



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:16 PM UTC

PDB ID : 5D92 / pdb\_00005d92  
Title : Structure of a phosphatidylinositolphosphate (PIP) synthase from Renibacterium Salmoninarum  
Authors : Clarke, O.B.; Tomasek, D.T.; Jorge, C.D.; Belcher Dufrisne, M.; Kim, M.; Banerjee, S.; Rajashankar, K.R.; Hendrickson, W.A.; Santos, H.; Mancina, F.  
Deposited on : 2015-08-18  
Resolution : 3.62 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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (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

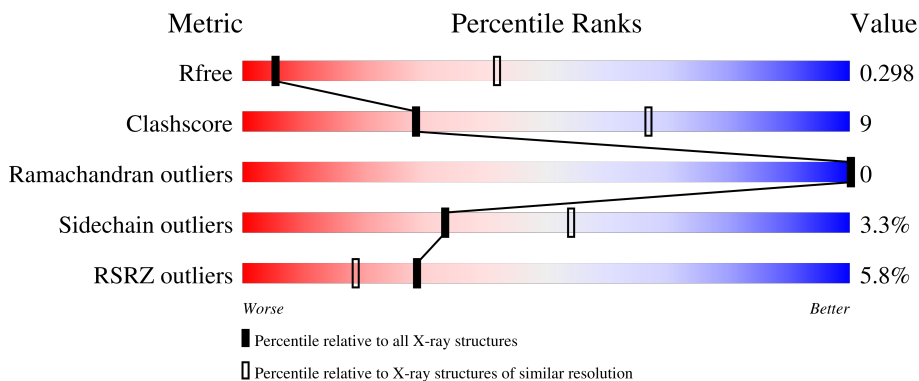
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

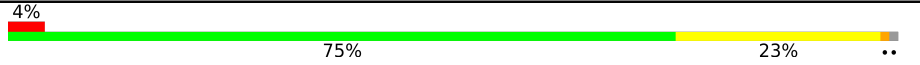



The reported resolution of this entry is 3.62 Å.

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	1062 (3.72-3.52)
Clashscore	190562	1092 (3.72-3.52)
Ramachandran outliers	187476	1057 (3.72-3.52)
Sidechain outliers	187428	1055 (3.72-3.52)
RSRZ outliers	180081	1060 (3.72-3.52)

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	342	 4% 75% 23% ..
1	B	342	 9% 79% 20% .
1	C	342	 8% 75% 21% ..
1	D	342	 3% 74% 25% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
2	8K6	D	310	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10844 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 AF2299 protein, Phosphatidylinositol synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	D	342	Total 2605	C 1716	N 414	O 470	S 5	0	0	0
1	A	340	Total 2591	C 1707	N 414	O 465	S 5	0	0	0
1	B	342	Total 2602	C 1715	N 413	O 469	S 5	0	0	0
1	C	334	Total 2551	C 1683	N 405	O 458	S 5	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

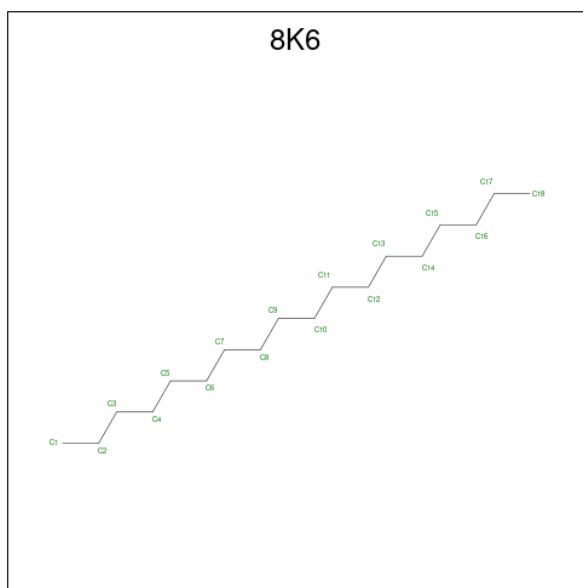
Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	GLY	-	linker	UNP O27985
D	-1	SER	-	linker	UNP O27985
D	0	GLY	-	linker	UNP O27985
D	1	SER	-	linker	UNP O27985
D	15	LEU	MET	conflict	UNP A9WSF5
D	22	ALA	VAL	conflict	UNP A9WSF5
D	23	ASP	ARG	conflict	UNP A9WSF5
D	75	LEU	GLN	conflict	UNP A9WSF5
D	77	PHE	ASP	conflict	UNP A9WSF5
D	79	GLU	PRO	conflict	UNP A9WSF5
A	-2	GLY	-	linker	UNP O27985
A	-1	SER	-	linker	UNP O27985
A	0	GLY	-	linker	UNP O27985
A	1	SER	-	linker	UNP O27985
A	15	LEU	MET	conflict	UNP A9WSF5
A	22	ALA	VAL	conflict	UNP A9WSF5
A	23	ASP	ARG	conflict	UNP A9WSF5
A	75	LEU	GLN	conflict	UNP A9WSF5
A	77	PHE	ASP	conflict	UNP A9WSF5
A	79	GLU	PRO	conflict	UNP A9WSF5
B	-2	GLY	-	linker	UNP O27985

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	SER	-	linker	UNP O27985
B	0	GLY	-	linker	UNP O27985
B	1	SER	-	linker	UNP O27985
B	15	LEU	MET	conflict	UNP A9WSF5
B	22	ALA	VAL	conflict	UNP A9WSF5
B	23	ASP	ARG	conflict	UNP A9WSF5
B	75	LEU	GLN	conflict	UNP A9WSF5
B	77	PHE	ASP	conflict	UNP A9WSF5
B	79	GLU	PRO	conflict	UNP A9WSF5
C	-2	GLY	-	linker	UNP O27985
C	-1	SER	-	linker	UNP O27985
C	0	GLY	-	linker	UNP O27985
C	1	SER	-	linker	UNP O27985
C	15	LEU	MET	conflict	UNP A9WSF5
C	22	ALA	VAL	conflict	UNP A9WSF5
C	23	ASP	ARG	conflict	UNP A9WSF5
C	75	LEU	GLN	conflict	UNP A9WSF5
C	77	PHE	ASP	conflict	UNP A9WSF5
C	79	GLU	PRO	conflict	UNP A9WSF5

- Molecule 2 is Octadecane (CCD ID: 8K6) (formula: C<sub>18</sub>H<sub>38</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	D	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	B	1	Total C 7 7	0	0
2	B	1	Total C 7 7	0	0
2	B	1	Total C 7 7	0	0

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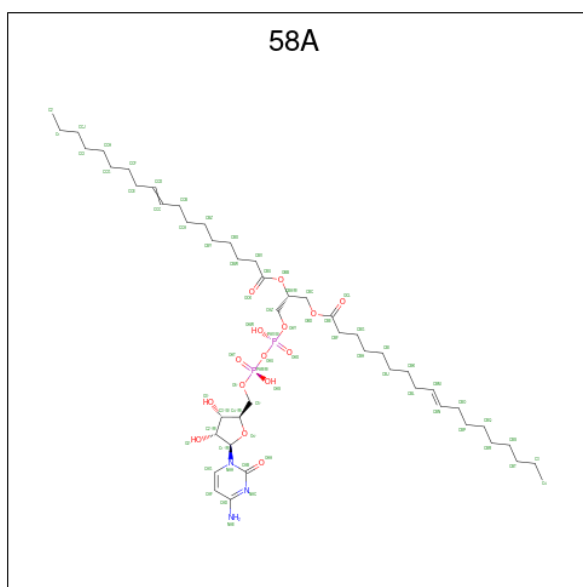
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C 7 7	0	0
2	B	1	Total C 7 7	0	0
2	B	1	Total C 7 7	0	0
2	C	1	Total C 7 7	0	0
2	C	1	Total C 7 7	0	0
2	C	1	Total C 7 7	0	0
2	C	1	Total C 7 7	0	0
2	C	1	Total C 7 7	0	0
2	C	1	Total C 7 7	0	0
2	C	1	Total C 7 7	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	2	Total Mg 2 2	0	0
3	A	2	Total Mg 2 2	0	0
3	B	2	Total Mg 2 2	0	0
3	C	2	Total Mg 2 2	0	0

- Molecule 4 is 5'-O-[(R)-{[(S)-{(2R)-2,3-bis[(9E)-octadec-9-enoyloxy]propoxy}(hydroxy)phosphoryl]oxy}(hydroxy)phosphoryl]cytidine (CCD ID: 58A) (formula: C<sub>48</sub>H<sub>85</sub>N<sub>3</sub>O<sub>15</sub>P<sub>2</sub>).

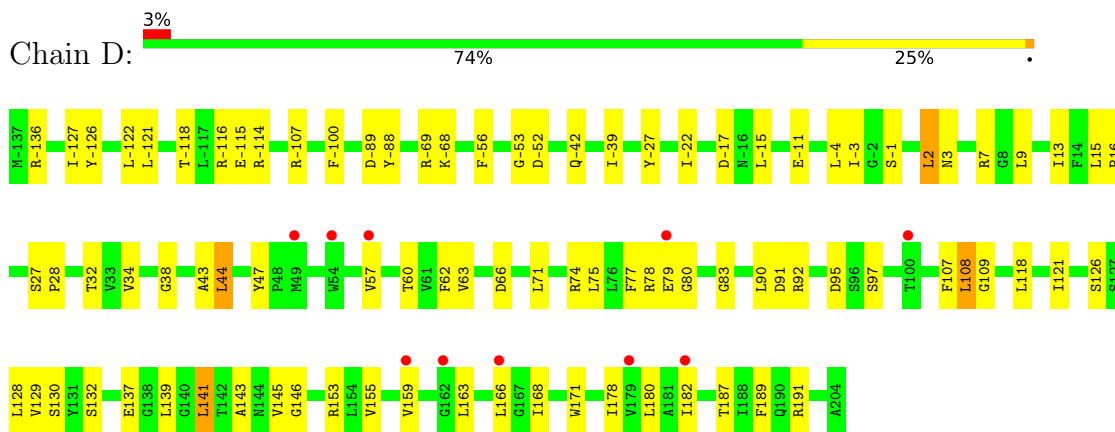


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	D	1	Total 64	44	3	15	2	0	0
4	A	1	Total 64	44	3	15	2	0	0
4	B	1	Total 64	44	3	15	2	0	0
4	C	1	Total 64	44	3	15	2	0	0

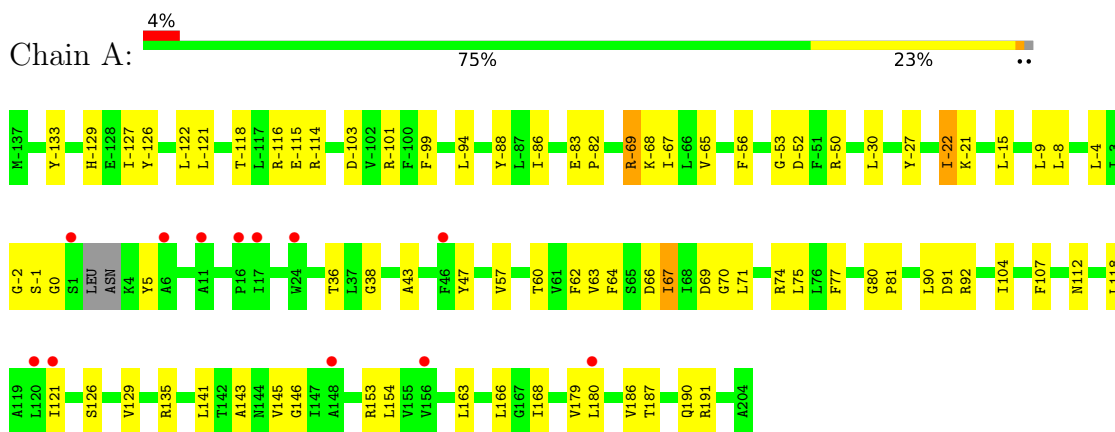
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

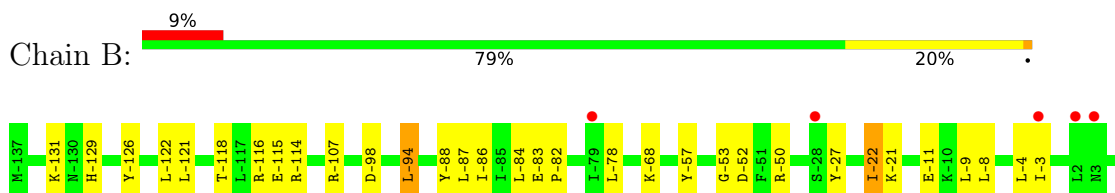
- Molecule 1: AF2299 protein, Phosphatidylinositol synthase

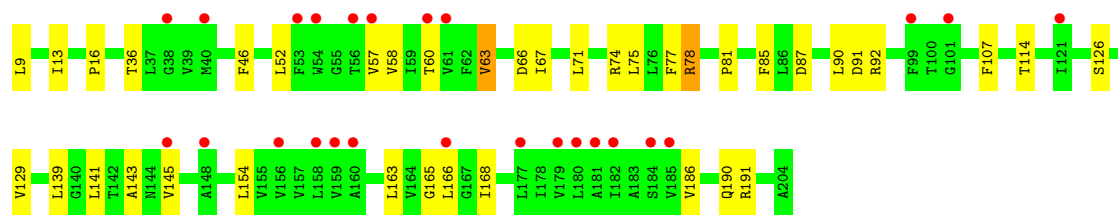


- Molecule 1: AF2299 protein, Phosphatidylinositol synthase

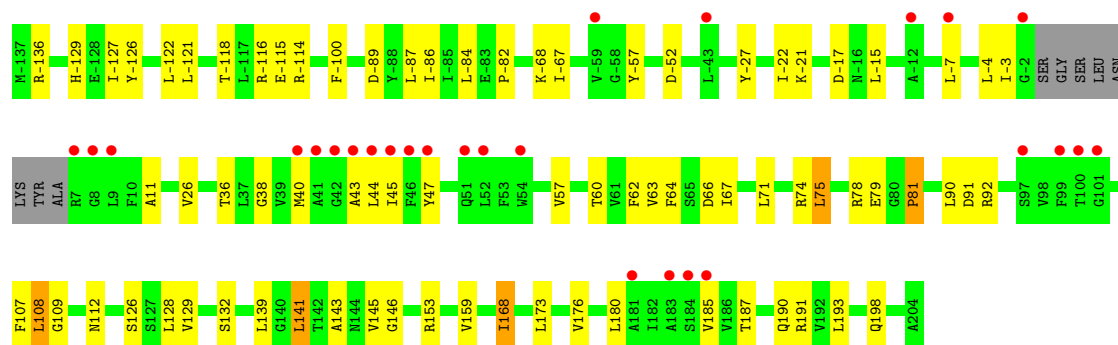
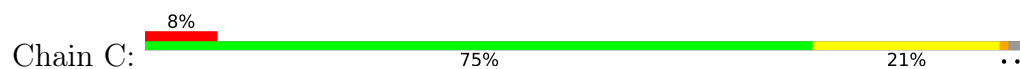


- Molecule 1: AF2299 protein, Phosphatidylinositol synthase





● Molecule 1: AF2299 protein, Phosphatidylinositol synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.00Å 62.49Å 169.76Å 90.00° 99.77° 90.00°	Depositor
Resolution (Å)	166.97 – 3.62 166.97 – 3.62	Depositor EDS
% Data completeness (in resolution range)	98.4 (166.97-3.62) 99.1 (166.97-3.62)	Depositor EDS
$R_{merge}$	0.25	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.55 (at 3.58Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.280 , 0.300 0.279 , 0.298	Depositor DCC
$R_{free}$ test set	1045 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	72.9	Xtrriage
Anisotropy	0.626	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 57.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.84	EDS
Total number of atoms	10844	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	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 20.91 % 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 7.8532e-03. 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: 8K6, MG, 58A

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	0.36	0/2641	0.93	9/3596 (0.3%)
1	B	0.35	0/2653	0.94	10/3616 (0.3%)
1	C	0.37	0/2600	0.96	15/3542 (0.4%)
1	D	0.35	0/2656	0.92	4/3620 (0.1%)
All	All	0.36	0/10550	0.94	38/14374 (0.3%)

There are no bond length outliers.

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	80	GLY	CA-C-N	9.94	130.21	119.28
1	D	80	GLY	C-N-CA	9.94	130.21	119.28
1	B	145	VAL	N-CA-C	9.92	123.22	108.54
1	C	145	VAL	N-CA-C	9.88	123.17	108.54
1	D	145	VAL	N-CA-C	9.73	122.94	108.54

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	2591	0	2635	54	0
1	B	2602	0	2646	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2551	0	2603	42	0
1	D	2605	0	2650	54	0
2	A	56	0	80	2	0
2	B	42	0	60	1	0
2	C	49	0	70	3	0
2	D	84	0	120	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	64	0	68	5	0
4	B	64	0	68	1	0
4	C	64	0	68	5	0
4	D	64	0	68	8	0
All	All	10844	0	11136	193	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 193 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)
4:C:310:58A:C1'	4:C:310:58A:O4'	1.65	1.29
4:A:311:58A:O4'	4:A:311:58A:C1'	1.65	1.27
4:B:309:58A:C1'	4:B:309:58A:O4'	1.65	1.21
4:D:315:58A:C1'	4:D:315:58A:O4'	1.65	1.15
1:D:66:ASP:OD1	4:D:315:58A:OAW	1.62	1.14

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	336/342 (98%)	329 (98%)	7 (2%)	0	100	100
1	B	340/342 (99%)	334 (98%)	6 (2%)	0	100	100
1	C	330/342 (96%)	324 (98%)	6 (2%)	0	100	100
1	D	340/342 (99%)	334 (98%)	6 (2%)	0	100	100
All	All	1346/1368 (98%)	1321 (98%)	25 (2%)	0	100	100

There are no Ramachandran outliers to report.

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	268/283 (95%)	261 (97%)	7 (3%)	40	58
1	B	270/283 (95%)	262 (97%)	8 (3%)	36	56
1	C	266/283 (94%)	255 (96%)	11 (4%)	27	50
1	D	271/283 (96%)	261 (96%)	10 (4%)	30	52
All	All	1075/1132 (95%)	1039 (97%)	36 (3%)	33	54

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	44	LEU
1	C	168	ILE
1	C	63	VAL
1	C	107	PHE
1	A	5	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-130	ASN
1	B	190	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 45 ligands modelled in this entry, 8 are monoatomic - leaving 37 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
2	8K6	D	304	-	6,6,17	0.31	0	5,5,16	0.71	0
2	8K6	B	303	-	6,6,17	0.31	0	5,5,16	0.70	0
2	8K6	D	306	-	6,6,17	0.32	0	5,5,16	0.68	0
2	8K6	A	302	-	6,6,17	0.31	0	5,5,16	0.69	0
2	8K6	C	305	-	6,6,17	0.32	0	5,5,16	0.70	0
2	8K6	A	306	-	6,6,17	0.32	0	5,5,16	0.69	0
2	8K6	D	307	-	6,6,17	0.31	0	5,5,16	0.67	0
4	58A	C	310	3	65,65,69	2.62	17 (26%)	78,82,86	1.11	7 (8%)
2	8K6	C	304	-	6,6,17	0.32	0	5,5,16	0.69	0
4	58A	A	311	3	65,65,69	2.61	18 (27%)	78,82,86	1.09	6 (7%)
2	8K6	A	307	-	6,6,17	0.32	0	5,5,16	0.70	0
2	8K6	B	302	-	6,6,17	0.32	0	5,5,16	0.68	0
2	8K6	B	306	-	6,6,17	0.32	0	5,5,16	0.69	0
2	8K6	D	311	-	6,6,17	0.30	0	5,5,16	0.71	0
2	8K6	C	301	-	6,6,17	0.32	0	5,5,16	0.68	0
4	58A	D	315	3	65,65,69	2.63	18 (27%)	78,82,86	1.10	6 (7%)
2	8K6	D	308	-	6,6,17	0.33	0	5,5,16	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	58A	B	309	3	65,65,69	2.65	18 (27%)	78,82,86	1.10	5 (6%)
2	8K6	D	305	-	6,6,17	0.33	0	5,5,16	0.65	0
2	8K6	D	302	-	6,6,17	0.31	0	5,5,16	0.68	0
2	8K6	C	303	-	6,6,17	0.32	0	5,5,16	0.70	0
2	8K6	D	310	-	6,6,17	0.31	0	5,5,16	0.70	0
2	8K6	D	301	-	6,6,17	0.31	0	5,5,16	0.68	0
2	8K6	A	301	-	6,6,17	0.32	0	5,5,16	0.68	0
2	8K6	A	304	-	6,6,17	0.31	0	5,5,16	0.71	0
2	8K6	B	305	-	6,6,17	0.32	0	5,5,16	0.70	0
2	8K6	C	302	-	6,6,17	0.32	0	5,5,16	0.66	0
2	8K6	D	303	-	6,6,17	0.32	0	5,5,16	0.67	0
2	8K6	C	306	-	6,6,17	0.31	0	5,5,16	0.73	0
2	8K6	A	308	-	6,6,17	0.31	0	5,5,16	0.70	0
2	8K6	C	307	-	6,6,17	0.30	0	5,5,16	0.74	0
2	8K6	D	309	-	6,6,17	0.33	0	5,5,16	0.63	0
2	8K6	B	301	-	6,6,17	0.32	0	5,5,16	0.67	0
2	8K6	B	304	-	6,6,17	0.30	0	5,5,16	0.73	0
2	8K6	A	303	-	6,6,17	0.31	0	5,5,16	0.71	0
2	8K6	A	305	-	6,6,17	0.32	0	5,5,16	0.68	0
2	8K6	D	312	-	6,6,17	0.33	0	5,5,16	0.70	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	8K6	D	304	-	-	1/4/4/15	-
2	8K6	B	303	-	-	0/4/4/15	-
2	8K6	D	306	-	-	0/4/4/15	-
2	8K6	A	302	-	-	0/4/4/15	-
2	8K6	C	305	-	-	0/4/4/15	-
2	8K6	A	306	-	-	0/4/4/15	-
2	8K6	D	307	-	-	0/4/4/15	-
4	58A	C	310	3	-	29/61/77/81	0/2/2/2
2	8K6	C	304	-	-	0/4/4/15	-
4	58A	A	311	3	-	26/61/77/81	0/2/2/2
2	8K6	A	307	-	-	0/4/4/15	-
2	8K6	B	302	-	-	0/4/4/15	-
2	8K6	B	306	-	-	0/4/4/15	-
2	8K6	D	311	-	-	0/4/4/15	-
2	8K6	C	301	-	-	0/4/4/15	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	58A	D	315	3	-	37/61/77/81	0/2/2/2
2	8K6	D	308	-	-	0/4/4/15	-
4	58A	B	309	3	-	31/61/77/81	0/2/2/2
2	8K6	D	305	-	-	2/4/4/15	-
2	8K6	D	302	-	-	1/4/4/15	-
2	8K6	C	303	-	-	0/4/4/15	-
2	8K6	D	310	-	-	0/4/4/15	-
2	8K6	D	301	-	-	1/4/4/15	-
2	8K6	A	301	-	-	0/4/4/15	-
2	8K6	A	304	-	-	0/4/4/15	-
2	8K6	B	305	-	-	0/4/4/15	-
2	8K6	C	302	-	-	3/4/4/15	-
2	8K6	D	303	-	-	0/4/4/15	-
2	8K6	C	306	-	-	0/4/4/15	-
2	8K6	A	308	-	-	0/4/4/15	-
2	8K6	C	307	-	-	0/4/4/15	-
2	8K6	D	309	-	-	2/4/4/15	-
2	8K6	B	301	-	-	1/4/4/15	-
2	8K6	B	304	-	-	0/4/4/15	-
2	8K6	A	303	-	-	0/4/4/15	-
2	8K6	A	305	-	-	0/4/4/15	-
2	8K6	D	312	-	-	0/4/4/15	-

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	315	58A	O4'-C1'	10.14	1.65	1.42
4	A	311	58A	O4'-C1'	10.14	1.65	1.42
4	B	309	58A	O4'-C1'	10.14	1.65	1.42
4	C	310	58A	O4'-C1'	10.09	1.65	1.42
4	C	310	58A	O4'-C4'	-6.45	1.30	1.45

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	311	58A	OBB-CBU-CBV	4.09	120.32	111.48
4	B	309	58A	OBB-CBU-CBV	4.02	120.18	111.48
4	D	315	58A	OBB-CBU-CBV	4.00	120.14	111.48
4	C	310	58A	OBB-CBU-CBV	3.94	120.00	111.48
4	C	310	58A	OBD-CBE-CBF	2.88	120.60	111.83

There are no chirality outliers.

5 of 134 torsion outliers are listed below:

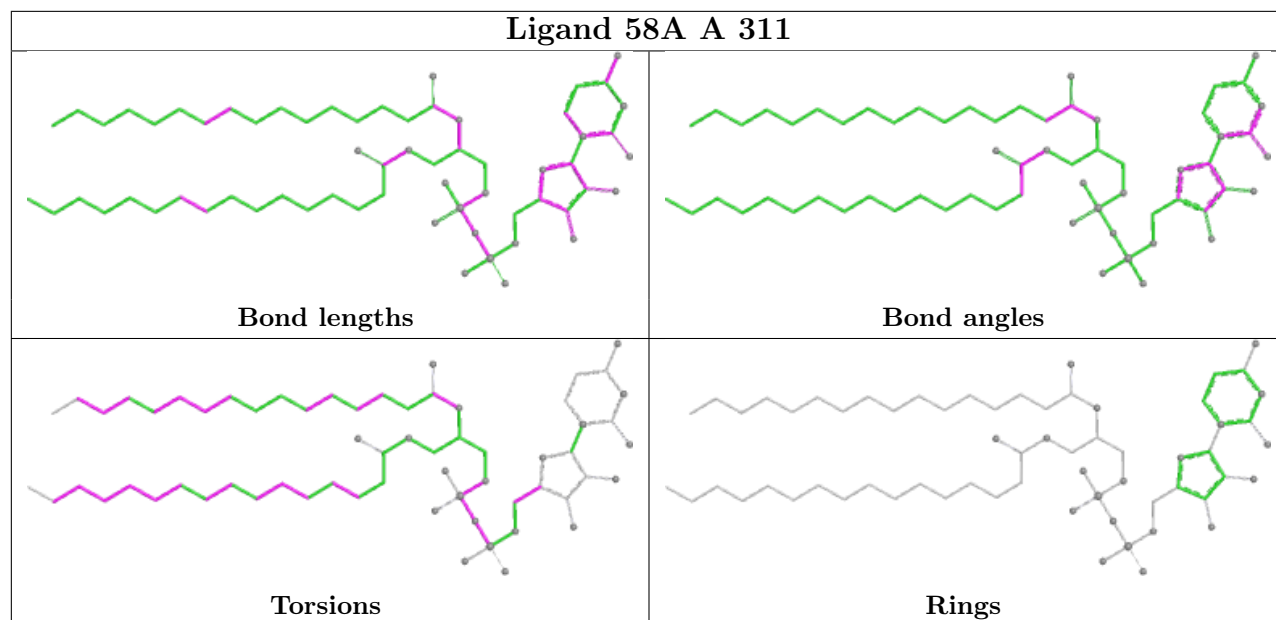
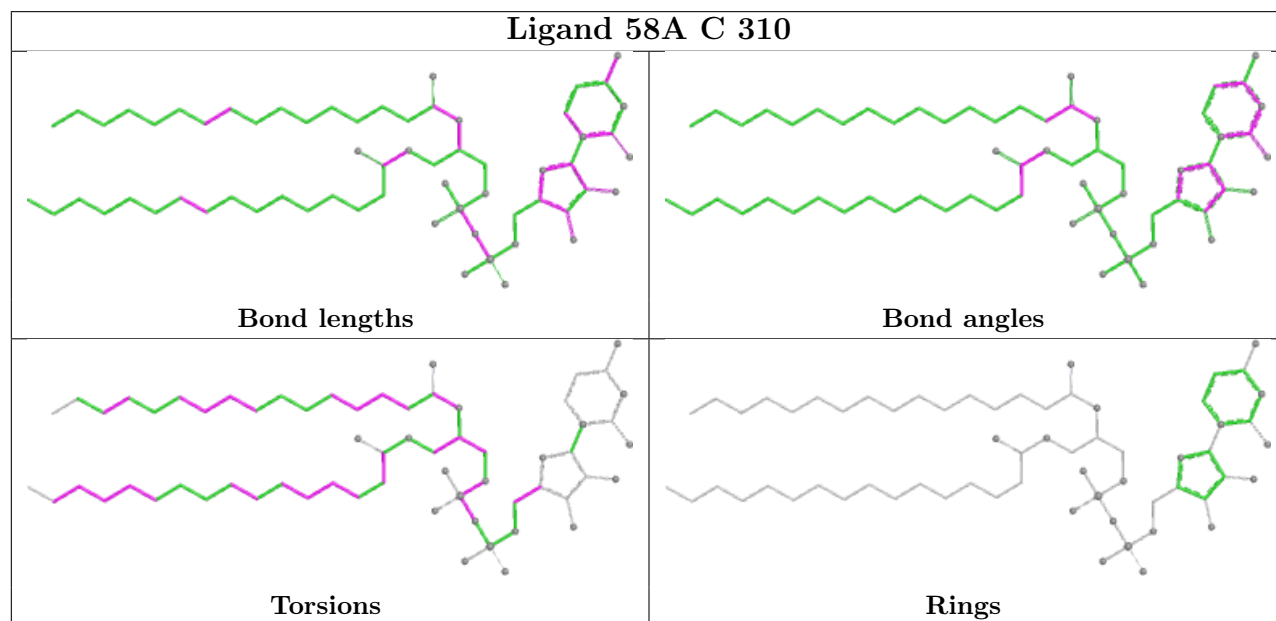
Mol	Chain	Res	Type	Atoms
4	D	315	58A	O4'-C4'-C5'-O5'
4	D	315	58A	C3'-C4'-C5'-O5'
4	D	315	58A	CAZ-OAY-PAV-OAU
4	D	315	58A	CAZ-OAY-PAV-OAX
4	D	315	58A	CAZ-OAY-PAV-OAW

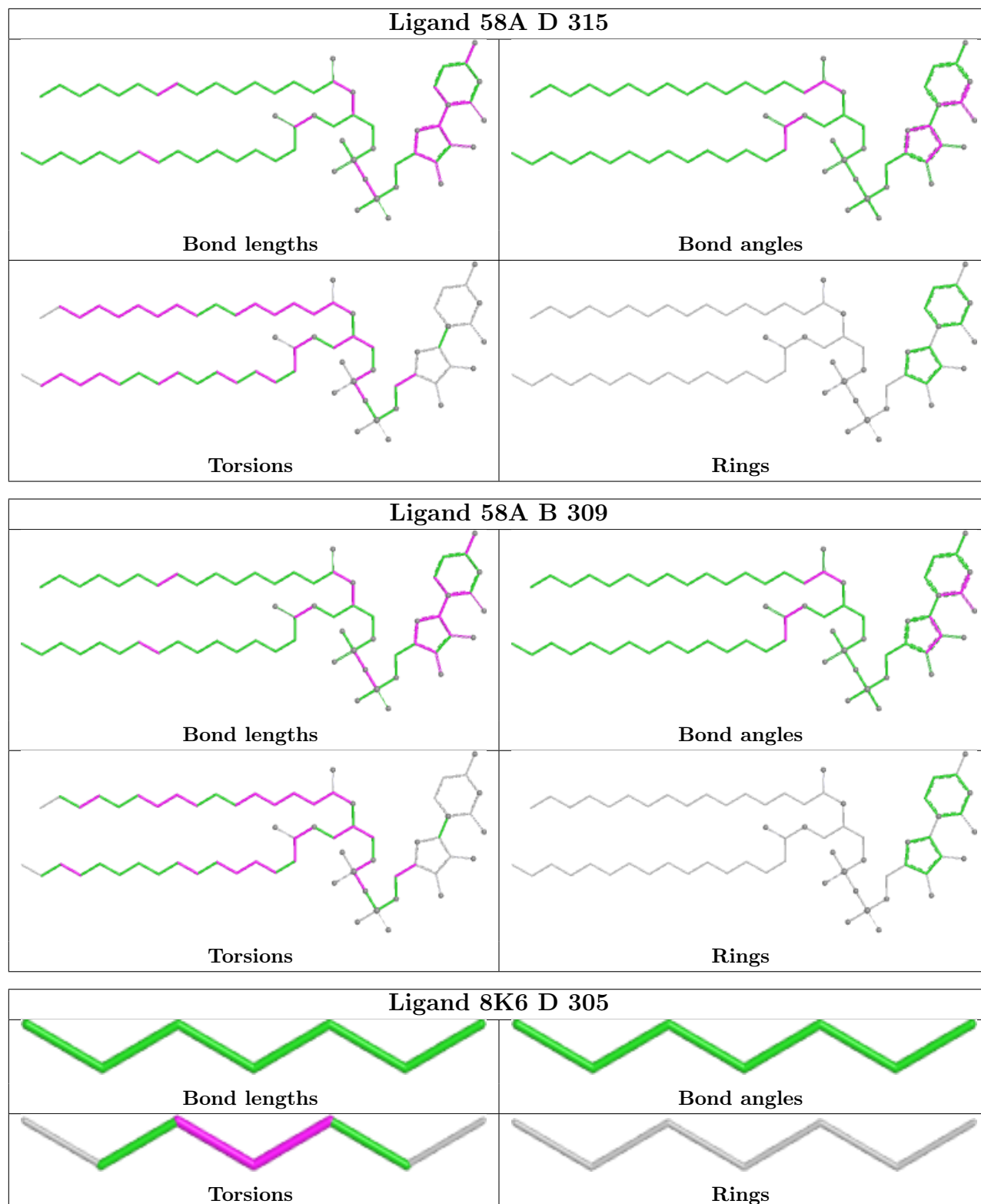
There are no ring outliers.

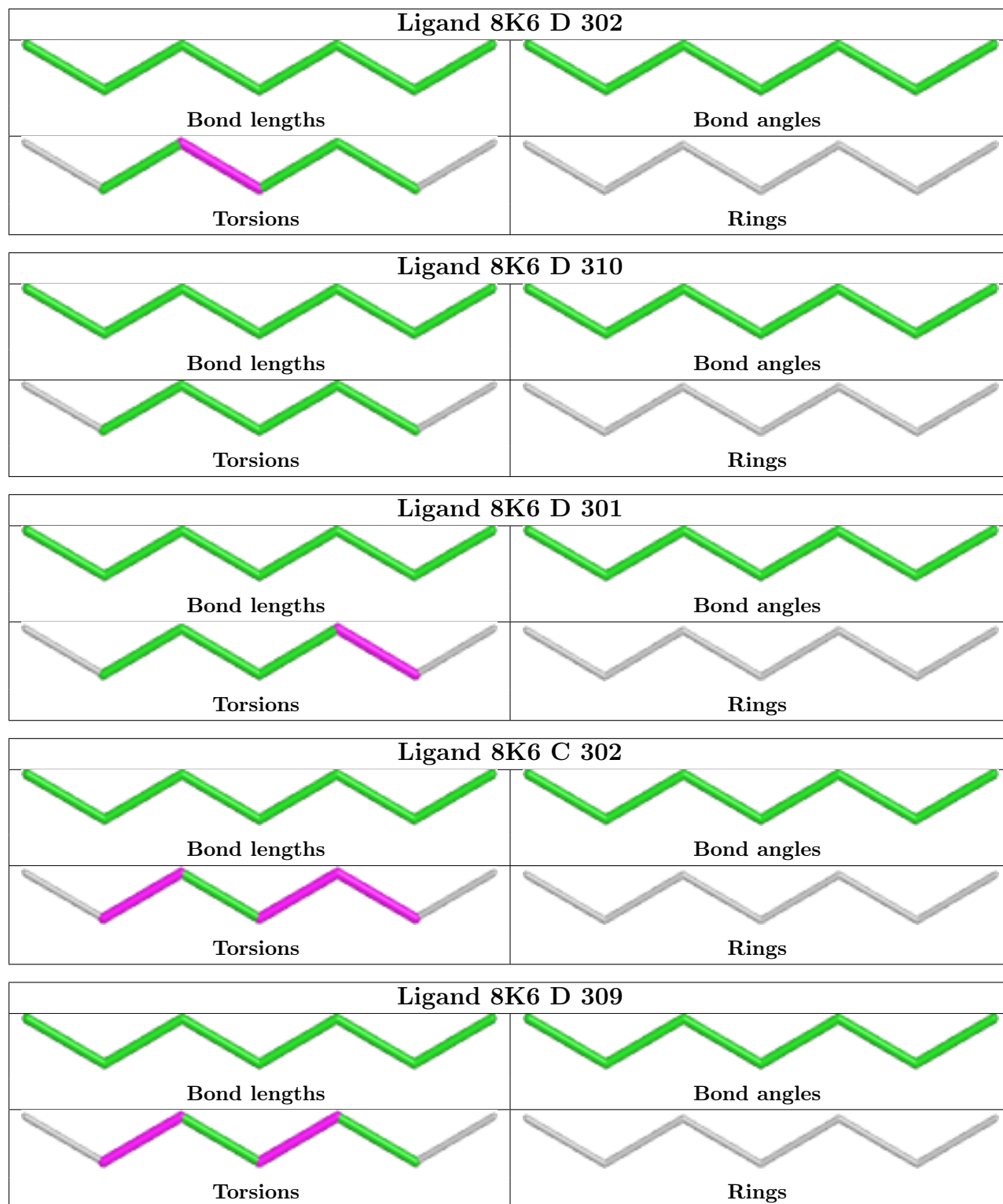
12 monomers are involved in 26 short contacts:

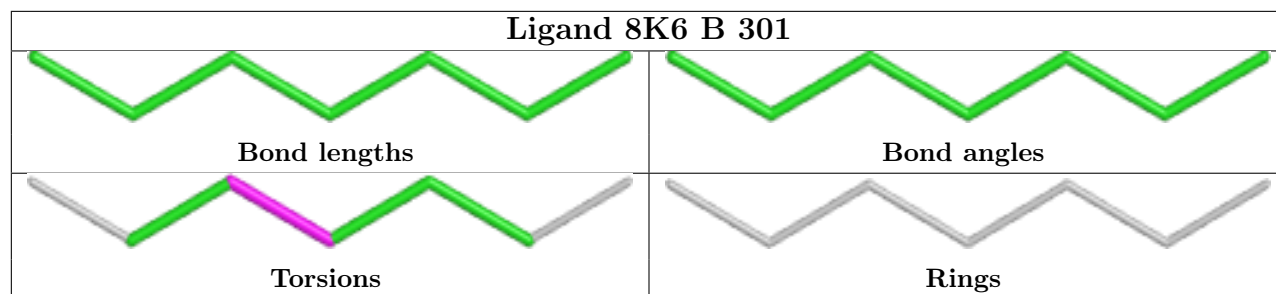
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	306	8K6	1	0
2	D	307	8K6	1	0
4	C	310	58A	5	0
2	C	304	8K6	1	0
4	A	311	58A	5	0
2	B	306	8K6	1	0
2	C	301	8K6	1	0
4	D	315	58A	8	0
4	B	309	58A	1	0
2	A	301	8K6	1	0
2	C	302	8K6	1	0
2	C	306	8K6	1	0

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 [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<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	340/342 (99%)	0.64	12 (3%) 47 28	38, 68, 106, 154	0
1	B	342/342 (100%)	0.71	30 (8%) 15 12	37, 69, 119, 151	0
1	C	334/342 (97%)	0.82	27 (8%) 18 13	44, 87, 149, 176	0
1	D	342/342 (100%)	0.63	10 (2%) 53 32	35, 66, 127, 152	0
All	All	1358/1368 (99%)	0.70	79 (5%) 29 18	35, 70, 134, 176	0

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	57	VAL	4.3
1	A	156	VAL	4.2
1	C	43	ALA	3.8
1	B	156	VAL	3.5
1	D	179	VAL	3.5

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

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [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.

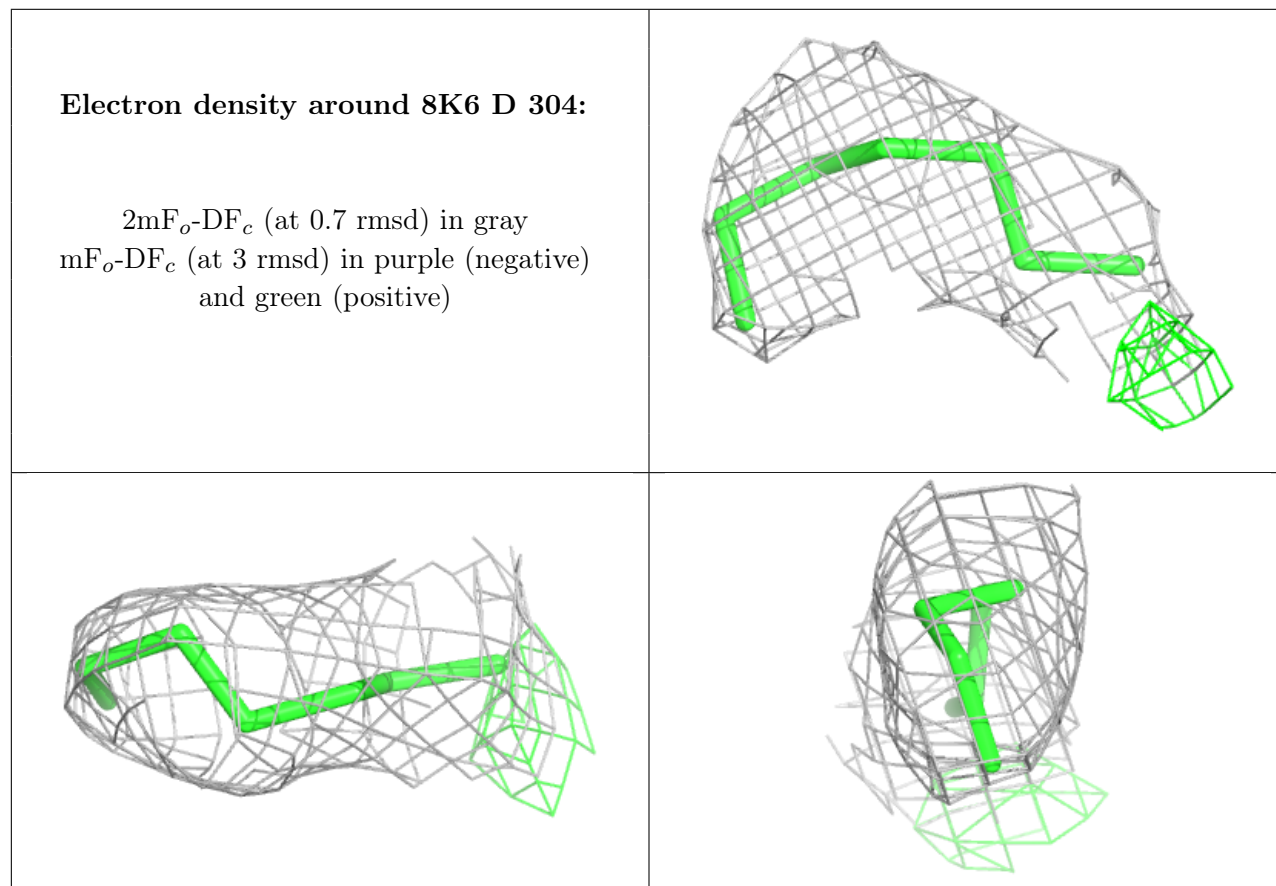
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	8K6	C	301	7/18	0.43	0.34	61,69,83,92	0
2	8K6	D	304	7/18	0.57	0.33	60,74,85,91	0
2	8K6	B	303	7/18	0.64	0.33	50,51,57,64	0
2	8K6	D	312	7/18	0.67	0.27	51,52,54,61	0
2	8K6	C	306	7/18	0.68	0.38	63,65,70,79	0
2	8K6	D	307	7/18	0.72	0.24	38,40,44,44	0
2	8K6	C	302	7/18	0.73	0.28	44,51,58,60	0
2	8K6	B	305	7/18	0.73	0.32	57,68,77,90	0
2	8K6	D	306	7/18	0.74	0.24	40,41,46,47	0
2	8K6	D	310	7/18	0.74	0.40	63,73,75,90	0
2	8K6	B	306	7/18	0.75	0.28	47,51,52,53	0
2	8K6	D	308	7/18	0.76	0.24	32,33,41,44	0
2	8K6	D	301	7/18	0.77	0.28	36,36,40,43	0
2	8K6	B	301	7/18	0.78	0.27	37,39,41,42	0
2	8K6	A	301	7/18	0.79	0.22	40,40,44,46	0
2	8K6	A	302	7/18	0.80	0.20	46,49,54,65	0
2	8K6	D	309	7/18	0.80	0.28	55,57,64,76	0
2	8K6	C	307	7/18	0.80	0.26	46,50,56,60	0
2	8K6	D	305	7/18	0.81	0.24	26,28,31,34	0
2	8K6	B	302	7/18	0.81	0.23	27,28,29,29	0
2	8K6	A	306	7/18	0.81	0.31	44,48,54,63	0
2	8K6	C	303	7/18	0.82	0.24	44,47,54,56	0
2	8K6	C	304	7/18	0.82	0.29	51,53,55,57	0
2	8K6	D	311	7/18	0.82	0.27	61,62,69,84	0
2	8K6	D	303	7/18	0.82	0.20	37,38,40,40	0
2	8K6	A	305	7/18	0.83	0.27	45,48,50,56	0
2	8K6	A	307	7/18	0.84	0.18	33,35,39,39	0
2	8K6	A	303	7/18	0.84	0.23	35,37,40,41	0
2	8K6	D	302	7/18	0.85	0.23	40,45,48,48	0
2	8K6	A	304	7/18	0.85	0.41	36,38,41,44	0
4	58A	C	310	64/68	0.86	0.19	59,73,101,139	0
2	8K6	B	304	7/18	0.87	0.17	36,37,39,42	0
2	8K6	A	308	7/18	0.87	0.19	35,36,37,37	0
2	8K6	C	305	7/18	0.88	0.31	63,66,71,71	0
4	58A	B	309	64/68	0.89	0.20	55,75,116,127	0
4	58A	D	315	64/68	0.89	0.17	56,67,84,126	0
3	MG	A	309	1/1	0.90	0.12	59,59,59,59	0
4	58A	A	311	64/68	0.90	0.16	48,63,91,113	0
3	MG	D	313	1/1	0.93	0.14	64,64,64,64	0
3	MG	C	308	1/1	0.93	0.11	70,70,70,70	0
3	MG	B	307	1/1	0.95	0.15	63,63,63,63	0
3	MG	B	308	1/1	0.96	0.06	63,63,63,63	0
3	MG	D	314	1/1	0.96	0.05	63,63,63,63	0

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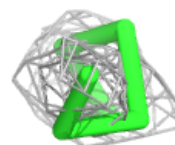
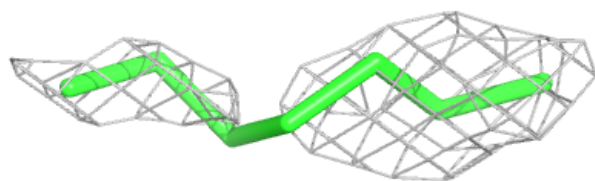
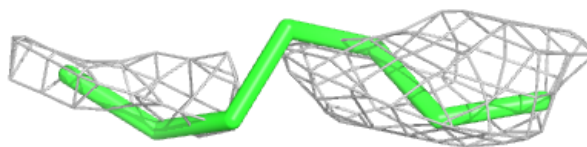
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MG	C	309	1/1	0.97	0.04	69,69,69,69	0
3	MG	A	310	1/1	0.99	0.08	61,61,61,61	0

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 8K6 C 302:**

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

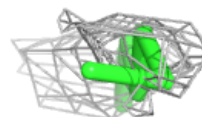
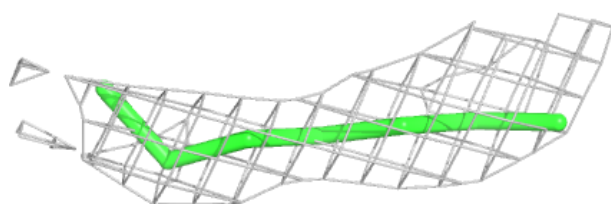
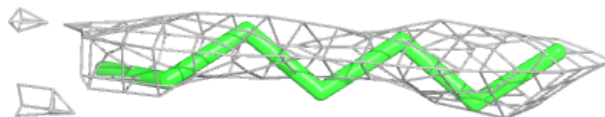
**Electron density around 8K6 D 310:**

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

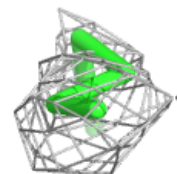
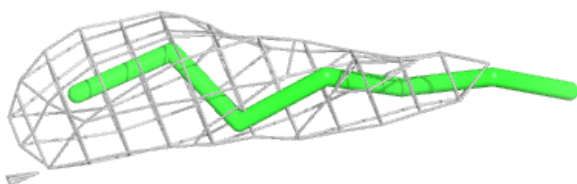
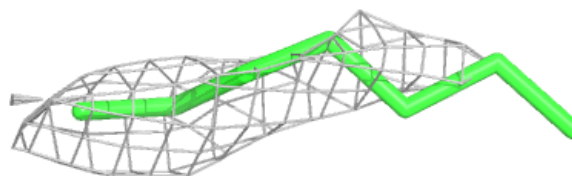


**Electron density around 8K6 D 301:**

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

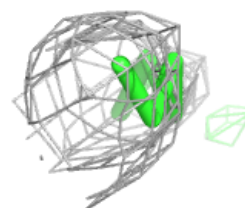
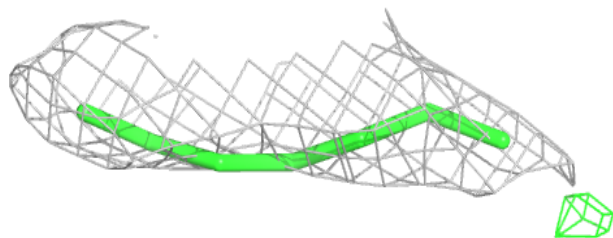
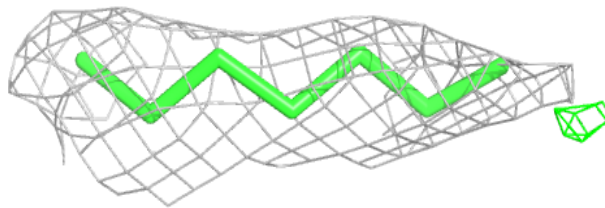
**Electron density around 8K6 B 301:**

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

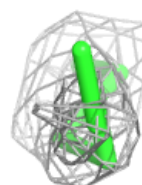
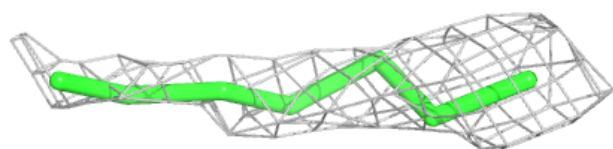
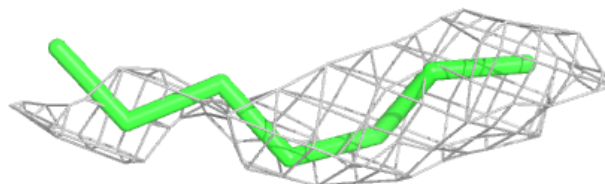


**Electron density around 8K6 D 309:**

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

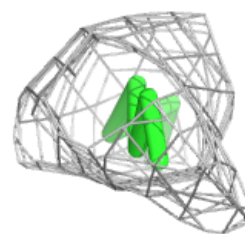
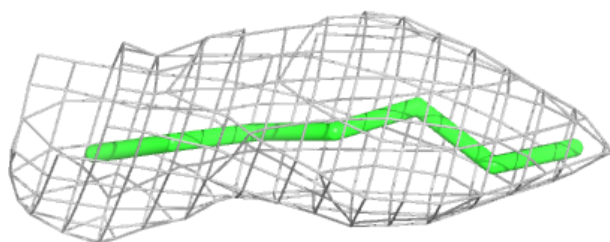
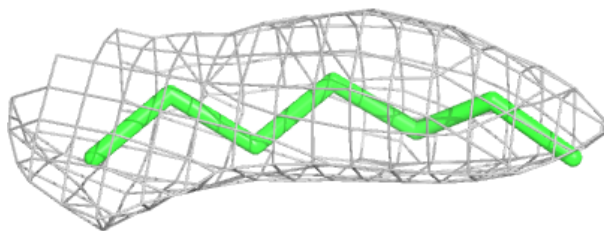
**Electron density around 8K6 D 305:**

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

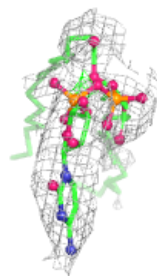
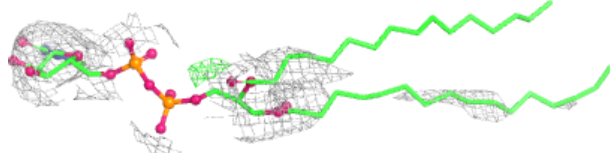
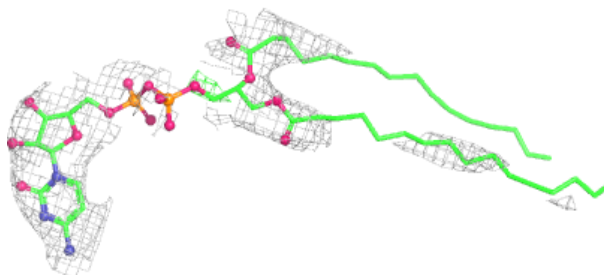


**Electron density around 8K6 D 302:**

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

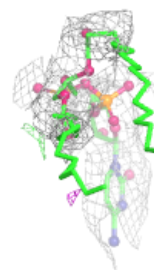
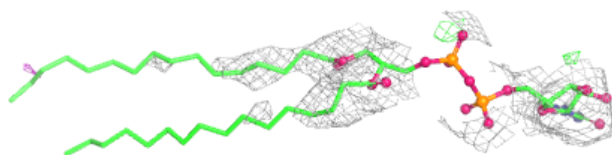
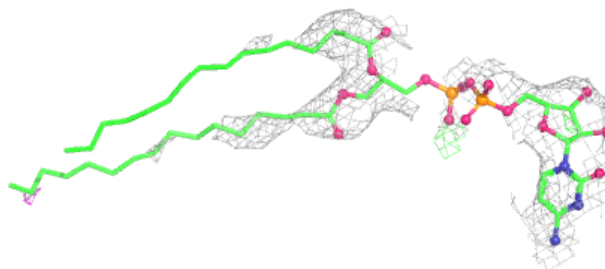
**Electron density around 58A C 310:**

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

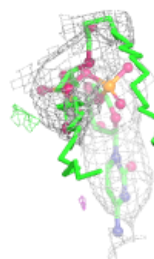
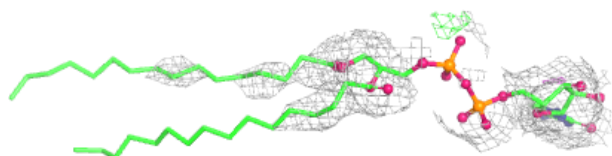
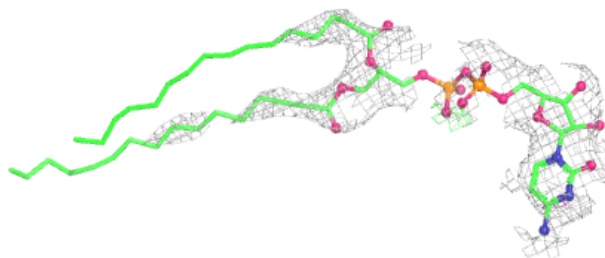


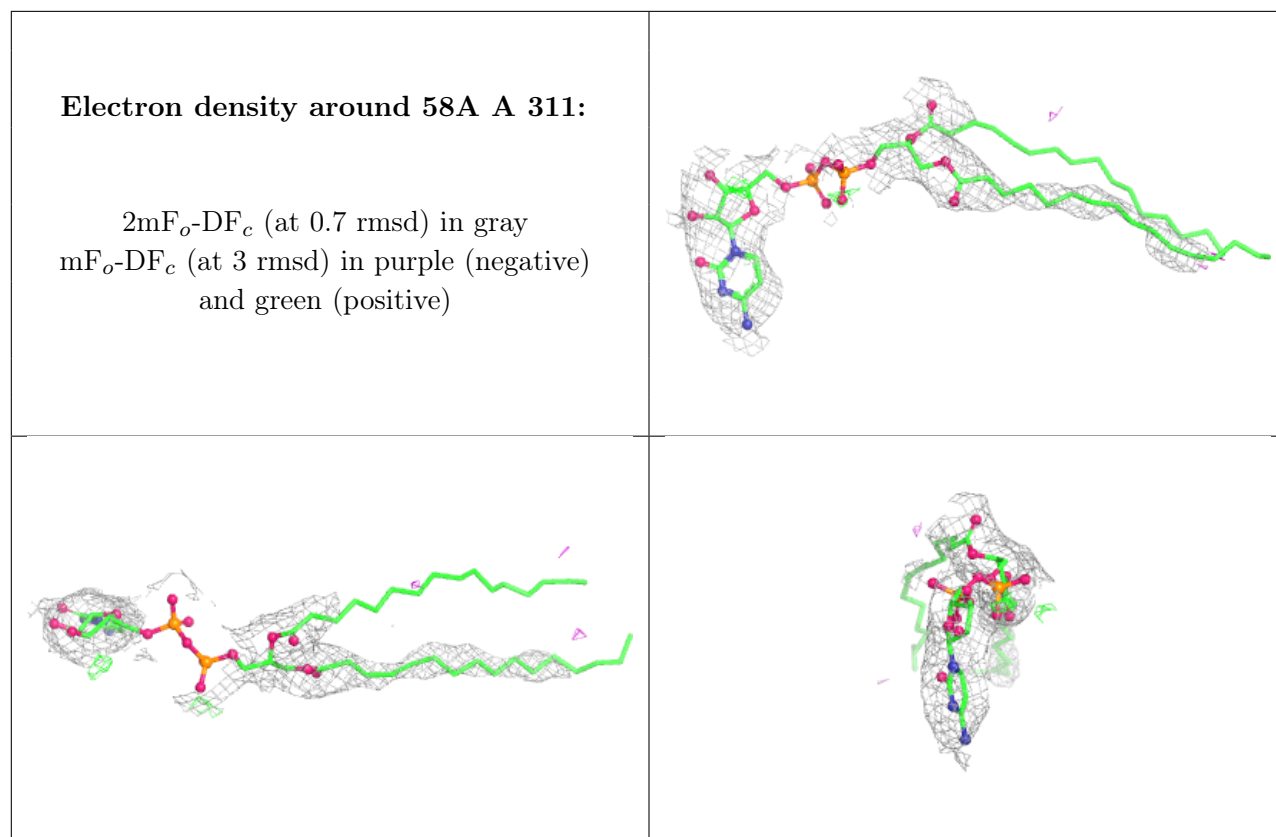
**Electron density around 58A B 309:**

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

**Electron density around 58A D 315:**

$2mF_o-DF_c$  (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.