



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 24, 2025 – 11:10 pm BST

PDB ID : 9GJ9 / pdb_00009gj9
Title : Crystal structure of methionine gamma-lyase from *Brevibacterium sandarakinum* in complex with PLP and norleucine at pH 6.5
Authors : Kopecny, D.; Ferchaud, N.; Briozzo, P.
Deposited on : 2024-08-21
Resolution : 2.49 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 Phenix2.0rc1
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1

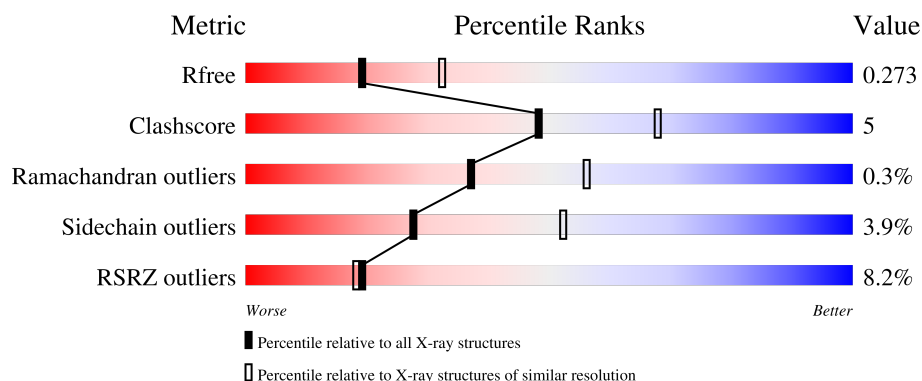
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)

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	413	<div> <div>7%</div> <div>80%</div> <div>12%</div> <div>7%</div> </div>
1	B	413	<div> <div>9%</div> <div>79%</div> <div>13%</div> <div>7%</div> </div>
1	C	413	<div> <div>8%</div> <div>78%</div> <div>15%</div> <div>6%</div> </div>
1	D	413	<div> <div>6%</div> <div>81%</div> <div>12%</div> <div>7%</div> </div>
1	E	413	<div> <div>8%</div> <div>80%</div> <div>13%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	413	<div><div></div><div>8%</div><div>78%</div><div>13%</div><div>8%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16999 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 Cystathionine gamma-synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	P	S	0	0	0
			2805	1755	497	538	1	14			
1	B	386	Total	C	N	O	P	S	0	0	0
			2822	1763	501	544	1	13			
1	C	388	Total	C	N	O	P	S	0	0	0
			2838	1773	504	547	1	13			
1	D	386	Total	C	N	O	P	S	0	0	0
			2825	1767	500	543	1	14			
1	E	385	Total	C	N	O	P	S	0	0	0
			2817	1759	500	544	1	13			
1	F	380	Total	C	N	O	P	S	0	0	0
			2786	1743	493	536	1	13			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A1H1YBL2
A	-18	GLY	-	expression tag	UNP A0A1H1YBL2
A	-17	SER	-	expression tag	UNP A0A1H1YBL2
A	-16	SER	-	expression tag	UNP A0A1H1YBL2
A	-15	HIS	-	expression tag	UNP A0A1H1YBL2
A	-14	HIS	-	expression tag	UNP A0A1H1YBL2
A	-13	HIS	-	expression tag	UNP A0A1H1YBL2
A	-12	HIS	-	expression tag	UNP A0A1H1YBL2
A	-11	HIS	-	expression tag	UNP A0A1H1YBL2
A	-10	HIS	-	expression tag	UNP A0A1H1YBL2
A	-9	SER	-	expression tag	UNP A0A1H1YBL2
A	-8	SER	-	expression tag	UNP A0A1H1YBL2
A	-7	GLY	-	expression tag	UNP A0A1H1YBL2
A	-6	LEU	-	expression tag	UNP A0A1H1YBL2
A	-5	VAL	-	expression tag	UNP A0A1H1YBL2
A	-4	PRO	-	expression tag	UNP A0A1H1YBL2
A	-3	ARG	-	expression tag	UNP A0A1H1YBL2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A0A1H1YBL2
A	-1	SER	-	expression tag	UNP A0A1H1YBL2
A	0	HIS	-	expression tag	UNP A0A1H1YBL2
B	-19	MET	-	initiating methionine	UNP A0A1H1YBL2
B	-18	GLY	-	expression tag	UNP A0A1H1YBL2
B	-17	SER	-	expression tag	UNP A0A1H1YBL2
B	-16	SER	-	expression tag	UNP A0A1H1YBL2
B	-15	HIS	-	expression tag	UNP A0A1H1YBL2
B	-14	HIS	-	expression tag	UNP A0A1H1YBL2
B	-13	HIS	-	expression tag	UNP A0A1H1YBL2
B	-12	HIS	-	expression tag	UNP A0A1H1YBL2
B	-11	HIS	-	expression tag	UNP A0A1H1YBL2
B	-10	HIS	-	expression tag	UNP A0A1H1YBL2
B	-9	SER	-	expression tag	UNP A0A1H1YBL2
B	-8	SER	-	expression tag	UNP A0A1H1YBL2
B	-7	GLY	-	expression tag	UNP A0A1H1YBL2
B	-6	LEU	-	expression tag	UNP A0A1H1YBL2
B	-5	VAL	-	expression tag	UNP A0A1H1YBL2
B	-4	PRO	-	expression tag	UNP A0A1H1YBL2
B	-3	ARG	-	expression tag	UNP A0A1H1YBL2
B	-2	GLY	-	expression tag	UNP A0A1H1YBL2
B	-1	SER	-	expression tag	UNP A0A1H1YBL2
B	0	HIS	-	expression tag	UNP A0A1H1YBL2
C	-19	MET	-	initiating methionine	UNP A0A1H1YBL2
C	-18	GLY	-	expression tag	UNP A0A1H1YBL2
C	-17	SER	-	expression tag	UNP A0A1H1YBL2
C	-16	SER	-	expression tag	UNP A0A1H1YBL2
C	-15	HIS	-	expression tag	UNP A0A1H1YBL2
C	-14	HIS	-	expression tag	UNP A0A1H1YBL2
C	-13	HIS	-	expression tag	UNP A0A1H1YBL2
C	-12	HIS	-	expression tag	UNP A0A1H1YBL2
C	-11	HIS	-	expression tag	UNP A0A1H1YBL2
C	-10	HIS	-	expression tag	UNP A0A1H1YBL2
C	-9	SER	-	expression tag	UNP A0A1H1YBL2
C	-8	SER	-	expression tag	UNP A0A1H1YBL2
C	-7	GLY	-	expression tag	UNP A0A1H1YBL2
C	-6	LEU	-	expression tag	UNP A0A1H1YBL2
C	-5	VAL	-	expression tag	UNP A0A1H1YBL2
C	-4	PRO	-	expression tag	UNP A0A1H1YBL2
C	-3	ARG	-	expression tag	UNP A0A1H1YBL2
C	-2	GLY	-	expression tag	UNP A0A1H1YBL2
C	-1	SER	-	expression tag	UNP A0A1H1YBL2

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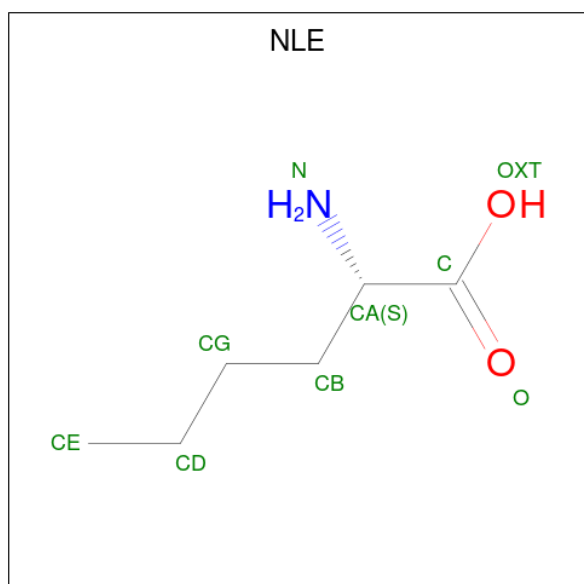
Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP A0A1H1YBL2
D	-19	MET	-	initiating methionine	UNP A0A1H1YBL2
D	-18	GLY	-	expression tag	UNP A0A1H1YBL2
D	-17	SER	-	expression tag	UNP A0A1H1YBL2
D	-16	SER	-	expression tag	UNP A0A1H1YBL2
D	-15	HIS	-	expression tag	UNP A0A1H1YBL2
D	-14	HIS	-	expression tag	UNP A0A1H1YBL2
D	-13	HIS	-	expression tag	UNP A0A1H1YBL2
D	-12	HIS	-	expression tag	UNP A0A1H1YBL2
D	-11	HIS	-	expression tag	UNP A0A1H1YBL2
D	-10	HIS	-	expression tag	UNP A0A1H1YBL2
D	-9	SER	-	expression tag	UNP A0A1H1YBL2
D	-8	SER	-	expression tag	UNP A0A1H1YBL2
D	-7	GLY	-	expression tag	UNP A0A1H1YBL2
D	-6	LEU	-	expression tag	UNP A0A1H1YBL2
D	-5	VAL	-	expression tag	UNP A0A1H1YBL2
D	-4	PRO	-	expression tag	UNP A0A1H1YBL2
D	-3	ARG	-	expression tag	UNP A0A1H1YBL2
D	-2	GLY	-	expression tag	UNP A0A1H1YBL2
D	-1	SER	-	expression tag	UNP A0A1H1YBL2
D	0	HIS	-	expression tag	UNP A0A1H1YBL2
E	-19	MET	-	initiating methionine	UNP A0A1H1YBL2
E	-18	GLY	-	expression tag	UNP A0A1H1YBL2
E	-17	SER	-	expression tag	UNP A0A1H1YBL2
E	-16	SER	-	expression tag	UNP A0A1H1YBL2
E	-15	HIS	-	expression tag	UNP A0A1H1YBL2
E	-14	HIS	-	expression tag	UNP A0A1H1YBL2
E	-13	HIS	-	expression tag	UNP A0A1H1YBL2
E	-12	HIS	-	expression tag	UNP A0A1H1YBL2
E	-11	HIS	-	expression tag	UNP A0A1H1YBL2
E	-10	HIS	-	expression tag	UNP A0A1H1YBL2
E	-9	SER	-	expression tag	UNP A0A1H1YBL2
E	-8	SER	-	expression tag	UNP A0A1H1YBL2
E	-7	GLY	-	expression tag	UNP A0A1H1YBL2
E	-6	LEU	-	expression tag	UNP A0A1H1YBL2
E	-5	VAL	-	expression tag	UNP A0A1H1YBL2
E	-4	PRO	-	expression tag	UNP A0A1H1YBL2
E	-3	ARG	-	expression tag	UNP A0A1H1YBL2
E	-2	GLY	-	expression tag	UNP A0A1H1YBL2
E	-1	SER	-	expression tag	UNP A0A1H1YBL2
E	0	HIS	-	expression tag	UNP A0A1H1YBL2
F	-19	MET	-	initiating methionine	UNP A0A1H1YBL2

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-18	GLY	-	expression tag	UNP A0A1H1YBL2
F	-17	SER	-	expression tag	UNP A0A1H1YBL2
F	-16	SER	-	expression tag	UNP A0A1H1YBL2
F	-15	HIS	-	expression tag	UNP A0A1H1YBL2
F	-14	HIS	-	expression tag	UNP A0A1H1YBL2
F	-13	HIS	-	expression tag	UNP A0A1H1YBL2
F	-12	HIS	-	expression tag	UNP A0A1H1YBL2
F	-11	HIS	-	expression tag	UNP A0A1H1YBL2
F	-10	HIS	-	expression tag	UNP A0A1H1YBL2
F	-9	SER	-	expression tag	UNP A0A1H1YBL2
F	-8	SER	-	expression tag	UNP A0A1H1YBL2
F	-7	GLY	-	expression tag	UNP A0A1H1YBL2
F	-6	LEU	-	expression tag	UNP A0A1H1YBL2
F	-5	VAL	-	expression tag	UNP A0A1H1YBL2
F	-4	PRO	-	expression tag	UNP A0A1H1YBL2
F	-3	ARG	-	expression tag	UNP A0A1H1YBL2
F	-2	GLY	-	expression tag	UNP A0A1H1YBL2
F	-1	SER	-	expression tag	UNP A0A1H1YBL2
F	0	HIS	-	expression tag	UNP A0A1H1YBL2

- Molecule 2 is NORLEUCINE (CCD ID: NLE) (formula: $C_6H_{13}NO_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			9	6	1	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			9	6	1	2		
2	C	1	Total	C	N	O	0	0
			9	6	1	2		
2	D	1	Total	C	N	O	0	0
			9	6	1	2		
2	E	1	Total	C	N	O	0	0
			9	6	1	2		
2	F	1	Total	C	N	O	0	0
			9	6	1	2		

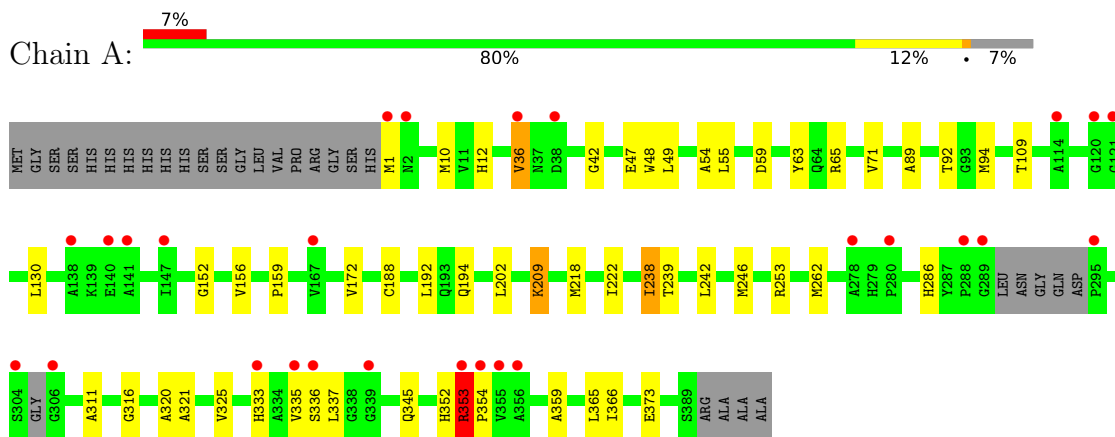
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	20	Total	O	0	0
			20	20		
3	B	7	Total	O	0	0
			7	7		
3	C	6	Total	O	0	0
			6	6		
3	D	8	Total	O	0	0
			8	8		
3	E	7	Total	O	0	0
			7	7		
3	F	4	Total	O	0	0
			4	4		

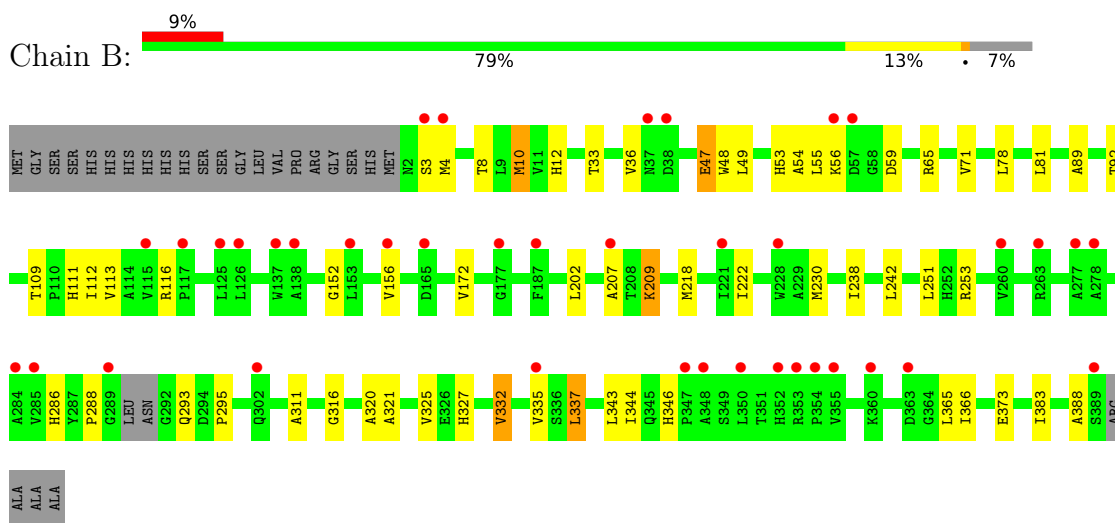
3 Residue-property plots [i](#)

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.

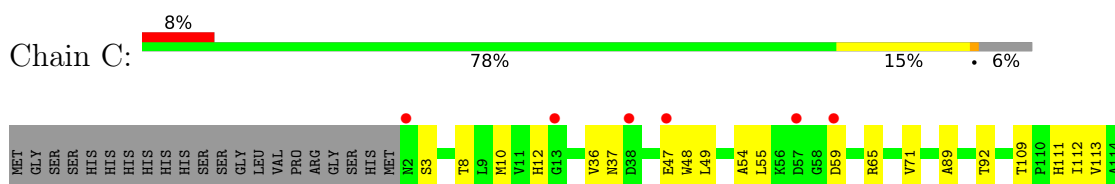
- Molecule 1: Cystathionine gamma-synthase

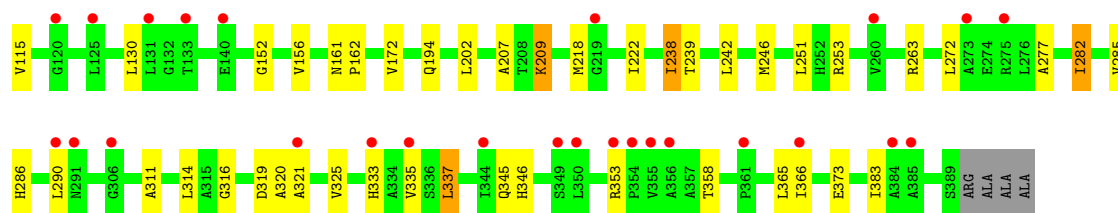


- Molecule 1: Cystathionine gamma-synthase

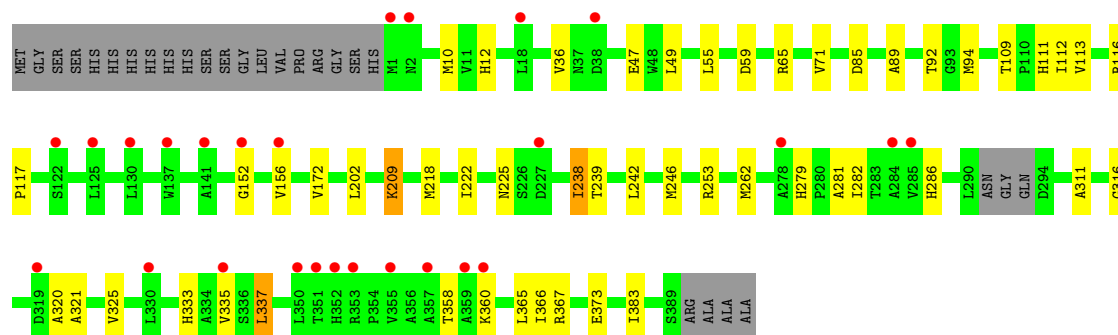
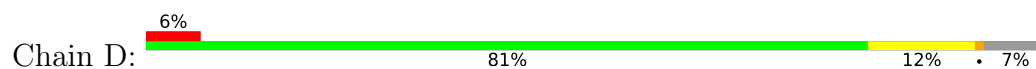


- Molecule 1: Cystathionine gamma-synthase

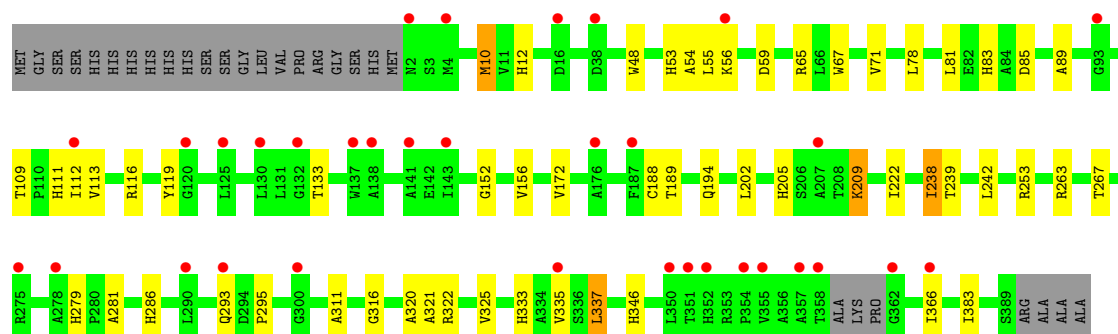
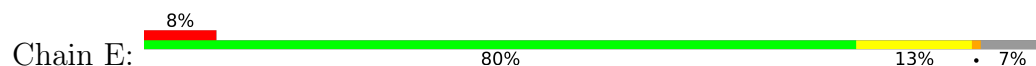




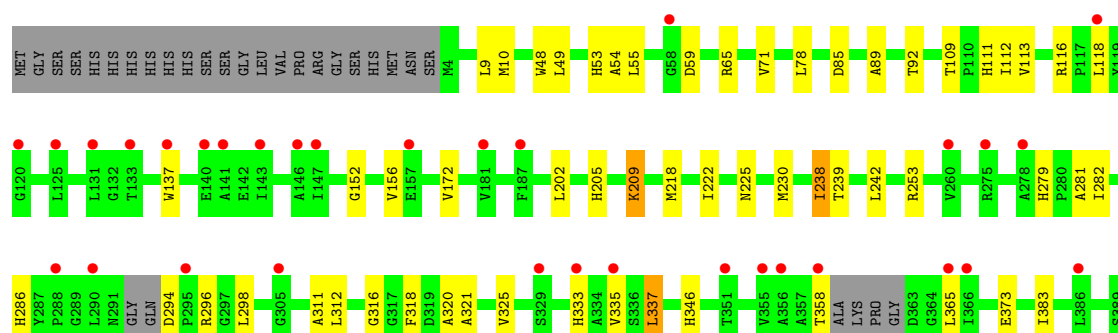
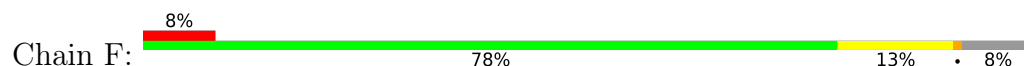
• Molecule 1: Cystathionine gamma-synthase



• Molecule 1: Cystathionine gamma-synthase



• Molecule 1: Cystathionine gamma-synthase



ARG
ALA
ALA
ALA

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	132.57Å 229.73Å 155.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	114.87 – 2.49 114.87 – 2.49	Depositor EDS
% Data completeness (in resolution range)	41.5 (114.87-2.49) 41.5 (114.87-2.49)	Depositor EDS
R_{merge}	0.33	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.48Å)	Xtriage
Refinement program	BUSTER 2.10.4	Depositor
R, R_{free}	0.255 , 0.287 0.246 , 0.273	Depositor DCC
R_{free} test set	1706 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.435	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.098 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.090 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	16999	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.93 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.3141e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: LLP, NLE

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	0.53	0/2833	0.98	1/3867 (0.0%)
1	B	0.54	0/2851	0.96	1/3894 (0.0%)
1	C	0.53	0/2868	0.98	2/3919 (0.1%)
1	D	0.54	0/2854	0.97	1/3898 (0.0%)
1	E	0.54	0/2845	0.96	1/3886 (0.0%)
1	F	0.53	0/2813	0.97	1/3842 (0.0%)
All	All	0.54	0/17064	0.97	7/23306 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	335	VAL	N-CA-C	7.00	113.70	106.21
1	E	335	VAL	N-CA-C	6.99	113.69	106.21
1	C	335	VAL	N-CA-C	6.93	113.62	106.21
1	D	335	VAL	N-CA-C	6.92	113.62	106.21
1	A	335	VAL	N-CA-C	6.89	113.59	106.21
1	B	335	VAL	N-CA-C	6.84	113.53	106.21
1	C	47	GLU	CB-CG-CD	5.03	121.15	112.60

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	2805	0	2775	35	0
1	B	2822	0	2782	38	0
1	C	2838	0	2800	37	0
1	D	2825	0	2794	33	0
1	E	2817	0	2774	35	0
1	F	2786	0	2748	37	0
2	A	9	0	12	0	0
2	B	9	0	12	0	0
2	C	9	0	12	0	0
2	D	9	0	12	0	0
2	E	9	0	12	1	0
2	F	9	0	12	0	0
3	A	20	0	0	0	0
3	B	7	0	0	0	0
3	C	6	0	0	0	0
3	D	8	0	0	0	0
3	E	7	0	0	0	0
3	F	4	0	0	0	0
All	All	16999	0	16745	181	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 (181) 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:D:286:HIS:HB2	1:D:311:ALA:HB3	1.57	0.83
1:B:56:LYS:HZ2	1:E:56:LYS:CE	1.92	0.83
1:F:318:PHE:CB	1:F:358:THR:HB	2.16	0.75
1:C:286:HIS:HB2	1:C:311:ALA:HB3	1.70	0.74
1:F:78:LEU:HD21	1:F:205:HIS:HD2	1.51	0.74
1:D:358:THR:HA	1:D:360:LYS:HZ3	1.54	0.72
1:A:286:HIS:HB2	1:A:311:ALA:HB3	1.71	0.72
1:B:56:LYS:HZ2	1:E:56:LYS:HE3	1.55	0.72
1:B:286:HIS:HB2	1:B:311:ALA:HB3	1.73	0.71
1:E:253:ARG:HH11	1:F:253:ARG:NH1	1.89	0.71
1:B:56:LYS:HZ2	1:E:56:LYS:NZ	1.88	0.70
1:E:253:ARG:NH1	1:F:253:ARG:HH11	1.89	0.70
1:E:253:ARG:NH1	1:F:253:ARG:NH1	2.41	0.69
1:A:352:HIS:ND1	1:E:85:ASP:OD2	2.26	0.67
1:F:286:HIS:HB2	1:F:311:ALA:HB3	1.77	0.67
1:F:318:PHE:HB2	1:F:358:THR:HB	1.76	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209:LLP:OP3	1:D:65:ARG:NH1	2.30	0.64
1:E:286:HIS:HB2	1:E:311:ALA:HB3	1.79	0.63
1:D:116:ARG:HG3	1:D:117:PRO:HA	1.79	0.63
1:F:78:LEU:HD21	1:F:205:HIS:CD2	2.34	0.63
1:F:321:ALA:HB3	1:F:346:HIS:CE1	2.34	0.62
1:C:321:ALA:HB3	1:C:346:HIS:CE1	2.35	0.61
1:B:332:VAL:HG13	1:B:343:LEU:HD23	1.82	0.61
1:A:253:ARG:NH1	1:D:253:ARG:HH11	2.00	0.59
1:B:56:LYS:NZ	1:E:56:LYS:NZ	2.50	0.59
1:E:78:LEU:HD21	1:E:205:HIS:HD2	1.67	0.59
1:E:321:ALA:HB3	1:E:346:HIS:CE1	2.37	0.59
1:F:48:TRP:NE1	1:F:54:ALA:O	2.35	0.58
1:B:48:TRP:NE1	1:B:54:ALA:O	2.36	0.58
1:B:373:GLU:OE2	1:C:12:HIS:NE2	2.26	0.57
1:E:48:TRP:NE1	1:E:54:ALA:O	2.36	0.57
1:A:209:LLP:HB2	1:A:337:LEU:HG	1.87	0.57
1:A:49:LEU:HD11	1:A:55:LEU:HD13	1.85	0.57
1:A:253:ARG:HH11	1:D:253:ARG:NH1	2.03	0.56
1:A:253:ARG:NH1	1:D:253:ARG:NH1	2.54	0.56
1:F:325:VAL:HG11	1:F:333:HIS:CE1	2.42	0.55
1:B:47:GLU:OE2	1:E:53:HIS:NE2	2.36	0.55
1:B:288:PRO:HA	1:B:293:GLN:HG2	1.89	0.55
1:F:318:PHE:HB3	1:F:358:THR:HB	1.89	0.55
1:F:53:HIS:CD2	1:F:230:MET:HE2	2.42	0.54
1:E:10:MET:HE3	1:E:81:LEU:HD22	1.89	0.54
1:C:48:TRP:NE1	1:C:54:ALA:O	2.36	0.54
1:B:12:HIS:NE2	1:C:373:GLU:OE2	2.35	0.53
1:C:49:LEU:HD11	1:C:55:LEU:HD13	1.89	0.53
1:B:53:HIS:CD2	1:B:230:MET:HE2	2.44	0.53
1:C:156:VAL:HG21	1:C:172:VAL:HG11	1.90	0.53
1:B:325:VAL:HG12	1:B:344:ILE:HG12	1.90	0.53
1:D:311:ALA:HB1	1:D:365:LEU:HD11	1.91	0.52
1:F:156:VAL:HG21	1:F:172:VAL:HG11	1.92	0.52
1:B:49:LEU:HD11	1:B:55:LEU:HD13	1.91	0.52
1:D:279:HIS:HB3	1:D:282:ILE:HG22	1.92	0.51
1:C:319:ASP:OD2	1:C:358:THR:O	2.27	0.51
1:C:321:ALA:HB1	1:C:366:ILE:HD11	1.91	0.51
1:A:192:LEU:HD13	1:A:262:MET:HE3	1.92	0.51
1:D:156:VAL:HG21	1:D:172:VAL:HG11	1.92	0.51
1:A:373:GLU:OE2	1:D:12:HIS:NE2	2.32	0.51
1:C:92:THR:HG22	1:C:218:MET:HE3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:92:THR:HG22	1:D:218:MET:HE3	1.93	0.51
1:F:325:VAL:HG13	1:F:333:HIS:CG	2.45	0.51
1:F:49:LEU:HD11	1:F:55:LEU:HD13	1.93	0.51
1:F:53:HIS:HD2	1:F:230:MET:HE2	1.76	0.51
1:E:156:VAL:HG21	1:E:172:VAL:HG11	1.92	0.51
1:E:55:LEU:HD22	1:E:67:TRP:CD1	2.46	0.50
1:B:92:THR:HG22	1:B:218:MET:HE3	1.94	0.50
1:A:92:THR:HG22	1:A:218:MET:HE3	1.93	0.50
1:C:277:ALA:HA	1:C:282:ILE:HD11	1.94	0.49
1:A:48:TRP:NE1	1:A:54:ALA:O	2.40	0.49
1:F:209:LLP:HB2	1:F:337:LEU:HG	1.95	0.49
1:A:238:ILE:HD12	1:A:239:THR:HG23	1.95	0.49
1:C:209:LLP:HB2	1:C:337:LEU:HG	1.94	0.49
1:F:111:HIS:HE1	1:F:113:VAL:HG22	1.78	0.49
1:C:325:VAL:HG11	1:C:333:HIS:CE1	2.48	0.48
1:D:111:HIS:HE1	1:D:113:VAL:HG22	1.78	0.48
1:D:238:ILE:HD12	1:D:239:THR:HG23	1.95	0.48
1:A:359:ALA:HB3	1:E:83:HIS:ND1	2.28	0.48
1:E:238:ILE:HD12	1:E:239:THR:HG23	1.95	0.48
1:F:92:THR:HG22	1:F:218:MET:HE3	1.94	0.48
1:A:321:ALA:HB1	1:A:366:ILE:HD11	1.95	0.48
1:C:238:ILE:HD12	1:C:239:THR:HG23	1.95	0.48
1:A:156:VAL:HG21	1:A:172:VAL:HG11	1.94	0.48
1:D:65:ARG:HA	1:D:242:LEU:HD11	1.96	0.48
1:C:325:VAL:CG1	1:C:333:HIS:CG	2.97	0.48
1:E:12:HIS:NE2	1:F:373:GLU:OE2	2.37	0.48
1:A:325:VAL:CG1	1:A:333:HIS:CG	2.97	0.48
1:C:111:HIS:HE1	1:C:113:VAL:HG22	1.79	0.48
1:A:325:VAL:HG11	1:A:333:HIS:CE1	2.48	0.48
1:A:325:VAL:HG13	1:A:333:HIS:CG	2.48	0.48
1:E:111:HIS:HE1	1:E:113:VAL:HG22	1.79	0.48
1:F:325:VAL:CG1	1:F:333:HIS:CG	2.96	0.48
1:B:71:VAL:HG13	1:B:89:ALA:HB3	1.95	0.47
1:B:53:HIS:HD2	1:B:230:MET:HE2	1.78	0.47
1:C:71:VAL:HG13	1:C:89:ALA:HB3	1.96	0.47
1:F:71:VAL:HG13	1:F:89:ALA:HB3	1.96	0.47
1:F:238:ILE:HD12	1:F:239:THR:HG23	1.95	0.47
1:B:65:ARG:HA	1:B:242:LEU:HD11	1.96	0.47
1:C:319:ASP:CG	1:C:358:THR:O	2.57	0.47
1:C:325:VAL:HG13	1:C:333:HIS:CG	2.49	0.47
1:A:71:VAL:HG13	1:A:89:ALA:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:209:LLP:HB2	1:B:337:LEU:HG	1.96	0.47
1:D:209:LLP:HB2	1:D:337:LEU:HG	1.96	0.47
1:B:111:HIS:HE1	1:B:113:VAL:HG22	1.80	0.47
1:B:321:ALA:HB1	1:B:366:ILE:HD11	1.96	0.47
1:C:65:ARG:HA	1:C:242:LEU:HD11	1.97	0.47
1:D:71:VAL:HG13	1:D:89:ALA:HB3	1.97	0.47
1:E:209:LLP:HB2	1:E:337:LEU:HG	1.96	0.47
1:E:71:VAL:HG13	1:E:89:ALA:HB3	1.96	0.46
1:A:333:HIS:CE1	1:A:345:GLN:HA	2.50	0.46
1:F:65:ARG:HA	1:F:242:LEU:HD11	1.97	0.46
1:F:316:GLY:HA3	1:F:320:ALA:HB2	1.96	0.46
1:A:109:THR:HB	1:A:152:GLY:CA	2.46	0.46
1:C:65:ARG:NH1	1:D:209:LLP:OP3	2.48	0.46
1:A:63:TYR:OH	1:B:209:LLP:OP3	2.27	0.46
1:A:333:HIS:CD2	1:B:36:VAL:CG2	2.99	0.46
1:E:109:THR:HB	1:E:152:GLY:CA	2.46	0.46
1:A:65:ARG:HA	1:A:242:LEU:HD11	1.98	0.46
1:B:109:THR:HB	1:B:152:GLY:CA	2.46	0.46
1:D:109:THR:HB	1:D:152:GLY:CA	2.46	0.46
1:D:321:ALA:HB1	1:D:366:ILE:HD11	1.97	0.46
1:C:333:HIS:CD2	1:D:36:VAL:CG2	2.99	0.46
1:F:109:THR:HB	1:F:152:GLY:CA	2.46	0.46
1:B:316:GLY:HA3	1:B:320:ALA:HB2	1.98	0.46
1:C:109:THR:HB	1:C:152:GLY:CA	2.46	0.46
1:D:49:LEU:HD11	1:D:55:LEU:HD13	1.98	0.46
1:A:246:MET:HE2	1:D:246:MET:HE2	1.98	0.45
1:A:65:ARG:NH2	1:B:209:LLP:OP2	2.50	0.45
1:C:333:HIS:CE1	1:C:345:GLN:HA	2.52	0.45
1:E:321:ALA:HB1	1:E:366:ILE:HD11	1.99	0.45
1:E:321:ALA:CB	1:E:346:HIS:CE1	2.98	0.45
1:B:156:VAL:HG21	1:B:172:VAL:HG11	1.98	0.45
1:F:118:LEU:HD12	1:F:137:TRP:HZ3	1.82	0.45
1:A:316:GLY:HA3	1:A:320:ALA:HB2	1.98	0.45
1:E:65:ARG:HA	1:E:242:LEU:HD11	1.99	0.44
1:C:316:GLY:HA3	1:C:320:ALA:HB2	1.98	0.44
1:E:253:ARG:HH12	1:F:253:ARG:HH11	1.65	0.44
1:D:325:VAL:CG1	1:D:333:HIS:CG	3.01	0.44
1:C:311:ALA:HB1	1:C:365:LEU:HD11	1.99	0.44
1:A:336:SER:HB2	1:B:33:THR:HB	2.00	0.44
1:A:353:ARG:HB2	1:A:354:PRO:HD3	1.99	0.44
1:E:325:VAL:CG1	1:E:333:HIS:CG	3.01	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:311:ALA:HB1	1:F:365:LEU:HD11	2.00	0.44
1:B:311:ALA:HB1	1:B:365:LEU:HD11	2.00	0.44
1:A:94:MET:N	1:A:209:LLP:OP2	2.50	0.43
1:B:321:ALA:HB3	1:B:346:HIS:CE1	2.53	0.43
1:E:316:GLY:HA3	1:E:320:ALA:HB2	1.99	0.43
1:F:325:VAL:CG1	1:F:333:HIS:CE1	3.01	0.43
1:B:8:THR:HG23	1:C:373:GLU:HG2	2.00	0.43
1:B:56:LYS:HZ2	1:E:56:LYS:HZ1	1.66	0.43
1:F:282:ILE:HD13	1:F:312:LEU:HD22	2.00	0.43
1:C:321:ALA:CB	1:C:346:HIS:CE1	3.01	0.43
1:B:10:MET:HG3	1:B:81:LEU:HD11	2.01	0.43
1:D:316:GLY:HA3	1:D:320:ALA:HB2	2.00	0.43
1:A:159:PRO:HD3	1:A:188:CYS:SG	2.59	0.42
1:F:296:ARG:HB3	1:F:298:LEU:HD13	2.00	0.42
1:A:12:HIS:NE2	1:D:373:GLU:OE2	2.38	0.42
1:B:327:HIS:CE1	1:B:388:ALA:HB1	2.54	0.42
1:B:373:GLU:HG2	1:C:8:THR:HG23	2.01	0.42
1:E:253:ARG:HH11	1:F:253:ARG:HH12	1.66	0.42
1:E:119:TYR:OH	2:E:401:NLE:N	2.53	0.42
1:E:202:LEU:HD23	1:E:222:ILE:HG21	2.01	0.42
1:C:246:MET:HE2	1:D:246:MET:SD	2.60	0.41
1:D:94:MET:HE3	1:D:209:LLP:H5'2	2.02	0.41
1:A:202:LEU:HD23	1:A:222:ILE:HG21	2.01	0.41
1:E:279:HIS:CE1	1:E:281:ALA:HB3	2.56	0.41
1:B:253:ARG:HH21	1:C:253:ARG:NH2	2.19	0.41
1:D:202:LEU:HD23	1:D:222:ILE:HG21	2.02	0.41
1:C:36:VAL:CG2	1:D:333:HIS:CE1	3.03	0.41
1:F:202:LEU:HD23	1:F:222:ILE:HG21	2.02	0.41
1:B:202:LEU:HD23	1:B:222:ILE:HG21	2.02	0.41
1:E:263:ARG:NH1	1:E:267:THR:OG1	2.54	0.41
1:A:36:VAL:HG11	1:A:42:GLY:HA3	2.03	0.41
1:C:115:VAL:HG22	1:C:156:VAL:HG22	2.03	0.41
1:C:161:ASN:HA	1:C:162:PRO:HA	1.88	0.40
1:C:202:LEU:HD23	1:C:222:ILE:HG21	2.02	0.40
1:A:311:ALA:HB1	1:A:365:LEU:HD11	2.03	0.40
1:C:207:ALA:HB1	1:C:251:LEU:HD22	2.04	0.40
1:F:279:HIS:CE1	1:F:281:ALA:HB3	2.56	0.40
1:B:207:ALA:HB1	1:B:251:LEU:HD22	2.04	0.40
1:F:85:ASP:HB2	1:F:225:ASN:HA	2.04	0.40
1:D:85:ASP:HB2	1:D:225:ASN:HA	2.04	0.40
1:D:279:HIS:CE1	1:D:281:ALA:HB3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:325:VAL:HG13	1:D:333:HIS:CG	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	376/413 (91%)	366 (97%)	9 (2%)	1 (0%)	37	56
1	B	381/413 (92%)	367 (96%)	12 (3%)	2 (0%)	25	44
1	C	385/413 (93%)	372 (97%)	12 (3%)	1 (0%)	37	56
1	D	381/413 (92%)	368 (97%)	13 (3%)	0	100	100
1	E	380/413 (92%)	366 (96%)	12 (3%)	2 (0%)	25	44
1	F	373/413 (90%)	362 (97%)	11 (3%)	0	100	100
All	All	2276/2478 (92%)	2201 (97%)	69 (3%)	6 (0%)	37	56

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	3	SER
1	B	295	PRO
1	C	3	SER
1	E	189	THR
1	A	353	ARG
1	E	295	PRO

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	282/304 (93%)	273 (97%)	9 (3%)	34	60
1	B	283/304 (93%)	272 (96%)	11 (4%)	27	52
1	C	285/304 (94%)	269 (94%)	16 (6%)	17	36
1	D	284/304 (93%)	275 (97%)	9 (3%)	34	60
1	E	283/304 (93%)	271 (96%)	12 (4%)	25	49
1	F	280/304 (92%)	271 (97%)	9 (3%)	34	60
All	All	1697/1824 (93%)	1631 (96%)	66 (4%)	27	52

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	10	MET
1	A	36	VAL
1	A	47	GLU
1	A	59	ASP
1	A	130	LEU
1	A	194	GLN
1	A	238	ILE
1	A	353	ARG
1	B	4	MET
1	B	10	MET
1	B	47	GLU
1	B	59	ASP
1	B	78	LEU
1	B	112	ILE
1	B	116	ARG
1	B	238	ILE
1	B	332	VAL
1	B	337	LEU
1	B	383	ILE
1	C	10	MET
1	C	37	ASN
1	C	59	ASP
1	C	112	ILE
1	C	130	LEU
1	C	194	GLN

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Mol	Chain	Res	Type
1	C	238	ILE
1	C	263	ARG
1	C	272	LEU
1	C	282	ILE
1	C	285	VAL
1	C	290	LEU
1	C	314	LEU
1	C	337	LEU
1	C	353	ARG
1	C	383	ILE
1	D	10	MET
1	D	47	GLU
1	D	59	ASP
1	D	112	ILE
1	D	238	ILE
1	D	262	MET
1	D	337	LEU
1	D	367	ARG
1	D	383	ILE
1	E	10	MET
1	E	59	ASP
1	E	112	ILE
1	E	116	ARG
1	E	133	THR
1	E	188	CYS
1	E	194	GLN
1	E	238	ILE
1	E	293	GLN
1	E	322	ARG
1	E	337	LEU
1	E	383	ILE
1	F	9	LEU
1	F	10	MET
1	F	59	ASP
1	F	112	ILE
1	F	116	ARG
1	F	238	ILE
1	F	294	ASP
1	F	337	LEU
1	F	383	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	HIS
1	A	194	GLN
1	A	333	HIS
1	B	198	HIS
1	B	266	GLN
1	C	64	GLN
1	C	266	GLN
1	C	333	HIS
1	C	346	HIS
1	C	352	HIS
1	D	266	GLN
1	E	205	HIS
1	F	53	HIS
1	F	198	HIS
1	F	266	GLN
1	F	352	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	LLP	B	209	1	23,24,25	1.38	1 (4%)	25,32,34	0.76	1 (4%)
1	LLP	F	209	1	23,24,25	1.36	1 (4%)	25,32,34	0.81	1 (4%)
1	LLP	D	209	1	23,24,25	1.38	1 (4%)	25,32,34	0.84	1 (4%)
1	LLP	E	209	1	23,24,25	1.41	1 (4%)	25,32,34	0.76	1 (4%)
1	LLP	C	209	1	23,24,25	1.42	1 (4%)	25,32,34	0.76	1 (4%)
1	LLP	A	209	1	23,24,25	1.37	1 (4%)	25,32,34	0.87	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	LLP	B	209	1	-	4/16/17/19	0/1/1/1
1	LLP	F	209	1	-	3/16/17/19	0/1/1/1
1	LLP	D	209	1	-	3/16/17/19	0/1/1/1
1	LLP	E	209	1	-	3/16/17/19	0/1/1/1
1	LLP	C	209	1	-	3/16/17/19	0/1/1/1
1	LLP	A	209	1	-	5/16/17/19	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	209	LLP	C4'-NZ	6.24	1.48	1.27
1	C	209	LLP	C4'-NZ	6.24	1.48	1.27
1	D	209	LLP	C4'-NZ	6.07	1.47	1.27
1	B	209	LLP	C4'-NZ	6.06	1.47	1.27
1	A	209	LLP	C4'-NZ	6.03	1.47	1.27
1	F	209	LLP	C4'-NZ	5.97	1.47	1.27

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	209	LLP	OP4-C5'-C5	2.70	114.49	109.35
1	A	209	LLP	OP4-C5'-C5	2.70	114.49	109.35
1	F	209	LLP	OP4-C5'-C5	2.43	113.99	109.35
1	E	209	LLP	OP4-C5'-C5	2.27	113.67	109.35
1	C	209	LLP	OP4-C5'-C5	2.20	113.53	109.35
1	B	209	LLP	OP4-C5'-C5	2.02	113.20	109.35

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	209	LLP	N-CA-CB-CG
1	A	209	LLP	C-CA-CB-CG
1	B	209	LLP	N-CA-CB-CG
1	B	209	LLP	C-CA-CB-CG
1	C	209	LLP	N-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
1	C	209	LLP	C-CA-CB-CG
1	D	209	LLP	N-CA-CB-CG
1	D	209	LLP	C-CA-CB-CG
1	E	209	LLP	N-CA-CB-CG
1	E	209	LLP	C-CA-CB-CG
1	F	209	LLP	N-CA-CB-CG
1	F	209	LLP	C-CA-CB-CG
1	A	209	LLP	C4-C4'-NZ-CE
1	B	209	LLP	C4-C4'-NZ-CE
1	C	209	LLP	C4-C4'-NZ-CE
1	D	209	LLP	C4-C4'-NZ-CE
1	E	209	LLP	C4-C4'-NZ-CE
1	F	209	LLP	C4-C4'-NZ-CE
1	A	209	LLP	CD-CE-NZ-C4'
1	A	209	LLP	C3-C4-C4'-NZ
1	B	209	LLP	CD-CE-NZ-C4'

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	209	LLP	3	0
1	F	209	LLP	1	0
1	D	209	LLP	3	0
1	E	209	LLP	1	0
1	C	209	LLP	2	0
1	A	209	LLP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	$\# Z > 2$
2	NLE	D	401	-	7,8,8	0.77	0	8,9,9	1.01	0
2	NLE	E	401	-	7,8,8	0.85	0	8,9,9	0.93	0
2	NLE	F	401	-	7,8,8	0.95	0	8,9,9	0.81	0
2	NLE	B	401	-	7,8,8	0.87	0	8,9,9	0.94	0
2	NLE	A	401	-	7,8,8	0.90	0	8,9,9	0.79	0
2	NLE	C	401	-	7,8,8	0.80	0	8,9,9	0.86	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
2	NLE	D	401	-	-	2/8/8/8	-
2	NLE	E	401	-	-	3/8/8/8	-
2	NLE	F	401	-	-	2/8/8/8	-
2	NLE	B	401	-	-	3/8/8/8	-
2	NLE	A	401	-	-	3/8/8/8	-
2	NLE	C	401	-	-	1/8/8/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	NLE	CA-CB-CG-CD
2	E	401	NLE	CA-CB-CG-CD
2	D	401	NLE	CA-CB-CG-CD
2	E	401	NLE	CE-CD-CG-CB
2	A	401	NLE	CE-CD-CG-CB
2	C	401	NLE	CE-CD-CG-CB
2	F	401	NLE	CE-CD-CG-CB
2	D	401	NLE	CE-CD-CG-CB
2	B	401	NLE	CE-CD-CG-CB
2	A	401	NLE	O-C-CA-CB
2	A	401	NLE	OXT-C-CA-CB

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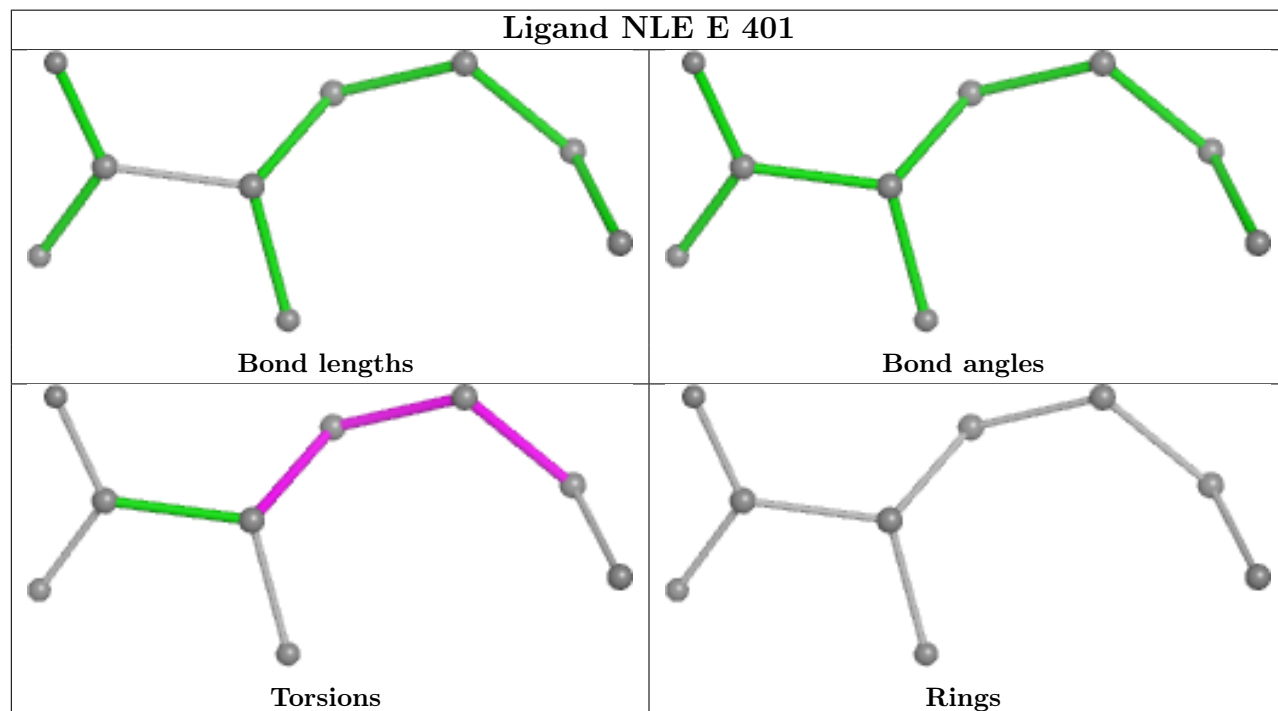
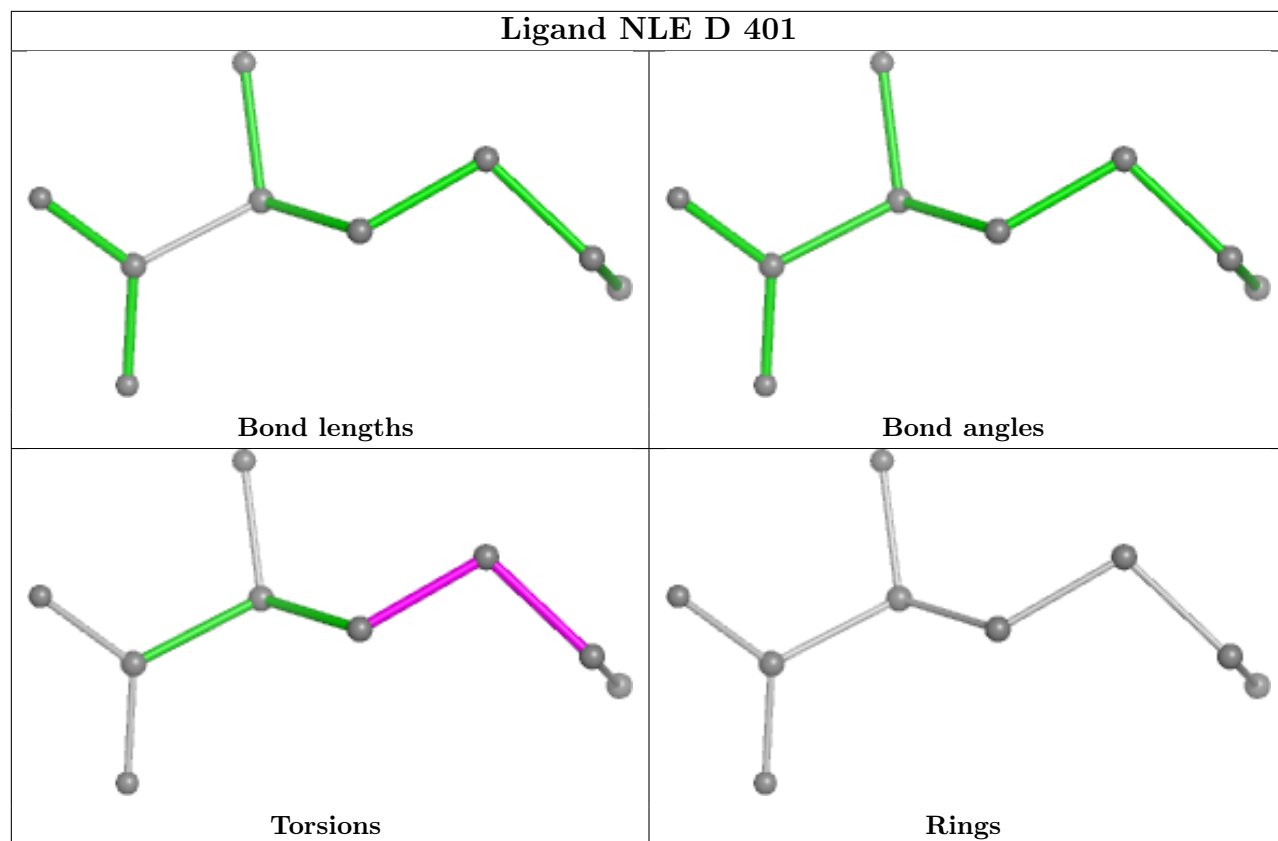
Mol	Chain	Res	Type	Atoms
2	B	401	NLE	O-C-CA-N
2	E	401	NLE	C-CA-CB-CG
2	F	401	NLE	N-CA-CB-CG

There are no ring outliers.

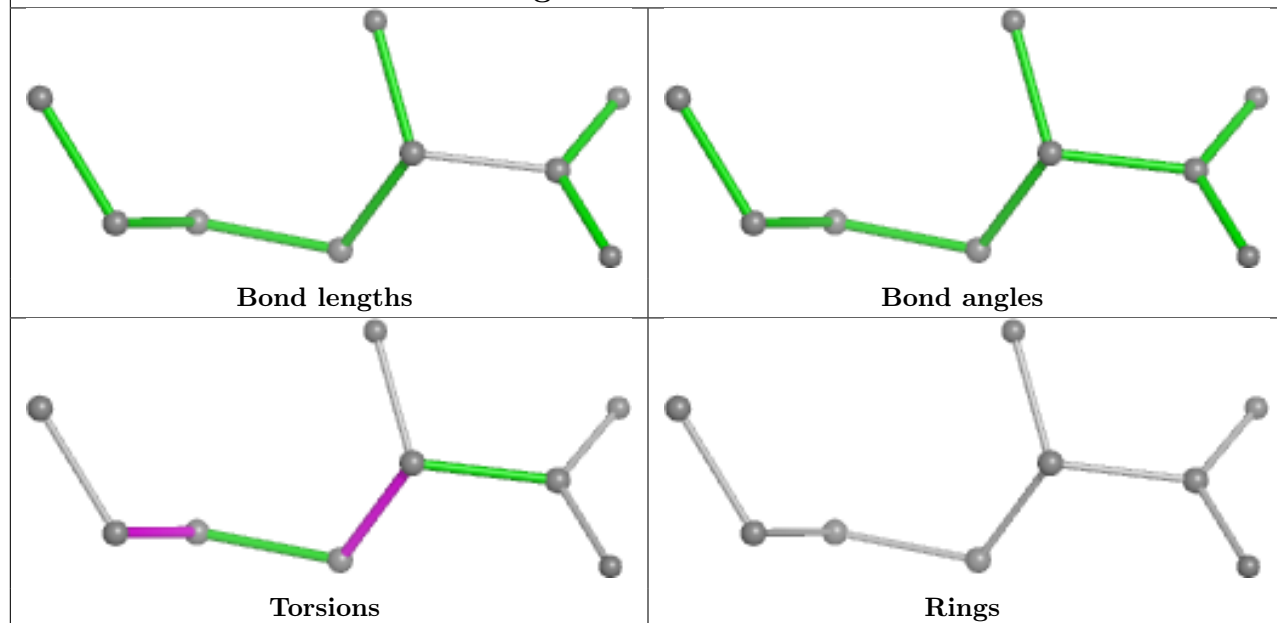
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	401	NLE	1	0

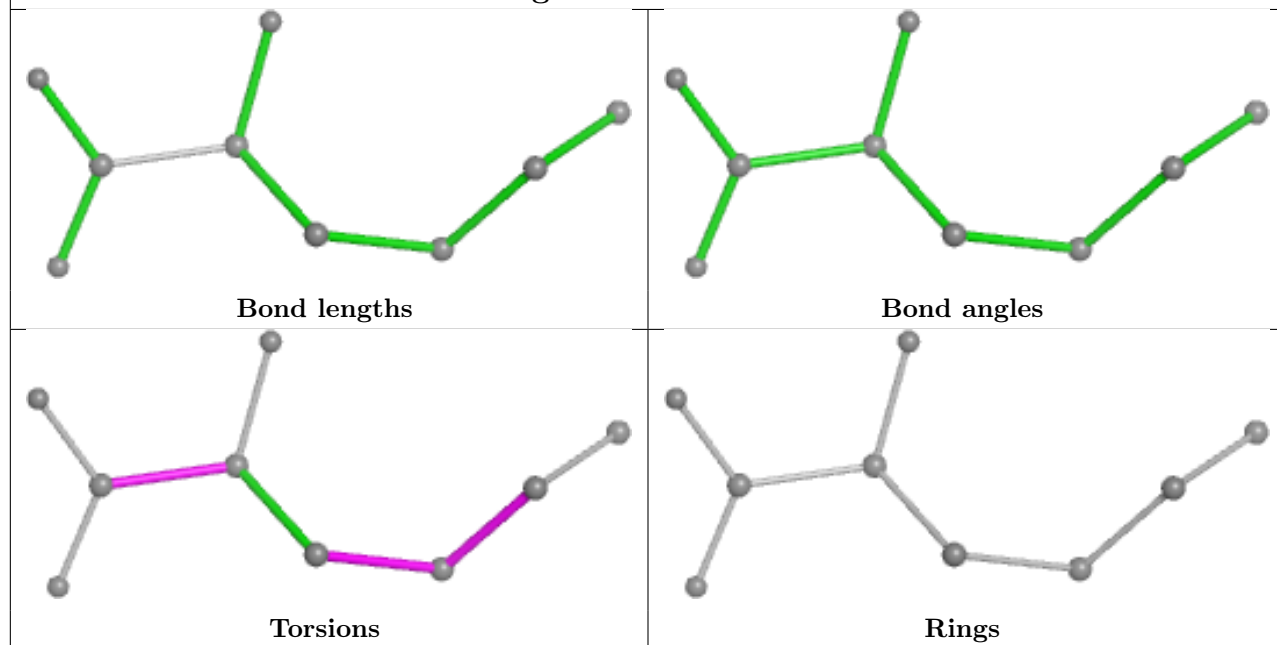
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

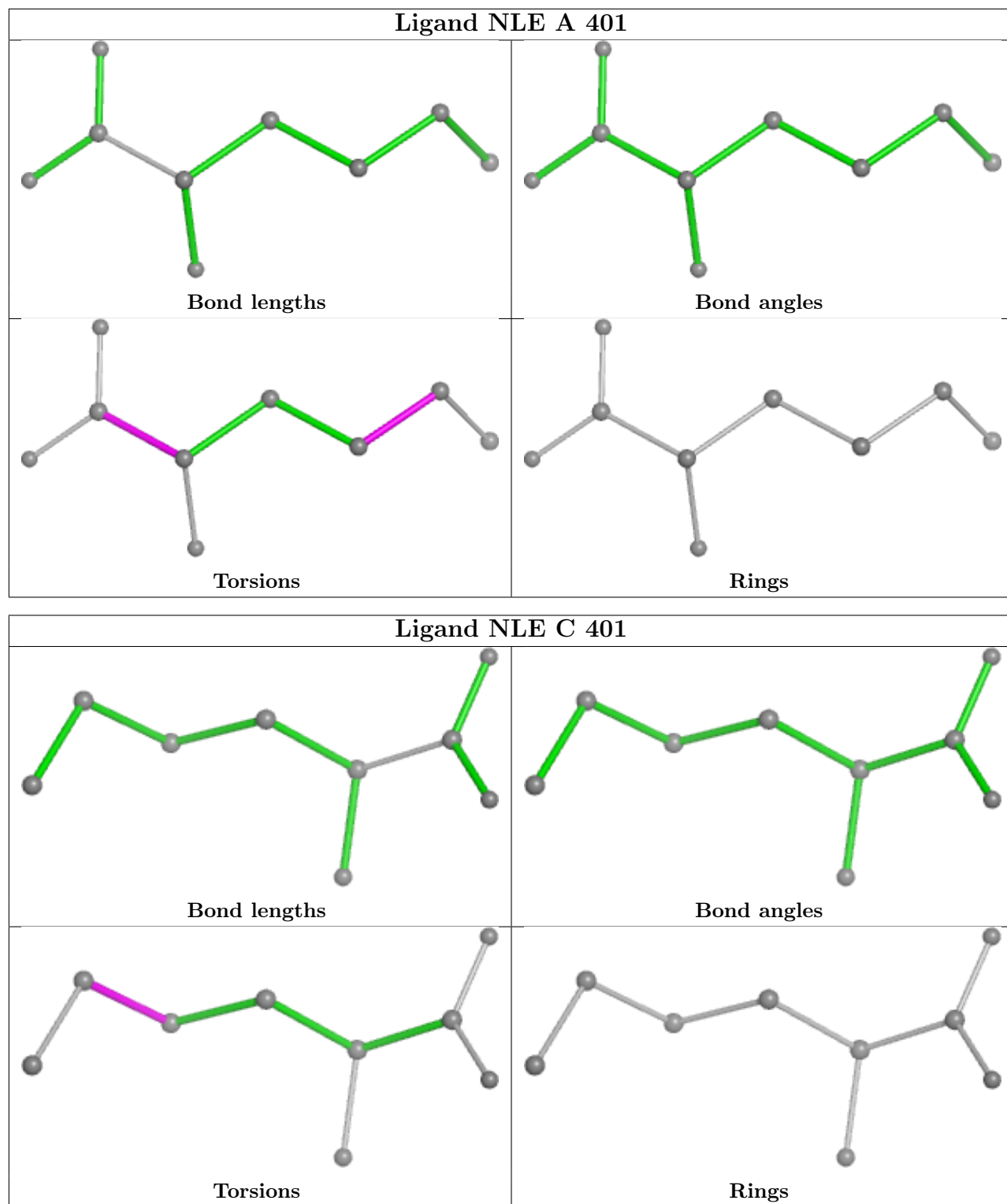


Ligand NLE F 401



Ligand NLE B 401





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

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	A	382/413 (92%)	0.69	27 (7%) 23 22	32, 50, 71, 80	0
1	B	385/413 (93%)	0.82	39 (10%) 14 13	36, 57, 75, 86	0
1	C	387/413 (93%)	0.76	32 (8%) 19 18	34, 55, 74, 83	0
1	D	385/413 (93%)	0.74	26 (6%) 25 23	33, 55, 77, 88	0
1	E	384/413 (92%)	0.80	33 (8%) 18 17	36, 58, 80, 102	0
1	F	379/413 (91%)	0.82	32 (8%) 18 17	39, 57, 78, 90	0
All	All	2302/2478 (92%)	0.77	189 (8%) 19 18	32, 56, 76, 102	0

All (189) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	278	ALA	6.5
1	F	355	VAL	5.4
1	E	355	VAL	4.4
1	C	355	VAL	4.3
1	A	289	GLY	4.1
1	A	38	ASP	4.0
1	E	2	ASN	3.9
1	B	335	VAL	3.9
1	E	335	VAL	3.9
1	E	351	THR	3.8
1	D	2	ASN	3.7
1	C	335	VAL	3.7
1	A	278	ALA	3.7
1	F	278	ALA	3.7
1	F	290	LEU	3.6
1	E	38	ASP	3.6
1	A	354	PRO	3.6
1	A	2	ASN	3.6
1	F	356	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	359	ALA	3.5
1	A	355	VAL	3.5
1	F	140	GLU	3.4
1	E	350	LEU	3.4
1	F	305	GLY	3.4
1	E	120	GLY	3.4
1	D	335	VAL	3.4
1	E	207	ALA	3.4
1	E	362	GLY	3.4
1	F	335	VAL	3.4
1	D	278	ALA	3.3
1	C	120	GLY	3.3
1	A	335	VAL	3.2
1	C	356	ALA	3.2
1	D	284	ALA	3.2
1	C	2	ASN	3.1
1	A	36	VAL	3.1
1	B	355	VAL	3.1
1	A	121	GLY	3.1
1	E	300	GLY	3.1
1	D	319	ASP	3.1
1	D	355	VAL	3.1
1	A	141	ALA	3.1
1	B	263	ARG	3.0
1	D	352	HIS	3.0
1	E	358	THR	3.0
1	C	350	LEU	3.0
1	B	38	ASP	3.0
1	A	114	ALA	3.0
1	D	350	LEU	3.0
1	B	354	PRO	3.0
1	C	321	ALA	3.0
1	A	1	MET	3.0
1	A	353	ARG	2.9
1	C	140	GLU	2.9
1	B	138	ALA	2.9
1	D	141	ALA	2.9
1	F	120	GLY	2.8
1	F	386	LEU	2.8
1	D	353	ARG	2.8
1	F	141	ALA	2.8
1	E	56	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	284	ALA	2.8
1	D	357	ALA	2.8
1	A	295	PRO	2.8
1	A	356	ALA	2.8
1	A	120	GLY	2.7
1	C	290	LEU	2.7
1	F	295	PRO	2.7
1	A	306	GLY	2.7
1	F	288	PRO	2.7
1	B	115	VAL	2.6
1	B	348	ALA	2.6
1	C	38	ASP	2.6
1	D	285	VAL	2.6
1	F	118	LEU	2.5
1	C	354	PRO	2.5
1	D	38	ASP	2.5
1	E	187	PHE	2.5
1	B	360	LYS	2.5
1	F	260	VAL	2.5
1	B	3	SER	2.5
1	F	329	SER	2.5
1	F	351	THR	2.5
1	C	353	ARG	2.5
1	C	125	LEU	2.5
1	F	125	LEU	2.5
1	A	336	SER	2.5
1	D	351	THR	2.5
1	F	275	ARG	2.5
1	B	187	PHE	2.5
1	B	126	LEU	2.5
1	D	156	VAL	2.5
1	C	385	ALA	2.5
1	F	137	TRP	2.5
1	B	165	ASP	2.5
1	E	357	ALA	2.4
1	C	273	ALA	2.4
1	B	289	GLY	2.4
1	A	280	PRO	2.4
1	B	207	ALA	2.4
1	C	384	ALA	2.4
1	F	143	ILE	2.4
1	C	131	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	333	HIS	2.3
1	D	1	MET	2.3
1	B	260	VAL	2.3
1	A	304	SER	2.3
1	A	339	GLY	2.3
1	E	354	PRO	2.3
1	F	157	GLU	2.3
1	E	141	ALA	2.3
1	B	153	LEU	2.3
1	B	389	SER	2.3
1	C	13	GLY	2.3
1	F	58	GLY	2.3
1	F	131	LEU	2.3
1	E	16	ASP	2.3
1	B	353	ARG	2.3
1	E	275	ARG	2.3
1	A	288	PRO	2.3
1	C	333	HIS	2.2
1	B	56	LYS	2.2
1	E	137	TRP	2.2
1	B	302	GLN	2.2
1	E	352	HIS	2.2
1	B	177	GLY	2.2
1	E	93	GLY	2.2
1	B	228	TRP	2.2
1	A	147	ILE	2.2
1	E	143	ILE	2.2
1	F	146	ALA	2.2
1	B	352	HIS	2.2
1	D	360	LYS	2.2
1	F	365	LEU	2.2
1	C	133	THR	2.2
1	F	187	PHE	2.2
1	B	37	ASN	2.2
1	B	363	ASP	2.2
1	B	137	TRP	2.2
1	B	277	ALA	2.2
1	E	130	LEU	2.2
1	B	4	MET	2.2
1	D	152	GLY	2.2
1	E	132	GLY	2.2
1	C	291	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	293	GLN	2.2
1	E	112	ILE	2.2
1	F	366	ILE	2.2
1	A	167	VAL	2.2
1	B	156	VAL	2.2
1	B	285	VAL	2.2
1	C	219	GLY	2.1
1	C	275	ARG	2.1
1	C	59	ASP	2.1
1	C	366	ILE	2.1
1	B	125	LEU	2.1
1	B	350	LEU	2.1
1	D	18	LEU	2.1
1	D	125	LEU	2.1
1	D	130	LEU	2.1
1	E	4	MET	2.1
1	C	57	ASP	2.1
1	E	366	ILE	2.1
1	F	333	HIS	2.1
1	D	330	LEU	2.1
1	E	125	LEU	2.1
1	E	176	ALA	2.1
1	C	361	PRO	2.1
1	A	140	GLU	2.1
1	B	57	ASP	2.1
1	F	181	VAL	2.1
1	A	138	ALA	2.1
1	E	278	ALA	2.1
1	B	347	PRO	2.1
1	F	358	THR	2.1
1	B	221	ILE	2.1
1	C	260	VAL	2.0
1	E	290	LEU	2.0
1	E	138	ALA	2.0
1	C	306	GLY	2.0
1	D	137	TRP	2.0
1	B	117	PRO	2.0
1	F	133	THR	2.0
1	D	122	SER	2.0
1	F	147	ILE	2.0
1	D	227	ASP	2.0
1	C	47	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	349	SER	2.0
1	C	344	ILE	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
1	LLP	E	209	24/25	0.91	0.13	40,52,53,53	0
1	LLP	F	209	24/25	0.91	0.13	43,57,58,58	0
1	LLP	D	209	24/25	0.93	0.10	36,46,46,46	0
1	LLP	B	209	24/25	0.94	0.09	38,46,46,47	0
1	LLP	C	209	24/25	0.95	0.09	40,45,46,47	0
1	LLP	A	209	24/25	0.96	0.09	36,42,42,43	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

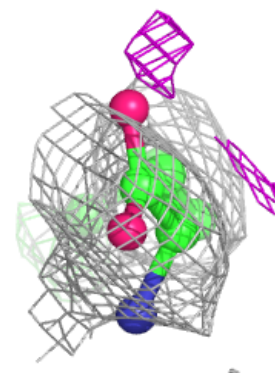
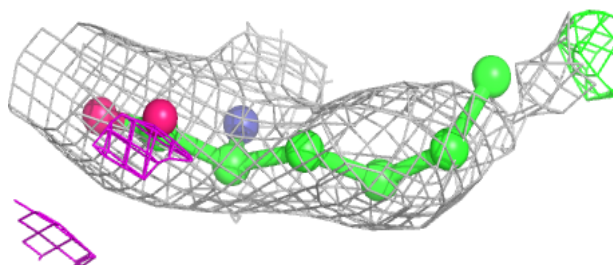
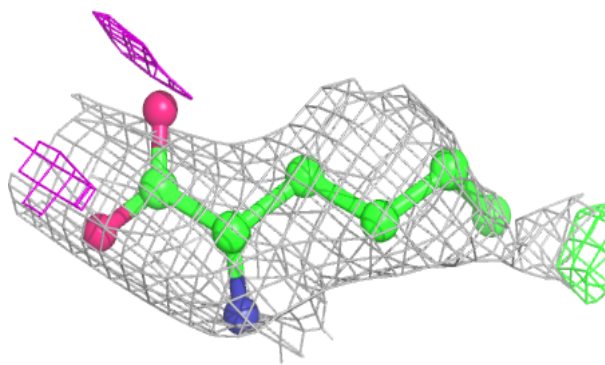
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	NLE	A	401	9/9	0.80	0.21	58,59,61,61	0
2	NLE	B	401	9/9	0.85	0.15	56,57,59,59	0
2	NLE	C	401	9/9	0.88	0.16	53,54,56,56	0
2	NLE	F	401	9/9	0.88	0.15	55,56,58,58	0
2	NLE	D	401	9/9	0.89	0.16	54,54,56,56	0
2	NLE	E	401	9/9	0.94	0.11	55,56,58,58	0

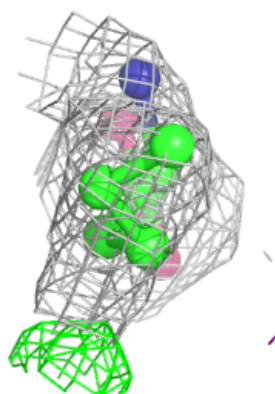
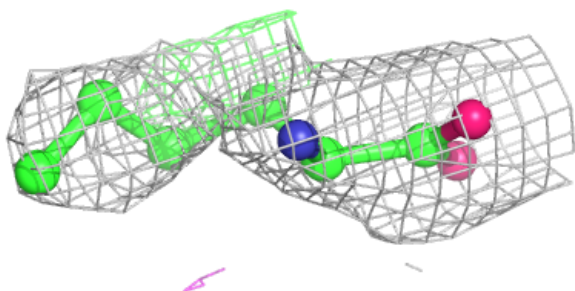
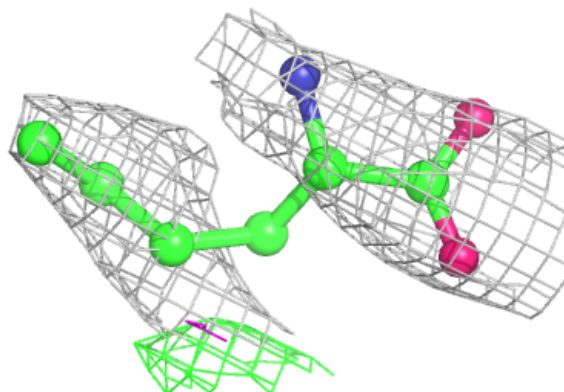
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NLE A 401:

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

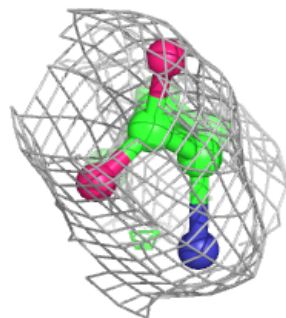
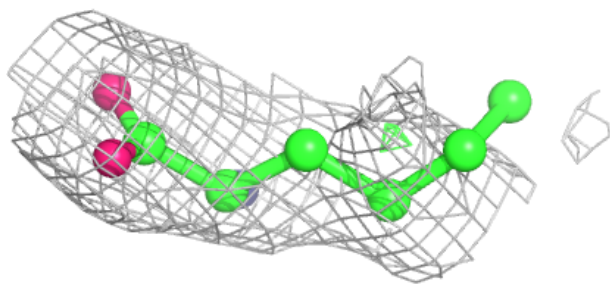
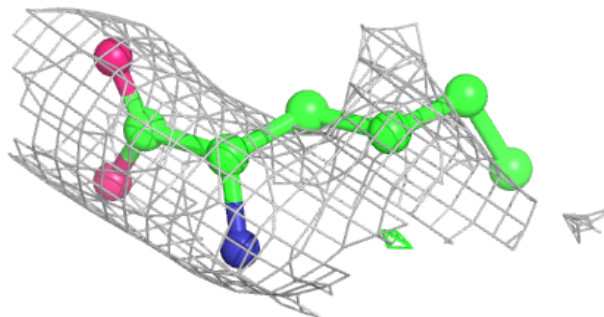
**Electron density around NLE B 401:**

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

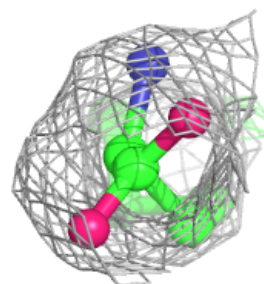
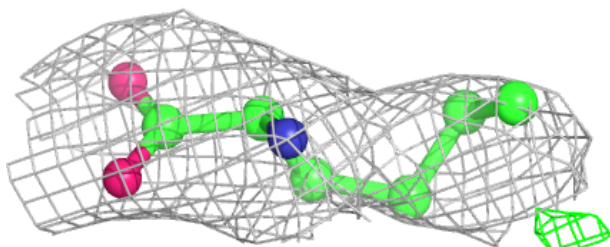
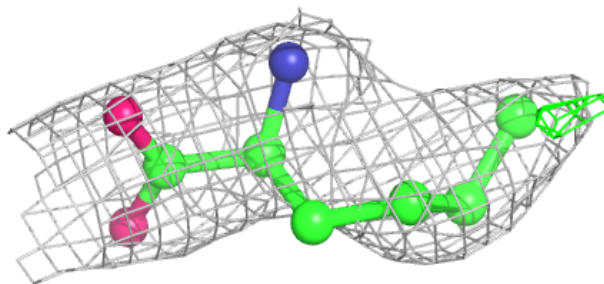


Electron density around NLE C 401:

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

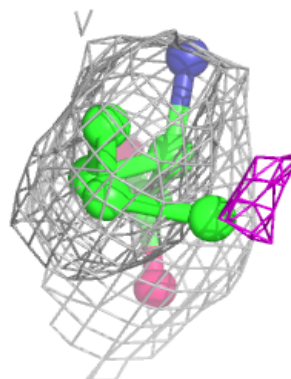
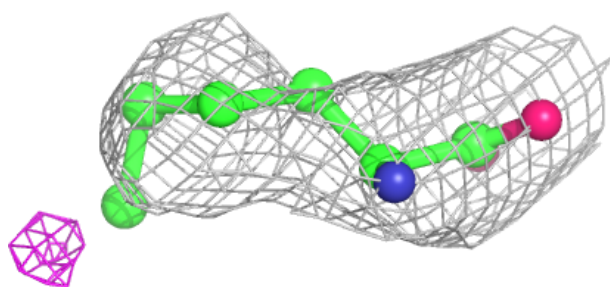
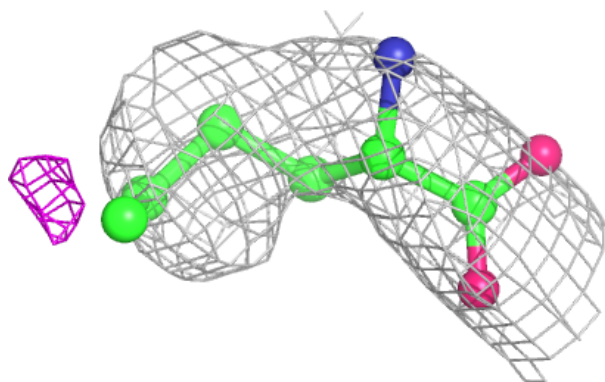
**Electron density around NLE F 401:**

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

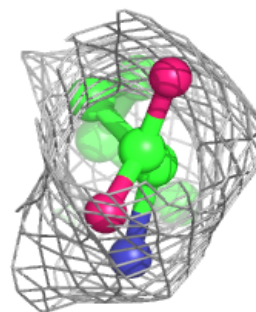
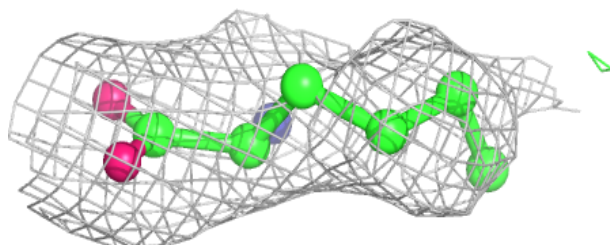
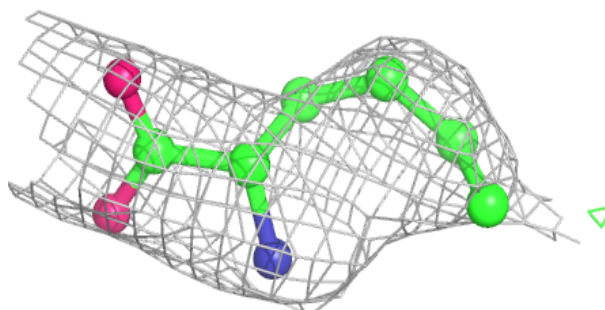


Electron density around NLE D 401:

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

**Electron density around NLE E 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.