



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 9, 2023 – 11:40 PM EDT

PDB ID : 7LPS  
Title : Crystal structure of DDB1-CRBN-ALV1 complex bound to Helios (IKZF2 ZF2)  
Authors : Nowak, R.P.; Fischer, E.S.  
Deposited on : 2021-02-12  
Resolution : 3.78 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](mailto: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>.

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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)  
Xtrriage (Phenix) : 1.13  
EDS : 2.35.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

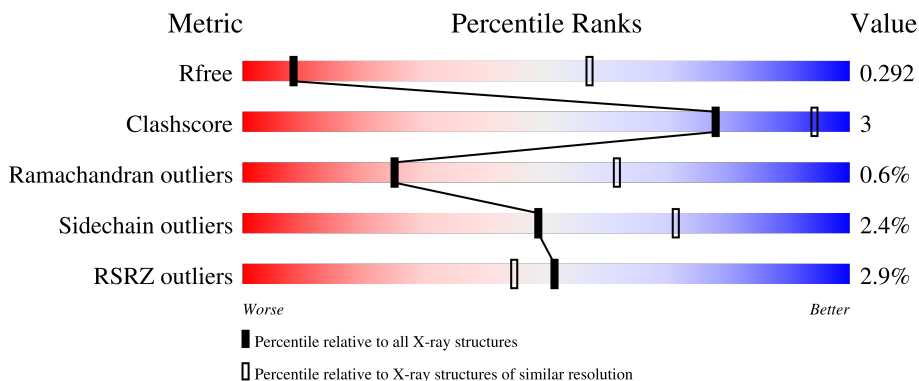
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.78 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))
$R_{free}$	130704	1038 (3.96-3.60)
Clashscore	141614	1100 (3.96-3.60)
Ramachandran outliers	138981	1062 (3.96-3.60)
Sidechain outliers	138945	1058 (3.96-3.60)
RSRZ outliers	127900	1009 (3.98-3.58)

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  $\geq 3$ , 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	1140	
1	D	1140	
1	G	1140	
1	J	1140	
2	B	390	

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Mol	Chain	Length	Quality of chain
2	E	390	<p>85% 12% ..</p>
2	H	390	<p>85% 12% ..</p>
2	K	390	<p>86% 11% .</p>
3	C	29	<p>93% 7%</p>
3	F	29	<p>97% .</p>
3	I	29	<p>93% 7%</p>
3	L	29	<p>90% 7% .</p>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 37550 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 DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	781	6066	3857	1014	1161	34	0	0	0
1	D	781	6066	3857	1014	1161	34	0	0	0
1	G	779	6051	3848	1011	1158	34	0	0	0
1	J	779	6051	3848	1011	1158	34	0	0	0

- Molecule 2 is a protein called Protein cereblon.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	381	3068	1954	521	569	24	0	0	0
2	E	381	3068	1954	521	569	24	0	0	0
2	H	381	3068	1954	521	569	24	0	0	0
2	K	381	3068	1954	521	569	24	0	0	0

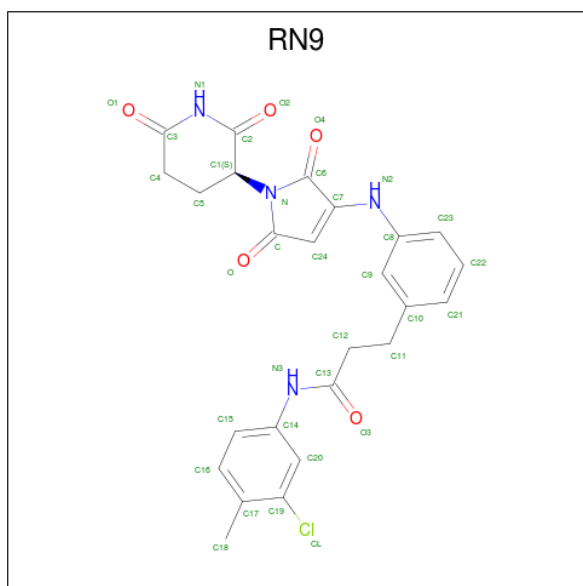
- Molecule 3 is a protein called Zinc finger protein Helios.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	29	226	139	47	38	2	0	0	0
3	F	28	222	137	46	37	2	0	0	0
3	I	29	226	139	47	38	2	0	0	0
3	L	28	222	137	46	37	2	0	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	C	1	Total	Zn	0	0
			1	1		
4	E	1	Total	Zn	0	0
			1	1		
4	F	1	Total	Zn	0	0
			1	1		
4	H	1	Total	Zn	0	0
			1	1		
4	I	1	Total	Zn	0	0
			1	1		
4	K	1	Total	Zn	0	0
			1	1		
4	L	1	Total	Zn	0	0
			1	1		

- Molecule 5 is 3-[3-[[1-[(3 {S})-2,6-bis(oxidanylidene)piperidin-3-yl]-2,5-bis(oxidanylidene)pyrrol-3-yl]amino]phenyl]-{N}-(3-chloranyl-4-methyl-phenyl)propanamide (three-letter code: RN9) (formula: C<sub>25</sub>H<sub>23</sub>ClN<sub>4</sub>O<sub>5</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
5	B	1	Total	C	Cl	N	O	0	0
			35	25	1	4	5		
5	E	1	Total	C	Cl	N	O	0	0
			35	25	1	4	5		

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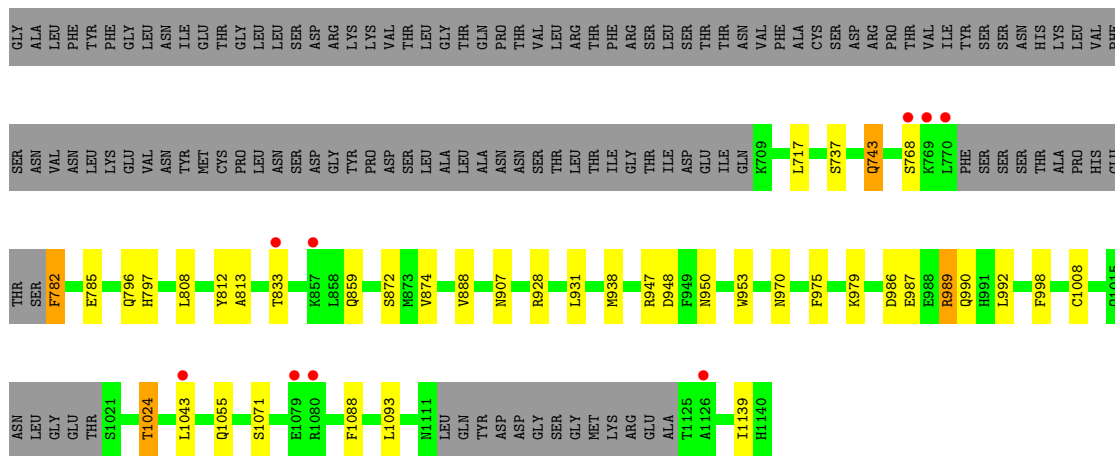
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Cl	N			O
5	H	1	Total 35	C 25	Cl 1	N 4	O 5	0	0
5	K	1	Total 35	C 25	Cl 1	N 4	O 5	0	0

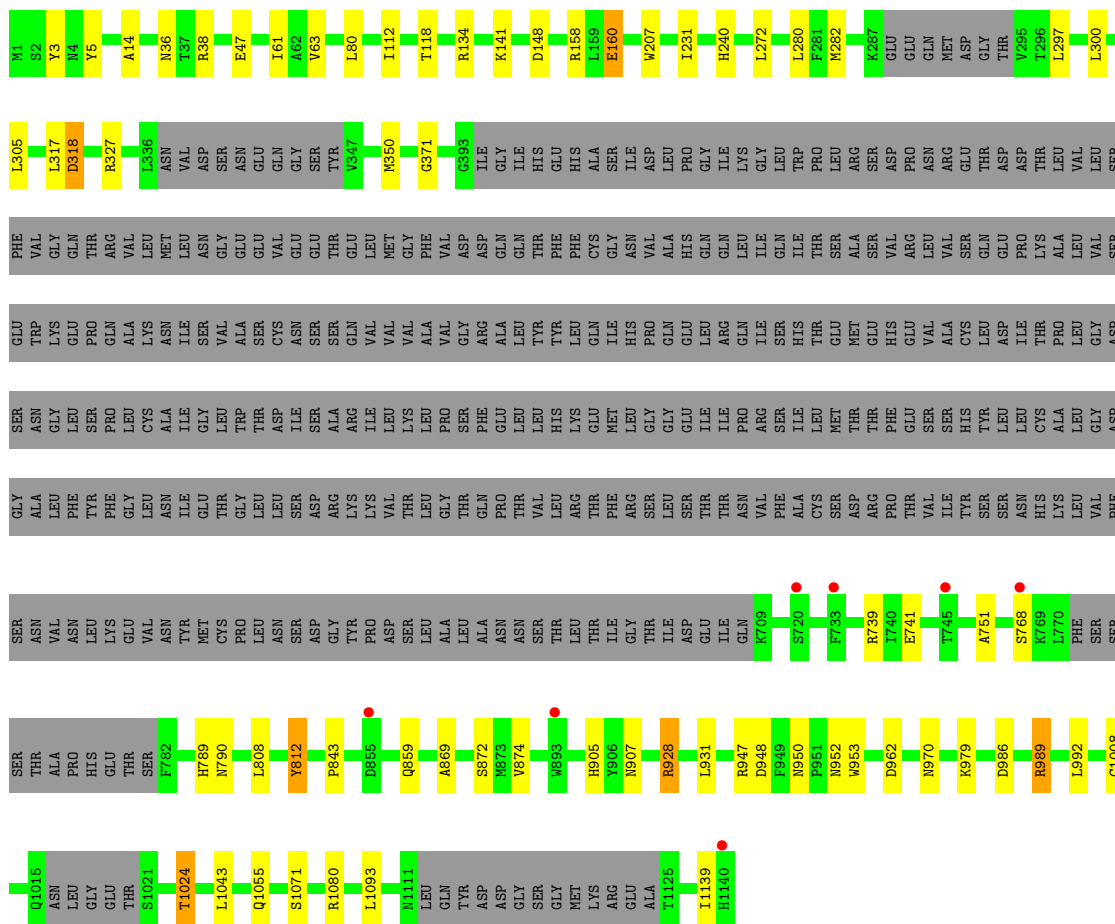




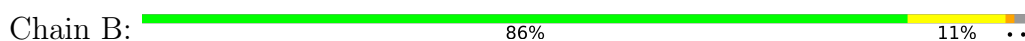




● Molecule 1: DNA damage-binding protein 1

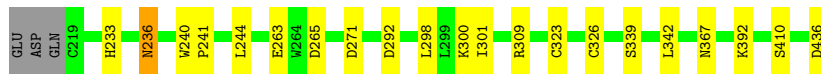
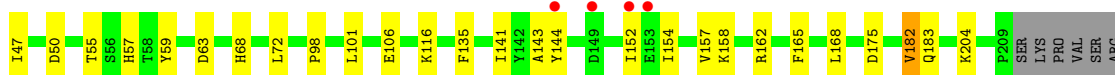
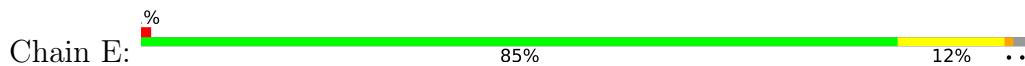


● Molecule 2: Protein cereblon

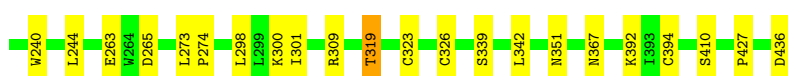
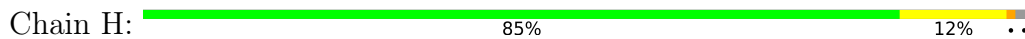




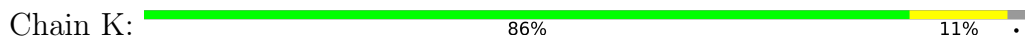
• Molecule 2: Protein cereblon



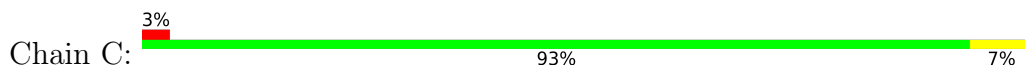
• Molecule 2: Protein cereblon



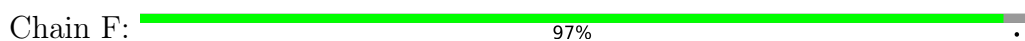
• Molecule 2: Protein cereblon



• Molecule 3: Zinc finger protein Helios



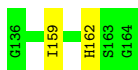
• Molecule 3: Zinc finger protein Helios






- Molecule 3: Zinc finger protein Helios

Chain I:  93% 7%



- Molecule 3: Zinc finger protein Helios

Chain L:  90% 7%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	151.80Å 117.29Å 196.71Å 90.00° 97.30° 90.00°	Depositor
Resolution (Å)	150.57 – 3.78 150.57 – 3.78	Depositor EDS
% Data completeness (in resolution range)	97.6 (150.57-3.78) 97.6 (150.57-3.78)	Depositor EDS
$R_{merge}$	0.37	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.49 (at 3.78Å)	Xtrriage
Refinement program	BUSTER 2.10.4 (11-DEC-2020)	Depositor
R, $R_{free}$	0.289 , 0.303 0.275 , 0.292	Depositor DCC
$R_{free}$ test set	3410 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	105.6	Xtrriage
Anisotropy	0.102	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 45.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.34$ , $\langle L^2 \rangle = 0.17$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	37550	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	124.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.27 % 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 1.1724e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: RN9, ZN

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	0.23	0/6173	0.42	0/8361
1	D	0.22	0/6173	0.43	0/8361
1	G	0.22	0/6158	0.42	0/8340
1	J	0.22	0/6158	0.42	0/8340
2	B	0.22	0/3141	0.42	0/4264
2	E	0.22	0/3141	0.42	0/4264
2	H	0.21	0/3141	0.42	0/4264
2	K	0.21	0/3141	0.41	0/4264
3	C	0.19	0/231	0.42	0/307
3	F	0.20	0/227	0.39	0/302
3	I	0.20	0/231	0.40	0/307
3	L	0.19	0/227	0.38	0/302
All	All	0.22	0/38142	0.42	0/51676

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6066	0	5984	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	6066	0	5984	39	0
1	G	6051	0	5969	37	0
1	J	6051	0	5969	40	0
2	B	3068	0	3036	27	0
2	E	3068	0	3036	27	0
2	H	3068	0	3038	22	0
2	K	3068	0	3036	22	0
3	C	226	0	217	1	0
3	F	222	0	214	0	0
3	I	226	0	217	1	0
3	L	222	0	214	2	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0
5	B	35	0	0	1	0
5	E	35	0	0	0	0
5	H	35	0	0	1	0
5	K	35	0	0	0	0
All	All	37550	0	36914	218	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 218 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:70:LYS:HB2	2:E:63:ASP:HB3	1.55	0.88
2:B:68:HIS:CD2	1:D:197:LEU:HD13	2.12	0.85
1:J:739:ARG:NH1	1:J:790:ASN:HD21	1.83	0.76
1:D:14:ALA:HB1	1:D:327:ARG:HD2	1.71	0.70
1:A:14:ALA:HB1	1:A:327:ARG:HD2	1.74	0.69

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	767/1140 (67%)	727 (95%)	35 (5%)	5 (1%)	22	59
1	D	767/1140 (67%)	729 (95%)	33 (4%)	5 (1%)	22	59
1	G	765/1140 (67%)	734 (96%)	26 (3%)	5 (1%)	22	59
1	J	765/1140 (67%)	736 (96%)	24 (3%)	5 (1%)	22	59
2	B	377/390 (97%)	364 (97%)	11 (3%)	2 (0%)	29	65
2	E	377/390 (97%)	363 (96%)	12 (3%)	2 (0%)	29	65
2	H	377/390 (97%)	362 (96%)	13 (3%)	2 (0%)	29	65
2	K	377/390 (97%)	365 (97%)	10 (3%)	2 (0%)	29	65
3	C	27/29 (93%)	25 (93%)	2 (7%)	0	100	100
3	F	26/29 (90%)	24 (92%)	2 (8%)	0	100	100
3	I	27/29 (93%)	25 (93%)	2 (7%)	0	100	100
3	L	26/29 (90%)	24 (92%)	2 (8%)	0	100	100
All	All	4678/6236 (75%)	4478 (96%)	172 (4%)	28 (1%)	25	61

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	318	ASP
2	B	50	ASP
1	D	318	ASP
2	E	50	ASP
1	G	318	ASP

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	664/999 (66%)	648 (98%)	16 (2%)	49	71
1	D	664/999 (66%)	645 (97%)	19 (3%)	42	67
1	G	662/999 (66%)	646 (98%)	16 (2%)	49	71
1	J	662/999 (66%)	645 (97%)	17 (3%)	46	70
2	B	344/354 (97%)	336 (98%)	8 (2%)	50	72
2	E	344/354 (97%)	337 (98%)	7 (2%)	55	75
2	H	344/354 (97%)	336 (98%)	8 (2%)	50	72
2	K	344/354 (97%)	338 (98%)	6 (2%)	60	79
3	C	24/24 (100%)	24 (100%)	0	100	100
3	F	24/24 (100%)	24 (100%)	0	100	100
3	I	24/24 (100%)	24 (100%)	0	100	100
3	L	24/24 (100%)	24 (100%)	0	100	100
All	All	4124/5508 (75%)	4027 (98%)	97 (2%)	49	71

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	859	GLN
2	H	319	THR
1	G	874	VAL
1	G	1071	SER
1	J	112	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	990	GLN
2	H	325	GLN
2	H	79	GLN
1	J	240	HIS
1	D	970	ASN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	RN9	E	1002	-	38,38,38	1.90	12 (31%)	53,54,54	2.18	15 (28%)
5	RN9	B	502	-	38,38,38	1.91	11 (28%)	53,54,54	2.30	10 (18%)
5	RN9	K	1002	-	38,38,38	1.90	12 (31%)	53,54,54	2.29	11 (20%)
5	RN9	H	502	-	38,38,38	1.88	14 (36%)	53,54,54	2.29	11 (20%)

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	RN9	E	1002	-	-	6/17/46/46	0/4/4/4
5	RN9	B	502	-	-	2/17/46/46	0/4/4/4
5	RN9	K	1002	-	-	1/17/46/46	0/4/4/4
5	RN9	H	502	-	-	2/17/46/46	0/4/4/4

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	502	RN9	C13-N3	4.92	1.46	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	1002	RN9	C13-N3	4.79	1.46	1.35
5	H	502	RN9	C13-N3	4.77	1.46	1.35
5	K	1002	RN9	C7-N2	4.57	1.46	1.36
5	K	1002	RN9	C13-N3	4.55	1.45	1.35

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	502	RN9	C6-C7-N2	11.11	124.76	115.68
5	H	502	RN9	C6-C7-N2	10.60	124.35	115.68
5	K	1002	RN9	C6-C7-N2	10.09	123.93	115.68
5	E	1002	RN9	C6-C7-N2	7.52	121.83	115.68
5	E	1002	RN9	C3-N1-C2	-5.87	118.44	126.61

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	1002	RN9	C15-C14-N3-C13
5	E	1002	RN9	C20-C14-N3-C13
5	E	1002	RN9	C11-C12-C13-O3
5	E	1002	RN9	C11-C12-C13-N3
5	K	1002	RN9	C10-C11-C12-C13

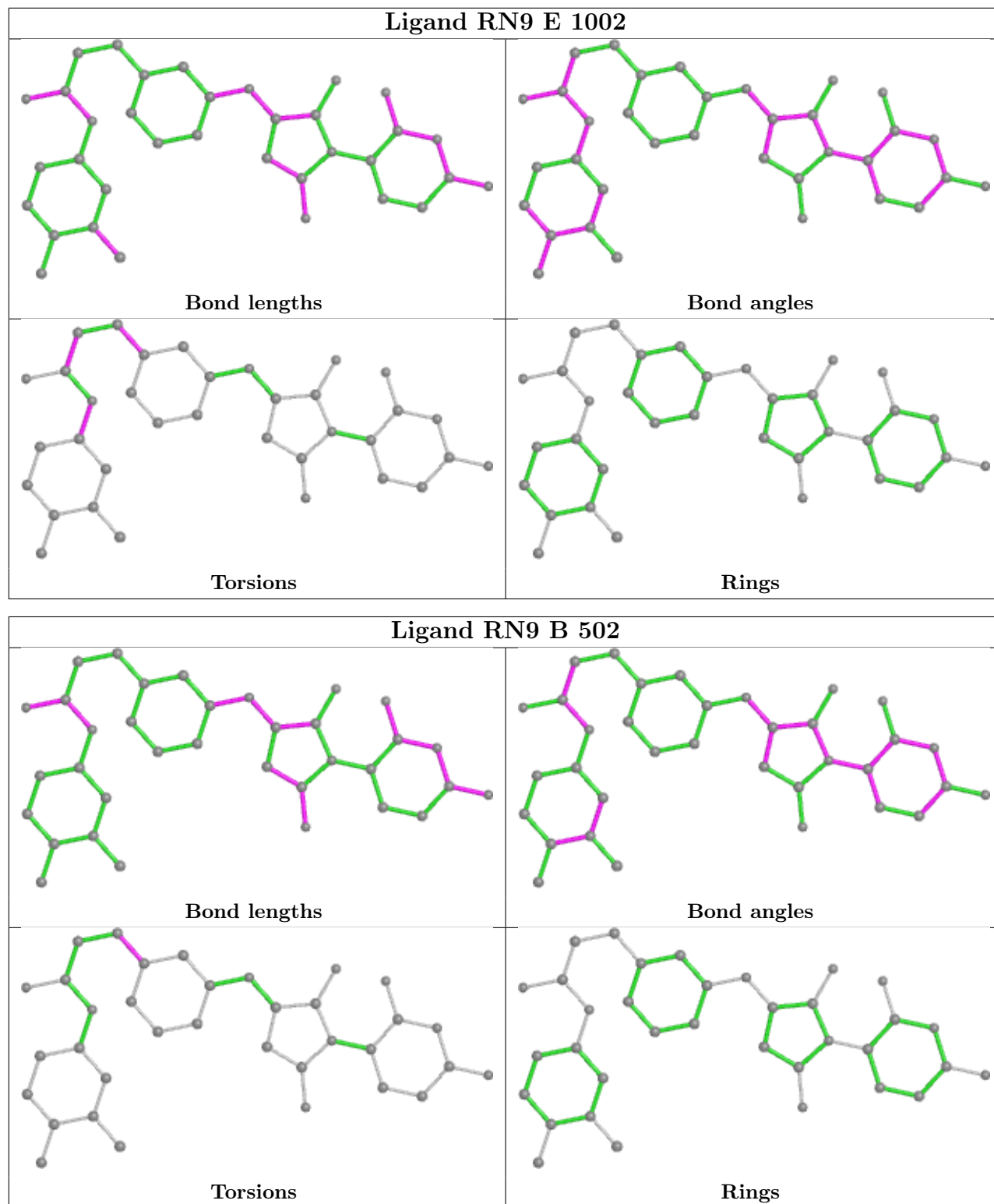
There are no ring outliers.

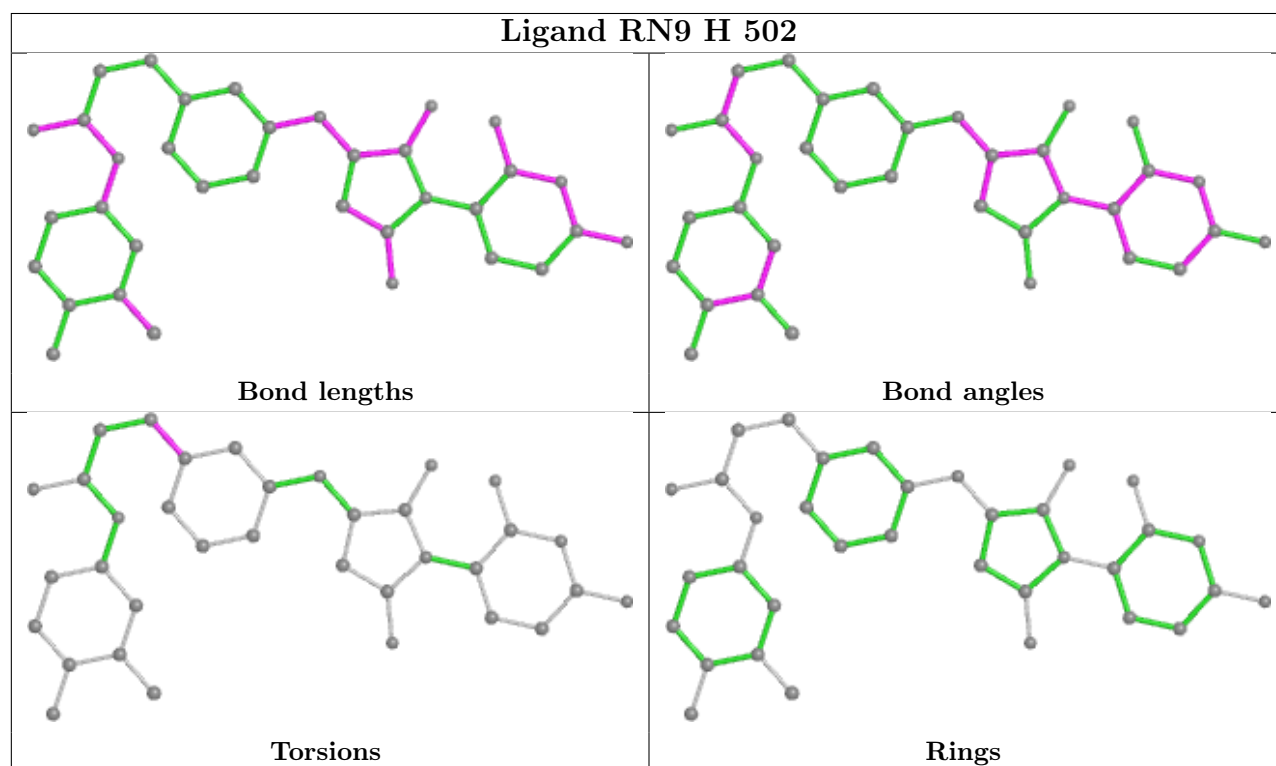
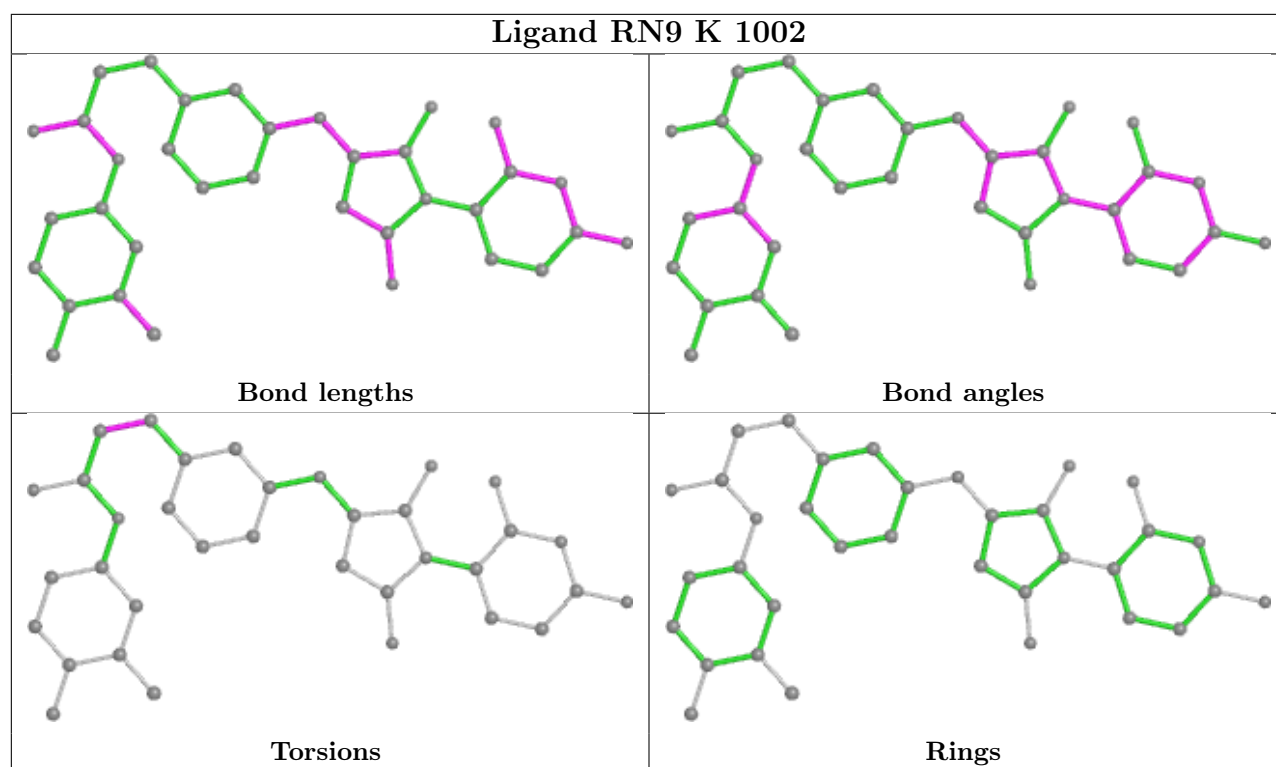
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	502	RN9	1	0
5	H	502	RN9	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.





## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	781/1140 (68%)	0.07	14 (1%) 68 65	66, 119, 172, 226	0
1	D	781/1140 (68%)	0.56	95 (12%) 4 4	99, 169, 249, 284	0
1	G	779/1140 (68%)	0.10	14 (1%) 68 65	64, 120, 179, 212	0
1	J	779/1140 (68%)	0.04	7 (0%) 84 82	58, 103, 168, 199	0
2	B	381/390 (97%)	-0.06	0 100 100	73, 106, 168, 199	0
2	E	381/390 (97%)	0.02	4 (1%) 82 80	74, 112, 179, 216	0
2	H	381/390 (97%)	-0.08	0 100 100	58, 100, 160, 220	0
2	K	381/390 (97%)	0.00	1 (0%) 94 94	67, 101, 153, 192	0
3	C	29/29 (100%)	-0.28	1 (3%) 45 40	89, 108, 157, 182	0
3	F	28/29 (96%)	-0.22	0 100 100	82, 116, 161, 197	0
3	I	29/29 (100%)	-0.37	0 100 100	89, 112, 172, 192	0
3	L	28/29 (96%)	-0.25	0 100 100	91, 106, 131, 136	0
All	All	4758/6236 (76%)	0.11	136 (2%) 51 45	58, 117, 195, 284	0

The worst 5 of 136 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	238	THR	6.0
1	D	317	LEU	5.4
1	D	321	VAL	5.3
1	D	830	ILE	5.2
1	D	247	ALA	5.1

### 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](#)

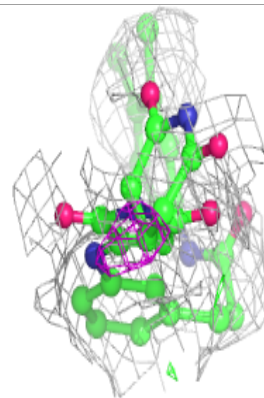
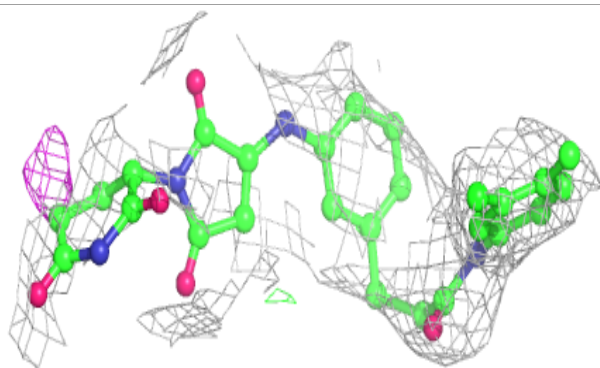
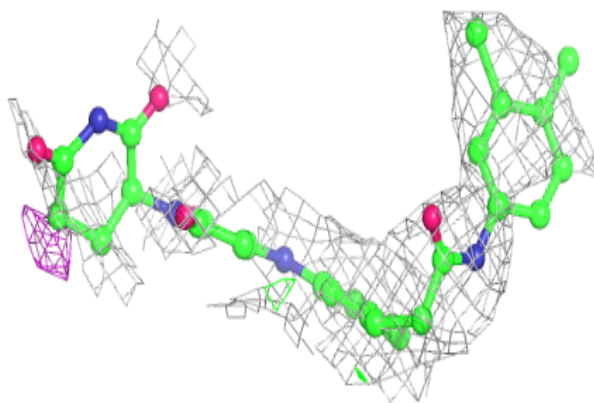
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	RN9	H	502	35/35	0.87	0.28	92,109,127,142	0
5	RN9	B	502	35/35	0.88	0.28	89,105,123,138	0
5	RN9	K	1002	35/35	0.89	0.35	91,107,125,140	0
5	RN9	E	1002	35/35	0.92	0.34	90,122,151,154	0
4	ZN	L	201	1/1	0.97	0.13	83,83,83,83	0
4	ZN	C	201	1/1	0.98	0.18	95,95,95,95	0
4	ZN	F	201	1/1	0.98	0.14	82,82,82,82	0
4	ZN	H	501	1/1	0.98	0.22	75,75,75,75	0
4	ZN	I	201	1/1	0.98	0.18	95,95,95,95	0
4	ZN	K	1001	1/1	0.98	0.20	89,89,89,89	0
4	ZN	E	1001	1/1	0.99	0.19	87,87,87,87	0
4	ZN	B	501	1/1	0.99	0.21	84,84,84,84	0

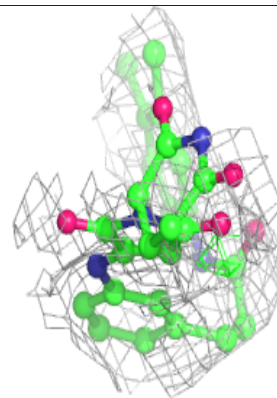
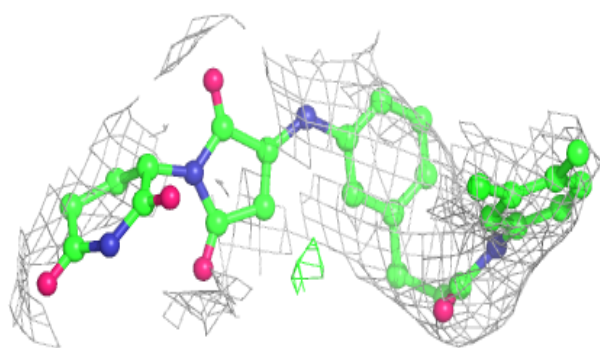
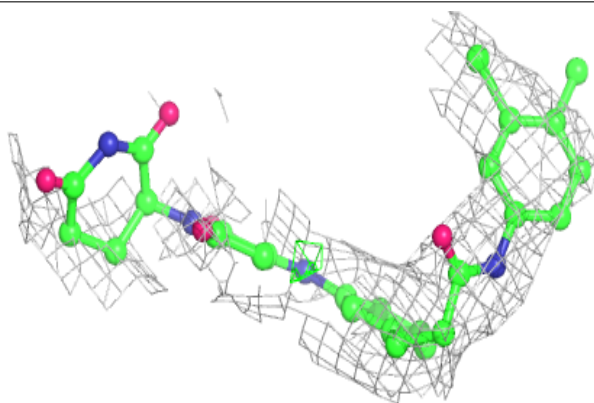
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around RN9 H 502:**

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

**Electron density around RN9 B 502:**

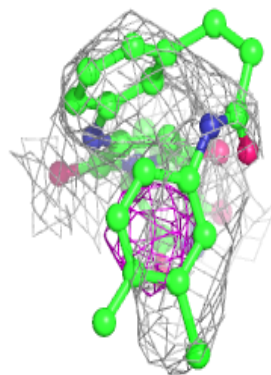
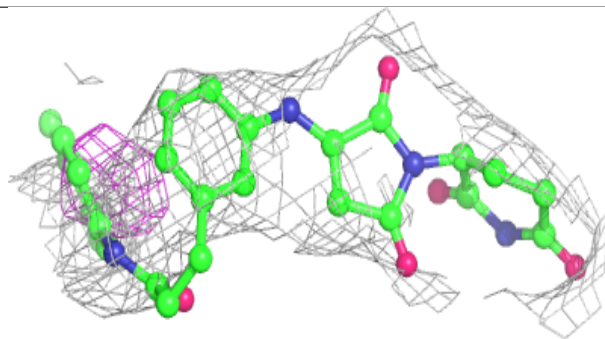
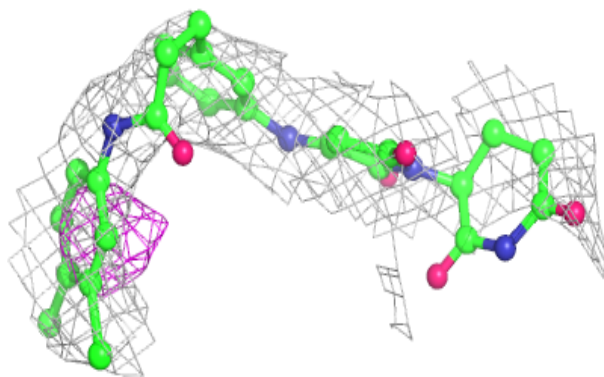
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



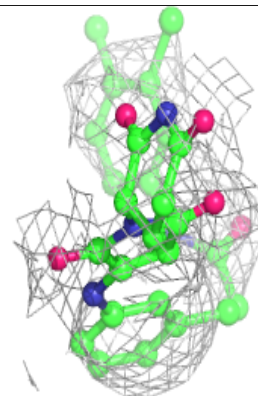
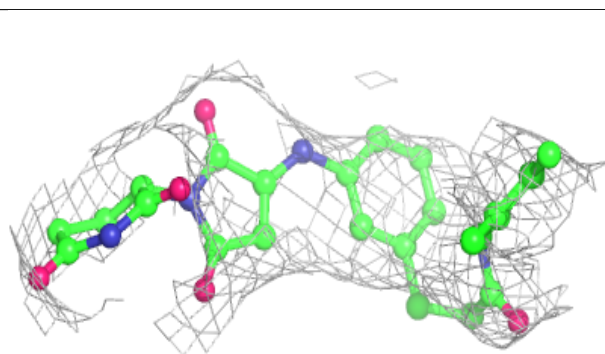
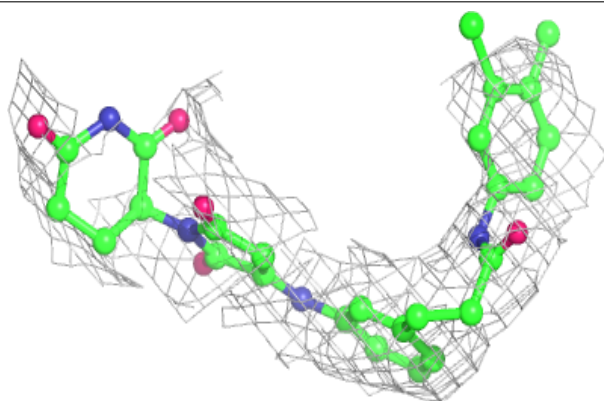


**Electron density around RN9 K 1002:**

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

**Electron density around RN9 E 1002:**

$2mF_o-DF_c$  (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.