



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:24 AM UTC

PDB ID : 7AYZ / pdb_00007ayz
Title : Structure of the mouse 8-oxoguanine DNA Glycosylase mOGG1 in complex with activator TH10785
Authors : Masuyer, G.; Davies, J.R.; Stenmark, P.
Deposited on : 2020-11-13
Resolution : 2.60 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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

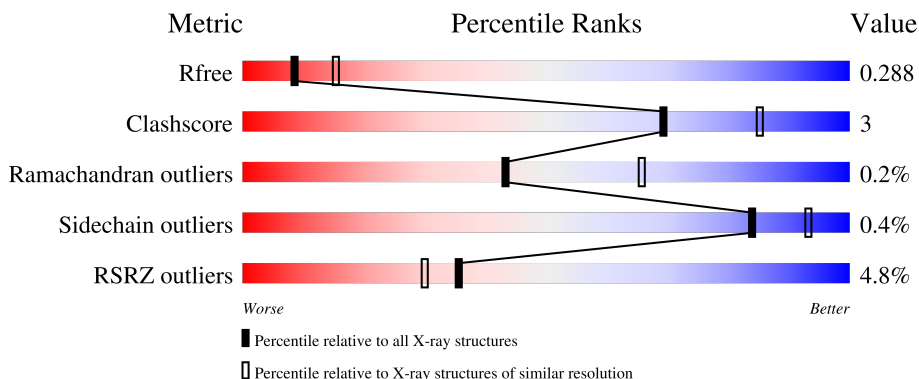
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	318	 2% 91% 7% .
1	BBB	318	 3% 87% 11% .
1	CCC	318	 10% 89% 9% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7509 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.

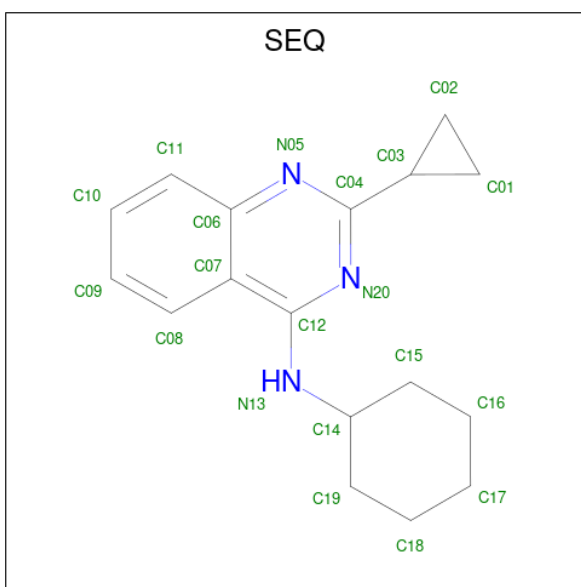
- Molecule 1 is a protein called N-glycosylase/DNA lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	311	Total	C	N	O	S	0	0	0
			2484	1581	448	444	11			
1	BBB	310	Total	C	N	O	S	0	0	0
			2472	1573	446	442	11			
1	CCC	313	Total	C	N	O	S	0	0	0
			2425	1540	433	441	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	8	GLY	-	expression tag	UNP O08760
AAA	10	HIS	SER	conflict	UNP O08760
BBB	8	GLY	-	expression tag	UNP O08760
BBB	10	HIS	SER	conflict	UNP O08760
CCC	8	GLY	-	expression tag	UNP O08760
CCC	10	HIS	SER	conflict	UNP O08760

- Molecule 2 is {N}-cyclohexyl-2-cyclopropyl-quinazolin-4-amine (CCD ID: SEQ) (formula: C₁₇H₂₁N₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AAA	1	Total	C	N	0	0
			20	17	3		
2	BBB	1	Total	C	N	0	0
			20	17	3		
2	CCC	1	Total	C	N	0	0
			20	17	3		

- Molecule 3 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	1	Total	Ni	0	0
			1	1		

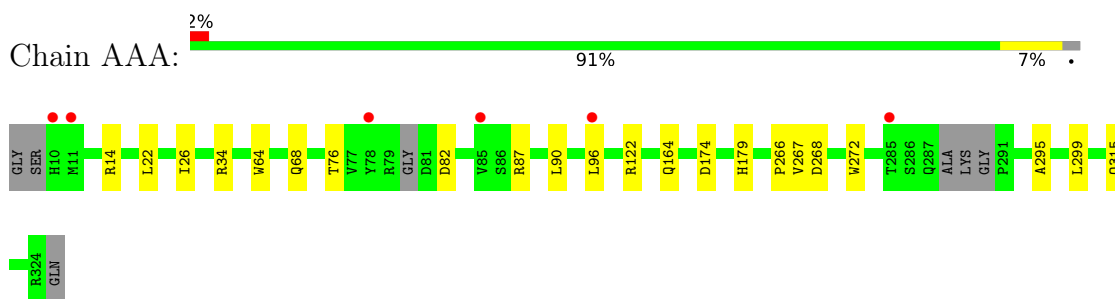
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	30	Total	O	0	0
			30	30		
4	BBB	24	Total	O	0	0
			24	24		
4	CCC	13	Total	O	0	0
			13	13		

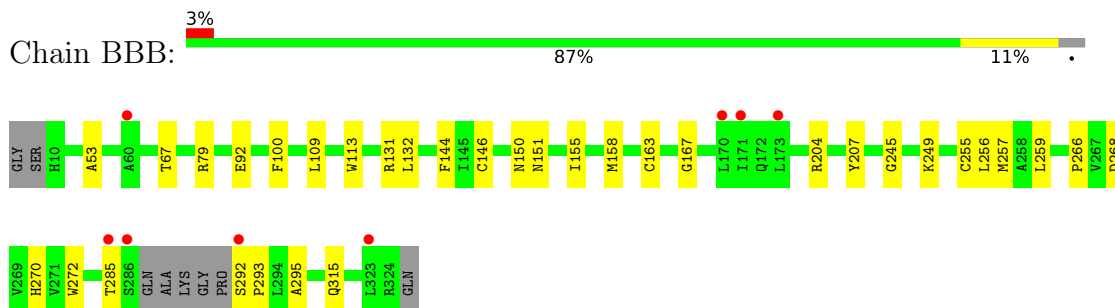
3 Residue-property plots [i](#)

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.

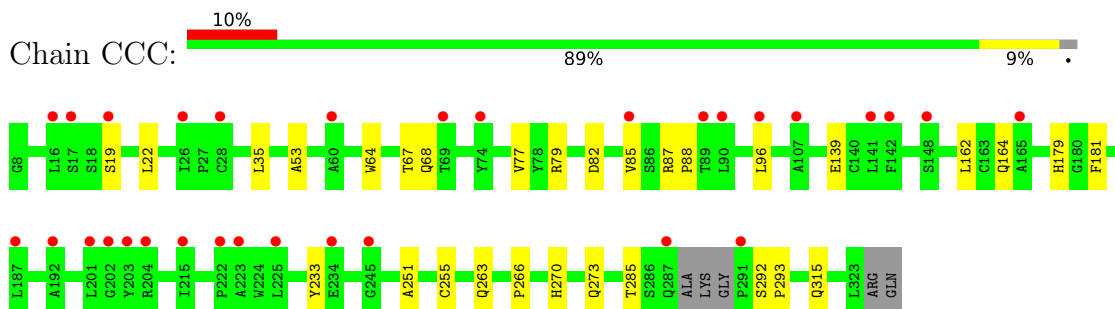
- Molecule 1: N-glycosylase/DNA lyase



- Molecule 1: N-glycosylase/DNA lyase



- Molecule 1: N-glycosylase/DNA lyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.83Å 81.80Å 170.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.87 – 2.60 73.87 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (73.87-2.60) 99.9 (73.87-2.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.237 , 0.286 0.238 , 0.288	Depositor DCC
R_{free} test set	1850 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å ²)	65.5	Xtriage
Anisotropy	0.484	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 31.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7509	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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: SEQ, NI

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	1.00	1/2553 (0.0%)	1.43	0/3473
1	BBB	1.00	0/2541	1.46	0/3458
1	CCC	1.03	0/2493	1.50	0/3401
All	All	1.01	1/7587 (0.0%)	1.46	0/10332

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	26	ILE	N-CA	5.30	1.50	1.45

There are no bond angle outliers.

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	AAA	2484	0	2427	13	0
1	BBB	2472	0	2415	23	0
1	CCC	2425	0	2309	16	0
2	AAA	20	0	0	0	0
2	BBB	20	0	0	0	0
2	CCC	20	0	0	0	0
3	AAA	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AAA	30	0	0	0	0
4	BBB	24	0	0	0	0
4	CCC	13	0	0	0	0
All	All	7509	0	7151	51	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 3.

All (51) 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:AAA:266:PRO:HD2	1:AAA:315:GLN:NE2	2.04	0.72
1:CCC:266:PRO:HD2	1:CCC:315:GLN:HE22	1.54	0.72
1:AAA:22:LEU:HA	1:AAA:87:ARG:HG2	1.74	0.69
1:BBB:266:PRO:HD2	1:BBB:315:GLN:HE22	1.56	0.69
1:CCC:64:TRP:CZ3	1:CCC:96:LEU:HD11	2.28	0.68
1:BBB:163:CYS:O	1:BBB:167:GLY:N	2.26	0.67
1:CCC:77:VAL:HG23	1:CCC:88:PRO:HG3	1.78	0.64
1:AAA:266:PRO:HD2	1:AAA:315:GLN:HE22	1.64	0.62
1:CCC:22:LEU:HD21	1:CCC:85:VAL:HG12	1.83	0.60
1:BBB:150:ASN:HD21	1:BBB:158:MET:CE	2.18	0.57
1:AAA:267:VAL:HG13	1:AAA:299:LEU:HD23	1.88	0.55
1:BBB:255:CYS:HA	1:BBB:259:LEU:HB2	1.90	0.54
1:BBB:207:TYR:CG	1:BBB:245:GLY:HA3	2.43	0.54
1:BBB:144:PHE:CZ	1:BBB:257:MET:HE1	2.43	0.53
1:BBB:272:TRP:HH2	1:BBB:295:ALA:HB1	1.72	0.53
1:BBB:146:CYS:HA	1:BBB:204:ARG:HD3	1.92	0.52
1:BBB:100:PHE:O	1:BBB:131:ARG:HD3	2.10	0.52
1:BBB:249:LYS:HD2	1:BBB:268:ASP:HB3	1.92	0.51
1:BBB:151:ASN:O	1:BBB:155:ILE:HG13	2.11	0.51
1:BBB:150:ASN:HD21	1:BBB:158:MET:HE3	1.75	0.50
1:AAA:22:LEU:CA	1:AAA:87:ARG:HG2	2.41	0.49
1:AAA:34:ARG:HA	1:AAA:68:GLN:HE22	1.77	0.48
1:AAA:122:ARG:NH2	1:BBB:270:HIS:CE1	2.82	0.48
1:BBB:292:SER:N	1:BBB:293:PRO:CD	2.76	0.48
1:AAA:272:TRP:HH2	1:AAA:295:ALA:HB1	1.80	0.47
1:CCC:139:GLU:HG3	1:CCC:181:PHE:CD1	2.49	0.47
1:CCC:35:LEU:H	1:CCC:68:GLN:HE22	1.62	0.46
1:CCC:79:ARG:NH2	1:CCC:87:ARG:O	2.49	0.46
1:CCC:19:SER:HB3	1:CCC:22:LEU:HB2	1.98	0.45
1:CCC:251:ALA:O	1:CCC:255:CYS:SG	2.74	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CCC:164:GLN:HA	1:CCC:179:HIS:CD2	2.52	0.45
1:AAA:164:GLN:HA	1:AAA:179:HIS:CG	2.51	0.45
1:AAA:90:LEU:C	1:AAA:90:LEU:HD23	2.43	0.44
1:BBB:53:ALA:O	1:BBB:67:THR:OG1	2.30	0.44
1:CCC:53:ALA:O	1:CCC:67:THR:OG1	2.22	0.44
1:CCC:162:LEU:C	1:CCC:162:LEU:HD23	2.43	0.44
1:BBB:163:CYS:O	1:BBB:167:GLY:CA	2.67	0.43
1:AAA:64:TRP:CZ2	1:AAA:96:LEU:HD11	2.53	0.43
1:CCC:233:TYR:HB2	1:CCC:263:GLN:NE2	2.34	0.43
1:CCC:266:PRO:HD2	1:CCC:315:GLN:NE2	2.30	0.43
1:BBB:266:PRO:HD2	1:BBB:315:GLN:NE2	2.30	0.42
1:BBB:132:LEU:HD21	1:BBB:256:LEU:HG	2.02	0.42
1:BBB:163:CYS:O	1:BBB:167:GLY:HA3	2.20	0.41
1:CCC:292:SER:HB2	1:CCC:293:PRO:HD2	2.02	0.41
1:AAA:14:ARG:NH1	1:AAA:76:THR:OG1	2.53	0.41
1:BBB:53:ALA:O	1:BBB:67:THR:CB	2.69	0.40
1:BBB:109:LEU:HB3	1:BBB:113:TRP:CH2	2.55	0.40
1:CCC:270:HIS:O	1:CCC:273:GLN:HB3	2.21	0.40
1:BBB:144:PHE:CE2	1:BBB:257:MET:HE1	2.56	0.40
1:AAA:268:ASP:OD1	1:AAA:268:ASP:C	2.65	0.40
1:BBB:79:ARG:NH2	1:BBB:92:GLU:OE1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AAA	305/318 (96%)	289 (95%)	15 (5%)	1 (0%)	36	58
1	BBB	306/318 (96%)	288 (94%)	18 (6%)	0	100	100
1	CCC	309/318 (97%)	291 (94%)	17 (6%)	1 (0%)	36	58
All	All	920/954 (96%)	868 (94%)	50 (5%)	2 (0%)	43	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	CCC	285	THR
1	AAA	82	ASP

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	263/266 (99%)	262 (100%)	1 (0%)	84	93
1	BBB	261/266 (98%)	260 (100%)	1 (0%)	84	93
1	CCC	249/266 (94%)	248 (100%)	1 (0%)	84	93
All	All	773/798 (97%)	770 (100%)	3 (0%)	84	93

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	174	ASP
1	BBB	285	THR
1	CCC	82	ASP

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 [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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$
2	SEQ	CCC	401	-	21,23,23	1.18	3 (14%)	27,32,32	2.01	7 (25%)
2	SEQ	BBB	401	-	21,23,23	1.06	0	27,32,32	1.83	5 (18%)
2	SEQ	AAA	401	-	21,23,23	1.10	2 (9%)	27,32,32	1.63	5 (18%)

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
2	SEQ	CCC	401	-	-	0/8/18/18	0/4/4/4
2	SEQ	BBB	401	-	-	2/8/18/18	0/4/4/4
2	SEQ	AAA	401	-	-	0/8/18/18	0/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	CCC	401	SEQ	C12-C07	2.32	1.47	1.44
2	AAA	401	SEQ	C09-C08	2.21	1.41	1.36
2	CCC	401	SEQ	C09-C08	2.21	1.41	1.36
2	CCC	401	SEQ	C10-C11	2.10	1.41	1.36
2	AAA	401	SEQ	C12-C07	2.05	1.47	1.44

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	CCC	401	SEQ	C04-N05-C06	5.43	120.09	116.50
2	BBB	401	SEQ	C04-N05-C06	5.13	119.90	116.50
2	AAA	401	SEQ	C12-C07-C06	4.32	118.41	115.86
2	CCC	401	SEQ	C12-C07-C06	4.30	118.40	115.86
2	CCC	401	SEQ	C07-C06-N05	-4.25	118.30	122.80
2	BBB	401	SEQ	C12-C07-C06	4.03	118.24	115.86
2	BBB	401	SEQ	C07-C06-N05	-3.85	118.73	122.80
2	AAA	401	SEQ	C07-C06-N05	-3.75	118.83	122.80
2	AAA	401	SEQ	C04-N05-C06	3.29	118.68	116.50
2	CCC	401	SEQ	C16-C15-C14	2.83	116.17	111.09
2	CCC	401	SEQ	C12-N13-C14	-2.75	119.24	124.06
2	BBB	401	SEQ	C07-C12-N20	-2.61	118.15	122.07
2	BBB	401	SEQ	C12-N13-C14	-2.61	119.49	124.06
2	CCC	401	SEQ	C07-C12-N20	-2.53	118.28	122.07
2	AAA	401	SEQ	C07-C12-N20	-2.40	118.47	122.07
2	AAA	401	SEQ	C12-N13-C14	-2.22	120.17	124.06
2	CCC	401	SEQ	C17-C16-C15	2.02	115.57	111.42

There are no chirality outliers.

All (2) torsion outliers are listed below:

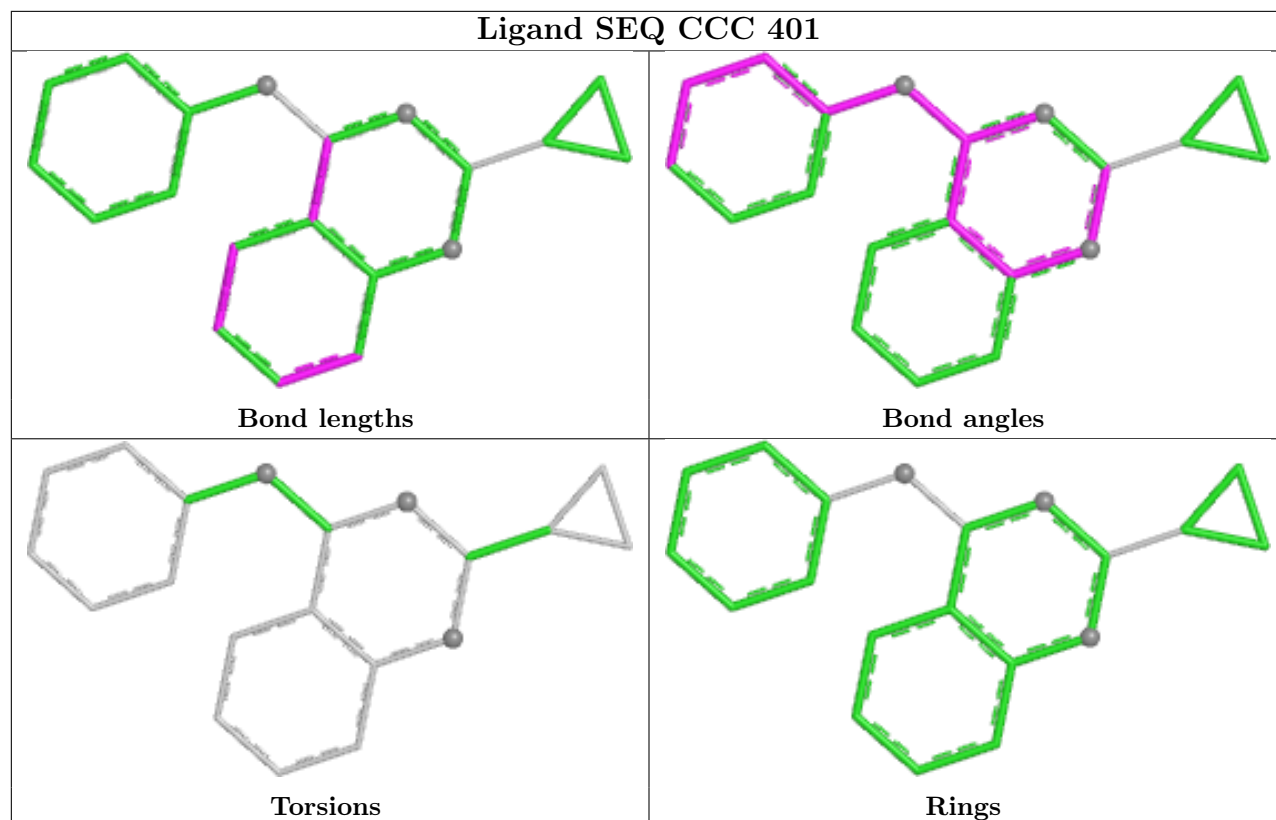
Mol	Chain	Res	Type	Atoms
2	BBB	401	SEQ	C01-C03-C04-N05
2	BBB	401	SEQ	C01-C03-C04-N20

There are no ring outliers.

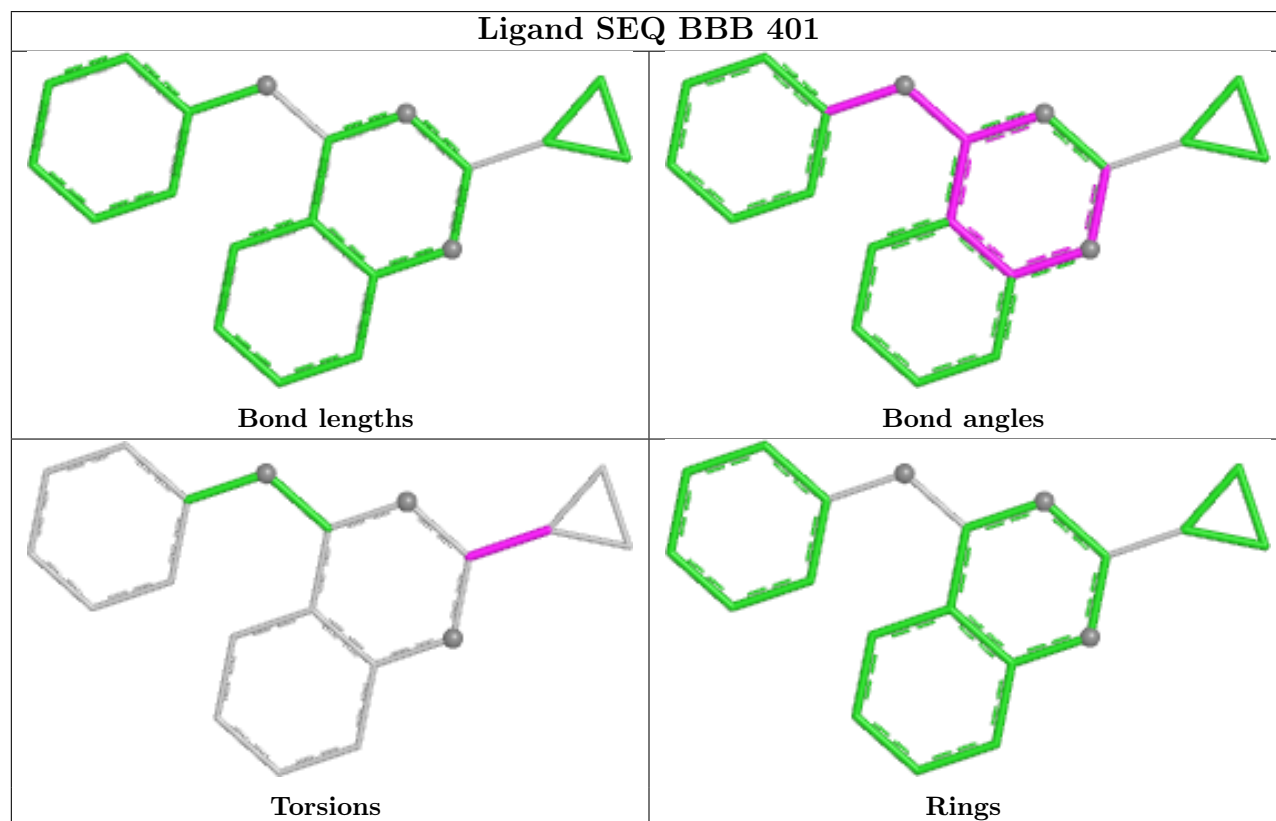
No monomer is involved in short contacts.

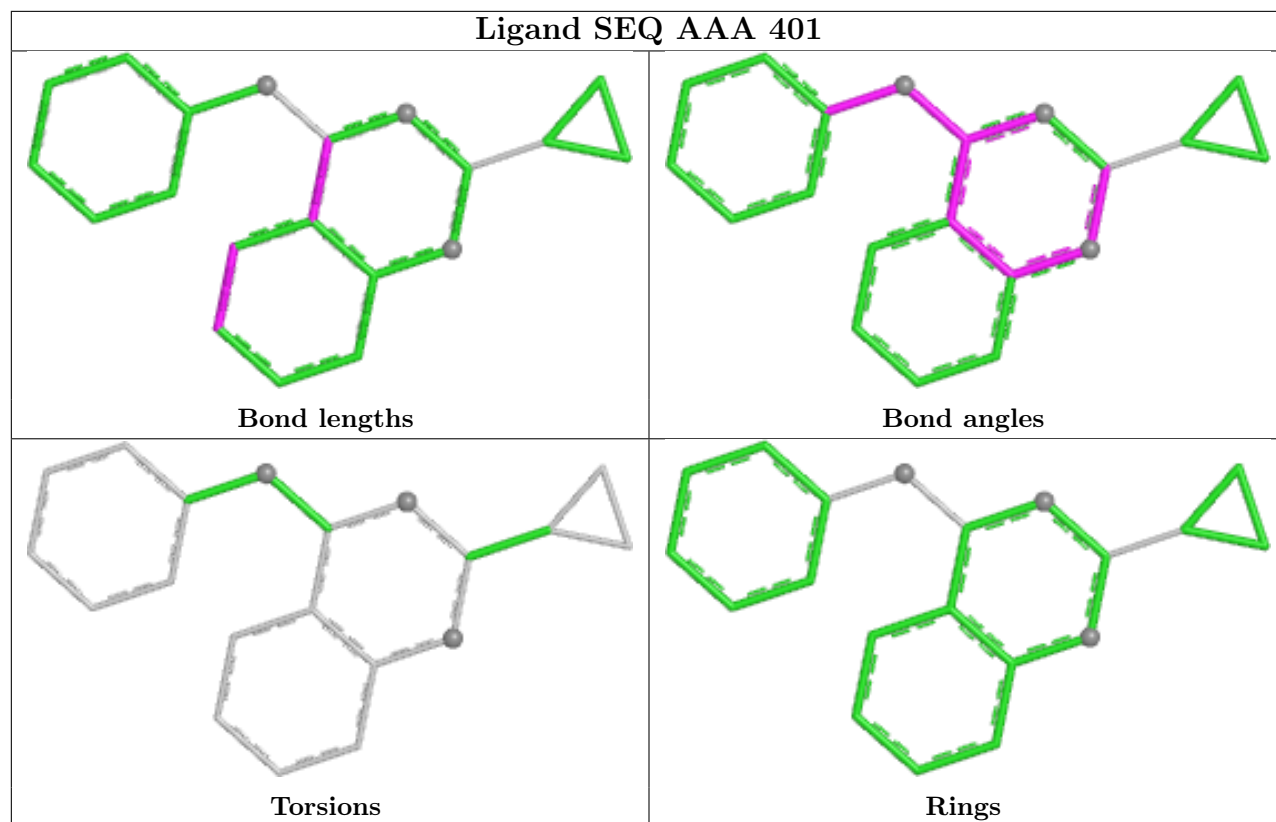
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand SEQ CCC 401



Ligand SEQ BBB 401





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	311/318 (97%)	0.09	6 (1%) 66 61	42, 65, 114, 147	0
1	BBB	310/318 (97%)	0.34	8 (2%) 57 51	46, 73, 112, 140	0
1	CCC	313/318 (98%)	0.79	31 (9%) 13 10	47, 90, 144, 167	0
All	All	934/954 (97%)	0.41	45 (4%) 35 30	42, 76, 134, 167	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	286	SER	3.6
1	AAA	85	VAL	3.3
1	CCC	291	PRO	3.3
1	CCC	85	VAL	3.2
1	CCC	234	GLU	3.0
1	BBB	323	LEU	3.0
1	CCC	28	CYS	2.9
1	CCC	225	LEU	2.9
1	CCC	202	GLY	2.8
1	CCC	16	LEU	2.7
1	CCC	287	GLN	2.7
1	CCC	90	LEU	2.7
1	CCC	26	ILE	2.7
1	CCC	19	SER	2.6
1	CCC	223	ALA	2.6
1	CCC	142	PHE	2.6
1	CCC	192	ALA	2.5
1	CCC	17	SER	2.5
1	BBB	285	THR	2.5
1	CCC	215	ILE	2.5
1	AAA	78	TYR	2.4
1	CCC	96	LEU	2.3
1	BBB	60	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	CCC	69	THR	2.3
1	BBB	171	ILE	2.3
1	AAA	96	LEU	2.3
1	CCC	74	TYR	2.3
1	CCC	107	ALA	2.2
1	CCC	222	PRO	2.2
1	BBB	292	SER	2.2
1	CCC	141	LEU	2.2
1	CCC	201	LEU	2.2
1	CCC	187	LEU	2.1
1	CCC	148	SER	2.1
1	CCC	165	ALA	2.1
1	BBB	173	LEU	2.1
1	CCC	60	ALA	2.1
1	AAA	285	THR	2.1
1	AAA	11	MET	2.1
1	CCC	245	GLY	2.1
1	AAA	10	HIS	2.1
1	CCC	203	TYR	2.1
1	CCC	89	THR	2.0
1	CCC	204	ARG	2.0
1	BBB	170	LEU	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
2	SEQ	CCC	401	20/20	0.89	0.14	84,97,103,104	0

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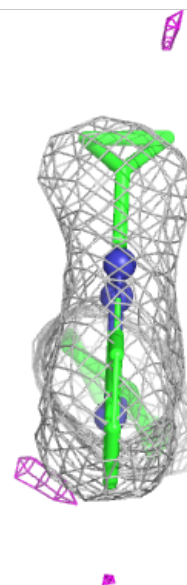
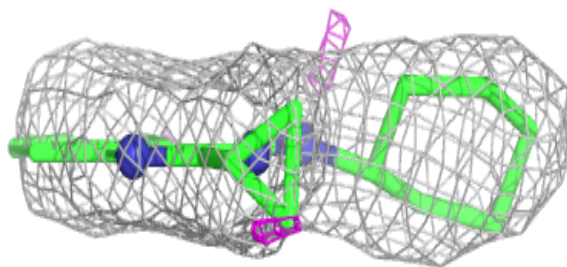
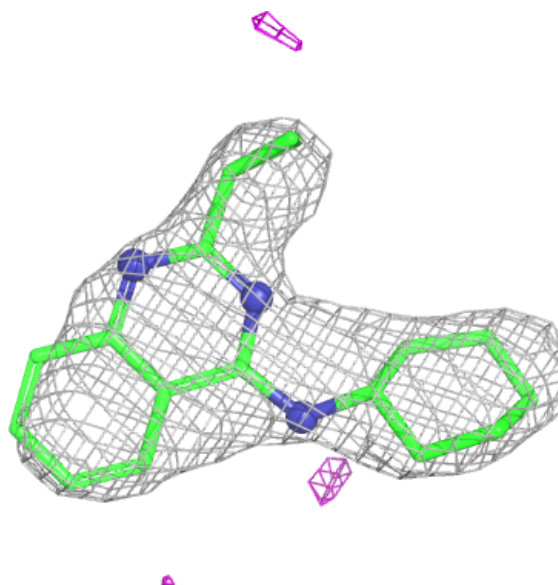
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SEQ	BBB	401	20/20	0.92	0.11	57,69,75,78	0
2	SEQ	AAA	401	20/20	0.94	0.08	44,48,55,55	0
3	NI	AAA	402	1/1	1.00	0.03	52,52,52,52	0

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.

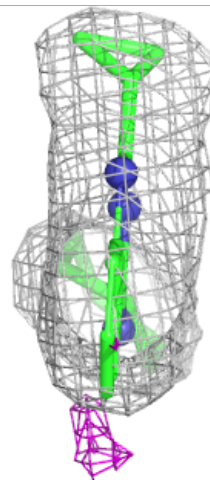
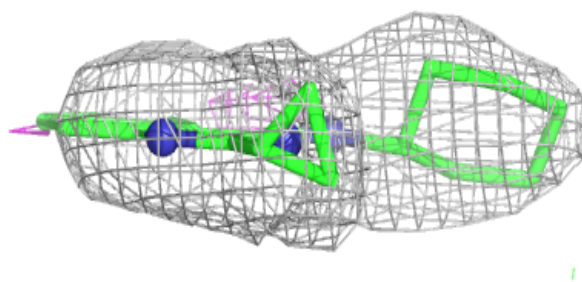
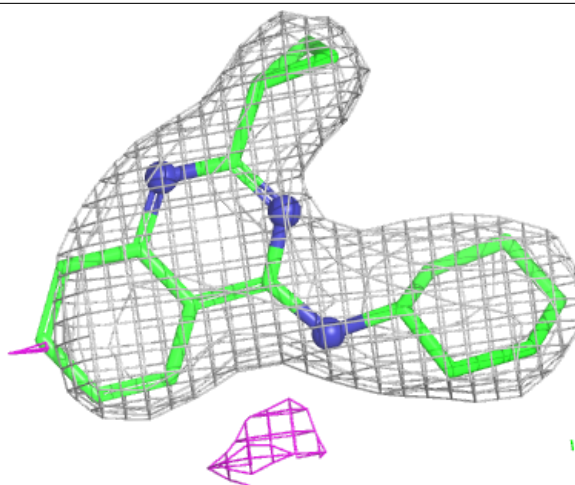
Electron density around SEQ CCC 401:

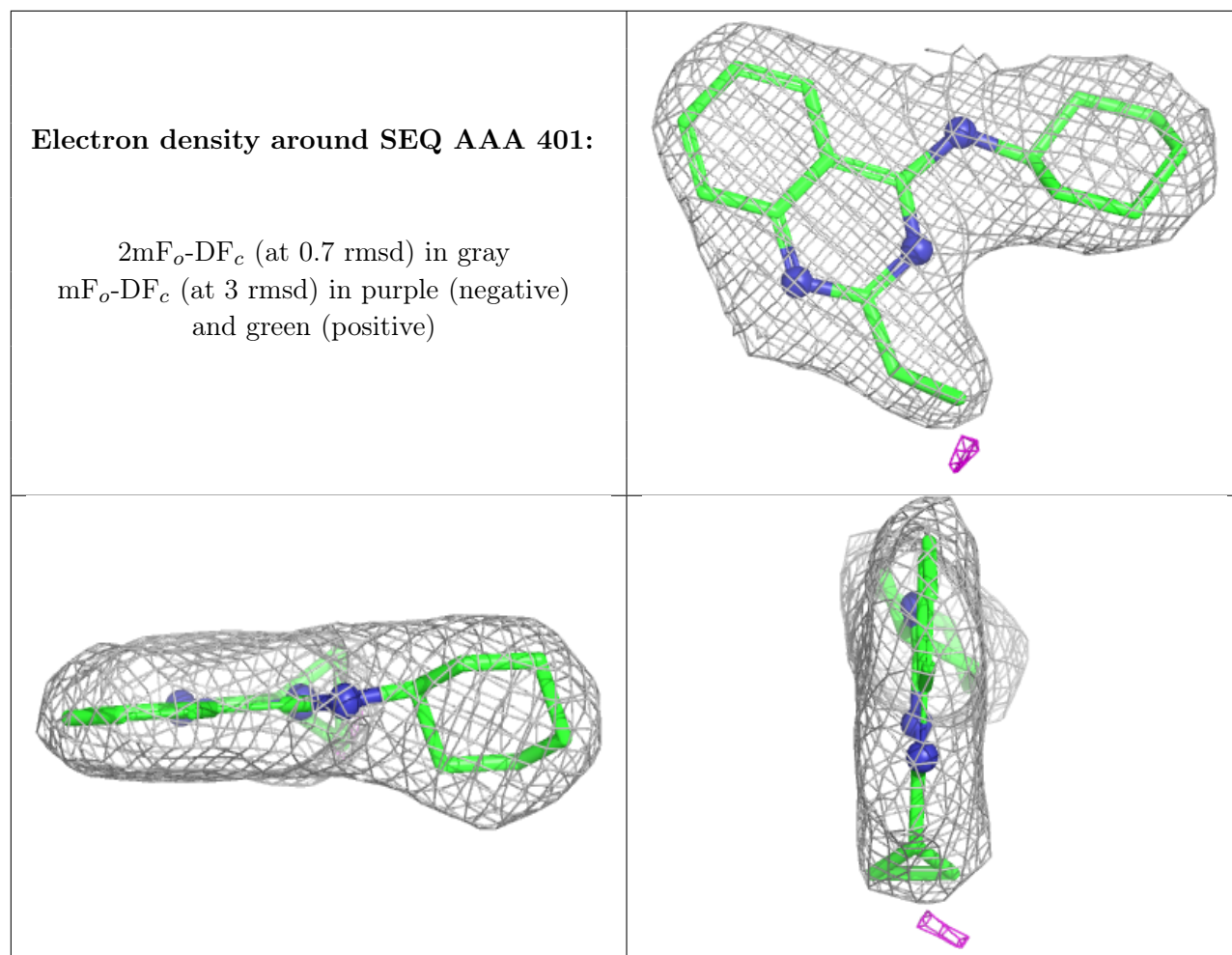
2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around SEQ BBB 401:

$2mF_o-DF_c$ (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.