



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:44 AM UTC

PDB ID : 7EYI / pdb_00007eyi
Title : Crystal structure of ZBTB7A in complex with gamma-globin -200 sequence element with C-194A mutation
Authors : Yang, Y.; Shi, Y.Y.
Deposited on : 2021-05-31
Resolution : 2.40 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

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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

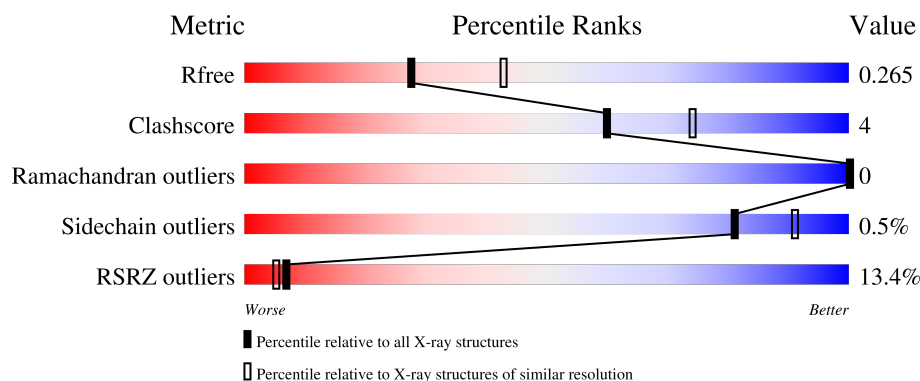
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	G	130	8% 77% 8% 15%
1	H	130	20% 72% 14% 14%
2	A	18	56% 33% 11%
2	C	18	6% 72% 28%
3	B	18	83% 6% 11%

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Mol	Chain	Length	Quality of chain
3	D	18	6% 83% 17%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3251 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 Zinc finger and BTB domain-containing protein 7A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	111	Total	C	N	O	S	0	0	0
			905	560	182	150	13			
1	H	112	Total	C	N	O	S	0	0	0
			911	563	183	152	13			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	378	GLY	-	expression tag	UNP O95365
G	379	SER	-	expression tag	UNP O95365
G	380	HIS	-	expression tag	UNP O95365
G	381	MET	-	expression tag	UNP O95365
G	507	TRP	-	expression tag	UNP O95365
H	378	GLY	-	expression tag	UNP O95365
H	379	SER	-	expression tag	UNP O95365
H	380	HIS	-	expression tag	UNP O95365
H	381	MET	-	expression tag	UNP O95365
H	507	TRP	-	expression tag	UNP O95365

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*TP*AP*GP*GP*GP*CP*CP*CP*CP*TP*TP*CP*CP*CP*AP*AP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	16	Total	C	N	O	P	0	0	0
			321	152	58	95	16			
2	C	18	Total	C	N	O	P	0	0	0
			362	172	65	107	18			

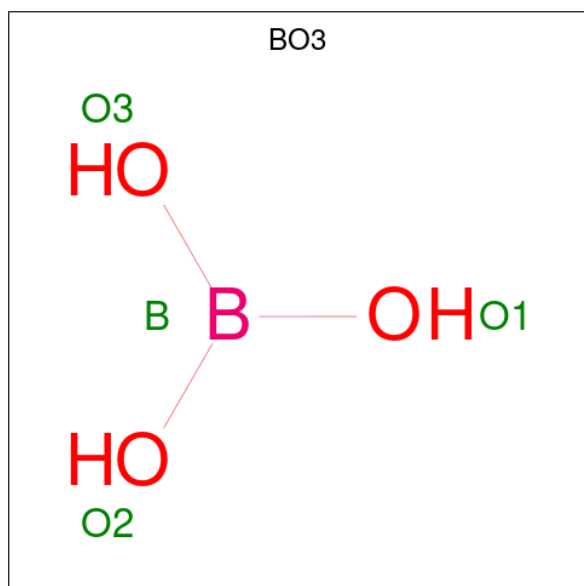
- Molecule 3 is a DNA chain called DNA (5'-D(*TP*GP*TP*TP*GP*GP*GP*AP*AP*GP*GP*GP*GP*CP*CP*CP*TP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	16	Total	C	N	O	P	0	0	0
			335	157	65	97	16			
3	D	18	Total	C	N	O	P	0	0	0
			376	177	72	109	18			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	4	Total	Zn	0	0
			4	4		
4	H	4	Total	Zn	0	0
			4	4		

- Molecule 5 is BORIC ACID (CCD ID: BO3) (formula: BH₃O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	B	O	0	0
			4	1	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	3	Total	O	0	0
			3	3		

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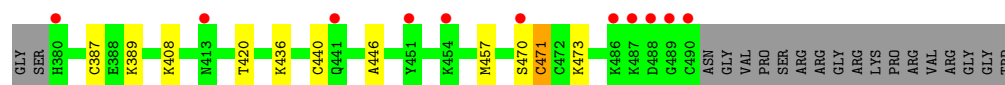
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	10	Total	O	0	0
			10	10		
6	A	3	Total	O	0	0
			3	3		
6	B	3	Total	O	0	0
			3	3		
6	C	5	Total	O	0	0
			5	5		
6	D	5	Total	O	0	0
			5	5		

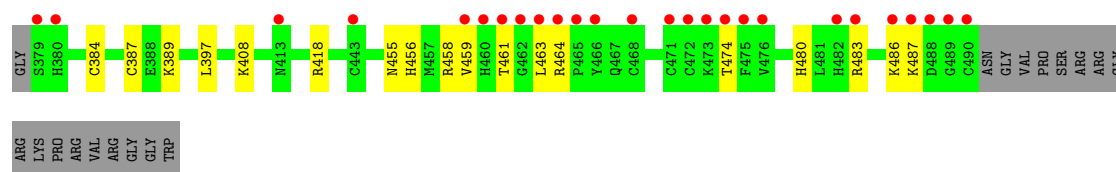
3 Residue-property plots [i](#)

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.

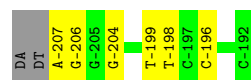
- Molecule 1: Zinc finger and BTB domain-containing protein 7A



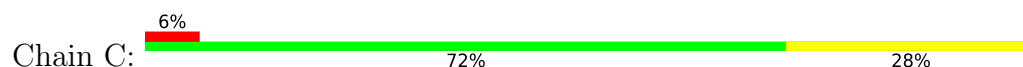
- Molecule 1: Zinc finger and BTB domain-containing protein 7A



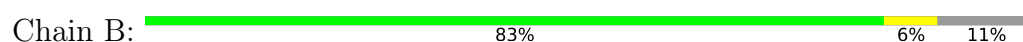
- Molecule 2: DNA (5'-D(*AP*TP*AP*GP*GP*GP*CP*CP*CP*CP*TP*TP*CP*CP*CP*AP*AP*C)-3')



- Molecule 2: DNA (5'-D(*AP*TP*AP*GP*GP*GP*CP*CP*CP*CP*TP*TP*CP*CP*CP*AP*AP*C)-3')

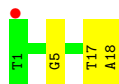
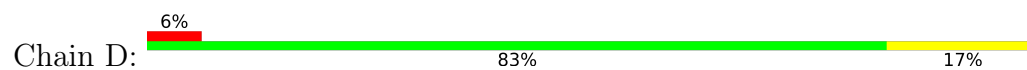


- Molecule 3: DNA (5'-D(*TP*GP*TP*TP*GP*GP*GP*AP*AP*GP*GP*GP*GP*CP*CP*CP*TP*A)-3')





- Molecule 3: DNA (5'-D(*TP*GP*TP*TP*GP*GP*GP*AP*AP*GP*GP*GP*GP*CP*CP*CP*TP*A)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	67.44Å 67.44Å 228.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.72 – 2.40 33.72 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.2 (33.72-2.40) 92.2 (33.72-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.95 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.16	Depositor
R, R_{free}	0.222 , 0.267 0.222 , 0.265	Depositor DCC
R_{free} test set	1029 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	39.0	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3251	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.82% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BO3, 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	G	0.34	0/927	0.53	1/1239 (0.1%)
1	H	0.11	0/933	0.31	0/1247
2	A	0.71	1/358 (0.3%)	0.68	0/548
2	C	0.17	0/404	0.34	0/619
3	B	0.18	0/376	0.33	0/580
3	D	0.17	0/422	0.33	0/651
All	All	0.32	1/3420 (0.0%)	0.43	1/4884 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	-204	DG	O3'-P	-5.12	1.53	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	471	CYS	CB-CA-C	-9.22	92.69	110.11

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	G	905	0	898	6	0
1	H	911	0	904	10	0
2	A	321	0	179	3	0
2	C	362	0	202	3	0
3	B	335	0	180	1	0
3	D	376	0	203	2	0
4	G	4	0	0	0	0
4	H	4	0	0	0	0
5	B	4	0	3	1	0
6	A	3	0	0	0	0
6	B	3	0	0	0	0
6	C	5	0	0	0	0
6	D	5	0	0	0	0
6	G	3	0	0	0	0
6	H	10	0	0	0	0
All	All	3251	0	2569	23	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 4.

All (23) 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:H:455:ASN:OD1	1:H:458:ARG:NH1	2.29	0.66
1:H:486:LYS:HG2	2:A:-196:DC:H5''	1.82	0.61
1:G:408:LYS:HG2	1:G:420:THR:HG22	1.83	0.61
1:H:408:LYS:O	1:H:418:ARG:NH1	2.37	0.58
1:H:461:THR:HB	1:H:463:LEU:HD12	1.85	0.58
1:G:436:LYS:HB2	1:G:446:ALA:HB1	1.88	0.54
1:H:480:HIS:NE2	3:D:5:DG:N7	2.49	0.53
2:C:-201:DC:H2'	2:C:-200:DC:C6	2.45	0.51
1:G:440:CYS:SG	1:G:457:MET:HE1	2.51	0.51
1:H:483:ARG:O	1:H:487:LYS:HB2	2.10	0.51
2:A:-199:DT:H2'	2:A:-198:DT:C6	2.46	0.50
1:H:456:HIS:O	1:H:459:VAL:HG22	2.12	0.48
1:G:471:CYS:HB3	1:G:473:LYS:H	1.78	0.48
2:C:-200:DC:H2'	2:C:-199:DT:C6	2.49	0.47
1:G:387:CYS:SG	1:G:389:LYS:HB2	2.55	0.46
1:H:387:CYS:SG	1:H:389:LYS:HB2	2.57	0.45
3:D:17:DT:H2''	3:D:18:DA:C8	2.54	0.43
2:A:-207:DA:H2''	2:A:-206:DG:C8	2.54	0.42
1:G:471:CYS:SG	1:G:473:LYS:HB2	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:6:DG:O6	5:B:101:BO3:O2	2.37	0.42
1:H:384:CYS:HA	1:H:397:LEU:HD11	2.03	0.41
1:H:464:ARG:HB3	1:H:474:THR:HG22	2.02	0.41
2:C:-197:DC:H2'	2:C:-196:DC:C6	2.55	0.41

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	G	109/130 (84%)	107 (98%)	2 (2%)	0	100	100
1	H	110/130 (85%)	105 (96%)	5 (4%)	0	100	100
All	All	219/260 (84%)	212 (97%)	7 (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	G	100/114 (88%)	99 (99%)	1 (1%)	68	84
1	H	101/114 (89%)	101 (100%)	0	100	100
All	All	201/228 (88%)	200 (100%)	1 (0%)	81	91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	470	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	441	GLN
1	G	467	GLN
1	G	482	HIS
1	H	413	ASN
1	H	442	GLN
1	H	482	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 9 ligands modelled in this entry, 8 are monoatomic - leaving 1 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	BO3	B	101	-	3,3,3	0.04	0	3,3,3	0.05	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

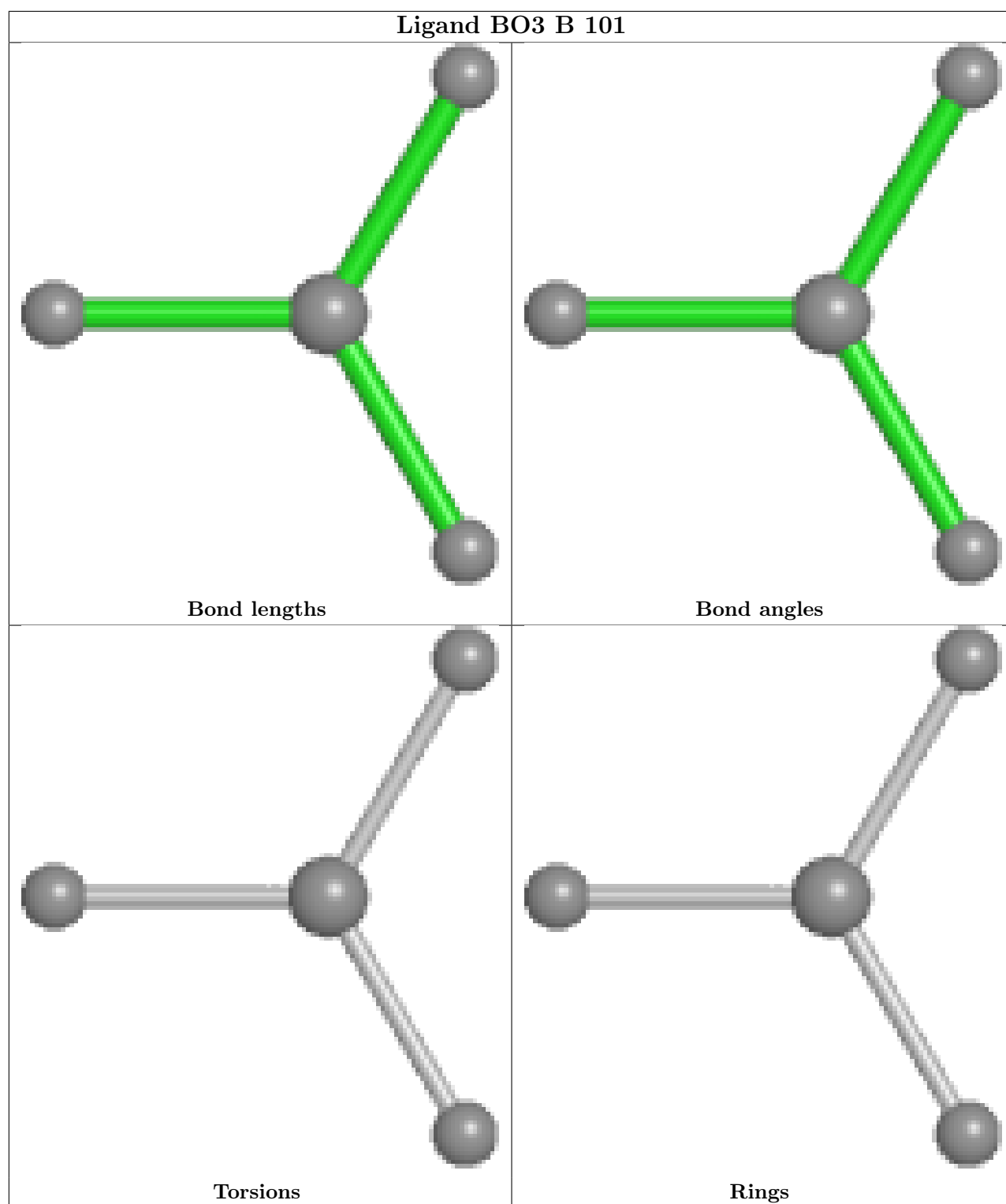
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	101	BO3	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

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, 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	G	111/130 (85%)	0.53	11 (9%) 13 9	26, 39, 75, 149	0
1	H	112/130 (86%)	0.95	26 (23%) 2 1	19, 39, 107, 162	0
2	A	16/18 (88%)	0.25	0 100 100	42, 49, 92, 124	0
2	C	18/18 (100%)	0.04	1 (5%) 30 26	34, 41, 58, 71	0
3	B	16/18 (88%)	-0.01	0 100 100	32, 43, 94, 117	0
3	D	18/18 (100%)	0.22	1 (5%) 30 26	27, 46, 69, 83	0
All	All	291/332 (87%)	0.60	39 (13%) 7 5	19, 41, 95, 162	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	489	GLY	5.3
1	G	489	GLY	5.0
1	H	490	CYS	5.0
1	H	488	ASP	4.6
1	H	379	SER	4.4
1	H	486	LYS	4.4
1	H	462	GLY	4.3
1	H	463	LEU	4.3
1	H	487	LYS	4.0
1	H	465	PRO	3.9
1	G	490	CYS	3.7
2	C	-209	DA	3.6
1	H	475	PHE	3.5
1	H	380	HIS	3.4
1	H	461	THR	3.3
1	G	487	LYS	3.2
1	H	474	THR	3.0
1	G	486	LYS	3.0
1	H	483	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	H	472	CYS	3.0
1	H	413	ASN	3.0
1	H	482	HIS	3.0
1	H	471	CYS	2.9
3	D	1	DT	2.9
1	G	380	HIS	2.8
1	G	488	ASP	2.8
1	H	464	ARG	2.7
1	H	468	CYS	2.7
1	G	454	LYS	2.6
1	H	466	TYR	2.6
1	G	470	SER	2.5
1	G	441	GLN	2.5
1	H	459	VAL	2.3
1	H	473	LYS	2.3
1	G	451	TYR	2.3
1	H	460	HIS	2.2
1	G	413	ASN	2.1
1	H	443	CYS	2.1
1	H	476	VAL	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, 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
4	ZN	G	604	1/1	0.89	0.11	79,79,79,79	0
4	ZN	H	604	1/1	0.89	0.11	107,107,107,107	0
5	BO3	B	101	4/4	0.91	0.12	27,31,32,38	0

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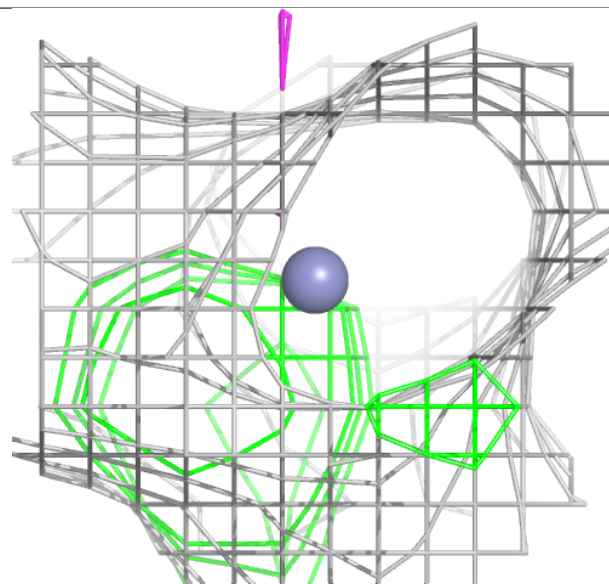
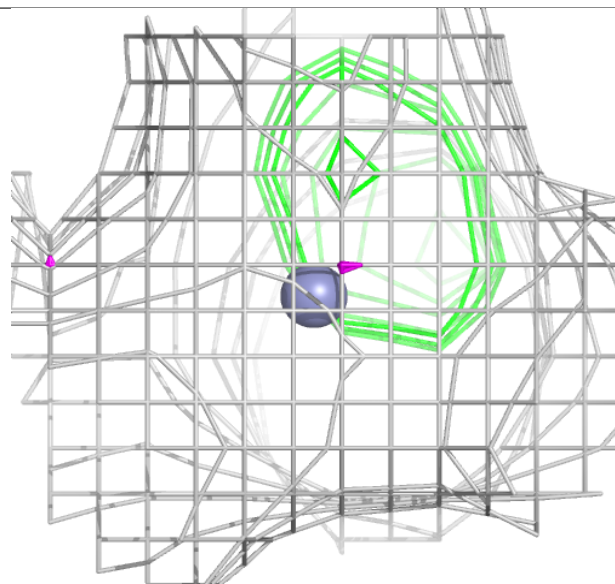
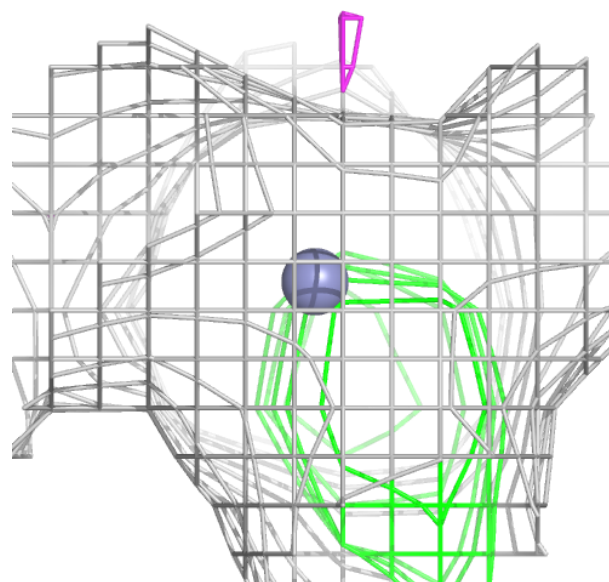
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ZN	G	602	1/1	0.94	0.06	40,40,40,40	0
4	ZN	H	601	1/1	0.97	0.04	32,32,32,32	0
4	ZN	G	603	1/1	0.98	0.03	36,36,36,36	0
4	ZN	H	602	1/1	0.98	0.03	42,42,42,42	0
4	ZN	G	601	1/1	0.99	0.02	27,27,27,27	0
4	ZN	H	603	1/1	0.99	0.03	23,23,23,23	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.

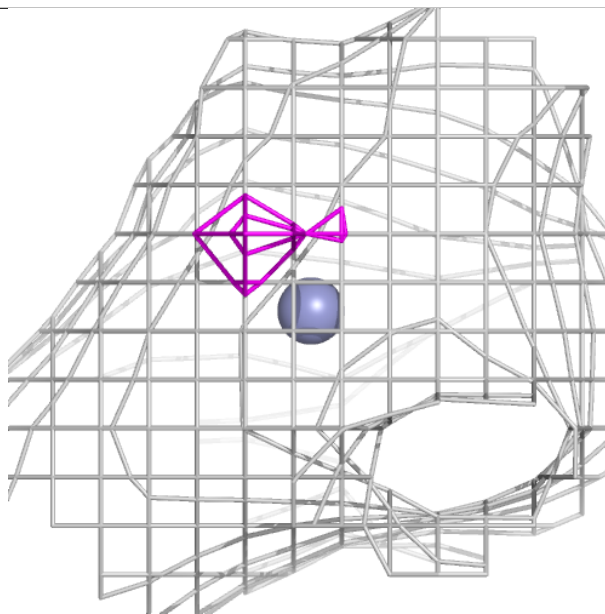
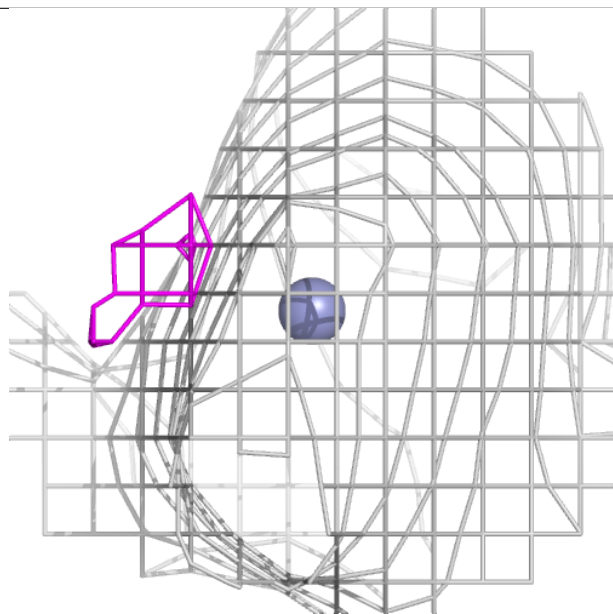
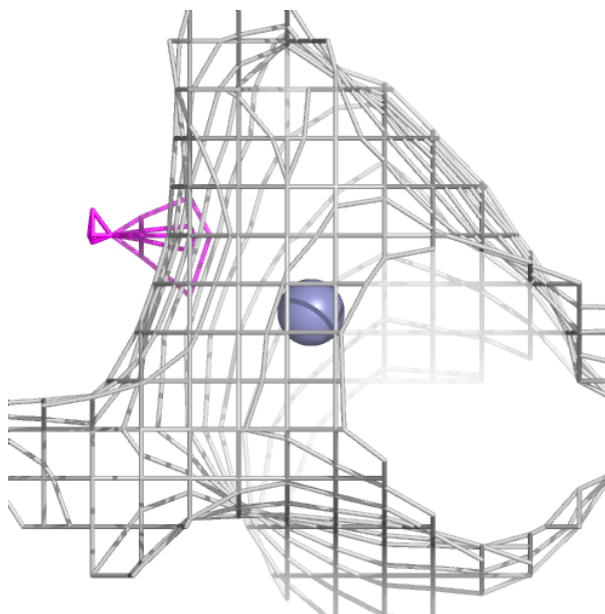
Electron density around ZN G 604:

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



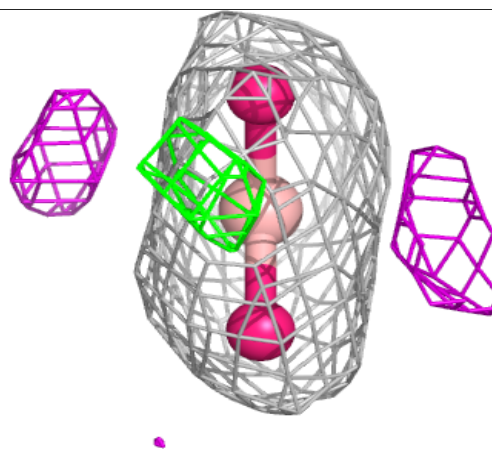
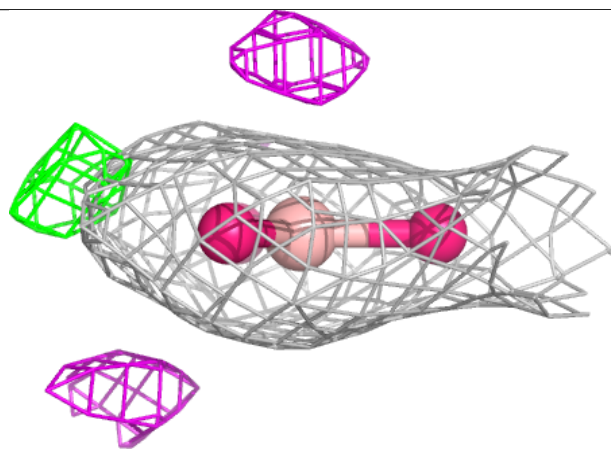
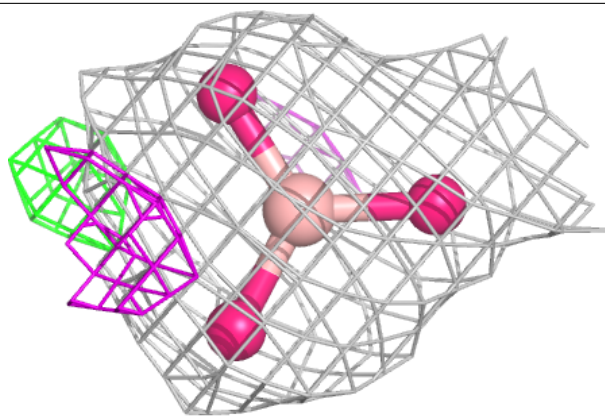
Electron density around ZN H 604:

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



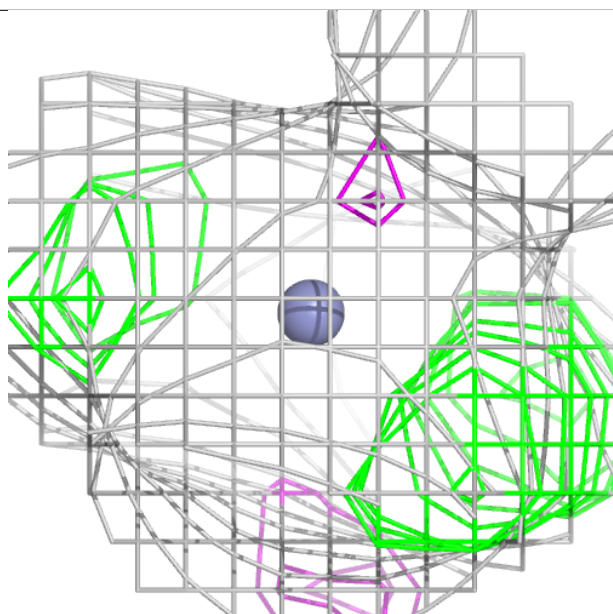
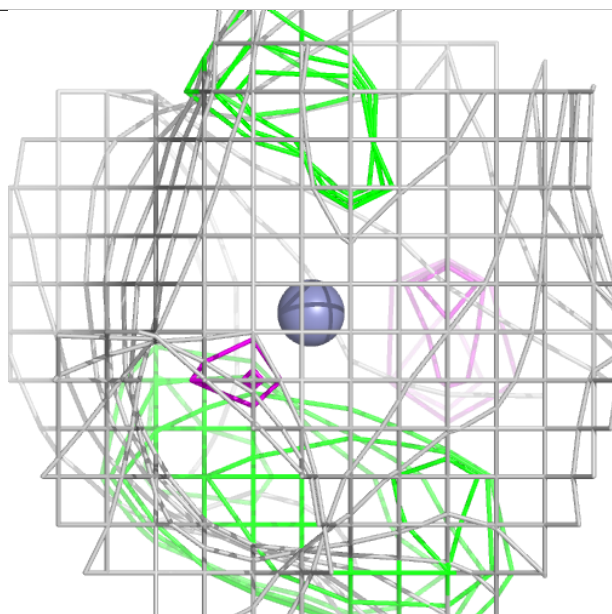
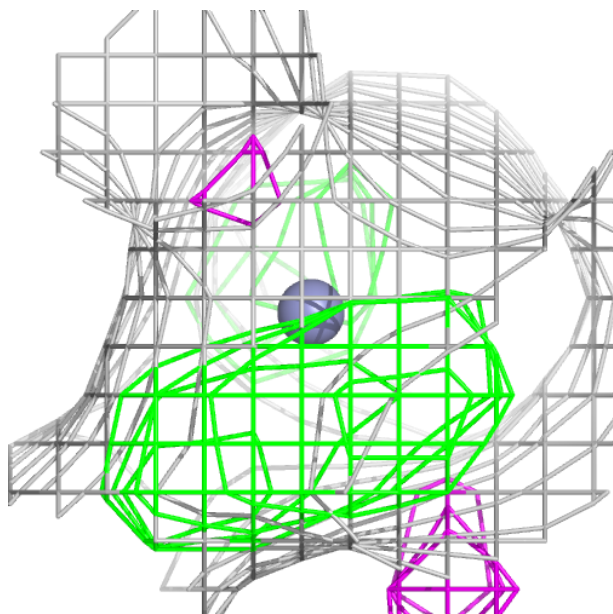
Electron density around BO3 B 101:

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



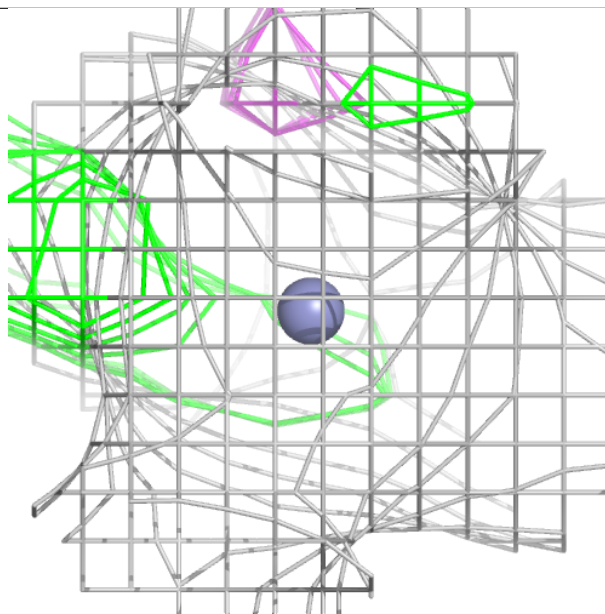
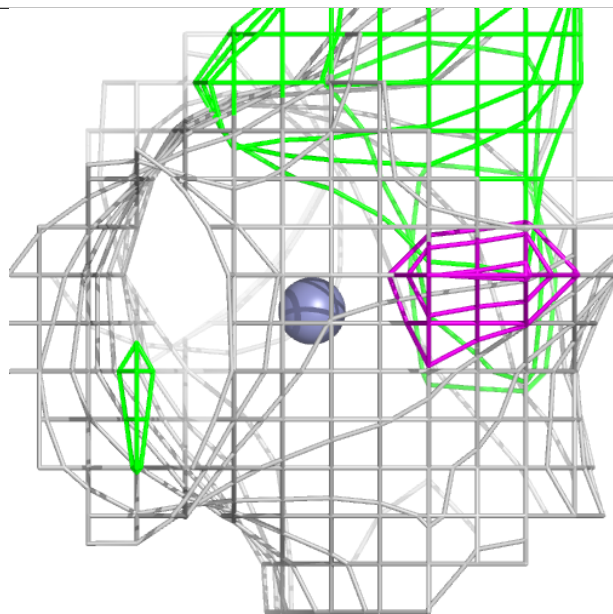
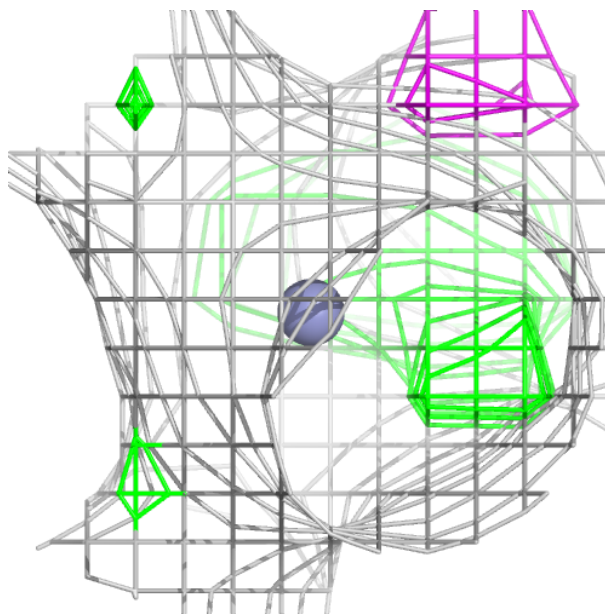
Electron density around ZN G 602:

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



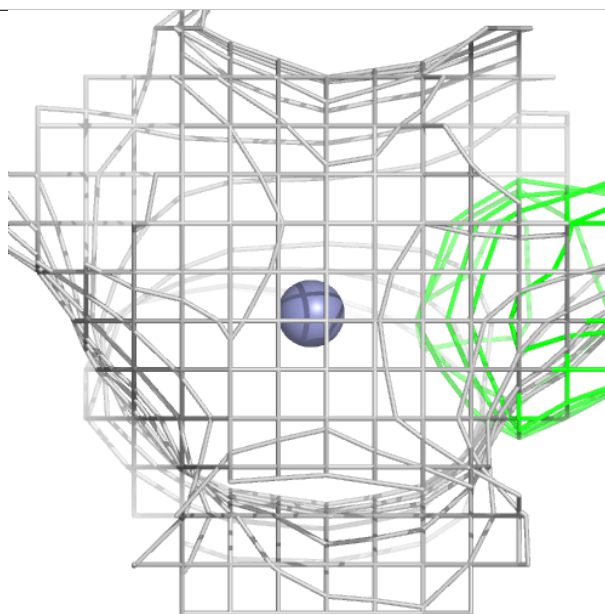
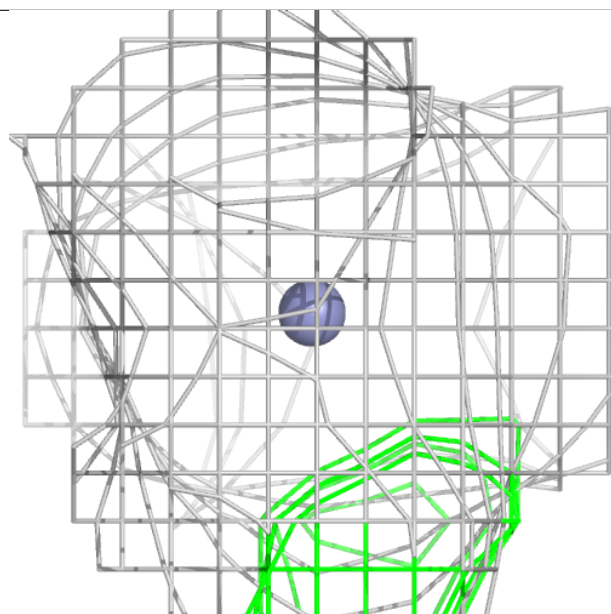
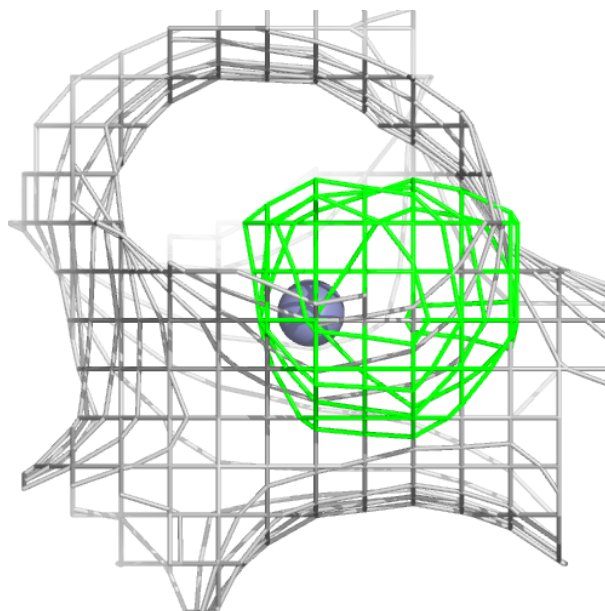
Electron density around ZN H 601:

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



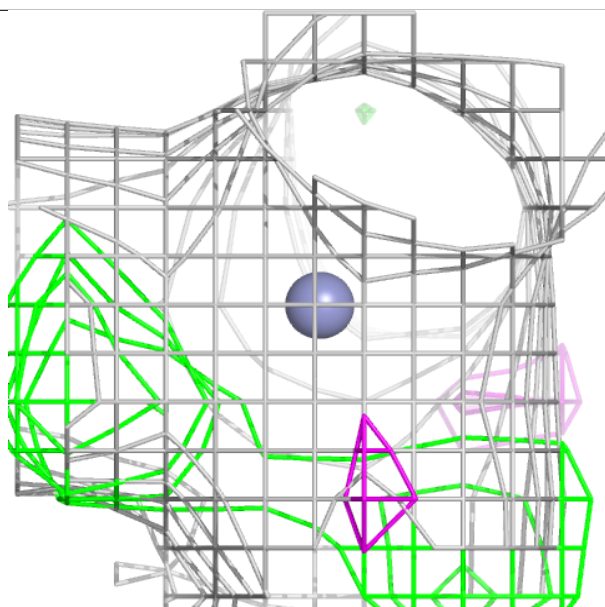
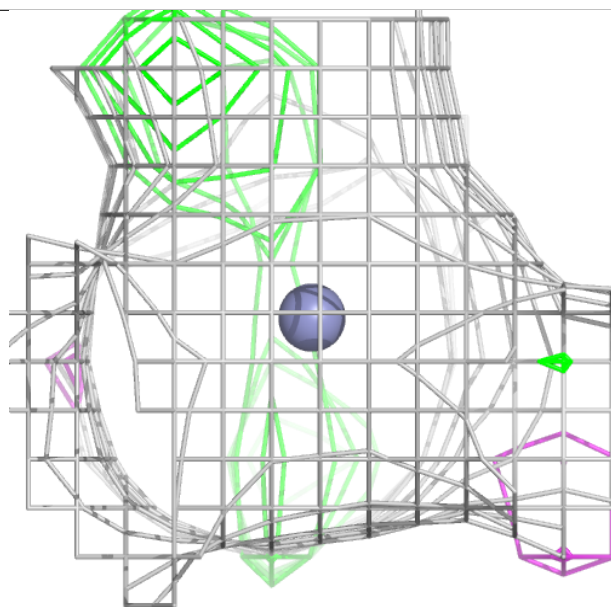
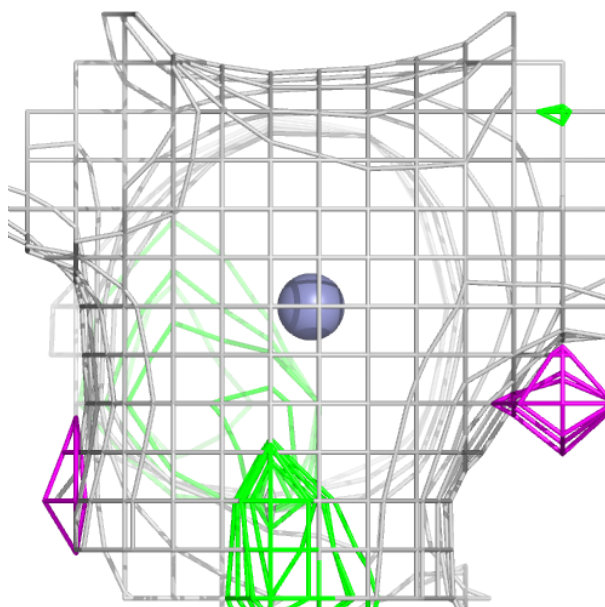
Electron density around ZN G 603:

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



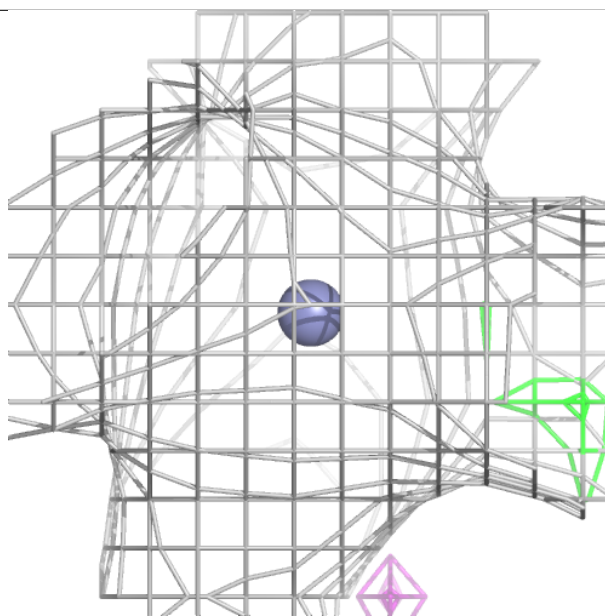
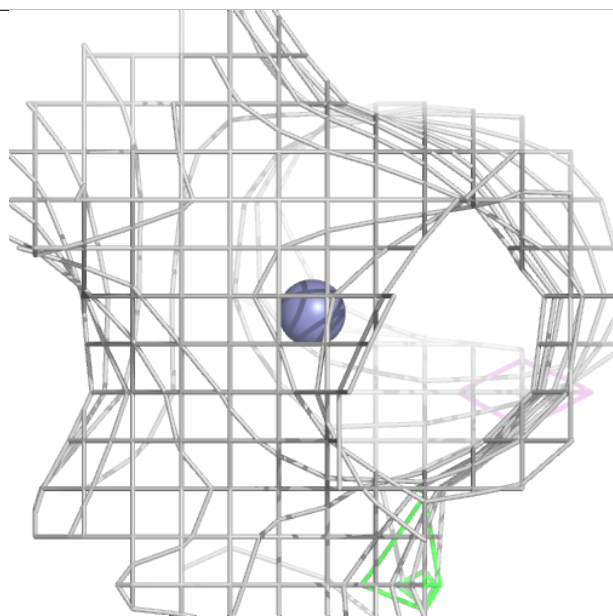
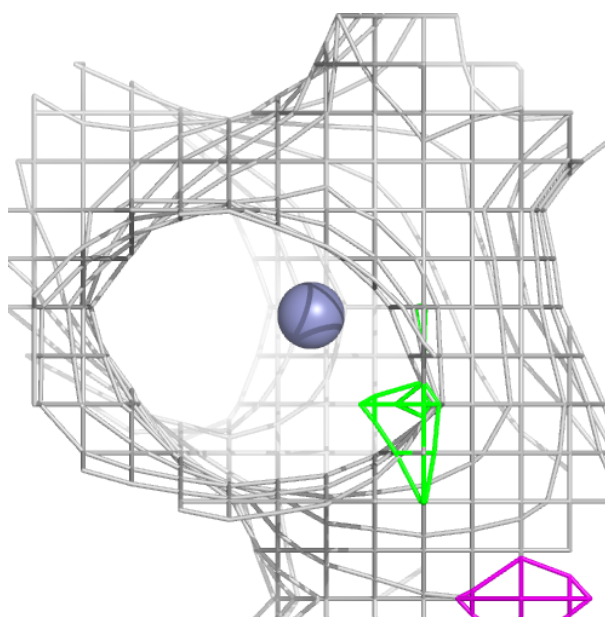
Electron density around ZN H 602:

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



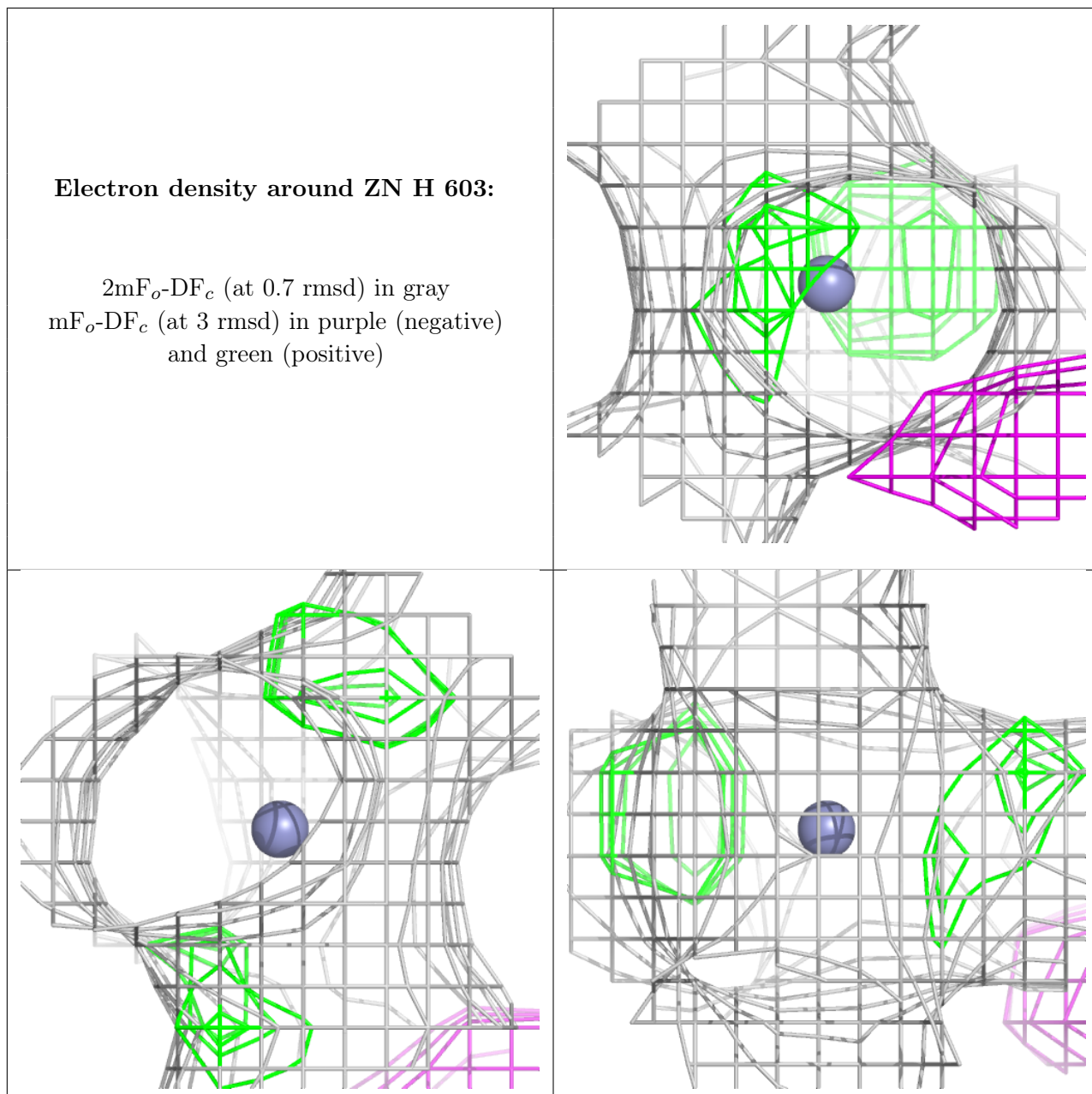
Electron density around ZN G 601:

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



Electron density around ZN H 603:

$2mF_o-DF_c$ (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.