



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 27, 2026 – 05:46 PM UTC

PDB ID : 8RYI / pdb_00008ryi
Title : Metformin hydrolase from Aminobacter niigataensis MD1 with urea in the active site
Authors : Fleming, J.R.; Lutz, H.; Bachmann, A.; Mayans, O.
Deposited on : 2024-02-08
Resolution : 2.06 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
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

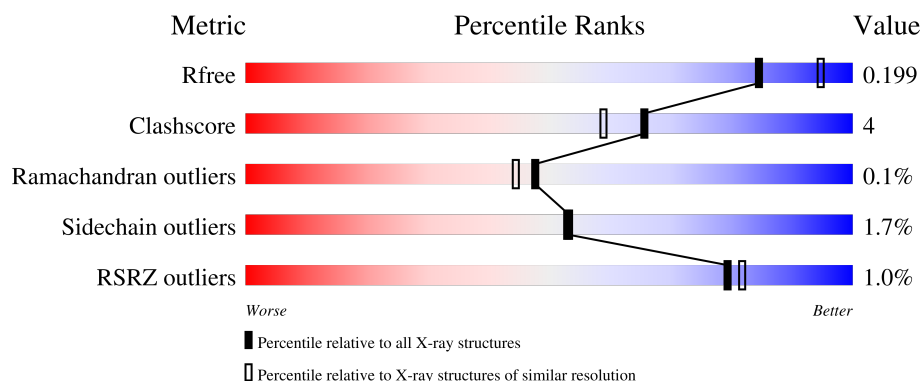
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	348	% 86% 7% • 6%
1	C	348	% 86% 10% • •
1	D	348	% 88% 7% • 5%
1	F	348	3% 83% 9% • 7%
2	B	376	 85% 8% 7%

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Mol	Chain	Length	Quality of chain
2	E	376	87% 8% . .

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16808 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 Arginase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	336	Total	C	N	O	S	0	2	0
			2588	1627	453	489	19			
1	A	326	Total	C	N	O	S	0	4	0
			2534	1596	443	475	20			
1	F	324	Total	C	N	O	S	0	0	0
			2490	1565	436	471	18			
1	D	332	Total	C	N	O	S	0	5	0
			2585	1625	456	484	20			

- Molecule 2 is a protein called Agmatinase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	350	Total	C	N	O	S	0	5	0
			2774	1743	489	519	23			
2	E	361	Total	C	N	O	S	0	9	0
			2882	1812	504	542	24			

There are 40 discrepancies between the modelled and reference sequences:

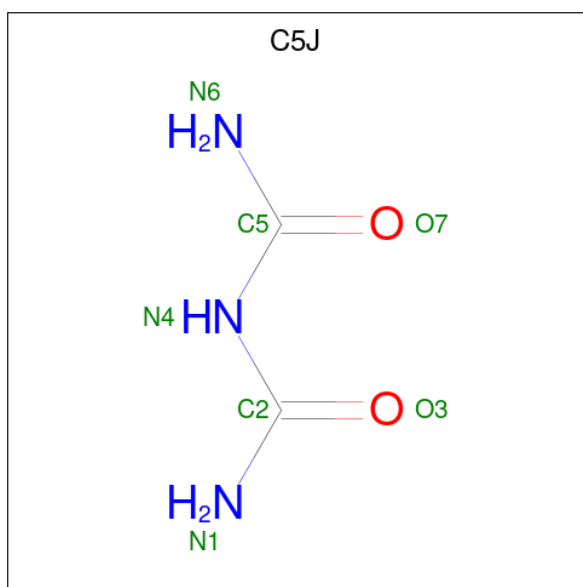
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	MET	-	initiating methionine	UNP A0A9E9PQ69
B	-17	ALA	-	expression tag	UNP A0A9E9PQ69
B	-16	TRP	-	expression tag	UNP A0A9E9PQ69
B	-15	SER	-	expression tag	UNP A0A9E9PQ69
B	-14	HIS	-	expression tag	UNP A0A9E9PQ69
B	-13	PRO	-	expression tag	UNP A0A9E9PQ69
B	-12	GLN	-	expression tag	UNP A0A9E9PQ69
B	-11	PHE	-	expression tag	UNP A0A9E9PQ69
B	-10	GLU	-	expression tag	UNP A0A9E9PQ69
B	-9	LYS	-	expression tag	UNP A0A9E9PQ69
B	-8	VAL	-	expression tag	UNP A0A9E9PQ69
B	-7	GLU	-	expression tag	UNP A0A9E9PQ69

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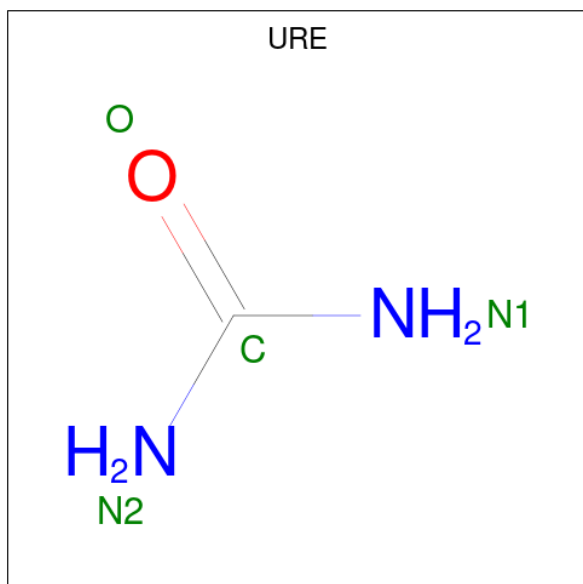
Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	ASN	-	expression tag	UNP A0A9E9PQ69
B	-5	LEU	-	expression tag	UNP A0A9E9PQ69
B	-4	TYR	-	expression tag	UNP A0A9E9PQ69
B	-3	PHE	-	expression tag	UNP A0A9E9PQ69
B	-2	GLN	-	expression tag	UNP A0A9E9PQ69
B	-1	GLY	-	expression tag	UNP A0A9E9PQ69
B	0	ALA	-	expression tag	UNP A0A9E9PQ69
B	324	ASP	TYR	conflict	UNP A0A9E9PQ69
E	-18	MET	-	initiating methionine	UNP A0A9E9PQ69
E	-17	ALA	-	expression tag	UNP A0A9E9PQ69
E	-16	TRP	-	expression tag	UNP A0A9E9PQ69
E	-15	SER	-	expression tag	UNP A0A9E9PQ69
E	-14	HIS	-	expression tag	UNP A0A9E9PQ69
E	-13	PRO	-	expression tag	UNP A0A9E9PQ69
E	-12	GLN	-	expression tag	UNP A0A9E9PQ69
E	-11	PHE	-	expression tag	UNP A0A9E9PQ69
E	-10	GLU	-	expression tag	UNP A0A9E9PQ69
E	-9	LYS	-	expression tag	UNP A0A9E9PQ69
E	-8	VAL	-	expression tag	UNP A0A9E9PQ69
E	-7	GLU	-	expression tag	UNP A0A9E9PQ69
E	-6	ASN	-	expression tag	UNP A0A9E9PQ69
E	-5	LEU	-	expression tag	UNP A0A9E9PQ69
E	-4	TYR	-	expression tag	UNP A0A9E9PQ69
E	-3	PHE	-	expression tag	UNP A0A9E9PQ69
E	-2	GLN	-	expression tag	UNP A0A9E9PQ69
E	-1	GLY	-	expression tag	UNP A0A9E9PQ69
E	0	ALA	-	expression tag	UNP A0A9E9PQ69
E	324	ASP	TYR	conflict	UNP A0A9E9PQ69

- Molecule 3 is dicarbonimidic diamide (CCD ID: C5J) (formula: $C_2H_5N_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			7	2	3	2		
3	E	1	Total	C	N	O	0	0
			7	2	3	2		

- Molecule 4 is UREA (CCD ID: URE) (formula: $\text{CH}_4\text{N}_2\text{O}$) (labeled as "Ligand of Interest" by depositor).



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

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

- Molecule 5 is NICKEL (II) ION (CCD ID: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Ni	0	0
			2	2		
5	E	2	Total	Ni	0	0
			2	2		

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	1	Total	Ca	0	0
			1	1		

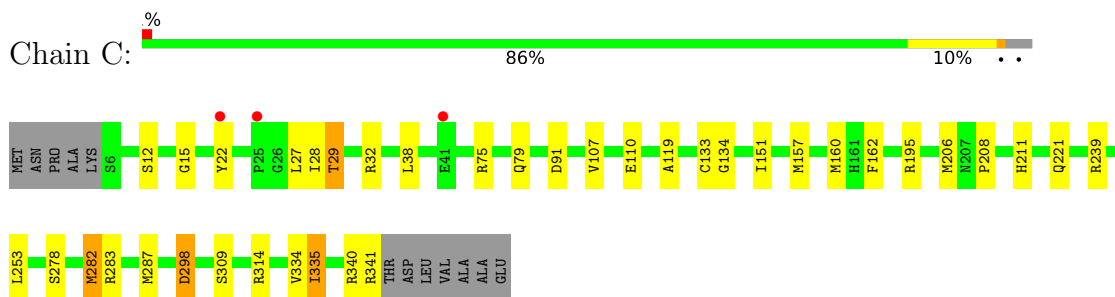
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	129	Total	O	0	0
			129	129		
7	B	254	Total	O	0	0
			254	254		
7	A	136	Total	O	0	0
			136	136		
7	E	268	Total	O	0	0
			268	268		
7	F	30	Total	O	0	0
			30	30		
7	D	111	Total	O	0	0
			111	111		

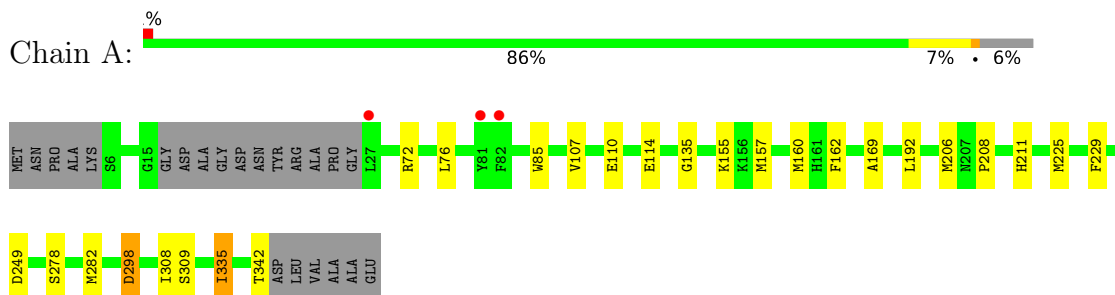
3 Residue-property plots [i](#)

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.

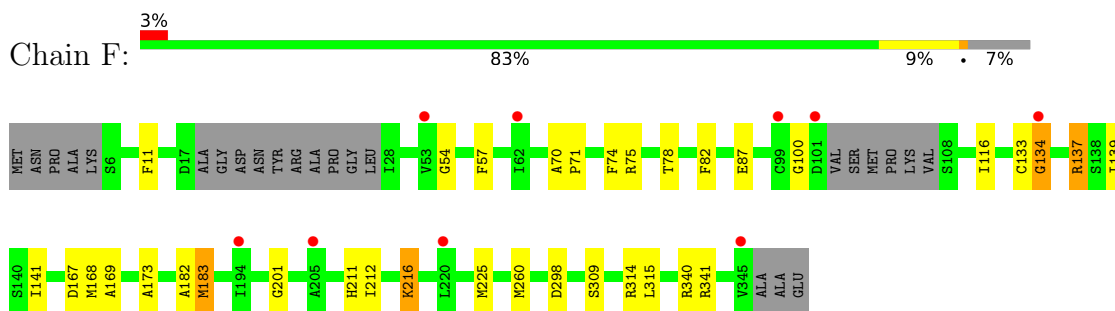
- Molecule 1: Arginase family protein



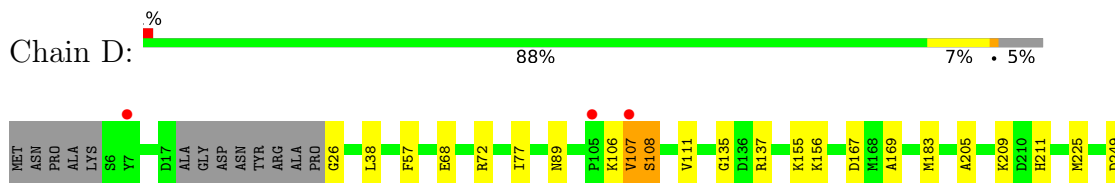
- Molecule 1: Arginase family protein



- Molecule 1: Arginase family protein

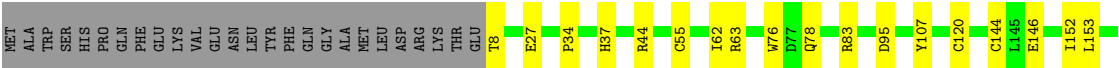
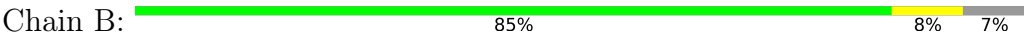


- Molecule 1: Arginase family protein

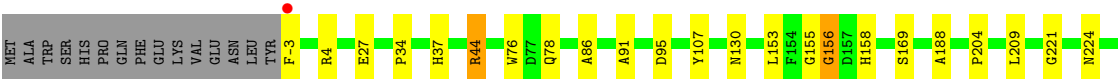
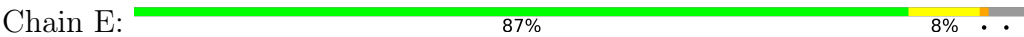




● Molecule 2: Agmatinase family protein



● Molecule 2: Agmatinase family protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	163.99Å 86.52Å 168.41Å 90.00° 113.99° 90.00°	Depositor
Resolution (Å)	29.97 – 2.06 29.97 – 2.06	Depositor EDS
% Data completeness (in resolution range)	98.0 (29.97-2.06) 98.0 (29.97-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 2.06Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.169 , 0.199 0.169 , 0.199	Depositor DCC
R_{free} test set	6574 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	45.5	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	16808	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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: C5J, URE, CA, 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	A	0.31	0/2594	0.53	1/3506 (0.0%)
1	C	0.36	0/2648	0.55	2/3582 (0.1%)
1	D	0.28	0/2645	0.50	0/3574
1	F	0.21	0/2539	0.42	0/3432
2	B	0.41	0/2852	0.59	0/3867
2	E	0.40	0/2976	0.59	0/4031
All	All	0.34	0/16254	0.53	3/21992 (0.0%)

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
1	C	0	1
2	E	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	135	GLY	N-CA-C	-5.86	99.28	113.18
1	C	133	CYS	CA-C-N	-5.46	116.68	122.30
1	C	133	CYS	C-N-CA	-5.46	116.68	122.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	134	GLY	Peptide
2	E	155	GLY	Peptide

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	2534	0	2506	16	0
1	C	2588	0	2543	23	0
1	D	2585	0	2557	21	0
1	F	2490	0	2442	25	0
2	B	2774	0	2663	18	0
2	E	2882	0	2780	33	0
3	B	7	0	0	0	0
3	E	7	0	0	0	0
4	B	4	0	4	0	0
4	E	4	0	4	0	0
5	B	2	0	0	0	0
5	E	2	0	0	0	0
6	E	1	0	0	0	0
7	A	136	0	0	0	0
7	B	254	0	0	3	0
7	C	129	0	0	1	0
7	D	111	0	0	2	0
7	E	268	0	0	3	0
7	F	30	0	0	0	0
All	All	16808	0	15499	120	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 120 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:F:133:CYS:SG	1:F:134:GLY:N	2.53	0.81
1:C:91:ASP:HB2	1:C:335:ILE:HD11	1.68	0.75
1:D:108:SER:HB2	1:D:111:VAL:HB	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:95[B]:ASP:OD1	7:B:501:HOH:O	2.04	0.74
2:B:44[A]:ARG:NH2	2:E:95[A]:ASP:OD1	2.24	0.70

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	326/348 (94%)	317 (97%)	9 (3%)	0	100	100
1	C	336/348 (97%)	325 (97%)	11 (3%)	0	100	100
1	D	333/348 (96%)	323 (97%)	9 (3%)	1 (0%)	36	30
1	F	318/348 (91%)	308 (97%)	9 (3%)	1 (0%)	36	30
2	B	353/376 (94%)	341 (97%)	12 (3%)	0	100	100
2	E	368/376 (98%)	352 (96%)	15 (4%)	1 (0%)	36	30
All	All	2034/2144 (95%)	1966 (97%)	65 (3%)	3 (0%)	48	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	134	GLY
1	D	107	VAL
2	E	156	GLY

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	269/279 (96%)	264 (98%)	5 (2%)	50	49
1	C	272/279 (98%)	263 (97%)	9 (3%)	33	28
1	D	274/279 (98%)	271 (99%)	3 (1%)	65	68
1	F	262/279 (94%)	258 (98%)	4 (2%)	57	58
2	B	297/315 (94%)	291 (98%)	6 (2%)	48	47
2	E	310/315 (98%)	307 (99%)	3 (1%)	68	71
All	All	1684/1746 (96%)	1654 (98%)	30 (2%)	53	51

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	317	ASP
1	D	107	VAL
1	A	298	ASP
1	D	298	ASP
1	F	183	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	79	GLN
1	F	150	HIS
1	D	177	ASN
1	F	161	HIS
2	B	348	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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	$\# Z > 2$
3	C5J	E	401	-	6,6,6	0.78	0	6,7,7	1.22	0
4	URE	E	402	5	3,3,3	0.06	0	3,3,3	0.03	0
3	C5J	B	401	-	6,6,6	0.87	0	6,7,7	1.13	0
4	URE	B	402	5	3,3,3	0.36	0	3,3,3	0.08	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
3	C5J	E	401	-	-	0/4/4/4	-
3	C5J	B	401	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

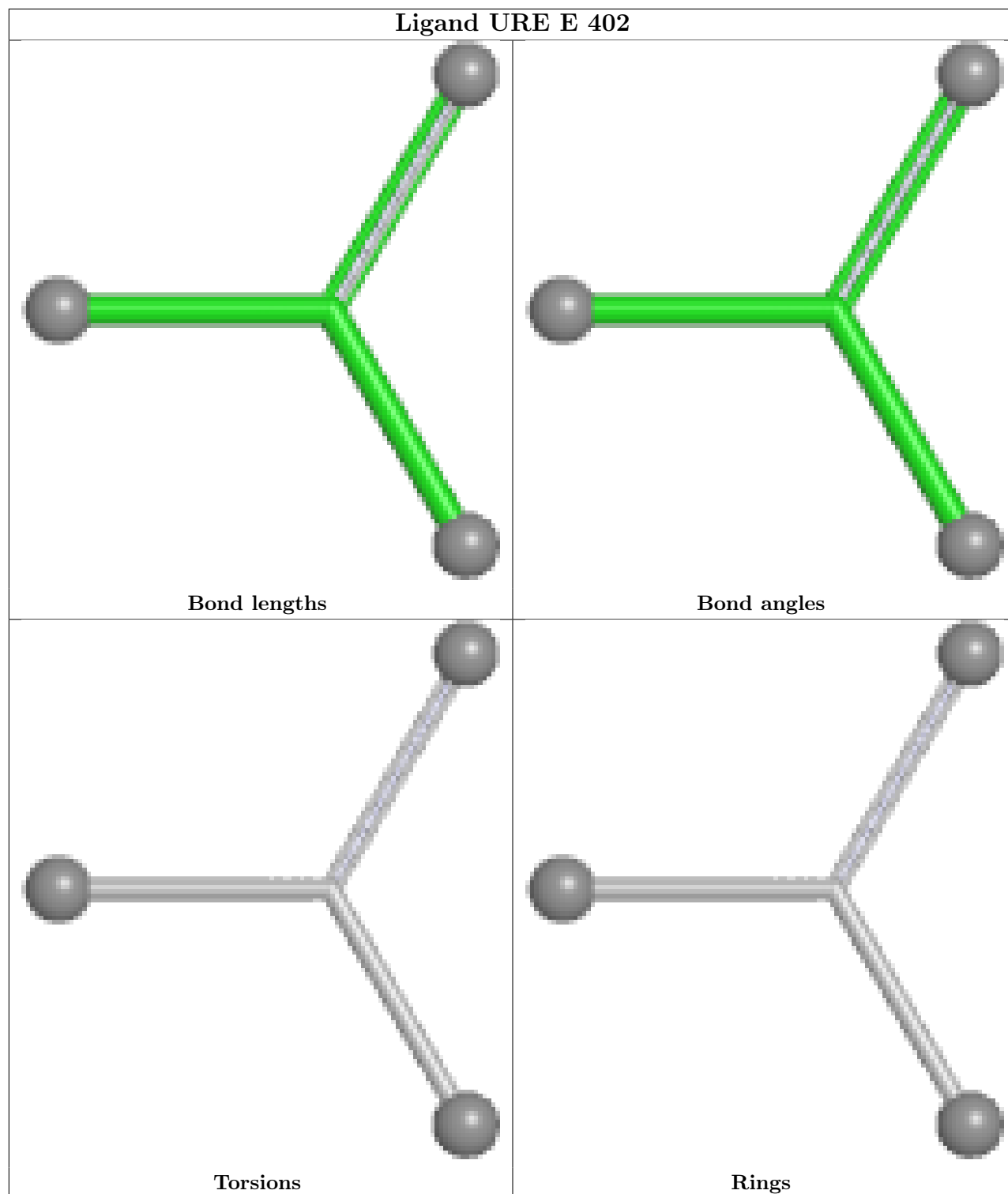
There are no torsion outliers.

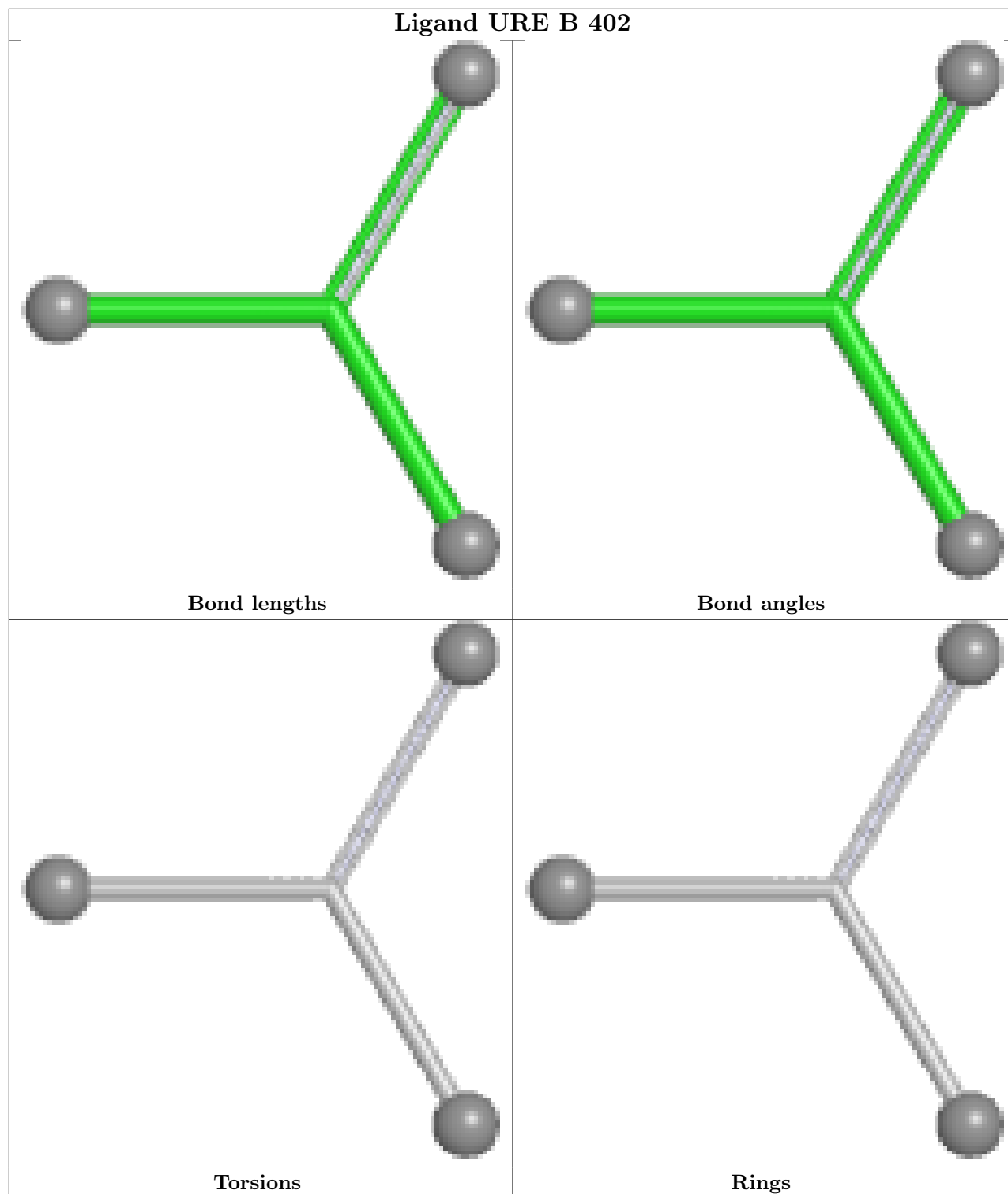
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	326/348 (93%)	-0.20	3 (0%) 81 83	29, 56, 82, 117	4 (1%)
1	C	336/348 (96%)	-0.07	3 (0%) 81 83	34, 62, 116, 172	2 (0%)
1	D	332/348 (95%)	-0.10	5 (1%) 72 74	33, 61, 88, 145	5 (1%)
1	F	324/348 (93%)	0.53	9 (2%) 55 56	58, 100, 136, 160	0
2	B	350/376 (93%)	-0.58	0 100 100	21, 41, 54, 83	5 (1%)
2	E	361/376 (96%)	-0.48	1 (0%) 90 92	22, 43, 63, 87	9 (2%)
All	All	2029/2144 (94%)	-0.16	21 (1%) 79 82	21, 55, 118, 172	25 (1%)

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	99	CYS	3.5
1	C	41	GLU	3.4
1	D	308	ILE	2.8
1	F	220	LEU	2.7
1	F	101	ASP	2.7

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

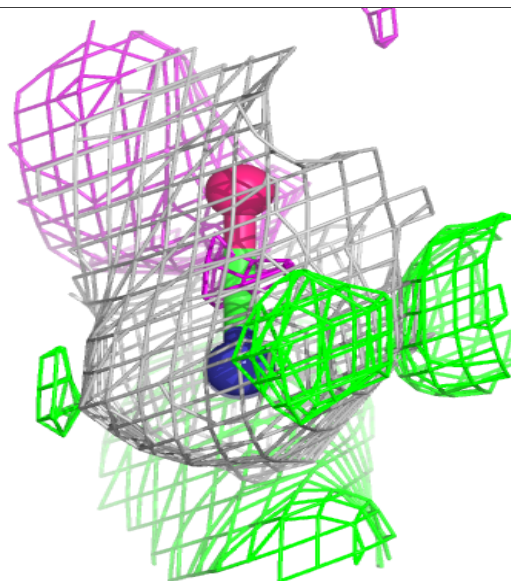
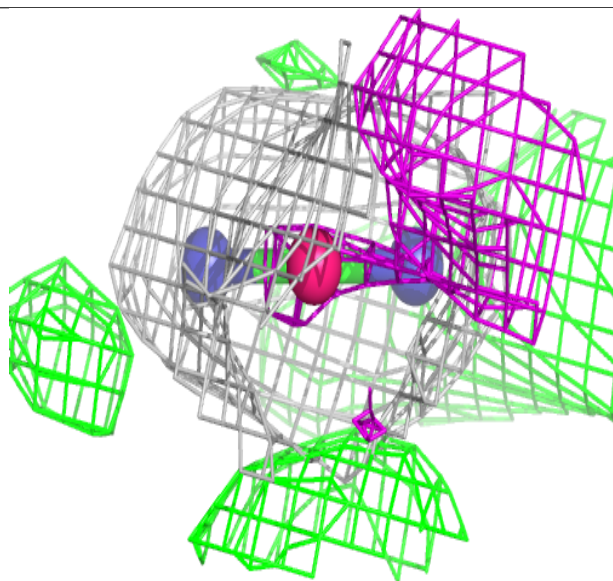
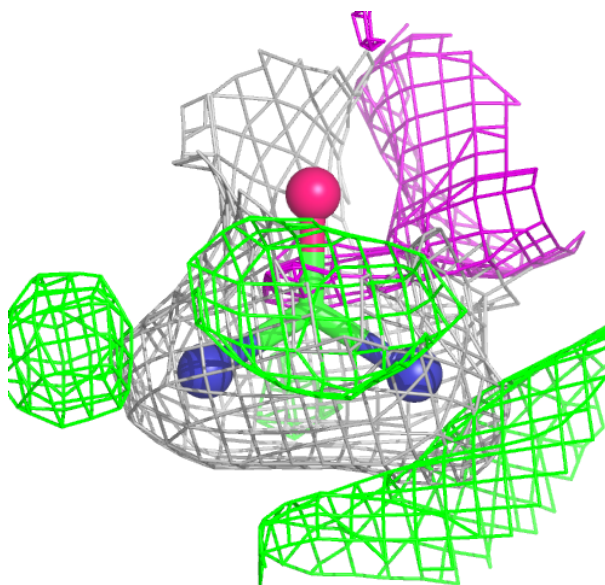
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	URE	B	402	4/4	0.83	0.18	56,62,66,68	0
3	C5J	B	401	7/7	0.88	0.09	48,49,50,50	0
3	C5J	E	401	7/7	0.92	0.07	42,44,45,45	0
4	URE	E	402	4/4	0.92	0.15	82,83,84,84	0
5	NI	B	403	1/1	0.99	0.04	49,49,49,49	0
5	NI	B	404	1/1	0.99	0.11	58,58,58,58	0
5	NI	E	403	1/1	0.99	0.04	56,56,56,56	0
5	NI	E	404	1/1	0.99	0.06	63,63,63,63	0
6	CA	E	405	1/1	0.99	0.03	37,37,37,37	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.

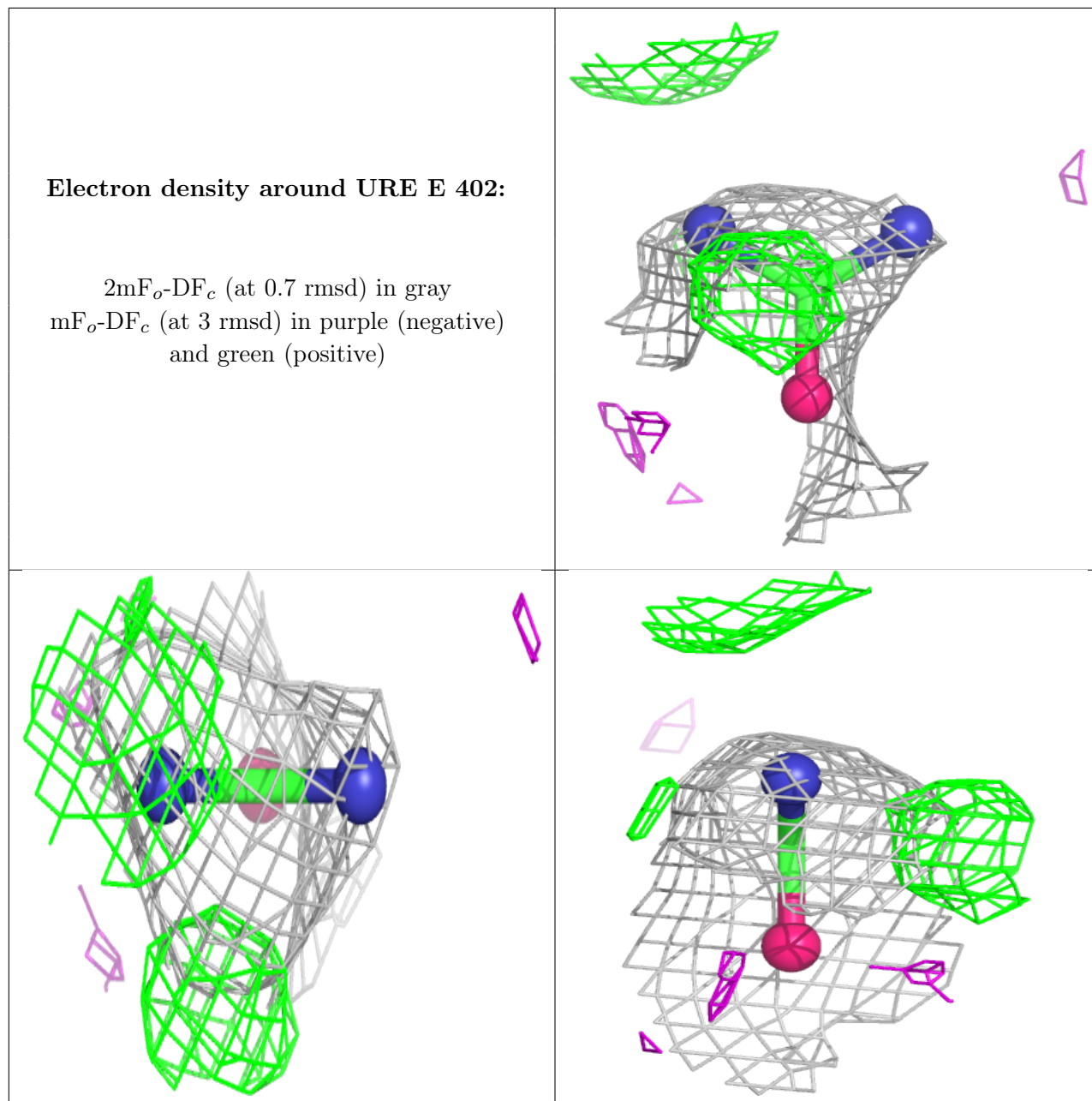
Electron density around URE B 402:

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



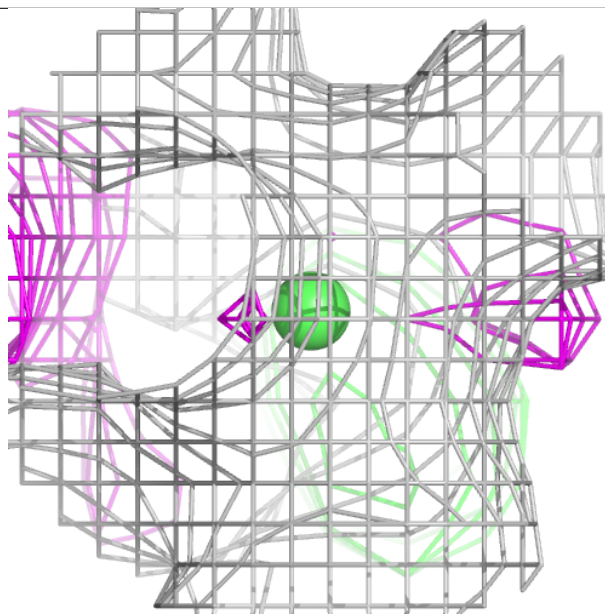
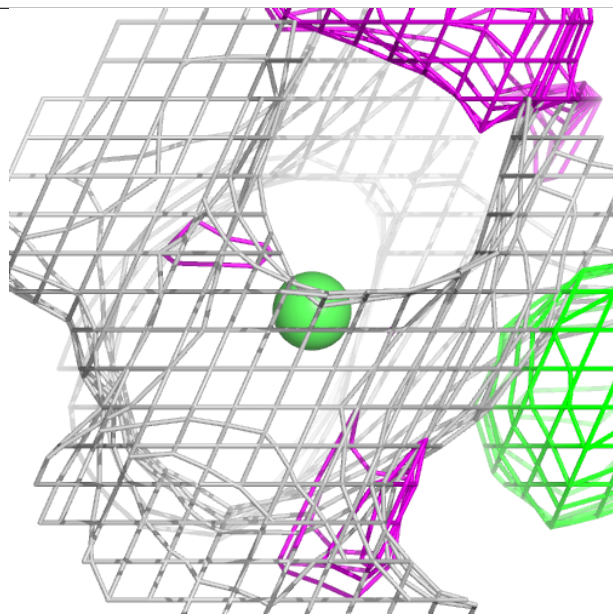
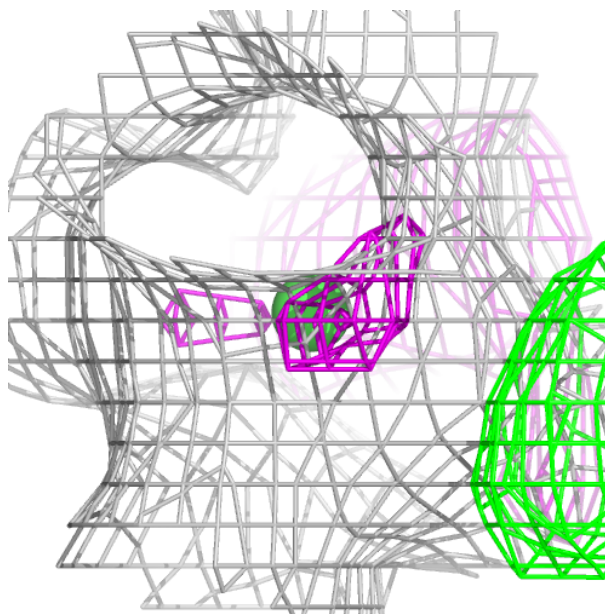
Electron density around URE E 402:

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



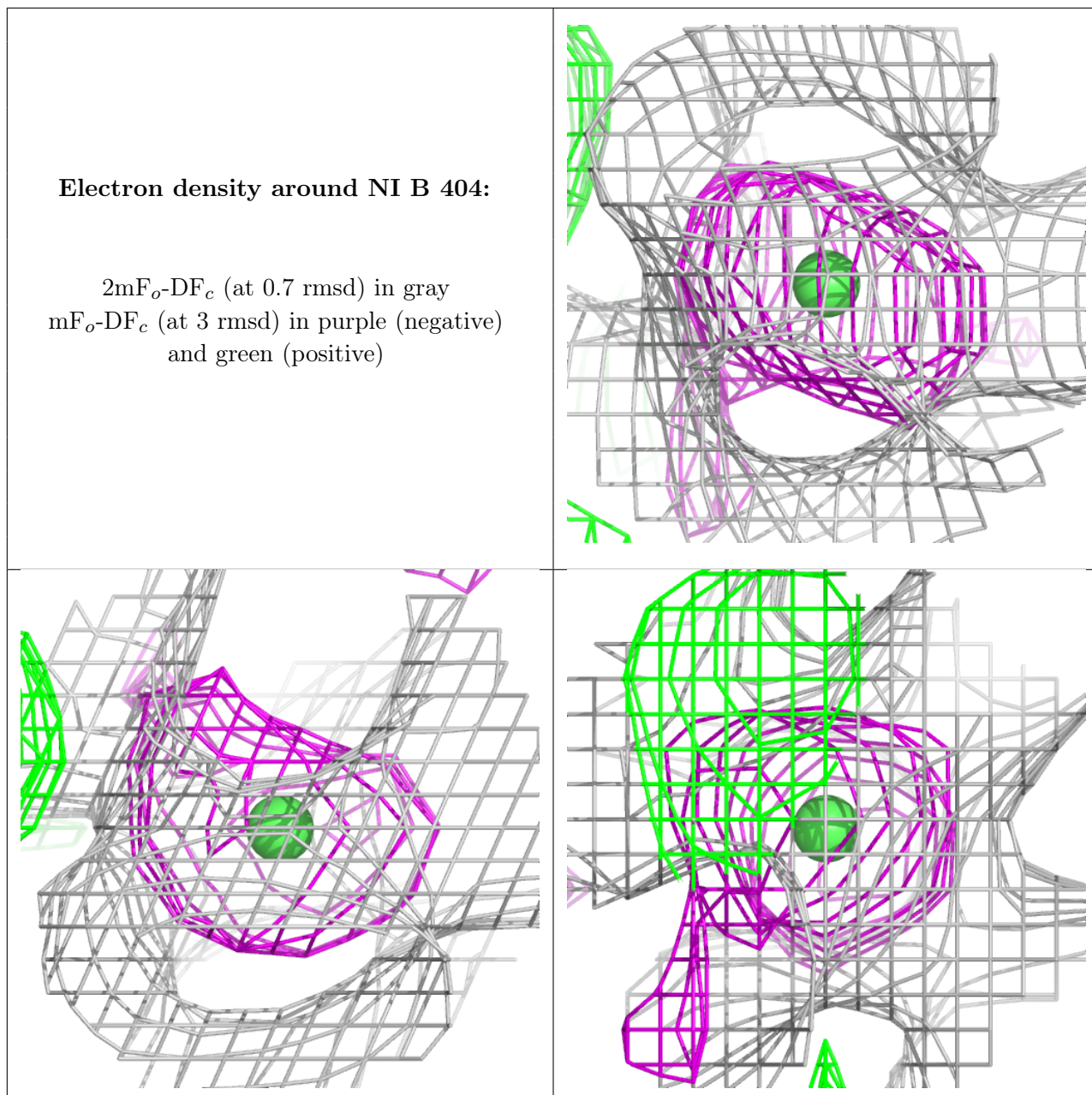
Electron density around NI B 403:

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



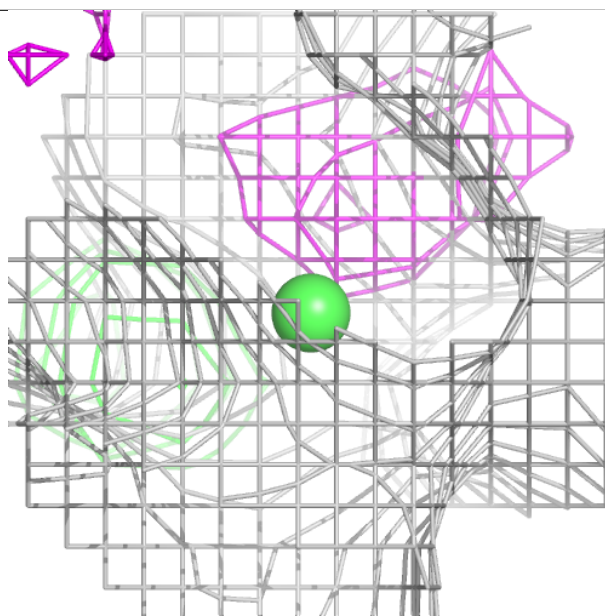
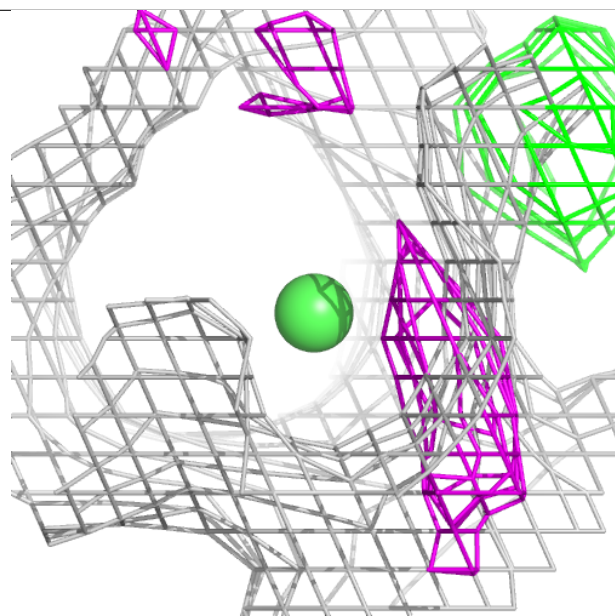
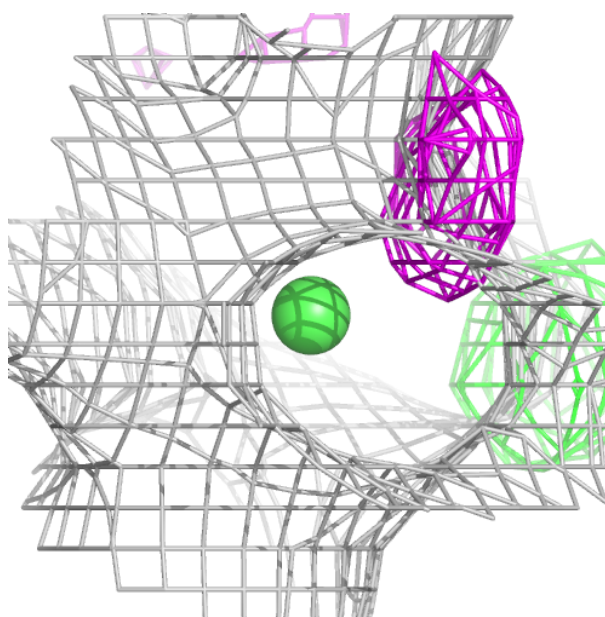
Electron density around NI B 404:

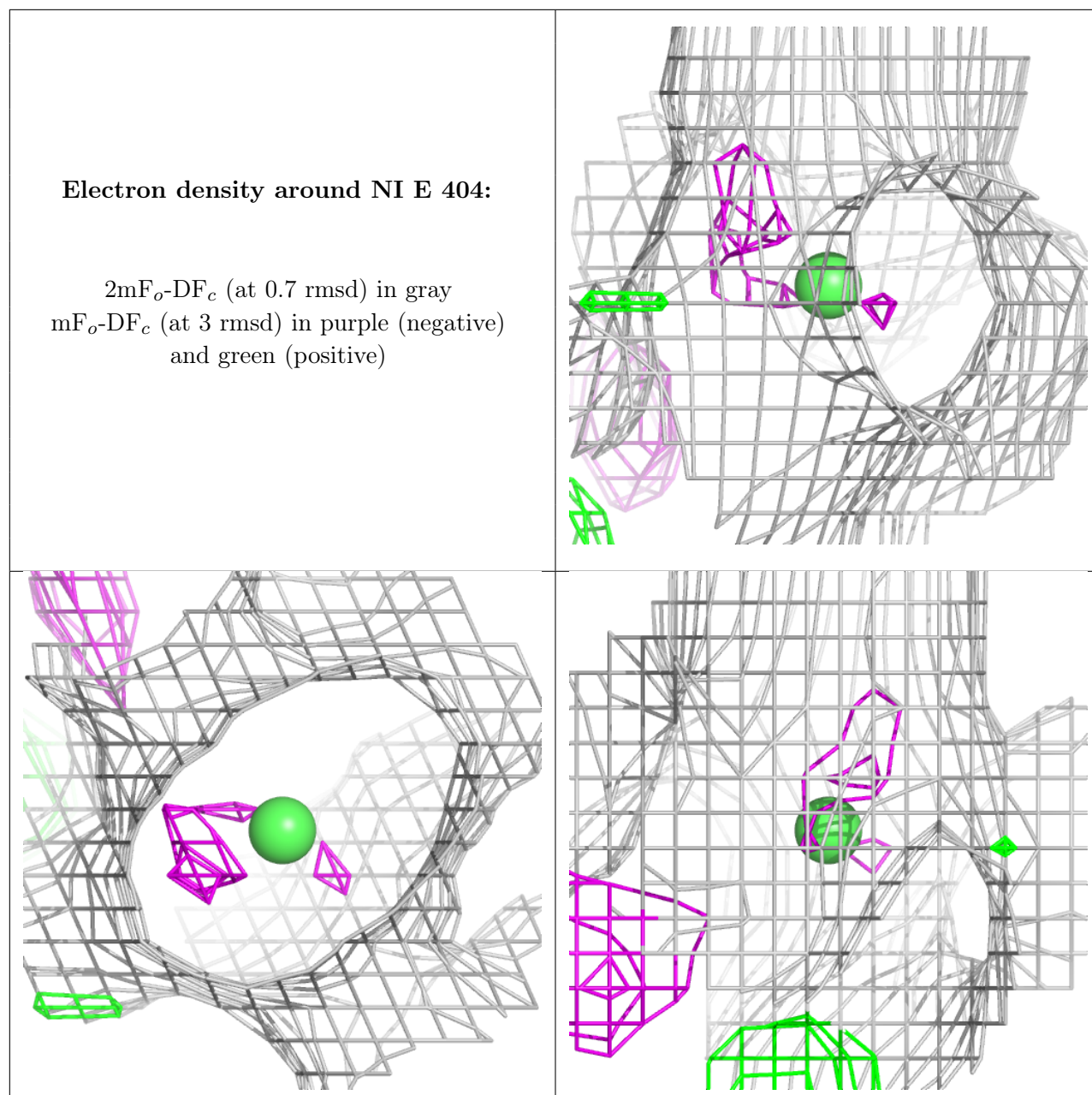
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around NI E 403:

$2mF_o-DF_c$ (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.