



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2023 – 06:01 PM EDT

PDB ID : 5WDL
Title : A processive dipeptidyl aminopeptidase secreted from an established commensal bacterium *P. distasonis*
Authors : Wolan, D.W.; Xu, J.H.; Solania, A.; Chatterjee, S.; Jiang, Z.; ODonoghue, A.J.
Deposited on : 2017-07-05
Resolution : 2.62 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

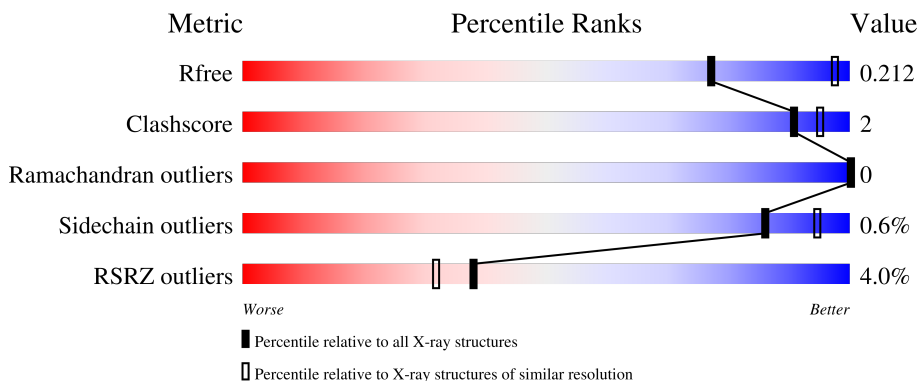
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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.



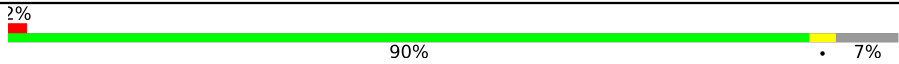
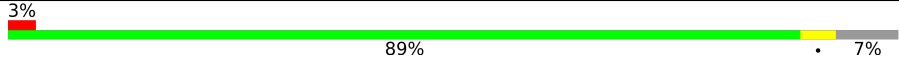
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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	401	
1	B	401	
1	C	401	
1	D	401	

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Mol	Chain	Length	Quality of chain
1	E	401	 2% 90% 7%
1	F	401	 3% 89% 7%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 18292 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 Aminopeptidase C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	372	2906	1847	473	569	17	0	1	0
1	B	368	2884	1835	471	561	17	0	0	0
1	C	367	2838	1804	461	556	17	0	0	0
1	D	373	2889	1836	470	566	17	0	0	0
1	E	373	2942	1877	481	567	17	0	1	0
1	F	373	2945	1875	481	572	17	0	0	0

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	MET	-	expression tag	UNP A6LE66
A	6	GLY	-	expression tag	UNP A6LE66
A	7	SER	-	expression tag	UNP A6LE66
A	8	ASP	-	expression tag	UNP A6LE66
A	9	LYS	-	expression tag	UNP A6LE66
A	10	ILE	-	expression tag	UNP A6LE66
A	11	HIS	-	expression tag	UNP A6LE66
A	12	HIS	-	expression tag	UNP A6LE66
A	13	HIS	-	expression tag	UNP A6LE66
A	14	HIS	-	expression tag	UNP A6LE66
A	15	HIS	-	expression tag	UNP A6LE66
A	16	HIS	-	expression tag	UNP A6LE66
A	17	GLU	-	expression tag	UNP A6LE66
A	18	ASN	-	expression tag	UNP A6LE66
A	19	LEU	-	expression tag	UNP A6LE66
A	20	TYR	-	expression tag	UNP A6LE66
A	21	PHE	-	expression tag	UNP A6LE66

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Chain	Residue	Modelled	Actual	Comment	Reference
A	22	GLN	-	expression tag	UNP A6LE66
B	5	MET	-	expression tag	UNP A6LE66
B	6	GLY	-	expression tag	UNP A6LE66
B	7	SER	-	expression tag	UNP A6LE66
B	8	ASP	-	expression tag	UNP A6LE66
B	9	LYS	-	expression tag	UNP A6LE66
B	10	ILE	-	expression tag	UNP A6LE66
B	11	HIS	-	expression tag	UNP A6LE66
B	12	HIS	-	expression tag	UNP A6LE66
B	13	HIS	-	expression tag	UNP A6LE66
B	14	HIS	-	expression tag	UNP A6LE66
B	15	HIS	-	expression tag	UNP A6LE66
B	16	HIS	-	expression tag	UNP A6LE66
B	17	GLU	-	expression tag	UNP A6LE66
B	18	ASN	-	expression tag	UNP A6LE66
B	19	LEU	-	expression tag	UNP A6LE66
B	20	TYR	-	expression tag	UNP A6LE66
B	21	PHE	-	expression tag	UNP A6LE66
B	22	GLN	-	expression tag	UNP A6LE66
C	5	MET	-	expression tag	UNP A6LE66
C	6	GLY	-	expression tag	UNP A6LE66
C	7	SER	-	expression tag	UNP A6LE66
C	8	ASP	-	expression tag	UNP A6LE66
C	9	LYS	-	expression tag	UNP A6LE66
C	10	ILE	-	expression tag	UNP A6LE66
C	11	HIS	-	expression tag	UNP A6LE66
C	12	HIS	-	expression tag	UNP A6LE66
C	13	HIS	-	expression tag	UNP A6LE66
C	14	HIS	-	expression tag	UNP A6LE66
C	15	HIS	-	expression tag	UNP A6LE66
C	16	HIS	-	expression tag	UNP A6LE66
C	17	GLU	-	expression tag	UNP A6LE66
C	18	ASN	-	expression tag	UNP A6LE66
C	19	LEU	-	expression tag	UNP A6LE66
C	20	TYR	-	expression tag	UNP A6LE66
C	21	PHE	-	expression tag	UNP A6LE66
C	22	GLN	-	expression tag	UNP A6LE66
D	5	MET	-	expression tag	UNP A6LE66
D	6	GLY	-	expression tag	UNP A6LE66
D	7	SER	-	expression tag	UNP A6LE66
D	8	ASP	-	expression tag	UNP A6LE66
D	9	LYS	-	expression tag	UNP A6LE66

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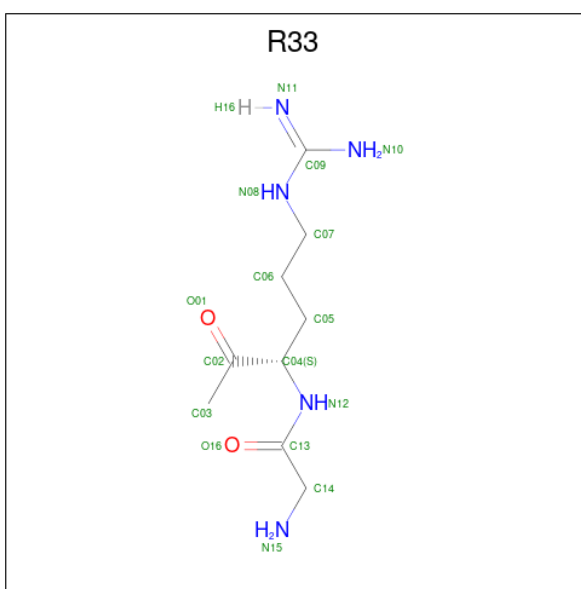
Chain	Residue	Modelled	Actual	Comment	Reference
D	10	ILE	-	expression tag	UNP A6LE66
D	11	HIS	-	expression tag	UNP A6LE66
D	12	HIS	-	expression tag	UNP A6LE66
D	13	HIS	-	expression tag	UNP A6LE66
D	14	HIS	-	expression tag	UNP A6LE66
D	15	HIS	-	expression tag	UNP A6LE66
D	16	HIS	-	expression tag	UNP A6LE66
D	17	GLU	-	expression tag	UNP A6LE66
D	18	ASN	-	expression tag	UNP A6LE66
D	19	LEU	-	expression tag	UNP A6LE66
D	20	TYR	-	expression tag	UNP A6LE66
D	21	PHE	-	expression tag	UNP A6LE66
D	22	GLN	-	expression tag	UNP A6LE66
E	5	MET	-	expression tag	UNP A6LE66
E	6	GLY	-	expression tag	UNP A6LE66
E	7	SER	-	expression tag	UNP A6LE66
E	8	ASP	-	expression tag	UNP A6LE66
E	9	LYS	-	expression tag	UNP A6LE66
E	10	ILE	-	expression tag	UNP A6LE66
E	11	HIS	-	expression tag	UNP A6LE66
E	12	HIS	-	expression tag	UNP A6LE66
E	13	HIS	-	expression tag	UNP A6LE66
E	14	HIS	-	expression tag	UNP A6LE66
E	15	HIS	-	expression tag	UNP A6LE66
E	16	HIS	-	expression tag	UNP A6LE66
E	17	GLU	-	expression tag	UNP A6LE66
E	18	ASN	-	expression tag	UNP A6LE66
E	19	LEU	-	expression tag	UNP A6LE66
E	20	TYR	-	expression tag	UNP A6LE66
E	21	PHE	-	expression tag	UNP A6LE66
E	22	GLN	-	expression tag	UNP A6LE66
F	5	MET	-	expression tag	UNP A6LE66
F	6	GLY	-	expression tag	UNP A6LE66
F	7	SER	-	expression tag	UNP A6LE66
F	8	ASP	-	expression tag	UNP A6LE66
F	9	LYS	-	expression tag	UNP A6LE66
F	10	ILE	-	expression tag	UNP A6LE66
F	11	HIS	-	expression tag	UNP A6LE66
F	12	HIS	-	expression tag	UNP A6LE66
F	13	HIS	-	expression tag	UNP A6LE66
F	14	HIS	-	expression tag	UNP A6LE66
F	15	HIS	-	expression tag	UNP A6LE66

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Chain	Residue	Modelled	Actual	Comment	Reference
F	16	HIS	-	expression tag	UNP A6LE66
F	17	GLU	-	expression tag	UNP A6LE66
F	18	ASN	-	expression tag	UNP A6LE66
F	19	LEU	-	expression tag	UNP A6LE66
F	20	TYR	-	expression tag	UNP A6LE66
F	21	PHE	-	expression tag	UNP A6LE66
F	22	GLN	-	expression tag	UNP A6LE66

- Molecule 2 is N-[(3S)-6-carbamimidamido-2-oxohexan-3-yl]glycinamide (three-letter code: R33) (formula: C₉H₁₉N₅O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			16	9	5	2		
2	B	1	Total	C	N	O	0	0
			16	9	5	2		
2	C	1	Total	C	N	O	0	0
			16	9	5	2		
2	D	1	Total	C	N	O	0	0
			16	9	5	2		
2	E	1	Total	C	N	O	0	0
			16	9	5	2		
2	F	1	Total	C	N	O	0	0
			16	9	5	2		

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total K 2 2	0	0
3	B	2	Total K 2 2	0	0
3	C	2	Total K 2 2	0	0
3	D	2	Total K 2 2	0	0
3	E	2	Total K 2 2	0	0
3	F	2	Total K 2 2	0	0

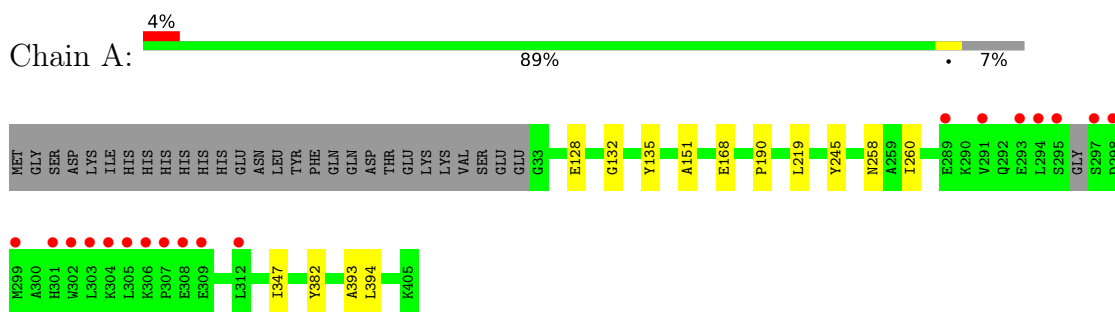
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	116	Total O 116 116	0	0
4	B	103	Total O 103 103	0	0
4	C	79	Total O 79 79	0	0
4	D	114	Total O 114 114	0	0
4	E	170	Total O 170 170	0	0
4	F	198	Total O 198 198	0	0

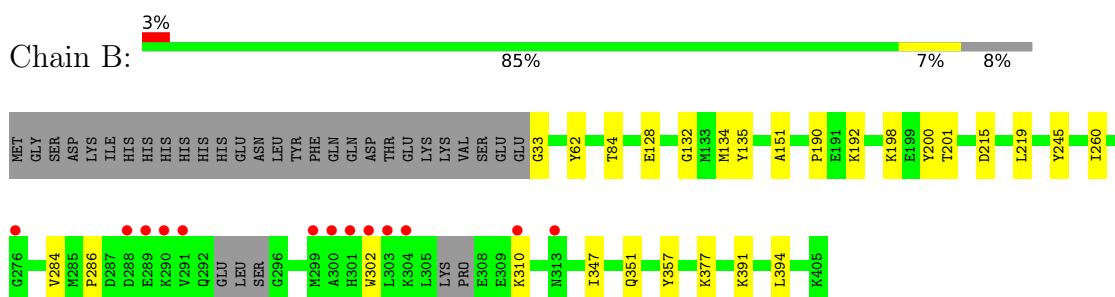
3 Residue-property plots [i](#)

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.

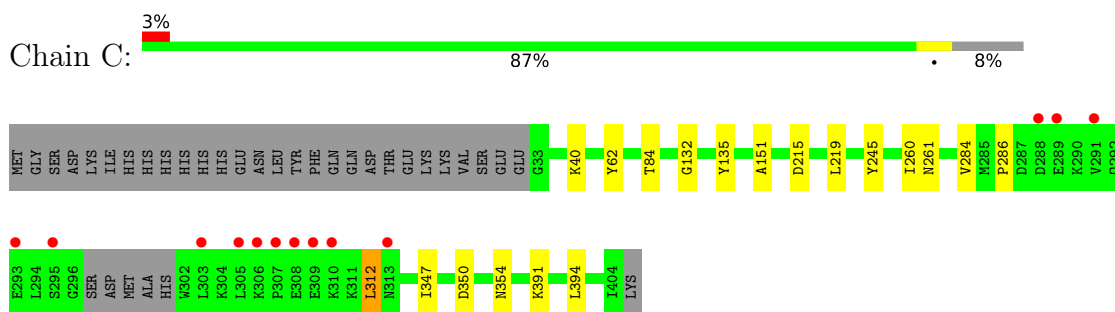
- Molecule 1: Aminopeptidase C



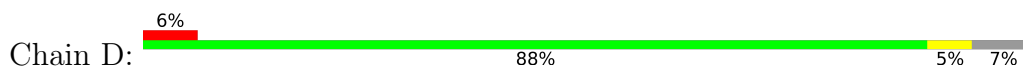
- Molecule 1: Aminopeptidase C

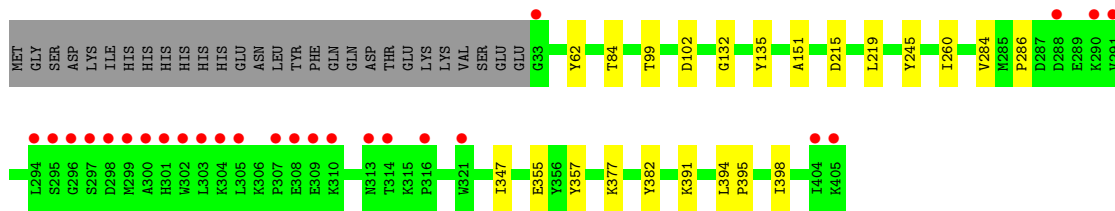


- Molecule 1: Aminopeptidase C

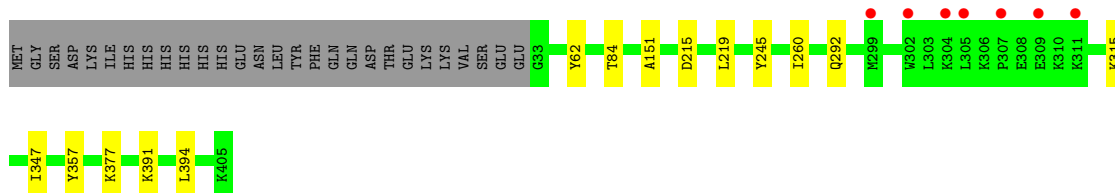
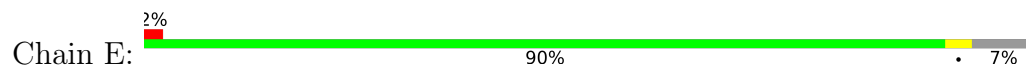


- Molecule 1: Aminopeptidase C

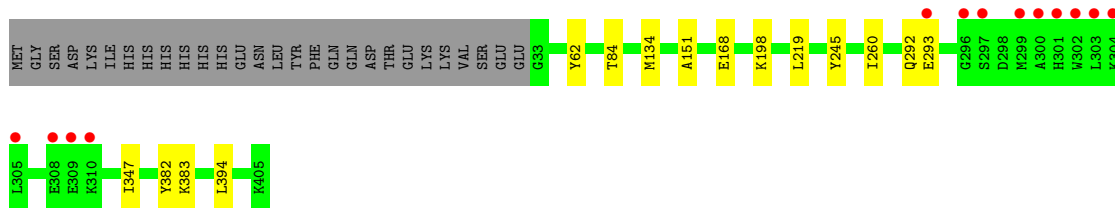
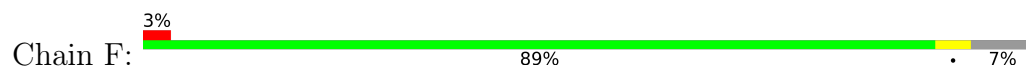




- Molecule 1: Aminopeptidase C



- Molecule 1: Aminopeptidase C



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.84Å 140.30Å 221.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.10 – 2.62 49.10 – 2.63	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.10-2.62) 98.5 (49.10-2.63)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.61Å)	Xtrriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.171 , 0.212 0.171 , 0.212	Depositor DCC
R_{free} test set	4875 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtrriage
Anisotropy	0.215	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18292	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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: R33, K

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	0.25	0/2983	0.43	0/4050
1	B	0.25	0/2958	0.44	0/4013
1	C	0.25	0/2912	0.43	0/3961
1	D	0.26	0/2966	0.44	0/4033
1	E	0.29	0/3025	0.45	0/4104
1	F	0.25	0/3022	0.45	0/4098
All	All	0.26	0/17866	0.44	0/24259

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	2906	0	2691	7	0
1	B	2884	0	2683	14	0
1	C	2838	0	2602	11	0
1	D	2889	0	2648	12	0
1	E	2942	0	2762	7	0
1	F	2945	0	2777	8	0
2	A	16	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	16	0	0	0	0
2	C	16	0	0	0	0
2	D	16	0	0	0	0
2	E	16	0	0	0	0
2	F	16	0	0	0	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
3	E	2	0	0	0	0
3	F	2	0	0	0	0
4	A	116	0	0	0	0
4	B	103	0	0	0	0
4	C	79	0	0	0	0
4	D	114	0	0	0	0
4	E	170	0	0	0	0
4	F	198	0	0	0	0
All	All	18292	0	16163	56	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 (56) 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:D:215:ASP:HA	1:D:391:LYS:HE2	1.76	0.68
1:C:215:ASP:HA	1:C:391:LYS:HE2	1.77	0.64
1:E:215:ASP:HA	1:E:391:LYS:HE2	1.86	0.58
1:D:260:ILE:HG21	1:D:347:ILE:HG13	1.86	0.57
1:E:62:TYR:OH	1:E:84:THR:OG1	2.20	0.57
1:B:219:LEU:HD11	1:B:394:LEU:HD21	1.87	0.56
1:E:219:LEU:HD11	1:E:394:LEU:HD21	1.88	0.55
1:D:62:TYR:OH	1:D:84:THR:OG1	2.15	0.55
1:C:219:LEU:HD11	1:C:394:LEU:HD21	1.89	0.54
1:B:215:ASP:HA	1:B:391:LYS:HE2	1.90	0.54
1:D:219:LEU:HD11	1:D:394:LEU:HD21	1.91	0.53
1:A:258:ASN:ND2	1:A:393:ALA:O	2.41	0.52
1:F:219:LEU:HD11	1:F:394:LEU:HD21	1.91	0.51
1:A:219:LEU:HD23	1:A:245:TYR:HB2	1.93	0.51
1:A:128:GLU:HB3	1:A:190:PRO:HG3	1.94	0.50
1:B:33:GLY:O	1:B:351:GLN:NE2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:ILE:HG21	1:B:347:ILE:HG13	1.91	0.50
1:C:260:ILE:HG21	1:C:347:ILE:HG13	1.92	0.50
1:D:219:LEU:HD23	1:D:245:TYR:HB2	1.92	0.50
1:F:260:ILE:HG21	1:F:347:ILE:HG13	1.93	0.50
1:C:151:ALA:HB1	1:D:151:ALA:HB1	1.93	0.50
1:B:357:TYR:CE2	1:B:377:LYS:HG2	2.47	0.50
1:A:219:LEU:HD11	1:A:394:LEU:HD21	1.94	0.50
1:B:302:TRP:CH2	1:B:310:LYS:HB3	2.47	0.50
1:C:284:VAL:HG23	1:C:286:PRO:HD3	1.93	0.49
1:F:62:TYR:OH	1:F:84:THR:OG1	2.20	0.49
1:C:312:LEU:H	1:C:312:LEU:HD12	1.79	0.48
1:C:219:LEU:HD23	1:C:245:TYR:HB2	1.96	0.48
1:B:284:VAL:HG23	1:B:286:PRO:HD3	1.96	0.47
1:A:151:ALA:HB1	1:B:151:ALA:HB1	1.95	0.47
1:D:132:GLY:HA2	1:D:135:TYR:CZ	2.50	0.47
1:A:260:ILE:HG21	1:A:347:ILE:HG13	1.96	0.47
1:B:219:LEU:HD23	1:B:245:TYR:HB2	1.96	0.46
1:C:62:TYR:OH	1:C:84:THR:OG1	2.17	0.46
1:E:357:TYR:CE2	1:E:377:LYS:HG2	2.50	0.46
1:A:132:GLY:HA2	1:A:135:TYR:CZ	2.51	0.46
1:D:284:VAL:HG23	1:D:286:PRO:HD3	1.99	0.45
1:B:62:TYR:HH	1:B:84:THR:HG1	1.52	0.45
1:C:132:GLY:HA2	1:C:135:TYR:CZ	2.52	0.45
1:F:168:GLU:H	1:F:168:GLU:CD	2.21	0.44
1:B:132:GLY:HA2	1:B:135:TYR:CZ	2.52	0.44
1:D:355:GLU:HB3	1:D:377:LYS:HE3	2.00	0.44
1:D:357:TYR:CE2	1:D:377:LYS:HG2	2.53	0.43
1:C:40:LYS:NZ	1:C:261:ASN:O	2.51	0.43
1:E:219:LEU:HD23	1:E:245:TYR:HB2	2.01	0.42
1:F:383:LYS:HA	1:F:383:LYS:HD3	1.90	0.42
1:B:198:LYS:HD3	1:B:200:TYR:CZ	2.55	0.42
1:D:395:PRO:HG2	1:D:398:ILE:HD12	2.02	0.41
1:E:151:ALA:HB1	1:F:151:ALA:HB1	2.01	0.41
1:F:219:LEU:HD23	1:F:245:TYR:HB2	2.03	0.41
1:B:128:GLU:HB3	1:B:190:PRO:HG3	2.03	0.41
1:E:260:ILE:HG21	1:E:347:ILE:HG13	2.02	0.40
1:F:198:LYS:HE3	1:F:198:LYS:HB2	1.89	0.40
1:D:99:THR:HB	1:D:102:ASP:HB2	2.03	0.40
1:B:192:LYS:HD3	1:B:201:THR:HG22	2.02	0.40
1:C:350:ASP:OD1	1:C:354:ASN:N	2.53	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	369/401 (92%)	366 (99%)	3 (1%)	0	100	100
1	B	362/401 (90%)	358 (99%)	4 (1%)	0	100	100
1	C	363/401 (90%)	359 (99%)	4 (1%)	0	100	100
1	D	371/401 (92%)	367 (99%)	4 (1%)	0	100	100
1	E	372/401 (93%)	368 (99%)	4 (1%)	0	100	100
1	F	371/401 (92%)	367 (99%)	4 (1%)	0	100	100
All	All	2208/2406 (92%)	2185 (99%)	23 (1%)	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	299/346 (86%)	296 (99%)	3 (1%)	76	89
1	B	298/346 (86%)	297 (100%)	1 (0%)	92	97
1	C	290/346 (84%)	289 (100%)	1 (0%)	92	97
1	D	294/346 (85%)	293 (100%)	1 (0%)	92	97
1	E	306/346 (88%)	304 (99%)	2 (1%)	84	93
1	F	309/346 (89%)	305 (99%)	4 (1%)	69	85
All	All	1796/2076 (86%)	1784 (99%)	12 (1%)	86	93

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	168[A]	GLU
1	A	168[B]	GLU
1	A	382	TYR
1	B	134	MET
1	C	312	LEU
1	D	382	TYR
1	E	292	GLN
1	E	315	LYS
1	F	134	MET
1	F	292	GLN
1	F	293	GLU
1	F	382	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 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	R33	F	501	1	14,15,15	2.44	3 (21%)	10,18,18	0.70	0
2	R33	B	501	1	14,15,15	2.56	5 (35%)	10,18,18	0.78	0
2	R33	E	501	1	14,15,15	2.45	4 (28%)	10,18,18	0.87	0
2	R33	A	501	1	14,15,15	2.47	4 (28%)	10,18,18	0.74	0
2	R33	D	501	1	14,15,15	2.45	4 (28%)	10,18,18	0.80	0
2	R33	C	501	1	14,15,15	2.49	4 (28%)	10,18,18	0.62	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	R33	F	501	1	-	1/17/17/17	-
2	R33	B	501	1	-	4/17/17/17	-
2	R33	E	501	1	-	1/17/17/17	-
2	R33	A	501	1	-	1/17/17/17	-
2	R33	D	501	1	-	5/17/17/17	-
2	R33	C	501	1	-	2/17/17/17	-

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	R33	C09-N08	6.27	1.45	1.33
2	B	501	R33	C09-N08	6.23	1.45	1.33
2	A	501	R33	C09-N08	6.19	1.45	1.33
2	F	501	R33	C09-N08	6.16	1.45	1.33
2	E	501	R33	C09-N08	6.16	1.45	1.33
2	D	501	R33	C09-N08	6.10	1.45	1.33
2	C	501	R33	C13-N12	5.51	1.45	1.34
2	A	501	R33	C13-N12	5.45	1.45	1.34
2	B	501	R33	C13-N12	5.45	1.45	1.34
2	E	501	R33	C13-N12	5.41	1.45	1.34
2	D	501	R33	C13-N12	5.40	1.45	1.34
2	F	501	R33	C13-N12	5.38	1.45	1.34
2	B	501	R33	C09-N11	3.36	1.45	1.32
2	A	501	R33	C09-N10	2.66	1.45	1.34
2	F	501	R33	C09-N10	2.66	1.45	1.34
2	D	501	R33	C09-N10	2.66	1.45	1.34
2	C	501	R33	C09-N10	2.66	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	501	R33	C09-N10	2.64	1.45	1.34
2	B	501	R33	C09-N10	-2.20	1.25	1.34
2	C	501	R33	O16-C13	-2.15	1.18	1.23
2	D	501	R33	O16-C13	-2.12	1.18	1.23
2	A	501	R33	O16-C13	-2.07	1.19	1.23
2	E	501	R33	O16-C13	-2.05	1.19	1.23
2	B	501	R33	O16-C13	-2.01	1.19	1.23

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

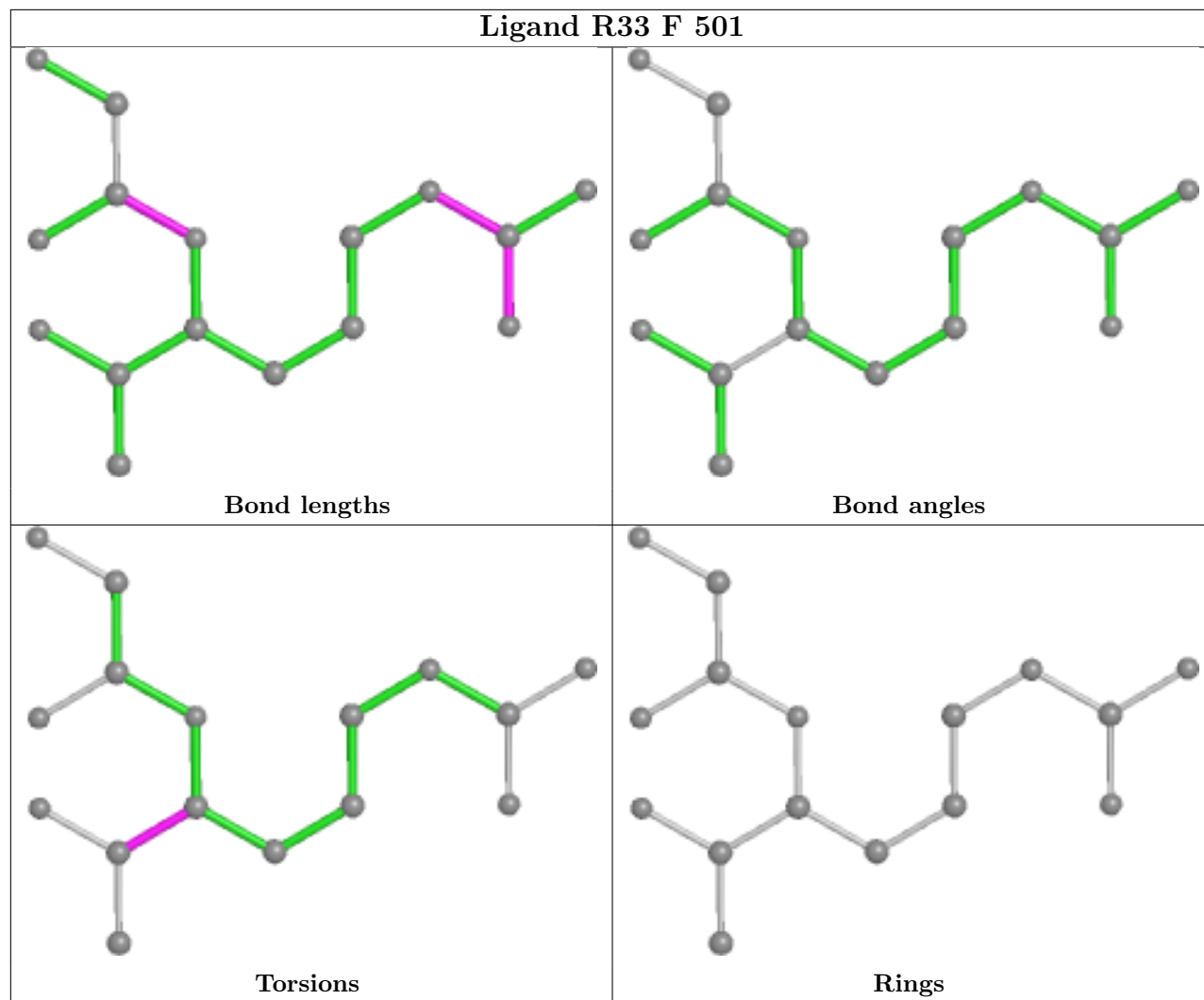
Mol	Chain	Res	Type	Atoms
2	A	501	R33	C03-C02-C04-N12
2	C	501	R33	C03-C02-C04-N12
2	D	501	R33	C03-C02-C04-N12
2	E	501	R33	C03-C02-C04-N12
2	F	501	R33	C03-C02-C04-N12
2	B	501	R33	N12-C04-C05-C06
2	D	501	R33	N12-C04-C05-C06
2	D	501	R33	C05-C06-C07-N08
2	B	501	R33	C02-C04-C05-C06
2	D	501	R33	C02-C04-C05-C06
2	D	501	R33	C04-C05-C06-C07
2	B	501	R33	C04-C05-C06-C07
2	B	501	R33	C06-C07-N08-C09
2	C	501	R33	C06-C07-N08-C09

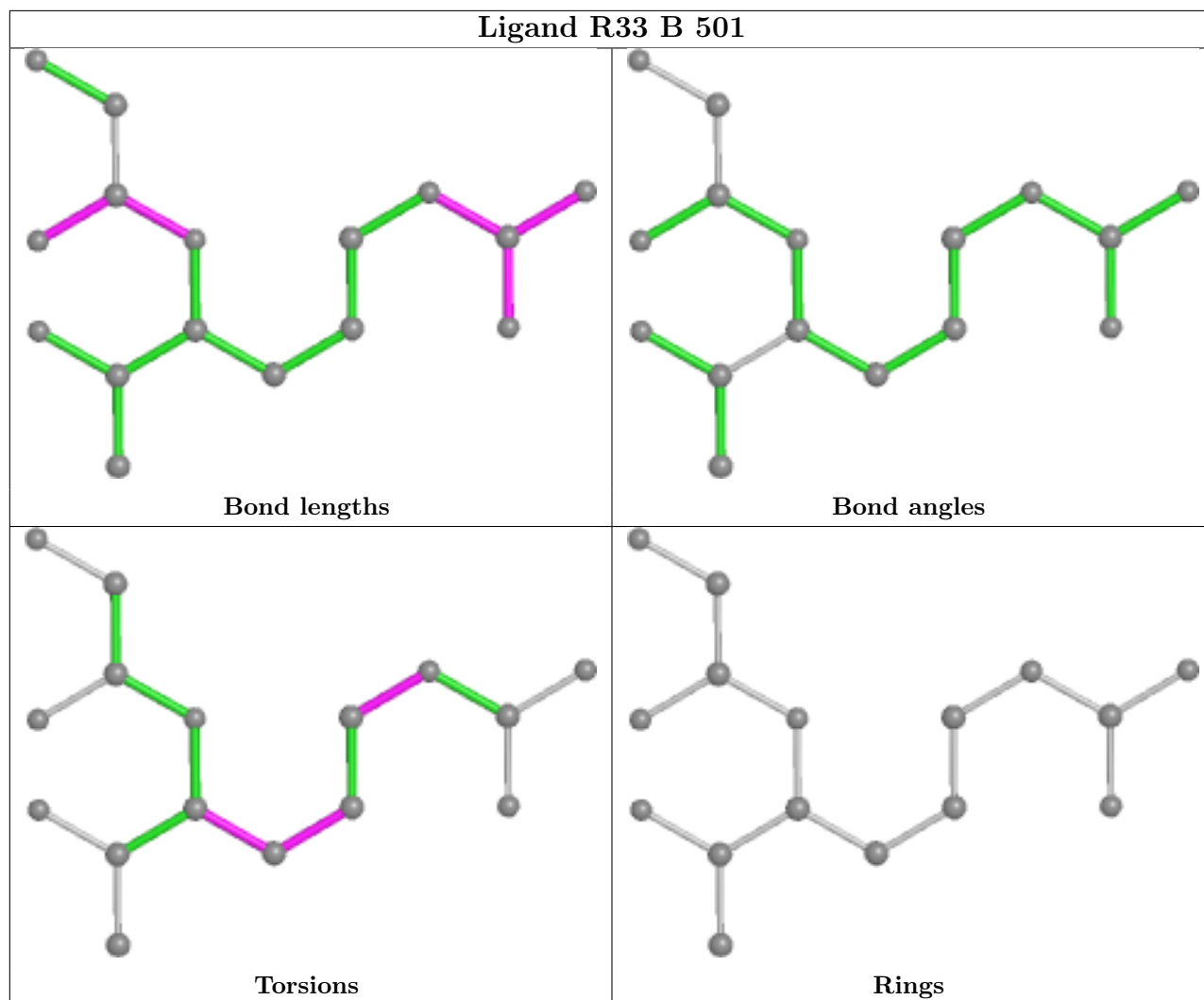
There are no ring outliers.

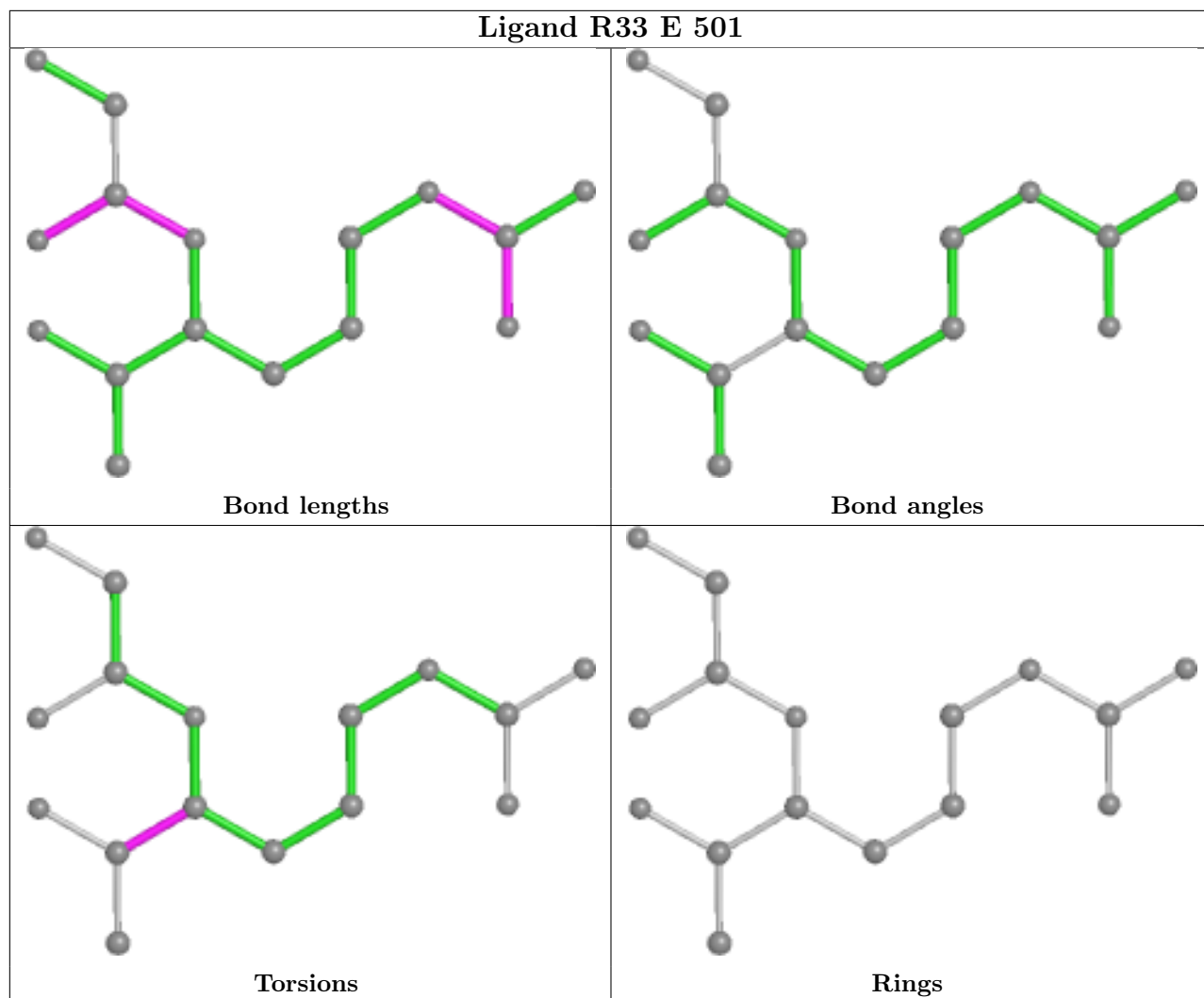
No monomer is involved in short contacts.

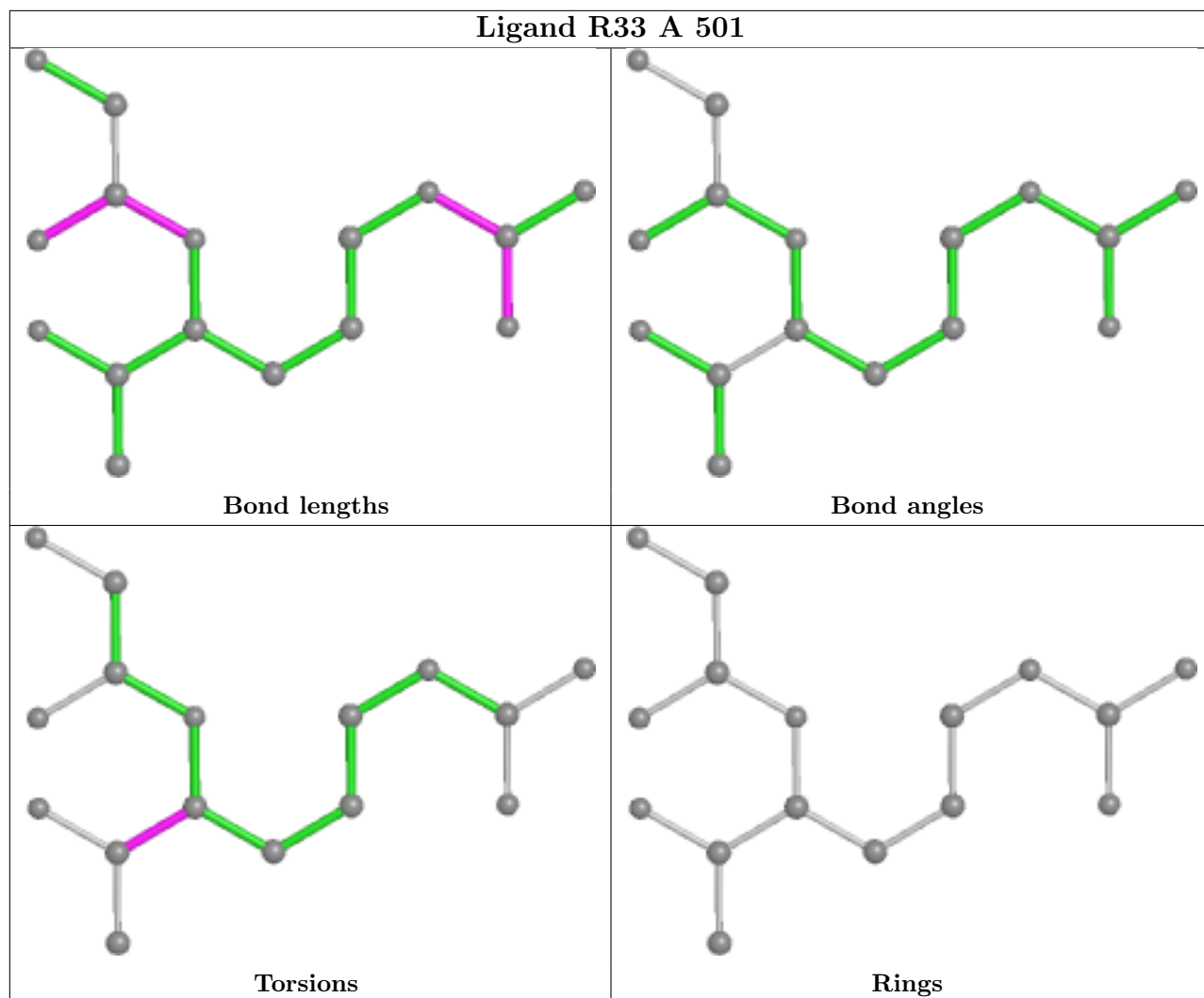
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

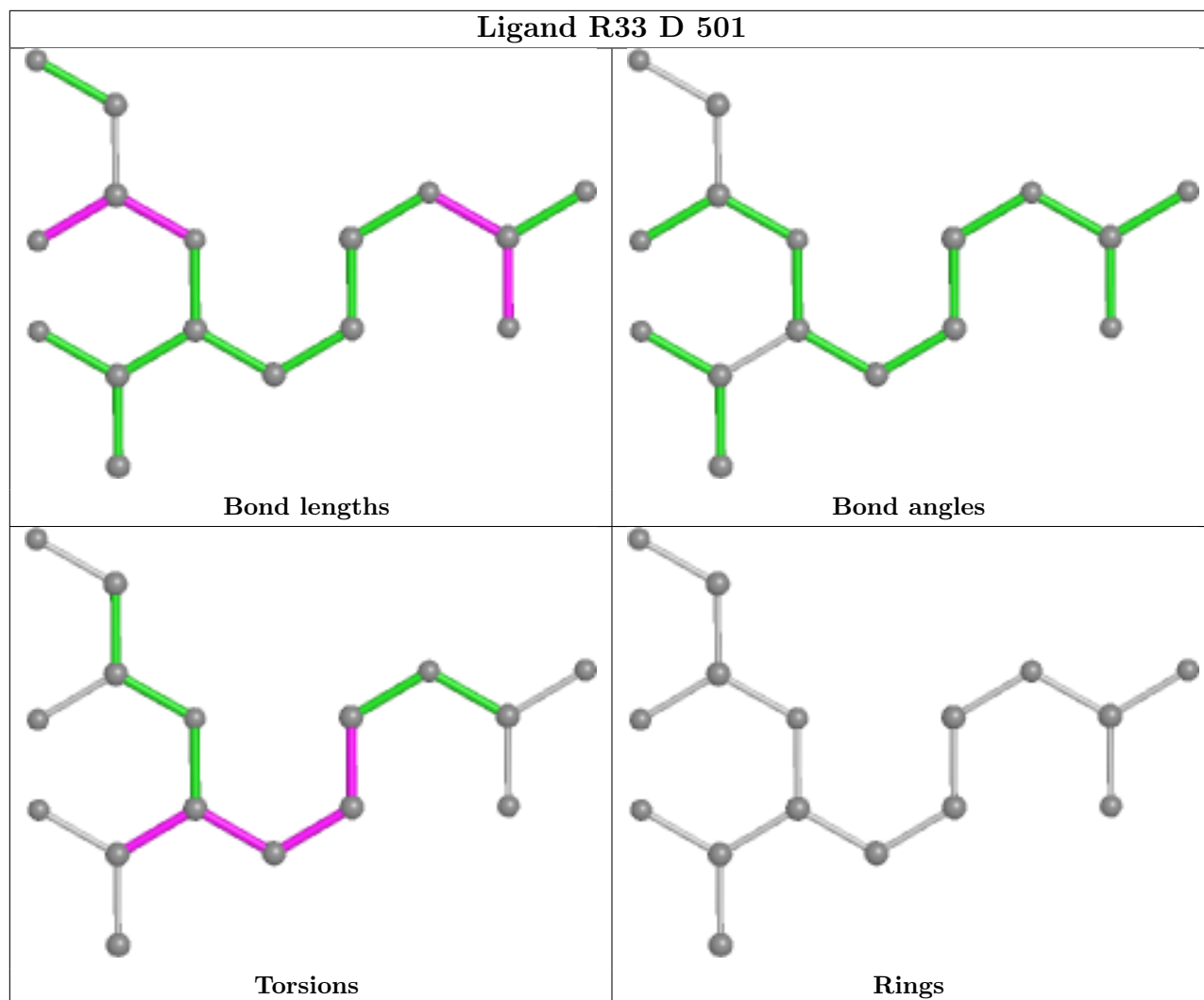
equivalents in the CSD to analyse the geometry.

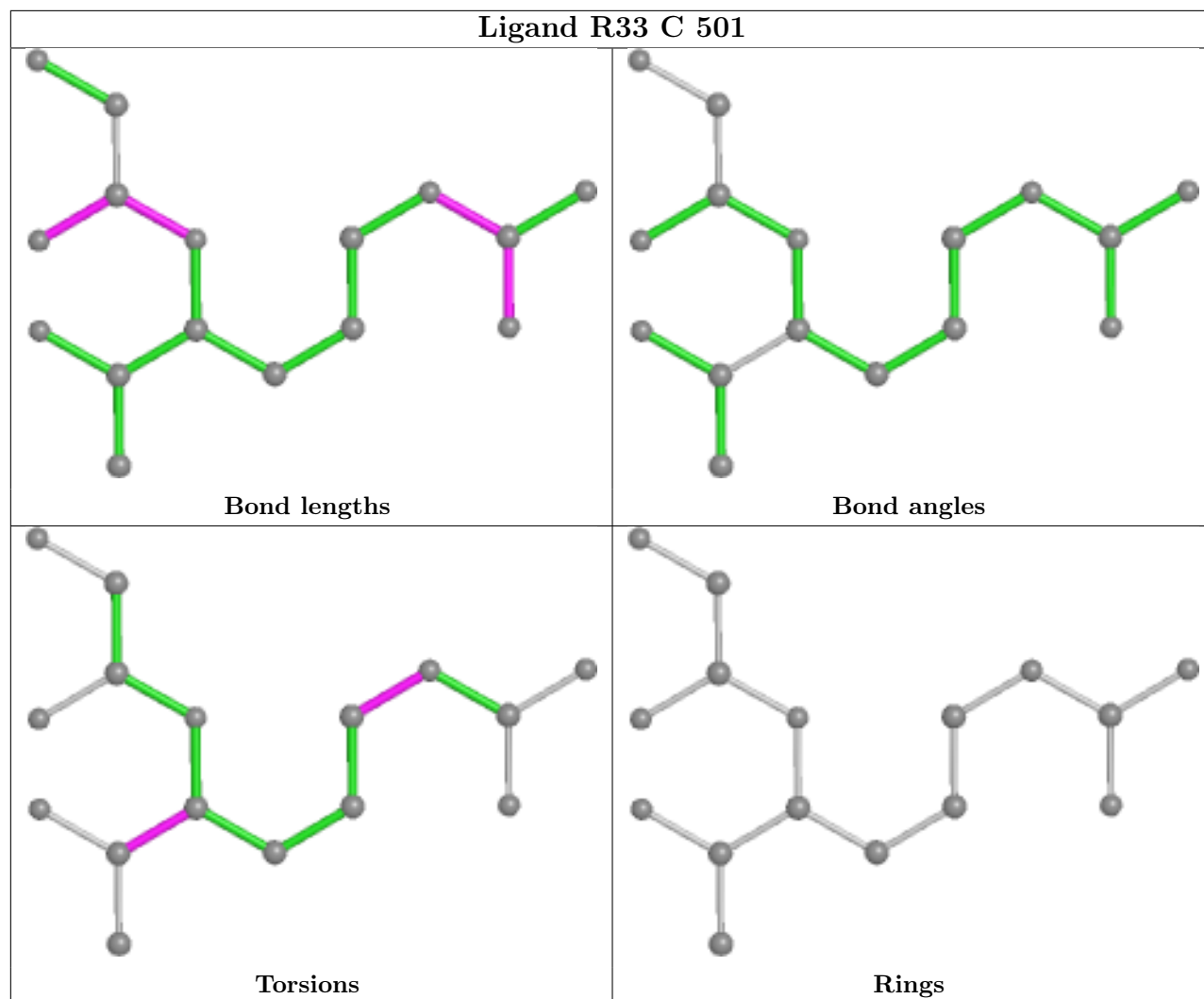












5.7 Other polymers [i](#)

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	372/401 (92%)	-0.16	18 (4%) 30 24	21, 41, 86, 104	0
1	B	368/401 (91%)	-0.23	13 (3%) 44 37	22, 36, 74, 97	0
1	C	367/401 (91%)	-0.18	13 (3%) 44 37	24, 46, 81, 100	0
1	D	373/401 (93%)	-0.04	26 (6%) 16 12	24, 41, 84, 101	0
1	E	373/401 (93%)	-0.48	7 (1%) 66 62	19, 28, 71, 91	0
1	F	373/401 (93%)	-0.39	13 (3%) 44 37	18, 26, 68, 102	0
All	All	2226/2406 (92%)	-0.25	90 (4%) 38 32	18, 36, 79, 104	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	300	ALA	6.8
1	D	302	TRP	5.8
1	C	309	GLU	5.1
1	D	294	LEU	5.1
1	D	300	ALA	5.0
1	C	291	VAL	5.0
1	D	299	MET	4.9
1	D	307	PRO	4.9
1	A	308	GLU	4.9
1	B	300	ALA	4.9
1	C	307	PRO	4.7
1	D	297	SER	4.7
1	F	305	LEU	4.7
1	F	303	LEU	4.3
1	A	309	GLU	4.2
1	F	304	LYS	4.1
1	E	309	GLU	4.1
1	A	302	TRP	4.1
1	A	305	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	309	GLU	3.9
1	B	288	ASP	3.9
1	D	308	GLU	3.9
1	B	289	GLU	3.8
1	D	296	GLY	3.8
1	B	303	LEU	3.7
1	D	314	THR	3.7
1	D	295	SER	3.7
1	D	304	LYS	3.6
1	A	294	LEU	3.6
1	F	299	MET	3.6
1	D	305	LEU	3.4
1	A	291	VAL	3.4
1	C	305	LEU	3.4
1	B	302	TRP	3.3
1	E	305	LEU	3.1
1	D	288	ASP	3.1
1	A	307	PRO	3.1
1	D	290	LYS	3.1
1	F	302	TRP	3.1
1	F	293	GLU	3.0
1	F	301	HIS	3.0
1	B	299	MET	3.0
1	D	405	LYS	2.9
1	C	308	GLU	2.9
1	A	293	GLU	2.9
1	A	301	HIS	2.9
1	C	306	LYS	2.9
1	A	304	LYS	2.8
1	B	301	HIS	2.8
1	A	306	LYS	2.8
1	F	310	LYS	2.8
1	A	297	SER	2.7
1	E	302	TRP	2.7
1	F	309	GLU	2.7
1	B	290	LYS	2.7
1	A	298	ASP	2.7
1	B	310	LYS	2.7
1	E	304	LYS	2.7
1	C	288	ASP	2.6
1	D	303	LEU	2.6
1	D	33	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	299	MET	2.6
1	D	301	HIS	2.6
1	E	311	LYS	2.5
1	D	313	ASN	2.5
1	C	310	LYS	2.5
1	C	313	ASN	2.5
1	F	297	SER	2.5
1	D	310	LYS	2.4
1	A	289	GLU	2.4
1	C	303	LEU	2.4
1	C	289	GLU	2.4
1	A	295	SER	2.3
1	B	313	ASN	2.3
1	D	316	PRO	2.3
1	E	307	PRO	2.3
1	C	293	GLU	2.3
1	D	321	TRP	2.3
1	B	304	LYS	2.2
1	B	291	VAL	2.2
1	A	312	LEU	2.2
1	F	296	GLY	2.2
1	A	303	LEU	2.2
1	D	404	ILE	2.2
1	F	308	GLU	2.1
1	E	299	MET	2.1
1	C	295	SER	2.1
1	B	276	GLY	2.1
1	D	291	VAL	2.0
1	D	298	ASP	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

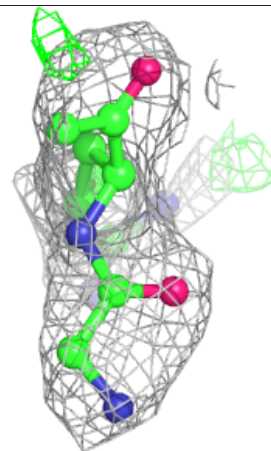
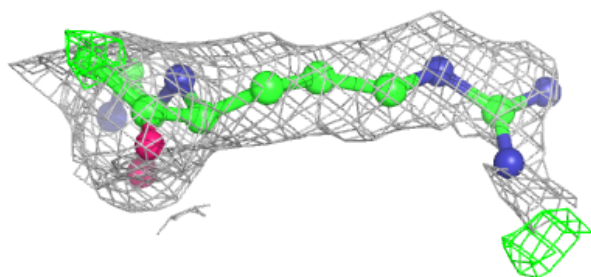
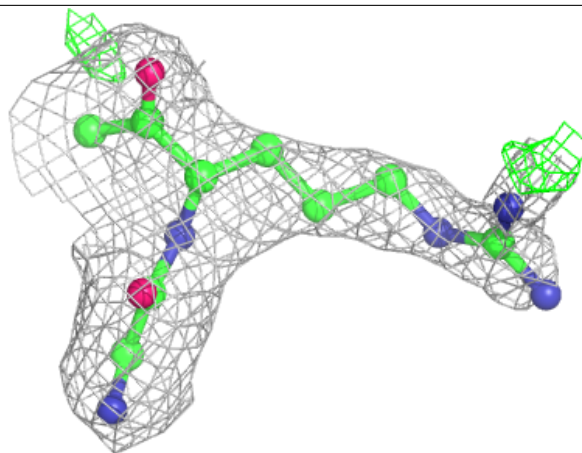
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	K	C	502	1/1	0.89	0.12	49,49,49,49	0
2	R33	C	501	16/16	0.91	0.18	38,48,63,72	0
2	R33	B	501	16/16	0.91	0.25	40,46,77,78	0
3	K	D	502	1/1	0.91	0.18	46,46,46,46	0
2	R33	A	501	16/16	0.94	0.17	31,41,64,67	0
3	K	B	502	1/1	0.94	0.11	42,42,42,42	0
3	K	B	503	1/1	0.95	0.10	43,43,43,43	0
3	K	A	503	1/1	0.95	0.10	33,33,33,33	0
2	R33	E	501	16/16	0.95	0.20	29,35,55,56	0
2	R33	D	501	16/16	0.96	0.16	35,45,68,69	0
3	K	A	502	1/1	0.97	0.09	50,50,50,50	0
2	R33	F	501	16/16	0.97	0.16	21,29,62,69	0
3	K	E	502	1/1	0.97	0.16	35,35,35,35	0
3	K	D	503	1/1	0.98	0.07	43,43,43,43	0
3	K	F	502	1/1	0.98	0.15	31,31,31,31	0
3	K	E	503	1/1	0.99	0.11	33,33,33,33	0
3	K	C	503	1/1	0.99	0.12	49,49,49,49	0
3	K	F	503	1/1	0.99	0.16	24,24,24,24	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.

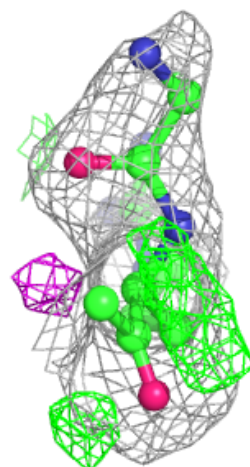
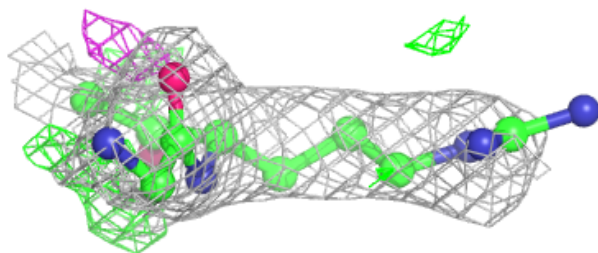
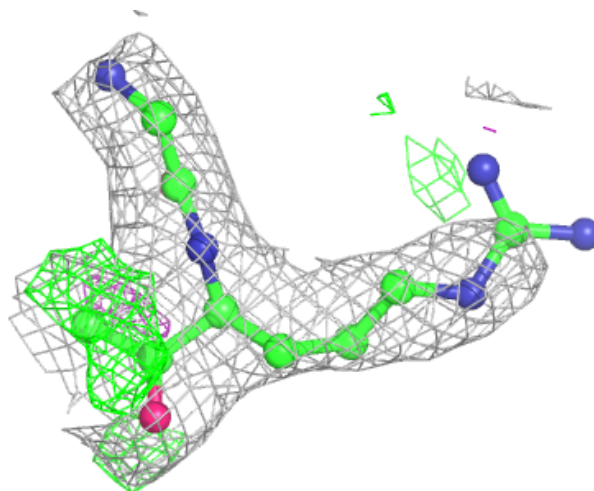
Electron density around R33 C 501:

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



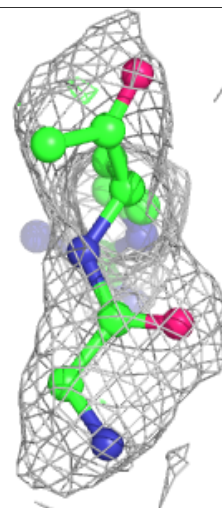
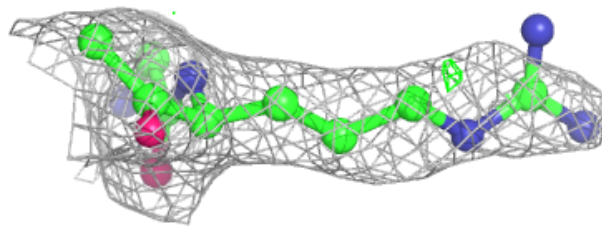
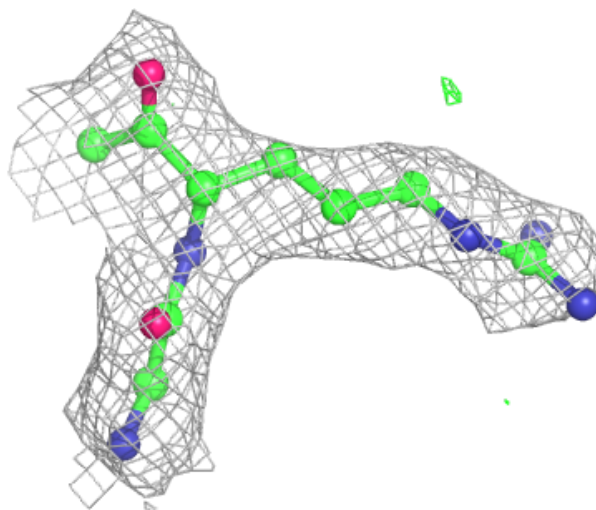
Electron density around R33 B 501:

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



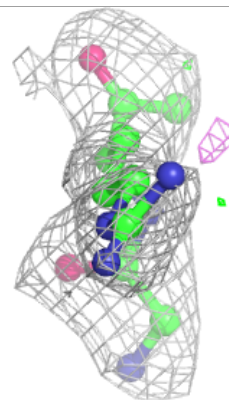
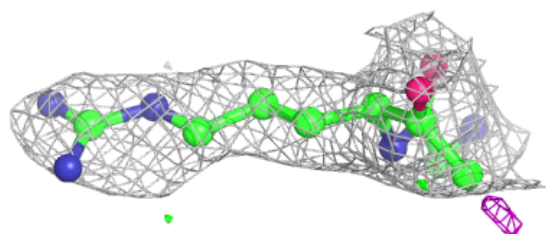
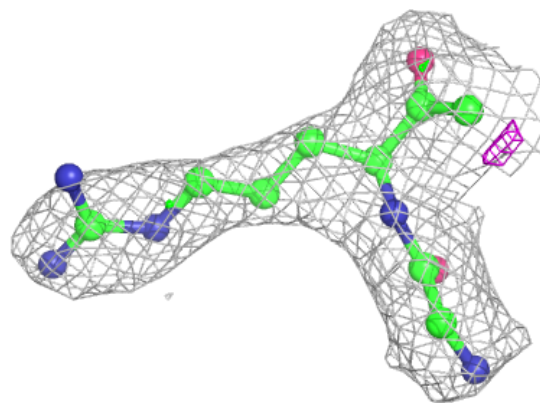
Electron density around R33 A 501:

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



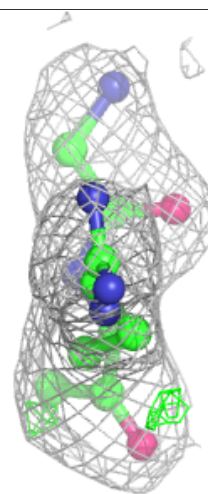
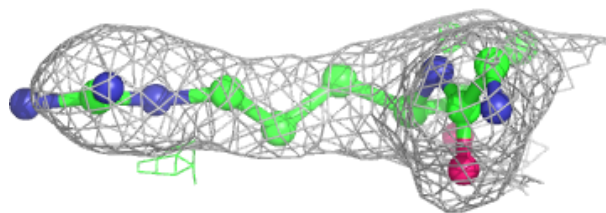
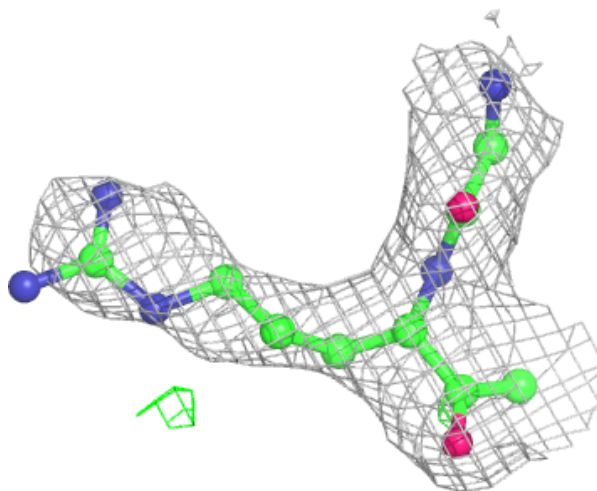
Electron density around R33 E 501:

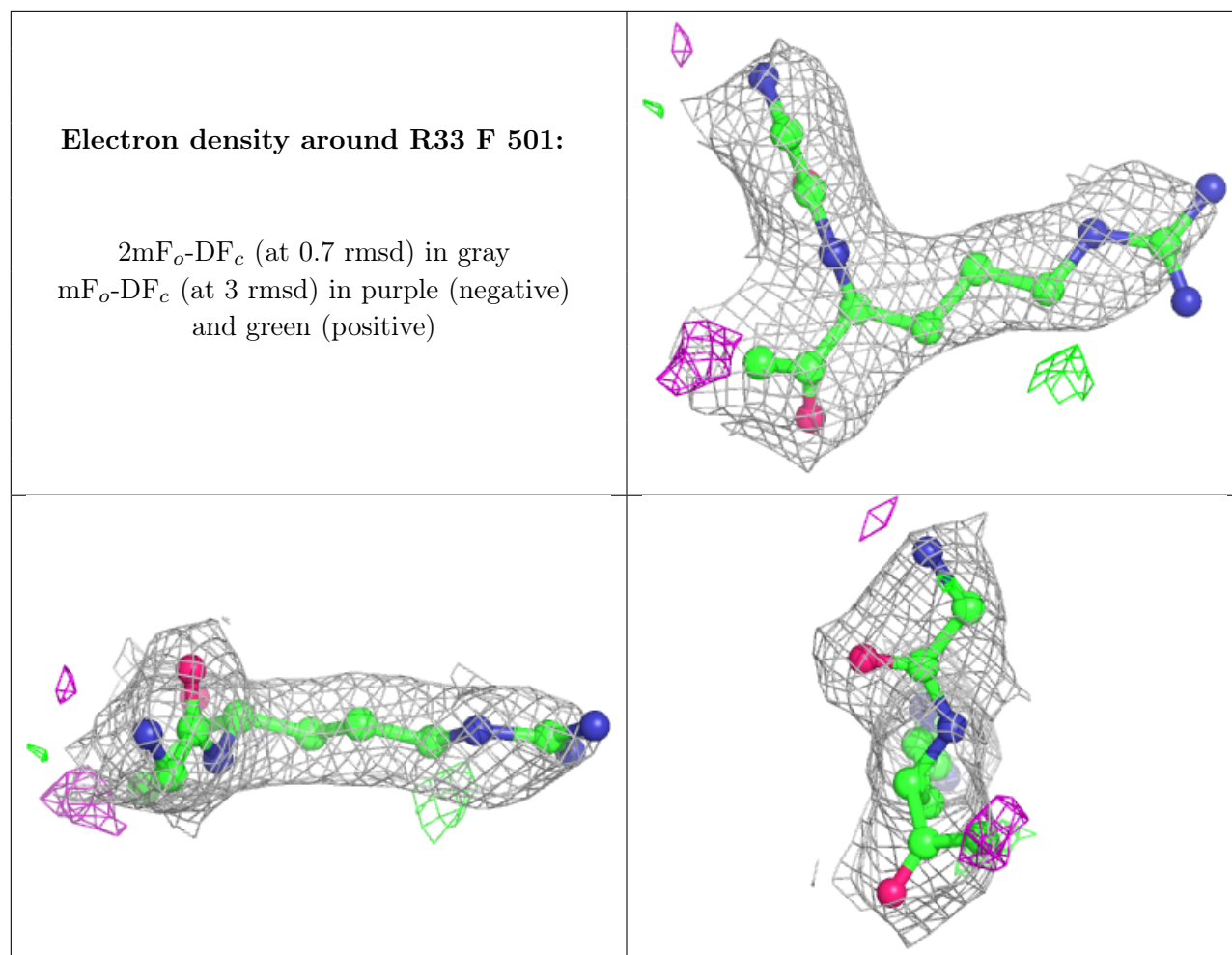
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around R33 D 501:

$2mF_o-DF_c$ (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.