



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 14, 2025 – 01:10 pm BST

PDB ID : 9G3T / pdb\_00009g3t  
Title : Structure of the PRO-PRO endopeptidase (PPEP-3) E153A Y189F from *Geobacillus thermodenitrificans*  
Authors : Claushuis, B.; Wojtalla, F.; van Leeuwen, H.; Corver, J.; Baumann, U.; Hensbergen, P.  
Deposited on : 2024-07-12  
Resolution : 1.60 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
Mogul	:	1.8.4, CSD as541be (2020)
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)	:	2.44

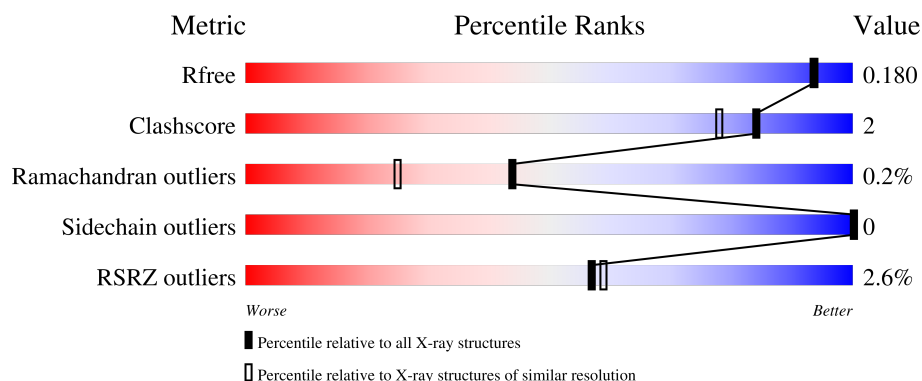
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


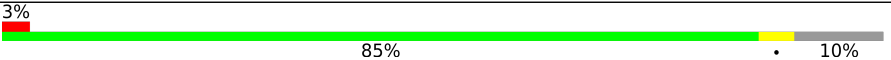
The reported resolution of this entry is 1.60 Å.

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	4274 (1.60-1.60)
Clashscore	180529	4682 (1.60-1.60)
Ramachandran outliers	177936	4583 (1.60-1.60)
Sidechain outliers	177891	4582 (1.60-1.60)
RSRZ outliers	164620	4272 (1.60-1.60)

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	230	 % 89% 7%
1	B	230	 3% 85% 10%

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7184 atoms, of which 3416 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 ATLF-like domain-containing protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	215	Total	C	H	N	O	S	0	5	0
			3492	1135	1718	310	327	2			
1	B	206	Total	C	H	N	O	S	0	1	0
			3308	1077	1626	291	313	1			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	MET	-	initiating methionine	UNP A4IN Y2
A	7	GLY	-	expression tag	UNP A4IN Y2
A	8	SER	-	expression tag	UNP A4IN Y2
A	9	SER	-	expression tag	UNP A4IN Y2
A	10	HIS	-	expression tag	UNP A4IN Y2
A	11	HIS	-	expression tag	UNP A4IN Y2
A	12	HIS	-	expression tag	UNP A4IN Y2
A	13	HIS	-	expression tag	UNP A4IN Y2
A	14	HIS	-	expression tag	UNP A4IN Y2
A	15	HIS	-	expression tag	UNP A4IN Y2
A	16	SER	-	expression tag	UNP A4IN Y2
A	17	SER	-	expression tag	UNP A4IN Y2
A	18	GLY	-	expression tag	UNP A4IN Y2
A	19	LEU	-	expression tag	UNP A4IN Y2
A	20	VAL	-	expression tag	UNP A4IN Y2
A	21	PRO	-	expression tag	UNP A4IN Y2
A	22	ARG	-	expression tag	UNP A4IN Y2
A	23	GLY	-	expression tag	UNP A4IN Y2
A	24	SER	-	expression tag	UNP A4IN Y2
A	25	HIS	-	expression tag	UNP A4IN Y2
A	26	MET	-	expression tag	UNP A4IN Y2
A	154	ALA	GLU	engineered mutation	UNP A4IN Y2
A	190	PHE	TYR	engineered mutation	UNP A4IN Y2
B	6	MET	-	initiating methionine	UNP A4IN Y2
B	7	GLY	-	expression tag	UNP A4IN Y2

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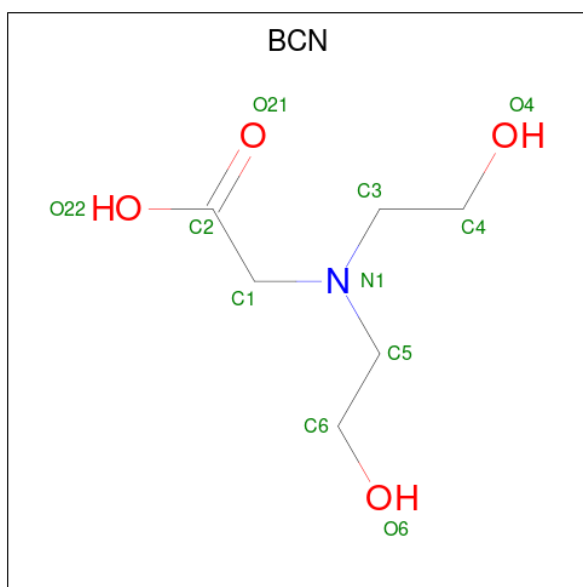
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Chain	Residue	Modelled	Actual	Comment	Reference
B	8	SER	-	expression tag	UNP A4IN Y2
B	9	SER	-	expression tag	UNP A4IN Y2
B	10	HIS	-	expression tag	UNP A4IN Y2
B	11	HIS	-	expression tag	UNP A4IN Y2
B	12	HIS	-	expression tag	UNP A4IN Y2
B	13	HIS	-	expression tag	UNP A4IN Y2
B	14	HIS	-	expression tag	UNP A4IN Y2
B	15	HIS	-	expression tag	UNP A4IN Y2
B	16	SER	-	expression tag	UNP A4IN Y2
B	17	SER	-	expression tag	UNP A4IN Y2
B	18	GLY	-	expression tag	UNP A4IN Y2
B	19	LEU	-	expression tag	UNP A4IN Y2
B	20	VAL	-	expression tag	UNP A4IN Y2
B	21	PRO	-	expression tag	UNP A4IN Y2
B	22	ARG	-	expression tag	UNP A4IN Y2
B	23	GLY	-	expression tag	UNP A4IN Y2
B	24	SER	-	expression tag	UNP A4IN Y2
B	25	HIS	-	expression tag	UNP A4IN Y2
B	26	MET	-	expression tag	UNP A4IN Y2
B	154	ALA	GLU	engineered mutation	UNP A4IN Y2
B	190	PHE	TYR	engineered mutation	UNP A4IN Y2

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

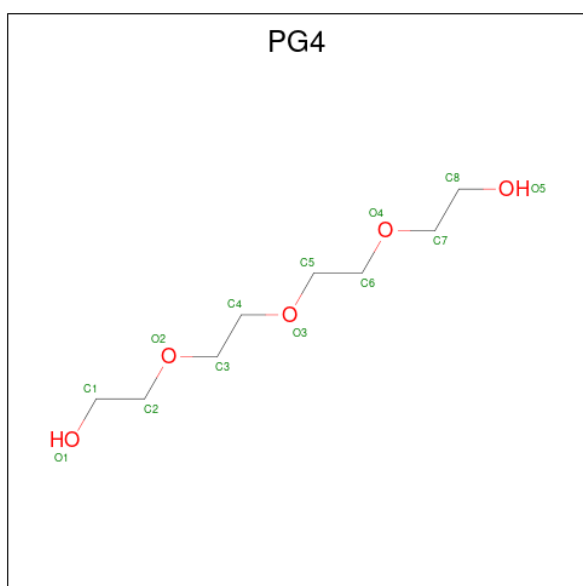
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

- Molecule 3 is BICINE (CCD ID: BCN) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			23	6	12	1	4		
3	B	1	Total	C	H	N	O	0	0
			23	6	12	1	4		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula:  $C_8H_{18}O_5$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			31	8	18	5		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		

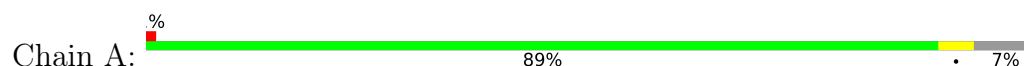
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	137	Total	O	0	0
			137	137		
6	B	117	Total	O	0	0
			117	117		

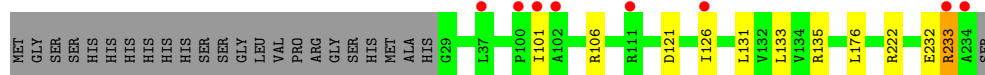
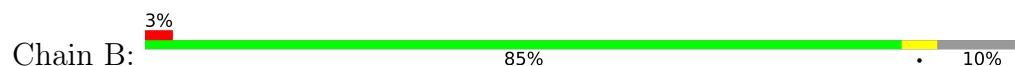
### 3 Residue-property plots [i](#)

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: ATLF-like domain-containing protein



- Molecule 1: ATLF-like domain-containing protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	125.62Å 125.62Å 63.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	62.81 – 1.60 62.81 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (62.81-1.60) 100.0 (62.81-1.60)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.38 (at 1.60Å)	Xtriage
Refinement program	PHENIX (1.21.2_5419: ???)	Depositor
R, $R_{free}$	0.157 , 0.177 0.158 , 0.180	Depositor DCC
$R_{free}$ test set	64980 reflections (3.47%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.2	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 42.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7184	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.12% 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: ZN, PG4, BCN, PEG

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	0.41	0/1832	0.56	0/2489
1	B	0.39	0/1731	0.58	0/2353
All	All	0.40	0/3563	0.57	0/4842

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	1774	1718	1724	7	0
1	B	1682	1626	1628	8	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	11	12	10	0	0
3	B	11	12	11	0	0
4	A	13	18	18	1	0
5	B	21	30	30	2	0
6	A	137	0	0	2	0
6	B	117	0	0	0	0
All	All	3768	3416	3421	15	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 (15) 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:B:101:ILE:HD13	1:B:131:LEU:HD23	1.76	0.66
1:A:94[A]:ASN:HB3	1:A:95:PRO:HD2	1.81	0.62
1:A:105:LEU:HD11	4:A:703:PG4:H22	1.85	0.59
1:B:101:ILE:HD11	1:B:133:LEU:HD11	1.83	0.59
1:B:135:ARG:HH21	5:B:301:PEG:H32	1.68	0.59
1:A:85:HIS:HE1	6:A:804:HOH:O	1.92	0.51
1:A:93:THR:HG22	5:B:301:PEG:H31	1.96	0.47
1:B:106:ARG:HG3	1:B:121:ASP:OD2	2.14	0.46
1:A:96:ILE:HG21	1:A:126[A]:ILE:HD12	1.97	0.46
1:B:126:ILE:HG13	1:B:126:ILE:O	2.15	0.45
1:B:232:GLU:O	1:B:233:ARG:CB	2.66	0.43
1:B:176:LEU:CD2	1:B:222:ARG:HB3	2.48	0.43
1:B:176:LEU:HD22	1:B:222:ARG:HB3	2.01	0.42
1:A:22:ARG:HB3	6:A:838:HOH:O	2.20	0.41
1:A:176:LEU:CD2	1:A:222:ARG:HB3	2.51	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	218/230 (95%)	215 (99%)	3 (1%)	0	100	100
1	B	205/230 (89%)	204 (100%)	0	1 (0%)	25	10
All	All	423/460 (92%)	419 (99%)	3 (1%)	1 (0%)	44	25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	233	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	188/197 (95%)	188 (100%)	0	100	100
1	B	178/197 (90%)	178 (100%)	0	100	100
All	All	366/394 (93%)	366 (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 (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	166	HIS
1	B	86	HIS

### 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 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	PEG	B	304	-	6,6,6	0.23	0	5,5,5	0.14	0
5	PEG	B	305	-	6,6,6	0.23	0	5,5,5	0.36	0
5	PEG	B	301	-	6,6,6	0.24	0	5,5,5	0.66	0
4	PG4	A	703	-	12,12,12	0.26	0	11,11,11	0.28	0
3	BCN	A	702	2	10,10,10	1.15	1 (10%)	11,11,11	1.04	0
3	BCN	B	303	2	10,10,10	1.17	1 (10%)	11,11,11	1.28	1 (9%)

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	PEG	B	304	-	-	2/4/4/4	-
5	PEG	B	305	-	-	2/4/4/4	-
5	PEG	B	301	-	-	2/4/4/4	-
4	PG4	A	703	-	-	6/10/10/10	-
3	BCN	A	702	2	-	0/10/10/10	-
3	BCN	B	303	2	-	4/10/10/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	702	BCN	C1-C2	2.40	1.56	1.51
3	B	303	BCN	C1-C2	2.36	1.56	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	303	BCN	C6-C5-N1	2.71	123.14	113.40

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	303	BCN	C6-C5-N1-C1
5	B	305	PEG	O1-C1-C2-O2
4	A	703	PG4	O3-C5-C6-O4
4	A	703	PG4	O2-C3-C4-O3
5	B	301	PEG	O2-C3-C4-O4
5	B	304	PEG	O2-C3-C4-O4
3	B	303	BCN	N1-C3-C4-O4
5	B	301	PEG	O1-C1-C2-O2
5	B	305	PEG	O2-C3-C4-O4
4	A	703	PG4	C1-C2-O2-C3
4	A	703	PG4	C5-C6-O4-C7
4	A	703	PG4	C3-C4-O3-C5
5	B	304	PEG	C1-C2-O2-C3
3	B	303	BCN	C6-C5-N1-C3
3	B	303	BCN	N1-C5-C6-O6
4	A	703	PG4	C6-C5-O3-C4

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	301	PEG	2	0
4	A	703	PG4	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, 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	215/230 (93%)	-0.27	3 (1%) 73 76	11, 25, 47, 70	5 (2%)
1	B	206/230 (89%)	-0.18	8 (3%) 44 44	16, 27, 57, 92	1 (0%)
All	All	421/460 (91%)	-0.23	11 (2%) 57 59	11, 26, 52, 92	6 (1%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	101	ILE	5.3
1	A	21	PRO	5.0
1	B	102	ALA	3.8
1	B	100	PRO	3.4
1	A	37	LEU	3.0
1	A	61	PHE	2.7
1	B	126	ILE	2.7
1	B	37	LEU	2.6
1	B	234	ALA	2.6
1	B	111	ARG	2.2
1	B	233	ARG	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

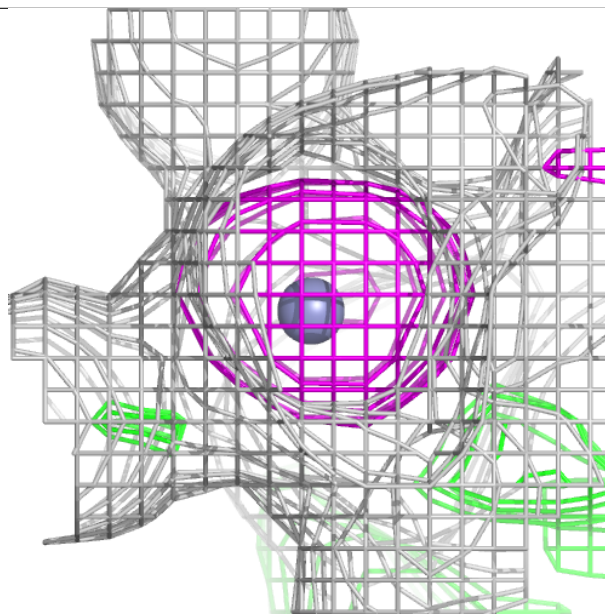
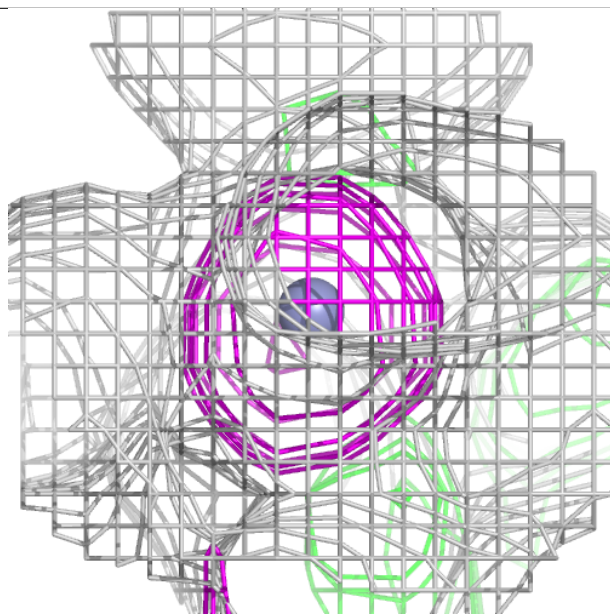
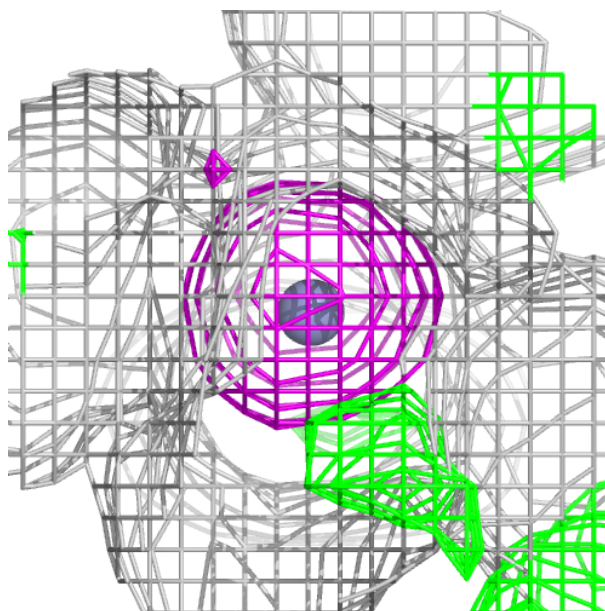
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
5	PEG	B	301	7/7	0.83	0.24	25,41,63,63	17
5	PEG	B	304	7/7	0.83	0.15	47,60,86,86	0
4	PG4	A	703	13/13	0.84	0.17	41,63,75,76	0
5	PEG	B	305	7/7	0.85	0.16	53,69,76,76	0
3	BCN	A	702	11/11	0.86	0.16	25,44,56,61	23
3	BCN	B	303	11/11	0.92	0.11	25,37,54,64	0
2	ZN	A	701	1/1	1.00	0.09	21,21,21,21	0
2	ZN	B	302	1/1	1.00	0.10	19,19,19,19	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 701:**

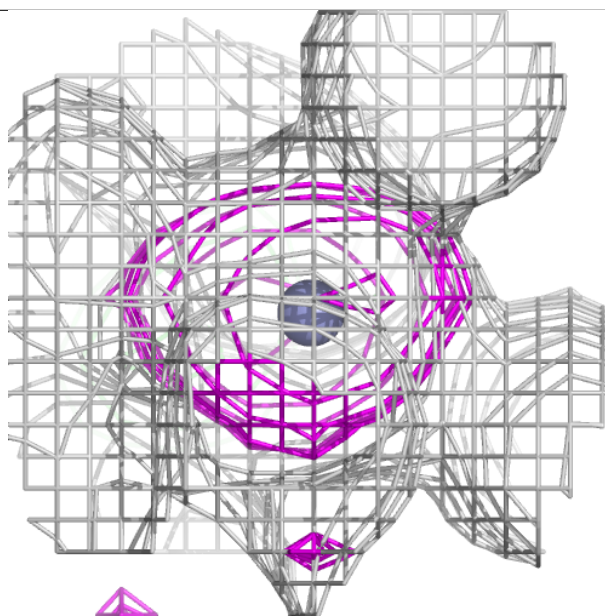
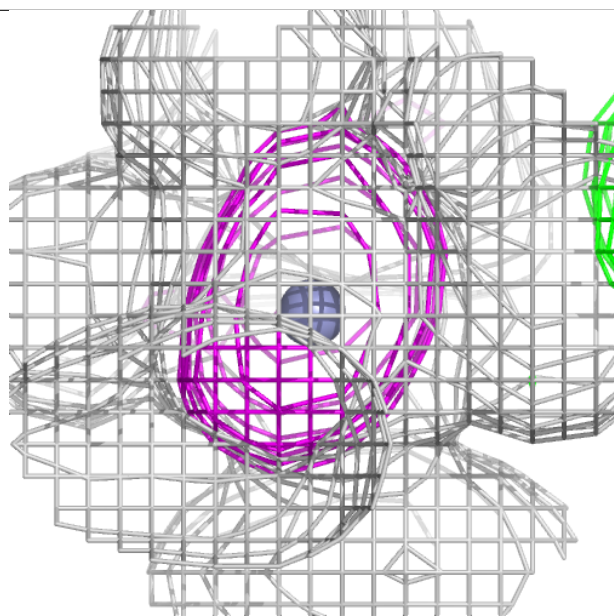
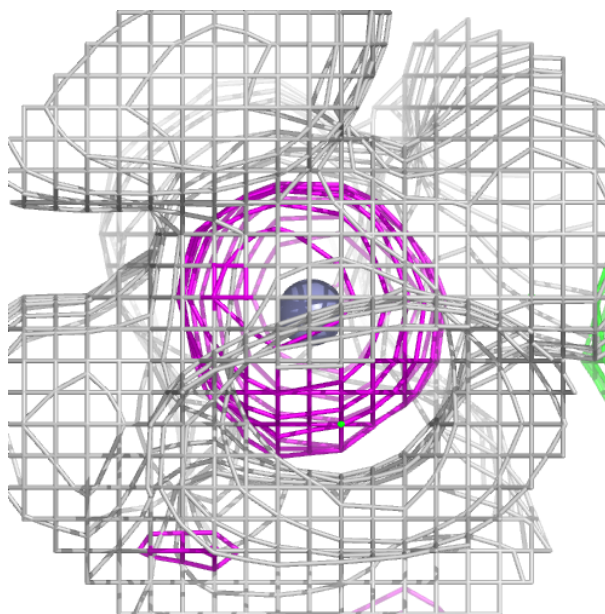
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around ZN B 302:**

$2mF_o-DF_c$  (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.