



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2021 – 06:34 AM EDT

PDB ID : 3BGL
Title : Hepatoselectivity of Statins: Design and synthesis of 4-sulfamoyl pyrroles as HMG-CoA reductase inhibitors
Authors : Finzel, B.C.; Pavlovsky, A.; Park, W.K.C.
Deposited on : 2007-11-26
Resolution : 2.23 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)
Xtrriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

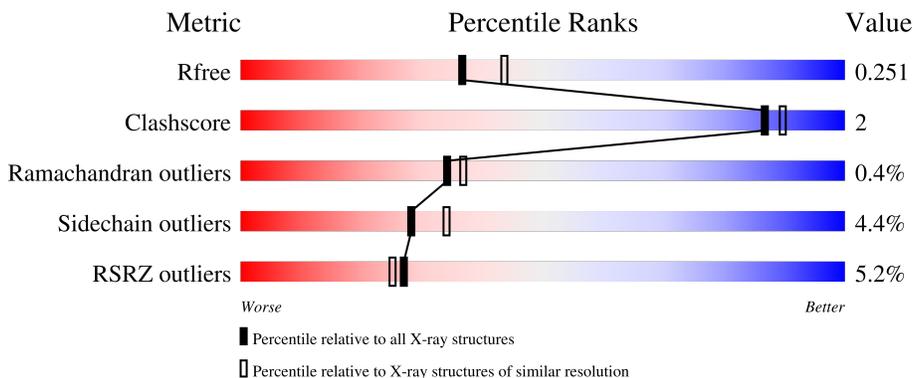
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	441	 3% 85% 9% 5%
1	B	441	 5% 87% 8% 5%
1	C	441	 9% 85% 8% 6%
1	D	441	 3% 86% 7% 7%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13232 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 3-hydroxy-3-methylglutaryl-coenzyme A reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	421	3133	1951	551	601	30	0	0	0
1	B	421	3133	1951	551	601	30	0	0	0
1	C	414	3073	1915	538	590	30	0	0	0
1	D	410	3050	1901	535	584	30	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

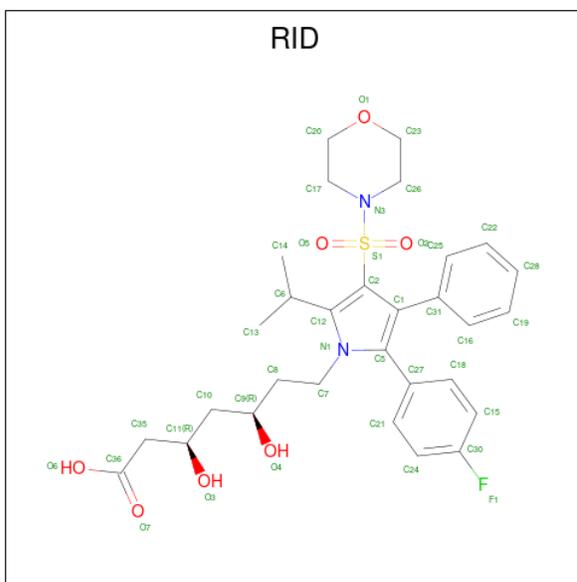
Chain	Residue	Modelled	Actual	Comment	Reference
A	435	HIS	-	expression tag	UNP P04035
A	436	HIS	-	expression tag	UNP P04035
A	437	HIS	-	expression tag	UNP P04035
A	438	HIS	-	expression tag	UNP P04035
A	439	HIS	-	expression tag	UNP P04035
A	440	HIS	-	expression tag	UNP P04035
A	485	ILE	MET	engineered mutation	UNP P04035
B	435	HIS	-	expression tag	UNP P04035
B	436	HIS	-	expression tag	UNP P04035
B	437	HIS	-	expression tag	UNP P04035
B	438	HIS	-	expression tag	UNP P04035
B	439	HIS	-	expression tag	UNP P04035
B	440	HIS	-	expression tag	UNP P04035
B	485	ILE	MET	engineered mutation	UNP P04035
C	435	HIS	-	expression tag	UNP P04035
C	436	HIS	-	expression tag	UNP P04035
C	437	HIS	-	expression tag	UNP P04035
C	438	HIS	-	expression tag	UNP P04035
C	439	HIS	-	expression tag	UNP P04035
C	440	HIS	-	expression tag	UNP P04035
C	485	ILE	MET	engineered mutation	UNP P04035

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Chain	Residue	Modelled	Actual	Comment	Reference
D	435	HIS	-	expression tag	UNP P04035
D	436	HIS	-	expression tag	UNP P04035
D	437	HIS	-	expression tag	UNP P04035
D	438	HIS	-	expression tag	UNP P04035
D	439	HIS	-	expression tag	UNP P04035
D	440	HIS	-	expression tag	UNP P04035
D	485	ILE	MET	engineered mutation	UNP P04035

- Molecule 2 is (3R,5R)-7-[2-(4-fluorophenyl)-5-(1-methylethyl)-4-(morpholin-4-ylsulfonyl)-3-phenyl-1H-pyrrol-1-yl]-3,5-dihydroxyheptanoic acid (three-letter code: RID) (formula: C₃₀H₃₇FN₂O₇S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
2	A	1	Total	C	F	N	O	S	0	0
			41	30	1	2	7	1		
2	B	1	Total	C	F	N	O	S	0	0
			41	30	1	2	7	1		
2	C	1	Total	C	F	N	O	S	0	0
			41	30	1	2	7	1		
2	D	1	Total	C	F	N	O	S	0	0
			41	30	1	2	7	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	191	Total	O	0	0
			191	191		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	169	Total 169	O 169	0	0
3	C	134	Total 134	O 134	0	0
3	D	185	Total 185	O 185	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.59Å 172.16Å 75.15Å 90.00° 117.24° 90.00°	Depositor
Resolution (Å)	30.00 – 2.23 29.85 – 2.23	Depositor EDS
% Data completeness (in resolution range)	82.2 (30.00-2.23) 82.2 (29.85-2.23)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.22Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.208 , 0.251 0.208 , 0.251	Depositor DCC
R_{free} test set	3345 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	26.2	Xtrriage
Anisotropy	0.843	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.031 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13232	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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:
RID

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	0.34	0/3179	0.62	4/4298 (0.1%)
1	B	0.34	0/3179	0.61	6/4298 (0.1%)
1	C	0.35	0/3116	0.60	7/4211 (0.2%)
1	D	0.34	0/3094	0.62	5/4182 (0.1%)
All	All	0.34	0/12568	0.61	22/16989 (0.1%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	790	ASP	CB-CG-OD2	5.96	123.66	118.30
1	C	601	ASP	CB-CG-OD2	5.78	123.50	118.30
1	B	547	ASP	CB-CG-OD2	5.64	123.38	118.30
1	A	547	ASP	CB-CG-OD2	5.62	123.36	118.30
1	D	653	ASP	CB-CG-OD2	5.57	123.31	118.30
1	B	829	ASP	CB-CG-OD2	5.56	123.30	118.30
1	A	623	ASP	CB-CG-OD2	5.52	123.27	118.30
1	D	516	ASP	CB-CG-OD2	5.50	123.25	118.30
1	D	601	ASP	CB-CG-OD2	5.36	123.13	118.30
1	B	516	ASP	CB-CG-OD2	5.36	123.12	118.30
1	B	623	ASP	CB-CG-OD2	5.27	123.04	118.30
1	C	690	ASP	CB-CG-OD2	5.26	123.03	118.30
1	C	547	ASP	CB-CG-OD2	5.23	123.00	118.30
1	A	516	ASP	CB-CG-OD2	5.22	123.00	118.30
1	D	623	ASP	CB-CG-OD2	5.20	122.98	118.30
1	C	790	ASP	CB-CG-OD2	5.19	122.97	118.30
1	C	623	ASP	CB-CG-OD2	5.17	122.96	118.30
1	C	829	ASP	CB-CG-OD2	5.16	122.94	118.30
1	B	653	ASP	CB-CG-OD2	5.12	122.91	118.30
1	D	829	ASP	CB-CG-OD2	5.11	122.90	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	653	ASP	CB-CG-OD2	5.11	122.90	118.30
1	C	653	ASP	CB-CG-OD2	5.07	122.86	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3133	0	3167	15	0
1	B	3133	0	3167	15	0
1	C	3073	0	3110	15	0
1	D	3050	0	3088	9	0
2	A	41	0	36	2	0
2	B	41	0	36	3	0
2	C	41	0	36	2	0
2	D	41	0	36	3	0
3	A	191	0	0	0	0
3	B	169	0	0	1	0
3	C	134	0	0	1	0
3	D	185	0	0	0	0
All	All	13232	0	12676	54	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 2.

All (54) 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:B:655:MET:SD	1:B:657:MET:HG3	2.42	0.59
1:A:655:MET:SD	1:A:657:MET:HG3	2.44	0.58
1:B:441:GLU:N	1:B:442:PRO:CD	2.68	0.56
1:A:472:ASN:O	1:A:473:ALA:HB3	2.07	0.54
2:A:2:RID:H13B	2:A:2:RID:O2	2.09	0.53
1:A:477:PRO:O	1:A:478:ALA:HB2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:448:CYS:HB3	1:D:462:LEU:HD22	1.91	0.53
1:B:590:ARG:HD2	3:B:989:HOH:O	2.09	0.52
1:C:596:LEU:HD13	1:C:602:SER:HA	1.93	0.51
1:A:581:SER:OG	1:A:840:ARG:HD2	2.12	0.50
1:B:555:MET:HE3	1:B:563:VAL:HG22	1.93	0.50
1:A:771:ASN:OD1	1:A:775:SER:OG	2.30	0.50
1:B:449:LEU:HD11	1:B:475:HIS:ND1	2.27	0.49
1:C:561:CYS:HB2	2:D:3:RID:C14	2.43	0.49
1:A:518:ASN:ND2	1:A:520:SER:OG	2.44	0.48
1:B:441:GLU:N	1:B:442:PRO:HD3	2.28	0.48
1:C:651:SER:HA	1:C:659:MET:HE3	1.96	0.48
1:D:752:HIS:CD2	1:D:853:LEU:HD23	2.50	0.47
1:C:468:ILE:HG22	1:C:468:ILE:O	2.13	0.47
1:C:771:ASN:OD1	1:C:775:SER:OG	2.33	0.46
1:B:712:ILE:HG13	1:B:851:LEU:HD11	1.98	0.46
2:B:1:RID:O2	2:B:1:RID:H14B	2.16	0.45
1:A:474:LYS:O	1:A:475:HIS:CB	2.64	0.45
1:A:551:PHE:CE2	1:A:841:ILE:HD11	2.52	0.45
1:C:561:CYS:HB2	2:D:3:RID:H14B	1.98	0.44
1:D:765:GLY:CA	1:D:814:GLN:HG2	2.48	0.44
1:A:561:CYS:HB2	2:B:1:RID:C14	2.48	0.44
1:C:819:GLN:HB3	1:D:508:SER:HB3	1.99	0.44
2:A:2:RID:C14	1:B:561:CYS:HB2	2.48	0.44
2:D:3:RID:O2	2:D:3:RID:H13B	2.16	0.44
1:B:638:ILE:O	1:C:796:THR:HG21	2.16	0.44
1:C:752:HIS:CD2	1:C:853:LEU:HD23	2.52	0.44
1:A:474:LYS:O	1:A:475:HIS:HB2	2.17	0.44
1:B:541:ALA:HB2	1:B:555:MET:HE1	2.00	0.44
1:A:796:THR:HG21	1:D:638:ILE:O	2.18	0.44
1:B:765:GLY:HA2	1:B:814:GLN:HG2	2.00	0.44
1:A:638:ILE:O	1:D:796:THR:HG21	2.18	0.43
1:B:541:ALA:HB2	1:B:555:MET:CE	2.49	0.42
2:C:4:RID:O2	2:C:4:RID:H14B	2.18	0.42
1:B:738:VAL:O	1:B:742:MET:HG2	2.19	0.42
1:B:460:LYS:HB2	1:B:486:GLU:HG2	2.00	0.42
1:C:608:TRP:CZ2	1:C:674:TYR:CD2	3.08	0.41
1:C:659:MET:SD	1:C:660:ILE:HD12	2.60	0.41
1:C:752:HIS:CD2	1:C:853:LEU:CD2	3.02	0.41
2:C:4:RID:O2	2:C:4:RID:H13B	2.20	0.41
1:A:861:HIS:HA	2:B:1:RID:H28	2.02	0.41
1:C:765:GLY:HA2	1:C:814:GLN:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:741:ALA:HB1	1:D:749:TYR:CE1	2.56	0.41
1:C:523:MET:CE	3:C:919:HOH:O	2.67	0.41
1:D:765:GLY:HA2	1:D:814:GLN:HG2	2.03	0.41
1:C:691:LYS:HZ3	1:C:767:ASP:CG	2.24	0.41
1:A:472:ASN:O	1:A:473:ALA:CB	2.69	0.40
1:A:846:VAL:O	1:A:850:GLU:HG2	2.21	0.40
1:D:702:ARG:O	1:D:799:SER:HA	2.22	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	419/441 (95%)	395 (94%)	19 (4%)	5 (1%)	13 9
1	B	419/441 (95%)	402 (96%)	17 (4%)	0	100 100
1	C	410/441 (93%)	390 (95%)	19 (5%)	1 (0%)	47 54
1	D	406/441 (92%)	392 (97%)	13 (3%)	1 (0%)	47 54
All	All	1654/1764 (94%)	1579 (96%)	68 (4%)	7 (0%)	34 37

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	474	LYS
1	A	786	PRO
1	A	475	HIS
1	A	478	ALA
1	C	514	TYR
1	D	525	ALA
1	A	477	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	335/355 (94%)	316 (94%)	19 (6%)	20	23
1	B	335/355 (94%)	321 (96%)	14 (4%)	30	36
1	C	329/355 (93%)	317 (96%)	12 (4%)	35	43
1	D	327/355 (92%)	314 (96%)	13 (4%)	31	38
All	All	1326/1420 (93%)	1268 (96%)	58 (4%)	28	34

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	441	GLU
1	A	443	ARG
1	A	449	LEU
1	A	467	ILE
1	A	470	LEU
1	A	486	GLU
1	A	498	LEU
1	A	512	LEU
1	A	515	ARG
1	A	630	ARG
1	A	638	ILE
1	A	649	SER
1	A	657	MET
1	A	669	SER
1	A	688	CYS
1	A	704	LYS
1	A	787	THR
1	A	788	ASN
1	A	814	GLN
1	B	446	GLU
1	B	447	GLU
1	B	452	LEU
1	B	482	GLU
1	B	486	GLU

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Mol	Chain	Res	Type
1	B	505	GLU
1	B	523	MET
1	B	633	LYS
1	B	659	MET
1	B	679	GLN
1	B	688	CYS
1	B	752	HIS
1	B	828	LYS
1	B	851	LEU
1	C	447	GLU
1	C	449	LEU
1	C	452	LEU
1	C	486	GLU
1	C	487	THR
1	C	523	MET
1	C	596	LEU
1	C	612	SER
1	C	638	ILE
1	C	681	LEU
1	C	688	CYS
1	C	828	LYS
1	D	448	CYS
1	D	469	GLN
1	D	470	LEU
1	D	482	GLU
1	D	487	THR
1	D	518	ASN
1	D	613	GLU
1	D	633	LYS
1	D	657	MET
1	D	688	CYS
1	D	791	LEU
1	D	828	LYS
1	D	851	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	488	HIS
1	A	518	ASN
1	A	567	ASN
1	A	632	GLN

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Mol	Chain	Res	Type
1	A	788	ASN
1	B	472	ASN
1	B	510	GLN
1	B	529	ASN
1	B	632	GLN
1	B	819	GLN
1	C	497	GLN
1	C	632	GLN
1	C	635	HIS
1	C	672	HIS
1	D	472	ASN
1	D	497	GLN
1	D	518	ASN
1	D	642	ASN
1	D	815	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	RID	D	3	-	37,44,44	1.88	3 (8%)	50,63,63	2.09	11 (22%)
2	RID	A	2	-	37,44,44	1.90	4 (10%)	50,63,63	1.72	8 (16%)
2	RID	C	4	-	37,44,44	1.91	3 (8%)	50,63,63	2.72	11 (22%)
2	RID	B	1	-	37,44,44	1.83	3 (8%)	50,63,63	2.11	14 (28%)

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	RID	D	3	-	-	11/29/45/45	0/4/4/4
2	RID	A	2	-	-	11/29/45/45	0/4/4/4
2	RID	C	4	-	-	8/29/45/45	0/4/4/4
2	RID	B	1	-	-	10/29/45/45	0/4/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	4	RID	C2-S1	-7.89	1.66	1.79
2	A	2	RID	S1-N3	-7.73	1.52	1.63
2	D	3	RID	C2-S1	-7.70	1.66	1.79
2	B	1	RID	C2-S1	-7.44	1.67	1.79
2	C	4	RID	S1-N3	-7.43	1.52	1.63
2	A	2	RID	C2-S1	-7.34	1.67	1.79
2	D	3	RID	S1-N3	-7.17	1.53	1.63
2	B	1	RID	S1-N3	-7.10	1.53	1.63
2	D	3	RID	C1-C5	2.35	1.46	1.40
2	C	4	RID	C1-C5	2.27	1.46	1.40
2	A	2	RID	C1-C5	2.19	1.46	1.40
2	A	2	RID	C12-C2	2.17	1.42	1.39
2	B	1	RID	C12-C2	2.08	1.42	1.39

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	RID	C26-N3-C17	10.89	124.22	112.17
2	C	4	RID	C20-C17-N3	9.22	113.61	108.18
2	D	3	RID	O2-S1-O5	-7.40	107.53	119.52
2	C	4	RID	O2-S1-O5	-7.12	107.99	119.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	RID	O2-S1-O5	-6.50	108.99	119.52
2	B	1	RID	C26-N3-C17	6.36	119.20	112.17
2	D	3	RID	C26-N3-C17	6.16	118.98	112.17
2	A	2	RID	O2-S1-O5	-6.02	109.76	119.52
2	A	2	RID	C26-N3-C17	4.87	117.56	112.17
2	D	3	RID	C23-C26-N3	4.21	110.66	108.18
2	B	1	RID	O5-S1-N3	4.19	110.50	106.69
2	C	4	RID	C2-S1-N3	3.97	111.67	103.46
2	B	1	RID	C5-N1-C12	3.82	111.29	108.78
2	A	2	RID	C2-S1-N3	3.65	111.01	103.46
2	C	4	RID	C7-C8-C9	-3.44	106.22	113.31
2	A	2	RID	C1-C5-C27	-3.43	119.21	128.64
2	B	1	RID	C21-C27-C5	-3.34	114.62	120.47
2	C	4	RID	C21-C27-C5	-3.19	114.88	120.47
2	D	3	RID	C5-N1-C12	3.19	110.87	108.78
2	C	4	RID	C1-C5-C27	-3.18	119.88	128.64
2	D	3	RID	C1-C5-C27	-2.98	120.44	128.64
2	D	3	RID	O5-S1-N3	2.97	109.40	106.69
2	B	1	RID	C7-C8-C9	-2.96	107.20	113.31
2	D	3	RID	C7-C8-C9	-2.94	107.24	113.31
2	D	3	RID	C2-S1-N3	2.78	109.21	103.46
2	B	1	RID	C2-S1-N3	2.75	109.15	103.46
2	B	1	RID	C11-C10-C9	-2.73	110.03	114.18
2	B	1	RID	C1-C5-C27	-2.71	121.19	128.64
2	D	3	RID	C21-C27-C5	-2.52	116.06	120.47
2	B	1	RID	C7-N1-C5	-2.51	120.85	124.83
2	A	2	RID	C21-C27-C5	-2.49	116.12	120.47
2	C	4	RID	C5-N1-C12	2.48	110.41	108.78
2	B	1	RID	C23-C26-N3	2.47	109.64	108.18
2	B	1	RID	C18-C27-C5	2.47	124.80	120.47
2	C	4	RID	C10-C11-C35	-2.41	108.39	113.19
2	D	3	RID	C10-C11-C35	-2.36	108.49	113.19
2	B	1	RID	O2-S1-C2	2.36	112.71	108.18
2	C	4	RID	O5-S1-N3	2.29	108.78	106.69
2	A	2	RID	O5-S1-N3	2.21	108.70	106.69
2	B	1	RID	C20-C17-N3	2.18	109.46	108.18
2	C	4	RID	C18-C27-C5	2.18	124.29	120.47
2	A	2	RID	C11-C10-C9	-2.15	110.91	114.18
2	A	2	RID	C5-N1-C12	2.14	110.18	108.78
2	D	3	RID	C10-C9-C8	-2.05	108.10	112.51

There are no chirality outliers.

All (40) torsion outliers are listed below:

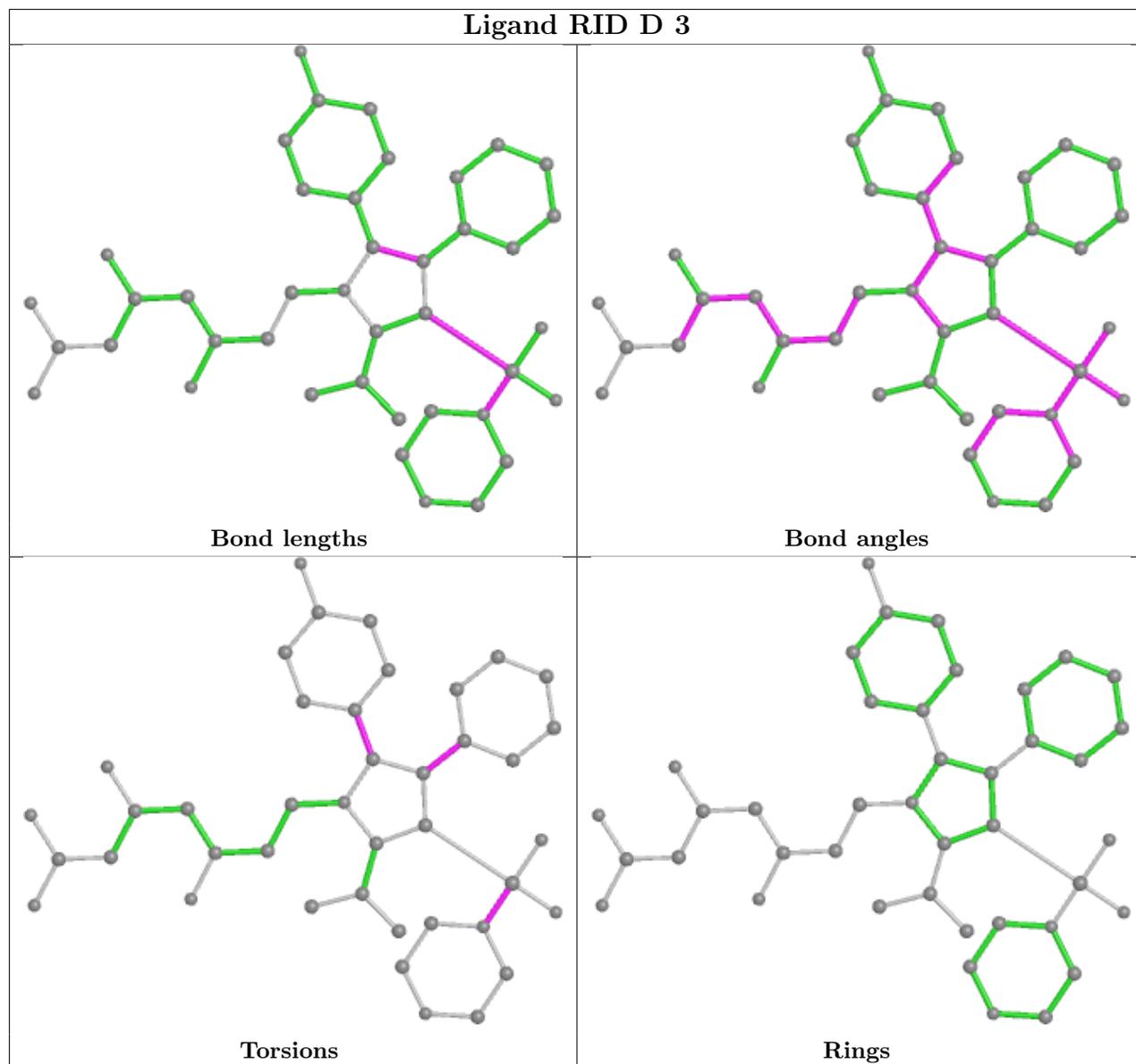
Mol	Chain	Res	Type	Atoms
2	A	2	RID	C21-C27-C5-N1
2	A	2	RID	C18-C27-C5-N1
2	D	3	RID	C26-N3-S1-O2
2	D	3	RID	C26-N3-S1-C2
2	D	3	RID	C26-N3-S1-O5
2	A	2	RID	C26-N3-S1-O2
2	B	1	RID	C17-N3-S1-O2
2	B	1	RID	C17-N3-S1-C2
2	C	4	RID	C26-N3-S1-O2
2	C	4	RID	C26-N3-S1-C2
2	A	2	RID	C26-N3-S1-C2
2	C	4	RID	C26-N3-S1-O5
2	A	2	RID	C18-C27-C5-C1
2	A	2	RID	C21-C27-C5-C1
2	B	1	RID	C17-N3-S1-O5
2	B	1	RID	C7-C8-C9-O4
2	B	1	RID	C7-C8-C9-C10
2	C	4	RID	C2-C1-C31-C25
2	B	1	RID	C2-C1-C31-C25
2	D	3	RID	C2-C1-C31-C16
2	D	3	RID	C18-C27-C5-C1
2	B	1	RID	C2-C1-C31-C16
2	D	3	RID	C21-C27-C5-C1
2	A	2	RID	C2-C1-C31-C25
2	C	4	RID	C2-C1-C31-C16
2	D	3	RID	C2-C1-C31-C25
2	C	4	RID	C18-C27-C5-C1
2	A	2	RID	C5-C1-C31-C16
2	D	3	RID	C18-C27-C5-N1
2	D	3	RID	C5-C1-C31-C25
2	D	3	RID	C5-C1-C31-C16
2	A	2	RID	C17-N3-S1-O2
2	B	1	RID	C18-C27-C5-C1
2	B	1	RID	C5-C1-C31-C25
2	B	1	RID	C5-C1-C31-C16
2	A	2	RID	C2-C1-C31-C16
2	C	4	RID	C5-C1-C31-C25
2	C	4	RID	C5-C1-C31-C16
2	D	3	RID	C17-N3-S1-O5
2	A	2	RID	C5-C1-C31-C25

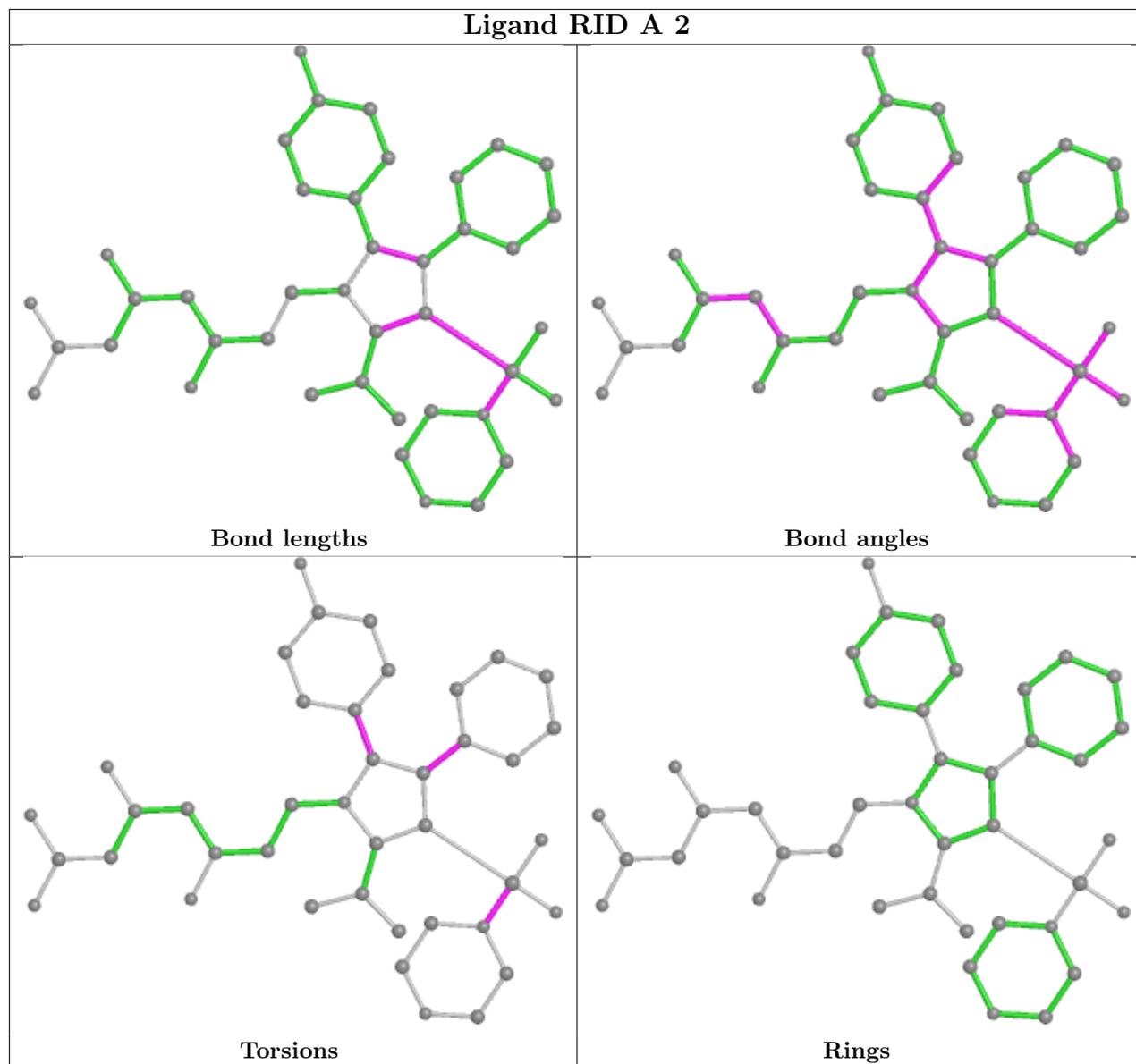
There are no ring outliers.

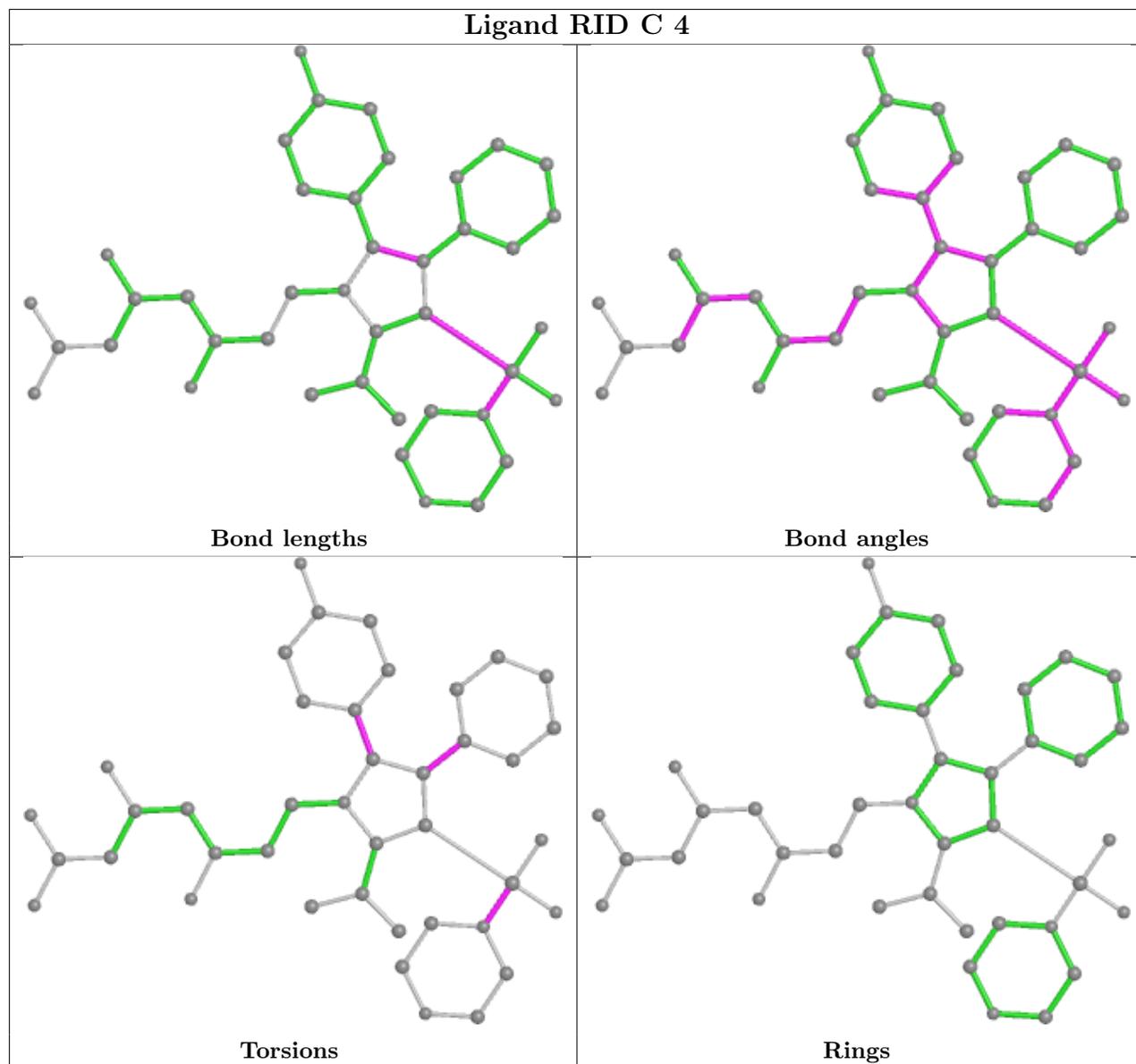
4 monomers are involved in 10 short contacts:

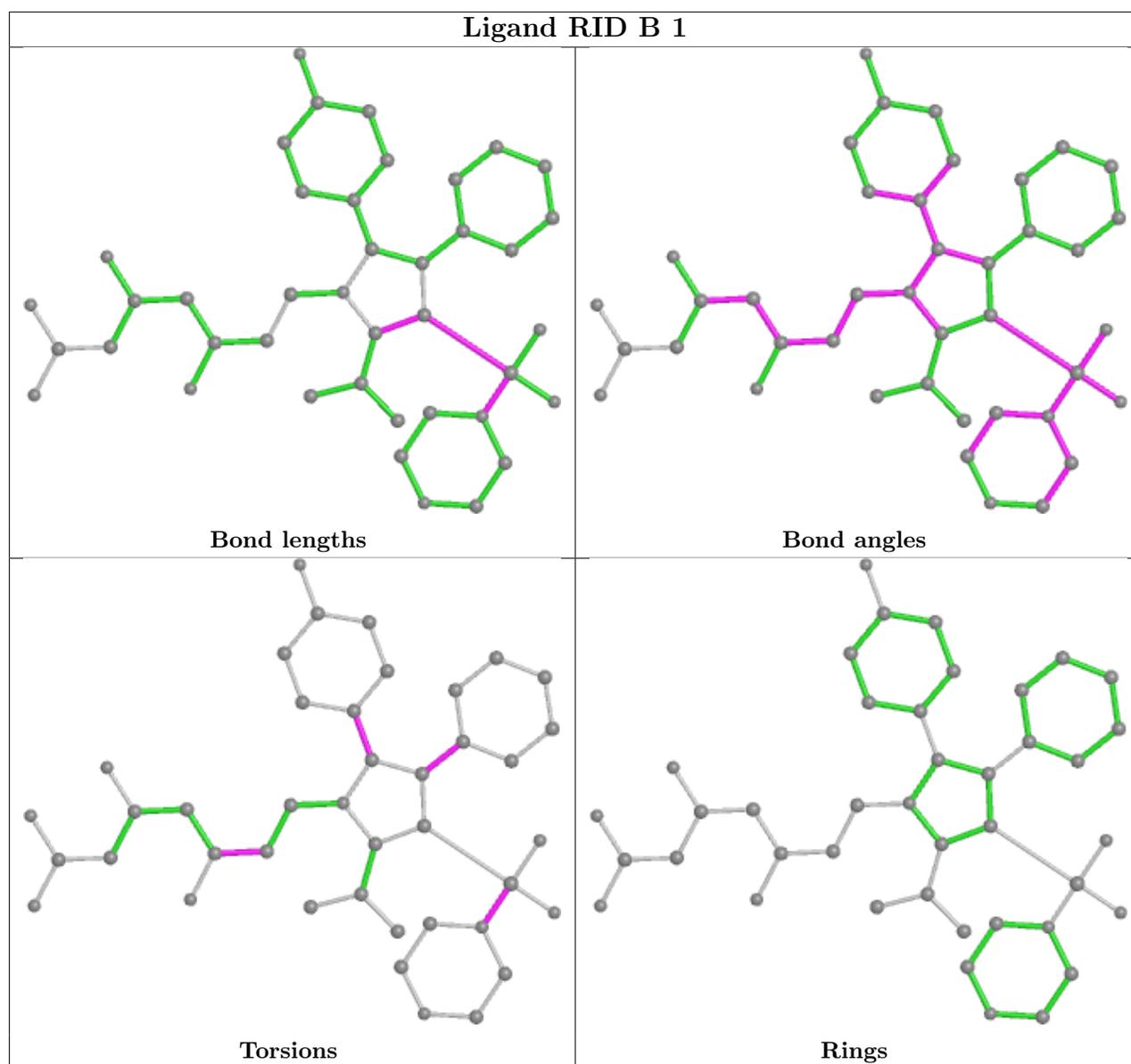
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	3	RID	3	0
2	A	2	RID	2	0
2	C	4	RID	2	0
2	B	1	RID	3	0

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	421/441 (95%)	-0.00	12 (2%) 51 49	22, 33, 46, 54	0
1	B	421/441 (95%)	0.16	22 (5%) 27 25	24, 34, 58, 64	0
1	C	414/441 (93%)	0.45	39 (9%) 8 7	24, 33, 65, 68	0
1	D	410/441 (92%)	0.05	14 (3%) 45 43	20, 33, 50, 64	0
All	All	1666/1764 (94%)	0.16	87 (5%) 27 25	20, 33, 54, 68	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	481	LEU	9.9
1	C	448	CYS	9.4
1	C	476	ILE	9.2
1	C	472	ASN	8.4
1	C	475	HIS	7.8
1	C	484	LEU	7.4
1	C	479	TYR	7.2
1	C	452	LEU	6.6
1	C	478	ALA	6.6
1	C	461	PHE	6.3
1	C	473	ALA	6.2
1	C	483	THR	6.1
1	C	458	GLY	6.1
1	C	447	GLU	6.1
1	C	446	GLU	6.0
1	B	861	HIS	6.0
1	C	454	ASN	5.9
1	C	444	PRO	5.6
1	C	453	GLY	5.4
1	C	450	GLN	5.4
1	D	461	PHE	5.3

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Mol	Chain	Res	Type	RSRZ
1	C	474	LYS	5.2
1	C	480	LYS	5.0
1	C	468	ILE	5.0
1	B	479	TYR	4.6
1	C	449	LEU	4.6
1	C	477	PRO	4.4
1	B	456	GLU	4.3
1	C	486	GLU	4.2
1	B	480	LYS	4.2
1	D	460	LYS	4.1
1	C	469	GLN	4.1
1	C	460	LYS	4.0
1	A	786	PRO	3.9
1	C	445	ASN	3.9
1	B	829	ASP	3.9
1	C	451	ILE	3.9
1	C	786	PRO	3.8
1	D	458	GLY	3.7
1	B	475	HIS	3.6
1	C	471	VAL	3.4
1	D	633	LYS	3.4
1	B	828	LYS	3.4
1	B	630	ARG	3.4
1	B	787	THR	3.3
1	B	473	ALA	3.3
1	C	828	LYS	3.2
1	C	482	GLU	3.2
1	C	462	LEU	3.2
1	A	474	LYS	3.1
1	D	828	LYS	3.1
1	B	450	GLN	3.1
1	C	459	ALA	3.1
1	D	448	CYS	3.1
1	A	787	THR	3.0
1	A	475	HIS	3.0
1	B	444	PRO	2.9
1	B	441	GLU	2.9
1	A	829	ASP	2.9
1	A	860	GLY	2.8
1	C	674	TYR	2.8
1	C	787	THR	2.8
1	C	470	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	457	LYS	2.7
1	C	465	ALA	2.7
1	D	524	GLY	2.7
1	D	484	LEU	2.6
1	D	447	GLU	2.6
1	A	524	GLY	2.5
1	B	461	PHE	2.5
1	B	483	THR	2.4
1	B	446	GLU	2.4
1	D	482	GLU	2.4
1	A	553	VAL	2.4
1	B	785	GLY	2.4
1	A	477	PRO	2.3
1	B	454	ASN	2.3
1	D	829	ASP	2.3
1	D	627	ARG	2.2
1	A	441	GLU	2.2
1	B	470	LEU	2.1
1	B	657	MET	2.1
1	A	473	ALA	2.1
1	D	479	TYR	2.1
1	B	484	LEU	2.1
1	D	672	HIS	2.0
1	A	446	GLU	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](#)

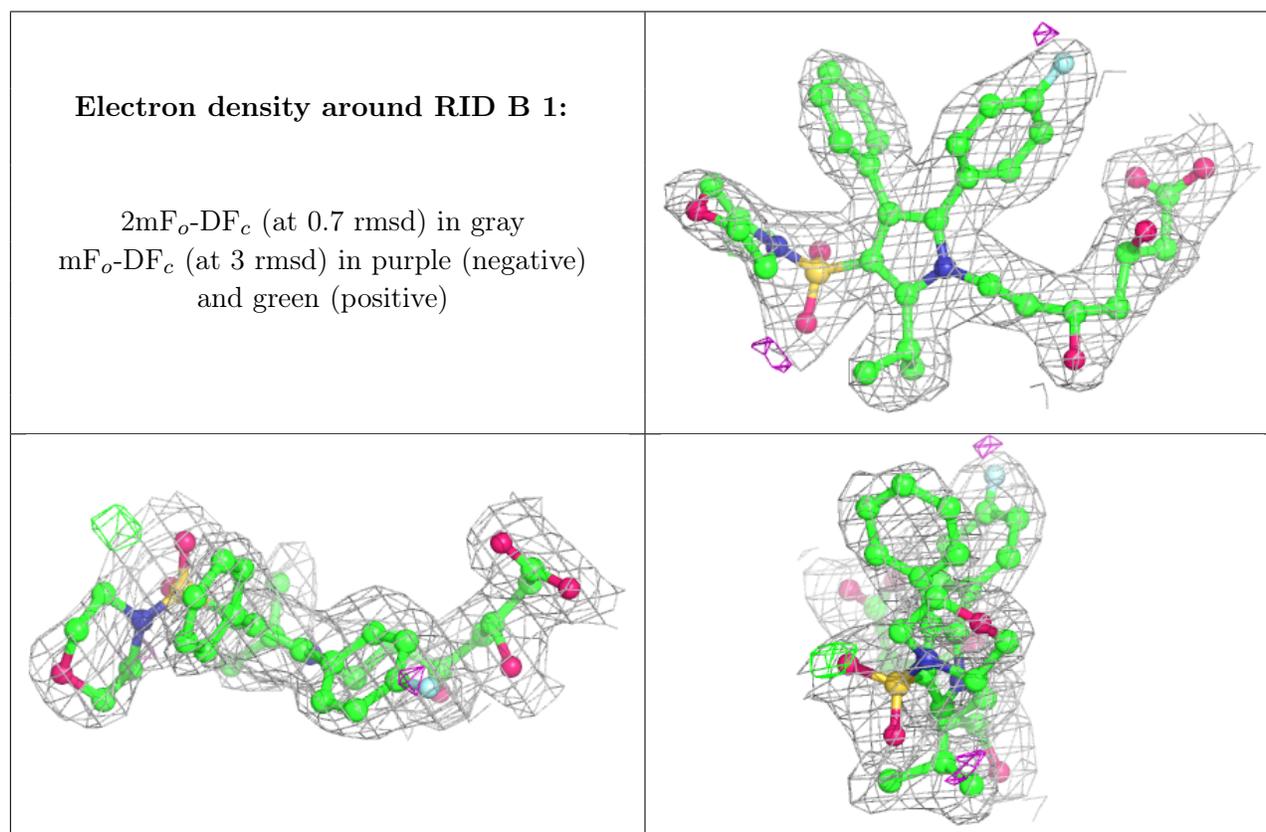
There are no monosaccharides in this entry.

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, 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.

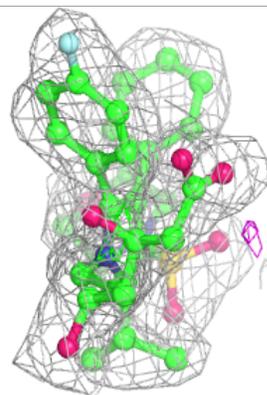
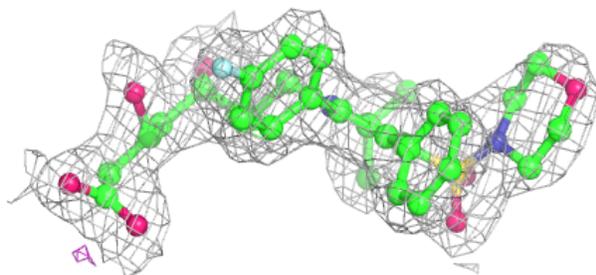
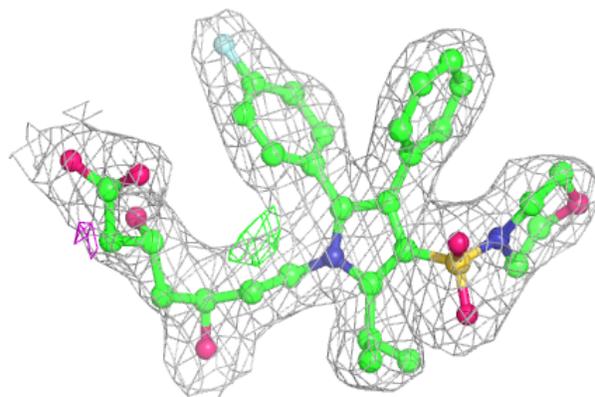
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	RID	B	1	41/41	0.91	0.15	29,37,43,44	0
2	RID	D	3	41/41	0.91	0.14	29,37,41,42	0
2	RID	C	4	41/41	0.92	0.15	24,32,38,38	0
2	RID	A	2	41/41	0.94	0.13	28,34,37,37	0

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.

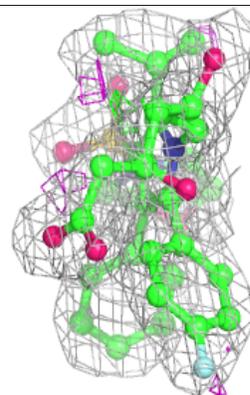
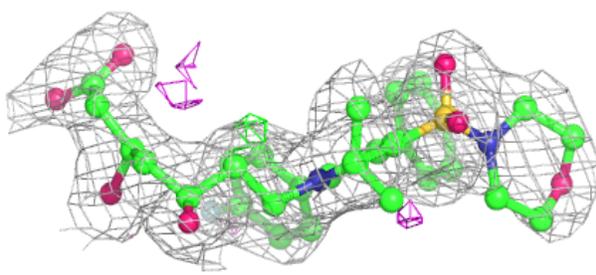
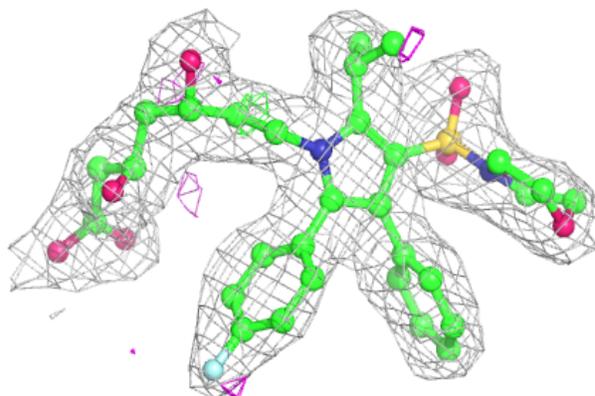


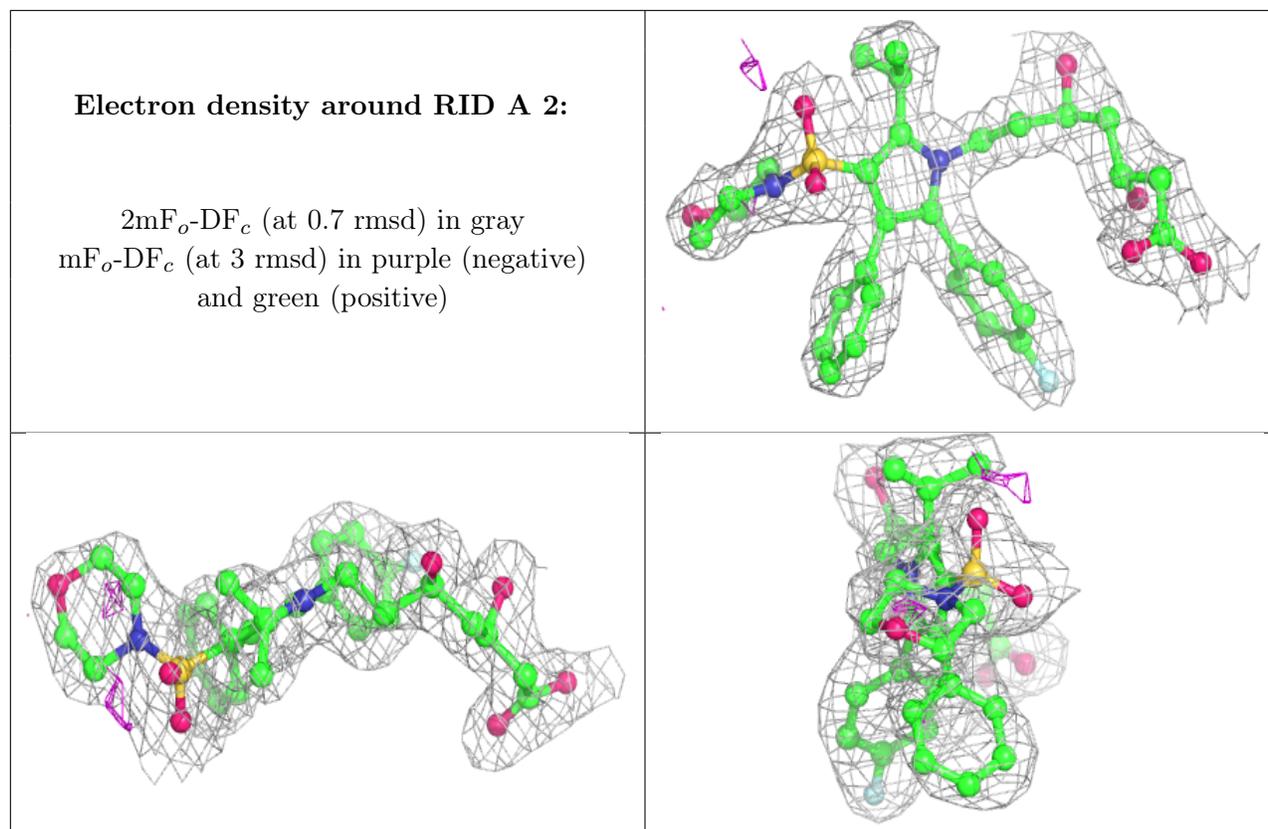
Electron density around RID D 3:

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

**Electron density around RID C 4:**

$2mF_o-DF_c$ (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.