Full wwPDB X-ray Structure Validation Report ⓘ

Sep 24, 2024 – 12:08 AM JST

PDB ID	:	8ZVH
Title	:	Crystal structure of AetD in complex with L-phenylalanine
Authors	:	Li, H.; Dai, L.; Zheng, H.B.; Chen, C.-C.; Guo, R.-T.
Deposited on	:	2024-06-11
Resolution	:	1.87 Å(reported)

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

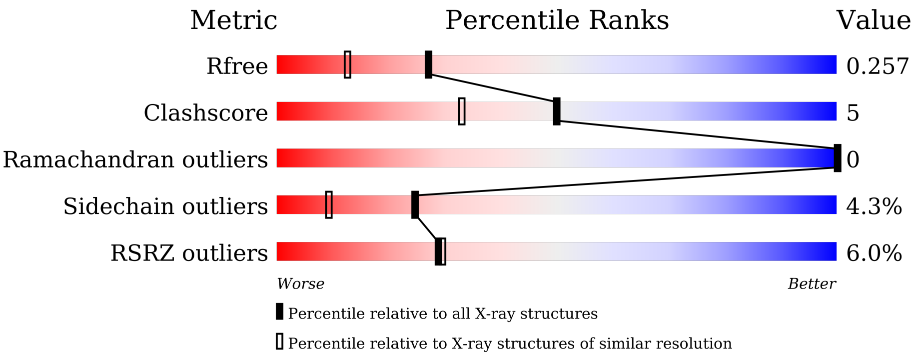
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.002 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

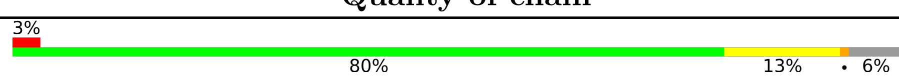
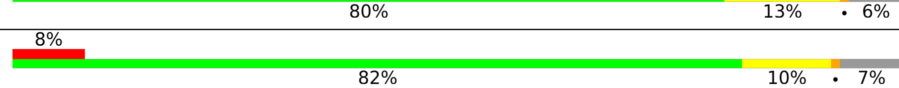
The reported resolution of this entry is 1.87 Å.

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}	164625	1090 (1.88-1.88)
Clashscore	180529	1144 (1.88-1.88)
Ramachandran outliers	177936	1135 (1.88-1.88)
Sidechain outliers	177891	1135 (1.88-1.88)
RSRZ outliers	164620	1090 (1.88-1.88)

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 <=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	250	
1	B	250	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4300 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 AetD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	235	Total 1935	C 1235	N 330	O 362	S 8	0	0	0
1	B	232	Total 1917	C 1225	N 327	O 357	S 8	0	0	0

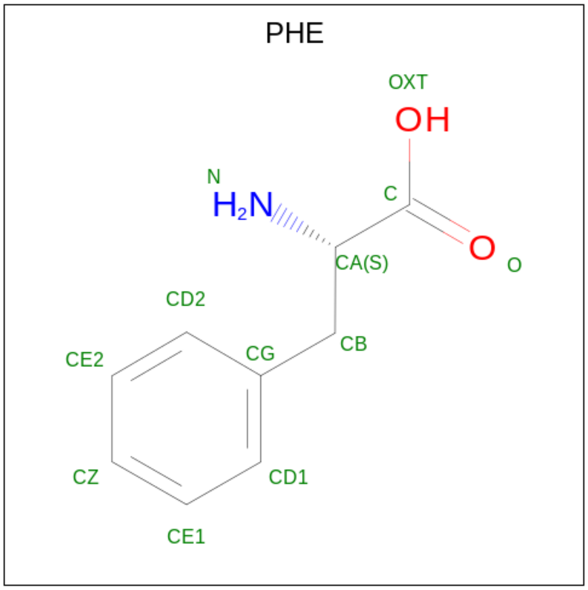
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	expression tag	UNP A0A861B387
A	-9	ALA	-	expression tag	UNP A0A861B387
A	-8	GLY	-	expression tag	UNP A0A861B387
A	-7	ALA	-	expression tag	UNP A0A861B387
A	-6	GLY	-	expression tag	UNP A0A861B387
A	-5	ALA	-	expression tag	UNP A0A861B387
A	-4	GLY	-	expression tag	UNP A0A861B387
A	-3	ALA	-	expression tag	UNP A0A861B387
A	-2	GLY	-	expression tag	UNP A0A861B387
A	-1	ALA	-	expression tag	UNP A0A861B387
A	0	GLY	-	expression tag	UNP A0A861B387
B	-10	GLY	-	expression tag	UNP A0A861B387
B	-9	ALA	-	expression tag	UNP A0A861B387
B	-8	GLY	-	expression tag	UNP A0A861B387
B	-7	ALA	-	expression tag	UNP A0A861B387
B	-6	GLY	-	expression tag	UNP A0A861B387
B	-5	ALA	-	expression tag	UNP A0A861B387
B	-4	GLY	-	expression tag	UNP A0A861B387
B	-3	ALA	-	expression tag	UNP A0A861B387
B	-2	GLY	-	expression tag	UNP A0A861B387
B	-1	ALA	-	expression tag	UNP A0A861B387
B	0	GLY	-	expression tag	UNP A0A861B387

- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Fe 1	0	0
2	B	1	Total 1	Fe 1	0	0

- Molecule 3 is PHENYLALANINE (three-letter code: PHE) (formula: $C_9H_{11}NO_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 12	C 9	N 1	O 2	0	0
3	B	1	Total 12	C 9	N 1	O 2	0	0

- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total 3	Ni 3	0	0
4	B	2	Total 2	Ni 2	0	0

- Molecule 5 is water.

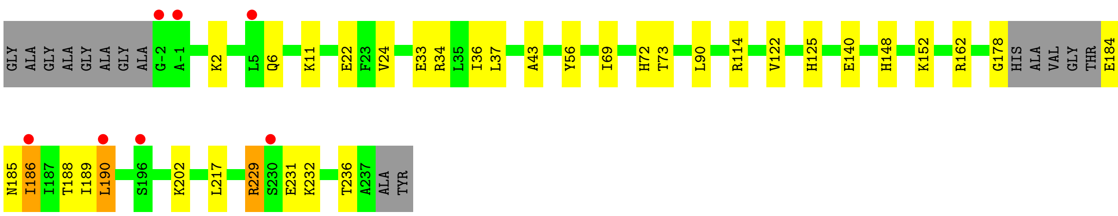
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	235	Total O 235 235	0	0
5	B	182	Total O 182 182	0	0

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.

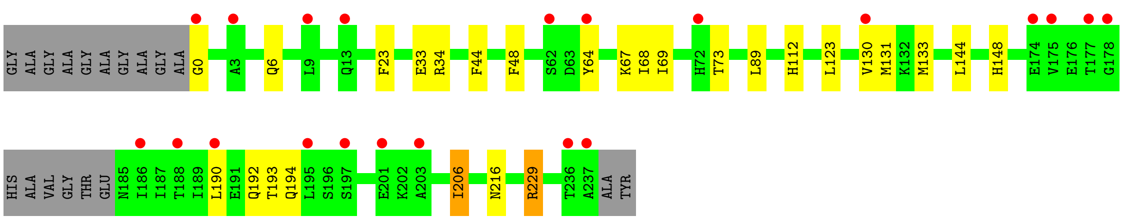
- Molecule 1: AetD

Chain A:



- Molecule 1: AetD

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α, β, γ	65.04Å 65.04Å 116.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.54 – 1.87 32.54 – 1.87	Depositor EDS
% Data completeness (in resolution range)	99.3 (32.54-1.87) 99.3 (32.54-1.87)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.61 (at 1.87Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.192 , 0.250 0.201 , 0.257	Depositor DCC
R_{free} test set	2019 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	28.1	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 47.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.040 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4300	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: FE2, 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	0.74	1/1975 (0.1%)	0.81	1/2666 (0.0%)
1	B	0.70	0/1957	0.81	0/2642
All	All	0.72	1/3932 (0.0%)	0.81	1/5308 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	140	GLU	CD-OE2	-5.16	1.20	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	56	TYR	CB-CG-CD1	5.02	124.01	121.00

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	A	1935	0	1911	25	0
1	B	1917	0	1897	15	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	12	0	8	0	0
3	B	12	0	8	2	0
4	A	3	0	0	0	0
4	B	2	0	0	0	0
5	A	235	0	0	10	0
5	B	182	0	0	2	0
All	All	4300	0	3824	40	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 5.

All (40) 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:A:189:ILE:HG13	5:A:485:HOH:O	1.91	0.71
1:A:186:ILE:CG2	1:A:188:THR:HG22	2.21	0.71
1:A:125:HIS:CE1	5:A:508:HOH:O	2.43	0.71
1:B:130:VAL:HA	1:B:133:MET:HE2	1.73	0.69
1:A:33:GLU:OE1	1:A:229:ARG:NH1	2.26	0.68
1:B:123:LEU:HD11	1:B:206:ILE:HD12	1.78	0.65
1:B:33:GLU:OE1	1:B:229:ARG:NH2	2.38	0.56
1:A:236:THR:HG22	5:A:463:HOH:O	2.05	0.56
1:A:190:LEU:N	1:A:190:LEU:CD2	2.69	0.55
1:A:162:ARG:NH1	5:A:405:HOH:O	2.40	0.55
1:B:0:GLY:N	5:B:405:HOH:O	2.40	0.53
1:A:186:ILE:HG23	5:A:421:HOH:O	2.08	0.52
1:A:186:ILE:HG21	1:A:188:THR:HG22	1.92	0.52
1:B:64:TYR:HA	1:B:67:LYS:HD2	1.90	0.52
1:B:123:LEU:HD11	1:B:206:ILE:CD1	2.41	0.51
1:B:48:PHE:CE2	3:B:302:PHE:HB2	2.47	0.50
1:B:148:HIS:NE2	5:B:402:HOH:O	2.34	0.50
1:A:11:LYS:NZ	5:A:408:HOH:O	2.45	0.49
1:A:231:GLU:OE2	5:A:401:HOH:O	2.20	0.48
1:A:152:LYS:HE3	5:A:551:HOH:O	2.14	0.47
1:A:184:GLU:HA	5:A:448:HOH:O	2.14	0.47
1:B:190:LEU:HD12	1:B:190:LEU:N	2.31	0.46
1:B:131:MET:HA	1:B:131:MET:HE2	1.99	0.45
1:A:69:ILE:O	1:A:73:THR:HG23	2.17	0.44
1:A:122:VAL:O	1:A:125:HIS:HD2	2.01	0.44
1:A:36:ILE:HD13	1:A:232:LYS:CA	2.48	0.44
1:A:24:VAL:O	1:A:34:ARG:HD2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:ALA:O	1:A:114:ARG:HA	2.18	0.43
1:A:186:ILE:HD12	1:A:186:ILE:HA	1.89	0.43
1:B:130:VAL:HG21	1:B:193:THR:HG21	2.00	0.43
1:A:190:LEU:N	1:A:190:LEU:HD23	2.33	0.43
1:A:72:HIS:HE1	1:A:186:ILE:HD12	1.83	0.43
1:B:44:PHE:CZ	3:B:302:PHE:CD1	3.07	0.43
1:A:178:GLY:HA3	1:A:186:ILE:HD11	2.00	0.42
1:A:148:HIS:CE1	5:A:574:HOH:O	2.71	0.42
1:A:217:LEU:C	1:A:217:LEU:HD23	2.39	0.42
1:B:69:ILE:O	1:B:73:THR:HG23	2.20	0.41
1:A:186:ILE:HG22	1:A:188:THR:HG22	2.01	0.40
1:B:23:PHE:CE2	1:B:34:ARG:HA	2.57	0.40
1:B:112:HIS:CG	1:B:216:ASN:HB3	2.57	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	231/250 (92%)	228 (99%)	3 (1%)	0	100	100
1	B	228/250 (91%)	220 (96%)	8 (4%)	0	100	100
All	All	459/500 (92%)	448 (98%)	11 (2%)	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	209/213 (98%)	199 (95%)	10 (5%)	21	7
1	B	208/213 (98%)	200 (96%)	8 (4%)	28	12
All	All	417/426 (98%)	399 (96%)	18 (4%)	25	9

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	6	GLN
1	A	22	GLU
1	A	37	LEU
1	A	90	LEU
1	A	185	ASN
1	A	186	ILE
1	A	190	LEU
1	A	202	LYS
1	A	229	ARG
1	B	6	GLN
1	B	68	ILE
1	B	89	LEU
1	B	144	LEU
1	B	192	GLN
1	B	194	GLN
1	B	206	ILE
1	B	229	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	112	HIS
1	A	185	ASN
1	B	6	GLN
1	B	194	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 7 are monoatomic - leaving 2 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	PHE	A	302	2	11,12,12	0.39	0	14,15,15	1.22	2 (14%)
3	PHE	B	302	2	11,12,12	0.47	0	14,15,15	1.48	1 (7%)

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	PHE	A	302	2	-	0/8/8/8	0/1/1/1
3	PHE	B	302	2	-	1/8/8/8	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	302	PHE	OXT-C-O	-4.84	113.09	124.09
3	A	302	PHE	OXT-C-CA	3.11	123.98	113.38
3	A	302	PHE	OXT-C-O	-2.86	117.59	124.09

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	302	PHE	C-CA-CB-CG

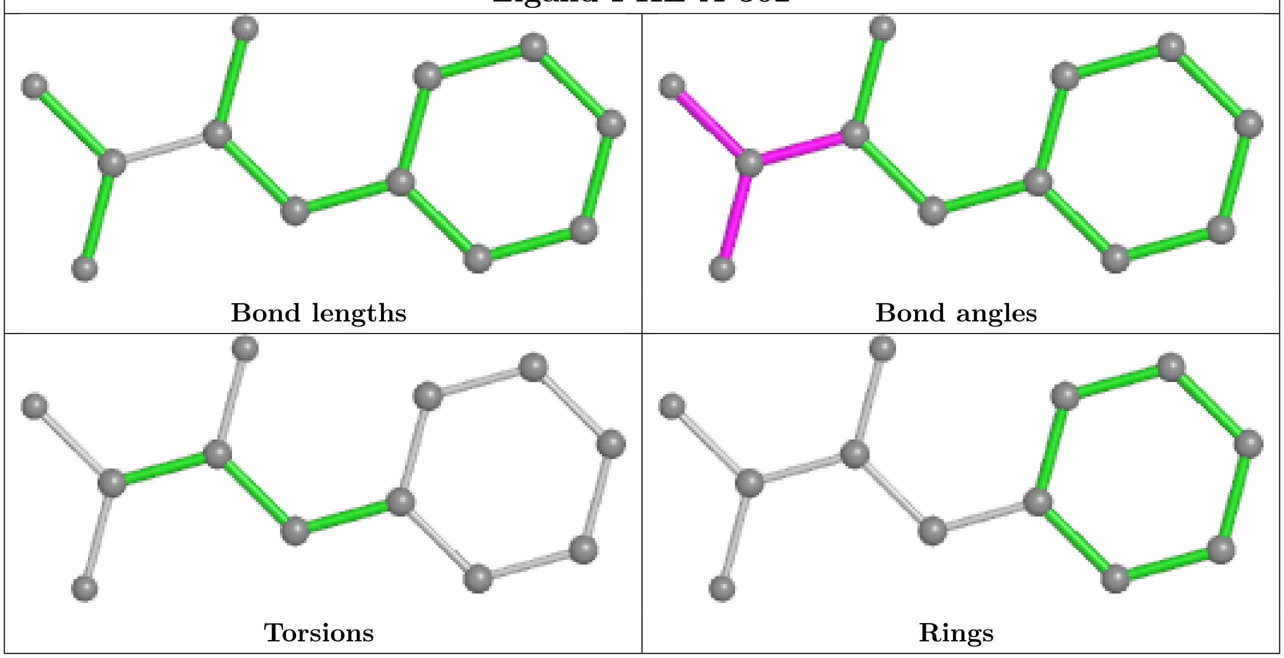
There are no ring outliers.

1 monomer is involved in 2 short contacts:

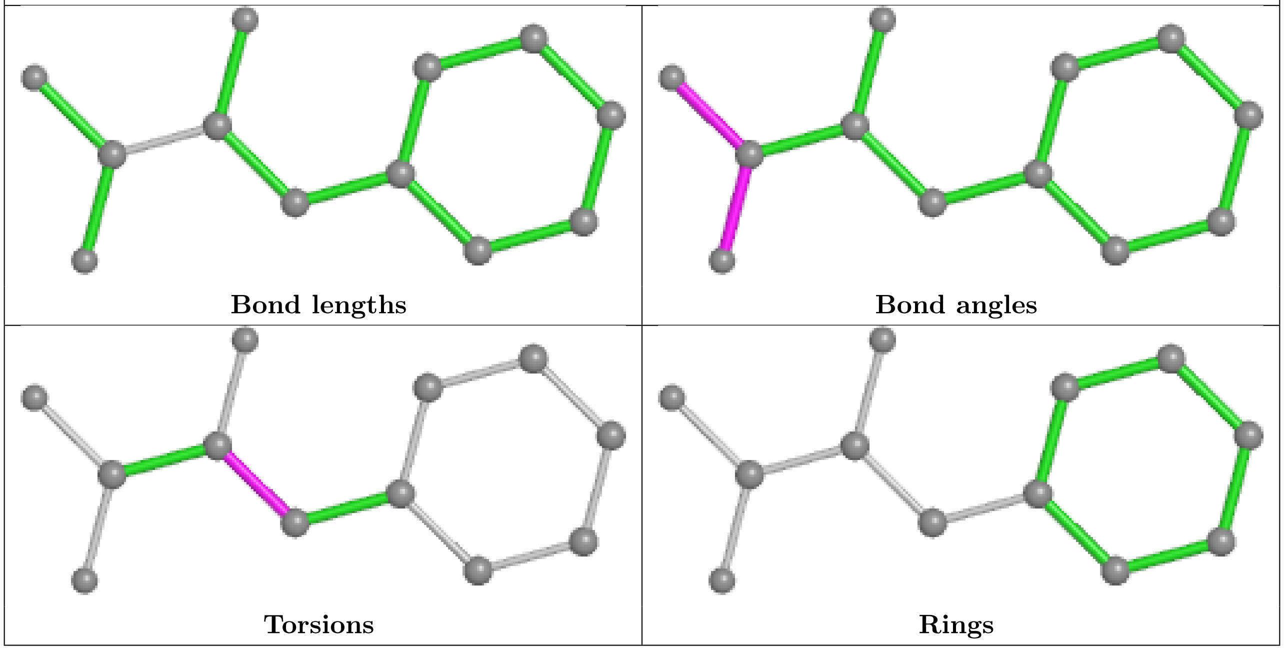
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	302	PHE	2	0

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 then 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 PHE A 302



Ligand PHE B 302



Bond lengths | Bond angles | Torsions | Rings

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^{th} 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	235/250 (94%)	0.26	7 (2%)	52	56	19, 30, 55, 78	0
1	B	232/250 (92%)	0.48	21 (9%)	16	18	18, 32, 67, 80	0
All	All	467/500 (93%)	0.37	28 (5%)	29	29	18, 31, 63, 80	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	190	LEU	4.3
1	B	190	LEU	4.2
1	B	9	LEU	3.5
1	B	175	VAL	3.3
1	B	177	THR	3.1
1	B	237	ALA	3.0
1	A	-1	ALA	2.9
1	B	3	ALA	2.8
1	B	0	GLY	2.8
1	B	236	THR	2.8
1	B	178	GLY	2.6
1	A	-2	GLY	2.6
1	B	186	ILE	2.6
1	B	195	LEU	2.5
1	B	72	HIS	2.4
1	B	197	SER	2.3
1	B	188	THR	2.2
1	A	5	LEU	2.2
1	A	186	ILE	2.2
1	A	230	SER	2.1
1	B	201	GLU	2.1
1	B	64	TYR	2.1
1	B	13	GLN	2.1
1	B	174	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	130	VAL	2.0
1	B	203	ALA	2.0
1	A	196	SER	2.0
1	B	62	SER	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 monosaccharides in this entry.

6.4 Ligands (i)

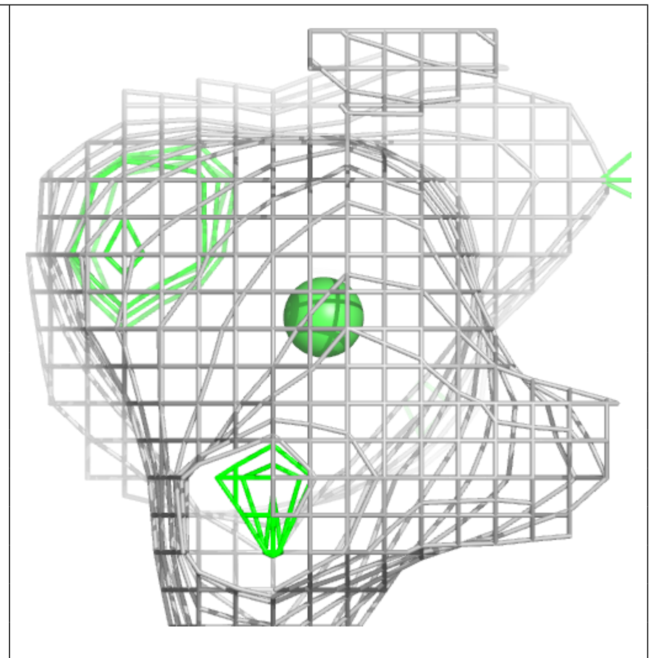
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

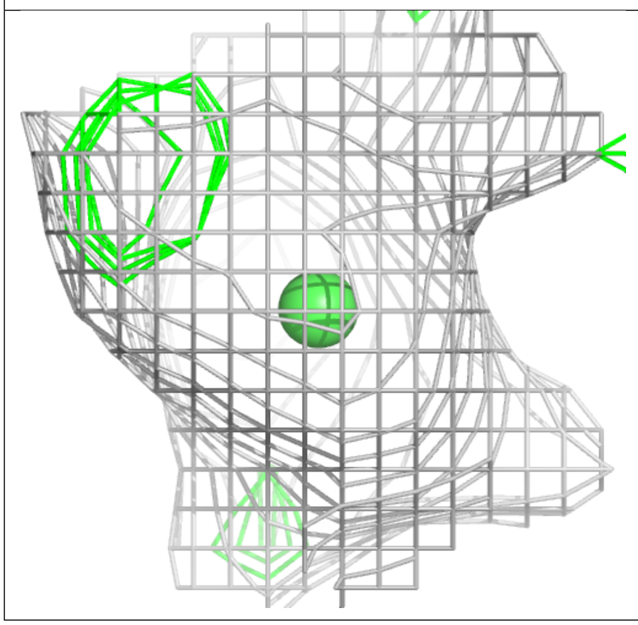
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NI	B	303	1/1	0.90	0.09	70,70,70,70	0
4	NI	A	304	1/1	0.92	0.09	48,48,48,48	0
3	PHE	B	302	12/12	0.92	0.09	25,32,38,39	0
3	PHE	A	302	12/12	0.96	0.06	21,25,29,30	0
4	NI	B	304	1/1	0.97	0.05	46,46,46,46	0
4	NI	A	305	1/1	0.99	0.03	44,44,44,44	0
2	FE2	B	301	1/1	0.99	0.02	28,28,28,28	0
2	FE2	A	301	1/1	0.99	0.04	22,22,22,22	0
4	NI	A	303	1/1	1.00	0.02	31,31,31,31	0

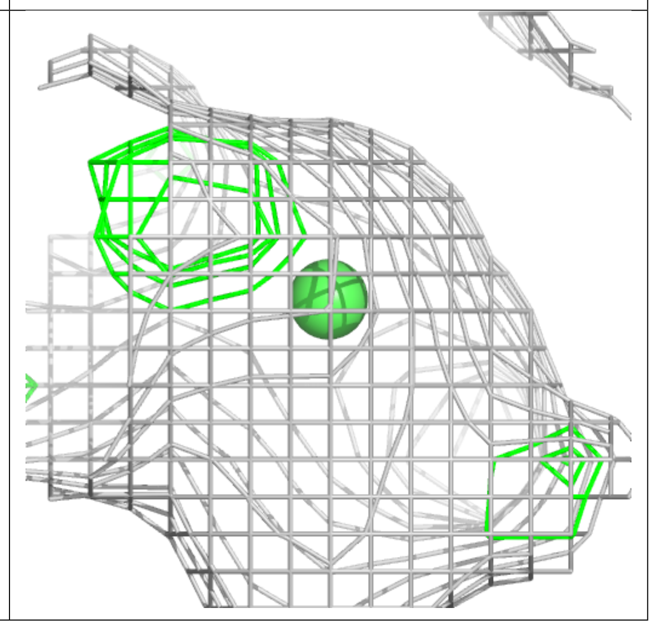
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

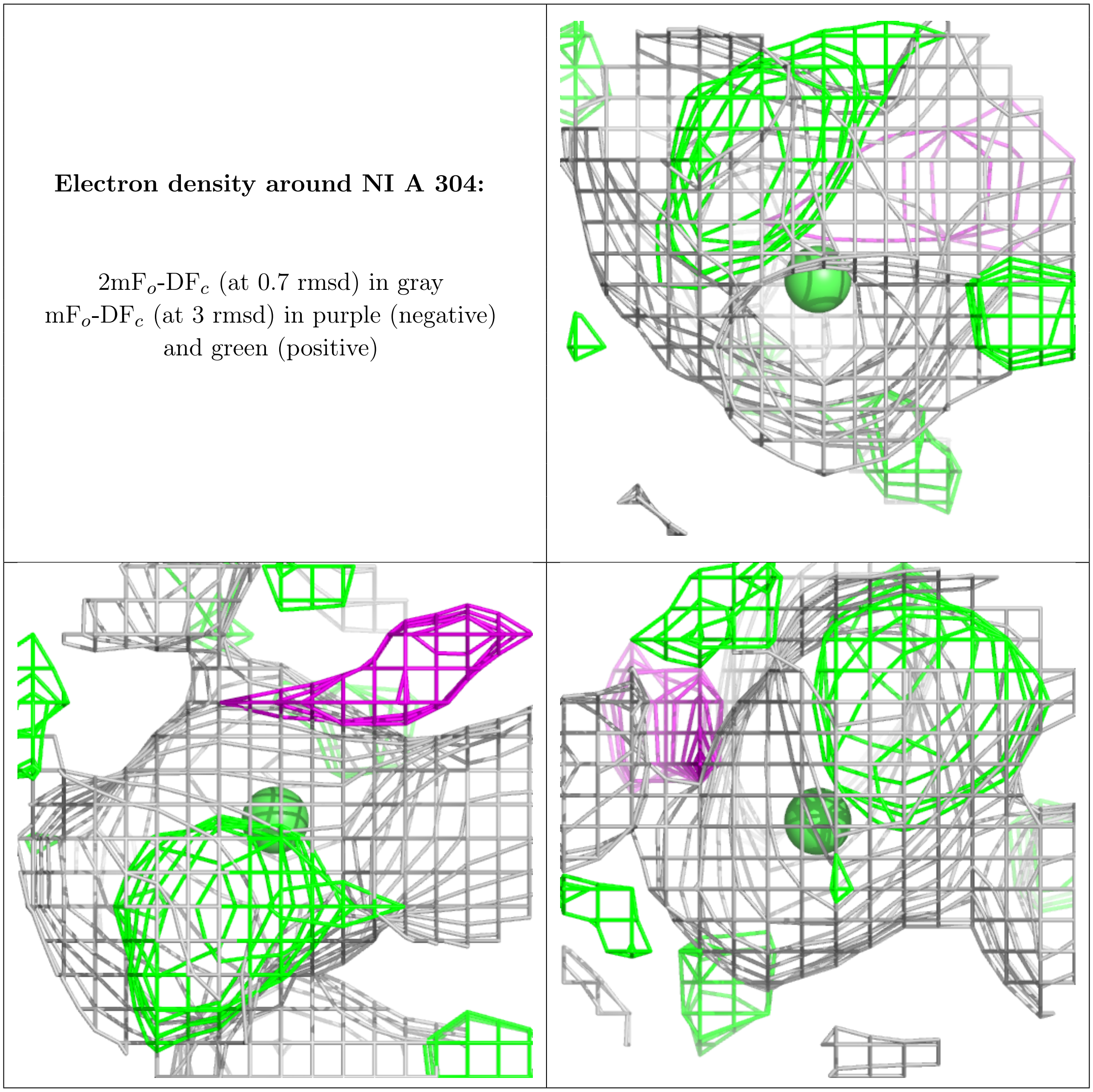
Electron density around NI B 303:

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







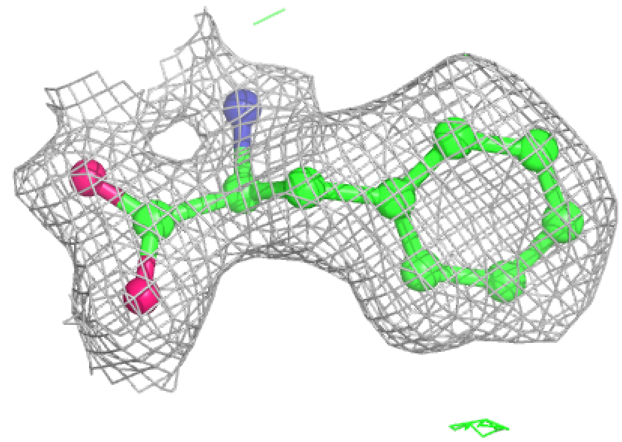


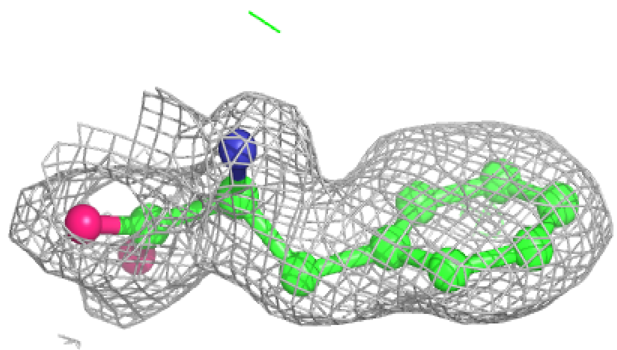
Electron density around NI A 304:

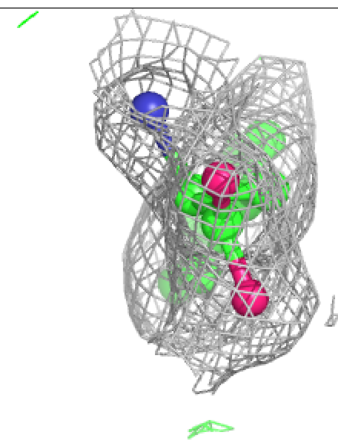
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around PHE B 302:

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

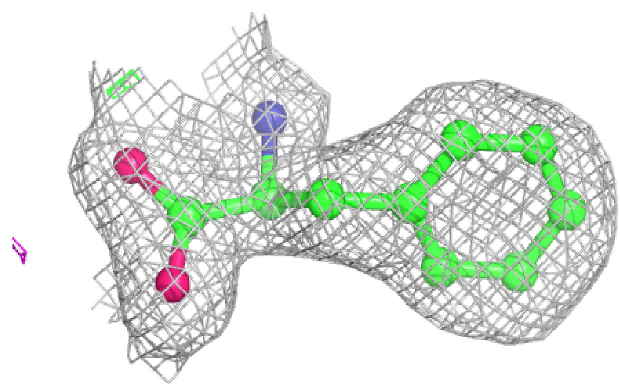


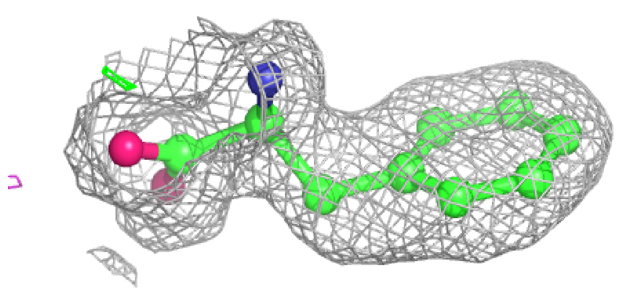


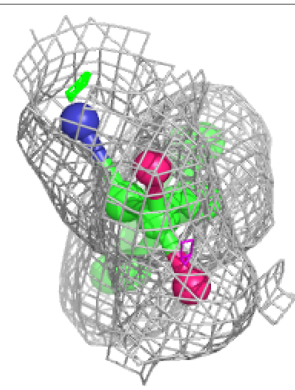


Electron density around PHE A 302:

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

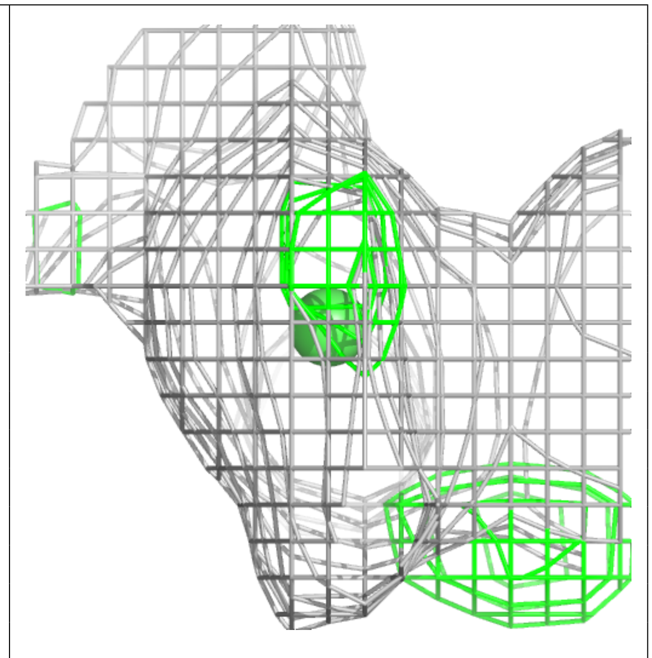


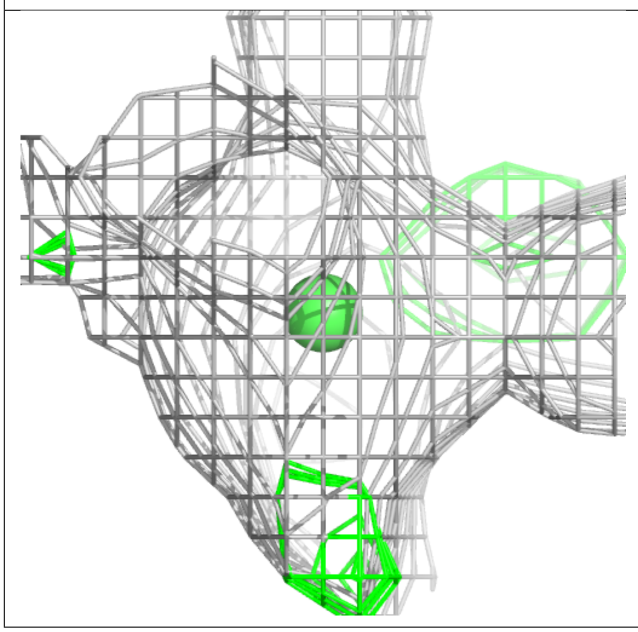


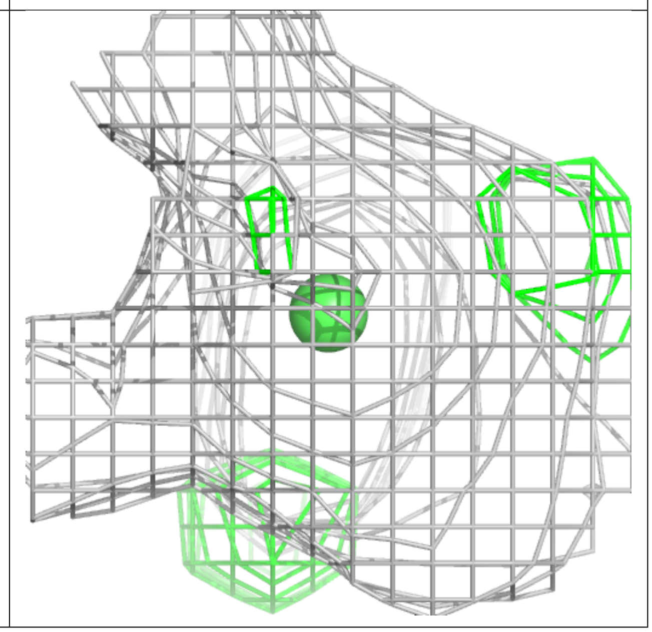


Electron density around NI B 304:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

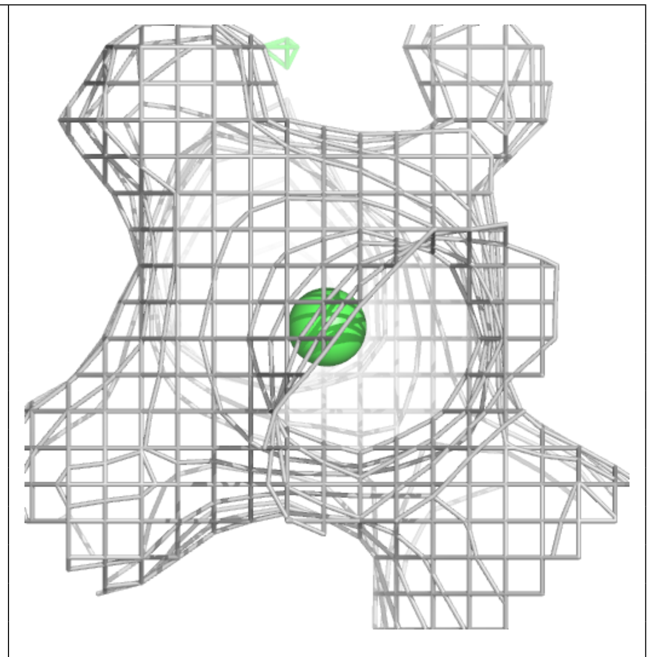


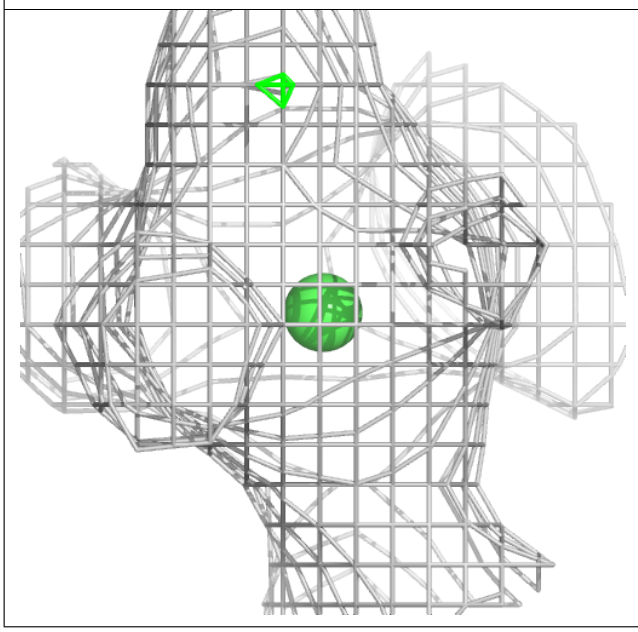


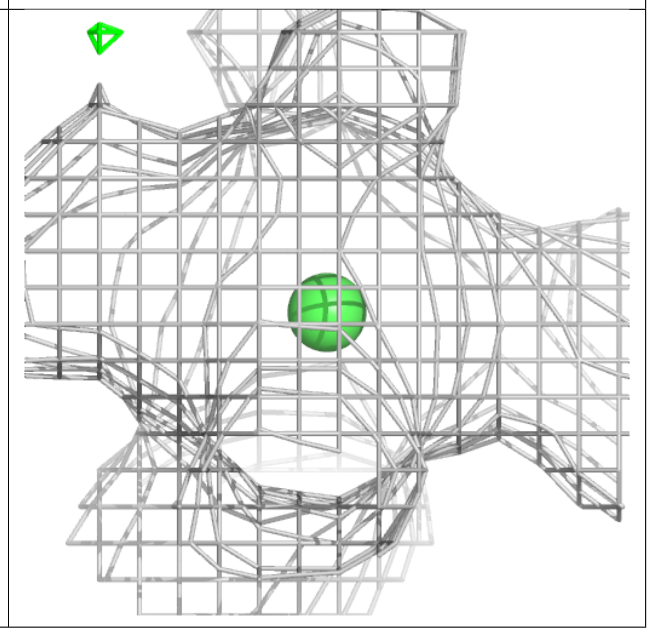


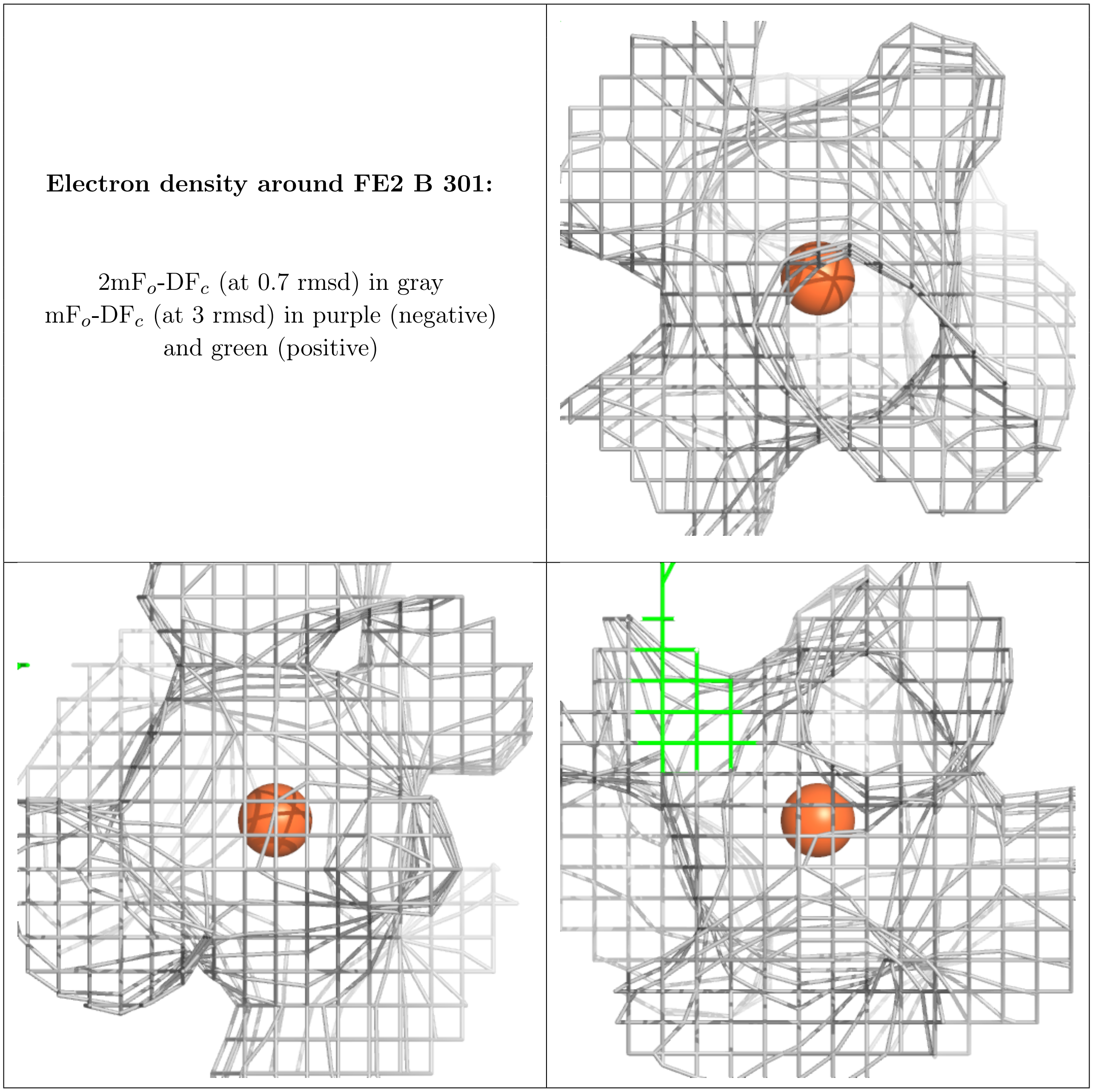
Electron density around NI A 305:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)







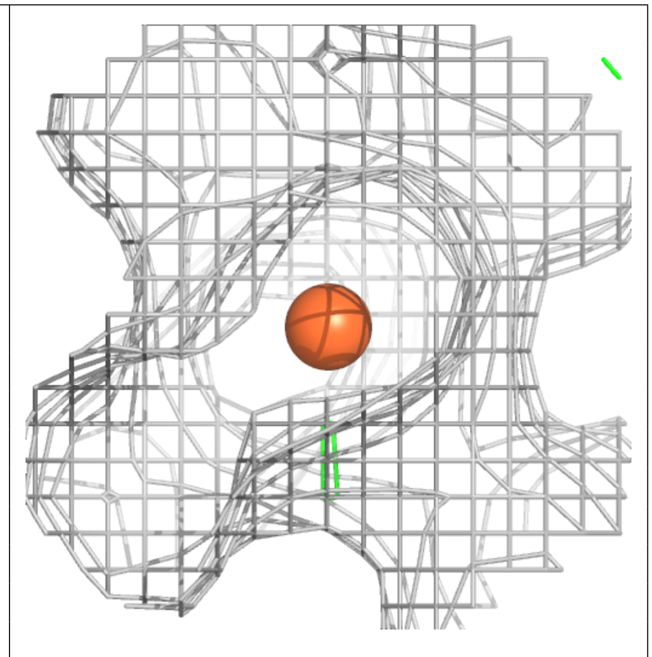


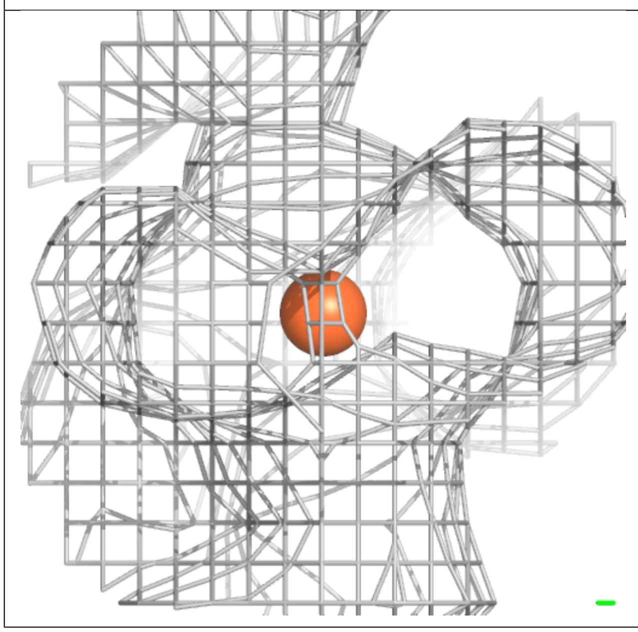
Electron density around FE2 B 301:

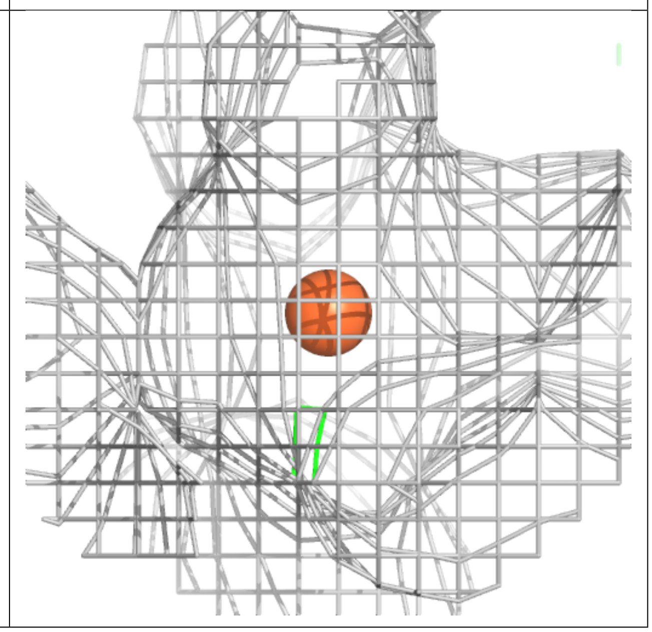
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around FE2 A 301:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

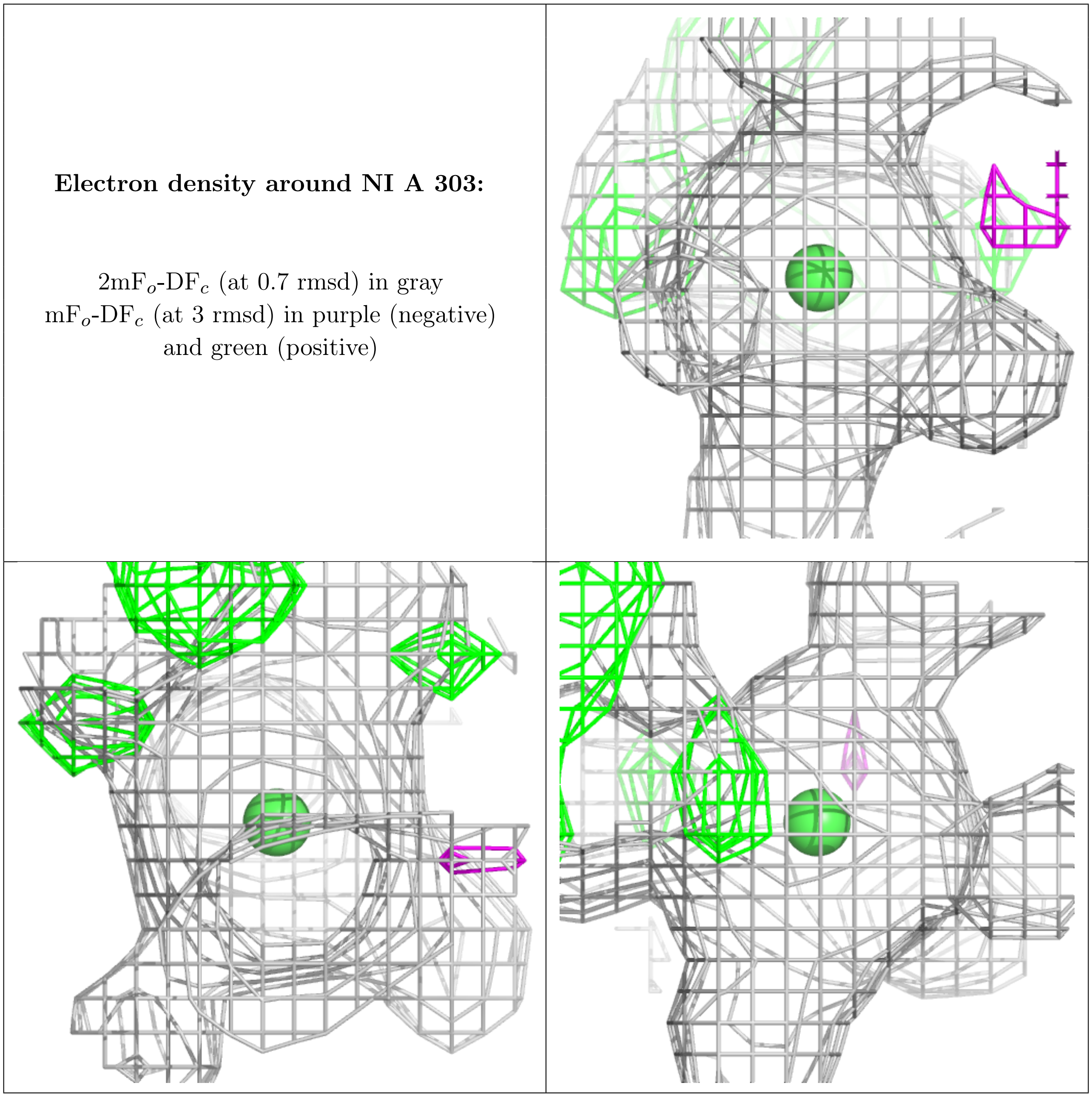






Electron density around NI A 303:

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.