



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 07:29 PM UTC

PDB ID : 1S64 / pdb_00001s64
Title : Rat protein geranylgeranyltransferase type-I complexed with L-778,123 and a sulfate anion
Authors : Reid, T.S.; Long, S.B.; Beese, L.S.
Deposited on : 2004-01-22
Resolution : 2.55 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

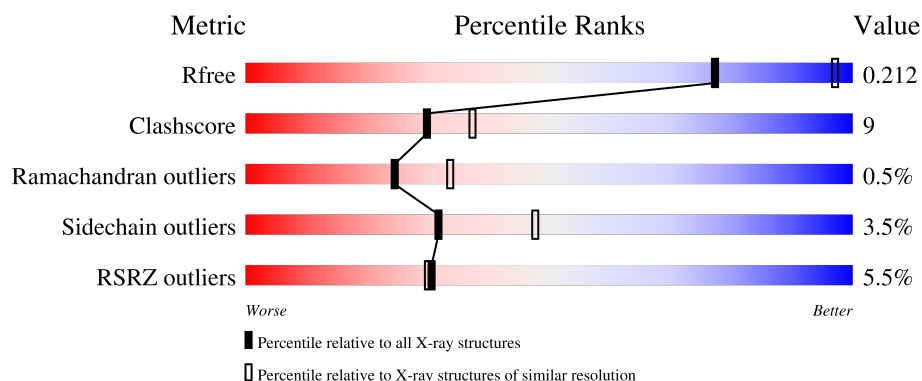
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	377	7% 67% 15% • 17%
1	C	377	3% 68% 15% • 17%
1	E	377	4% 63% 20% • 17%
1	G	377	8% 64% 19% • 17%
1	I	377	3% 66% 16% • 17%

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Mol	Chain	Length	Quality of chain
1	K	377	2% 67% 15% 17%
2	B	377	2% 68% 21% 8%
2	D	377	4% 72% 19% 8%
2	F	377	3% 72% 18% 8%
2	H	377	11% 67% 23% 8%
2	J	377	5% 72% 18% 8%
2	L	377	3% 75% 15% 8%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 33735 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 Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2626	1678	463	480	5			
1	C	314	Total	C	N	O	S	0	0	0
			2637	1686	458	488	5			
1	E	314	Total	C	N	O	S	0	0	0
			2642	1686	461	490	5			
1	G	314	Total	C	N	O	S	0	0	0
			2633	1683	459	486	5			
1	I	314	Total	C	N	O	S	0	0	0
			2651	1692	462	492	5			
1	K	314	Total	C	N	O	S	0	0	0
			2667	1700	466	496	5			

- Molecule 2 is a protein called Geranylgeranyl transferase type I beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	346	Total	C	N	O	S	0	0	0
			2693	1704	467	498	24			
2	D	346	Total	C	N	O	S	0	0	0
			2690	1705	463	498	24			
2	F	346	Total	C	N	O	S	0	0	0
			2714	1714	474	502	24			
2	H	346	Total	C	N	O	S	0	0	0
			2688	1701	463	500	24			
2	J	346	Total	C	N	O	S	0	0	0
			2709	1711	471	503	24			
2	L	346	Total	C	N	O	S	0	0	0
			2719	1717	473	505	24			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

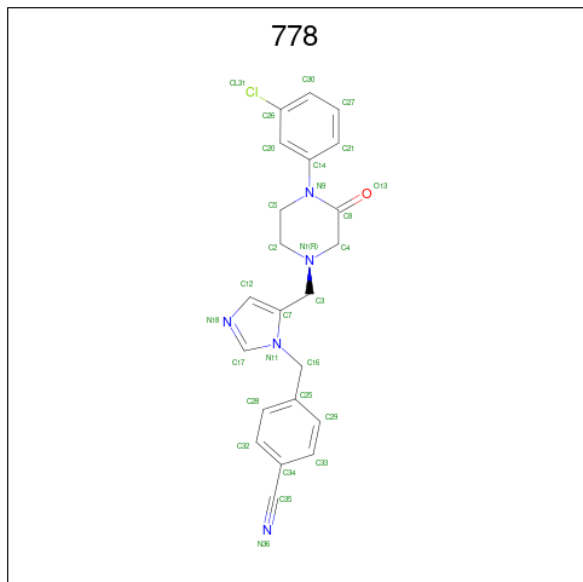
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		
3	F	1	Total	Zn	0	0
			1	1		
3	H	1	Total	Zn	0	0
			1	1		
3	J	1	Total	Zn	0	0
			1	1		
3	L	1	Total	Zn	0	0
			1	1		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	J	1	Total	O	S	0	0
			5	4	1		
4	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 4-[(5-{[4-(3-CHLOROPHENYL)-3-OXOPIPERAZIN-1-YL]METHYL}-1H-1MIDAZOL-1-YL)METHYL]BENZONITRILE (CCD ID: 778) (formula: $C_{22}H_{20}ClN_5O$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	Cl	N	O	0	0
			29	22	1	5	1		
5	D	1	Total	C	Cl	N	O	0	0
			29	22	1	5	1		
5	F	1	Total	C	Cl	N	O	0	0
			29	22	1	5	1		
5	H	1	Total	C	Cl	N	O	0	0
			29	22	1	5	1		
5	J	1	Total	C	Cl	N	O	0	0
			29	22	1	5	1		
5	L	1	Total	C	Cl	N	O	0	0
			29	22	1	5	1		

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	H	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	J	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
6	L	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	1	Total	Cl	0	0
			1	1		
7	D	1	Total	Cl	0	0
			1	1		
7	F	1	Total	Cl	0	0
			1	1		
7	G	1	Total	Cl	0	0
			1	1		
7	H	1	Total	Cl	0	0
			1	1		
7	I	1	Total	Cl	0	0
			1	1		

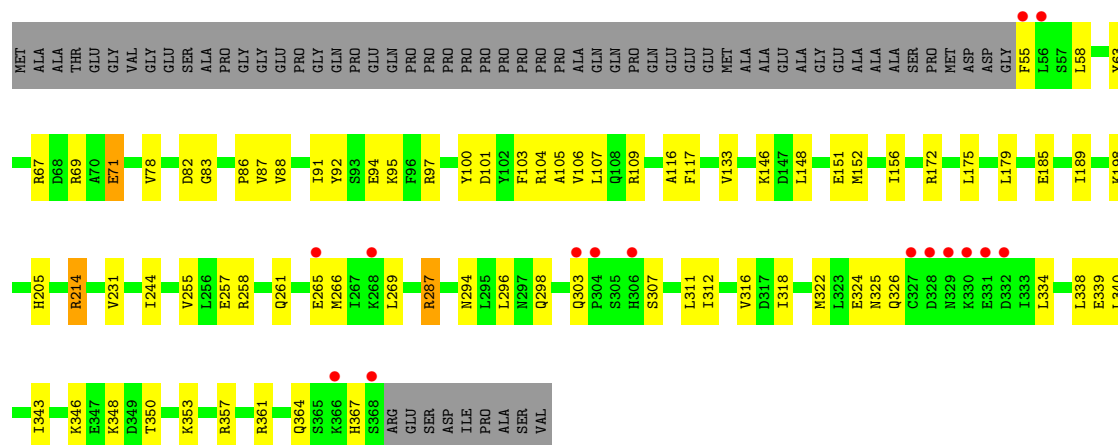
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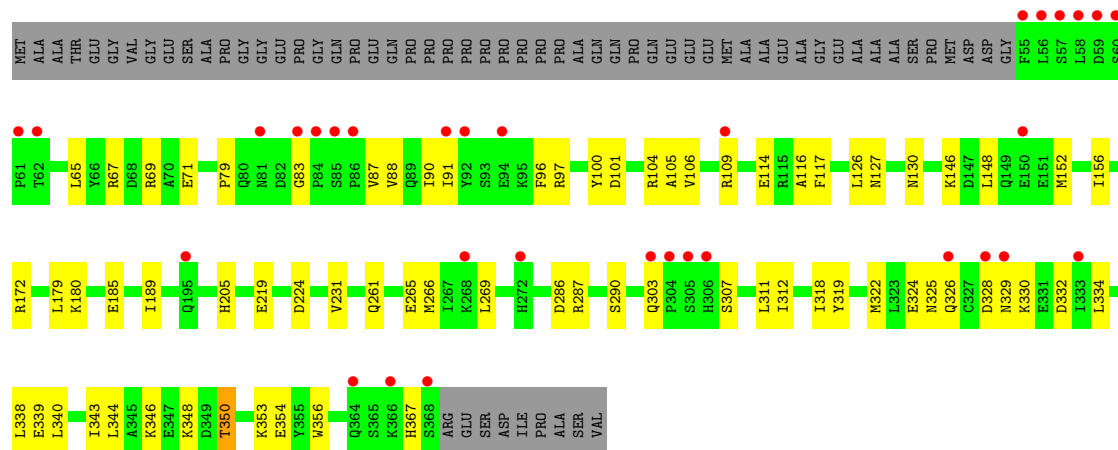
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	J	1	Total 1	Cl 1	0	0
7	K	1	Total 1	Cl 1	0	0
7	L	1	Total 1	Cl 1	0	0

- Molecule 8 is water.

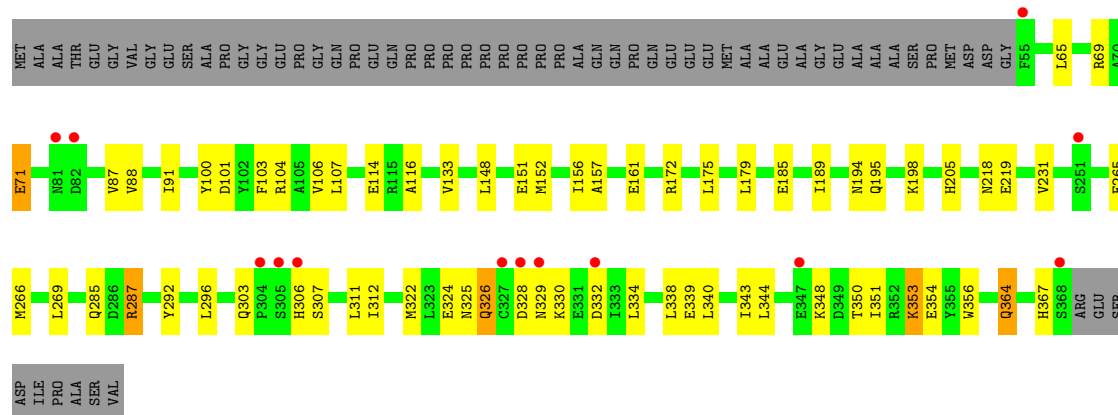
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	95	Total 95	O 95	0	0
8	B	74	Total 74	O 74	0	0
8	C	102	Total 102	O 102	0	0
8	D	123	Total 123	O 123	0	0
8	E	97	Total 97	O 97	0	0
8	F	114	Total 114	O 114	0	0
8	G	96	Total 96	O 96	0	0
8	H	65	Total 65	O 65	0	0
8	I	134	Total 134	O 134	0	0
8	J	102	Total 102	O 102	0	0
8	K	207	Total 207	O 207	0	0
8	L	166	Total 166	O 166	0	0



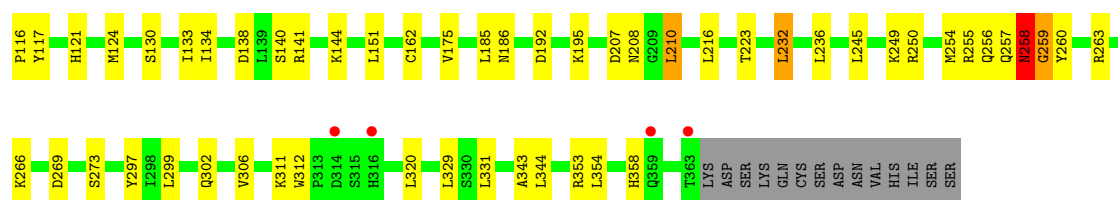
- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit



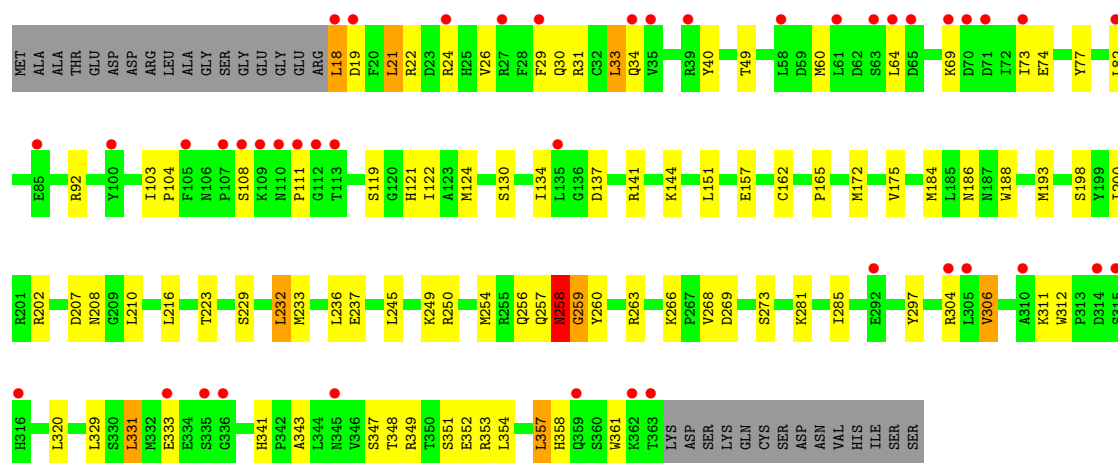
- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit



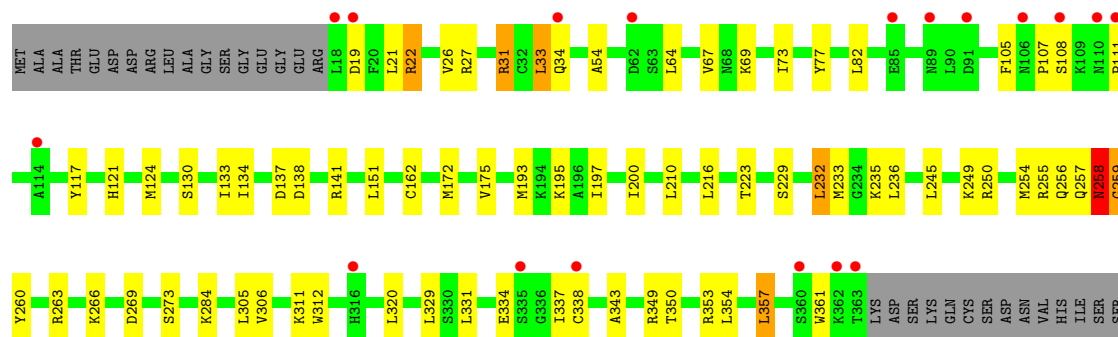
- Molecule 1: Protein farnesyltransferase/geranylgeranyltransferase type I alpha subunit



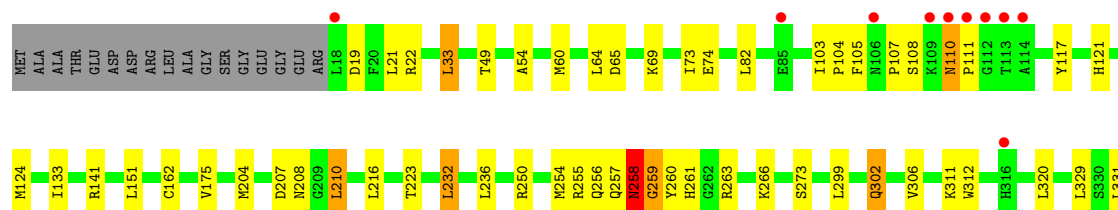
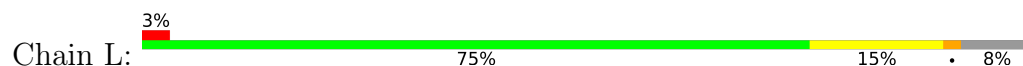
• Molecule 2: Geranylgeranyl transferase type I beta subunit

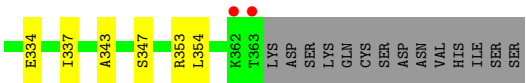


• Molecule 2: Geranylgeranyl transferase type I beta subunit



• Molecule 2: Geranylgeranyl transferase type I beta subunit





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	271.15Å 268.68Å 184.62Å 90.00° 131.55° 90.00°	Depositor
Resolution (Å)	30.00 – 2.55 30.00 – 2.55	Depositor EDS
% Data completeness (in resolution range)	93.4 (30.00-2.55) 93.3 (30.00-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.54Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.192 , 0.213 0.195 , 0.212	Depositor DCC
R_{free} test set	15041 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.086 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	33735	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% 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: CL, MES, ZN, SO4, 778

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	0.40	0/2692	0.82	2/3664 (0.1%)
1	C	0.41	0/2703	0.84	5/3677 (0.1%)
1	E	0.40	0/2708	0.83	4/3684 (0.1%)
1	G	0.41	0/2699	0.83	5/3672 (0.1%)
1	I	0.41	0/2717	0.83	4/3694 (0.1%)
1	K	0.46	0/2733	0.84	5/3713 (0.1%)
2	B	0.40	0/2754	0.91	6/3725 (0.2%)
2	D	0.42	0/2751	0.91	10/3720 (0.3%)
2	F	0.42	0/2775	0.91	6/3750 (0.2%)
2	H	0.39	0/2749	0.91	9/3720 (0.2%)
2	J	0.41	0/2770	0.90	7/3745 (0.2%)
2	L	0.46	1/2780 (0.0%)	0.91	6/3756 (0.2%)
All	All	0.42	1/32831 (0.0%)	0.87	69/44520 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
2	F	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	204	MET	SD-CE	5.63	1.93	1.79

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	259	GLY	N-CA-C	-10.25	97.95	112.60
2	H	259	GLY	N-CA-C	-10.06	98.21	112.60
2	F	259	GLY	N-CA-C	-9.97	98.34	112.60
2	D	259	GLY	N-CA-C	-9.90	98.44	112.60
2	L	259	GLY	N-CA-C	-9.86	98.50	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	297	TYR	Sidechain
2	F	297	TYR	Sidechain

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	2626	0	2518	43	0
1	C	2637	0	2529	38	0
1	E	2642	0	2534	53	0
1	G	2633	0	2524	52	0
1	I	2651	0	2551	45	0
1	K	2667	0	2577	38	0
2	B	2693	0	2589	61	0
2	D	2690	0	2588	42	0
2	F	2714	0	2624	44	0
2	H	2688	0	2573	63	0
2	J	2709	0	2610	44	0
2	L	2719	0	2632	34	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
3	J	1	0	0	0	0
3	L	1	0	0	0	0
4	B	5	0	0	0	0
4	D	5	0	0	0	0
4	F	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	5	0	0	0	0
4	J	5	0	0	0	0
4	L	5	0	0	0	0
5	B	29	0	20	0	0
5	D	29	0	20	0	0
5	F	29	0	20	0	0
5	H	29	0	20	0	0
5	J	29	0	20	0	0
5	L	29	0	20	0	0
6	B	12	0	13	0	0
6	D	12	0	13	2	0
6	F	12	0	13	0	0
6	H	12	0	13	0	0
6	J	12	0	13	0	0
6	L	12	0	13	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	F	1	0	0	0	0
7	G	1	0	0	1	0
7	H	1	0	0	0	0
7	I	1	0	0	1	0
7	J	1	0	0	0	0
7	K	1	0	0	1	0
7	L	1	0	0	0	0
8	A	95	0	0	2	0
8	B	74	0	0	2	0
8	C	102	0	0	2	0
8	D	123	0	0	3	0
8	E	97	0	0	1	0
8	F	114	0	0	1	0
8	G	96	0	0	3	0
8	H	65	0	0	3	0
8	I	134	0	0	3	0
8	J	102	0	0	2	0
8	K	207	0	0	5	0
8	L	166	0	0	0	0
All	All	33735	0	31047	541	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 9.

The worst 5 of 541 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:E:156:ILE:HG12	1:E:172:ARG:HH12	1.10	1.13
1:A:156:ILE:HG12	1:A:172:ARG:HH12	0.97	1.12
1:I:156:ILE:HG12	1:I:172:ARG:HH12	1.05	1.11
1:K:156:ILE:HG12	1:K:172:ARG:HH12	0.99	1.07
1:G:156:ILE:HG12	1:G:172:ARG:HH12	1.20	1.05

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	312/377 (83%)	289 (93%)	22 (7%)	1 (0%)	36	45
1	C	312/377 (83%)	294 (94%)	17 (5%)	1 (0%)	36	45
1	E	312/377 (83%)	288 (92%)	24 (8%)	0	100	100
1	G	312/377 (83%)	291 (93%)	21 (7%)	0	100	100
1	I	312/377 (83%)	292 (94%)	18 (6%)	2 (1%)	21	29
1	K	312/377 (83%)	294 (94%)	17 (5%)	1 (0%)	36	45
2	B	344/377 (91%)	325 (94%)	17 (5%)	2 (1%)	21	29
2	D	344/377 (91%)	329 (96%)	13 (4%)	2 (1%)	21	29
2	F	344/377 (91%)	327 (95%)	15 (4%)	2 (1%)	21	29
2	H	344/377 (91%)	326 (95%)	15 (4%)	3 (1%)	14	20
2	J	344/377 (91%)	329 (96%)	12 (4%)	3 (1%)	14	20
2	L	344/377 (91%)	332 (96%)	10 (3%)	2 (1%)	21	29
All	All	3936/4524 (87%)	3716 (94%)	201 (5%)	19 (0%)	24	34

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	326	GLN

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Mol	Chain	Res	Type
2	B	258	ASN
1	C	326	GLN
2	D	258	ASN
2	H	258	ASN

5.3.2 Protein sidechains ⓘ

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	279/338 (82%)	273 (98%)	6 (2%)	45	64
1	C	282/338 (83%)	275 (98%)	7 (2%)	42	60
1	E	284/338 (84%)	276 (97%)	8 (3%)	38	57
1	G	281/338 (83%)	276 (98%)	5 (2%)	51	70
1	I	286/338 (85%)	278 (97%)	8 (3%)	38	57
1	K	290/338 (86%)	279 (96%)	11 (4%)	29	44
2	B	287/326 (88%)	274 (96%)	13 (4%)	24	38
2	D	286/326 (88%)	276 (96%)	10 (4%)	32	48
2	F	292/326 (90%)	279 (96%)	13 (4%)	24	38
2	H	286/326 (88%)	273 (96%)	13 (4%)	24	38
2	J	291/326 (89%)	278 (96%)	13 (4%)	24	38
2	L	294/326 (90%)	281 (96%)	13 (4%)	25	38
All	All	3438/3984 (86%)	3318 (96%)	120 (4%)	32	48

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	71	GLU
2	L	110	ASN
2	H	306	VAL
2	L	65	ASP
2	L	329	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	80	GLN
1	K	285	GLN
1	G	297	ASN
1	K	234	ASN
2	L	257	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 33 ligands modelled in this entry, 15 are monoatomic - leaving 18 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	$\# Z > 2$
4	SO4	H	380	-	4,4,4	0.38	0	6,6,6	0.20	0
4	SO4	F	380	-	4,4,4	0.34	0	6,6,6	0.20	0
5	778	H	381	3	32,32,32	2.50	18 (56%)	39,44,44	2.67	12 (30%)
5	778	J	381	3	32,32,32	2.51	18 (56%)	39,44,44	2.64	12 (30%)
5	778	B	380	3	32,32,32	2.61	19 (59%)	39,44,44	2.65	11 (28%)
6	MES	D	382	-	12,12,12	9.71	8 (66%)	15,16,16	2.18	6 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	J	380	-	4,4,4	0.34	0	6,6,6	0.24	0
6	MES	H	382	-	12,12,12	9.70	8 (66%)	15,16,16	2.09	6 (40%)
4	SO4	L	380	-	4,4,4	0.33	0	6,6,6	0.20	0
6	MES	J	382	-	12,12,12	9.64	8 (66%)	15,16,16	2.24	7 (46%)
5	778	F	381	3	32,32,32	2.57	17 (53%)	39,44,44	2.69	12 (30%)
5	778	L	381	3	32,32,32	2.55	17 (53%)	39,44,44	2.63	12 (30%)
6	MES	L	382	-	12,12,12	9.88	9 (75%)	15,16,16	2.29	7 (46%)
4	SO4	B	379	-	4,4,4	0.37	0	6,6,6	0.08	0
5	778	D	381	3	32,32,32	2.52	19 (59%)	39,44,44	2.67	12 (30%)
6	MES	F	382	-	12,12,12	9.46	8 (66%)	15,16,16	2.25	7 (46%)
4	SO4	D	380	-	4,4,4	0.37	0	6,6,6	0.12	0
6	MES	B	381	-	12,12,12	9.55	8 (66%)	15,16,16	2.23	7 (46%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	778	H	381	3	-	0/14/27/27	0/4/4/4
5	778	J	381	3	-	0/14/27/27	0/4/4/4
5	778	B	380	3	-	0/14/27/27	0/4/4/4
6	MES	D	382	-	-	0/6/14/14	0/1/1/1
6	MES	H	382	-	-	0/6/14/14	0/1/1/1
6	MES	J	382	-	-	0/6/14/14	0/1/1/1
5	778	F	381	3	-	1/14/27/27	0/4/4/4
5	778	L	381	3	-	0/14/27/27	0/4/4/4
6	MES	L	382	-	-	0/6/14/14	0/1/1/1
5	778	D	381	3	-	0/14/27/27	0/4/4/4
6	MES	F	382	-	-	0/6/14/14	0/1/1/1
6	MES	B	381	-	-	0/6/14/14	0/1/1/1

The worst 5 of 157 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L	382	MES	C8-S	-25.82	1.41	1.77
6	D	382	MES	C8-S	-25.25	1.42	1.77
6	H	382	MES	C8-S	-25.14	1.42	1.77
6	J	382	MES	C8-S	-24.87	1.42	1.77
6	B	381	MES	C8-S	-24.37	1.43	1.77

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	381	778	C12-C7-N11	9.56	110.81	105.08
5	H	381	778	C12-C7-N11	9.46	110.75	105.08
5	F	381	778	C12-C7-N11	9.17	110.57	105.08
5	B	380	778	C12-C7-N11	9.12	110.55	105.08
5	J	381	778	C12-C7-N11	8.98	110.46	105.08

There are no chirality outliers.

All (1) torsion outliers are listed below:

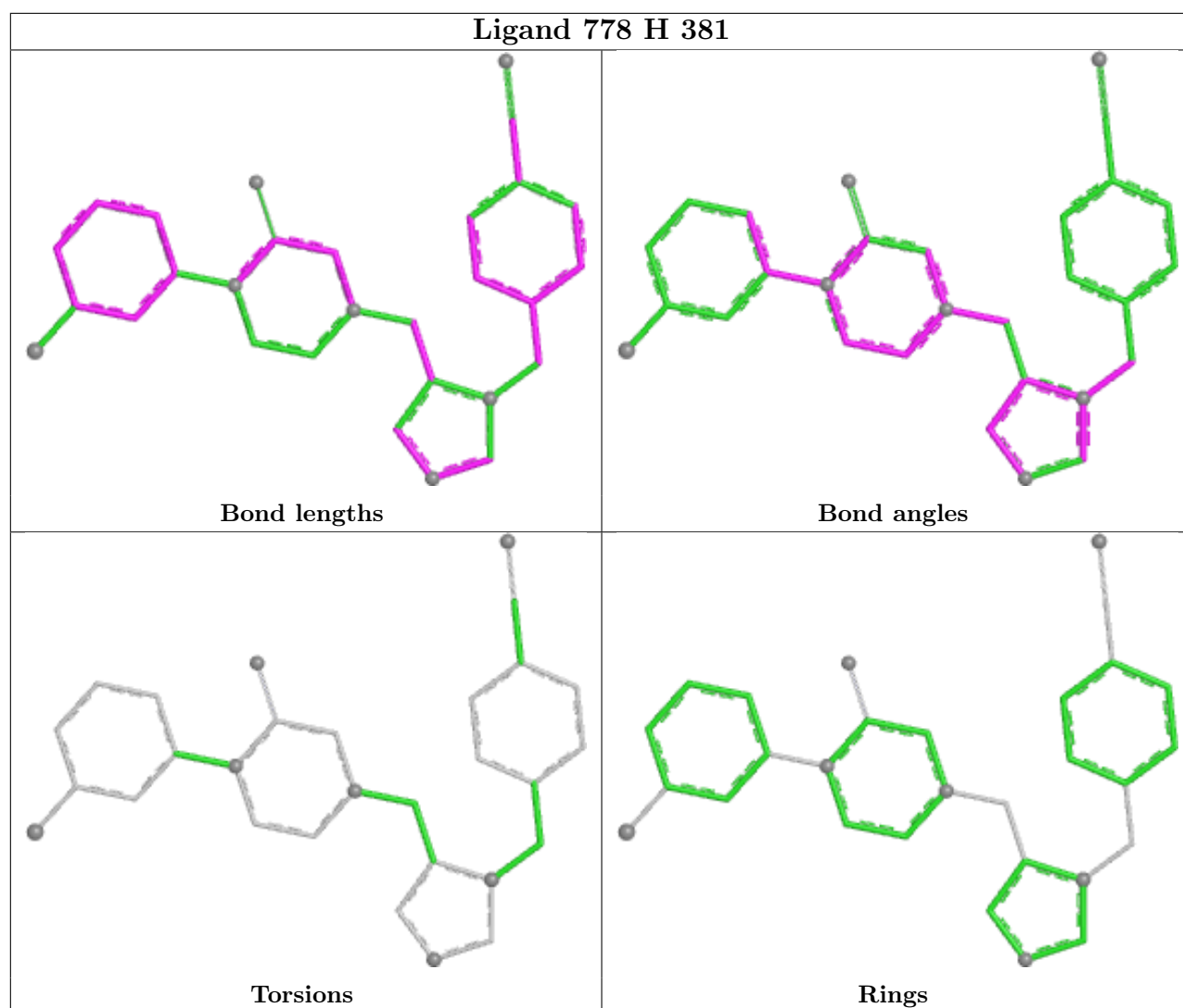
Mol	Chain	Res	Type	Atoms
5	F	381	778	C32-C34-C35-N36

There are no ring outliers.

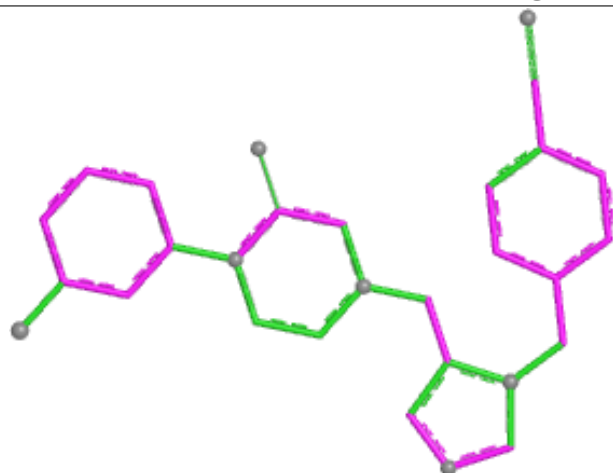
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	382	MES	2	0

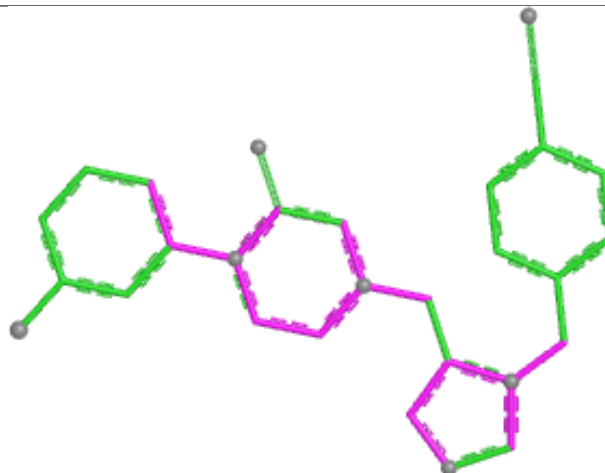
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



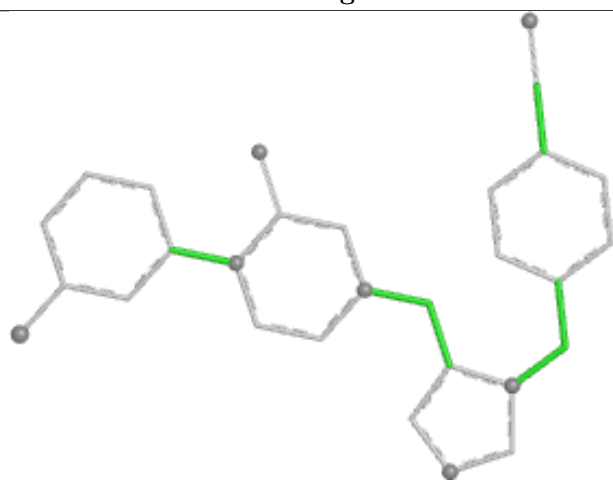
Ligand 778 J 381



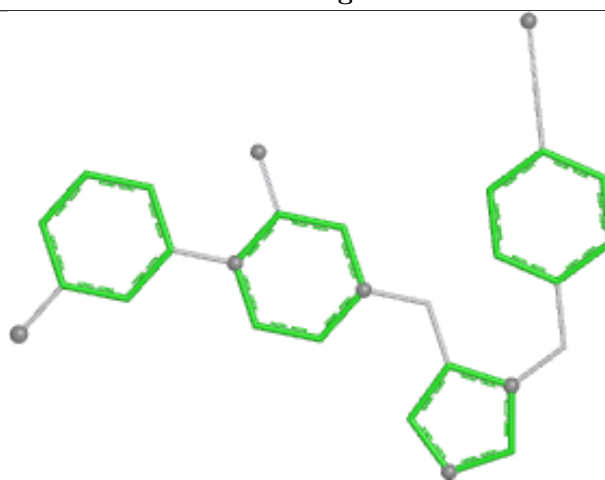
Bond lengths



Bond angles

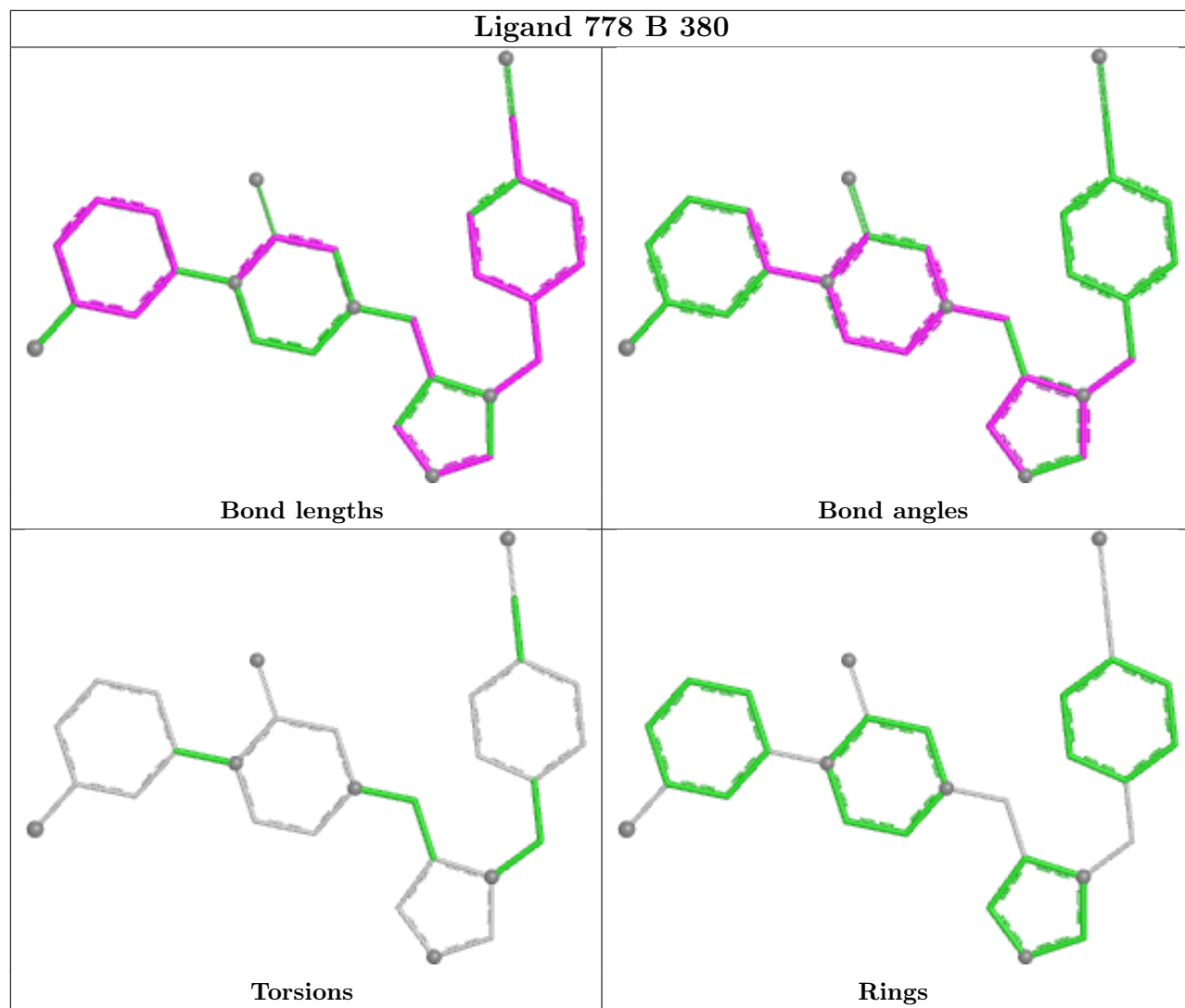


Torsions

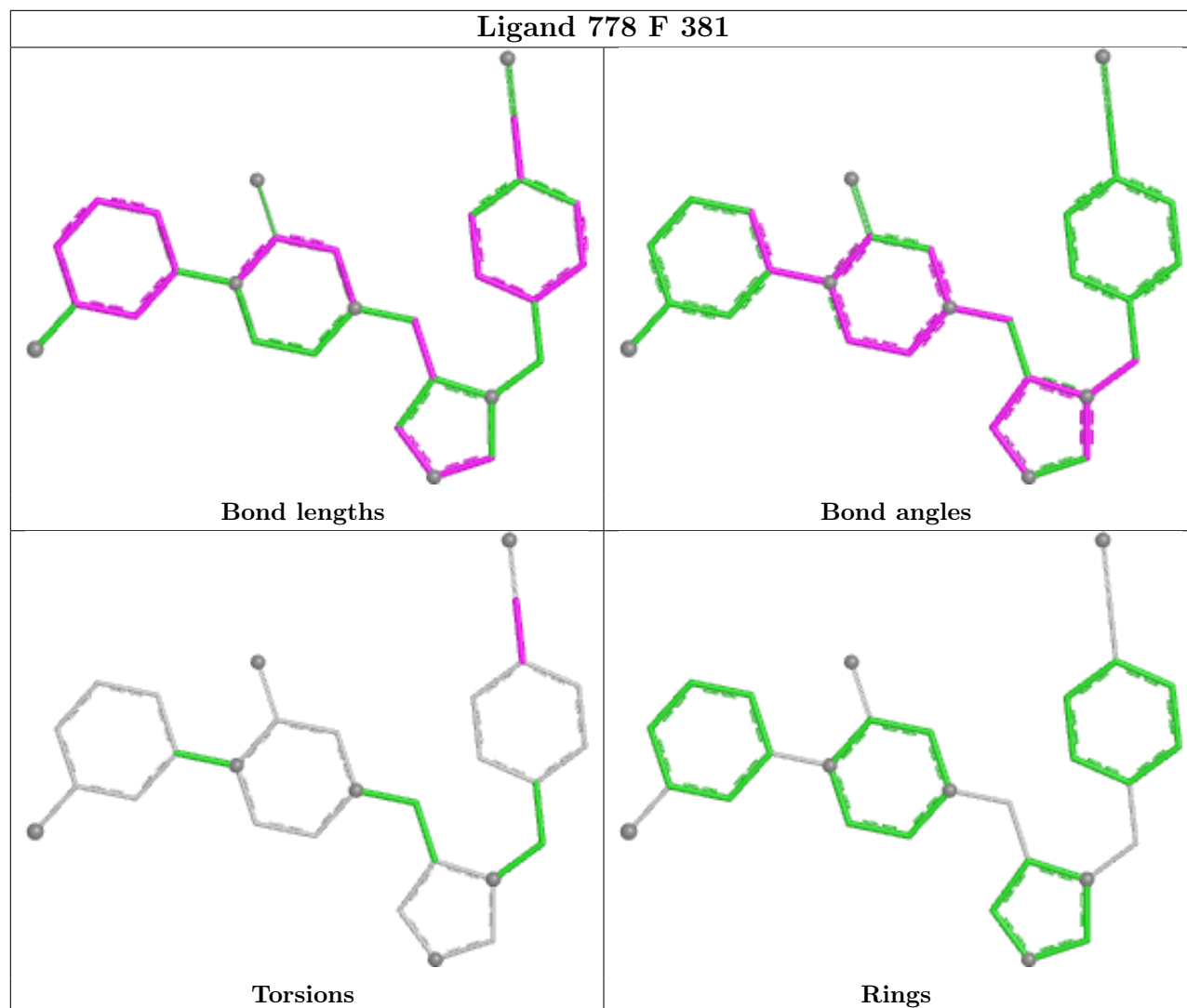


Rings

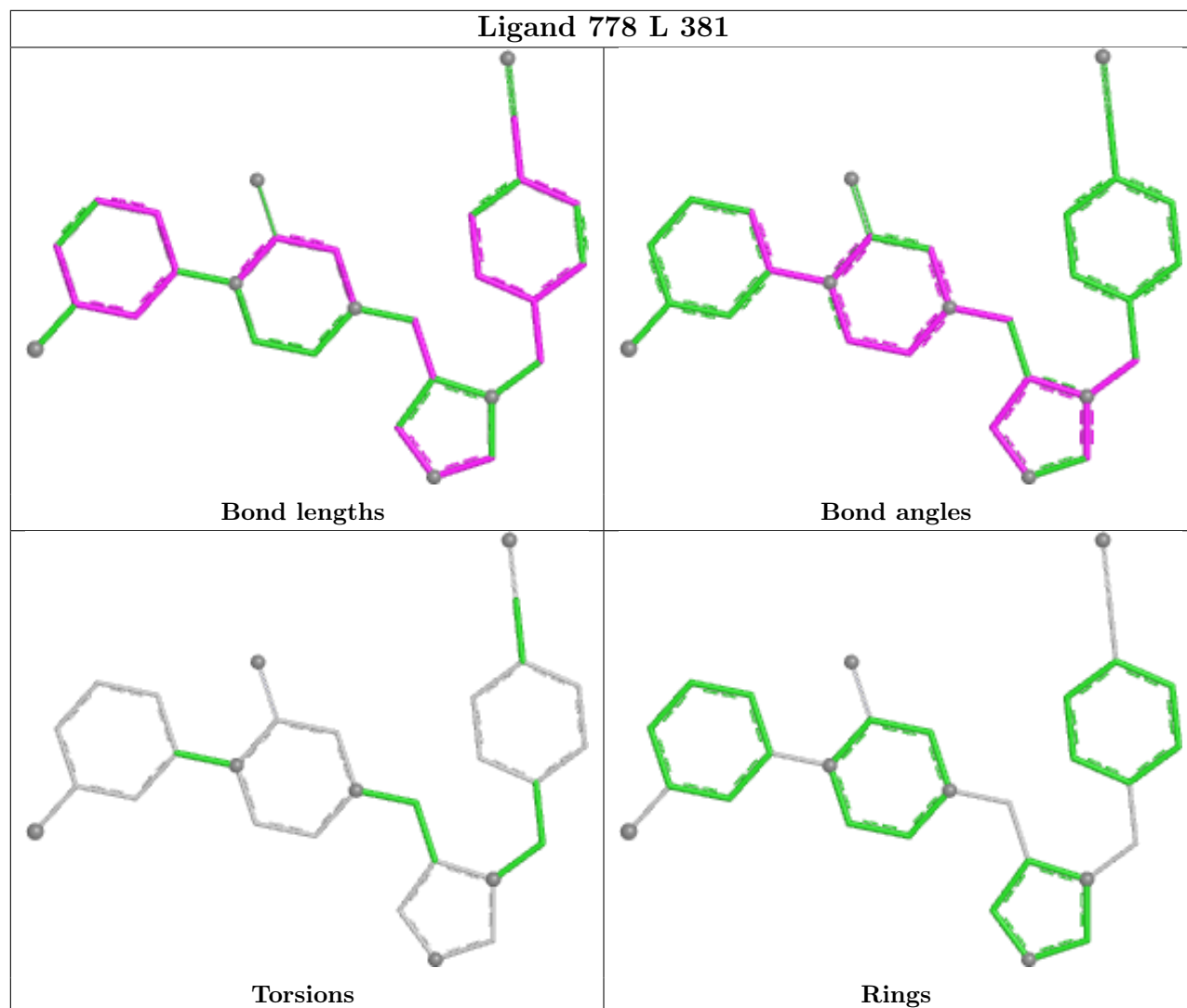
Ligand 778 B 380

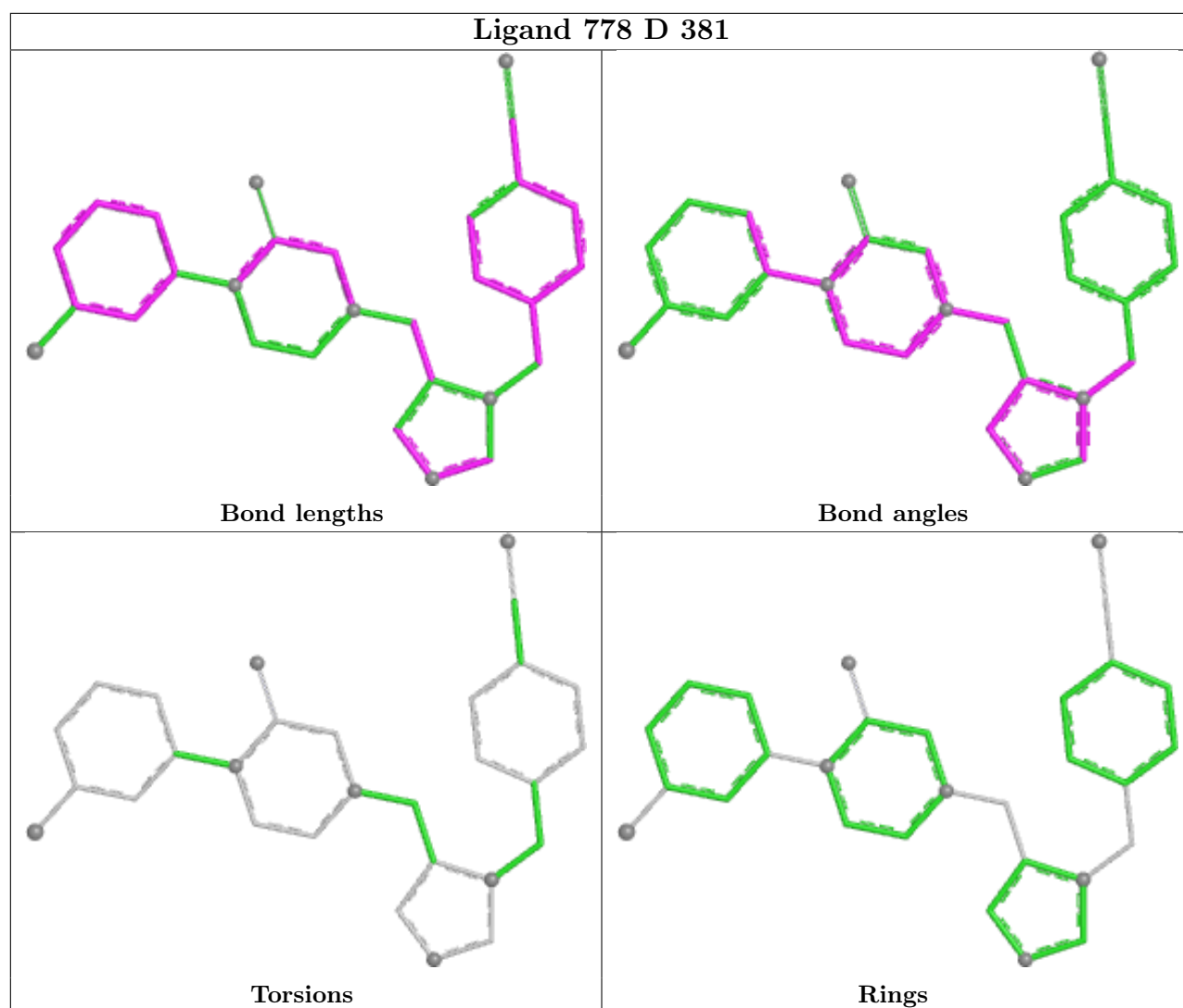


Ligand 778 F 381



Ligand 778 L 381





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, 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	314/377 (83%)	0.50	27 (8%) 16 15	41, 63, 97, 108	0
1	C	314/377 (83%)	0.39	13 (4%) 41 42	41, 59, 87, 108	0
1	E	314/377 (83%)	0.53	15 (4%) 35 35	44, 63, 91, 106	0
1	G	314/377 (83%)	0.63	32 (10%) 12 11	41, 64, 94, 110	0
1	I	314/377 (83%)	0.28	13 (4%) 41 42	34, 57, 87, 96	0
1	K	314/377 (83%)	-0.08	9 (2%) 53 55	31, 47, 72, 87	0
2	B	346/377 (91%)	0.22	9 (2%) 57 58	42, 57, 82, 102	0
2	D	346/377 (91%)	-0.02	14 (4%) 42 43	35, 51, 77, 91	0
2	F	346/377 (91%)	0.05	13 (3%) 44 45	36, 51, 77, 101	0
2	H	346/377 (91%)	0.94	43 (12%) 8 7	40, 71, 97, 114	0
2	J	346/377 (91%)	0.20	18 (5%) 33 32	35, 55, 84, 104	0
2	L	346/377 (91%)	-0.18	12 (3%) 47 48	29, 44, 71, 95	0
All	All	3960/4524 (87%)	0.28	218 (5%) 30 30	29, 57, 88, 114	0

The worst 5 of 218 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	55	PHE	8.4
1	C	55	PHE	8.1
2	H	18	LEU	7.0
2	F	18	LEU	6.9
1	E	55	PHE	6.2

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 ⓘ

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
5	778	B	380	29/29	0.85	0.12	39,46,53,56	0
5	778	J	381	29/29	0.85	0.11	29,39,42,42	0
5	778	L	381	29/29	0.85	0.10	27,33,36,39	0
5	778	F	381	29/29	0.87	0.12	36,45,52,52	0
5	778	D	381	29/29	0.88	0.12	35,45,47,51	0
5	778	H	381	29/29	0.88	0.12	42,48,51,54	0
6	MES	H	382	12/12	0.90	0.14	74,75,84,84	0
6	MES	L	382	12/12	0.90	0.16	69,71,76,77	0
6	MES	B	381	12/12	0.93	0.13	69,71,81,83	0
6	MES	J	382	12/12	0.93	0.13	70,72,81,81	0
6	MES	F	382	12/12	0.93	0.12	72,73,85,86	0
6	MES	D	382	12/12	0.94	0.12	71,72,78,78	0
7	CL	I	378	1/1	0.94	0.23	75,75,75,75	0
7	CL	C	378	1/1	0.96	0.22	61,61,61,61	0
7	CL	H	379	1/1	0.97	0.07	68,68,68,68	0
7	CL	G	378	1/1	0.97	0.18	61,61,61,61	0
7	CL	J	379	1/1	0.97	0.08	63,63,63,63	0
7	CL	K	378	1/1	0.97	0.16	67,67,67,67	0
4	SO4	D	380	5/5	0.98	0.07	51,52,54,55	0
4	SO4	F	380	5/5	0.98	0.08	53,54,58,58	0
4	SO4	H	380	5/5	0.98	0.06	60,61,62,62	0
7	CL	F	379	1/1	0.99	0.10	53,53,53,53	0
3	ZN	H	378	1/1	0.99	0.03	55,55,55,55	0
4	SO4	J	380	5/5	0.99	0.05	45,45,47,48	0
4	SO4	L	380	5/5	0.99	0.05	41,44,45,47	0
4	SO4	B	379	5/5	0.99	0.06	56,56,58,59	0
7	CL	D	379	1/1	0.99	0.06	52,52,52,52	0
7	CL	L	379	1/1	0.99	0.06	53,53,53,53	0
3	ZN	B	378	1/1	1.00	0.01	45,45,45,45	0
3	ZN	J	378	1/1	1.00	0.02	39,39,39,39	0
3	ZN	L	378	1/1	1.00	0.02	35,35,35,35	0
3	ZN	D	378	1/1	1.00	0.03	43,43,43,43	0

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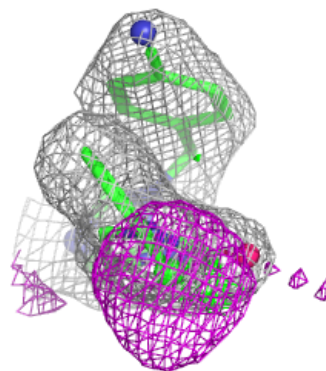
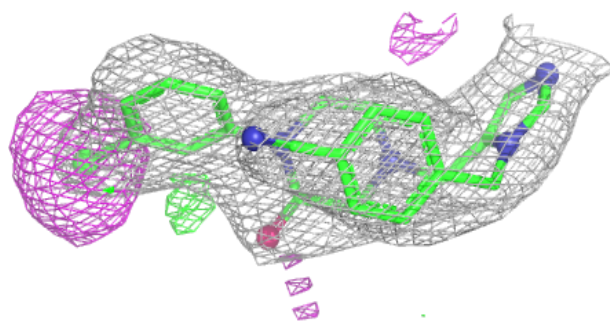
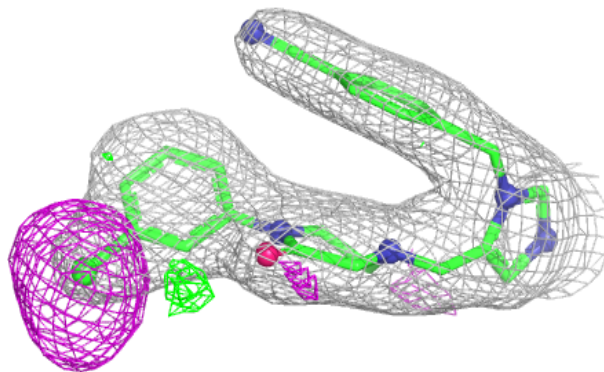
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZN	F	378	1/1	1.00	0.01	45,45,45,45	0

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.

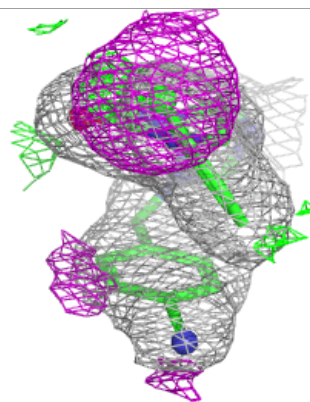
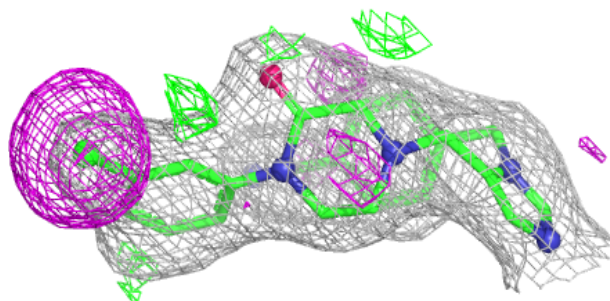
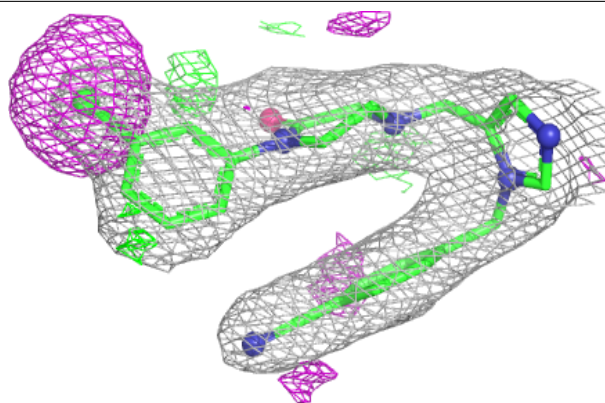
Electron density around 778 B 380:

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

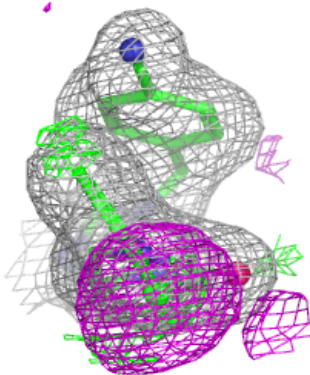
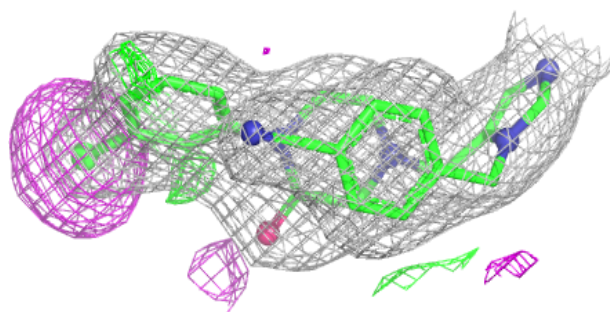
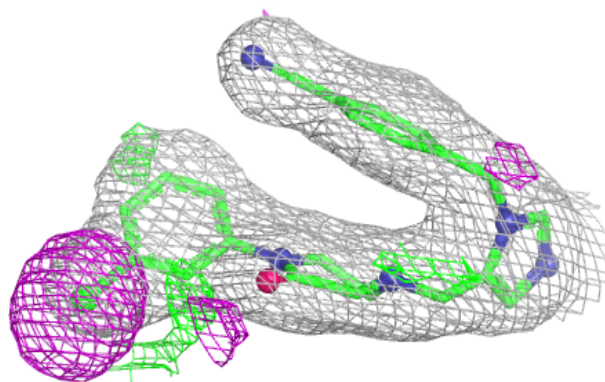


Electron density around 778 J 381:

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

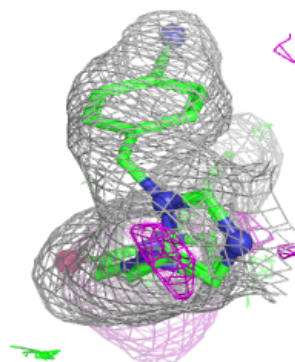
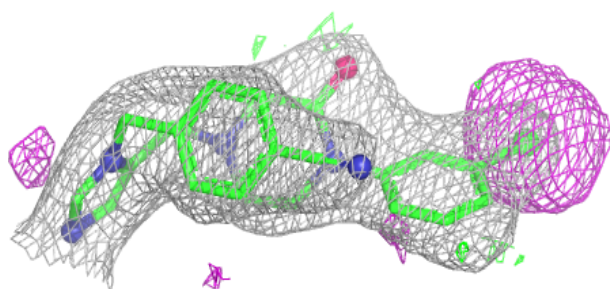
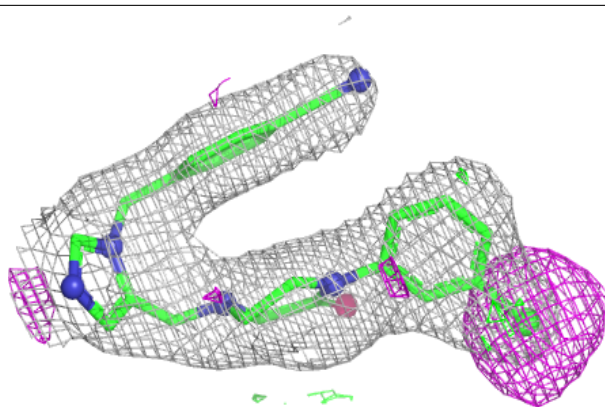
**Electron density around 778 L 381:**

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

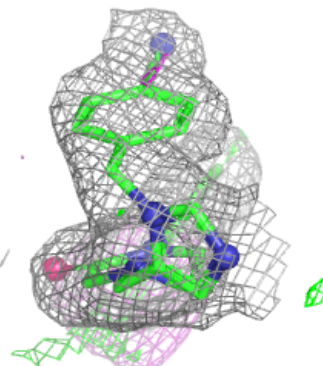
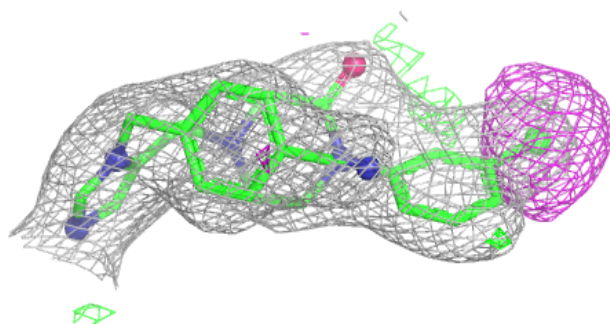
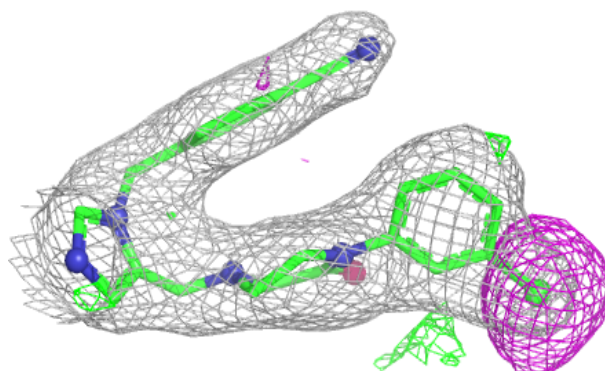


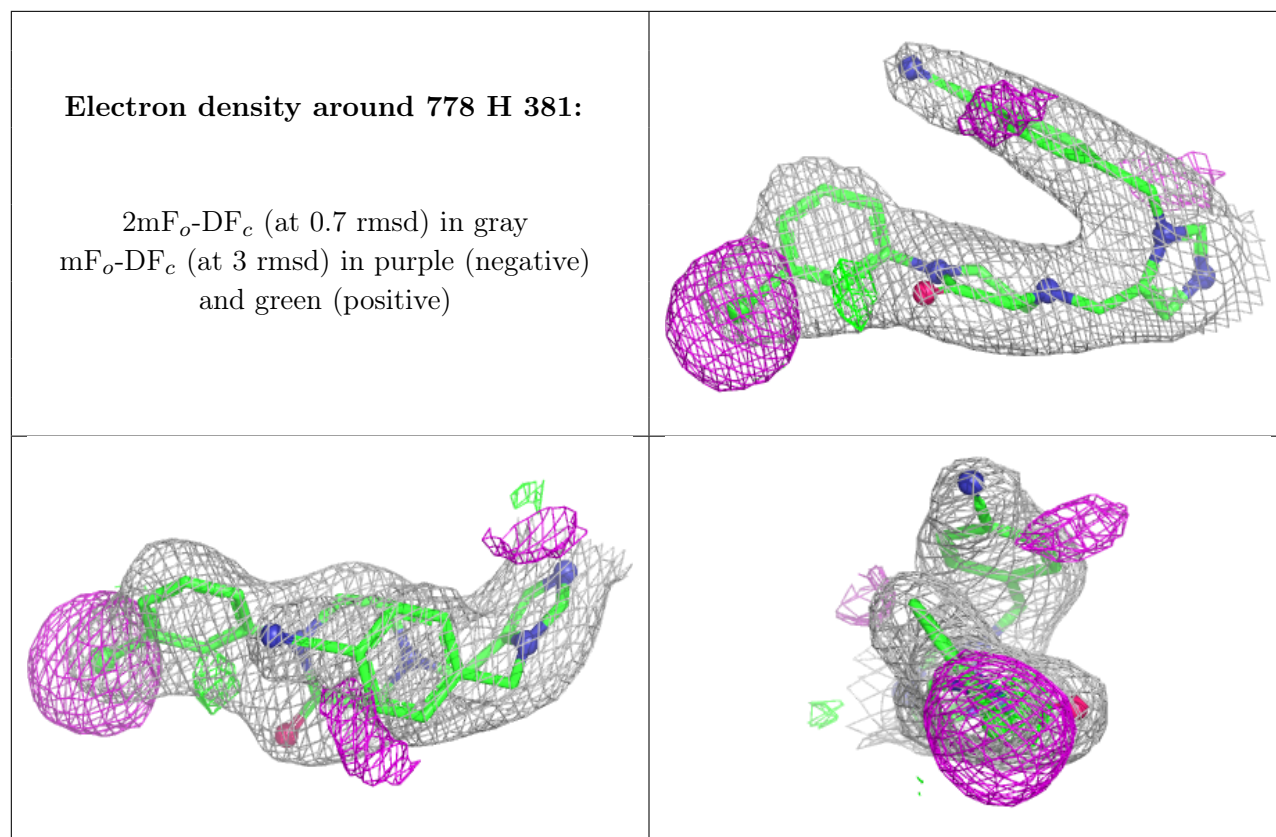
Electron density around 778 F 381:

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

**Electron density around 778 D 381:**

$2mF_o-DF_c$ (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.