



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 05:20 am BST

PDB ID : 4O01
Title : Crystal Structure of *D. radiodurans* Bacteriophytochrome Photosensory Core Module in its Illuminated Form
Authors : Takala, H.; Ihalainen, J.A.; Westenhoff, S.
Deposited on : 2013-12-13
Resolution : 3.24 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

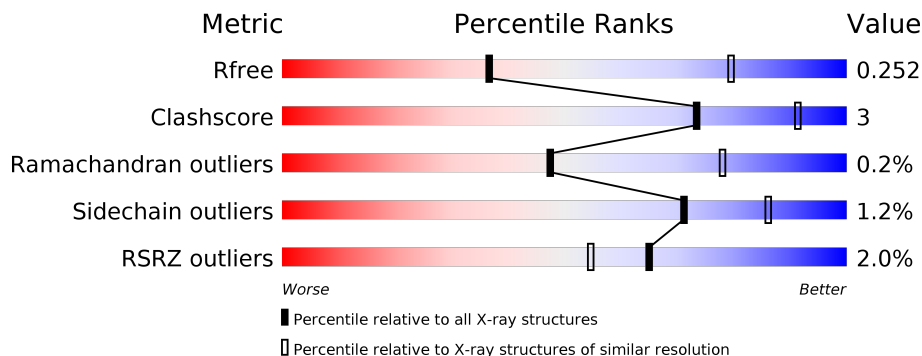
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.24 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	1619 (3.28-3.20)
Clashscore	141614	1755 (3.28-3.20)
Ramachandran outliers	138981	1728 (3.28-3.20)
Sidechain outliers	138945	1727 (3.28-3.20)
RSRZ outliers	127900	1567 (3.28-3.20)

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 on 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	523	
1	B	523	
1	C	523	
1	D	523	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 15128 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 Bacteriophytochrome.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	483	3691	2348	655	677	11	0	0	0
1	B	486	3719	2366	659	683	11	0	0	0
1	C	483	3691	2348	655	677	11	0	0	0
1	D	482	3683	2344	654	674	11	0	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP Q9RZA4
A	-12	ALA	-	EXPRESSION TAG	UNP Q9RZA4
A	-11	SER	-	EXPRESSION TAG	UNP Q9RZA4
A	-10	MET	-	EXPRESSION TAG	UNP Q9RZA4
A	-9	THR	-	EXPRESSION TAG	UNP Q9RZA4
A	-8	GLY	-	EXPRESSION TAG	UNP Q9RZA4
A	-7	GLY	-	EXPRESSION TAG	UNP Q9RZA4
A	-6	GLN	-	EXPRESSION TAG	UNP Q9RZA4
A	-5	GLN	-	EXPRESSION TAG	UNP Q9RZA4
A	-4	MET	-	EXPRESSION TAG	UNP Q9RZA4
A	-3	GLY	-	EXPRESSION TAG	UNP Q9RZA4
A	-2	ARG	-	EXPRESSION TAG	UNP Q9RZA4
A	-1	GLY	-	EXPRESSION TAG	UNP Q9RZA4
A	0	SER	-	EXPRESSION TAG	UNP Q9RZA4
A	503	GLU	-	EXPRESSION TAG	UNP Q9RZA4
A	504	HIS	-	EXPRESSION TAG	UNP Q9RZA4
A	505	HIS	-	EXPRESSION TAG	UNP Q9RZA4
A	506	HIS	-	EXPRESSION TAG	UNP Q9RZA4
A	507	HIS	-	EXPRESSION TAG	UNP Q9RZA4
A	508	HIS	-	EXPRESSION TAG	UNP Q9RZA4
A	509	HIS	-	EXPRESSION TAG	UNP Q9RZA4

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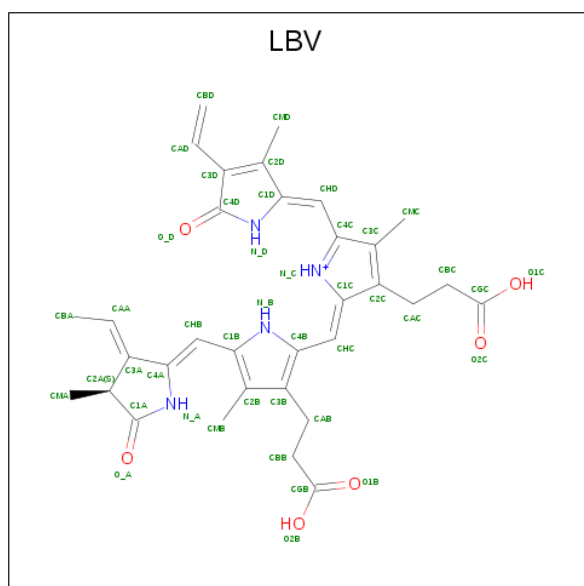
Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	MET	-	EXPRESSION TAG	UNP Q9RZA4
B	-12	ALA	-	EXPRESSION TAG	UNP Q9RZA4
B	-11	SER	-	EXPRESSION TAG	UNP Q9RZA4
B	-10	MET	-	EXPRESSION TAG	UNP Q9RZA4
B	-9	THR	-	EXPRESSION TAG	UNP Q9RZA4
B	-8	GLY	-	EXPRESSION TAG	UNP Q9RZA4
B	-7	GLY	-	EXPRESSION TAG	UNP Q9RZA4
B	-6	GLN	-	EXPRESSION TAG	UNP Q9RZA4
B	-5	GLN	-	EXPRESSION TAG	UNP Q9RZA4
B	-4	MET	-	EXPRESSION TAG	UNP Q9RZA4
B	-3	GLY	-	EXPRESSION TAG	UNP Q9RZA4
B	-2	ARG	-	EXPRESSION TAG	UNP Q9RZA4
B	-1	GLY	-	EXPRESSION TAG	UNP Q9RZA4
B	0	SER	-	EXPRESSION TAG	UNP Q9RZA4
B	503	GLU	-	EXPRESSION TAG	UNP Q9RZA4
B	504	HIS	-	EXPRESSION TAG	UNP Q9RZA4
B	505	HIS	-	EXPRESSION TAG	UNP Q9RZA4
B	506	HIS	-	EXPRESSION TAG	UNP Q9RZA4
B	507	HIS	-	EXPRESSION TAG	UNP Q9RZA4
B	508	HIS	-	EXPRESSION TAG	UNP Q9RZA4
B	509	HIS	-	EXPRESSION TAG	UNP Q9RZA4
C	-13	MET	-	EXPRESSION TAG	UNP Q9RZA4
C	-12	ALA	-	EXPRESSION TAG	UNP Q9RZA4
C	-11	SER	-	EXPRESSION TAG	UNP Q9RZA4
C	-10	MET	-	EXPRESSION TAG	UNP Q9RZA4
C	-9	THR	-	EXPRESSION TAG	UNP Q9RZA4
C	-8	GLY	-	EXPRESSION TAG	UNP Q9RZA4
C	-7	GLY	-	EXPRESSION TAG	UNP Q9RZA4
C	-6	GLN	-	EXPRESSION TAG	UNP Q9RZA4
C	-5	GLN	-	EXPRESSION TAG	UNP Q9RZA4
C	-4	MET	-	EXPRESSION TAG	UNP Q9RZA4
C	-3	GLY	-	EXPRESSION TAG	UNP Q9RZA4
C	-2	ARG	-	EXPRESSION TAG	UNP Q9RZA4
C	-1	GLY	-	EXPRESSION TAG	UNP Q9RZA4
C	0	SER	-	EXPRESSION TAG	UNP Q9RZA4
C	503	GLU	-	EXPRESSION TAG	UNP Q9RZA4
C	504	HIS	-	EXPRESSION TAG	UNP Q9RZA4
C	505	HIS	-	EXPRESSION TAG	UNP Q9RZA4
C	506	HIS	-	EXPRESSION TAG	UNP Q9RZA4
C	507	HIS	-	EXPRESSION TAG	UNP Q9RZA4
C	508	HIS	-	EXPRESSION TAG	UNP Q9RZA4
C	509	HIS	-	EXPRESSION TAG	UNP Q9RZA4

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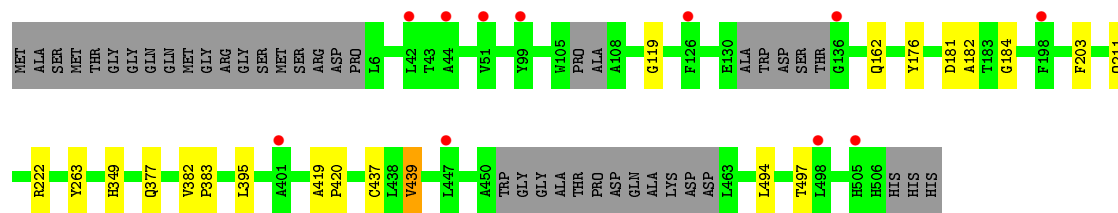
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-13	MET	-	EXPRESSION TAG	UNP Q9RZA4
D	-12	ALA	-	EXPRESSION TAG	UNP Q9RZA4
D	-11	SER	-	EXPRESSION TAG	UNP Q9RZA4
D	-10	MET	-	EXPRESSION TAG	UNP Q9RZA4
D	-9	THR	-	EXPRESSION TAG	UNP Q9RZA4
D	-8	GLY	-	EXPRESSION TAG	UNP Q9RZA4
D	-7	GLY	-	EXPRESSION TAG	UNP Q9RZA4
D	-6	GLN	-	EXPRESSION TAG	UNP Q9RZA4
D	-5	GLN	-	EXPRESSION TAG	UNP Q9RZA4
D	-4	MET	-	EXPRESSION TAG	UNP Q9RZA4
D	-3	GLY	-	EXPRESSION TAG	UNP Q9RZA4
D	-2	ARG	-	EXPRESSION TAG	UNP Q9RZA4
D	-1	GLY	-	EXPRESSION TAG	UNP Q9RZA4
D	0	SER	-	EXPRESSION TAG	UNP Q9RZA4
D	503	GLU	-	EXPRESSION TAG	UNP Q9RZA4
D	504	HIS	-	EXPRESSION TAG	UNP Q9RZA4
D	505	HIS	-	EXPRESSION TAG	UNP Q9RZA4
D	506	HIS	-	EXPRESSION TAG	UNP Q9RZA4
D	507	HIS	-	EXPRESSION TAG	UNP Q9RZA4
D	508	HIS	-	EXPRESSION TAG	UNP Q9RZA4
D	509	HIS	-	EXPRESSION TAG	UNP Q9RZA4

- Molecule 2 is 3-[2-[(Z)-[3-(2-carboxyethyl)-5-[(Z)-(4-ethenyl-3-methyl-5-oxidanylidene-pyrro- l-2-ylidene)methyl]-4-methyl-pyrrol-1-ium-2-ylidene]methyl]-5-[(Z)-[(3E)-3-ethylidene-4-m ethyl-5-oxidanylidene-pyrrolidin-2-ylidene]methyl]-4-methyl-1H-pyrrol-3-yl]propanoic acid (three-letter code: LBV) (formula: C₃₃H₃₇N₄O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	1
			86	66	8	12		
2	B	1	Total	C	N	O	0	1
			86	66	8	12		
2	C	1	Total	C	N	O	0	1
			86	66	8	12		
2	D	1	Total	C	N	O	0	1
			86	66	8	12		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.90Å 195.70Å 225.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.22 – 3.24 49.22 – 3.24	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.22-3.24) 100.0 (49.22-3.24)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	0.25	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 3.25Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.233 , 0.260 0.225 , 0.252	Depositor DCC
R_{free} test set	3094 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	131.2	Xtrriage
Anisotropy	0.166	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 98.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15128	wwPDB-VP
Average B, all atoms (Å ²)	158.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LBV

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	0.29	0/3787	0.51	0/5180
1	B	0.29	0/3816	0.50	0/5219
1	C	0.27	0/3787	0.50	0/5180
1	D	0.27	0/3779	0.50	0/5169
All	All	0.28	0/15169	0.50	0/20748

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	3691	0	3653	10	0
1	B	3719	0	3671	7	0
1	C	3691	0	3653	8	0
1	D	3683	0	3649	10	0
2	A	86	0	68	22	0
2	B	86	0	65	18	0
2	C	86	0	66	11	0
2	D	86	0	63	17	0
All	All	15128	0	14888	98	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.

All (98) 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)
2:B:600[B]:LBV:CMD	2:B:600[B]:LBV:CMC	1.75	1.59
2:A:600[B]:LBV:CMC	2:A:600[B]:LBV:HMD3	1.33	1.55
2:A:600[B]:LBV:CMC	2:A:600[B]:LBV:CMD	2.24	1.16
2:B:600[B]:LBV:CMD	2:B:600[B]:LBV:C3C	2.25	1.14
2:C:600[A]:LBV:N_D	2:C:600[A]:LBV:HMC1	1.69	1.05
2:D:600[A]:LBV:HMC1	2:D:600[A]:LBV:N_D	1.71	1.04
2:A:600[B]:LBV:HMC2	2:A:600[B]:LBV:CMD	1.86	1.03
2:A:600[B]:LBV:C3C	2:A:600[B]:LBV:HMD3	1.90	1.02
2:B:600[B]:LBV:C2D	2:B:600[B]:LBV:CMC	2.42	0.96
2:D:600[A]:LBV:CMC	2:D:600[A]:LBV:N_D	2.29	0.95
2:A:600[B]:LBV:HMD3	2:A:600[B]:LBV:HMC2	0.96	0.93
2:C:600[A]:LBV:N_D	2:C:600[A]:LBV:CMC	2.35	0.89
2:C:600[A]:LBV:C1D	2:C:600[A]:LBV:HMC1	2.07	0.83
2:B:600[B]:LBV:HAF	2:B:600[B]:LBV:HAE	1.28	0.81
2:D:600[A]:LBV:HMC1	2:D:600[A]:LBV:C1D	2.12	0.79
2:A:600[B]:LBV:HMC1	2:A:600[B]:LBV:HMD3	1.57	0.78
2:A:600[B]:LBV:HMC1	2:A:600[B]:LBV:C2D	2.14	0.77
2:A:600[A]:LBV:HMC1	2:A:600[A]:LBV:N_D	2.00	0.76
2:A:600[B]:LBV:C3C	2:A:600[B]:LBV:CMD	2.60	0.76
2:B:600[A]:LBV:HAE	2:B:600[A]:LBV:HAF	1.39	0.71
2:D:600[A]:LBV:CMC	2:D:600[A]:LBV:HAG	1.99	0.71
2:C:600[B]:LBV:HAE	2:C:600[B]:LBV:HAF	1.38	0.71
2:B:600[A]:LBV:N_D	2:B:600[A]:LBV:HMC1	2.04	0.71
2:D:600[B]:LBV:HAE	2:D:600[B]:LBV:HAF	1.38	0.71
2:A:600[A]:LBV:CMC	2:A:600[A]:LBV:N_D	2.57	0.66
2:B:600[B]:LBV:HHC1	2:B:600[B]:LBV:HBB1	1.79	0.65
2:A:600[B]:LBV:HBB1	2:A:600[B]:LBV:HHC1	1.79	0.65
2:A:600[B]:LBV:HAE	2:A:600[B]:LBV:HAF	1.43	0.64
2:B:600[A]:LBV:N_D	2:B:600[A]:LBV:CMC	2.61	0.64
2:C:600[A]:LBV:HAE	2:C:600[A]:LBV:HAF	1.45	0.64
2:B:600[B]:LBV:HMD2	2:B:600[B]:LBV:C3C	2.30	0.60
2:D:600[A]:LBV:HAE	2:D:600[A]:LBV:HAF	1.49	0.59
2:C:600[A]:LBV:C4D	2:C:600[A]:LBV:HMC1	2.31	0.59
2:B:600[A]:LBV:HHC1	2:B:600[A]:LBV:HBB1	1.85	0.59
2:B:600[A]:LBV:HBA2	2:B:600[A]:LBV:HMA1	1.86	0.58
2:C:600[A]:LBV:HAG	2:C:600[A]:LBV:CMC	2.16	0.57
2:B:600[B]:LBV:HMA1	2:B:600[B]:LBV:HBA2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:600[A]:LBV:HMA1	2:D:600[A]:LBV:HBA2	1.86	0.56
2:D:600[B]:LBV:HBA2	2:D:600[B]:LBV:HMA1	1.86	0.56
2:A:600[A]:LBV:HAF	2:A:600[A]:LBV:HAE	1.52	0.55
2:B:600[A]:LBV:C1D	2:B:600[A]:LBV:HMC1	2.37	0.55
2:A:600[A]:LBV:HMC1	2:A:600[A]:LBV:C1D	2.36	0.55
1:B:395:LEU:HD11	1:B:439:VAL:HG21	1.89	0.54
1:C:395:LEU:HD11	1:C:439:VAL:HG21	1.89	0.54
1:A:395:LEU:HD11	1:A:439:VAL:HG21	1.89	0.53
1:D:395:LEU:HD11	1:D:439:VAL:HG21	1.90	0.53
2:A:600[A]:LBV:CMC	2:A:600[A]:LBV:HAG	2.20	0.53
2:A:600[A]:LBV:HBB1	2:A:600[A]:LBV:HHC1	1.90	0.53
1:A:290:HIS:CE1	2:A:600[B]:LBV:HAD1	2.44	0.52
2:D:600[A]:LBV:HBB1	2:D:600[A]:LBV:HHC1	1.92	0.52
1:A:290:HIS:HE1	2:A:600[B]:LBV:HAD1	1.75	0.51
1:D:203:PHE:CD2	2:D:600[A]:LBV:HMD1	2.45	0.51
2:C:600[A]:LBV:HMA1	2:C:600[A]:LBV:HBA2	1.93	0.51
2:C:600[B]:LBV:HMA1	2:C:600[B]:LBV:HBA2	1.93	0.51
2:D:600[A]:LBV:HMC1	2:D:600[A]:LBV:C4D	2.41	0.49
2:D:600[A]:LBV:N_D	2:D:600[A]:LBV:C3C	2.75	0.49
2:D:600[B]:LBV:HHC1	2:D:600[B]:LBV:HBB1	1.96	0.48
1:A:419:ALA:N	1:A:420:PRO:CD	2.77	0.48
1:B:419:ALA:N	1:B:420:PRO:CD	2.77	0.47
1:C:419:ALA:N	1:C:420:PRO:CD	2.77	0.47
2:A:600[B]:LBV:HBB1	2:A:600[B]:LBV:CHC	2.45	0.47
2:B:600[B]:LBV:O_D	2:B:600[B]:LBV:HBD1	2.14	0.47
1:D:419:ALA:N	1:D:420:PRO:CD	2.78	0.46
2:D:600[A]:LBV:HAG	2:D:600[A]:LBV:C3C	2.29	0.46
1:A:211:GLN:N	1:A:211:GLN:OE1	2.49	0.46
1:C:211:GLN:OE1	1:C:211:GLN:N	2.49	0.45
2:B:600[B]:LBV:HBB1	2:B:600[B]:LBV:CHC	2.44	0.45
1:B:211:GLN:N	1:B:211:GLN:OE1	2.49	0.45
2:A:600[B]:LBV:HMA1	2:A:600[B]:LBV:HBA2	1.99	0.45
2:C:600[A]:LBV:C1D	2:C:600[A]:LBV:CMC	2.83	0.45
1:D:211:GLN:N	1:D:211:GLN:OE1	2.50	0.44
2:B:600[B]:LBV:C4C	2:B:600[B]:LBV:CMD	2.94	0.44
1:D:263:TYR:OH	2:D:600[A]:LBV:HMD3	2.17	0.44
2:A:600[B]:LBV:O_D	2:A:600[B]:LBV:HBD1	2.17	0.43
1:C:176:TYR:CE1	1:C:184:GLY:HA3	2.54	0.43
2:D:600[B]:LBV:HBD1	2:D:600[B]:LBV:O_D	2.17	0.43
1:A:494:LEU:HA	1:A:497:THR:HG22	2.00	0.43
1:B:494:LEU:HA	1:B:497:THR:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:600[A]:LBV:CMC	2:D:600[A]:LBV:C1D	2.85	0.43
1:A:176:TYR:CE1	1:A:184:GLY:HA3	2.54	0.42
1:B:176:TYR:CE1	1:B:184:GLY:HA3	2.54	0.42
1:C:181:ASP:O	1:C:182:ALA:HB3	2.19	0.42
2:B:600[A]:LBV:HAG	2:B:600[A]:LBV:CMC	2.30	0.42
1:D:494:LEU:HA	1:D:497:THR:HG22	2.01	0.42
1:C:494:LEU:HA	1:C:497:THR:HG22	2.01	0.42
1:B:181:ASP:O	1:B:182:ALA:HB3	2.21	0.41
1:C:382:VAL:HG13	1:C:383:PRO:HD2	2.02	0.41
1:A:382:VAL:HG13	1:A:383:PRO:HD2	2.03	0.41
1:D:176:TYR:CE1	1:D:184:GLY:HA3	2.55	0.41
1:A:181:ASP:O	1:A:182:ALA:HB3	2.20	0.41
1:A:208:ILE:HG12	2:A:600[B]:LBV:C4C	2.51	0.41
2:C:600[B]:LBV:HMC1	2:C:600[B]:LBV:C1D	2.25	0.41
1:D:181:ASP:O	1:D:182:ALA:HB3	2.21	0.41
2:B:600[B]:LBV:N_C	2:B:600[B]:LBV:N_B	2.63	0.41
1:D:382:VAL:HG13	1:D:383:PRO:HD2	2.03	0.41
1:B:349:HIS:HB3	1:B:377:GLN:HE22	1.87	0.40
1:C:227:THR:O	1:C:265:ARG:NH2	2.54	0.40
1:D:349:HIS:HB3	1:D:377:GLN:HE22	1.86	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	475/523 (91%)	459 (97%)	15 (3%)	1 (0%)	47 78
1	B	476/523 (91%)	458 (96%)	17 (4%)	1 (0%)	47 78
1	C	475/523 (91%)	457 (96%)	17 (4%)	1 (0%)	47 78
1	D	474/523 (91%)	457 (96%)	16 (3%)	1 (0%)	47 78
All	All	1900/2092 (91%)	1831 (96%)	65 (3%)	4 (0%)	47 78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	GLY
1	B	119	GLY
1	D	119	GLY
1	C	119	GLY

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	381/410 (93%)	376 (99%)	5 (1%)	69 85
1	B	384/410 (94%)	379 (99%)	5 (1%)	69 85
1	C	381/410 (93%)	377 (99%)	4 (1%)	76 88
1	D	380/410 (93%)	376 (99%)	4 (1%)	73 87
All	All	1526/1640 (93%)	1508 (99%)	18 (1%)	71 86

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

Mol	Chain	Res	Type
1	A	162	GLN
1	A	222	ARG
1	A	370	LEU
1	A	437	CYS
1	A	439	VAL
1	B	162	GLN
1	B	222	ARG
1	B	370	LEU
1	B	437	CYS
1	B	439	VAL
1	C	162	GLN
1	C	222	ARG
1	C	437	CYS
1	C	439	VAL
1	D	162	GLN
1	D	222	ARG

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Mol	Chain	Res	Type
1	D	437	CYS
1	D	439	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
1	A	290	HIS
1	A	335	HIS
1	A	377	GLN
1	A	484	HIS
1	B	138	HIS
1	B	335	HIS
1	B	377	GLN
1	B	484	HIS
1	C	335	HIS
1	C	484	HIS
1	D	335	HIS
1	D	377	GLN
1	D	484	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 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	LBV	A	600[B]	1	36,46,46	4.21	13 (36%)	41,67,67	3.49	16 (39%)
2	LBV	B	600[B]	1	36,46,46	4.20	13 (36%)	41,67,67	3.75	17 (41%)
2	LBV	C	600[A]	1	36,46,46	4.19	13 (36%)	41,67,67	3.56	13 (31%)
2	LBV	A	600[A]	1	36,46,46	4.23	13 (36%)	41,67,67	3.53	15 (36%)
2	LBV	C	600[B]	1	36,46,46	4.24	13 (36%)	41,67,67	3.59	15 (36%)
2	LBV	D	600[B]	1	36,46,46	4.16	13 (36%)	41,67,67	3.67	14 (34%)
2	LBV	D	600[A]	1	36,46,46	4.15	13 (36%)	41,67,67	3.58	14 (34%)
2	LBV	B	600[A]	1	36,46,46	4.22	13 (36%)	41,67,67	3.68	17 (41%)

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	LBV	A	600[B]	1	-	12/22/74/74	0/4/4/4
2	LBV	B	600[B]	1	-	12/22/74/74	0/4/4/4
2	LBV	C	600[A]	1	-	9/22/74/74	0/4/4/4
2	LBV	A	600[A]	1	-	10/22/74/74	0/4/4/4
2	LBV	C	600[B]	1	-	9/22/74/74	0/4/4/4
2	LBV	D	600[B]	1	-	12/22/74/74	0/4/4/4
2	LBV	D	600[A]	1	-	10/22/74/74	0/4/4/4
2	LBV	B	600[A]	1	-	10/22/74/74	0/4/4/4

All (104) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	600[B]	LBV	CHC-C1C	20.09	1.51	1.35
2	A	600[A]	LBV	CHC-C1C	20.04	1.51	1.35
2	B	600[A]	LBV	CHC-C1C	19.95	1.51	1.35
2	C	600[A]	LBV	CHC-C1C	19.91	1.51	1.35
2	A	600[B]	LBV	CHC-C1C	19.81	1.51	1.35
2	B	600[B]	LBV	CHC-C1C	19.73	1.51	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	600[A]	LBV	CHC-C1C	19.63	1.51	1.35
2	D	600[B]	LBV	CHC-C1C	19.57	1.51	1.35
2	B	600[A]	LBV	CHB-C4A	8.63	1.52	1.34
2	B	600[B]	LBV	CHB-C4A	8.61	1.52	1.34
2	A	600[B]	LBV	CHB-C4A	8.55	1.52	1.34
2	A	600[A]	LBV	CHB-C4A	8.53	1.52	1.34
2	C	600[B]	LBV	CHB-C4A	8.53	1.52	1.34
2	D	600[B]	LBV	CHB-C4A	8.50	1.52	1.34
2	C	600[A]	LBV	CHB-C4A	8.50	1.52	1.34
2	D	600[A]	LBV	CHB-C4A	8.43	1.52	1.34
2	D	600[A]	LBV	CHD-C1D	5.71	1.51	1.38
2	C	600[B]	LBV	CHD-C1D	5.70	1.51	1.38
2	B	600[A]	LBV	CHD-C1D	5.66	1.51	1.38
2	A	600[A]	LBV	CHD-C1D	5.65	1.51	1.38
2	C	600[A]	LBV	CHD-C1D	5.65	1.51	1.38
2	D	600[B]	LBV	CHD-C1D	5.64	1.51	1.38
2	B	600[B]	LBV	CHD-C1D	5.61	1.51	1.38
2	A	600[B]	LBV	CHD-C1D	5.49	1.51	1.38
2	C	600[B]	LBV	C3D-C2D	5.34	1.48	1.37
2	B	600[B]	LBV	C3D-C2D	5.30	1.48	1.37
2	D	600[B]	LBV	C3D-C2D	5.29	1.48	1.37
2	B	600[A]	LBV	C3D-C2D	5.28	1.48	1.37
2	D	600[A]	LBV	C3D-C2D	5.27	1.48	1.37
2	A	600[A]	LBV	C3D-C2D	5.25	1.47	1.37
2	C	600[A]	LBV	C3D-C2D	5.23	1.47	1.37
2	A	600[B]	LBV	C3D-C2D	5.21	1.47	1.37
2	A	600[B]	LBV	CHD-C4C	4.84	1.51	1.40
2	A	600[A]	LBV	CHD-C4C	4.83	1.51	1.40
2	B	600[A]	LBV	CHD-C4C	4.82	1.51	1.40
2	B	600[B]	LBV	CHD-C4C	4.78	1.51	1.40
2	C	600[B]	LBV	CHD-C4C	4.75	1.51	1.40
2	B	600[A]	LBV	C4A-N_A	4.68	1.45	1.37
2	D	600[B]	LBV	CHD-C4C	4.67	1.51	1.40
2	B	600[B]	LBV	C4A-N_A	4.62	1.45	1.37
2	A	600[A]	LBV	C4A-N_A	4.59	1.45	1.37
2	A	600[B]	LBV	C4A-N_A	4.53	1.45	1.37
2	D	600[A]	LBV	CHD-C4C	4.51	1.51	1.40
2	C	600[A]	LBV	CHD-C4C	4.51	1.51	1.40
2	D	600[B]	LBV	C4A-N_A	4.37	1.45	1.37
2	C	600[A]	LBV	C4A-N_A	4.37	1.45	1.37
2	D	600[A]	LBV	C4A-N_A	4.37	1.45	1.37
2	C	600[B]	LBV	C4A-N_A	4.37	1.45	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600[B]	LBV	C1D-C2D	3.23	1.50	1.45
2	D	600[B]	LBV	C1D-C2D	3.21	1.50	1.45
2	A	600[B]	LBV	C1D-C2D	3.18	1.50	1.45
2	C	600[B]	LBV	C1D-C2D	3.18	1.50	1.45
2	A	600[A]	LBV	C1D-C2D	3.05	1.50	1.45
2	B	600[A]	LBV	C1D-C2D	2.93	1.50	1.45
2	A	600[B]	LBV	O_D-C4D	2.91	1.29	1.23
2	C	600[B]	LBV	C1A-N_A	-2.90	1.33	1.37
2	C	600[A]	LBV	C1A-N_A	-2.86	1.33	1.37
2	B	600[B]	LBV	O_D-C4D	2.86	1.29	1.23
2	C	600[A]	LBV	C4B-CHC	2.84	1.52	1.41
2	C	600[A]	LBV	C1D-C2D	2.83	1.50	1.45
2	D	600[A]	LBV	C1D-C2D	2.82	1.50	1.45
2	A	600[B]	LBV	C4B-CHC	2.81	1.52	1.41
2	A	600[A]	LBV	C4B-CHC	2.81	1.52	1.41
2	C	600[B]	LBV	C4B-CHC	2.80	1.52	1.41
2	B	600[A]	LBV	C1B-CHB	2.78	1.51	1.41
2	D	600[A]	LBV	C4B-CHC	2.76	1.51	1.41
2	C	600[B]	LBV	O_D-C4D	2.76	1.28	1.23
2	A	600[B]	LBV	C1B-CHB	2.76	1.51	1.41
2	A	600[A]	LBV	C1B-CHB	2.75	1.51	1.41
2	C	600[A]	LBV	O_D-C4D	2.74	1.28	1.23
2	D	600[B]	LBV	O_D-C4D	2.74	1.28	1.23
2	B	600[B]	LBV	C1B-CHB	2.74	1.51	1.41
2	B	600[A]	LBV	O_D-C4D	2.74	1.28	1.23
2	D	600[B]	LBV	C1A-N_A	-2.73	1.34	1.37
2	D	600[B]	LBV	C4B-CHC	2.73	1.51	1.41
2	D	600[A]	LBV	C1A-N_A	-2.73	1.34	1.37
2	B	600[A]	LBV	C4B-CHC	2.72	1.51	1.41
2	B	600[B]	LBV	C4B-CHC	2.72	1.51	1.41
2	C	600[B]	LBV	C1B-CHB	2.69	1.51	1.41
2	D	600[A]	LBV	C1B-CHB	2.68	1.51	1.41
2	D	600[B]	LBV	C1B-CHB	2.67	1.51	1.41
2	C	600[A]	LBV	C1B-CHB	2.67	1.51	1.41
2	D	600[A]	LBV	O_D-C4D	2.65	1.28	1.23
2	C	600[A]	LBV	C1C-C2C	2.60	1.49	1.45
2	B	600[A]	LBV	C1C-C2C	2.55	1.49	1.45
2	A	600[A]	LBV	C1C-C2C	2.55	1.49	1.45
2	A	600[A]	LBV	O_D-C4D	2.54	1.28	1.23
2	B	600[B]	LBV	C1C-C2C	2.52	1.49	1.45
2	A	600[B]	LBV	C1C-C2C	2.51	1.49	1.45
2	D	600[A]	LBV	C4A-C3A	2.49	1.49	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600[B]	LBV	C1A-N_A	-2.49	1.34	1.37
2	C	600[B]	LBV	C4A-C3A	2.48	1.49	1.45
2	C	600[B]	LBV	C1C-C2C	2.47	1.49	1.45
2	A	600[A]	LBV	C1A-N_A	-2.47	1.34	1.37
2	C	600[A]	LBV	C4A-C3A	2.46	1.49	1.45
2	B	600[B]	LBV	C4A-C3A	2.46	1.49	1.45
2	D	600[B]	LBV	C4A-C3A	2.44	1.49	1.45
2	B	600[A]	LBV	C4A-C3A	2.41	1.49	1.45
2	B	600[B]	LBV	C1A-N_A	-2.41	1.34	1.37
2	D	600[A]	LBV	C1C-C2C	2.40	1.49	1.45
2	A	600[B]	LBV	C4A-C3A	2.32	1.49	1.45
2	D	600[B]	LBV	C1C-C2C	2.31	1.49	1.45
2	B	600[A]	LBV	C1A-N_A	-2.25	1.34	1.37
2	A	600[A]	LBV	C4A-C3A	2.21	1.49	1.45

All (121) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	600[B]	LBV	C4B-CHC-C1C	-14.04	112.03	128.81
2	D	600[B]	LBV	C4B-CHC-C1C	-13.61	112.55	128.81
2	C	600[B]	LBV	C4B-CHC-C1C	-13.36	112.85	128.81
2	B	600[A]	LBV	C4B-CHC-C1C	-13.16	113.09	128.81
2	A	600[A]	LBV	CHB-C4A-C3A	-12.68	104.22	127.12
2	C	600[A]	LBV	C4B-CHC-C1C	-12.61	113.74	128.81
2	B	600[A]	LBV	CHB-C4A-C3A	-12.54	104.47	127.12
2	D	600[A]	LBV	C4B-CHC-C1C	-12.44	113.95	128.81
2	D	600[B]	LBV	CHB-C4A-C3A	-12.38	104.75	127.12
2	B	600[B]	LBV	CHB-C4A-C3A	-12.32	104.86	127.12
2	D	600[A]	LBV	CHB-C4A-C3A	-12.27	104.95	127.12
2	A	600[B]	LBV	CHB-C4A-C3A	-12.09	105.28	127.12
2	C	600[B]	LBV	CHB-C4A-C3A	-12.08	105.31	127.12
2	A	600[B]	LBV	C4B-CHC-C1C	-12.01	114.46	128.81
2	C	600[A]	LBV	CHB-C4A-C3A	-11.97	105.50	127.12
2	A	600[A]	LBV	C4B-CHC-C1C	-11.26	115.36	128.81
2	D	600[A]	LBV	C1D-CHD-C4C	-7.38	110.05	128.08
2	C	600[A]	LBV	C1D-CHD-C4C	-7.06	110.83	128.08
2	B	600[A]	LBV	C1D-CHD-C4C	-6.76	111.57	128.08
2	A	600[A]	LBV	C1D-CHD-C4C	-6.28	112.75	128.08
2	D	600[A]	LBV	C3D-C4D-N_D	6.19	113.18	106.19
2	A	600[A]	LBV	C3D-C4D-N_D	6.19	113.18	106.19
2	C	600[A]	LBV	C3D-C4D-N_D	6.17	113.16	106.19
2	D	600[B]	LBV	C1D-CHD-C4C	-6.15	113.05	128.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	600[B]	LBV	C1D-CHD-C4C	-5.92	113.63	128.08
2	B	600[A]	LBV	C3D-C4D-N_D	5.86	112.81	106.19
2	D	600[B]	LBV	C3D-C4D-N_D	5.86	112.81	106.19
2	C	600[B]	LBV	C1D-CHD-C4C	-5.83	113.85	128.08
2	C	600[B]	LBV	C3D-C4D-N_D	5.81	112.75	106.19
2	B	600[B]	LBV	C3D-C4D-N_D	5.67	112.60	106.19
2	A	600[B]	LBV	C3D-C4D-N_D	5.19	112.05	106.19
2	A	600[B]	LBV	C1D-CHD-C4C	-4.72	116.56	128.08
2	C	600[A]	LBV	CHB-C4A-N_A	-4.57	115.05	130.40
2	D	600[A]	LBV	CHB-C4A-N_A	-4.57	115.05	130.40
2	C	600[B]	LBV	CHB-C4A-N_A	-4.51	115.25	130.40
2	B	600[A]	LBV	C2A-C3A-C4A	4.47	112.72	107.81
2	A	600[B]	LBV	CMD-C2D-C1D	4.41	129.68	124.17
2	D	600[B]	LBV	CHB-C4A-N_A	-4.39	115.64	130.40
2	A	600[B]	LBV	C3D-C2D-C1D	-4.37	102.75	108.03
2	A	600[A]	LBV	C2A-C3A-C4A	4.30	112.52	107.81
2	A	600[B]	LBV	CHB-C4A-N_A	-4.29	115.99	130.40
2	B	600[B]	LBV	C2A-C3A-C4A	4.21	112.43	107.81
2	B	600[B]	LBV	CHB-C4A-N_A	-4.17	116.39	130.40
2	A	600[B]	LBV	C2A-C3A-C4A	4.13	112.34	107.81
2	B	600[B]	LBV	CMD-C2D-C1D	4.02	129.18	124.17
2	B	600[B]	LBV	C3D-C2D-C1D	-3.97	103.23	108.03
2	B	600[A]	LBV	CHB-C4A-N_A	-3.95	117.12	130.40
2	B	600[A]	LBV	O_A-C1A-C2A	-3.95	122.46	126.28
2	A	600[A]	LBV	CHB-C4A-N_A	-3.92	117.22	130.40
2	A	600[A]	LBV	O_A-C1A-C2A	-3.72	122.69	126.28
2	D	600[B]	LBV	C2A-C3A-C4A	3.72	111.89	107.81
2	D	600[B]	LBV	CMD-C2D-C1D	3.70	128.78	124.17
2	D	600[B]	LBV	C3D-C2D-C1D	-3.69	103.57	108.03
2	B	600[B]	LBV	O_A-C1A-C2A	-3.68	122.73	126.28
2	A	600[A]	LBV	CAA-C3A-C4A	-3.68	121.92	126.36
2	A	600[A]	LBV	C4D-C3D-C2D	-3.66	103.23	107.92
2	C	600[B]	LBV	CAA-C3A-C4A	-3.65	121.95	126.36
2	D	600[B]	LBV	CAA-C3A-C4A	-3.64	121.97	126.36
2	C	600[A]	LBV	CAA-C3A-C4A	-3.62	121.99	126.36
2	C	600[B]	LBV	CMD-C2D-C1D	3.58	128.64	124.17
2	D	600[A]	LBV	C2A-C3A-C4A	3.57	111.73	107.81
2	D	600[A]	LBV	C4D-C3D-C2D	-3.54	103.38	107.92
2	C	600[B]	LBV	C3D-C2D-C1D	-3.51	103.78	108.03
2	A	600[B]	LBV	O_A-C1A-C2A	-3.51	122.89	126.28
2	C	600[A]	LBV	C4D-C3D-C2D	-3.48	103.46	107.92
2	D	600[A]	LBV	CAA-C3A-C4A	-3.47	122.17	126.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600[B]	LBV	CAA-C3A-C4A	-3.34	122.33	126.36
2	C	600[B]	LBV	C2A-C3A-C4A	3.32	111.45	107.81
2	C	600[A]	LBV	C2A-C3A-C4A	3.30	111.43	107.81
2	B	600[A]	LBV	C4D-C3D-C2D	-3.30	103.69	107.92
2	D	600[B]	LBV	O_A-C1A-C2A	-3.26	123.13	126.28
2	B	600[B]	LBV	CAA-C3A-C4A	-3.21	122.48	126.36
2	D	600[A]	LBV	O_A-C1A-C2A	-3.19	123.19	126.28
2	B	600[A]	LBV	CAA-C3A-C4A	-3.16	122.54	126.36
2	A	600[A]	LBV	CMD-C2D-C1D	3.11	128.05	124.17
2	B	600[A]	LBV	C3D-C2D-C1D	-3.06	104.34	108.03
2	C	600[B]	LBV	O_A-C1A-C2A	-3.05	123.33	126.28
2	C	600[A]	LBV	C3D-C2D-C1D	-2.90	104.52	108.03
2	C	600[B]	LBV	C4D-C3D-C2D	-2.87	104.24	107.92
2	D	600[A]	LBV	C3D-C2D-C1D	-2.85	104.59	108.03
2	A	600[A]	LBV	C3D-C2D-C1D	-2.84	104.60	108.03
2	C	600[A]	LBV	O_A-C1A-C2A	-2.83	123.55	126.28
2	D	600[B]	LBV	C4D-C3D-C2D	-2.82	104.31	107.92
2	B	600[A]	LBV	CMD-C2D-C1D	2.73	127.57	124.17
2	A	600[B]	LBV	C2D-C1D-N_D	2.71	110.95	106.99
2	B	600[B]	LBV	C2D-C1D-N_D	2.71	110.95	106.99
2	C	600[A]	LBV	O_D-C4D-C3D	-2.70	123.33	129.46
2	A	600[A]	LBV	CAB-CBB-CGB	-2.67	108.19	112.67
2	C	600[B]	LBV	O_D-C4D-C3D	-2.60	123.56	129.46
2	D	600[A]	LBV	O_D-C4D-C3D	-2.60	123.57	129.46
2	D	600[B]	LBV	O_D-C4D-C3D	-2.60	123.57	129.46
2	B	600[B]	LBV	CHC-C1C-N_C	-2.58	125.25	128.83
2	B	600[B]	LBV	C4D-C3D-C2D	-2.56	104.64	107.92
2	C	600[A]	LBV	CMD-C2D-C1D	2.55	127.35	124.17
2	D	600[B]	LBV	C2D-C1D-N_D	2.54	110.71	106.99
2	B	600[B]	LBV	O_D-C4D-C3D	-2.51	123.76	129.46
2	D	600[B]	LBV	CAB-CBB-CGB	-2.46	108.54	112.67
2	A	600[B]	LBV	O_D-C4D-C3D	-2.45	123.91	129.46
2	C	600[B]	LBV	C2D-C1D-N_D	2.41	110.52	106.99
2	C	600[A]	LBV	C2D-C1D-N_D	2.40	110.50	106.99
2	B	600[A]	LBV	C2D-C1D-N_D	2.36	110.44	106.99
2	B	600[A]	LBV	CAB-CBB-CGB	-2.36	108.72	112.67
2	A	600[A]	LBV	C2D-C1D-N_D	2.36	110.44	106.99
2	D	600[A]	LBV	C2D-C1D-N_D	2.35	110.42	106.99
2	D	600[A]	LBV	CAB-CBB-CGB	-2.32	108.77	112.67
2	B	600[A]	LBV	O_D-C4D-C3D	-2.24	124.39	129.46
2	B	600[A]	LBV	CBA-CAA-C3A	-2.20	120.29	126.72
2	D	600[A]	LBV	CMD-C2D-C1D	2.20	126.91	124.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	600[B]	LBV	C1C-N_C-C4C	2.19	110.64	106.51
2	A	600[B]	LBV	CHC-C1C-N_C	-2.16	125.83	128.83
2	B	600[B]	LBV	CMC-C3C-C4C	2.15	128.38	125.06
2	A	600[B]	LBV	CHD-C1D-N_D	-2.14	121.47	126.06
2	B	600[A]	LBV	CMC-C3C-C4C	2.11	128.32	125.06
2	C	600[B]	LBV	CAB-CBB-CGB	-2.10	109.15	112.67
2	B	600[B]	LBV	C1C-N_C-C4C	2.09	110.44	106.51
2	A	600[B]	LBV	CBA-CAA-C3A	-2.08	120.65	126.72
2	A	600[A]	LBV	CBA-CAA-C3A	-2.07	120.66	126.72
2	C	600[B]	LBV	C1C-N_C-C4C	2.04	110.36	106.51
2	A	600[A]	LBV	C1C-N_C-C4C	2.02	110.33	106.51
2	B	600[B]	LBV	CBA-CAA-C3A	-2.02	120.81	126.72
2	B	600[A]	LBV	C1C-N_C-C4C	2.00	110.28	106.51

There are no chirality outliers.

All (84) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	600[B]	LBV	C2B-C1B-CHB-C4A
2	A	600[B]	LBV	N_B-C1B-CHB-C4A
2	A	600[B]	LBV	C2B-C3B-CAB-CBB
2	A	600[B]	LBV	C4B-C3B-CAB-CBB
2	A	600[B]	LBV	N_A-C4A-CHB-C1B
2	A	600[B]	LBV	C3C-C4C-CHD-C1D
2	A	600[B]	LBV	N_C-C4C-CHD-C1D
2	B	600[B]	LBV	C2B-C1B-CHB-C4A
2	B	600[B]	LBV	N_B-C1B-CHB-C4A
2	B	600[B]	LBV	C2B-C3B-CAB-CBB
2	B	600[B]	LBV	C4B-C3B-CAB-CBB
2	B	600[B]	LBV	N_A-C4A-CHB-C1B
2	B	600[B]	LBV	N_C-C4C-CHD-C1D
2	C	600[A]	LBV	C2B-C1B-CHB-C4A
2	C	600[A]	LBV	N_B-C1B-CHB-C4A
2	C	600[A]	LBV	N_A-C4A-CHB-C1B
2	A	600[A]	LBV	C2B-C1B-CHB-C4A
2	A	600[A]	LBV	N_B-C1B-CHB-C4A
2	A	600[A]	LBV	C2B-C3B-CAB-CBB
2	A	600[A]	LBV	C4B-C3B-CAB-CBB
2	A	600[A]	LBV	N_A-C4A-CHB-C1B
2	A	600[A]	LBV	C3C-C4C-CHD-C1D
2	A	600[A]	LBV	N_C-C4C-CHD-C1D
2	C	600[B]	LBV	C2B-C1B-CHB-C4A

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Mol	Chain	Res	Type	Atoms
2	C	600[B]	LBV	N_B-C1B-CHB-C4A
2	C	600[B]	LBV	N_A-C4A-CHB-C1B
2	D	600[B]	LBV	C2B-C1B-CHB-C4A
2	D	600[B]	LBV	N_B-C1B-CHB-C4A
2	D	600[B]	LBV	C2B-C3B-CAB-CBB
2	D	600[B]	LBV	C4B-C3B-CAB-CBB
2	D	600[B]	LBV	N_A-C4A-CHB-C1B
2	D	600[B]	LBV	N_C-C4C-CHD-C1D
2	D	600[A]	LBV	C2B-C1B-CHB-C4A
2	D	600[A]	LBV	N_B-C1B-CHB-C4A
2	D	600[A]	LBV	C2B-C3B-CAB-CBB
2	D	600[A]	LBV	C4B-C3B-CAB-CBB
2	D	600[A]	LBV	N_A-C4A-CHB-C1B
2	D	600[A]	LBV	N_C-C4C-CHD-C1D
2	B	600[A]	LBV	C2B-C1B-CHB-C4A
2	B	600[A]	LBV	N_B-C1B-CHB-C4A
2	B	600[A]	LBV	C2B-C3B-CAB-CBB
2	B	600[A]	LBV	C4B-C3B-CAB-CBB
2	B	600[A]	LBV	N_A-C4A-CHB-C1B
2	B	600[A]	LBV	C3C-C4C-CHD-C1D
2	B	600[A]	LBV	N_C-C4C-CHD-C1D
2	C	600[B]	LBV	N_D-C1D-CHD-C4C
2	A	600[B]	LBV	C2D-C1D-CHD-C4C
2	B	600[B]	LBV	C2D-C1D-CHD-C4C
2	C	600[B]	LBV	C2D-C1D-CHD-C4C
2	D	600[B]	LBV	C2D-C1D-CHD-C4C
2	B	600[B]	LBV	C3C-C4C-CHD-C1D
2	D	600[B]	LBV	C3C-C4C-CHD-C1D
2	D	600[A]	LBV	C3C-C4C-CHD-C1D
2	D	600[B]	LBV	C2C-CAC-CBC-CGC
2	D	600[A]	LBV	C2C-CAC-CBC-CGC
2	C	600[A]	LBV	N_D-C1D-CHD-C4C
2	C	600[A]	LBV	N_C-C4C-CHD-C1D
2	C	600[B]	LBV	N_C-C4C-CHD-C1D
2	C	600[A]	LBV	C3C-C4C-CHD-C1D
2	C	600[B]	LBV	C3C-C4C-CHD-C1D
2	A	600[B]	LBV	C2C-CAC-CBC-CGC
2	B	600[B]	LBV	C2C-CAC-CBC-CGC
2	A	600[A]	LBV	C2C-CAC-CBC-CGC
2	A	600[B]	LBV	N_D-C1D-CHD-C4C
2	B	600[B]	LBV	N_D-C1D-CHD-C4C
2	D	600[B]	LBV	N_D-C1D-CHD-C4C

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Mol	Chain	Res	Type	Atoms
2	C	600[A]	LBV	C2D-C1D-CHD-C4C
2	B	600[B]	LBV	C1C-C2C-CAC-CBC
2	B	600[A]	LBV	C1C-C2C-CAC-CBC
2	B	600[B]	LBV	C3C-C2C-CAC-CBC
2	B	600[A]	LBV	C2C-CAC-CBC-CGC
2	B	600[A]	LBV	C3C-C2C-CAC-CBC
2	A	600[B]	LBV	C1C-C2C-CAC-CBC
2	D	600[B]	LBV	C1C-C2C-CAC-CBC
2	A	600[B]	LBV	C3C-C2C-CAC-CBC
2	C	600[A]	LBV	C2B-C3B-CAB-CBB
2	C	600[A]	LBV	C4B-C3B-CAB-CBB
2	C	600[B]	LBV	C2B-C3B-CAB-CBB
2	C	600[B]	LBV	C4B-C3B-CAB-CBB
2	D	600[A]	LBV	C1C-C2C-CAC-CBC
2	D	600[B]	LBV	C3C-C2C-CAC-CBC
2	A	600[A]	LBV	C1C-C2C-CAC-CBC
2	D	600[A]	LBV	C3C-C2C-CAC-CBC
2	A	600[A]	LBV	C3C-C2C-CAC-CBC

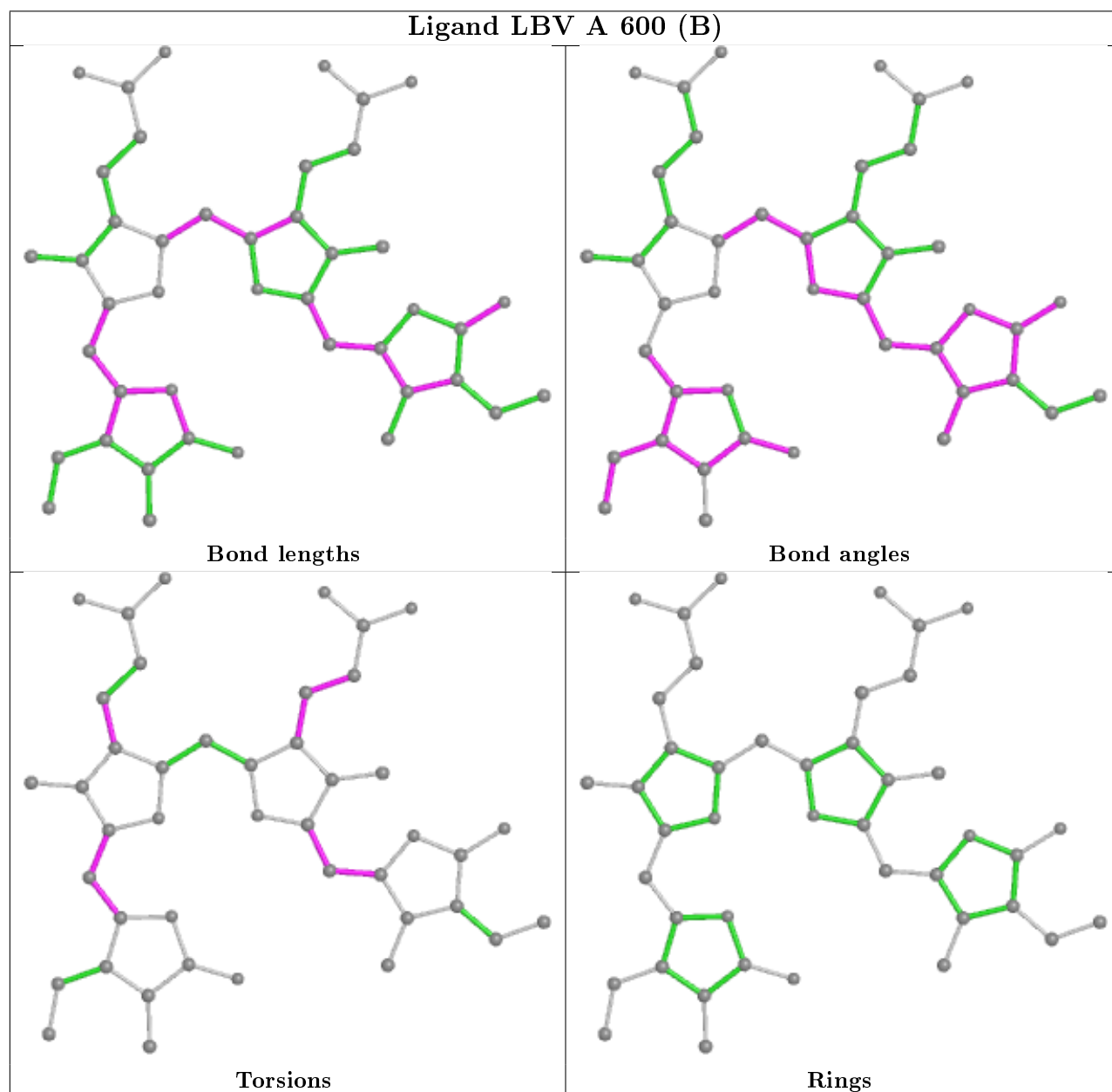
There are no ring outliers.

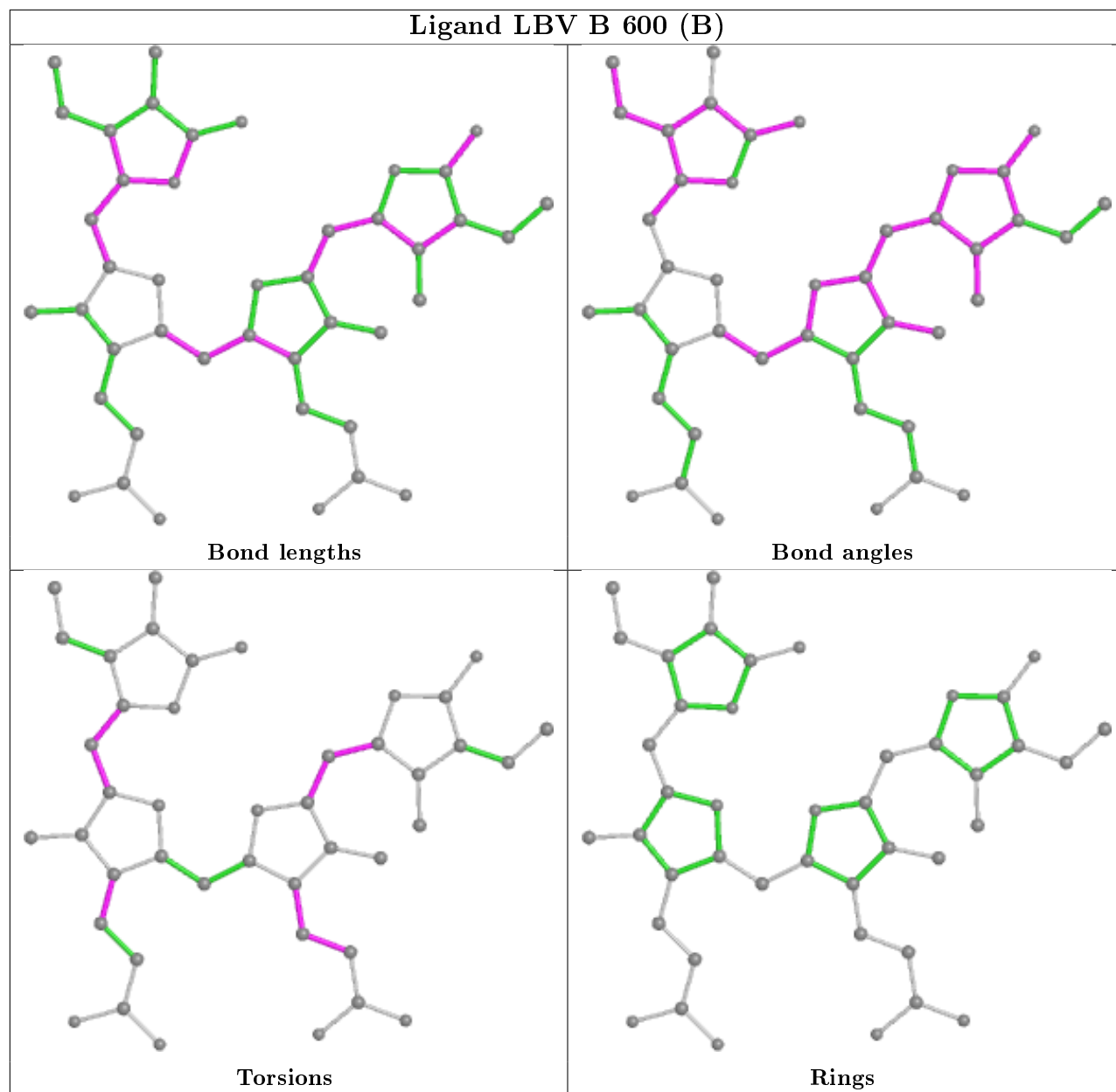
8 monomers are involved in 68 short contacts:

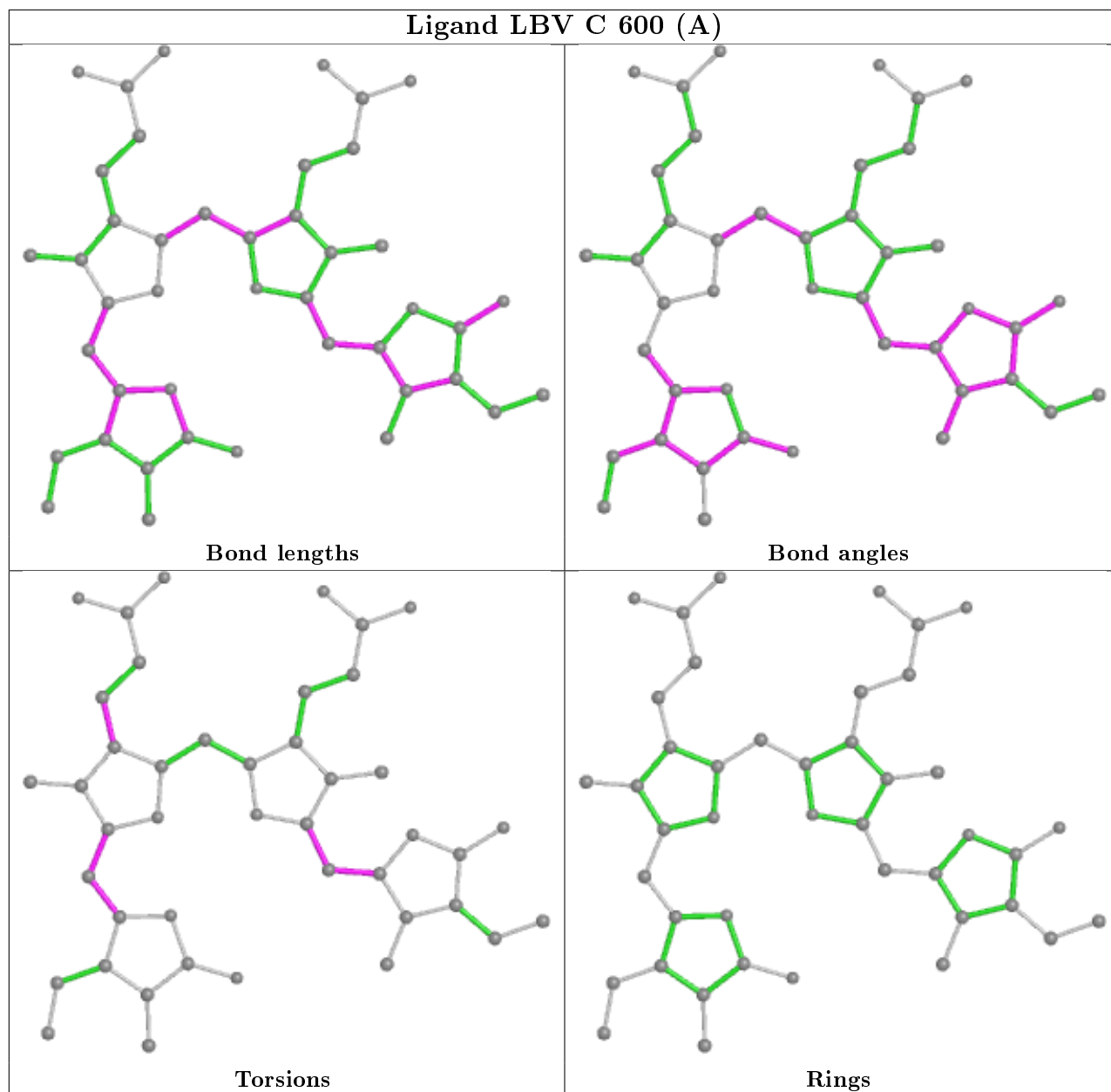
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600[B]	LBV	16	0
2	B	600[B]	LBV	11	0
2	C	600[A]	LBV	8	0
2	A	600[A]	LBV	6	0
2	C	600[B]	LBV	3	0
2	D	600[B]	LBV	4	0
2	D	600[A]	LBV	13	0
2	B	600[A]	LBV	7	0

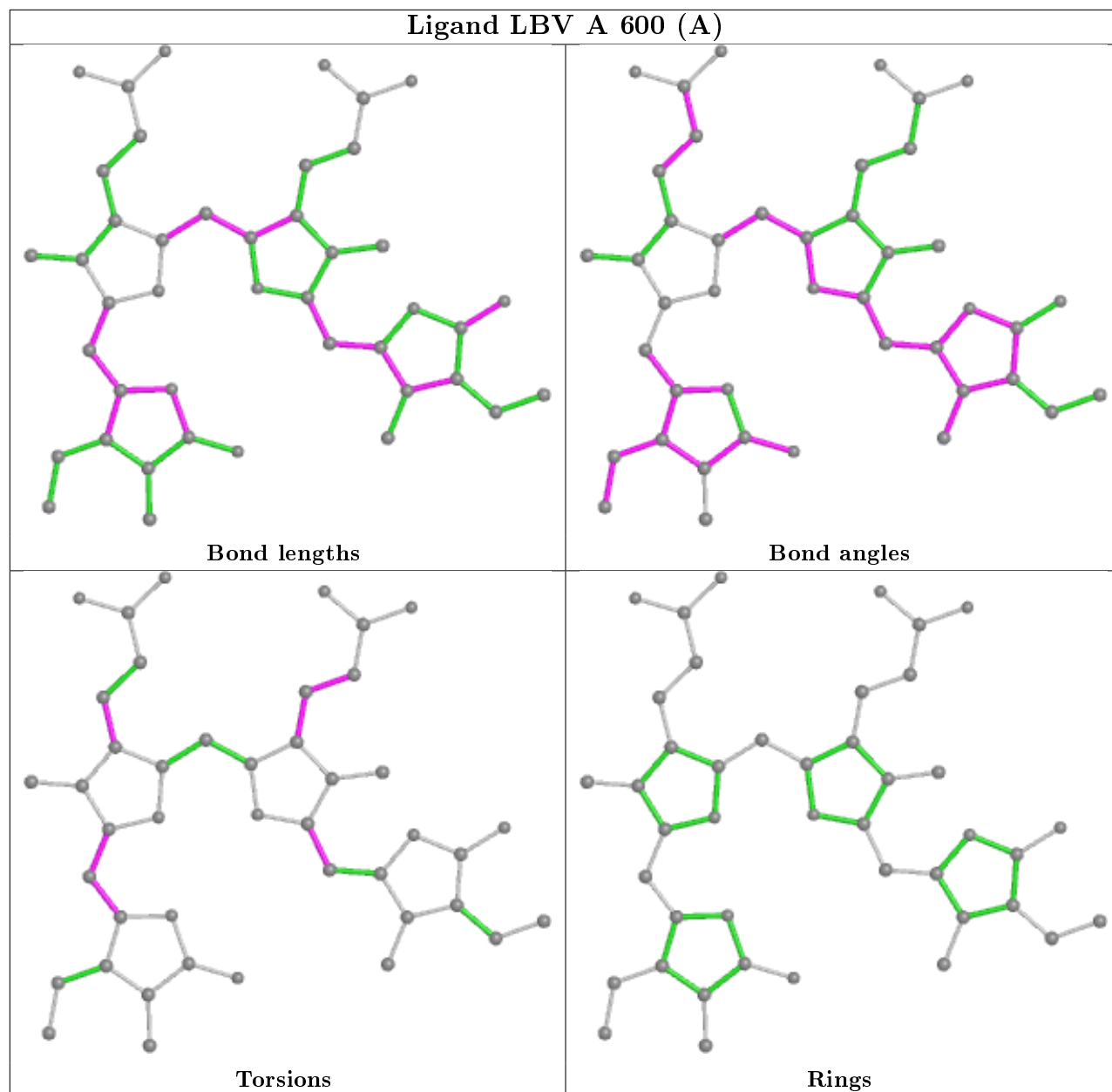
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

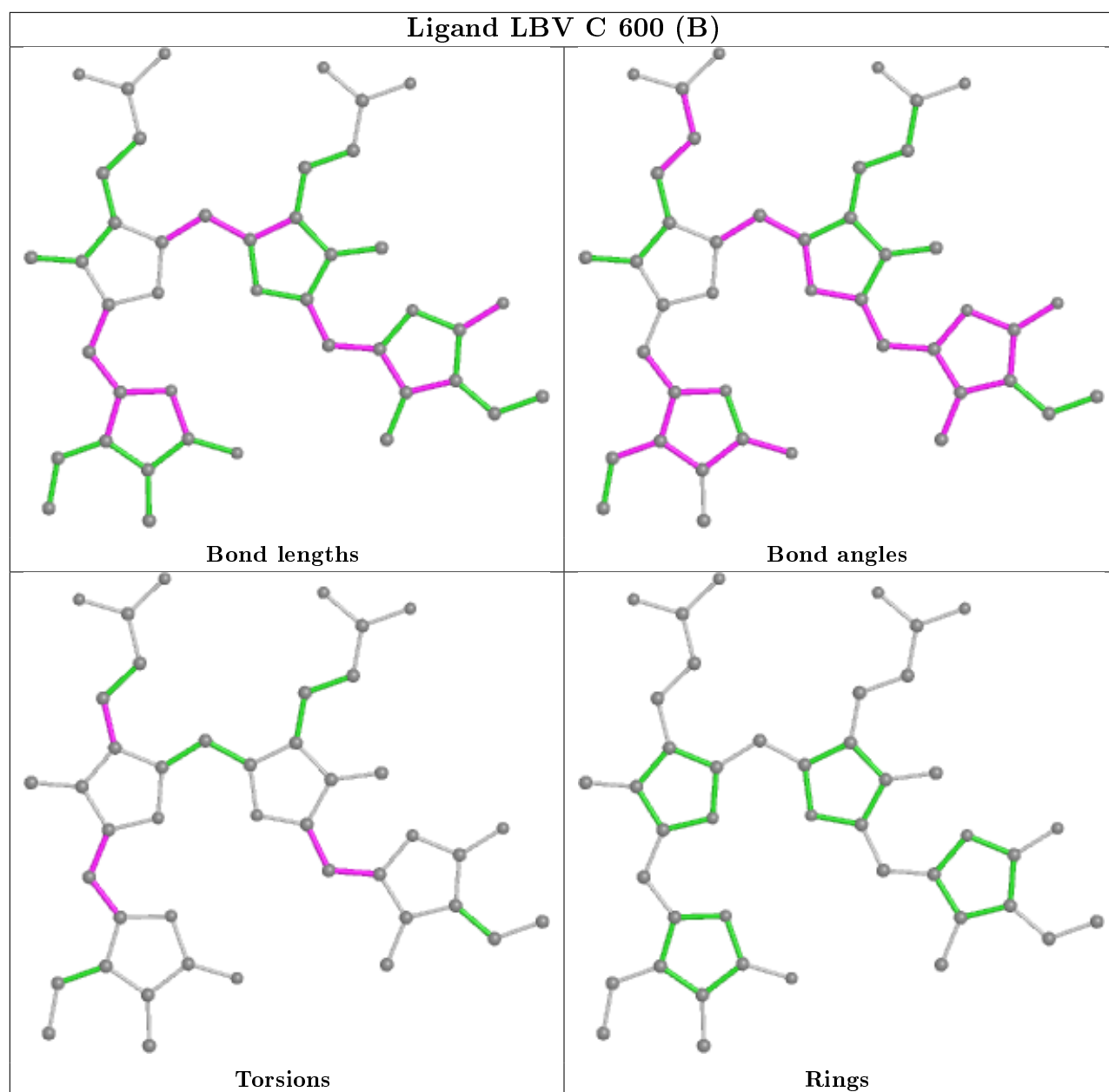
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

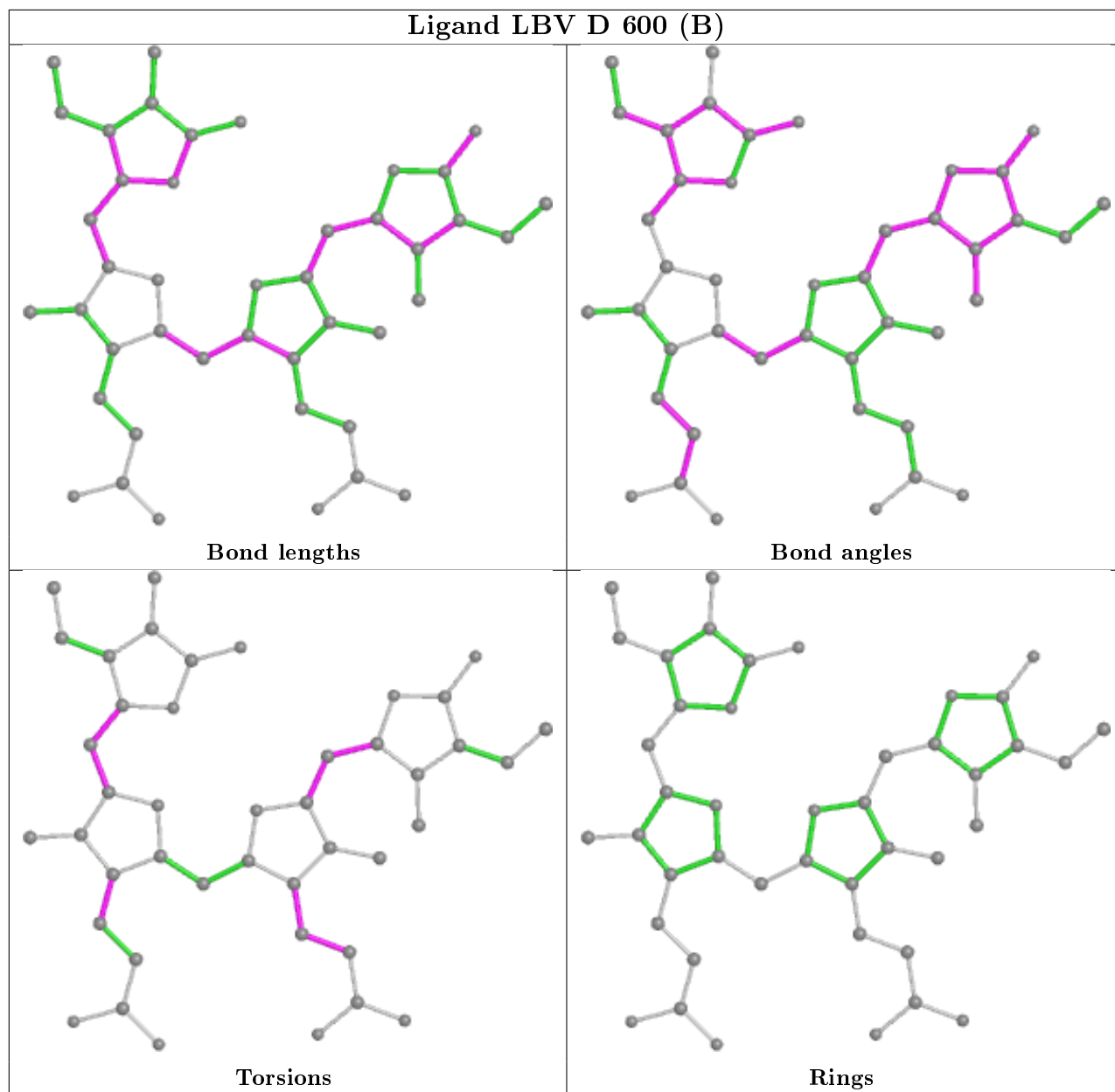


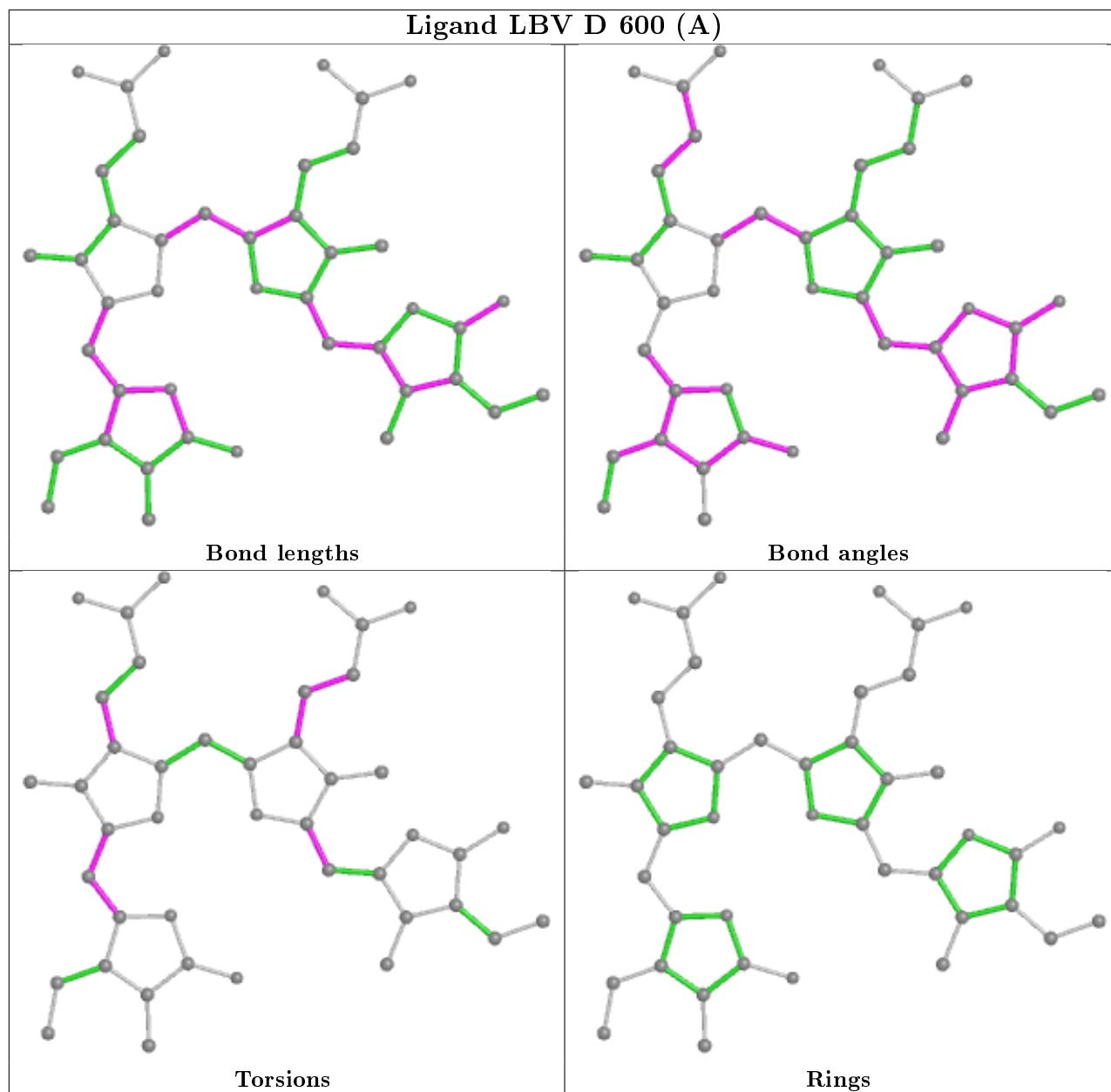


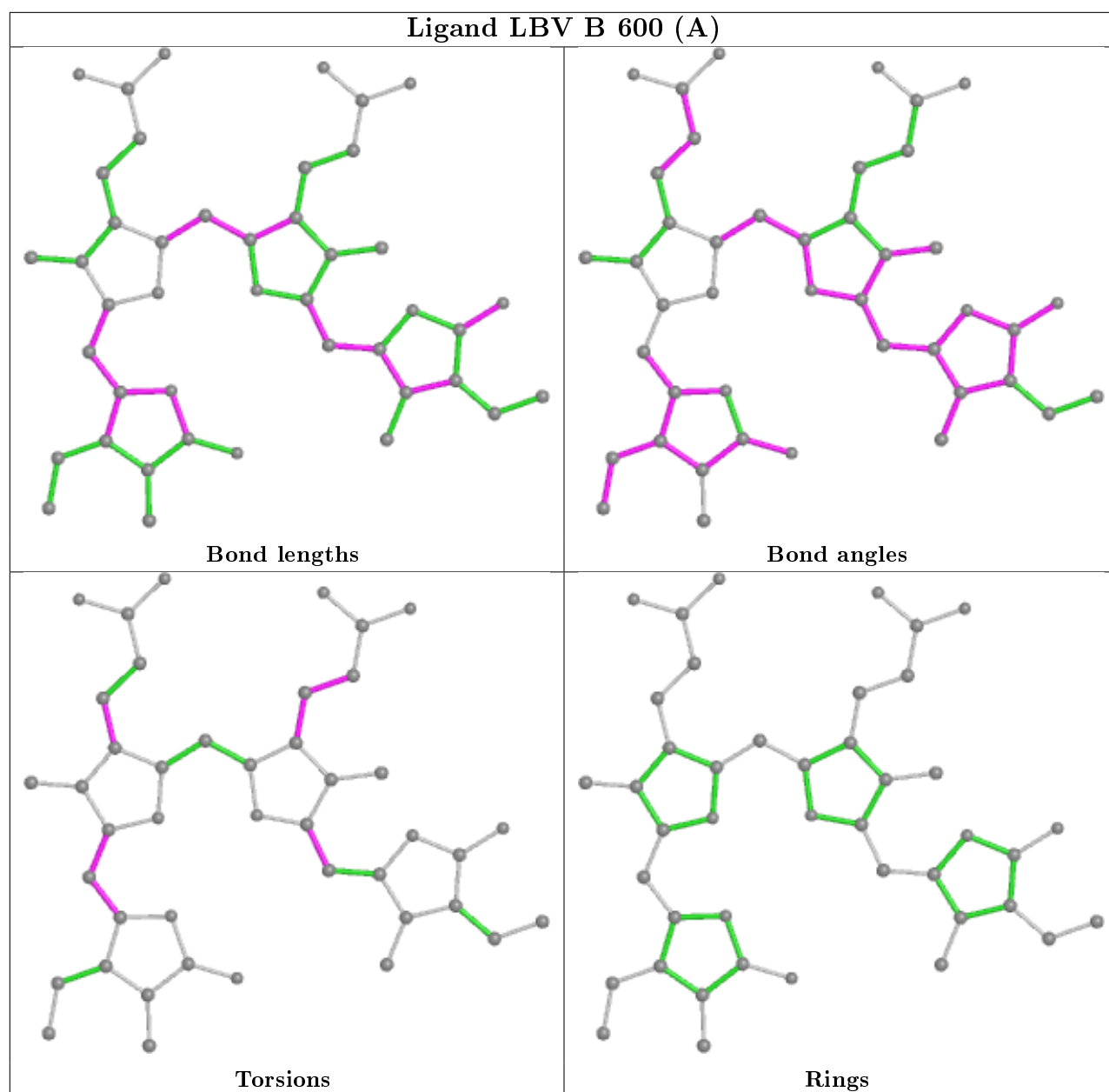












5.7 Other polymers [i](#)

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

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	483/523 (92%)	0.18	5 (1%) 82 75	88, 130, 194, 242	0
1	B	486/523 (92%)	0.13	9 (1%) 66 57	95, 135, 202, 252	0
1	C	483/523 (92%)	0.10	13 (2%) 54 42	125, 171, 212, 259	0
1	D	482/523 (92%)	0.11	11 (2%) 60 50	114, 175, 219, 265	0
All	All	1934/2092 (92%)	0.13	38 (1%) 65 54	88, 160, 210, 265	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	402	LEU	4.0
1	A	66	PRO	3.8
1	D	126	PHE	3.3
1	C	126	PHE	3.3
1	C	478	GLY	3.1
1	B	67	THR	3.0
1	C	295	TYR	2.9
1	C	401	ALA	2.9
1	D	99	TYR	2.8
1	D	136	GLY	2.8
1	D	505	HIS	2.7
1	B	66	PRO	2.7
1	B	77	LEU	2.7
1	A	71	GLY	2.7
1	B	132	TRP	2.7
1	B	134	SER	2.6
1	A	440	TRP	2.6
1	A	449	VAL	2.6
1	C	438	LEU	2.6
1	C	408	LEU	2.4
1	D	401	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	136	GLY	2.3
1	D	498	LEU	2.3
1	A	428	ILE	2.2
1	C	463	LEU	2.2
1	C	176	TYR	2.2
1	D	51	VAL	2.2
1	C	430	VAL	2.1
1	C	246	THR	2.1
1	C	498	LEU	2.1
1	D	447	LEU	2.1
1	D	42	LEU	2.1
1	D	198	PHE	2.1
1	C	491	ALA	2.1
1	D	44	ALA	2.1
1	B	401	ALA	2.0
1	B	359	LEU	2.0
1	C	40	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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	LBV	D	600[B]	43/43	0.85	0.51	141,179,193,205	43
2	LBV	D	600[A]	43/43	0.85	0.51	136,174,184,202	43
2	LBV	C	600[A]	43/43	0.87	0.39	133,168,193,198	43
2	LBV	C	600[B]	43/43	0.87	0.39	135,167,177,186	43
2	LBV	A	600[A]	43/43	0.90	0.32	96,109,125,138	43
2	LBV	A	600[B]	43/43	0.90	0.32	98,121,136,145	43

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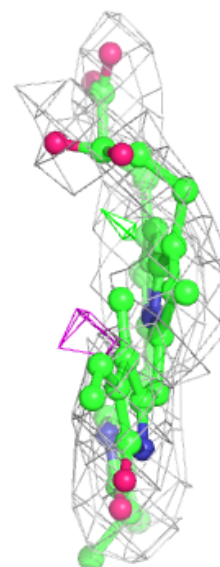
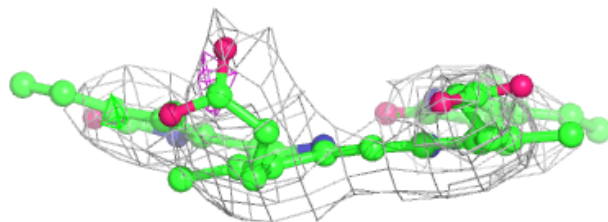
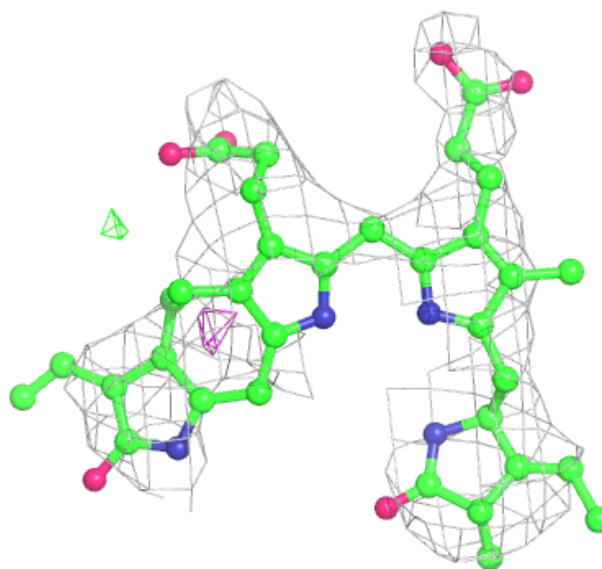
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	LBV	B	600[B]	43/43	0.91	0.35	109,125,144,151	43
2	LBV	B	600[A]	43/43	0.91	0.35	98,109,126,138	43

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.

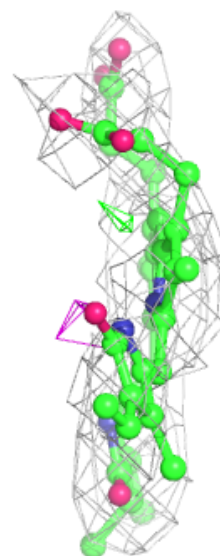
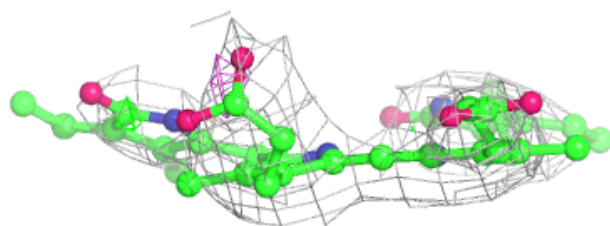
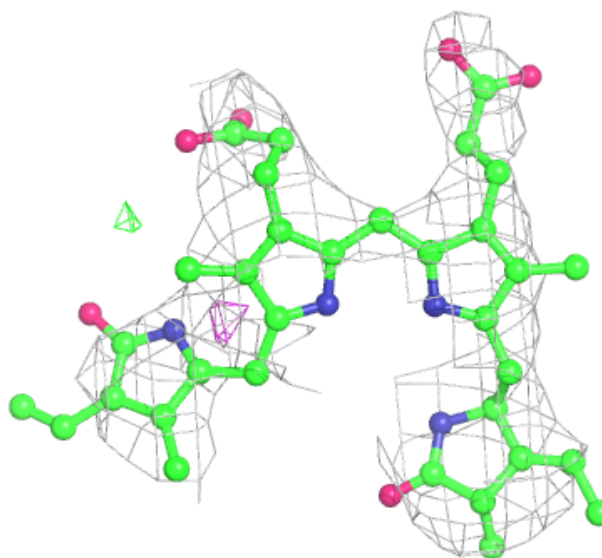
Electron density around LBV D 600 (B):

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



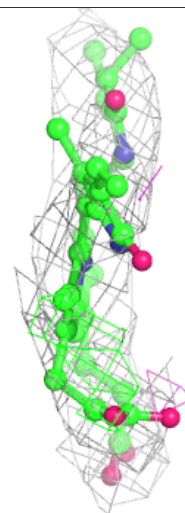
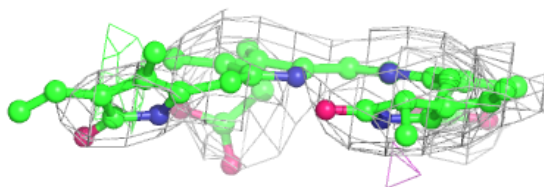
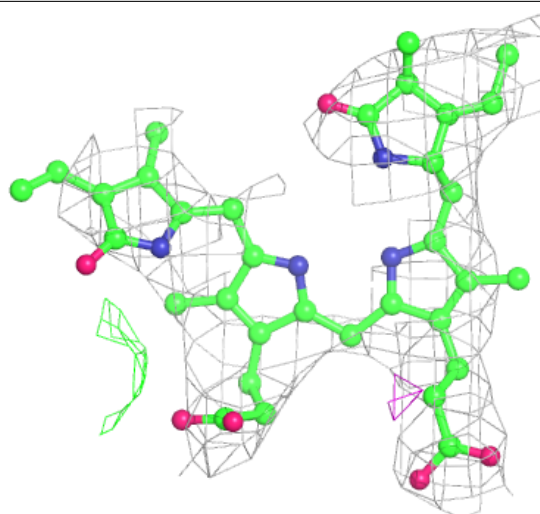
Electron density around LBV D 600 (A):

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



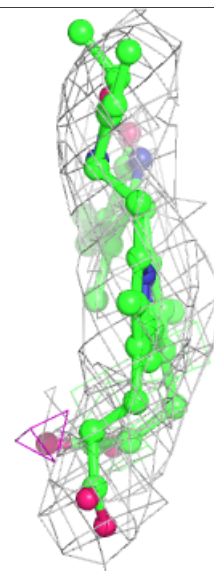
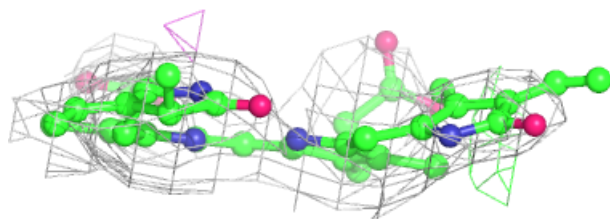
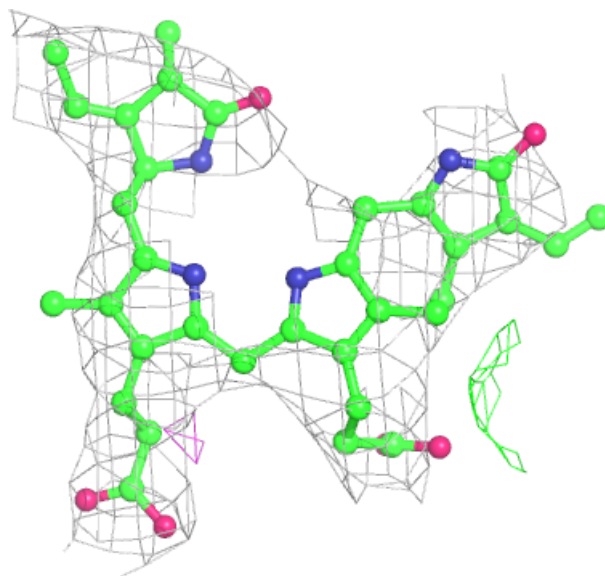
Electron density around LBV C 600 (A):

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



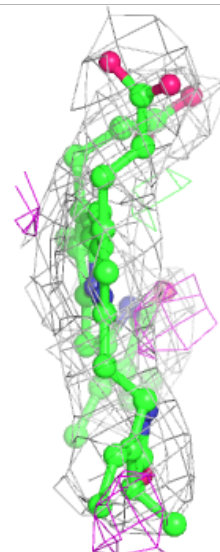
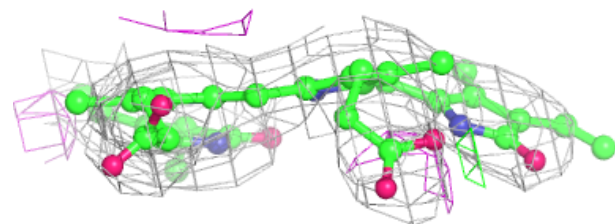
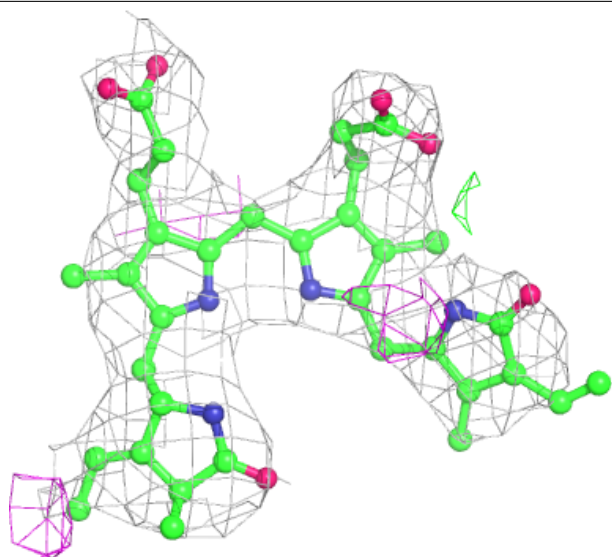
Electron density around LBV C 600 (B):

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



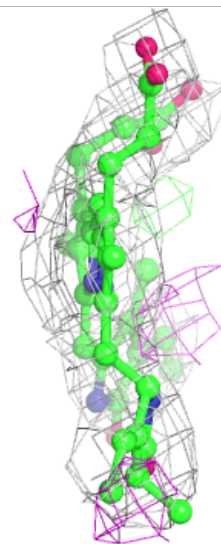
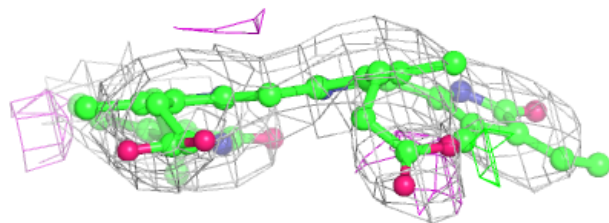
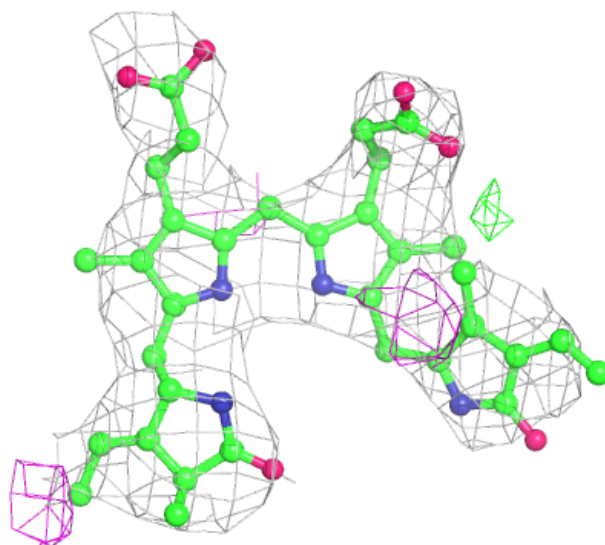
Electron density around LBV A 600 (A):

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



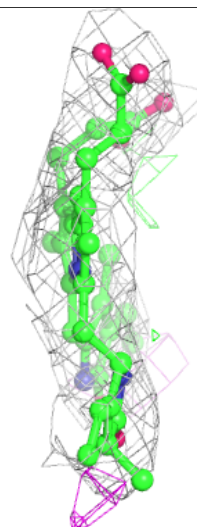
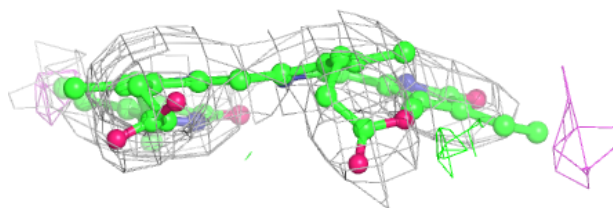
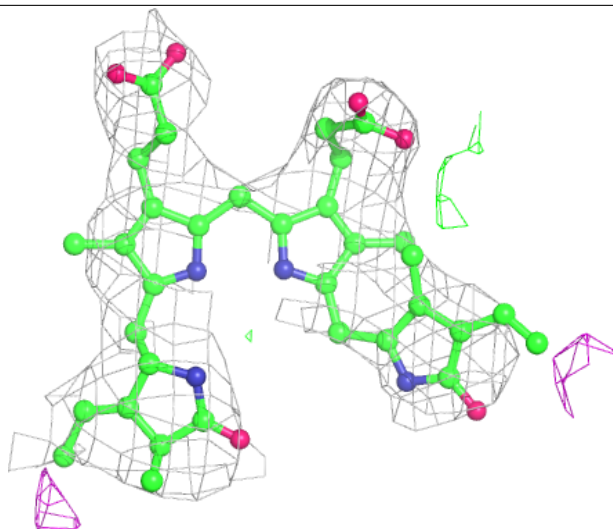
Electron density around LBV A 600 (B):

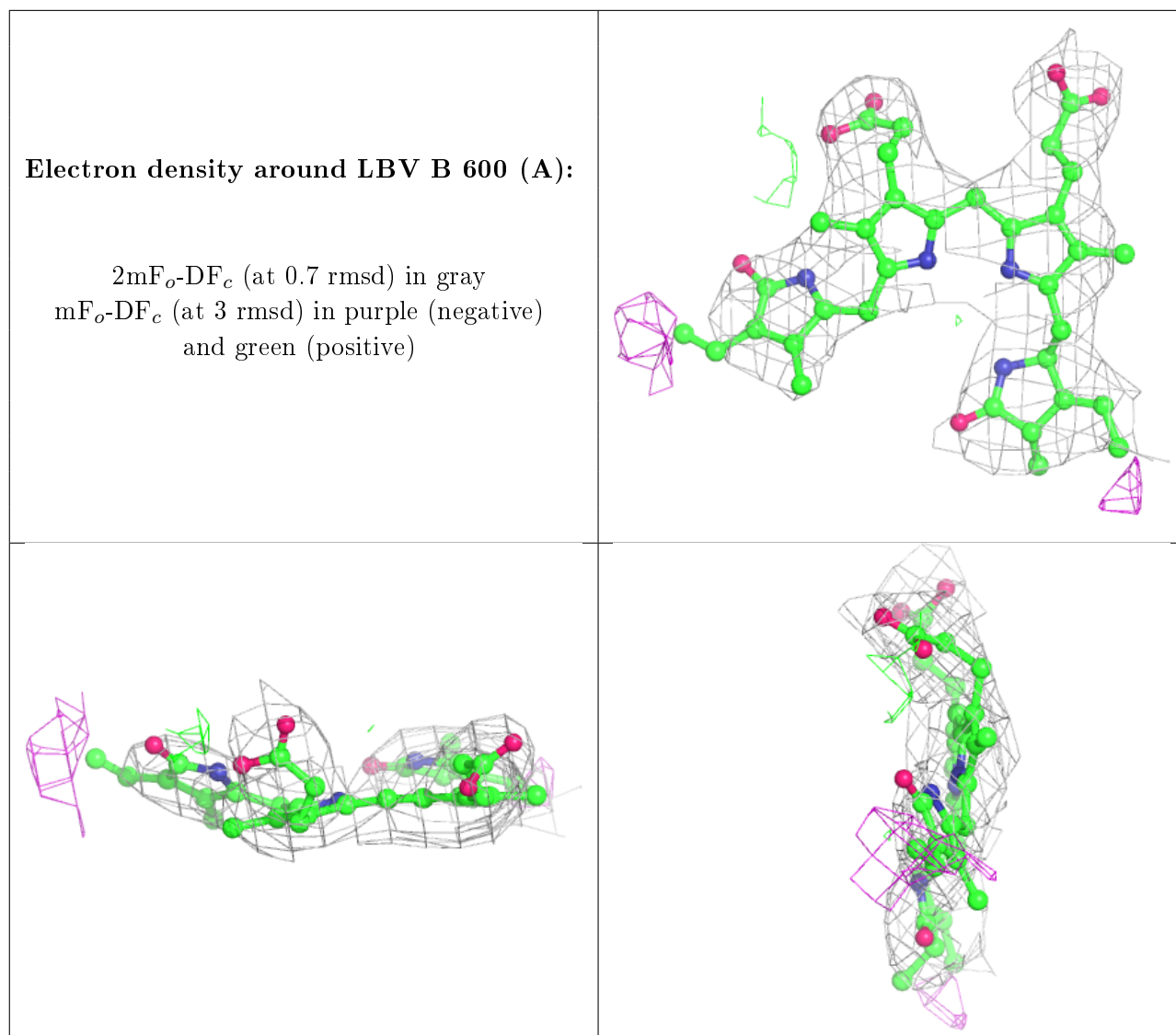
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around LBV B 600 (B):

$2mF_o-DF_c$ (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.