



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:15 AM UTC

PDB ID : 7S1T / pdb_00007s1t
Title : Structure of the human POT1-TPP1 complex
Authors : Aramburu, T.; Skordalakes, E.
Deposited on : 2021-09-02
Resolution : 2.90 Å(reported)

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

We welcome your comments at 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>.

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

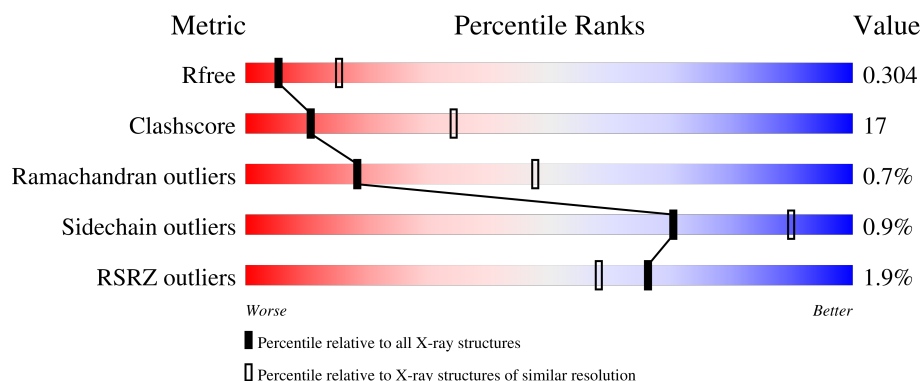
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	313	71% 25% .
1	D	313	65% 30% ..
1	G	313	66% 30% .
1	J	313	62% 35% .
2	B	93	51% 28% 20%

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Mol	Chain	Length	Quality of chain
2	E	93	2% 52% 28% 20%
2	H	93	3% 48% 28% 20%
2	K	93	3% 60% 19% 20%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11776 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 Protection of telomeres protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	302	Total	C	N	O	S	0	0	0
			2393	1528	398	451	16			
1	D	302	Total	C	N	O	S	0	0	0
			2393	1528	398	451	16			
1	G	302	Total	C	N	O	S	0	0	0
			2393	1528	398	451	16			
1	J	302	Total	C	N	O	S	0	0	0
			2393	1528	398	451	16			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	322	SER	-	expression tag	UNP Q9NUX5
A	323	ASN	-	expression tag	UNP Q9NUX5
A	324	ILE	-	expression tag	UNP Q9NUX5
D	322	SER	-	expression tag	UNP Q9NUX5
D	323	ASN	-	expression tag	UNP Q9NUX5
D	324	ILE	-	expression tag	UNP Q9NUX5
G	322	SER	-	expression tag	UNP Q9NUX5
G	323	ASN	-	expression tag	UNP Q9NUX5
G	324	ILE	-	expression tag	UNP Q9NUX5
J	322	SER	-	expression tag	UNP Q9NUX5
J	323	ASN	-	expression tag	UNP Q9NUX5
J	324	ILE	-	expression tag	UNP Q9NUX5

- Molecule 2 is a protein called Adrenocortical dysplasia protein homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	74	Total	C	N	O	S	0	0	0
			550	338	91	114	7			
2	E	74	Total	C	N	O	S	0	0	0
			550	338	91	114	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	74	Total	C	N	O	S	0	0	0
			550	338	91	114	7			
2	K	74	Total	C	N	O	S	0	0	0
			550	338	91	114	7			

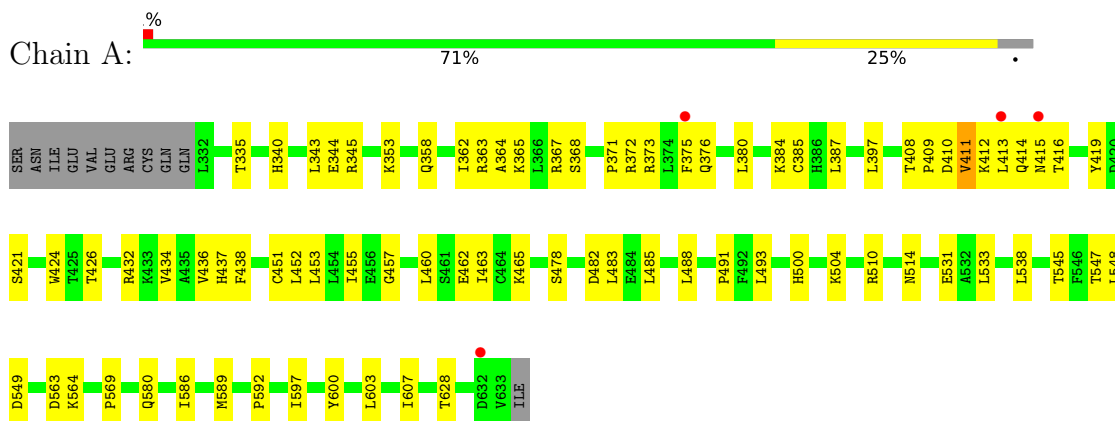
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		
3	G	1	Total	Zn	0	0
			1	1		
3	J	1	Total	Zn	0	0
			1	1		

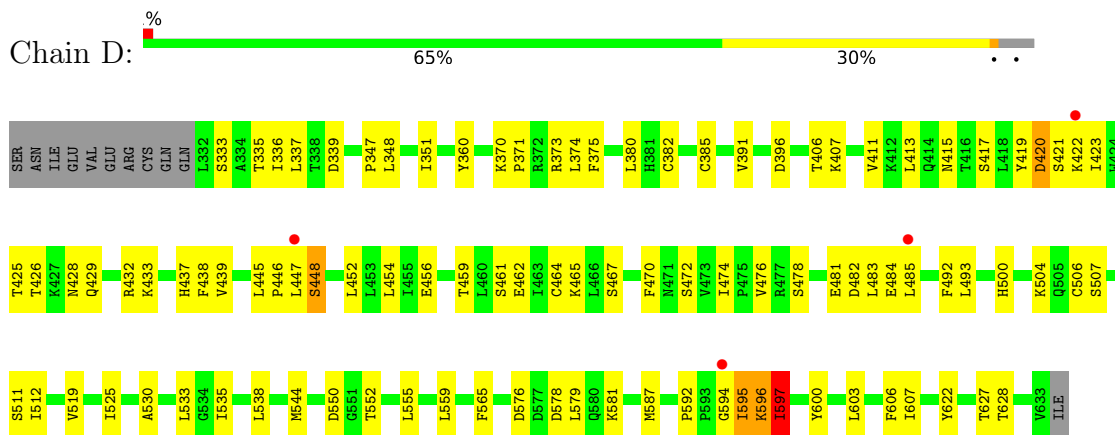
3 Residue-property plots

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.

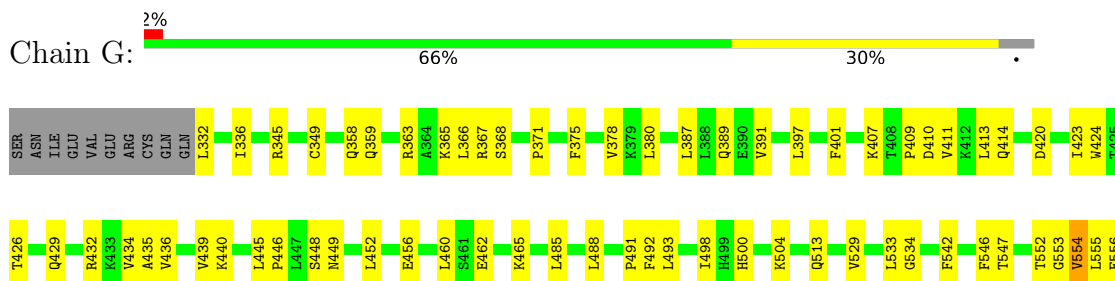
• Molecule 1: Protection of telomeres protein 1



• Molecule 1: Protection of telomeres protein 1

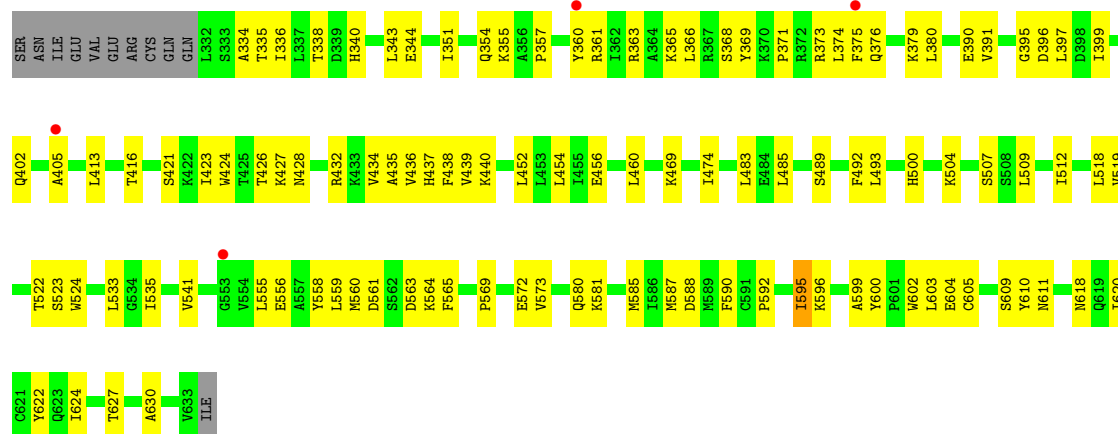


• Molecule 1: Protection of telomeres protein 1

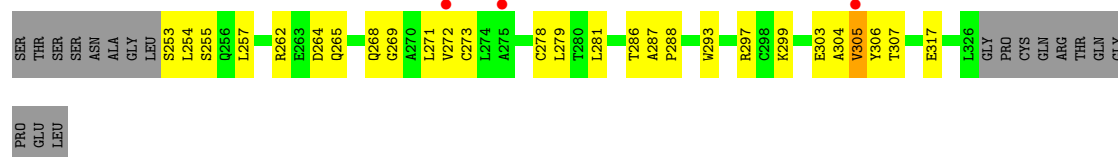




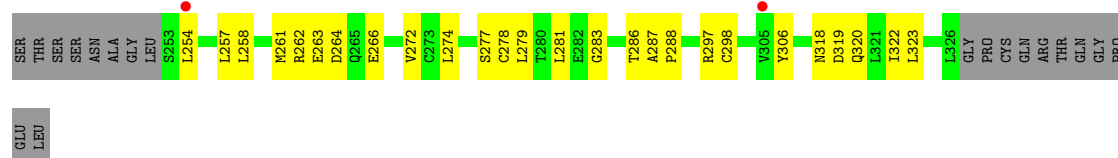
• Molecule 1: Protection of telomeres protein 1



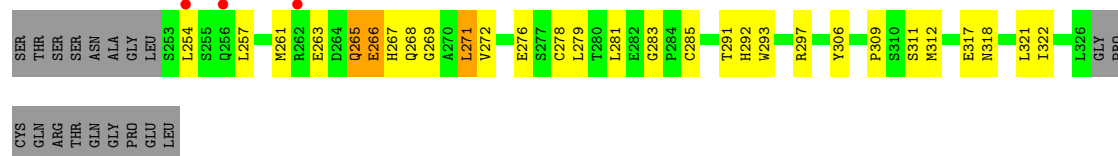
• Molecule 2: Adrenocortical dysplasia protein homolog



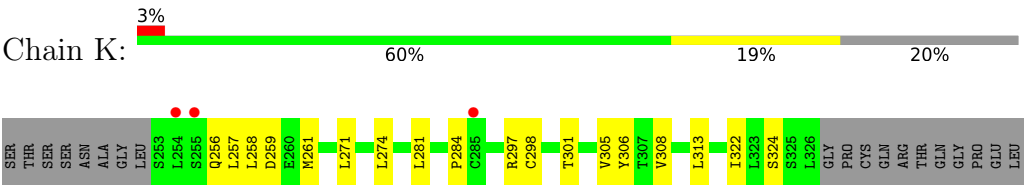
• Molecule 2: Adrenocortical dysplasia protein homolog



• Molecule 2: Adrenocortical dysplasia protein homolog



● Molecule 2: Adrenocortical dysplasia protein homolog



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	70.88Å 70.98Å 103.79Å 76.76° 84.61° 70.55°	Depositor
Resolution (Å)	36.44 – 2.90 36.44 – 2.90	Depositor EDS
% Data completeness (in resolution range)	89.7 (36.44-2.90) 89.7 (36.44-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.250 , 0.307 0.249 , 0.304	Depositor DCC
R_{free} test set	1848 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	69.0	Xtriage
Anisotropy	0.225	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11776	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.09% 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

5.1 Standard geometry

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	0.20	0/2443	0.45	0/3314
1	D	0.21	0/2443	0.47	3/3314 (0.1%)
1	G	0.27	0/2443	0.44	1/3314 (0.0%)
1	J	0.25	0/2443	0.47	1/3314 (0.0%)
2	B	0.51	0/558	0.61	1/760 (0.1%)
2	E	0.25	0/558	0.48	0/760
2	H	0.60	0/558	0.68	1/760 (0.1%)
2	K	0.14	0/558	0.31	0/760
All	All	0.28	0/12004	0.48	7/16296 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	271	LEU	N-CA-C	-7.16	101.87	111.96
1	G	564	LYS	N-CA-C	6.36	122.52	114.31
1	D	596	LYS	N-CA-C	6.07	119.45	110.46
1	D	597	ILE	N-CA-C	5.89	121.60	109.34
1	J	355	LYS	N-CA-C	5.25	117.07	110.24

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	2393	0	2404	87	0
1	D	2393	0	2404	92	0
1	G	2393	0	2404	83	0
1	J	2393	0	2404	88	0
2	B	550	0	537	27	0
2	E	550	0	537	32	0
2	H	550	0	537	30	0
2	K	550	0	537	19	0
3	A	1	0	0	0	0
3	D	1	0	0	0	0
3	G	1	0	0	0	0
3	J	1	0	0	0	0
All	All	11776	0	11764	392	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 17.

The worst 5 of 392 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:408:THR:CG2	1:A:409:PRO:HD2	1.61	1.31
1:G:359:GLN:OE1	1:G:608:LYS:HE2	1.48	1.09
1:J:375:PHE:HD1	2:K:297:ARG:HG2	1.17	1.05
1:J:375:PHE:CD1	2:K:297:ARG:HG2	1.91	1.05
1:A:408:THR:HG23	1:A:409:PRO:HD2	1.08	1.04

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	300/313 (96%)	276 (92%)	22 (7%)	2 (1%)	18 48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	300/313 (96%)	274 (91%)	21 (7%)	5 (2%)	7	26
1	G	300/313 (96%)	271 (90%)	28 (9%)	1 (0%)	36	65
1	J	300/313 (96%)	262 (87%)	37 (12%)	1 (0%)	36	65
2	B	72/93 (77%)	68 (94%)	4 (6%)	0	100	100
2	E	72/93 (77%)	67 (93%)	5 (7%)	0	100	100
2	H	72/93 (77%)	60 (83%)	11 (15%)	1 (1%)	9	30
2	K	72/93 (77%)	67 (93%)	5 (7%)	0	100	100
All	All	1488/1624 (92%)	1345 (90%)	133 (9%)	10 (1%)	18	48

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	448	SER
1	A	414	GLN
2	H	263	GLU
1	A	411	VAL
1	D	339	ASP

5.3.2 Protein sidechains ⓘ

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	275/286 (96%)	275 (100%)	0	100	100
1	D	275/286 (96%)	272 (99%)	3 (1%)	65	88
1	G	275/286 (96%)	274 (100%)	1 (0%)	84	94
1	J	275/286 (96%)	275 (100%)	0	100	100
2	B	64/79 (81%)	60 (94%)	4 (6%)	16	45
2	E	64/79 (81%)	64 (100%)	0	100	100
2	H	64/79 (81%)	60 (94%)	4 (6%)	16	45
2	K	64/79 (81%)	64 (100%)	0	100	100
All	All	1356/1460 (93%)	1344 (99%)	12 (1%)	70	90

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	307	THR
2	H	265	GLN
2	H	268	GLN
2	H	266	GLU
1	G	554	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	449	ASN
2	K	267	HIS
1	G	376	GLN
2	B	318	ASN
1	D	619	GLN

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 4 ligands modelled in this entry, 4 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, 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	302/313 (96%)	0.23	4 (1%) 75 67	40, 64, 112, 164	0
1	D	302/313 (96%)	0.24	4 (1%) 75 67	41, 68, 115, 161	0
1	G	302/313 (96%)	0.24	5 (1%) 69 61	39, 72, 105, 161	0
1	J	302/313 (96%)	0.40	4 (1%) 75 67	39, 77, 134, 158	0
2	B	74/93 (79%)	0.51	3 (4%) 41 33	48, 78, 101, 115	0
2	E	74/93 (79%)	0.46	2 (2%) 56 47	43, 79, 118, 125	0
2	H	74/93 (79%)	0.45	3 (4%) 41 33	51, 82, 107, 113	0
2	K	74/93 (79%)	0.51	3 (4%) 41 33	54, 82, 103, 171	0
All	All	1504/1624 (92%)	0.32	28 (1%) 66 58	39, 71, 121, 171	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	422	LYS	5.5
1	G	608	LYS	3.2
2	H	256	GLN	3.2
1	D	485	LEU	3.1
1	J	375	PHE	3.1

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 oligosaccharides in this entry.

6.4 Ligands

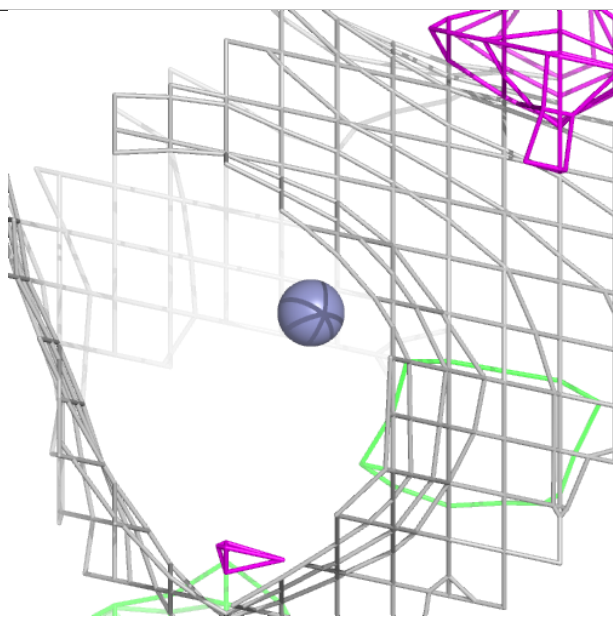
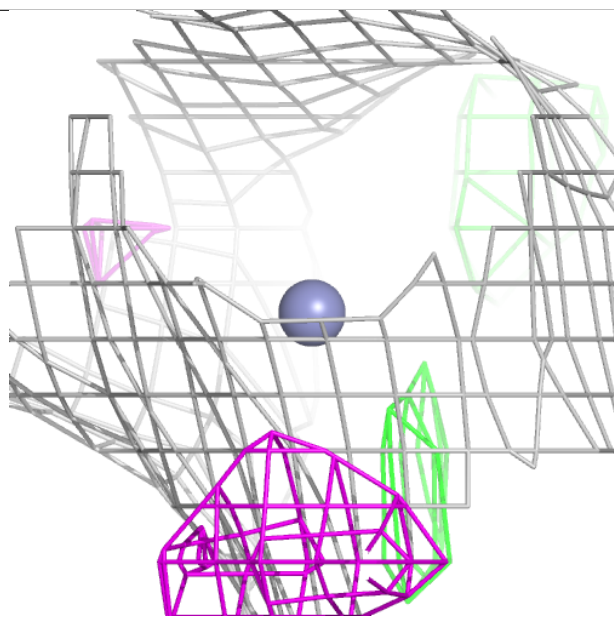
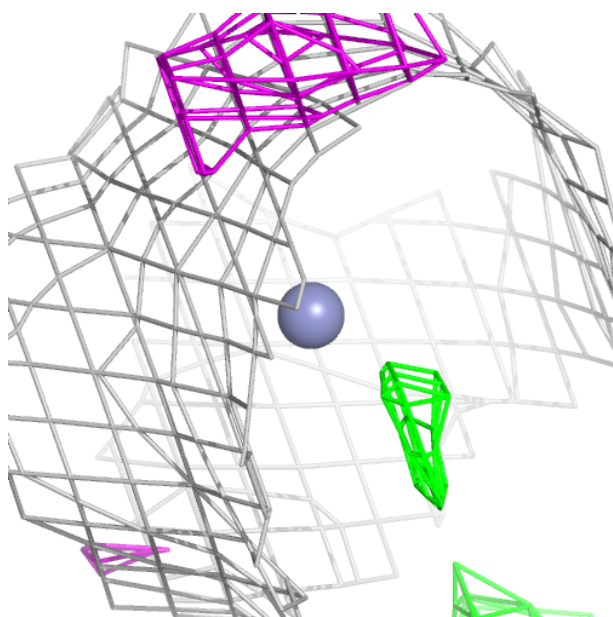
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ZN	D	701	1/1	0.97	0.05	69,69,69,69	0
3	ZN	G	701	1/1	0.97	0.09	72,72,72,72	0
3	ZN	A	701	1/1	0.98	0.04	61,61,61,61	0
3	ZN	J	701	1/1	0.98	0.06	69,69,69,69	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.

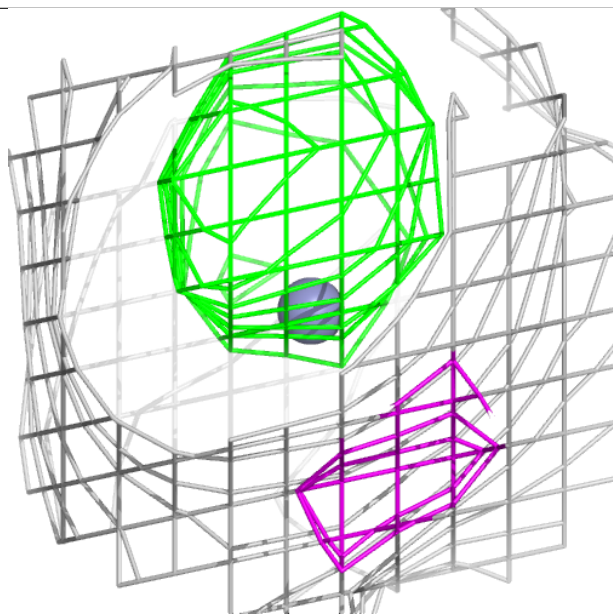
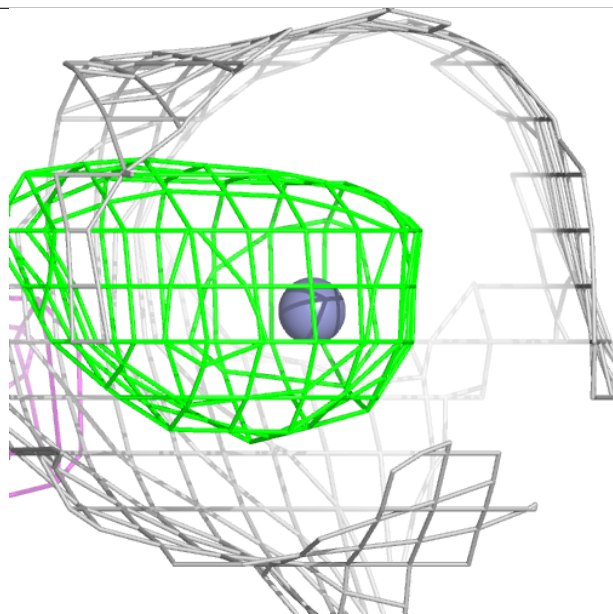
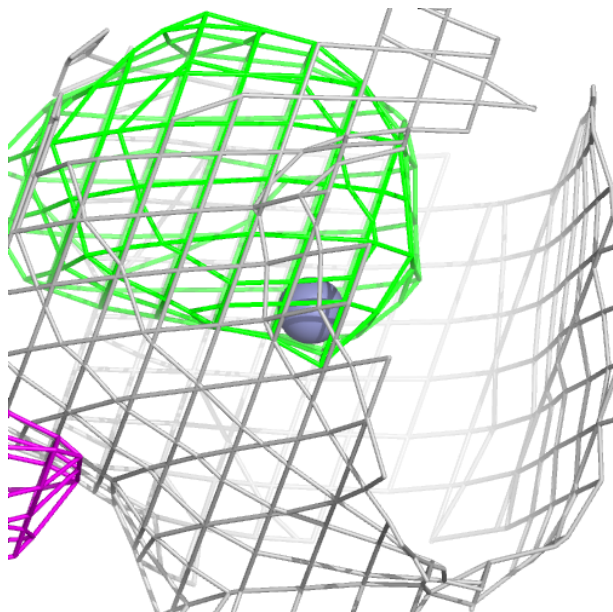
Electron density around ZN D 701:

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



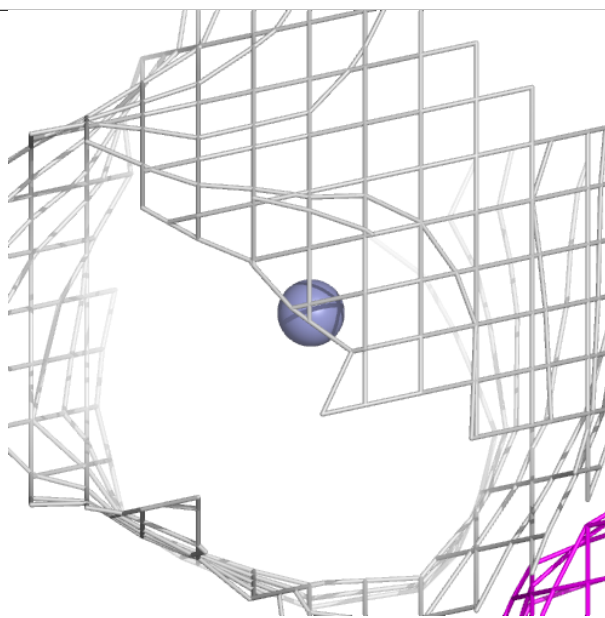
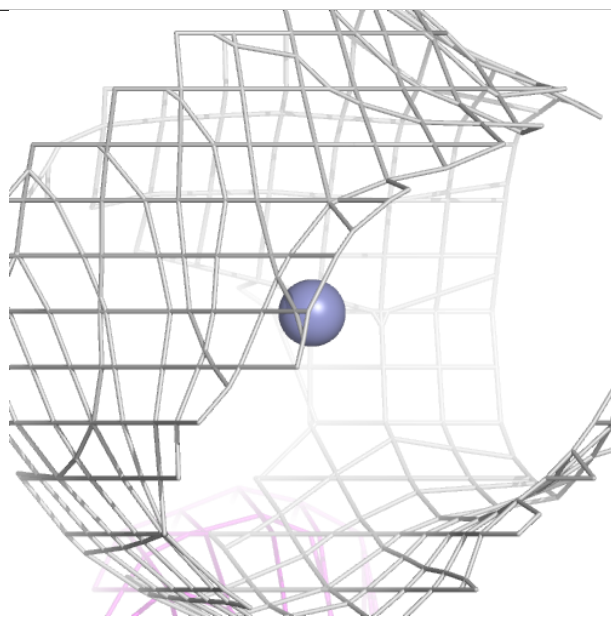
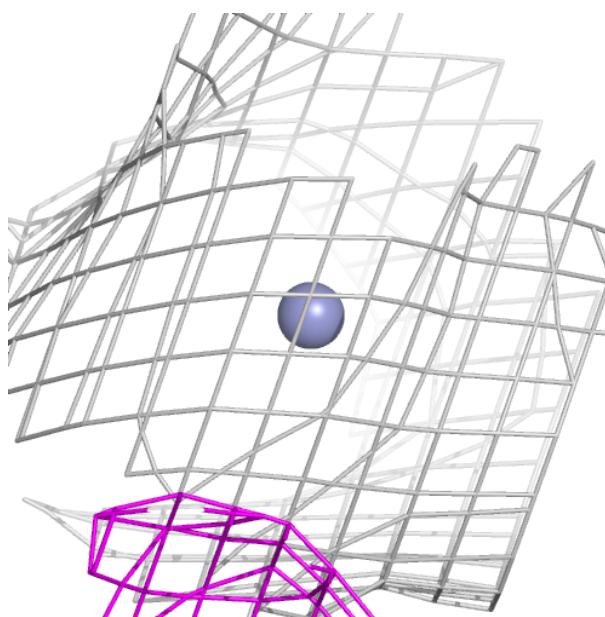
Electron density around ZN G 701:

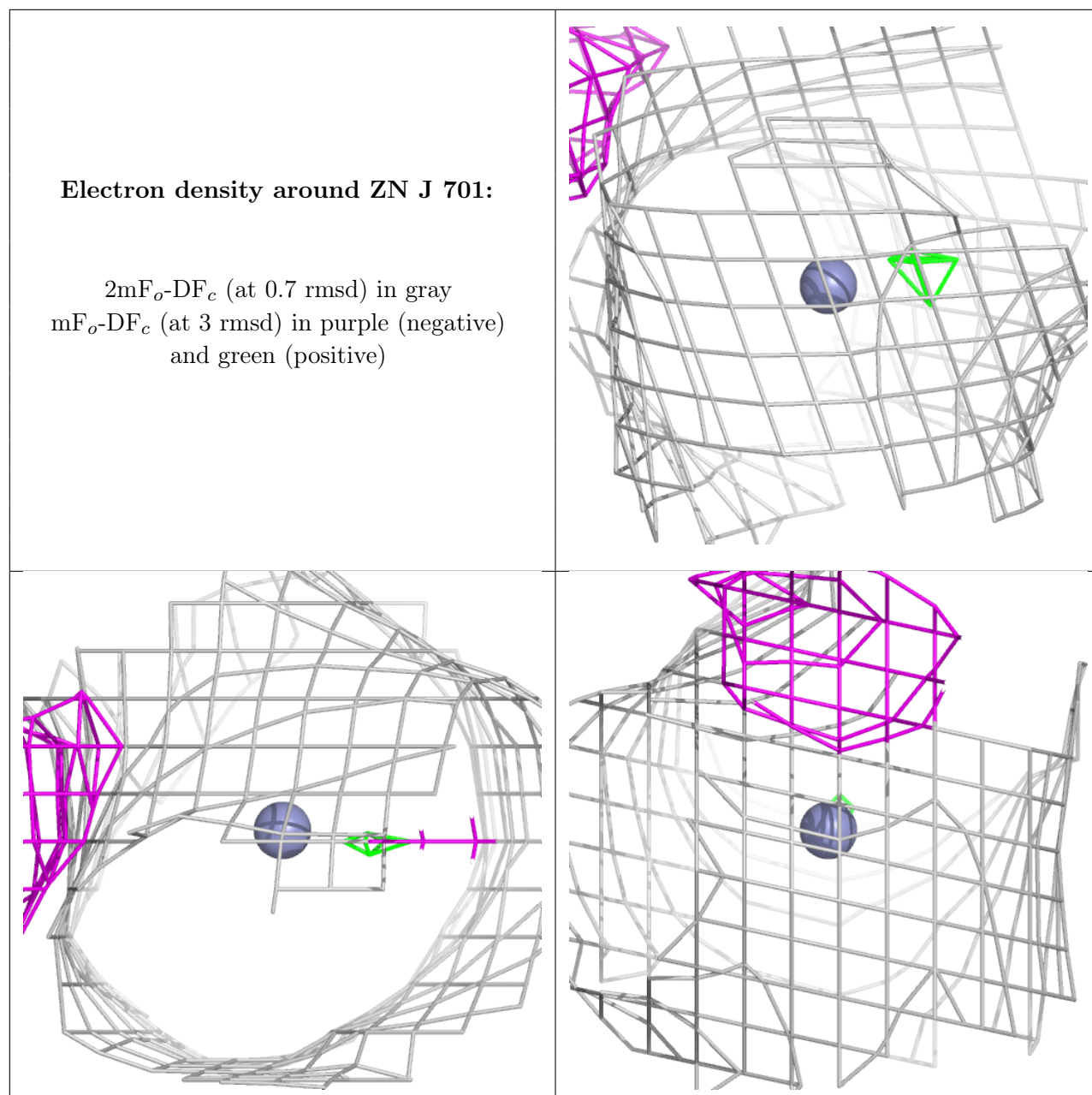
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN 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)





6.5 Other polymers ⓘ

There are no such residues in this entry.