



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 29, 2026 – 07:11 AM UTC

PDB ID : 7VB6 / pdb\_00007vb6  
Title : Crystal structure of hydroxynitrile lyase from *Linum usitatissimum* complexed with (R)-2-hydroxy-2-methylbutanenitrile  
Authors : Zheng, D.; Nakabayashi, M.; Asano, Y.  
Deposited on : 2021-08-30  
Resolution : 1.74 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  
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

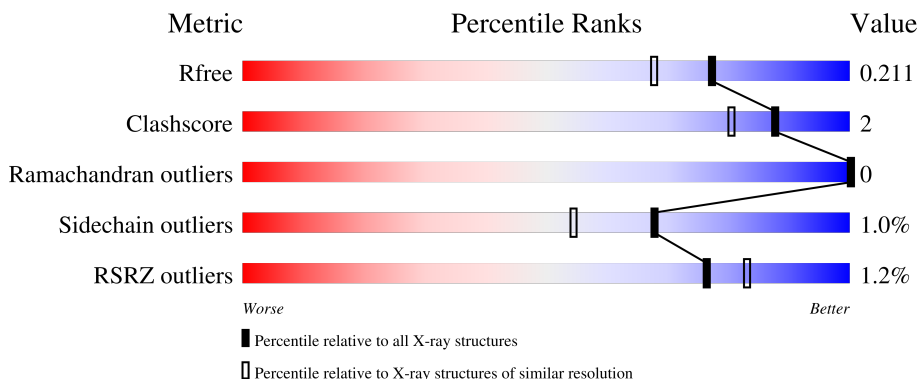
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.74 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	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	443	 86% 6% 8%
1	B	443	 89% 7%
1	C	443	 86% 6% 8%
1	D	443	 86% 6% 8%

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 14242 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 Aliphatic (R)-hydroxynitrile lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	408	Total 3121	C 1977	N 522	O 598	S 24	0	2	0
1	B	414	Total 3153	C 1994	N 527	O 608	S 24	0	1	0
1	C	408	Total 3110	C 1971	N 518	O 597	S 24	0	1	0
1	D	408	Total 3108	C 1967	N 518	O 599	S 24	0	1	0

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	initiating methionine	UNP P93243
A	-19	GLY	-	expression tag	UNP P93243
A	-18	SER	-	expression tag	UNP P93243
A	-17	SER	-	expression tag	UNP P93243
A	-16	HIS	-	expression tag	UNP P93243
A	-15	HIS	-	expression tag	UNP P93243
A	-14	HIS	-	expression tag	UNP P93243
A	-13	HIS	-	expression tag	UNP P93243
A	-12	HIS	-	expression tag	UNP P93243
A	-11	HIS	-	expression tag	UNP P93243
A	-10	SER	-	expression tag	UNP P93243
A	-9	SER	-	expression tag	UNP P93243
A	-8	GLY	-	expression tag	UNP P93243
A	-7	LEU	-	expression tag	UNP P93243
A	-6	VAL	-	expression tag	UNP P93243
A	-5	PRO	-	expression tag	UNP P93243
A	-4	ARG	-	expression tag	UNP P93243
A	-3	GLY	-	expression tag	UNP P93243
A	-2	SER	-	expression tag	UNP P93243
A	-1	HIS	-	expression tag	UNP P93243
A	0	MET	-	expression tag	UNP P93243

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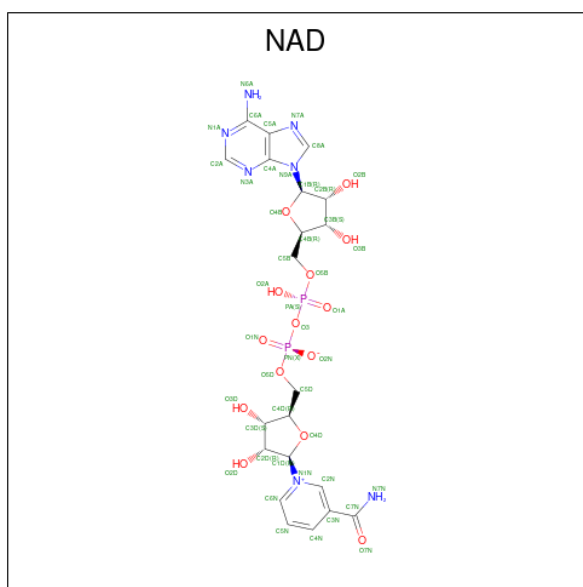
Chain	Residue	Modelled	Actual	Comment	Reference
A	117	THR	VAL	conflict	UNP P93243
B	-20	MET	-	initiating methionine	UNP P93243
B	-19	GLY	-	expression tag	UNP P93243
B	-18	SER	-	expression tag	UNP P93243
B	-17	SER	-	expression tag	UNP P93243
B	-16	HIS	-	expression tag	UNP P93243
B	-15	HIS	-	expression tag	UNP P93243
B	-14	HIS	-	expression tag	UNP P93243
B	-13	HIS	-	expression tag	UNP P93243
B	-12	HIS	-	expression tag	UNP P93243
B	-11	HIS	-	expression tag	UNP P93243
B	-10	SER	-	expression tag	UNP P93243
B	-9	SER	-	expression tag	UNP P93243
B	-8	GLY	-	expression tag	UNP P93243
B	-7	LEU	-	expression tag	UNP P93243
B	-6	VAL	-	expression tag	UNP P93243
B	-5	PRO	-	expression tag	UNP P93243
B	-4	ARG	-	expression tag	UNP P93243
B	-3	GLY	-	expression tag	UNP P93243
B	-2	SER	-	expression tag	UNP P93243
B	-1	HIS	-	expression tag	UNP P93243
B	0	MET	-	expression tag	UNP P93243
B	117	THR	VAL	conflict	UNP P93243
C	-20	MET	-	initiating methionine	UNP P93243
C	-19	GLY	-	expression tag	UNP P93243
C	-18	SER	-	expression tag	UNP P93243
C	-17	SER	-	expression tag	UNP P93243
C	-16	HIS	-	expression tag	UNP P93243
C	-15	HIS	-	expression tag	UNP P93243
C	-14	HIS	-	expression tag	UNP P93243
C	-13	HIS	-	expression tag	UNP P93243
C	-12	HIS	-	expression tag	UNP P93243
C	-11	HIS	-	expression tag	UNP P93243
C	-10	SER	-	expression tag	UNP P93243
C	-9	SER	-	expression tag	UNP P93243
C	-8	GLY	-	expression tag	UNP P93243
C	-7	LEU	-	expression tag	UNP P93243
C	-6	VAL	-	expression tag	UNP P93243
C	-5	PRO	-	expression tag	UNP P93243
C	-4	ARG	-	expression tag	UNP P93243
C	-3	GLY	-	expression tag	UNP P93243
C	-2	SER	-	expression tag	UNP P93243

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	HIS	-	expression tag	UNP P93243
C	0	MET	-	expression tag	UNP P93243
C	117	THR	VAL	conflict	UNP P93243
D	-20	MET	-	initiating methionine	UNP P93243
D	-19	GLY	-	expression tag	UNP P93243
D	-18	SER	-	expression tag	UNP P93243
D	-17	SER	-	expression tag	UNP P93243
D	-16	HIS	-	expression tag	UNP P93243
D	-15	HIS	-	expression tag	UNP P93243
D	-14	HIS	-	expression tag	UNP P93243
D	-13	HIS	-	expression tag	UNP P93243
D	-12	HIS	-	expression tag	UNP P93243
D	-11	HIS	-	expression tag	UNP P93243
D	-10	SER	-	expression tag	UNP P93243
D	-9	SER	-	expression tag	UNP P93243
D	-8	GLY	-	expression tag	UNP P93243
D	-7	LEU	-	expression tag	UNP P93243
D	-6	VAL	-	expression tag	UNP P93243
D	-5	PRO	-	expression tag	UNP P93243
D	-4	ARG	-	expression tag	UNP P93243
D	-3	GLY	-	expression tag	UNP P93243
D	-2	SER	-	expression tag	UNP P93243
D	-1	HIS	-	expression tag	UNP P93243
D	0	MET	-	expression tag	UNP P93243
D	117	THR	VAL	conflict	UNP P93243

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula:  $C_{21}H_{27}N_7O_{14}P_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	A	1	44	21	7	14	2	0	0
2	B	1	44	21	7	14	2	0	0
2	C	1	44	21	7	14	2	0	0
2	D	1	44	21	7	14	2	0	0

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

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

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

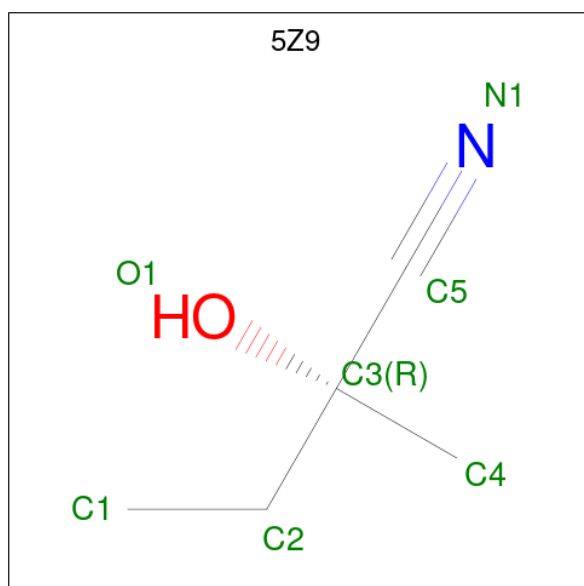
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0

- Molecule 5 is (2R)-2-methyl-2-oxidanyl-butanenitrile (CCD ID: 5Z9) (formula: C<sub>5</sub>H<sub>9</sub>NO) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O 7 5 1 1	0	0
5	B	1	Total C N O 7 5 1 1	0	0
5	C	1	Total C N O 7 5 1 1	0	0
5	D	1	Total C N O 7 5 1 1	0	0

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



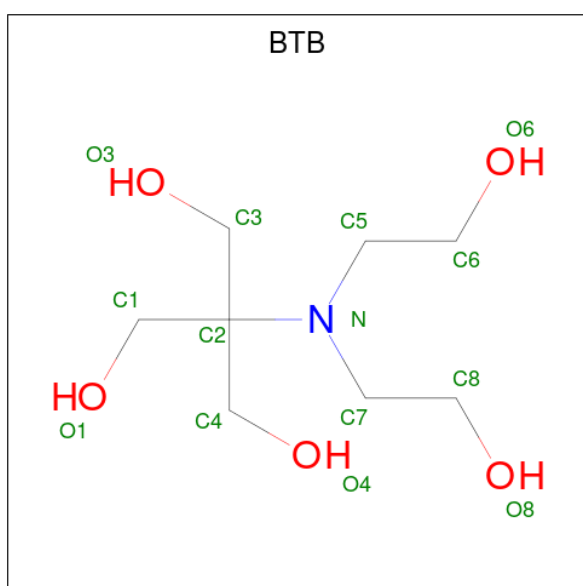
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	A	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	B	1	Total C O 4 2 2	0	0
6	D	1	Total C O 4 2 2	0	0

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula:  $C_8H_{19}NO_5$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	D	1	Total	C	N	O	0	0
			14	8	1	5		


- Molecule 9 is water.

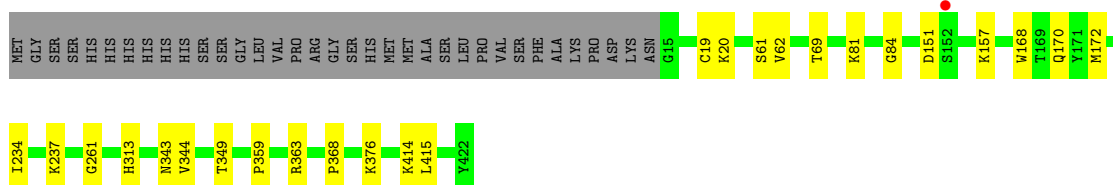
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	463	Total	O	0	0
			463	463		
9	B	481	Total	O	0	0
			481	481		
9	C	226	Total	O	0	0
			226	226		
9	D	252	Total	O	0	0
			252	252		

### 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.

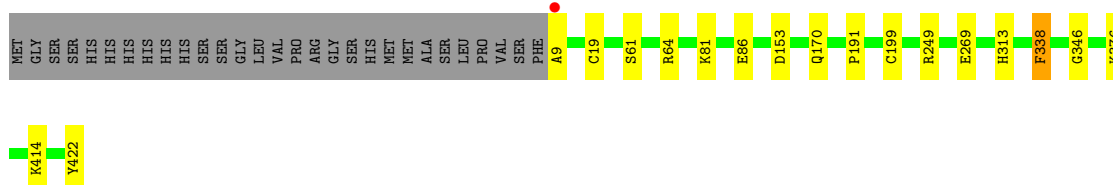
- Molecule 1: Aliphatic (R)-hydroxynitrile lyase

Chain A: 




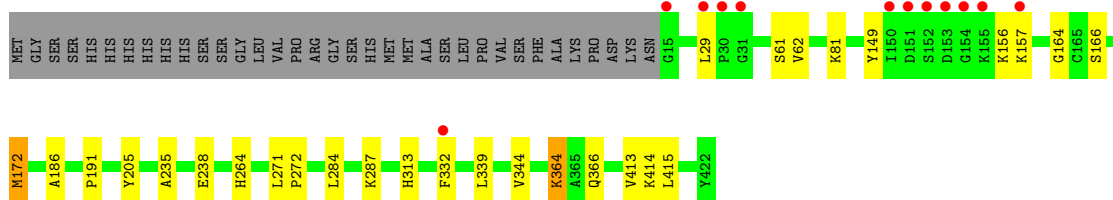
- Molecule 1: Aliphatic (R)-hydroxynitrile lyase

Chain B: 




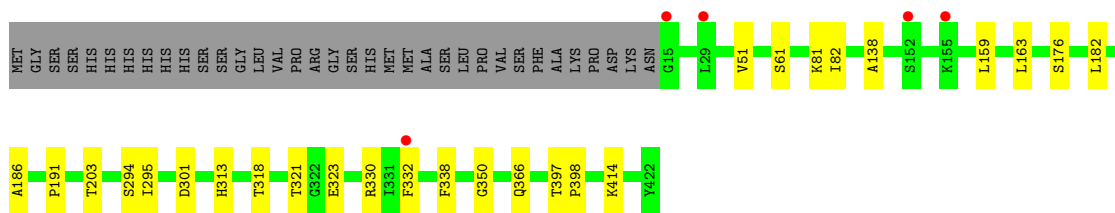
- Molecule 1: Aliphatic (R)-hydroxynitrile lyase

Chain C: 



- Molecule 1: Aliphatic (R)-hydroxynitrile lyase

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.18Å 52.10Å 169.85Å 90.00° 94.80° 90.00°	Depositor
Resolution (Å)	49.85 – 1.74 49.85 – 1.74	Depositor EDS
% Data completeness (in resolution range)	98.6 (49.85-1.74) 98.7 (49.85-1.74)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.29 (at 1.74Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.163 , 0.206 0.174 , 0.211	Depositor DCC
$R_{free}$ test set	8653 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.6	Xtrriage
Anisotropy	0.067	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 32.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14242	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.96% 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: EDO, 5Z9, ZN, BTB, MG, SNC, NAD, GOL

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	1.11	2/3170 (0.1%)	1.24	2/4284 (0.0%)
1	B	1.08	1/3202 (0.0%)	1.26	4/4328 (0.1%)
1	C	1.07	0/3159	1.33	2/4270 (0.0%)
1	D	1.06	1/3156 (0.0%)	1.29	4/4266 (0.1%)
All	All	1.08	4/12687 (0.0%)	1.28	12/17148 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	69	THR	C-O	5.36	1.30	1.24
1	D	295	ILE	C-O	5.26	1.30	1.24
1	A	234	ILE	C-O	5.11	1.29	1.24
1	B	346	GLY	C-O	5.07	1.29	1.23

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	151	ASP	CA-CB-CG	8.39	120.99	112.60
1	B	422	TYR	CA-C-O	-6.54	109.68	120.80
1	C	191	PRO	N-CA-C	6.39	118.49	110.70
1	D	321	THR	CA-C-N	5.78	125.59	120.10
1	D	321	THR	C-N-CA	5.78	125.59	120.10
1	D	191	PRO	N-CA-C	5.50	117.41	110.70
1	C	413	VAL	N-CA-C	-5.26	106.56	111.45
1	A	343	ASN	CB-CA-C	5.25	117.94	111.43
1	D	301	ASP	CA-CB-CG	5.24	117.84	112.60
1	B	64	ARG	N-CA-C	-5.15	105.79	111.71
1	B	338	PHE	CA-CB-CG	-5.10	108.70	113.80
1	B	191	PRO	N-CA-C	5.09	116.91	110.70

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	3121	0	3136	12	0
1	B	3153	0	3167	8	0
1	C	3110	0	3124	18	0
1	D	3108	0	3121	17	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	C	44	0	26	0	0
2	D	44	0	26	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	7	0	0	0	0
5	B	7	0	0	0	0
5	C	7	0	0	0	0
5	D	7	0	0	0	0
6	A	20	0	30	0	0
6	B	8	0	12	0	0
6	D	4	0	6	0	0
7	A	6	0	8	2	0
7	B	18	0	24	0	0
8	A	42	0	57	3	0
8	D	14	0	19	0	0
9	A	463	0	0	4	0
9	B	481	0	0	3	0
9	C	226	0	0	2	0
9	D	252	0	0	2	0
All	All	14242	0	12808	50	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 (50) 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)
8:A:514:BTB:H51	9:A:942:HOH:O	1.80	0.82
1:B:313:HIS:HD2	9:B:858:HOH:O	1.70	0.74
1:C:313:HIS:HD2	9:C:733:HOH:O	1.74	0.70
1:C:344:VAL:HG12	1:D:338:PHE:HZ	1.67	0.60
1:D:61:SER:HB2	1:D:414:LYS:HD2	1.84	0.58
1:A:344:VAL:HG12	1:B:338:PHE:HZ	1.70	0.56
1:C:149:TYR:CE1	1:C:157:LYS:HB2	2.40	0.56
1:B:313:HIS:HE1	9:B:974:HOH:O	1.88	0.55
1:D:313:HIS:HE1	9:D:821:HOH:O	1.88	0.55
1:A:61:SER:HB2	1:A:414:LYS:HD2	1.91	0.53
1:B:9:ALA:HB2	9:B:727:HOH:O	2.09	0.52
1:B:249:ARG:HB2	1:B:269:GLU:HG3	1.91	0.51
1:C:344:VAL:HG12	1:D:338:PHE:CZ	2.46	0.51
1:C:62:VAL:HG21	1:C:415:LEU:HD23	1.92	0.50
1:A:20:LYS:HE3	9:A:669:HOH:O	2.10	0.50
1:A:237:LYS:HD3	7:A:511:GOL:H12	1.94	0.49
1:D:182:LEU:HD12	1:D:182:LEU:N	2.28	0.48
1:C:332[B]:PHE:CD1	1:D:330:ARG:NH2	2.81	0.48
1:C:186:ALA:HA	1:C:366:GLN:NE2	2.29	0.48
1:A:157:LYS:HE2	9:A:614:HOH:O	2.13	0.47
1:B:19:CYS:HB2	1:B:170:GLN:HB2	1.96	0.47
1:B:61:SER:HB2	1:B:414:LYS:HD2	1.97	0.47
1:A:19:CYS:HB2	1:A:170:GLN:HB2	1.97	0.46
1:C:238:GLU:OE2	1:C:364:LYS:NZ	2.45	0.46
1:A:62:VAL:HG21	1:A:415:LEU:HD23	1.98	0.46
1:D:313:HIS:HD2	9:D:713:HOH:O	1.98	0.44
1:A:359:PRO:O	1:A:363[B]:ARG:HG3	2.17	0.44
1:D:186:ALA:HA	1:D:366:GLN:NE2	2.33	0.43
1:A:368:PRO:HD2	1:C:29:LEU:HD12	2.00	0.43
1:D:138:ALA:HA	1:D:163:LEU:O	2.18	0.43
1:A:313:HIS:HE1	9:A:990:HOH:O	2.01	0.43
1:B:86:GLU:OE2	1:B:199:CYS:HB3	2.18	0.43
1:C:61:SER:HB2	1:C:414:LYS:HD2	2.00	0.43
1:C:271:LEU:O	1:C:272:PRO:C	2.62	0.42
1:C:332[B]:PHE:CD1	1:D:330:ARG:CZ	3.02	0.42
1:C:339:LEU:HD22	1:D:323:GLU:HG2	2.00	0.42
1:C:166:SER:O	1:C:172:MET:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:264:HIS:CD2	1:C:284:LEU:HD22	2.54	0.42
1:C:332[A]:PHE:CE2	1:D:332:PHE:HB3	2.55	0.42
8:A:514:BTB:O8	8:A:514:BTB:H61	2.20	0.42
1:D:294:SER:O	1:D:318:THR:HA	2.20	0.41
1:A:84:GLY:HA3	1:A:168:TRP:CD1	2.55	0.41
8:A:514:BTB:H41	8:A:514:BTB:H52	1.98	0.41
1:C:205:TYR:CD2	1:C:235:ALA:HB2	2.56	0.41
1:A:261:GLY:O	7:A:511:GOL:C1	2.69	0.41
1:C:164:GLY:HA3	9:C:809:HOH:O	2.21	0.40
1:D:397:THR:N	1:D:398:PRO:CD	2.85	0.40
1:D:82:ILE:HD11	1:D:159:LEU:HD13	2.04	0.40
1:D:203:THR:HA	1:D:350:GLY:N	2.36	0.40
1:D:51:VAL:O	1:D:176:SER:OG	2.38	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	407/443 (92%)	397 (98%)	10 (2%)	0	100	100
1	B	412/443 (93%)	401 (97%)	11 (3%)	0	100	100
1	C	406/443 (92%)	391 (96%)	15 (4%)	0	100	100
1	D	406/443 (92%)	393 (97%)	13 (3%)	0	100	100
All	All	1631/1772 (92%)	1582 (97%)	49 (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	339/367 (92%)	335 (99%)	4 (1%)	63	47
1	B	343/367 (94%)	340 (99%)	3 (1%)	70	59
1	C	338/367 (92%)	333 (98%)	5 (2%)	57	38
1	D	338/367 (92%)	337 (100%)	1 (0%)	86	82
All	All	1358/1468 (92%)	1345 (99%)	13 (1%)	68	54

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	LYS
1	A	172	MET
1	A	349	THR
1	A	376	LYS
1	B	81	LYS
1	B	153	ASP
1	B	376	LYS
1	C	81	LYS
1	C	156	LYS
1	C	172	MET
1	C	287	LYS
1	C	364	LYS
1	D	81	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	366	GLN
1	B	14	ASN
1	B	44	GLN
1	B	130	GLN
1	B	131	ASN

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Mol	Chain	Res	Type
1	B	215	GLN
1	B	313	HIS
1	C	131	ASN
1	C	135	ASN
1	C	183	ASN
1	C	215	GLN
1	C	313	HIS
1	C	366	GLN
1	D	44	GLN
1	D	131	ASN
1	D	313	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](#)

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z  > 2$
1	SNC	C	265	1	4,7,8	0.75	0	2,7,9	1.34	0
1	SNC	B	265	1	4,7,8	0.85	0	2,7,9	0.28	0
1	SNC	A	265	1	4,7,8	0.85	0	2,7,9	0.53	0
1	SNC	D	265	1	4,7,8	0.90	0	2,7,9	1.22	0

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
1	SNC	C	265	1	-	0/0/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SNC	B	265	1	-	0/0/6/8	-
1	SNC	A	265	1	-	0/0/6/8	-
1	SNC	D	265	1	-	0/0/6/8	-

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.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 12 are monoatomic - leaving 24 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	5Z9	D	505	3	5,6,6	0.26	0	5,8,8	0.65	0
5	5Z9	B	505	3	5,6,6	1.39	1 (20%)	5,8,8	1.13	1 (20%)
8	BTB	A	512	-	13,13,13	1.52	3 (23%)	7,16,16	0.57	0
8	BTB	A	513	-	13,13,13	1.81	3 (23%)	7,16,16	0.60	0
6	EDO	A	506	-	3,3,3	0.15	0	2,2,2	0.07	0
2	NAD	B	501	-	46,48,48	0.78	2 (4%)	64,73,73	0.83	3 (4%)
8	BTB	D	507	-	13,13,13	1.27	3 (23%)	7,16,16	0.51	0
7	GOL	B	508	-	5,5,5	0.14	0	5,5,5	0.14	0
7	GOL	B	509	-	5,5,5	0.13	0	5,5,5	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	EDO	A	507	-	3,3,3	0.14	0	2,2,2	0.37	0
5	5Z9	A	505	3	5,6,6	0.58	0	5,8,8	1.23	1 (20%)
6	EDO	A	508	-	3,3,3	0.05	0	2,2,2	0.06	0
7	GOL	A	511	-	5,5,5	0.23	0	5,5,5	0.52	0
2	NAD	A	501	-	46,48,48	0.93	2 (4%)	64,73,73	0.87	2 (3%)
2	NAD	C	501	-	46,48,48	0.61	1 (2%)	64,73,73	0.74	1 (1%)
6	EDO	B	507	-	3,3,3	0.44	0	2,2,2	0.42	0
6	EDO	B	506	-	3,3,3	0.58	0	2,2,2	0.37	0
2	NAD	D	501	-	46,48,48	0.59	1 (2%)	64,73,73	0.94	5 (7%)
7	GOL	B	510	-	5,5,5	0.13	0	5,5,5	0.44	0
6	EDO	A	510	-	3,3,3	0.30	0	2,2,2	0.23	0
6	EDO	A	509	-	3,3,3	0.40	0	2,2,2	0.42	0
8	BTB	A	514	-	13,13,13	1.65	3 (23%)	7,16,16	1.26	2 (28%)
6	EDO	D	506	-	3,3,3	0.47	0	2,2,2	0.63	0
5	5Z9	C	505	3	5,6,6	0.24	0	5,8,8	0.96	0

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	5Z9	D	505	3	-	0/3/6/6	-
5	5Z9	B	505	3	-	0/3/6/6	-
8	BTB	A	512	-	-	3/21/21/21	-
8	BTB	A	513	-	-	2/21/21/21	-
6	EDO	A	506	-	-	1/1/1/1	-
2	NAD	B	501	-	-	4/30/62/62	0/5/5/5
8	BTB	D	507	-	-	7/21/21/21	-
7	GOL	B	508	-	-	4/4/4/4	-
7	GOL	B	509	-	-	2/4/4/4	-
6	EDO	A	507	-	-	0/1/1/1	-
5	5Z9	A	505	3	-	0/3/6/6	-
6	EDO	A	508	-	-	1/1/1/1	-
7	GOL	A	511	-	-	4/4/4/4	-
2	NAD	A	501	-	-	5/30/62/62	0/5/5/5
2	NAD	C	501	-	-	3/30/62/62	0/5/5/5
6	EDO	B	507	-	-	1/1/1/1	-
6	EDO	B	506	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	D	501	-	-	4/30/62/62	0/5/5/5
7	GOL	B	510	-	-	3/4/4/4	-
6	EDO	A	510	-	-	0/1/1/1	-
6	EDO	A	509	-	-	1/1/1/1	-
8	BTB	A	514	-	-	4/21/21/21	-
6	EDO	D	506	-	-	1/1/1/1	-
5	5Z9	C	505	3	-	0/3/6/6	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	513	BTB	C2-N	4.77	1.57	1.48
2	A	501	NAD	PA-O3	4.48	1.64	1.59
8	A	514	BTB	C2-N	4.22	1.56	1.48
8	A	512	BTB	C2-N	3.61	1.55	1.48
2	B	501	NAD	PN-O3	3.44	1.63	1.59
8	D	507	BTB	C2-N	3.00	1.54	1.48
2	A	501	NAD	C2N-N1N	2.97	1.38	1.35
8	A	514	BTB	C5-N	2.82	1.51	1.48
8	A	513	BTB	C5-N	2.79	1.51	1.48
8	A	512	BTB	C5-N	2.77	1.51	1.48
5	B	505	5Z9	C5-N1	2.76	1.18	1.14
8	D	507	BTB	C5-N	2.43	1.51	1.48
8	A	513	BTB	C7-N	2.41	1.51	1.48
8	A	512	BTB	C7-N	2.30	1.51	1.48
2	D	501	NAD	PA-O3	2.25	1.61	1.59
2	C	501	NAD	PA-O3	2.19	1.61	1.59
8	D	507	BTB	C7-N	2.10	1.50	1.48
8	A	514	BTB	C7-N	2.07	1.50	1.48
2	B	501	NAD	C5N-C4N	-2.02	1.35	1.38

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	NAD	C6N-N1N-C2N	-3.45	118.94	121.88
2	B	501	NAD	C6N-N1N-C2N	-2.83	119.47	121.88
2	C	501	NAD	C6N-N1N-C2N	-2.65	119.63	121.88
2	A	501	NAD	C6N-N1N-C2N	-2.40	119.84	121.88
2	D	501	NAD	O3-PA-O1A	-2.39	103.52	110.70
2	B	501	NAD	O4B-C1B-N9A	2.32	112.54	108.09
5	B	505	5Z9	O1-C3-C5	2.26	113.03	108.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	NAD	O2A-PA-O1A	2.23	122.81	112.44
8	A	514	BTB	O1-C1-C2	2.21	116.61	111.40
8	A	514	BTB	O3-C3-C2	2.12	116.38	111.40
2	A	501	NAD	O3-PA-O1A	-2.07	104.46	110.70
5	A	505	5Z9	O1-C3-C4	2.06	113.15	107.41
2	D	501	NAD	C5N-C4N-C3N	-2.06	118.34	120.36
2	D	501	NAD	O7N-C7N-C3N	-2.04	117.10	119.60
2	B	501	NAD	O7N-C7N-C3N	2.00	122.05	119.60

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	NAD	O4D-C1D-N1N-C2N
2	A	501	NAD	O4D-C1D-N1N-C6N
2	A	501	NAD	C2D-C1D-N1N-C2N
2	A	501	NAD	C2D-C1D-N1N-C6N
2	B	501	NAD	O4D-C1D-N1N-C2N
2	B	501	NAD	O4D-C1D-N1N-C6N
2	B	501	NAD	C2D-C1D-N1N-C2N
2	B	501	NAD	C2D-C1D-N1N-C6N
2	C	501	NAD	O4D-C1D-N1N-C2N
2	C	501	NAD	O4D-C1D-N1N-C6N
2	C	501	NAD	C2D-C1D-N1N-C2N
2	D	501	NAD	O4D-C1D-N1N-C2N
2	D	501	NAD	O4D-C1D-N1N-C6N
2	D	501	NAD	C2D-C1D-N1N-C2N
7	A	511	GOL	C1-C2-C3-O3
7	A	511	GOL	O2-C2-C3-O3
7	B	508	GOL	O1-C1-C2-O2
7	B	508	GOL	O1-C1-C2-C3
7	B	509	GOL	O1-C1-C2-C3
8	A	512	BTB	C1-C2-C3-O3
8	A	512	BTB	C4-C2-C3-O3
8	A	512	BTB	N-C2-C3-O3
8	A	513	BTB	N-C2-C4-O4
8	A	514	BTB	O1-C1-C2-C3
8	A	514	BTB	O1-C1-C2-C4
8	A	514	BTB	O1-C1-C2-N
8	D	507	BTB	C1-C2-N-C5
8	D	507	BTB	C3-C2-N-C5
8	D	507	BTB	C4-C2-N-C5

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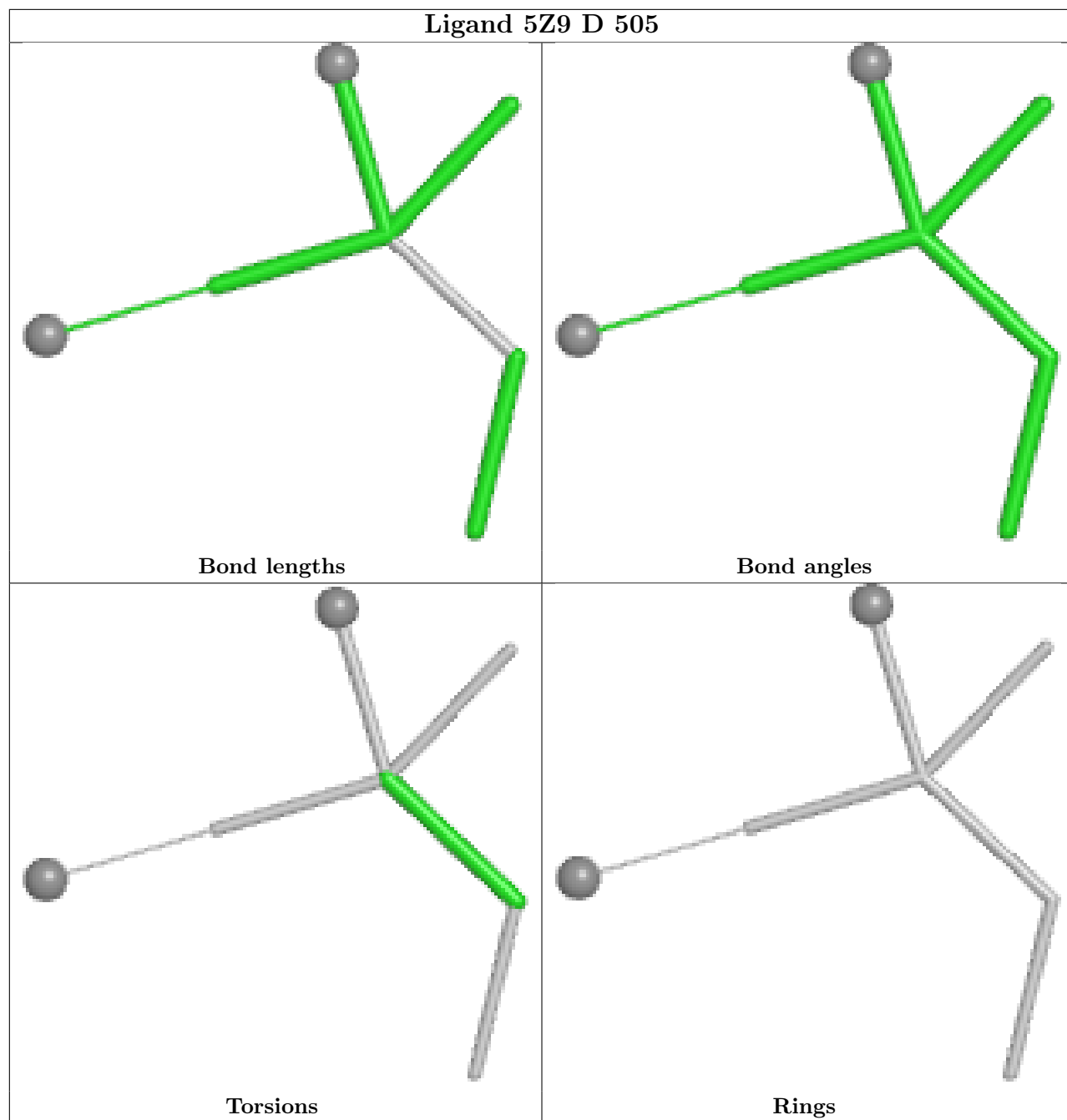
Mol	Chain	Res	Type	Atoms
8	D	507	BTB	C4-C2-N-C7
7	A	511	GOL	O1-C1-C2-C3
7	B	508	GOL	C1-C2-C3-O3
7	B	510	GOL	C1-C2-C3-O3
6	B	506	EDO	O1-C1-C2-O2
6	B	507	EDO	O1-C1-C2-O2
7	B	509	GOL	O1-C1-C2-O2
6	A	506	EDO	O1-C1-C2-O2
6	D	506	EDO	O1-C1-C2-O2
7	B	510	GOL	O2-C2-C3-O3
8	D	507	BTB	C6-C5-N-C7
8	A	514	BTB	N-C7-C8-O8
7	B	510	GOL	O1-C1-C2-C3
6	A	509	EDO	O1-C1-C2-O2
8	D	507	BTB	C1-C2-N-C7
7	A	511	GOL	O1-C1-C2-O2
8	A	513	BTB	C3-C2-C4-O4
2	D	501	NAD	C2D-C1D-N1N-C6N
7	B	508	GOL	O2-C2-C3-O3
6	A	508	EDO	O1-C1-C2-O2
2	A	501	NAD	O4B-C4B-C5B-O5B
8	D	507	BTB	C3-C2-N-C7

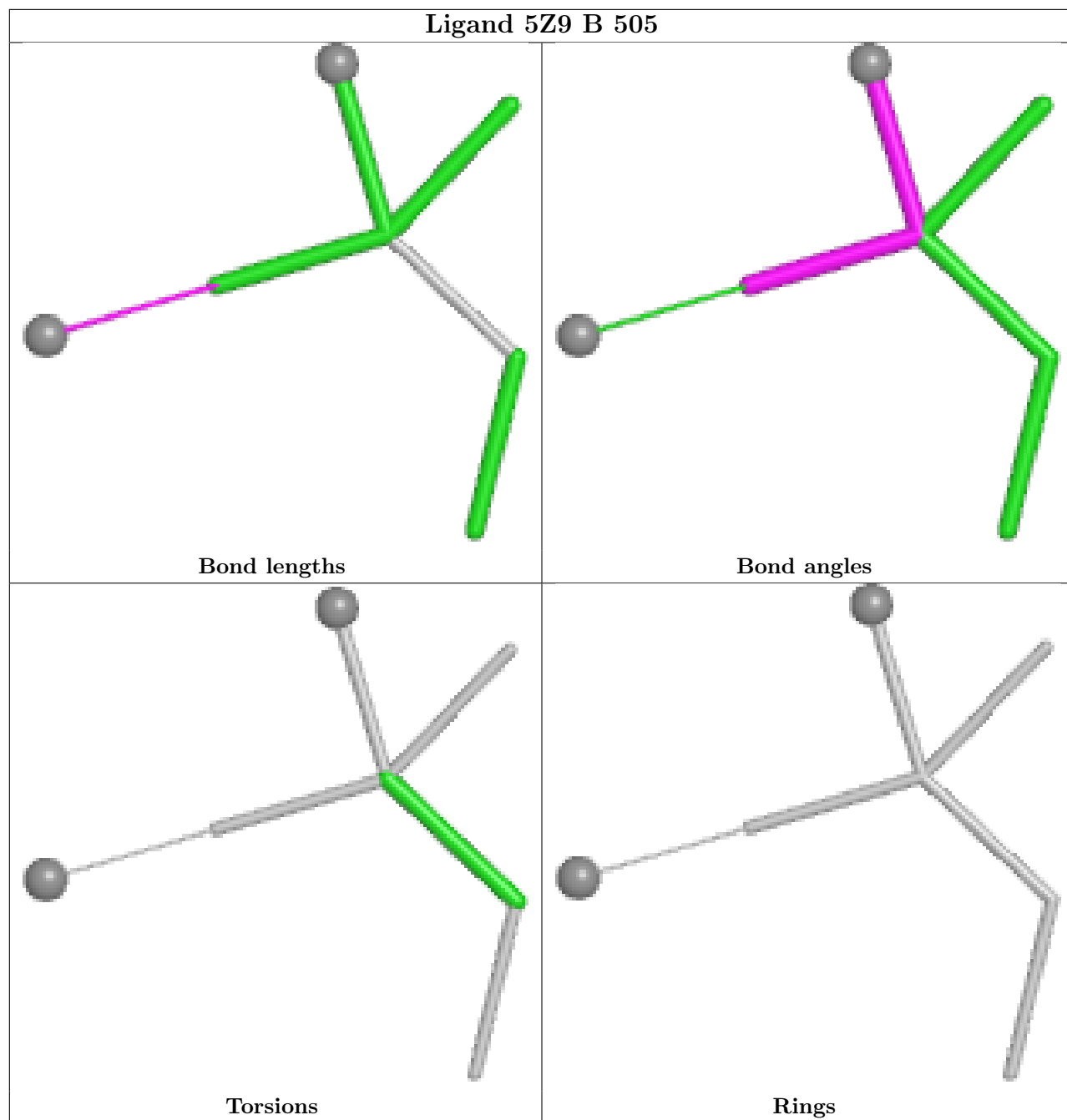
There are no ring outliers.

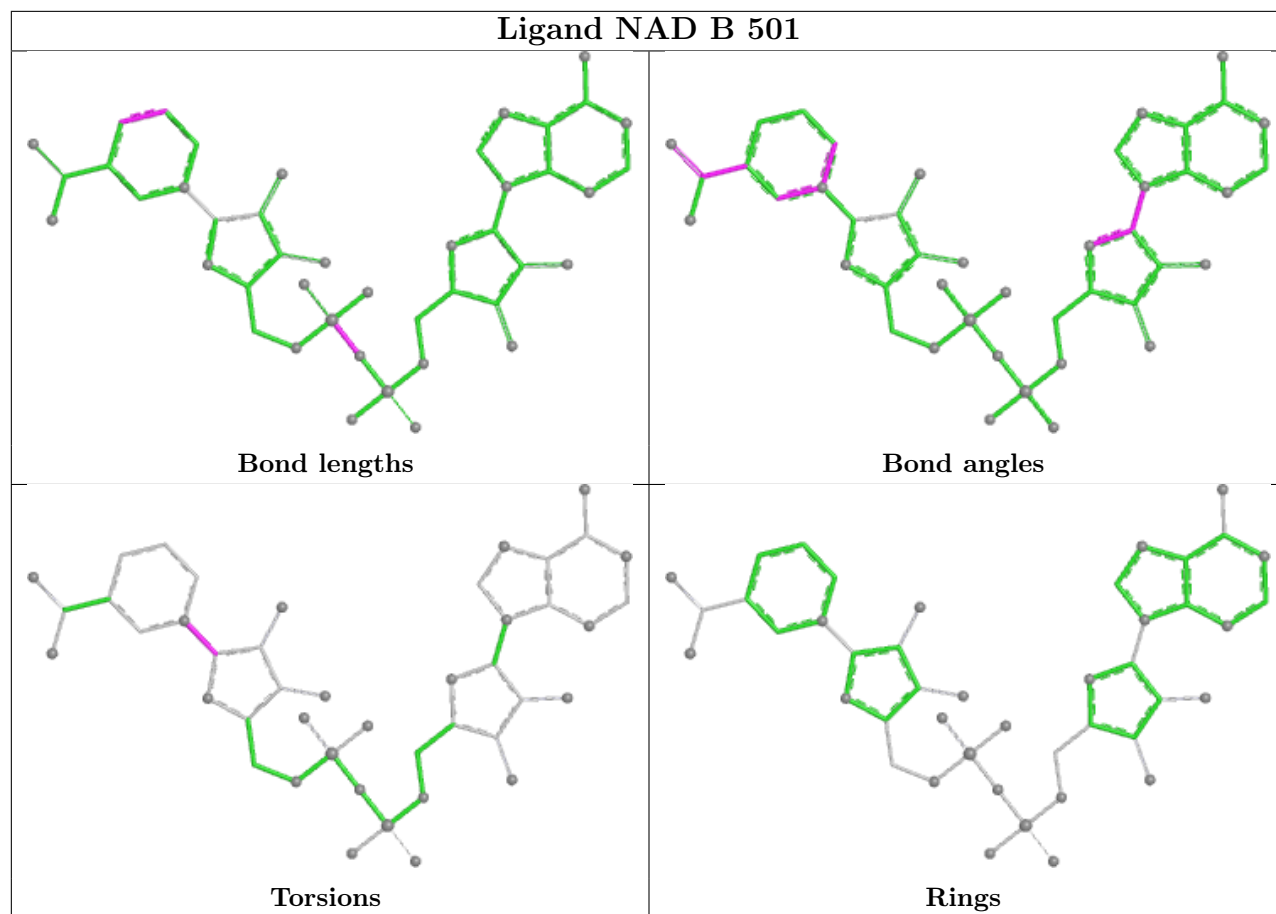
2 monomers are involved in 5 short contacts:

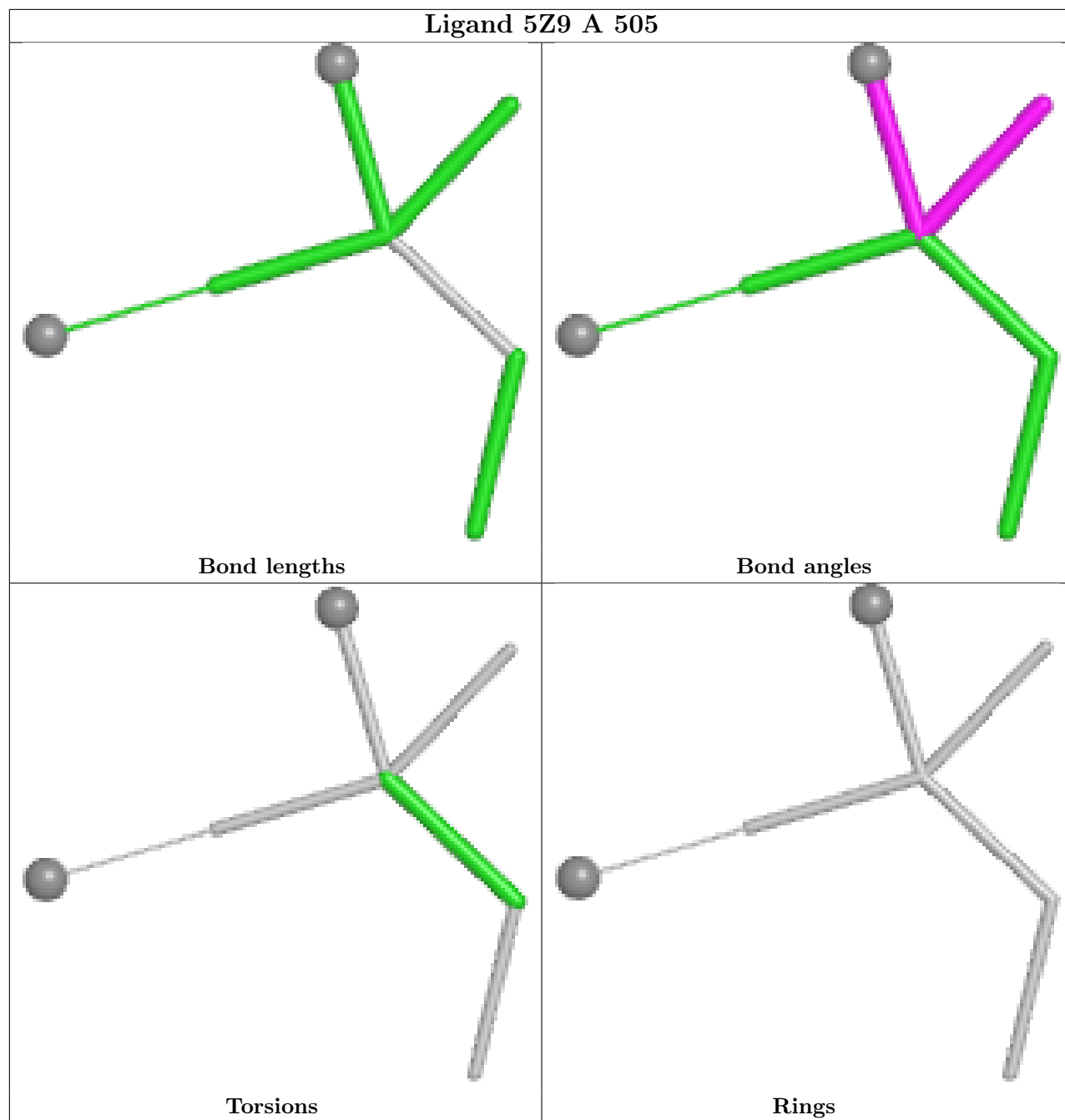
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	511	GOL	2	0
8	A	514	BTB	3	0

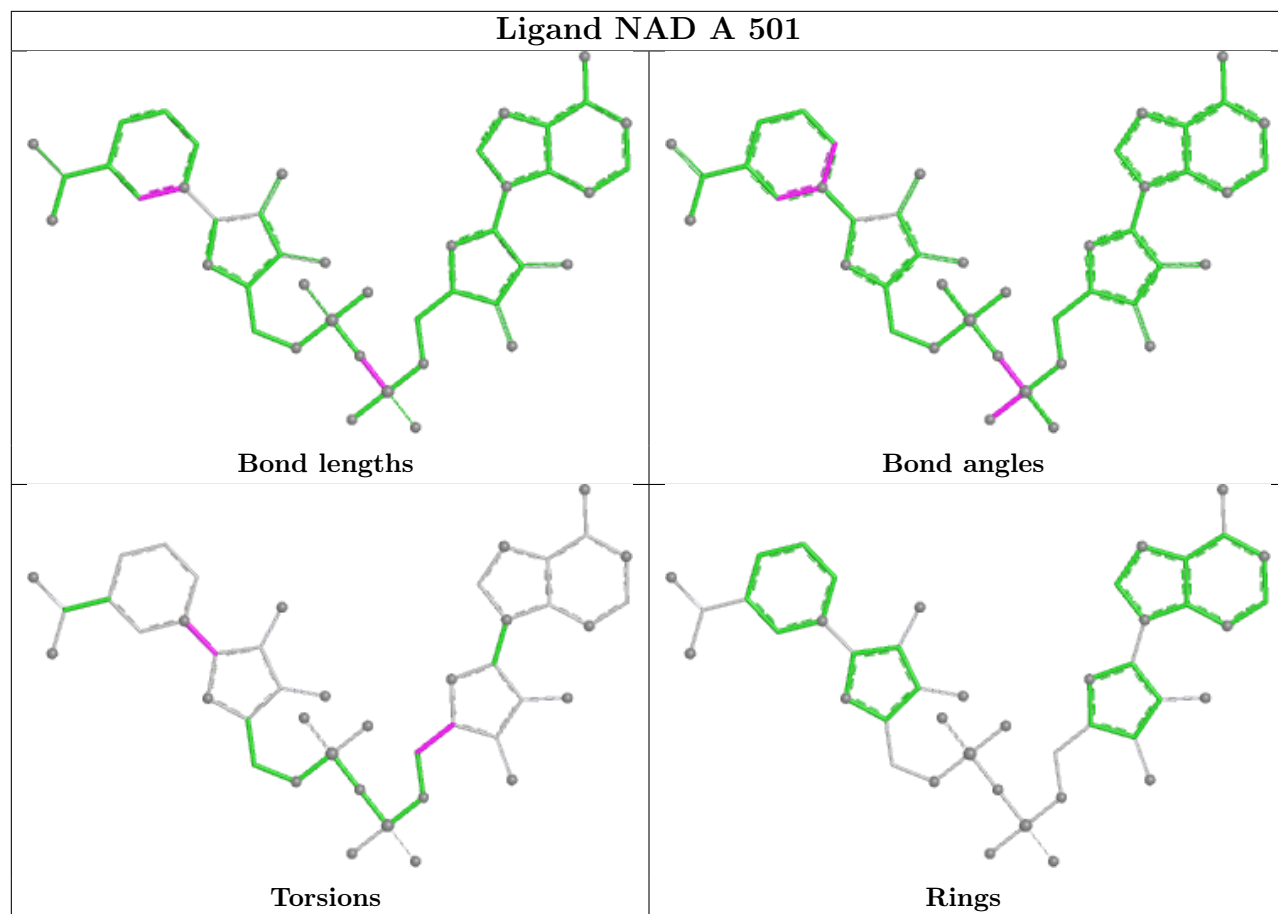
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

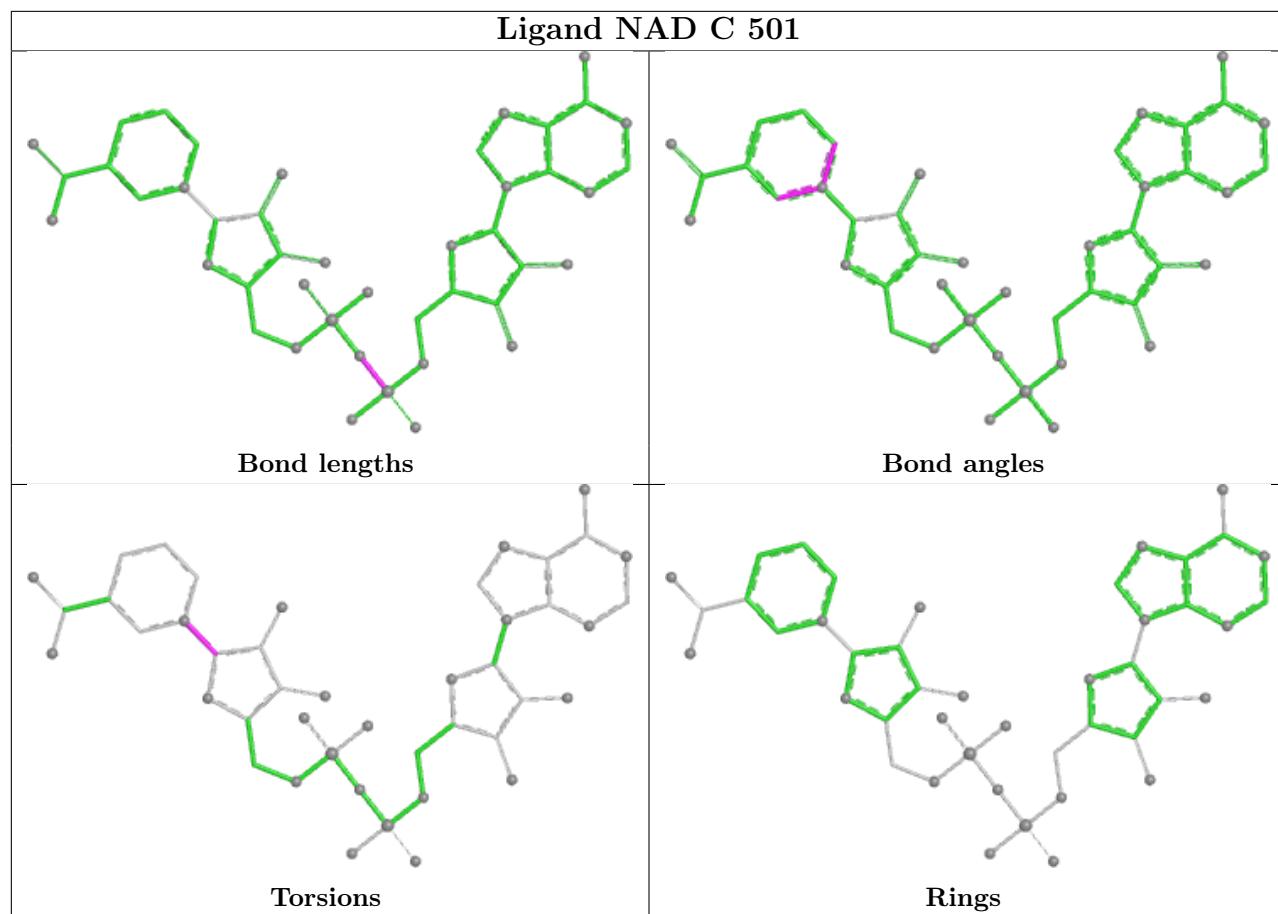


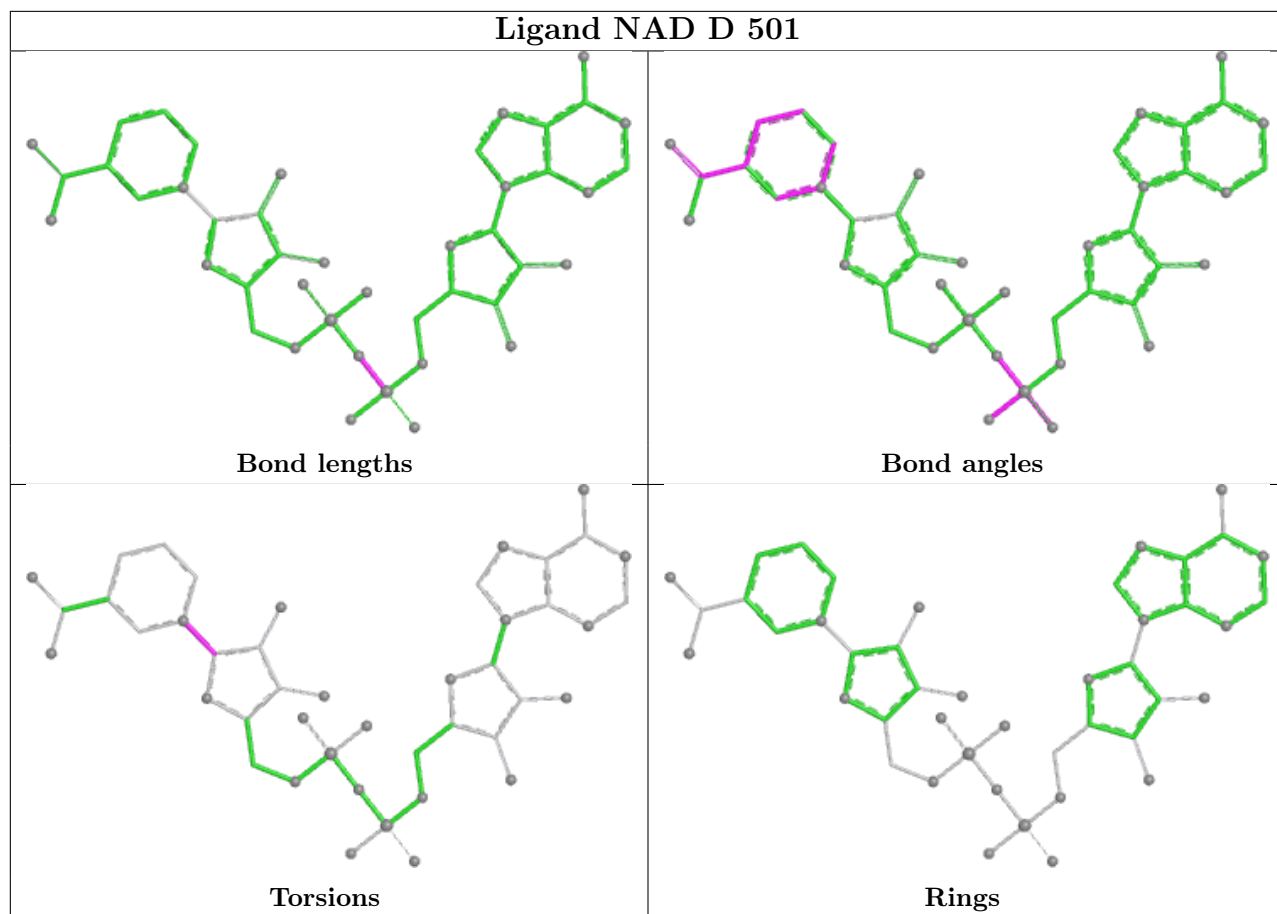


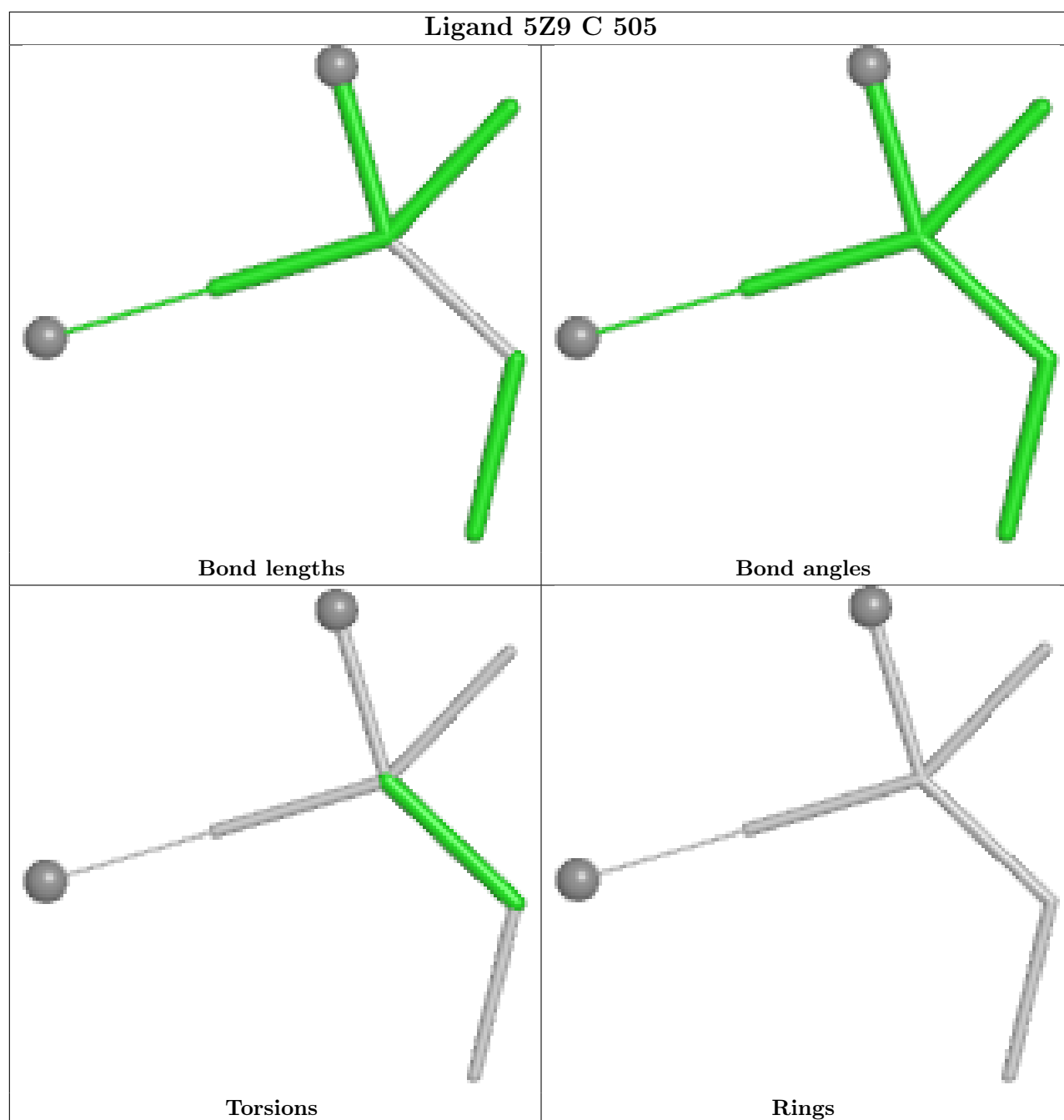












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [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	407/443 (91%)	-0.48	1 (0%) 91 93	9, 15, 26, 54	2 (0%)
1	B	413/443 (93%)	-0.46	1 (0%) 91 93	10, 15, 30, 63	1 (0%)
1	C	407/443 (91%)	0.33	12 (2%) 53 62	15, 29, 45, 75	1 (0%)
1	D	407/443 (91%)	0.09	5 (1%) 76 83	16, 26, 42, 70	1 (0%)
All	All	1634/1772 (92%)	-0.13	19 (1%) 76 83	9, 21, 40, 75	5 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	9	ALA	4.8
1	C	150	ILE	3.5
1	C	29	LEU	3.4
1	C	332[A]	PHE	3.4
1	D	332	PHE	2.8
1	C	154	GLY	2.8
1	C	152	SER	2.6
1	D	152	SER	2.5
1	C	30	PRO	2.5
1	D	29	LEU	2.4
1	C	155	LYS	2.4
1	C	15	GLY	2.3
1	D	155	LYS	2.2
1	C	31	GLY	2.1
1	A	152	SER	2.1
1	D	15	GLY	2.0
1	C	151	ASP	2.0
1	C	153	ASP	2.0
1	C	157	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SNC	C	265	8/9	0.88	0.12	26,30,37,42	0
1	SNC	B	265	8/9	0.96	0.06	12,15,22,25	0
1	SNC	D	265	8/9	0.96	0.08	17,22,24,31	0
1	SNC	A	265	8/9	0.98	0.05	15,16,21,32	0

## 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
6	EDO	B	506	4/4	0.79	0.18	33,37,38,41	0
7	GOL	B	509	6/6	0.79	0.14	32,38,43,51	0
8	BTB	A	513	14/14	0.79	0.15	26,36,40,41	0
8	BTB	D	507	14/14	0.79	0.15	40,60,65,69	0
7	GOL	A	511	6/6	0.80	0.16	41,44,44,46	0
6	EDO	A	509	4/4	0.80	0.16	33,40,41,46	0
6	EDO	A	508	4/4	0.81	0.14	50,52,54,55	0
6	EDO	D	506	4/4	0.81	0.16	43,43,47,47	0
6	EDO	A	506	4/4	0.82	0.16	42,46,47,47	0
8	BTB	A	514	14/14	0.84	0.16	40,55,65,66	0
7	GOL	B	510	6/6	0.85	0.12	39,45,45,50	0
6	EDO	B	507	4/4	0.86	0.13	43,45,47,49	0
7	GOL	B	508	6/6	0.88	0.12	34,38,41,44	0
6	EDO	A	510	4/4	0.89	0.12	34,38,39,40	0
8	BTB	A	512	14/14	0.92	0.10	25,30,36,37	0
6	EDO	A	507	4/4	0.93	0.10	24,33,35,38	0
5	5Z9	B	505	7/7	0.94	0.07	11,14,16,17	0
5	5Z9	C	505	7/7	0.96	0.07	19,23,24,25	0

*Continued on next page...*

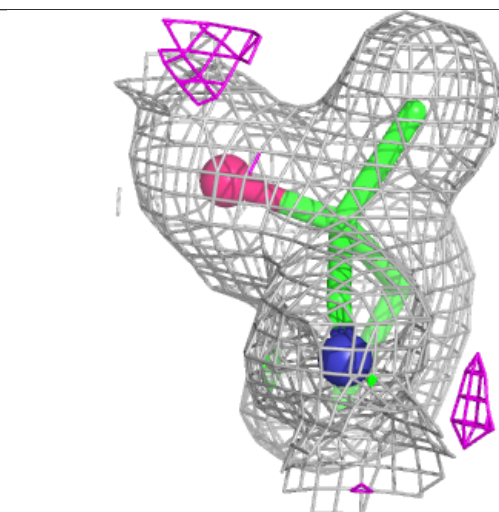
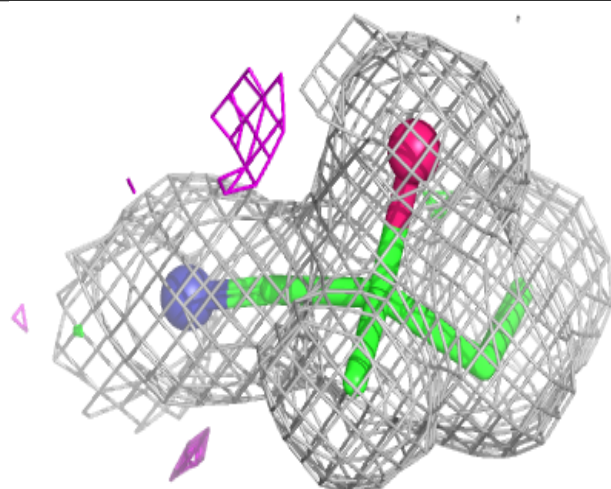
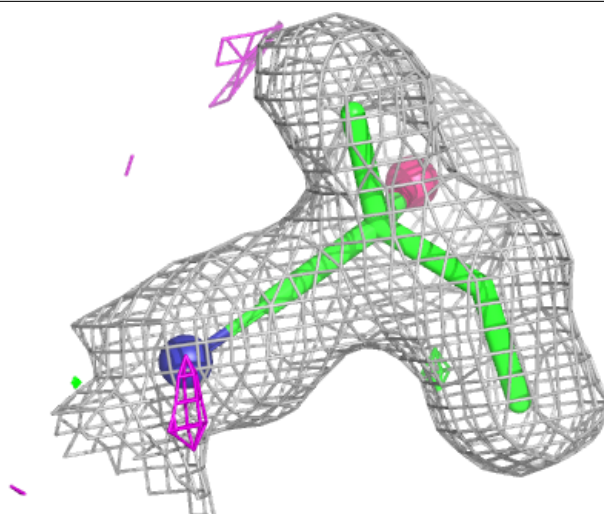
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	5Z9	D	505	7/7	0.96	0.07	21,24,27,27	0
2	NAD	D	501	44/44	0.97	0.05	17,21,23,25	0
5	5Z9	A	505	7/7	0.97	0.05	14,14,15,15	0
2	NAD	C	501	44/44	0.97	0.05	16,24,27,28	0
2	NAD	A	501	44/44	0.98	0.04	10,13,15,16	0
2	NAD	B	501	44/44	0.98	0.04	10,13,16,19	0
3	ZN	D	502	1/1	0.98	0.03	21,21,21,21	1
4	MG	D	504	1/1	0.98	0.04	34,34,34,34	0
3	ZN	A	502	1/1	0.99	0.02	14,14,14,14	0
4	MG	A	504	1/1	0.99	0.02	14,14,14,14	0
4	MG	B	504	1/1	0.99	0.07	16,16,16,16	0
4	MG	C	504	1/1	0.99	0.07	31,31,31,31	0
3	ZN	C	503	1/1	0.99	0.03	23,23,23,23	0
3	ZN	D	503	1/1	1.00	0.04	23,23,23,23	0
3	ZN	B	503	1/1	1.00	0.02	12,12,12,12	0
3	ZN	C	502	1/1	1.00	0.03	23,23,23,23	0
3	ZN	A	503	1/1	1.00	0.03	14,14,14,14	0
3	ZN	B	502	1/1	1.00	0.01	15,15,15,15	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.

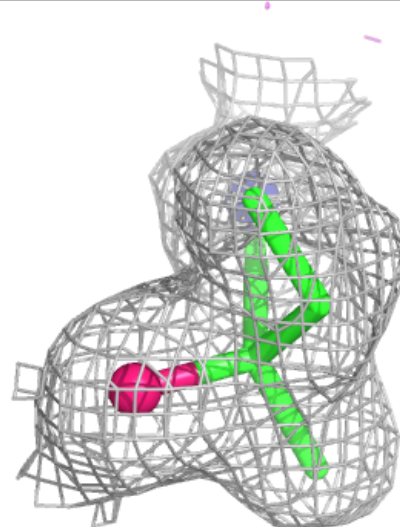
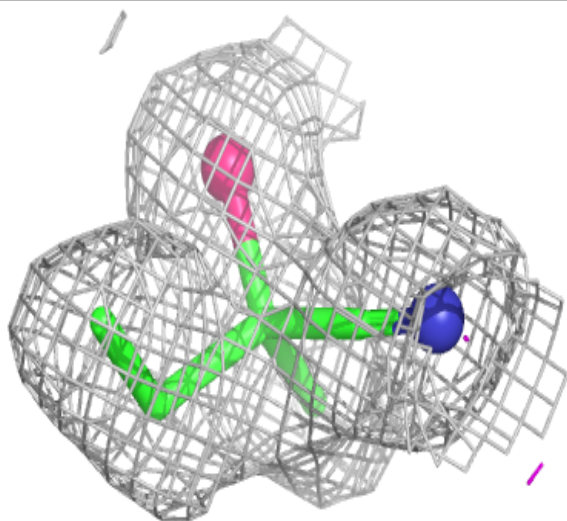
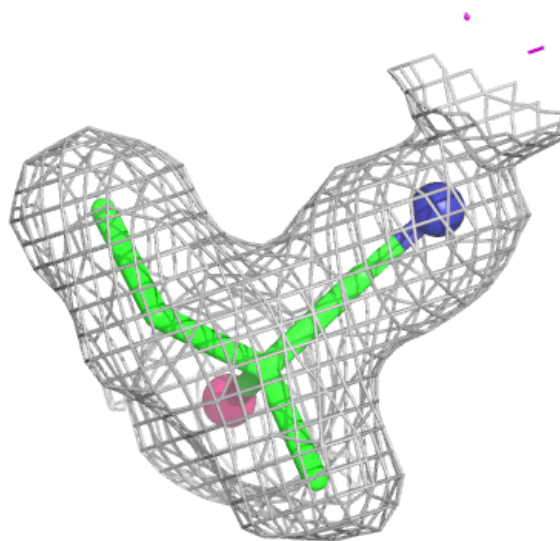
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and green (positive)



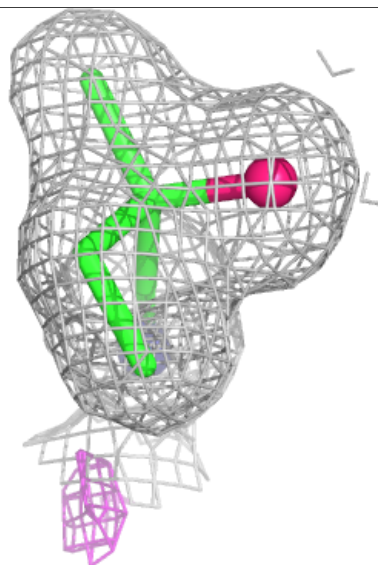
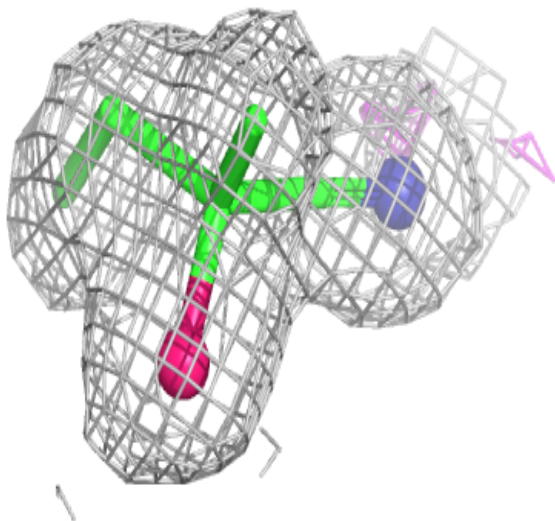
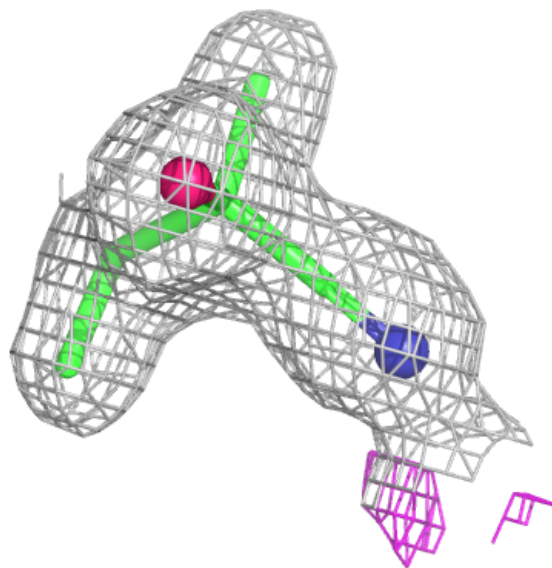
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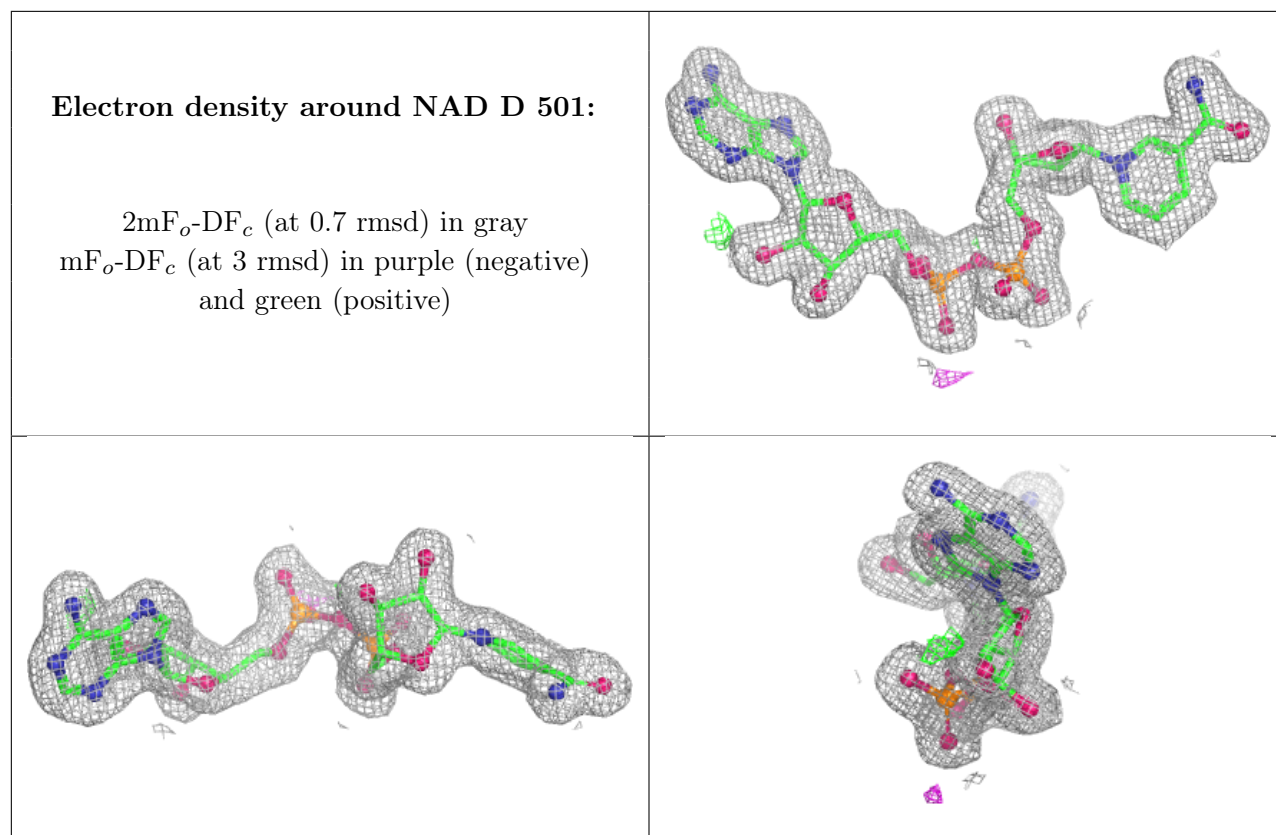
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and green (positive)



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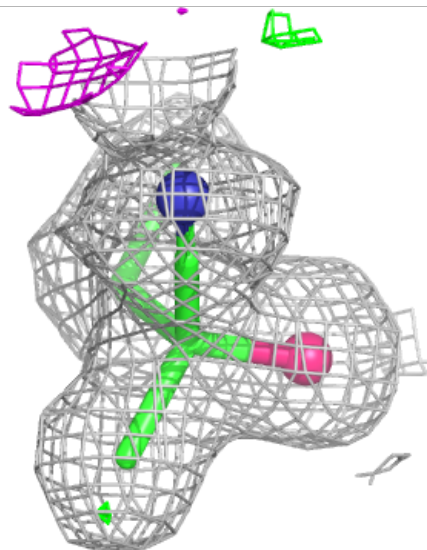
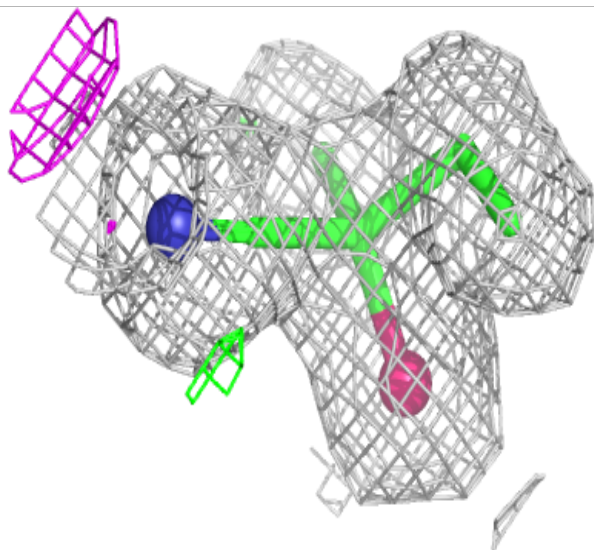
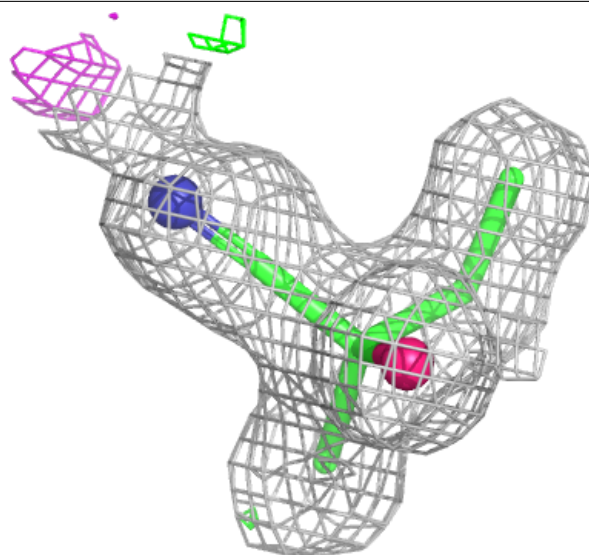
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and green (positive)





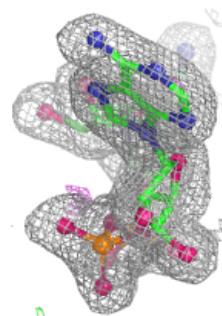
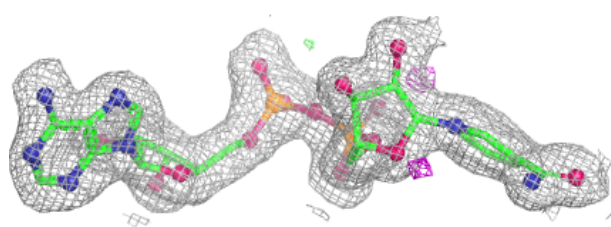
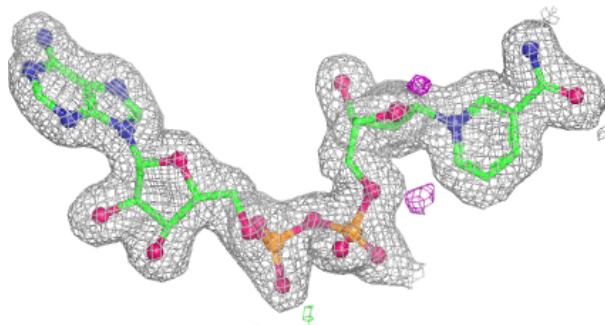
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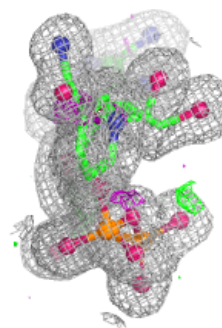
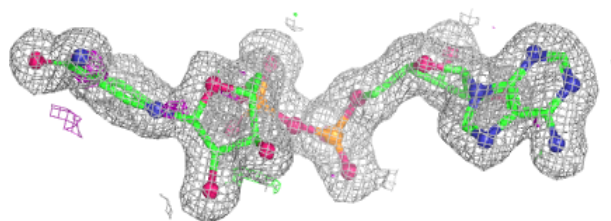
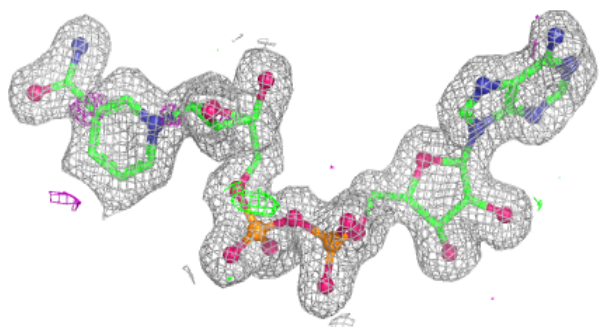


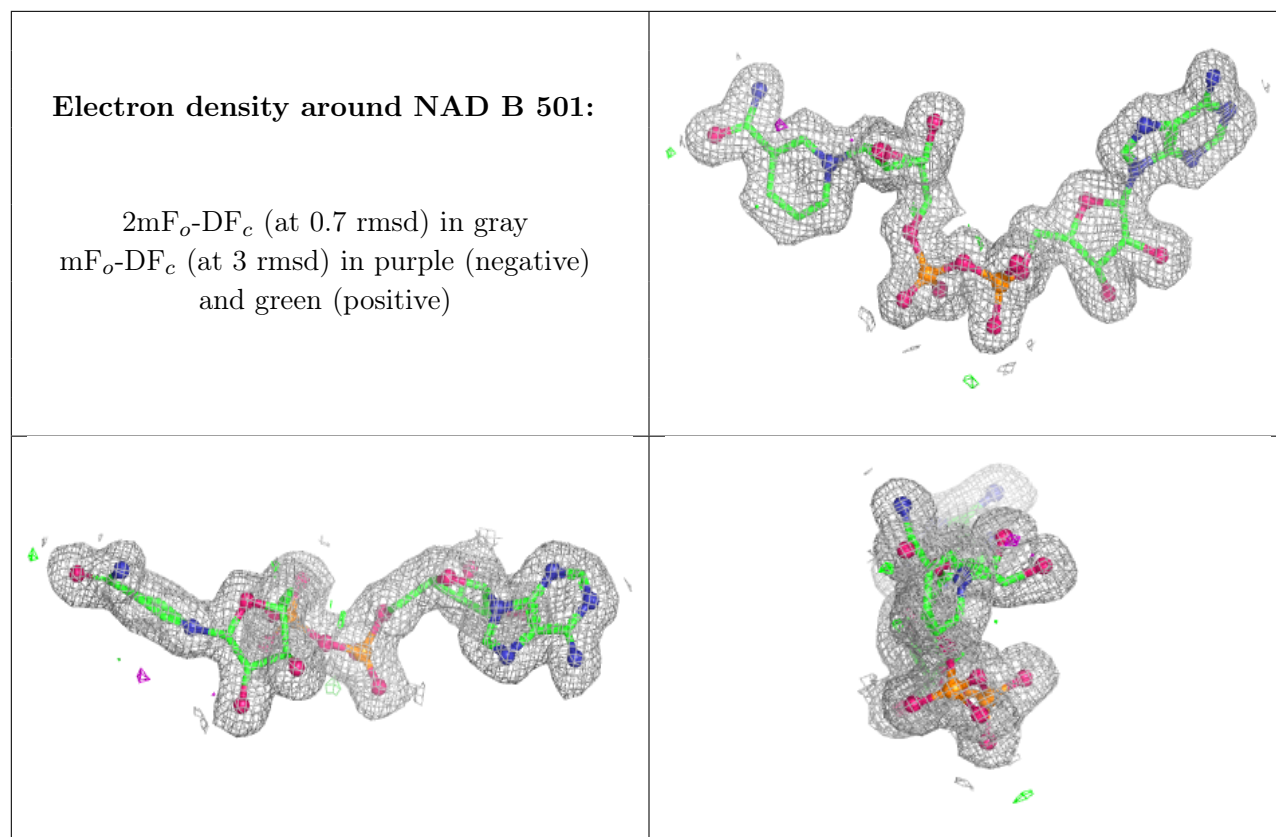
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and green (positive)

**Electron density around NAD A 501:**

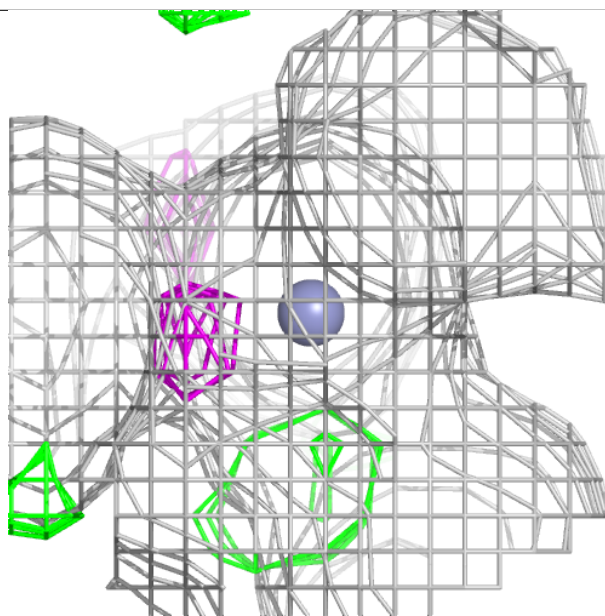
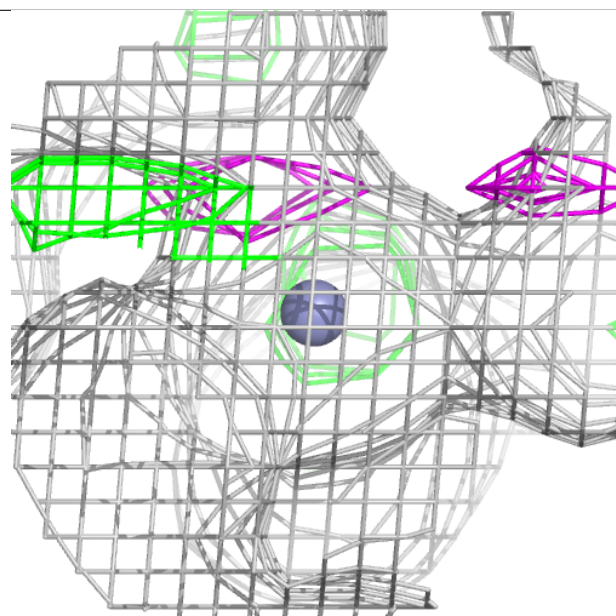
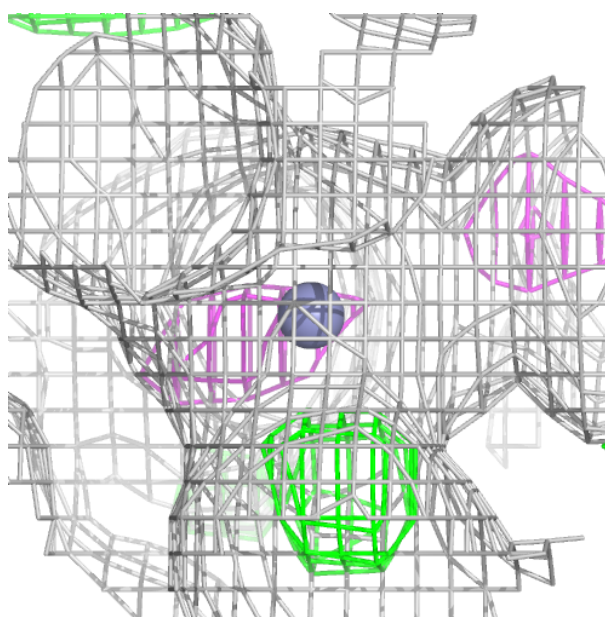
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and green (positive)





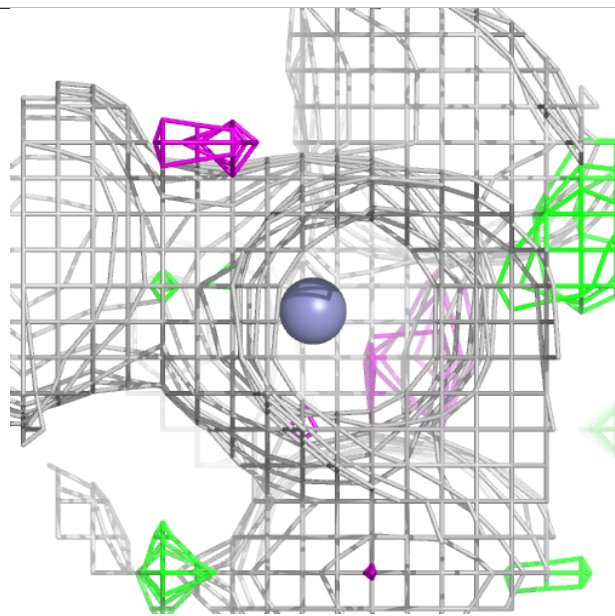
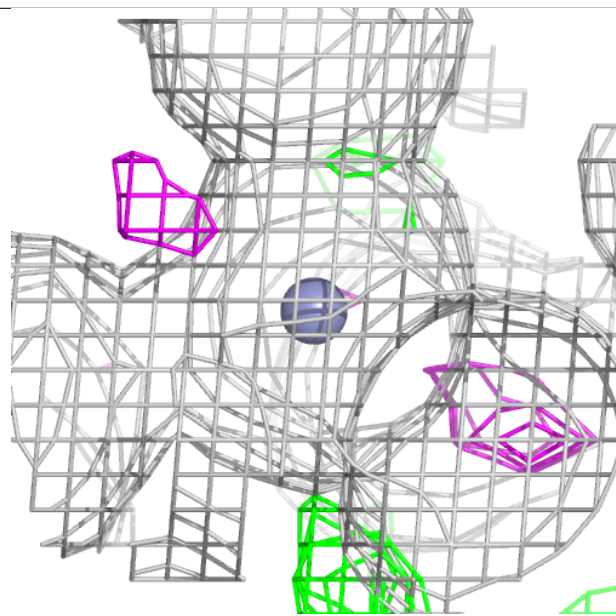
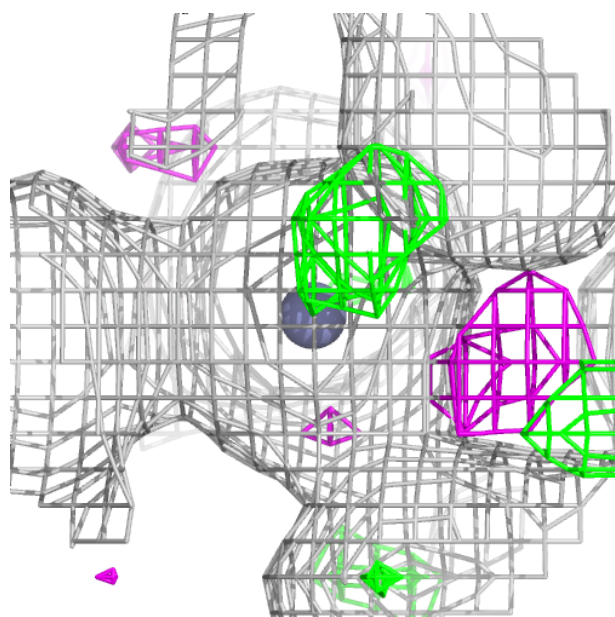
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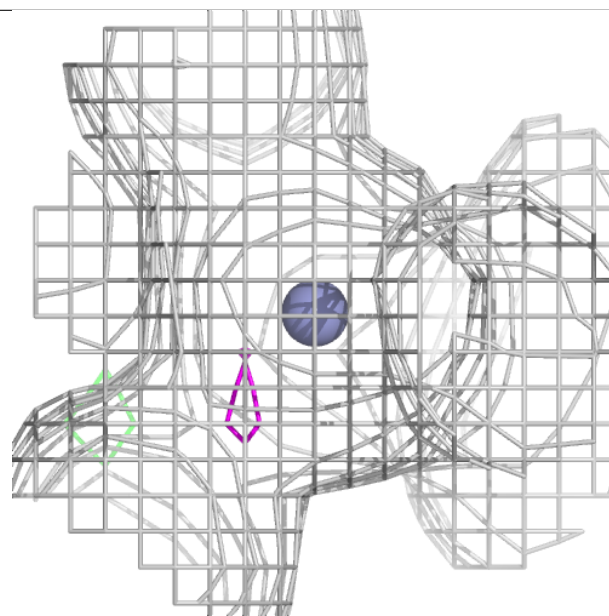
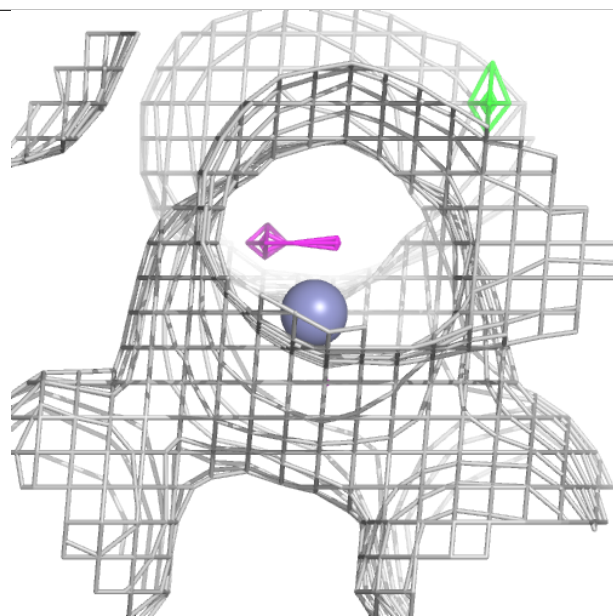
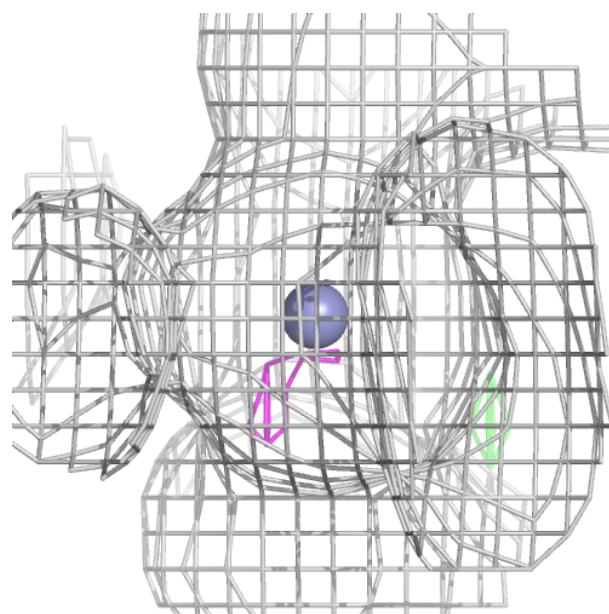
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and green (positive)



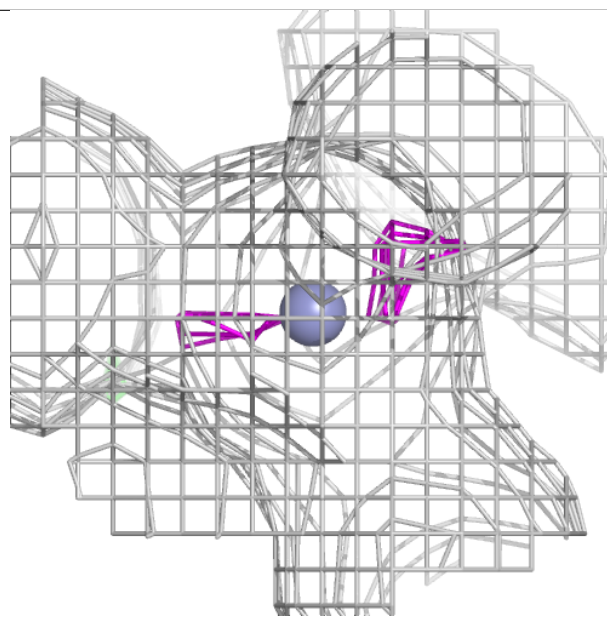
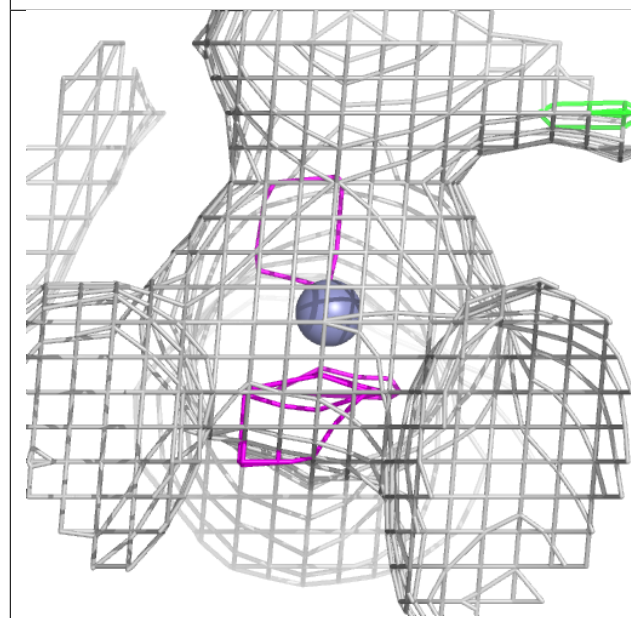
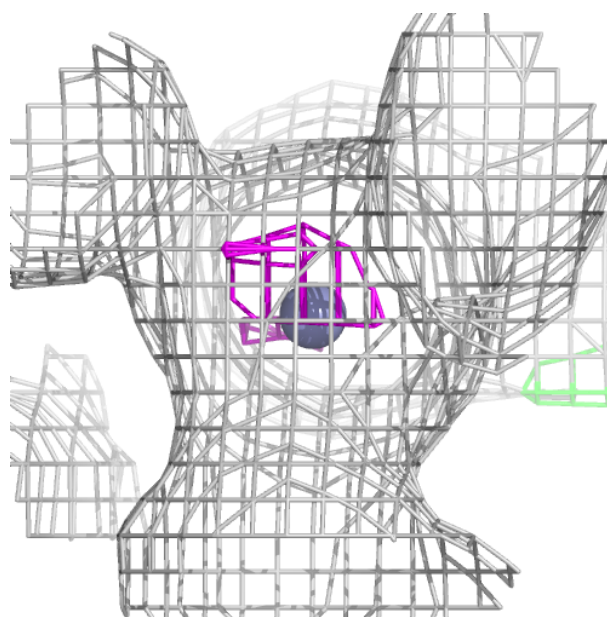
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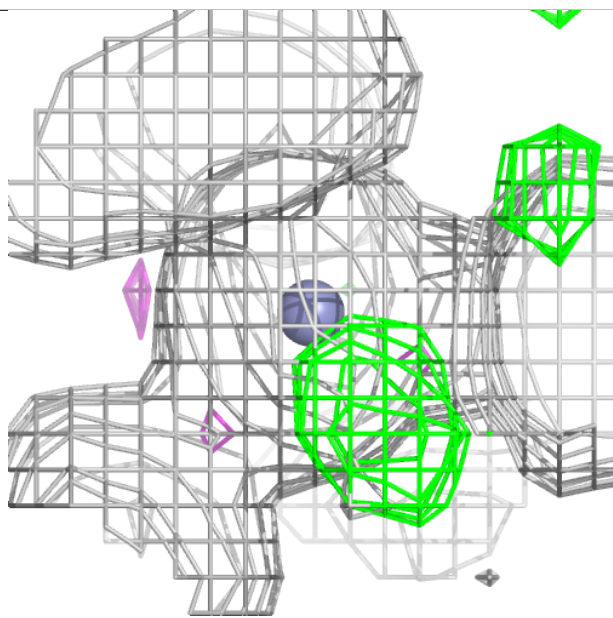
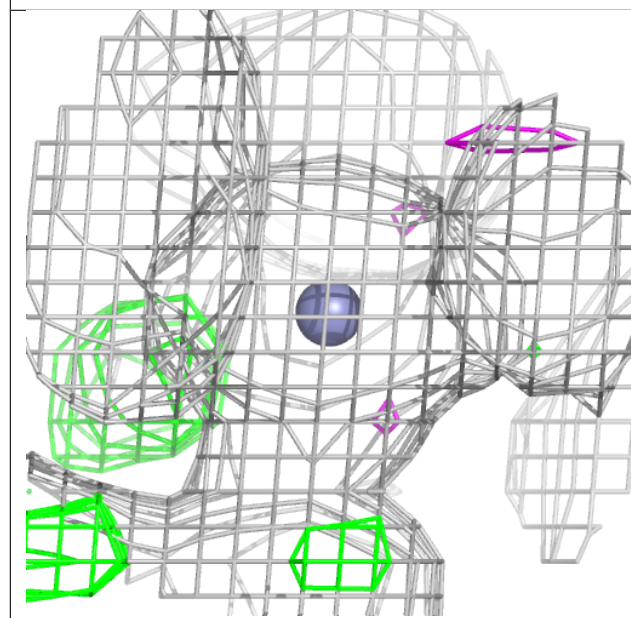
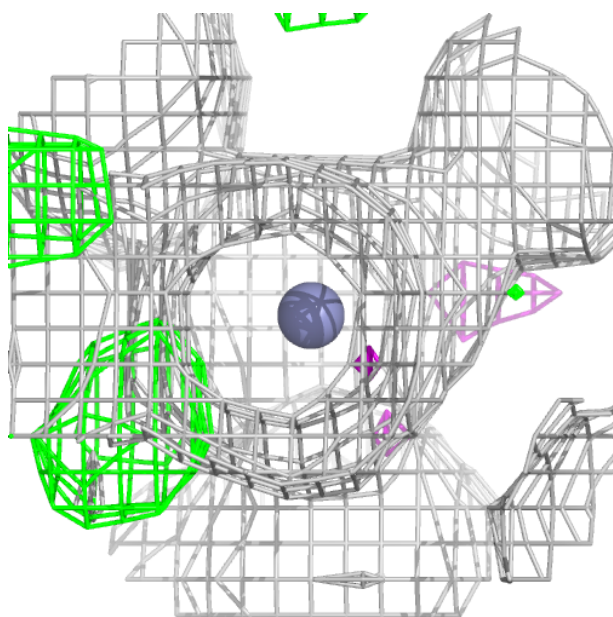
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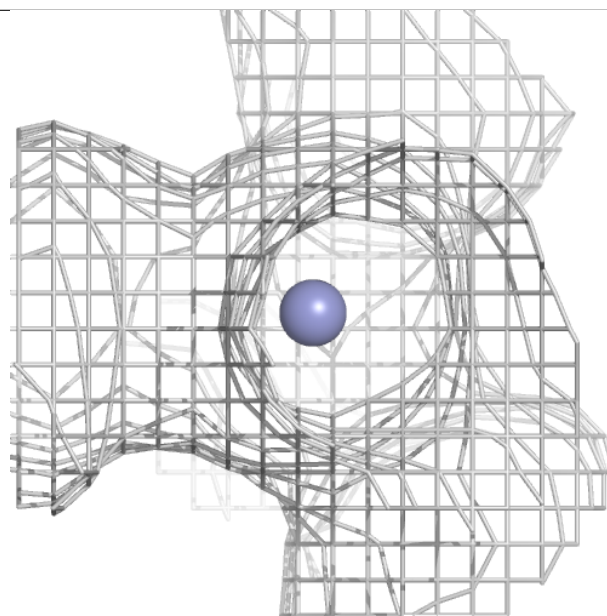
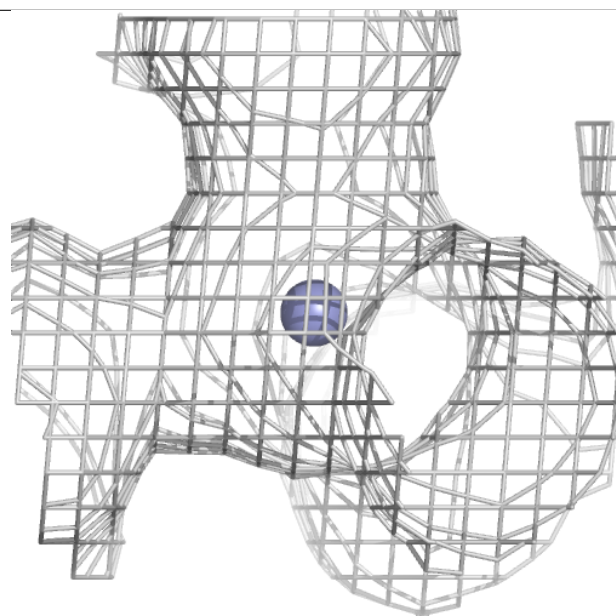
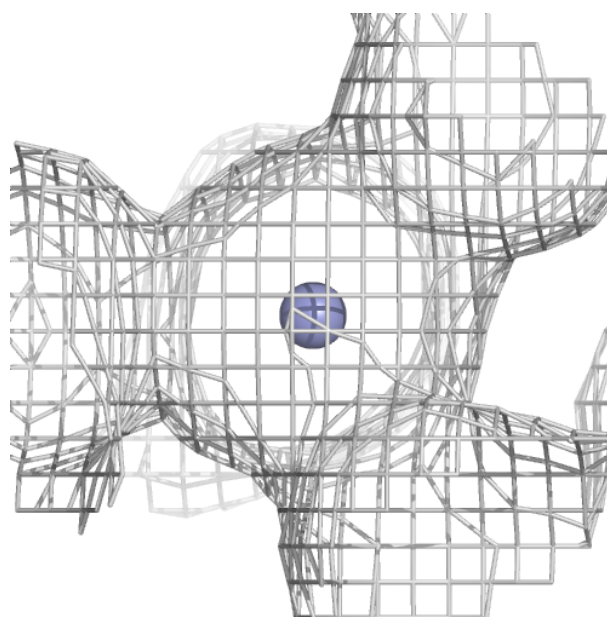
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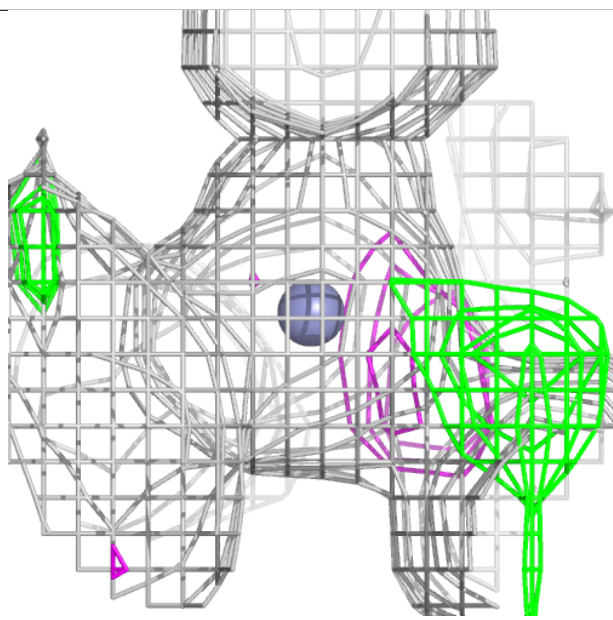
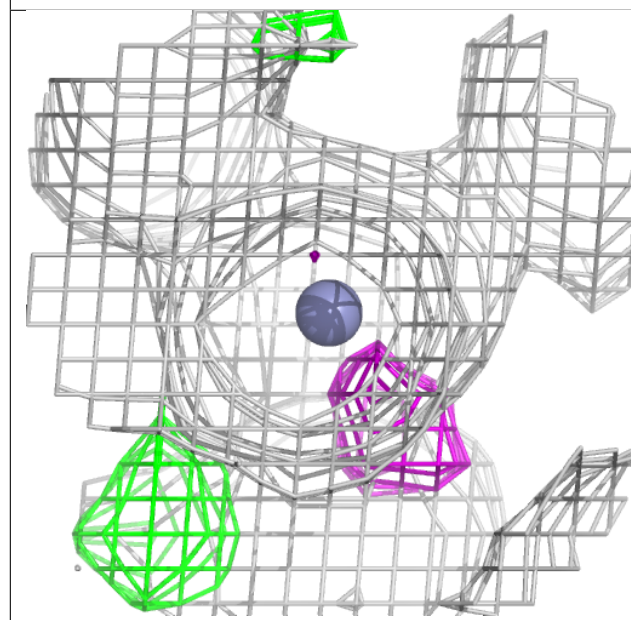
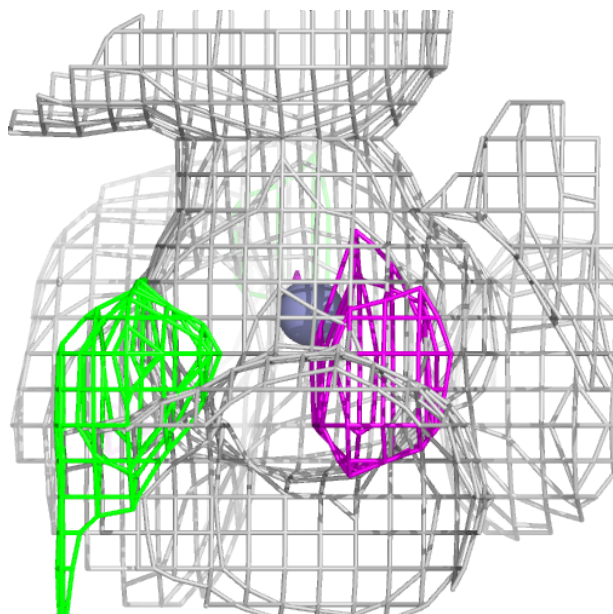
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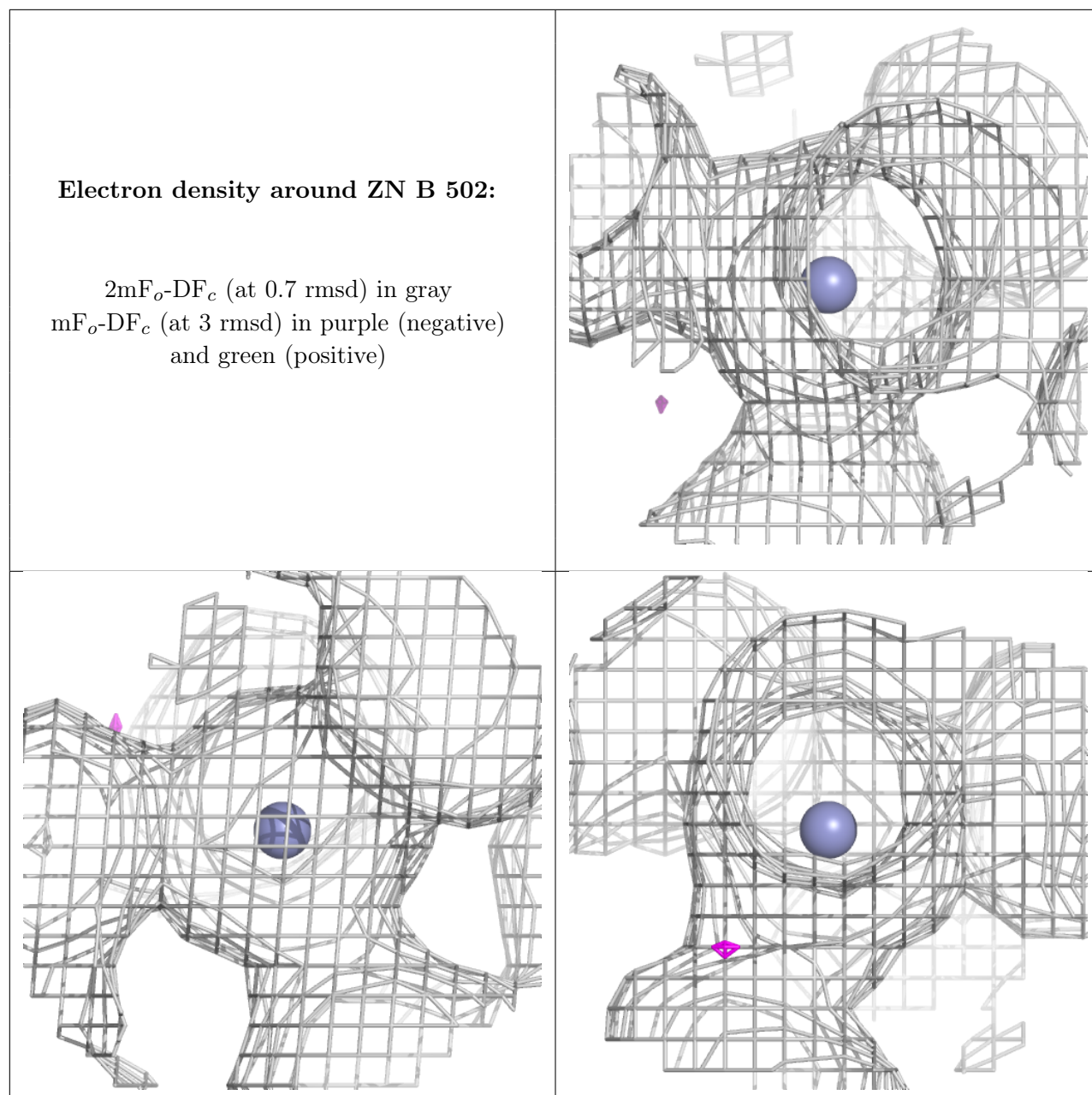
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and green (positive)



**Electron density around ZN A 503:**

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and green (positive)





## 6.5 Other polymers ⓘ

There are no such residues in this entry.