



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:07 AM UTC

PDB ID : 7A8Y / pdb_00007a8y
Title : X-ray crystal structure of Aspartate alpha-decarboxylase in complex with D-Serine
Authors : Yorke, B.A.; Raskar, T.
Deposited on : 2020-08-31
Resolution : 1.75 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

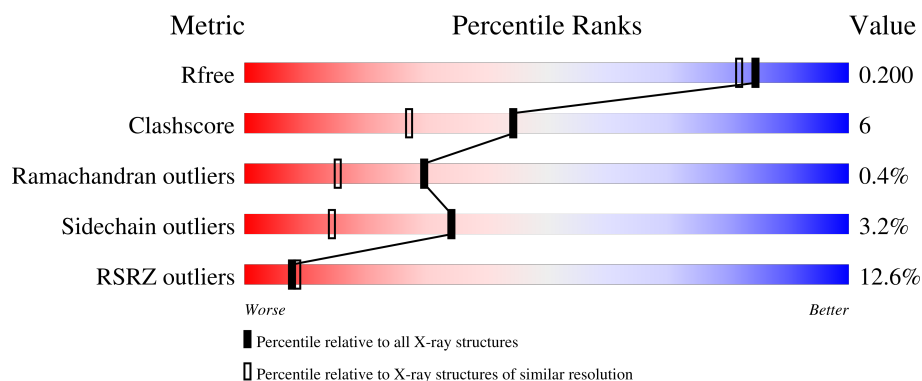
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	AAA	27	30% 67% 26% . .
1	DDD	27	30% 89% 7% .
2	BBB	95	7% 89% 11%
2	EaE	95	9% 91% 7% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DSN	BBB	201	-	-	-	X
3	DSN	EaE	203	-	X	-	X
5	SER	EaE	202	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 2163 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 Aspartate 1-decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	26	Total	C	N	O	S	0	3	0
			227	144	44	36	3			
1	DDD	25	Total	C	N	O	S	0	0	0
			203	127	40	34	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-2	ALA	-	expression tag	UNP A0A4Y8GT61
AAA	-1	GLY	-	expression tag	UNP A0A4Y8GT61
AAA	0	SER	-	expression tag	UNP A0A4Y8GT61
DDD	-2	ALA	-	expression tag	UNP A0A4Y8GT61
DDD	-1	GLY	-	expression tag	UNP A0A4Y8GT61
DDD	0	SER	-	expression tag	UNP A0A4Y8GT61

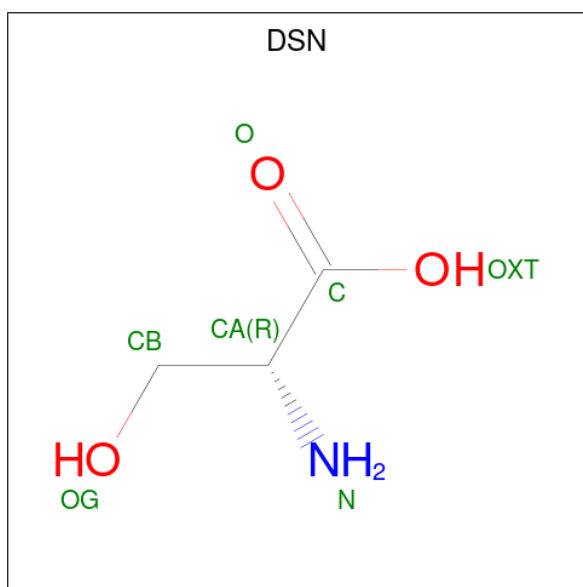
- Molecule 2 is a protein called Aspartate 1-decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	BBB	94	Total	C	N	O	S	0	6	0
			747	468	125	150	4			
2	EaE	94	Total	C	N	O	S	0	6	0
			748	467	128	149	4			

There are 2 discrepancies between the modelled and reference sequences:

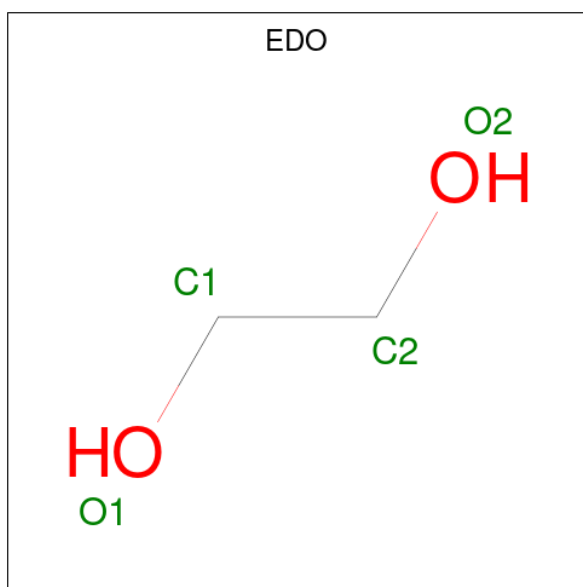
Chain	Residue	Modelled	Actual	Comment	Reference
BBB	92	THR	SER	conflict	UNP A0A4Y8GT61
EaE	92	THR	SER	conflict	UNP A0A4Y8GT61

- Molecule 3 is D-SERINE (CCD ID: DSN) (formula: $C_3H_7NO_3$) (labeled as "Ligand of Interest" by depositor).



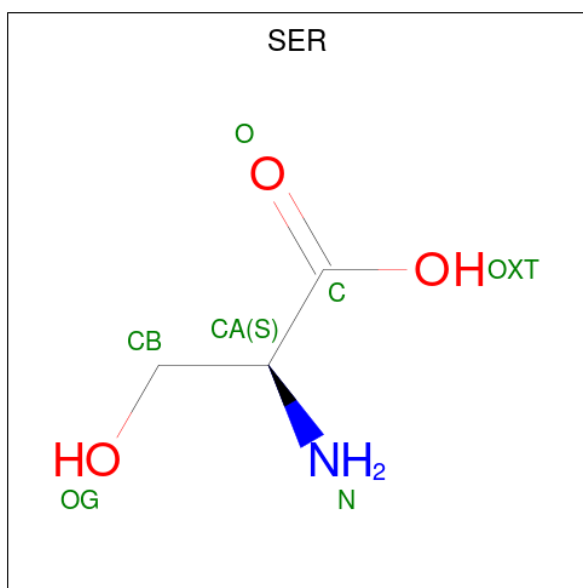
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	BBB	1	Total	C	N	O	0	0
			6	3	1	2		
3	BBB	1	Total	C	N	O	0	0
			7	3	1	3		
3	EaE	1	Total	C	N	O	0	0
			6	3	1	2		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	EaE	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is SERINE (CCD ID: SER) (formula: $C_3H_7NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	EaE	1	Total	C	N	O	0	0
			7	3	1	3		

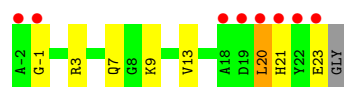
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	AAA	23	Total	O	0	0
			23	23		
6	BBB	88	Total	O	0	0
			88	88		
6	DDD	21	Total	O	0	0
			21	21		
6	EaE	76	Total	O	0	0
			76	76		

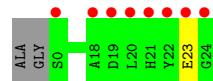
3 Residue-property plots [i](#)

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.

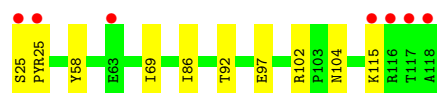
- Molecule 1: Aspartate 1-decarboxylase



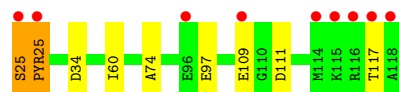
- Molecule 1: Aspartate 1-decarboxylase



- Molecule 2: Aspartate 1-decarboxylase



- Molecule 2: Aspartate 1-decarboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	71.30Å 71.30Å 216.65Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.98 – 1.75 46.98 – 1.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.98-1.75) 100.0 (46.98-1.75)	Depositor EDS
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.45 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.171 , 0.191 0.181 , 0.200	Depositor DCC
R_{free} test set	1702 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	18.5	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2163	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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: PYR, EDO, DSN

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	AAA	0.94	0/237	1.11	0/316
1	DDD	0.94	0/206	1.12	0/274
2	BBB	0.96	0/760	1.14	0/1031
2	EaE	0.97	0/761	1.19	0/1032
All	All	0.96	0/1964	1.16	0/2653

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	BBB	0	1
2	EaE	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	BBB	25[B]	PYR	Mainchain
2	EaE	25[B]	PYR	Mainchain

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	AAA	227	0	241	8	0
1	DDD	203	0	212	0	0
2	BBB	747	0	703	12	0
2	EaE	748	0	707	8	1
3	BBB	13	0	5	1	0
3	EaE	6	0	3	1	0
4	EaE	4	0	6	1	0
5	EaE	7	0	4	7	0
6	AAA	23	0	0	0	0
6	BBB	88	0	0	1	1
6	DDD	21	0	0	0	1
6	EaE	76	0	0	0	0
All	All	2163	0	1881	23	2

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 6.

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)
2:EaE:25[A]:SER:OG	2:EaE:60[A]:ILE:CD1	2.01	1.09
2:EaE:25[A]:SER:OG	2:EaE:60[A]:ILE:HD11	1.64	0.93
2:EaE:25[A]:SER:OG	2:EaE:60[A]:ILE:HD12	1.69	0.88
2:EaE:25[A]:SER:CB	2:EaE:60[A]:ILE:HD11	2.10	0.82
2:BBB:86[B]:ILE:CD1	5:EaE:202:SER:OG	2.30	0.79
2:BBB:86[B]:ILE:HD13	5:EaE:202:SER:OG	1.86	0.74
2:EaE:25[A]:SER:CB	2:EaE:60[A]:ILE:CD1	2.66	0.71
1:AAA:-1:GLY:O	2:EaE:97[A]:GLU:OE1	2.17	0.63
2:BBB:86[B]:ILE:HD12	5:EaE:202:SER:OG	2.09	0.52
2:EaE:34:ASP:OD1	4:EaE:201:EDO:H21	2.10	0.52
2:BBB:58:TYR:CE1	3:BBB:201:DSN:CB	2.96	0.49
2:BBB:86[A]:ILE:HG13	5:EaE:202:SER:OG	2.13	0.48
1:AAA:13[A]:VAL:HG22	2:BBB:69:ILE:HG13	1.97	0.47
2:EaE:74:ALA:HB3	5:EaE:202:SER:HB3	1.98	0.44
1:AAA:13[A]:VAL:CG2	2:BBB:69:ILE:HG13	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BBB:97[A]:GLU:HG3	6:BBB:359:HOH:O	2.18	0.43
1:AAA:9:LYS:NZ	3:EaE:203:DSN:H	2.17	0.42
1:AAA:7:GLN:NE2	2:BBB:104:ASN:HD22	2.18	0.42
2:BBB:86[B]:ILE:HD12	5:EaE:202:SER:HG	1.84	0.42
1:AAA:20:LEU:HD23	1:AAA:20:LEU:HA	1.95	0.41
2:BBB:86[A]:ILE:HG13	5:EaE:202:SER:CB	2.50	0.41
1:AAA:3:ARG:O	2:BBB:92:THR:HA	2.19	0.41
1:AAA:21[B]:HIS:CD2	1:AAA:21[B]:HIS:O	2.73	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EaE:111:ASP:OD2	2:EaE:111:ASP:OD2[9_554]	2.14	0.06
6:BBB:384:HOH:O	6:DDD:115:HOH:O[10_664]	2.18	0.02

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	AAA	27/27 (100%)	27 (100%)	0	0	100	100
1	DDD	23/27 (85%)	22 (96%)	1 (4%)	0	100	100
2	BBB	97/95 (102%)	94 (97%)	3 (3%)	0	100	100
2	EaE	97/95 (102%)	92 (95%)	4 (4%)	1 (1%)	12	3
All	All	244/244 (100%)	235 (96%)	8 (3%)	1 (0%)	30	15

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	EaE	117	THR

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	AAA	25/22 (114%)	23 (92%)	2 (8%)	11	2
1	DDD	22/22 (100%)	21 (96%)	1 (4%)	24	7
2	BBB	76/73 (104%)	74 (97%)	2 (3%)	40	20
2	EaE	76/73 (104%)	75 (99%)	1 (1%)	61	46
All	All	199/190 (105%)	193 (97%)	6 (3%)	34	16

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	20	LEU
1	AAA	23	GLU
2	BBB	102	ARG
2	BBB	115	LYS
1	DDD	23	GLU
2	EaE	109	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

5 ligands 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	$\# Z > 2$
5	SER	EaE	202	3	4,6,6	1.39	1 (25%)	2,7,7	1.77	1 (50%)
3	DSN	EaE	203	5	5,5,6	1.07	1 (20%)	6,6,7	1.50	2 (33%)
3	DSN	BBB	202	-	4,6,6	1.28	1 (25%)	2,7,7	2.17	1 (50%)
3	DSN	BBB	201	-	5,5,6	1.12	1 (20%)	6,6,7	1.23	1 (16%)
4	EDO	EaE	201	-	3,3,3	0.34	0	2,2,2	0.17	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	SER	EaE	202	3	-	0/6/6/6	-
3	DSN	EaE	203	5	-	4/4/4/6	-
3	DSN	BBB	202	-	-	2/6/6/6	-
3	DSN	BBB	201	-	-	0/4/4/6	-
4	EDO	EaE	201	-	-	1/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	EaE	202	SER	OXT-C	-2.77	1.21	1.30
3	BBB	202	DSN	OXT-C	-2.54	1.22	1.30
3	BBB	201	DSN	OXT-C	-2.33	1.23	1.30
3	EaE	203	DSN	OXT-C	-2.32	1.23	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	BBB	202	DSN	OXT-C-O	-2.94	117.40	124.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	EaE	203	DSN	OXT-C-O	-2.80	117.73	124.08
5	EaE	202	SER	OXT-C-O	-2.46	118.51	124.08
3	EaE	203	DSN	OXT-C-CA	2.25	121.53	113.79
3	BBB	201	DSN	OXT-C-O	-2.20	119.09	124.08

There are no chirality outliers.

All (7) torsion outliers are listed below:

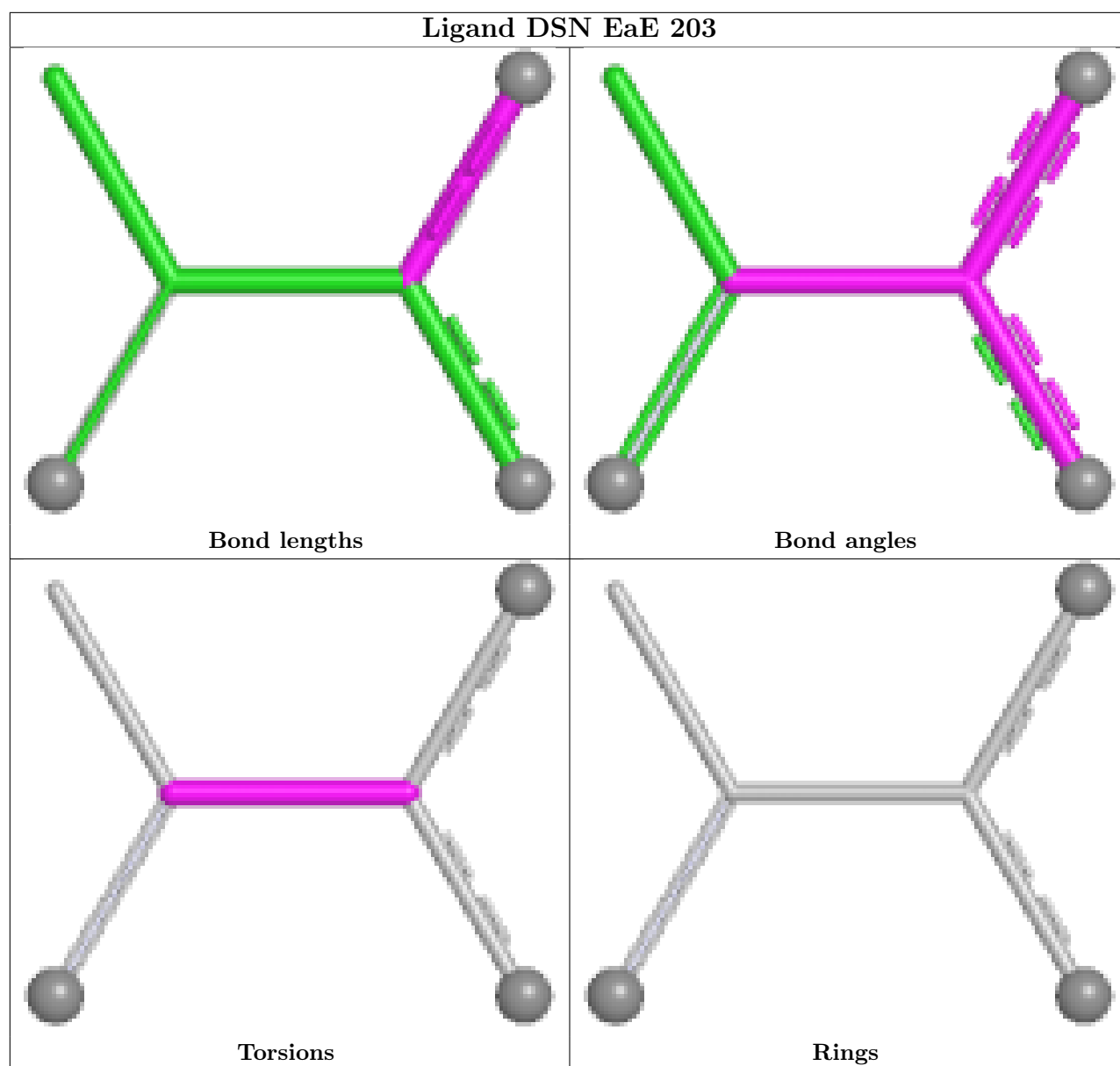
Mol	Chain	Res	Type	Atoms
3	BBB	202	DSN	O-C-CA-CB
3	BBB	202	DSN	OXT-C-CA-CB
3	EaE	203	DSN	O-C-CA-CB
3	EaE	203	DSN	OXT-C-CA-CB
4	EaE	201	EDO	O1-C1-C2-O2
3	EaE	203	DSN	O-C-CA-N
3	EaE	203	DSN	OXT-C-CA-N

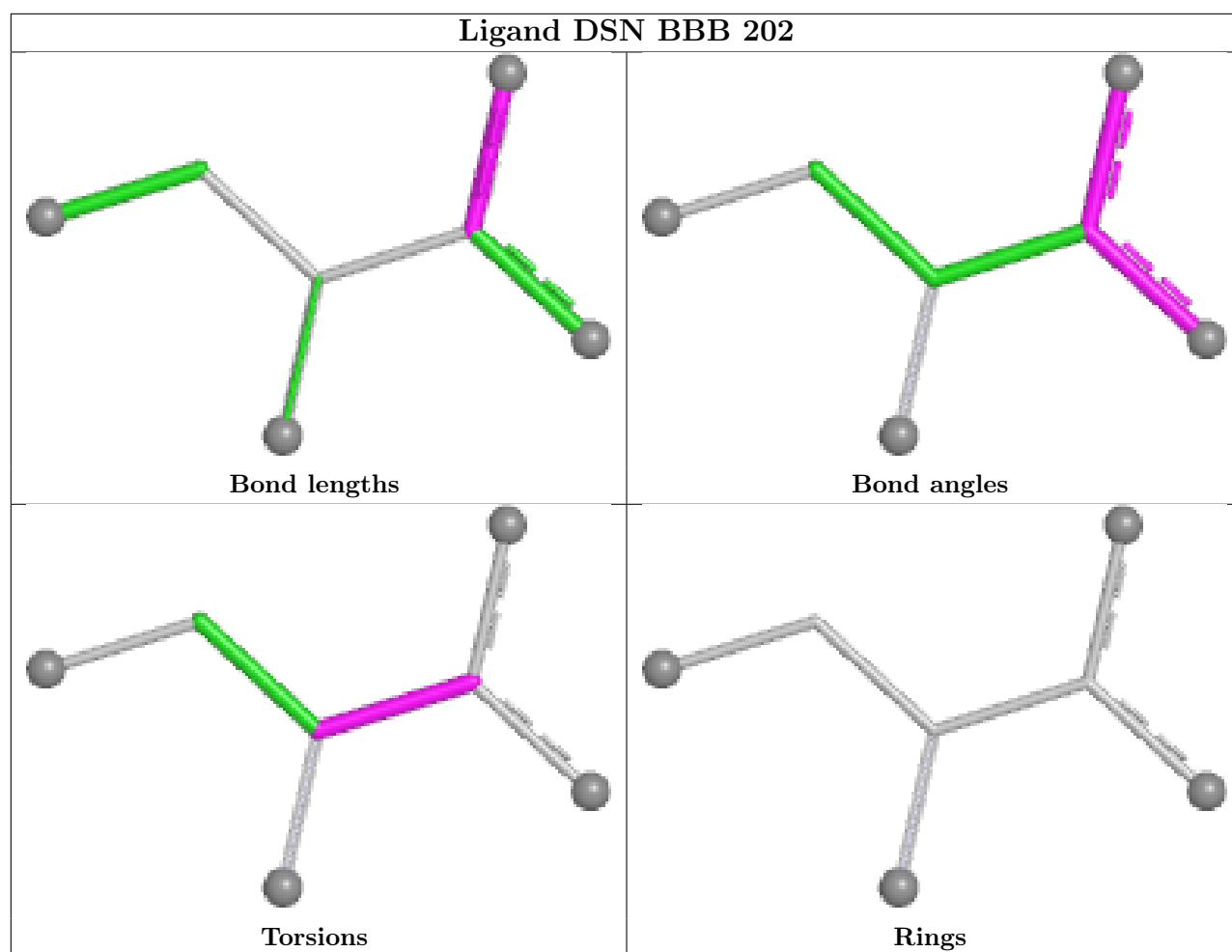
There are no ring outliers.

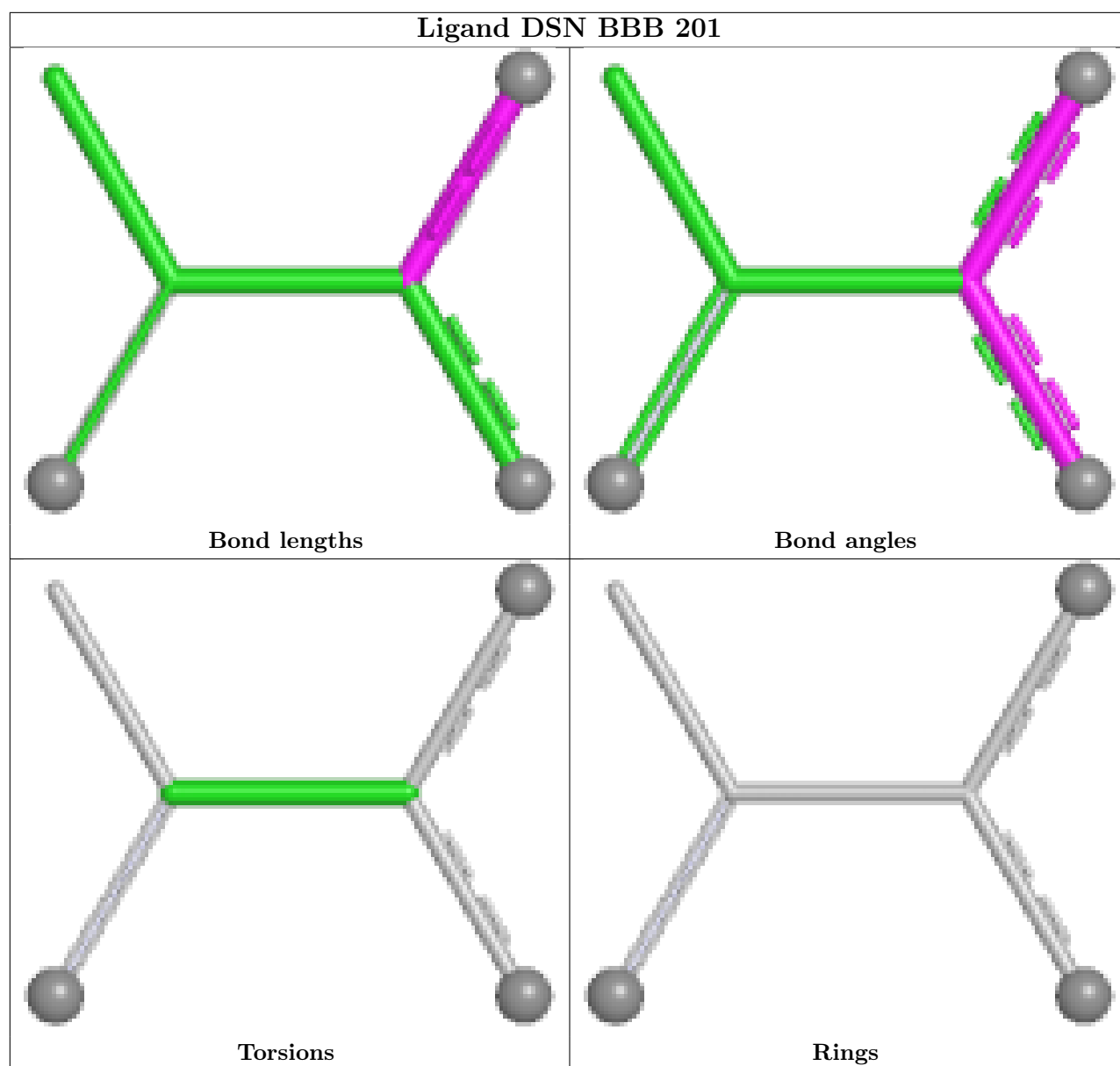
4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	EaE	202	SER	7	0
3	EaE	203	DSN	1	0
3	BBB	201	DSN	1	0
4	EaE	201	EDO	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 [i](#)

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	AAA	26/27 (96%)	0.99	8 (30%) 1 1	11, 18, 43, 55	3 (11%)
1	DDD	25/27 (92%)	1.18	8 (32%) 1 1	12, 22, 53, 61	0
2	BBB	93/95 (97%)	0.13	5 (5%) 31 35	7, 17, 30, 59	5 (5%)
2	EaE	93/95 (97%)	0.37	7 (7%) 20 23	8, 19, 40, 70	6 (6%)
All	All	237/244 (97%)	0.43	28 (11%) 8 10	7, 18, 43, 70	14 (5%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	EaE	117	THR	7.2
2	EaE	118	ALA	7.1
2	EaE	116	ARG	6.7
1	AAA	-2	ALA	6.5
2	BBB	117	THR	6.2
2	BBB	118	ALA	5.3
1	AAA	21[A]	HIS	4.7
1	DDD	0	SER	4.4
1	DDD	22	TYR	4.3
1	AAA	22	TYR	4.2
2	BBB	116	ARG	4.1
1	DDD	24	GLY	3.9
1	DDD	21	HIS	3.6
2	BBB	115	LYS	3.5
1	DDD	23	GLU	3.3
2	EaE	109	GLU	3.0
1	DDD	20	LEU	2.9
1	DDD	19	ASP	2.9
1	AAA	23	GLU	2.8
2	EaE	96	GLU	2.7
1	DDD	18	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
2	EaE	114	MET	2.4
2	BBB	63	GLU	2.3
1	AAA	20	LEU	2.3
2	EaE	115	LYS	2.3
1	AAA	19	ASP	2.3
1	AAA	18	ALA	2.1
1	AAA	-1	GLY	2.1

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 [i](#)

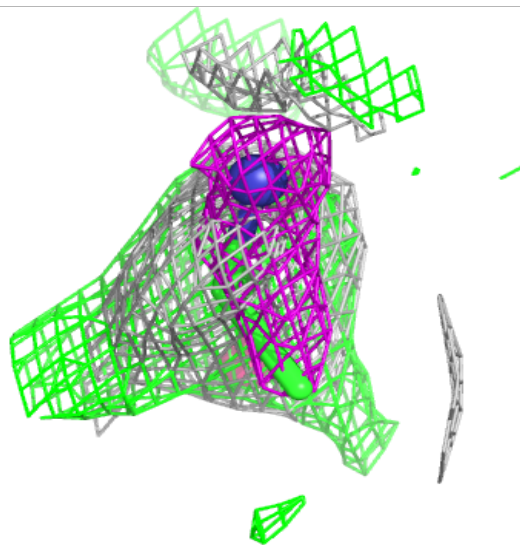
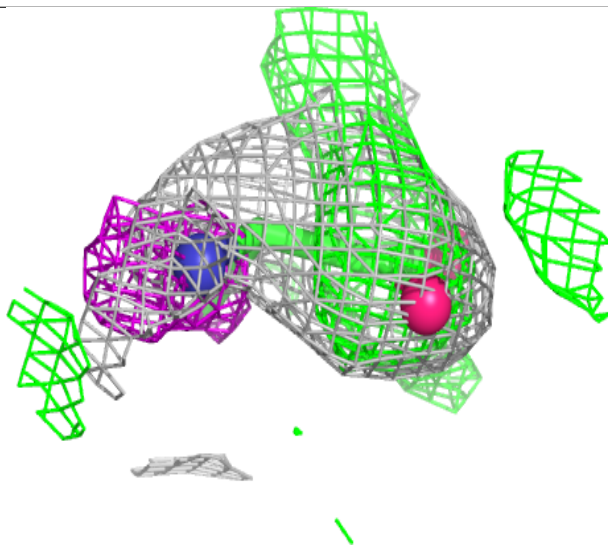
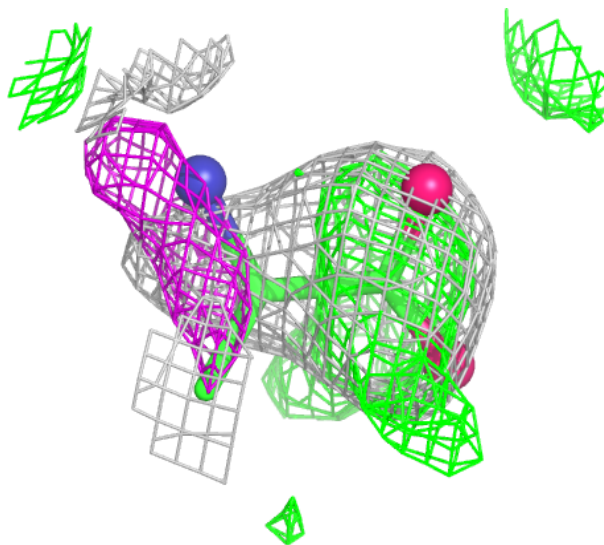
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	DSN	BBB	201	6/7	0.66	0.56	42,43,43,43	6
3	DSN	EaE	203	6/7	0.75	0.50	33,33,33,34	6
5	SER	EaE	202	7/7	0.75	0.35	30,33,34,36	7
3	DSN	BBB	202	7/7	0.76	0.27	26,26,29,32	7
4	EDO	EaE	201	4/4	0.89	0.16	26,31,32,35	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.

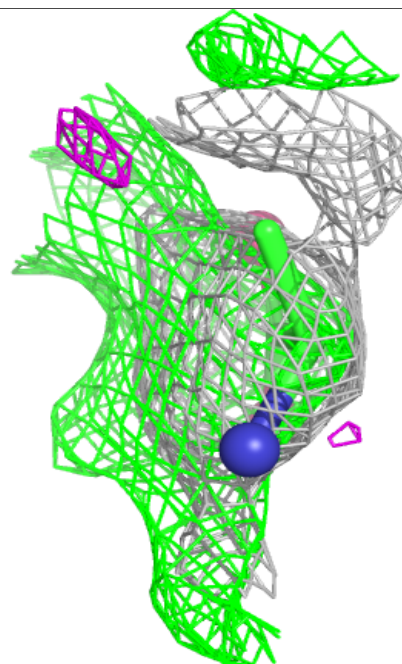
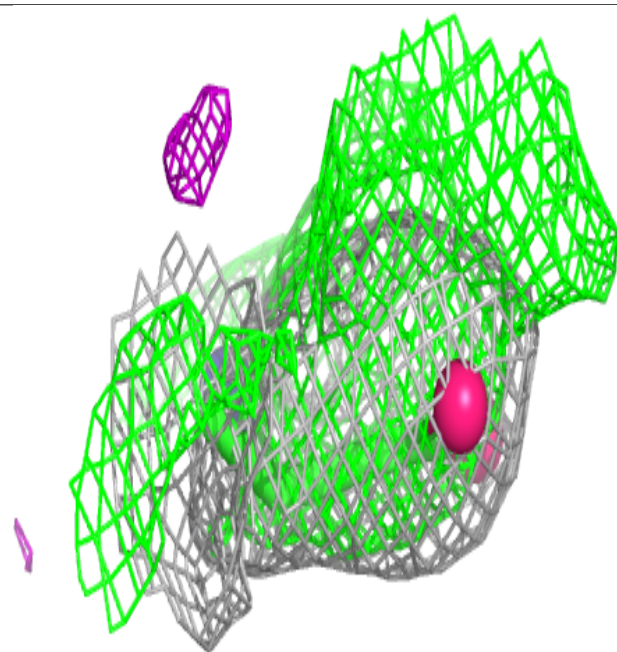
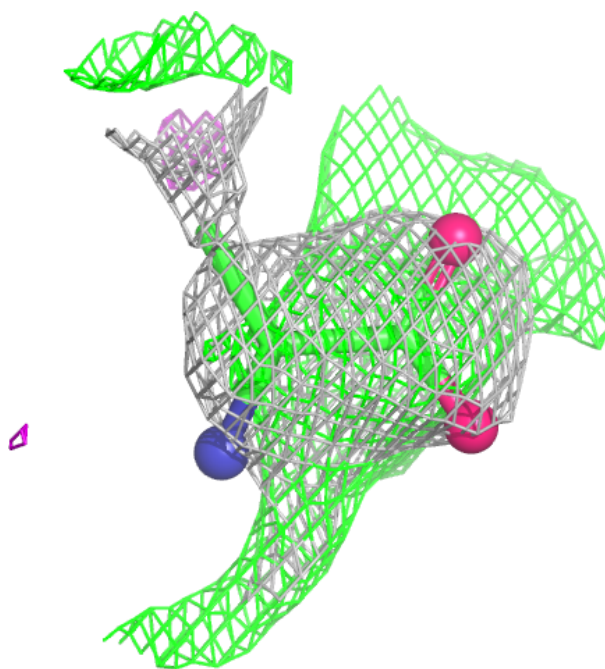
Electron density around DSN BBB 201:

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



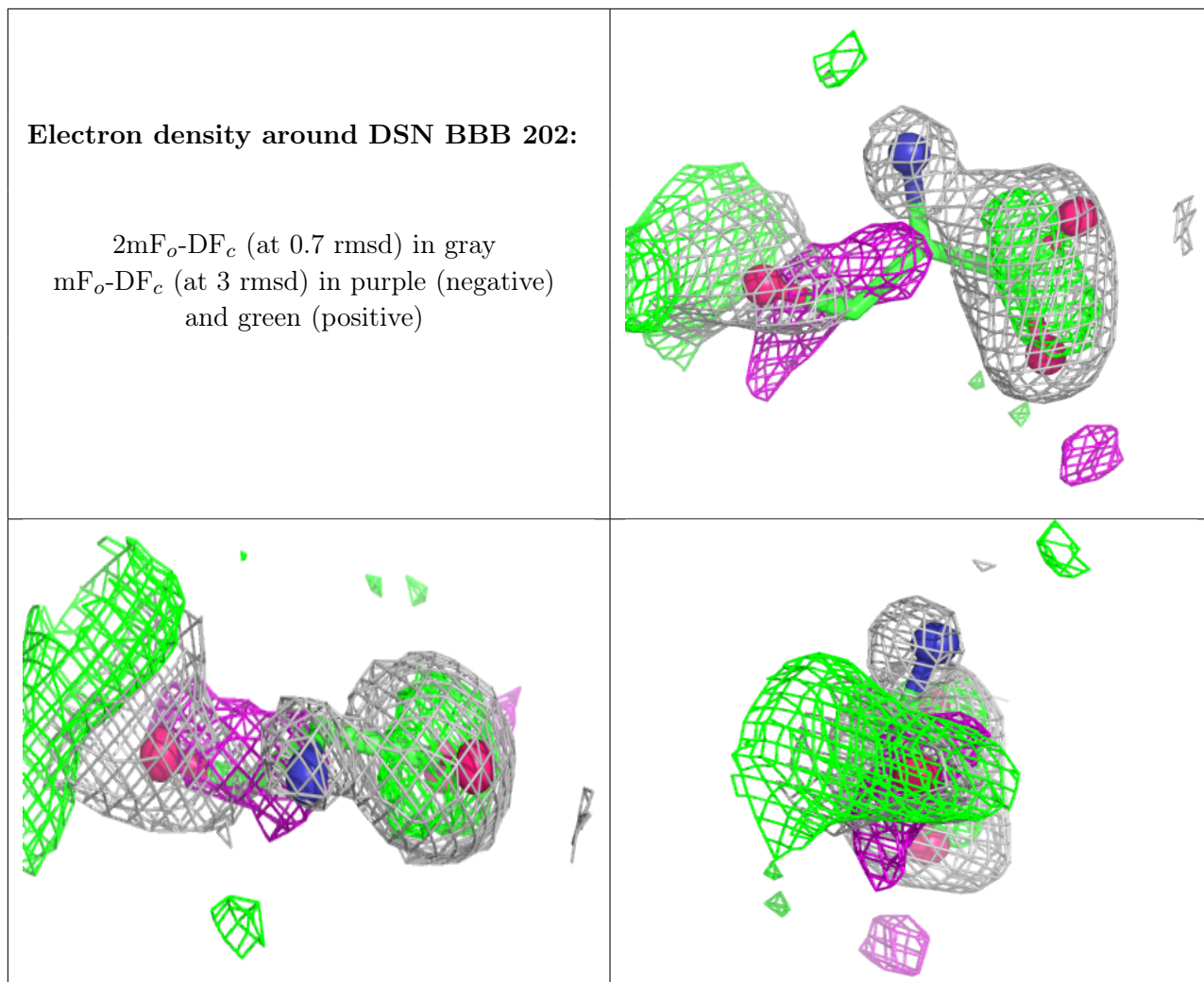
Electron density around DSN EaE 203:

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



Electron density around DSN BBB 202:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.