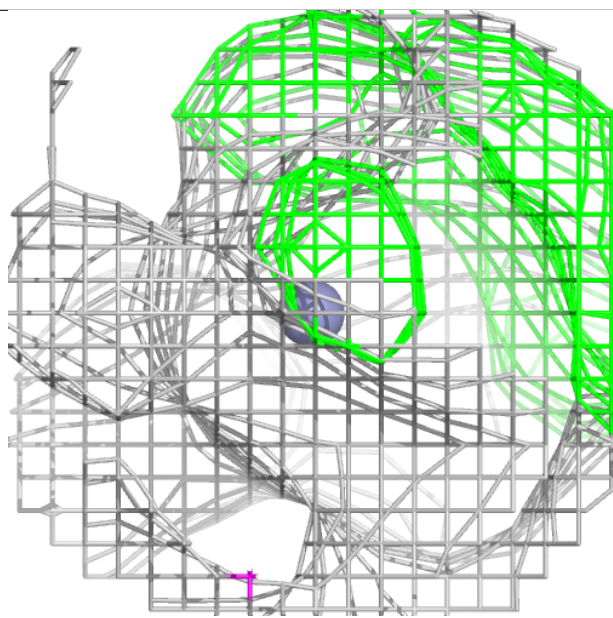
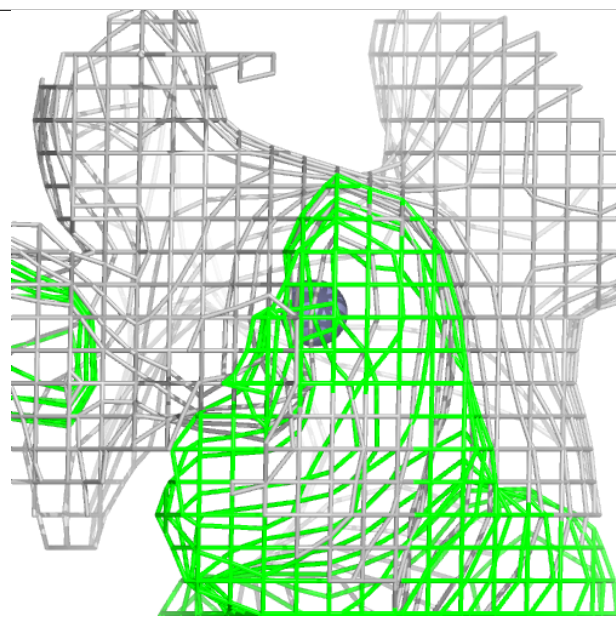
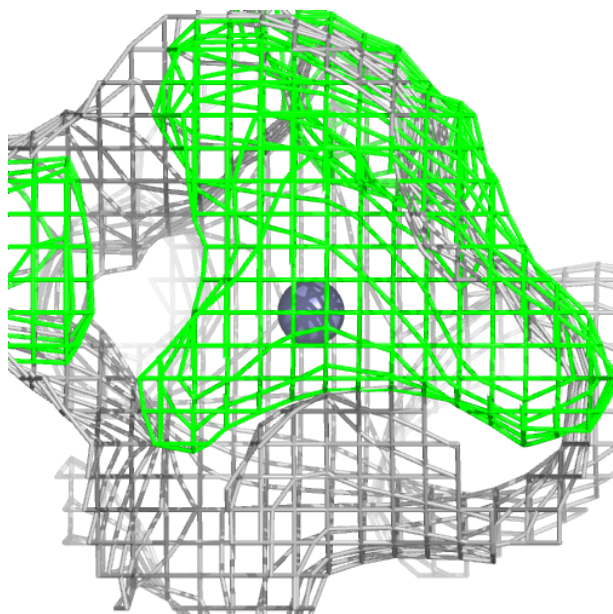
**Electron density around ZN A 1002 (B):**

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



**Electron density around ZN A 1002 (A):**

$2mF_o-DF_c$  (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.