



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 20, 2023 – 01:09 PM EDT

PDB ID : 5HK7  
Title : Bacterial sodium channel pore, 2.95 Angstrom resolution  
Authors : Shaya, D.; Findeisen, F.; Rohaim, A.; Minor, D.L.  
Deposited on : 2016-01-14  
Resolution : 2.95 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
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

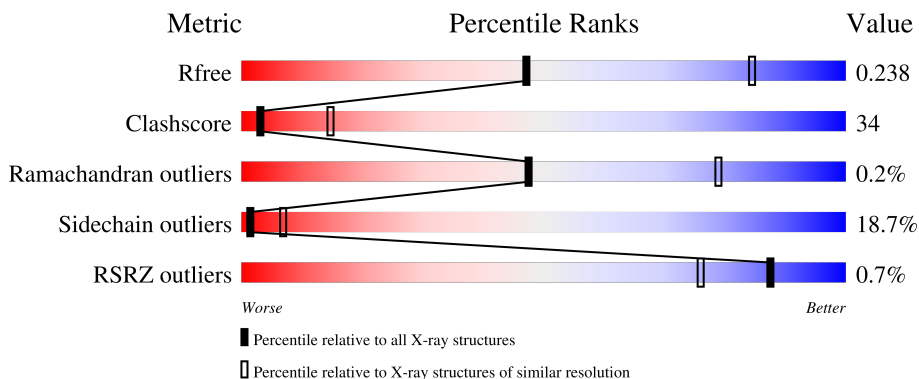
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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

Mol	Chain	Length	Quality of chain
1	A	152	
1	B	152	
1	C	152	
1	D	152	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	NA	C	305	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4667 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 Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	139	1132	750	181	195	6	0	1	0
1	B	138	1126	745	180	195	6	0	1	0
1	C	138	1122	742	178	196	6	0	0	0
1	D	138	1128	745	181	196	6	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	137	GLY	-	expression tag	UNP Q0ABW0
A	138	PRO	-	expression tag	UNP Q0ABW0
A	139	SER	-	expression tag	UNP Q0ABW0
A	140	SER	-	expression tag	UNP Q0ABW0
A	141	PRO	-	expression tag	UNP Q0ABW0
A	142	SER	-	expression tag	UNP Q0ABW0
B	137	GLY	-	expression tag	UNP Q0ABW0
B	138	PRO	-	expression tag	UNP Q0ABW0
B	139	SER	-	expression tag	UNP Q0ABW0
B	140	SER	-	expression tag	UNP Q0ABW0
B	141	PRO	-	expression tag	UNP Q0ABW0
B	142	SER	-	expression tag	UNP Q0ABW0
C	137	GLY	-	expression tag	UNP Q0ABW0
C	138	PRO	-	expression tag	UNP Q0ABW0
C	139	SER	-	expression tag	UNP Q0ABW0
C	140	SER	-	expression tag	UNP Q0ABW0
C	141	PRO	-	expression tag	UNP Q0ABW0
C	142	SER	-	expression tag	UNP Q0ABW0
D	137	GLY	-	expression tag	UNP Q0ABW0
D	138	PRO	-	expression tag	UNP Q0ABW0
D	139	SER	-	expression tag	UNP Q0ABW0

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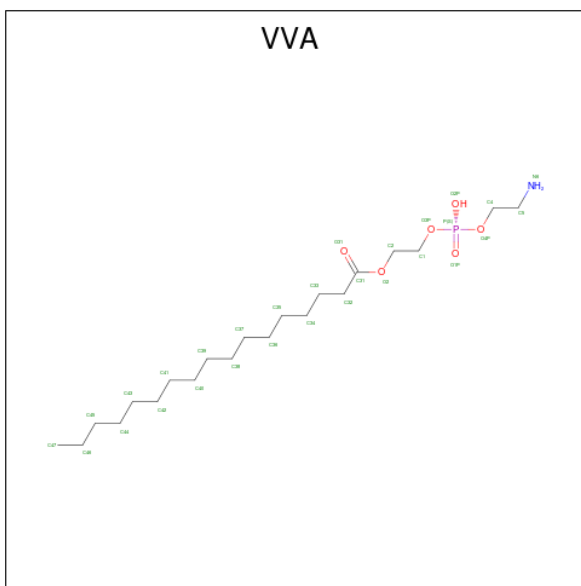
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Chain	Residue	Modelled	Actual	Comment	Reference
D	140	SER	-	expression tag	UNP Q0ABW0
D	141	PRO	-	expression tag	UNP Q0ABW0
D	142	SER	-	expression tag	UNP Q0ABW0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Cl 2 2	0	0

- Molecule 3 is 2-[[S)-(2-aminoethoxy)(hydroxy)phosphoryl]oxy}ethyl heptadecanoate (three-letter code: VVA) (formula: C<sub>21</sub>H<sub>44</sub>NO<sub>6</sub>P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 21 13 1 6 1	0	0
3	A	1	Total C 13 13	0	0
3	B	1	Total C N O P 21 13 1 6 1	0	0
3	B	1	Total C N O P 21 13 1 6 1	0	0
3	B	1	Total C 17 17	0	0
3	C	1	Total C N O P 21 13 1 6 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C 10 10	0	0
3	C	1	Total C 6 6	0	0
3	C	1	Total C 11 11	0	0
3	D	1	Total C 10 10	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0

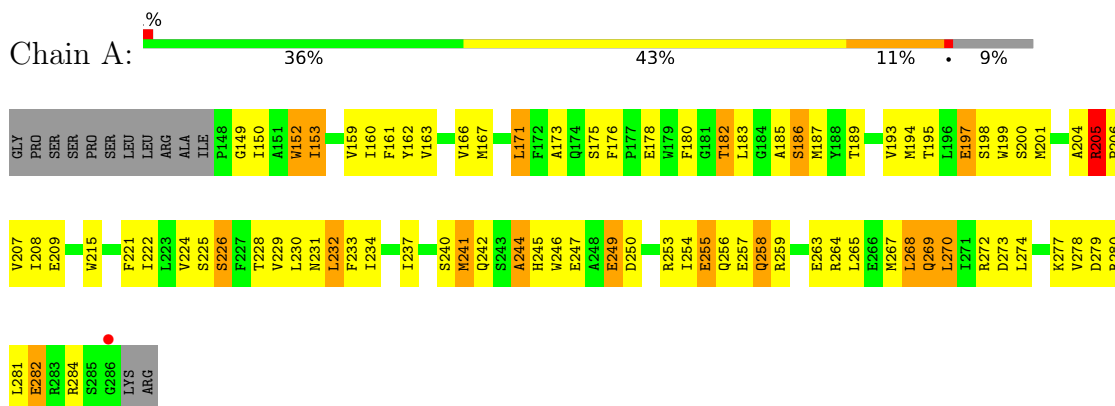
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O 1 1	0	0
5	B	1	Total O 1 1	0	0
5	C	1	Total O 1 1	0	0
5	D	1	Total O 1 1	0	0

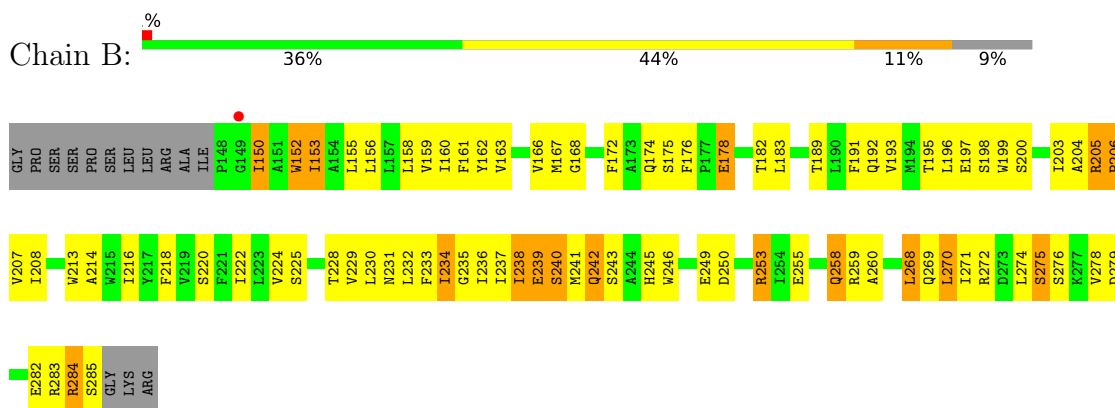
### 3 Residue-property plots

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.

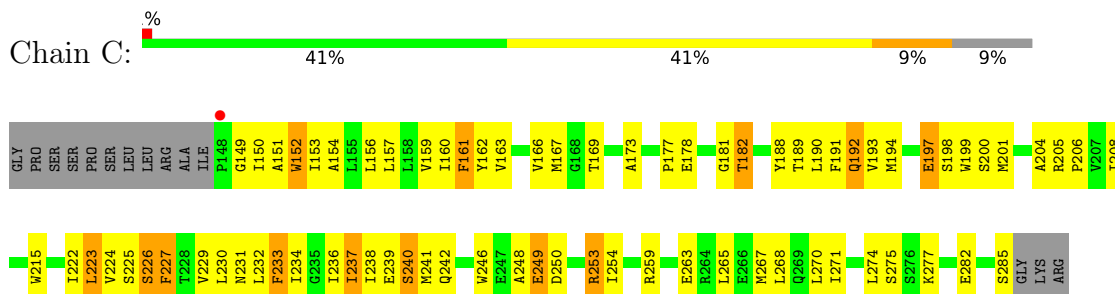
- Molecule 1: Ion transport protein



- Molecule 1: Ion transport protein

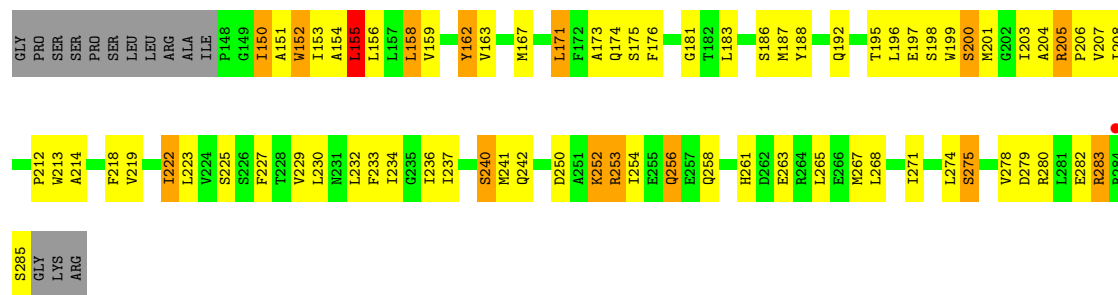


- Molecule 1: Ion transport protein



- Molecule 1: Ion transport protein

Chain D:  %





## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	153.51Å 160.52Å 166.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.95 15.00 – 2.95	Depositor EDS
% Data completeness (in resolution range)	97.9 (15.00-2.95) 98.7 (15.00-2.95)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.20	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.33 (at 2.96Å)	Xtrriage
Refinement program	REFMAC 5.8.0069	Depositor
R, $R_{free}$	0.205 , 0.236 0.205 , 0.238	Depositor DCC
$R_{free}$ test set	2185 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	89.3	Xtrriage
Anisotropy	0.141	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 81.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.027 for -h,-l,-k	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4667	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	92.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, CL, VVA

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	0.82	0/1167	1.04	4/1585 (0.3%)
1	B	0.79	0/1160	0.96	0/1575
1	C	0.86	0/1153	0.99	5/1566 (0.3%)
1	D	0.90	0/1159	1.05	5/1573 (0.3%)
All	All	0.84	0/4639	1.01	14/6299 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	LEU	CB-CG-CD1	-7.28	98.62	111.00
1	A	171	LEU	CB-CG-CD2	-6.42	100.08	111.00
1	A	270	LEU	CB-CG-CD2	6.30	121.71	111.00
1	D	171	LEU	CB-CG-CD1	-6.20	100.47	111.00
1	C	167	MET	CG-SD-CE	6.08	109.93	100.20
1	D	205	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	D	223	LEU	CA-CB-CG	-5.74	102.09	115.30
1	C	223	LEU	CA-CB-CG	-5.64	102.33	115.30
1	D	155	LEU	CB-CG-CD2	5.60	120.52	111.00
1	C	190	LEU	CB-CG-CD1	-5.23	102.11	111.00
1	C	265	LEU	CB-CG-CD2	-5.22	102.12	111.00
1	C	182	THR	N-CA-C	-5.13	97.14	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	ARG	CG-CD-NE	-5.12	101.04	111.80
1	D	167	MET	CG-SD-CE	5.06	108.30	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	244	ALA	Peptide

## 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	1132	0	1120	115	0
1	B	1126	0	1119	98	0
1	C	1122	0	1112	88	0
1	D	1128	0	1123	86	0
2	A	2	0	0	0	0
3	A	34	0	0	2	0
3	B	59	0	0	0	0
3	C	48	0	0	0	0
3	D	10	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
All	All	4667	0	4474	307	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 34.

All (307) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:VAL:HG12	1:A:233[A]:PHE:CE2	1.62	1.35
1:A:221:PHE:O	1:A:225:SER:HB3	1.50	1.12
1:A:229:VAL:CG1	1:A:233[A]:PHE:HE2	1.68	1.06
1:A:153:ILE:CG2	1:A:232:LEU:HD12	1.87	1.05
1:C:161:PHE:HE1	1:C:194:MET:CE	1.71	1.04
1:A:267:MET:HG2	1:B:268:LEU:HD23	1.41	1.01
1:A:229:VAL:CG1	1:A:233[A]:PHE:CE2	2.42	1.00
1:A:229:VAL:O	1:A:233[A]:PHE:CD2	2.14	1.00
1:A:229:VAL:HG12	1:A:233[A]:PHE:HE2	0.90	1.00
1:C:222:ILE:O	1:C:226:SER:OG	1.79	0.97
1:A:268:LEU:HD23	1:D:267:MET:HG2	1.47	0.97
1:C:161:PHE:HE1	1:C:194:MET:HE2	1.31	0.95
1:B:200:SER:O	1:B:205:ARG:HB2	1.67	0.93
1:A:233[B]:PHE:CE1	1:B:230:LEU:HD11	2.04	0.93
1:C:156:LEU:HD11	1:C:160:ILE:HD11	1.53	0.90
1:C:161:PHE:CE1	1:C:194:MET:CE	2.56	0.88
1:D:150:ILE:HD12	1:D:151:ALA:H	1.39	0.87
1:A:233[B]:PHE:CE2	1:D:233:PHE:HZ	1.92	0.87
1:A:180:PHE:HD1	1:A:186:SER:HG	1.19	0.87
1:C:177:PRO:HD2	1:C:178:GLU:OE1	1.74	0.86
1:C:150:ILE:HD12	1:C:151:ALA:N	1.92	0.85
1:B:241:MET:SD	1:C:241:MET:CE	2.67	0.82
1:A:267:MET:HG2	1:B:268:LEU:CD2	2.08	0.82
1:A:229:VAL:O	1:A:233[A]:PHE:HD2	1.63	0.82
1:B:162:TYR:O	1:B:166:VAL:HG23	1.79	0.82
1:B:178[A]:GLU:H	1:B:178[A]:GLU:CD	1.84	0.81
1:B:233:PHE:O	1:B:237:ILE:HG12	1.81	0.81
1:A:153:ILE:HG23	1:A:232:LEU:HD12	1.61	0.81
1:B:225:SER:O	1:B:229:VAL:HG23	1.82	0.79
1:B:249:GLU:O	1:B:253:ARG:HG3	1.83	0.79
1:A:233[B]:PHE:CD1	1:B:230:LEU:HD11	2.19	0.78
1:A:222:ILE:O	1:A:226:SER:HB2	1.83	0.77
1:B:272:ARG:HG2	1:B:272:ARG:HH21	1.50	0.75
1:A:233[B]:PHE:HZ	1:B:233:PHE:HE2	1.33	0.75
1:A:233[B]:PHE:HE2	1:D:233:PHE:HZ	1.35	0.75
1:C:208:ILE:HD12	1:C:215:TRP:HB3	1.69	0.74
1:A:268:LEU:HD23	1:D:267:MET:CG	2.19	0.73
1:B:241:MET:SD	1:C:241:MET:HE1	2.29	0.73
1:A:167:MET:O	1:A:171:LEU:HD12	1.88	0.73
1:A:204:ALA:O	1:A:208:ILE:HG13	1.89	0.73
1:A:268:LEU:HD11	1:A:272:ARG:NH2	2.04	0.73
1:C:156:LEU:CD1	1:C:160:ILE:HD11	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233[B]:PHE:HE1	1:B:230:LEU:HD11	1.54	0.73
1:A:153:ILE:HG23	1:A:232:LEU:CD1	2.17	0.73
1:A:249:GLU:HG3	1:A:250:ASP:N	2.04	0.73
1:A:233[B]:PHE:HE1	1:B:230:LEU:CD1	2.02	0.72
1:A:233[B]:PHE:CE1	1:B:230:LEU:CD1	2.73	0.72
1:D:218:PHE:O	1:D:222:ILE:HG13	1.89	0.72
1:A:153:ILE:CG2	1:A:232:LEU:CD1	2.66	0.72
1:C:267:MET:HB3	1:D:268:LEU:HD21	1.70	0.72
1:B:284:ARG:O	1:B:285:SER:O	2.08	0.72
1:C:204:ALA:O	1:C:208:ILE:HG12	1.89	0.72
1:B:241:MET:SD	1:C:241:MET:HE3	2.30	0.71
1:D:159:VAL:O	1:D:163:VAL:HG23	1.91	0.71
1:B:191:PHE:O	1:B:195:THR:HG23	1.90	0.70
1:B:218:PHE:O	1:B:222:ILE:HG12	1.91	0.70
1:A:149:GLY:O	1:A:152:TRP:HB2	1.91	0.70
1:A:244:ALA:HB2	1:B:238:ILE:HD13	1.74	0.69
1:C:241:MET:SD	1:D:241:MET:CE	2.80	0.69
1:D:171:LEU:HD13	1:D:213:TRP:HH2	1.57	0.69
1:D:250:ASP:HA	1:D:253:ARG:HD3	1.75	0.69
1:A:233[B]:PHE:HZ	1:B:233:PHE:CE2	2.10	0.68
1:C:161:PHE:CE1	1:C:194:MET:HE2	2.21	0.68
1:B:241:MET:HG2	1:C:241:MET:HE3	1.75	0.68
1:C:197:GLU:HG3	1:D:199:TRP:CD1	2.28	0.68
1:D:171:LEU:HD13	1:D:213:TRP:CH2	2.29	0.68
1:A:189:THR:O	1:A:193:VAL:HG23	1.93	0.68
1:C:151:ALA:HA	1:C:154:ALA:HB3	1.76	0.66
1:C:241:MET:SD	1:D:241:MET:HE1	2.35	0.66
1:B:258:GLN:OE1	1:B:258:GLN:HA	1.95	0.66
1:A:180:PHE:HD1	1:A:186:SER:OG	1.78	0.66
1:B:231:ASN:O	1:B:235:GLY:N	2.24	0.66
1:A:233[B]:PHE:CE2	1:D:233:PHE:CZ	2.82	0.65
1:B:271:ILE:O	1:B:275:SER:HB2	1.97	0.65
1:C:274:LEU:HD21	1:D:274:LEU:HD23	1.79	0.64
1:D:150:ILE:CD1	1:D:151:ALA:H	2.09	0.64
1:A:150:ILE:O	1:A:153:ILE:HG22	1.98	0.64
1:A:153:ILE:HG21	1:A:232:LEU:HD12	1.79	0.64
1:B:239:GLU:HG3	1:B:239:GLU:O	1.96	0.64
1:B:152:TRP:HA	1:B:152:TRP:CE3	2.32	0.64
1:C:162:TYR:O	1:C:166:VAL:HG23	1.98	0.63
1:A:221:PHE:O	1:A:225:SER:CB	2.39	0.63
1:D:153:ILE:O	1:D:156:LEU:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:276:SER:HA	1:B:279:ASP:HB2	1.81	0.63
1:D:252:LYS:O	1:D:256:GLN:HG2	1.99	0.62
1:A:241:MET:O	1:A:242:GLN:C	2.37	0.62
1:B:203:ILE:HG13	1:C:201:MET:CE	2.30	0.62
1:C:160:ILE:HG21	1:C:224:VAL:HG12	1.81	0.62
1:D:152:TRP:HA	1:D:152:TRP:CE3	2.34	0.62
1:A:159:VAL:O	1:A:163:VAL:HG23	2.00	0.61
1:D:253:ARG:HH11	1:D:253:ARG:HG3	1.64	0.61
1:D:253:ARG:HH11	1:D:253:ARG:CG	2.14	0.61
1:A:264:ARG:NH2	1:D:263:GLU:OE1	2.32	0.60
1:C:241:MET:SD	1:D:241:MET:HE3	2.42	0.60
1:B:152:TRP:HA	1:B:152:TRP:HE3	1.66	0.59
1:C:225:SER:O	1:C:229:VAL:HG23	2.02	0.59
1:C:237:ILE:HD12	1:D:234:ILE:HG12	1.84	0.59
1:A:149:GLY:O	1:A:152:TRP:CB	2.50	0.59
1:A:250:ASP:O	1:A:253:ARG:HG3	2.02	0.59
1:B:241:MET:CG	1:C:241:MET:HE3	2.32	0.59
1:B:189:THR:O	1:B:193:VAL:HG23	2.02	0.59
1:C:233:PHE:CD2	1:D:230:LEU:HD11	2.38	0.59
1:A:234:ILE:CD1	1:D:236:ILE:HG22	2.33	0.58
1:A:200:SER:O	1:A:205:ARG:HB2	2.03	0.58
1:C:236:ILE:O	1:C:240:SER:HB2	2.04	0.58
1:A:176:PHE:CZ	1:A:207:VAL:HA	2.38	0.57
1:A:193:VAL:HG13	1:A:199:TRP:HB2	1.86	0.57
1:C:169:THR:O	1:C:173:ALA:HB2	2.04	0.57
1:C:156:LEU:CD1	1:C:160:ILE:CD1	2.83	0.57
1:A:233[B]:PHE:HE2	1:D:233:PHE:CZ	2.18	0.57
1:C:156:LEU:HD11	1:C:160:ILE:CD1	2.32	0.57
1:B:270:LEU:N	1:B:270:LEU:HD23	2.20	0.57
1:B:197:GLU:OE1	1:B:198:SER:HB2	2.05	0.57
1:C:267:MET:HB3	1:D:268:LEU:CD2	2.35	0.57
1:C:208:ILE:CD1	1:C:215:TRP:HB3	2.35	0.56
1:A:195:THR:HB	1:B:196:LEU:HD13	1.87	0.56
1:C:263:GLU:OE2	1:D:261:HIS:ND1	2.39	0.56
1:B:238:ILE:HG22	1:B:239:GLU:N	2.21	0.56
1:D:205:ARG:HB2	1:D:206:PRO:HD2	1.88	0.56
1:A:194:MET:HG3	1:A:225:SER:OG	2.06	0.55
1:D:176:PHE:CZ	1:D:207:VAL:HA	2.41	0.55
1:C:200:SER:O	1:C:205:ARG:HG3	2.06	0.55
1:B:160:ILE:HD13	1:B:224:VAL:HG13	1.89	0.55
1:A:268:LEU:CD1	1:A:272:ARG:NH2	2.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:ARG:HH21	1:A:284:ARG:HB3	1.73	0.54
1:C:237:ILE:HD11	1:D:237:ILE:HD12	1.88	0.54
1:A:167:MET:O	1:A:171:LEU:CD1	2.53	0.54
1:A:269:GLN:OE1	1:A:269:GLN:HA	2.07	0.54
1:C:189:THR:O	1:C:193:VAL:HG23	2.06	0.54
1:A:233[B]:PHE:CZ	1:B:233:PHE:HE2	2.21	0.54
1:B:204:ALA:O	1:B:208:ILE:HG13	2.08	0.54
1:A:152:TRP:HA	1:A:152:TRP:CE3	2.43	0.54
1:A:205:ARG:NH1	1:D:192:GLN:OE1	2.41	0.54
1:C:270:LEU:HB2	1:D:271:ILE:HG21	1.91	0.53
1:C:161:PHE:CE1	1:C:194:MET:HE3	2.41	0.53
1:C:274:LEU:HD13	1:D:275:SER:HA	1.91	0.53
1:A:197:GLU:HG3	1:B:199:TRP:CD1	2.43	0.53
1:A:162:TYR:O	1:A:166:VAL:HG23	2.08	0.53
1:C:227:PHE:O	1:C:230:LEU:HB3	2.09	0.53
1:D:200:SER:HA	1:D:204:ALA:HB3	1.91	0.53
1:D:154:ALA:O	1:D:158:LEU:HD12	2.08	0.52
1:A:182:THR:HG23	1:A:185:ALA:HB2	1.90	0.52
1:B:192:GLN:NE2	1:B:197:GLU:O	2.41	0.52
1:B:155:LEU:O	1:B:159:VAL:HG23	2.10	0.52
1:C:249:GLU:HG3	1:C:250:ASP:N	2.24	0.52
1:A:256:GLN:NE2	1:B:253:ARG:NH2	2.57	0.52
1:A:256:GLN:OE1	1:B:253:ARG:NH2	2.41	0.52
1:B:250:ASP:O	1:B:253:ARG:HD3	2.09	0.52
1:D:242:GLN:O	1:D:242:GLN:HG3	2.09	0.52
1:A:246:TRP:O	1:A:250:ASP:HB2	2.10	0.52
1:C:197:GLU:OE2	1:C:198:SER:CB	2.57	0.52
1:C:271:ILE:HG13	1:D:271:ILE:HD13	1.91	0.52
1:A:183:LEU:O	1:A:187:MET:HG3	2.10	0.51
1:B:241:MET:HG2	1:C:241:MET:CE	2.40	0.51
1:D:195:THR:O	1:D:196:LEU:HB2	2.10	0.51
1:C:149:GLY:O	1:C:152:TRP:HB2	2.11	0.51
1:B:234:ILE:O	1:B:237:ILE:N	2.42	0.51
1:C:191:PHE:CD2	1:D:219:VAL:HG22	2.45	0.51
1:A:256:GLN:CD	1:B:253:ARG:NH2	2.63	0.51
1:D:278:VAL:HG12	1:D:278:VAL:O	2.10	0.51
1:A:241:MET:SD	1:B:241:MET:HE1	2.51	0.51
1:D:253:ARG:CG	1:D:253:ARG:NH1	2.73	0.51
1:C:248:ALA:O	1:C:249:GLU:C	2.49	0.51
1:D:230:LEU:O	1:D:233:PHE:HB3	2.11	0.51
1:A:280:ARG:O	1:A:281:LEU:C	2.47	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:162:TYR:CD1	1:D:162:TYR:C	2.85	0.51
1:A:279:ASP:O	1:A:282:GLU:HB3	2.11	0.50
1:B:197:GLU:HG3	1:C:199:TRP:CD1	2.46	0.50
1:B:272:ARG:HG2	1:B:272:ARG:NH2	2.22	0.50
1:D:205:ARG:HB2	1:D:206:PRO:CD	2.40	0.50
1:C:233:PHE:CD1	1:C:233:PHE:C	2.85	0.50
1:B:189:THR:HG23	1:B:203:ILE:HD13	1.92	0.50
1:A:233[B]:PHE:CZ	1:A:237:ILE:HD11	2.46	0.50
1:A:228:THR:O	1:A:228:THR:HG22	2.12	0.50
1:A:167:MET:O	1:A:171:LEU:CG	2.60	0.49
1:A:160:ILE:HD13	1:A:224:VAL:HG12	1.93	0.49
1:A:268:LEU:HD13	1:A:272:ARG:NH1	2.27	0.49
1:D:152:TRP:HA	1:D:152:TRP:HE3	1.75	0.49
1:A:241:MET:HE3	1:D:241:MET:SD	2.52	0.49
1:C:239:GLU:O	1:C:239:GLU:HG3	2.12	0.49
1:B:205:ARG:N	1:B:206:PRO:HD2	2.27	0.49
1:A:198:SER:HA	1:D:197:GLU:OE2	2.11	0.49
1:A:233[B]:PHE:CE2	1:A:237:ILE:CD1	2.96	0.49
1:C:223:LEU:HD23	1:C:223:LEU:HA	1.64	0.49
1:C:197:GLU:OE2	1:C:198:SER:HB2	2.12	0.48
1:C:230:LEU:O	1:C:233:PHE:HB3	2.12	0.48
1:D:150:ILE:HD12	1:D:151:ALA:N	2.20	0.48
1:C:159:VAL:O	1:C:163:VAL:HG23	2.13	0.48
1:A:200:SER:HA	1:A:204:ALA:HB3	1.96	0.48
1:A:241:MET:CE	1:D:241:MET:SD	3.02	0.48
1:B:245:HIS:CE1	1:C:246:TRP:HB3	2.49	0.48
1:D:283:ARG:C	1:D:285:SER:H	2.16	0.48
1:A:258:GLN:HA	1:A:258:GLN:OE1	2.13	0.47
1:D:213:TRP:CE3	1:D:214:ALA:HA	2.50	0.47
1:A:199:TRP:CD1	1:D:197:GLU:HG3	2.48	0.47
1:B:213:TRP:CE3	1:B:214:ALA:HA	2.49	0.47
1:A:208:ILE:HG22	1:A:208:ILE:O	2.14	0.47
1:A:194:MET:CE	3:A:303:VVA:C36	2.93	0.47
1:A:274:LEU:HD11	1:B:278:VAL:HG21	1.96	0.47
1:D:151:ALA:HA	1:D:154:ALA:HB3	1.97	0.47
1:A:167:MET:HG3	1:A:171:LEU:HD11	1.96	0.47
1:B:236:ILE:HG22	1:C:234:ILE:CD1	2.45	0.47
1:C:160:ILE:HG21	1:C:224:VAL:CG1	2.45	0.47
1:B:270:LEU:HD23	1:B:270:LEU:H	1.79	0.47
1:C:188:TYR:HH	1:D:200:SER:HG	1.63	0.46
1:B:240:SER:HB3	1:C:238:ILE:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:153:ILE:HD13	1:C:231:ASN:CB	2.45	0.46
1:D:155:LEU:O	1:D:155:LEU:HG	2.14	0.46
1:D:278:VAL:O	1:D:278:VAL:CG1	2.63	0.46
1:A:206:PRO:O	1:A:209:GLU:HB2	2.16	0.46
1:A:245:HIS:CE1	1:B:246:TRP:HB3	2.51	0.46
1:A:284:ARG:HH11	1:B:282:GLU:CG	2.28	0.46
1:D:150:ILE:CD1	1:D:151:ALA:N	2.77	0.46
1:D:208:ILE:O	1:D:212:PRO:HA	2.16	0.46
1:A:270:LEU:O	1:A:273:ASP:HB2	2.16	0.45
1:A:274:LEU:HD13	1:B:275:SER:HA	1.97	0.45
1:C:177:PRO:O	1:C:181:GLY:HA3	2.15	0.45
1:B:242:GLN:HA	1:B:246:TRP:HB2	1.98	0.45
1:B:272:ARG:HH21	1:B:272:ARG:CG	2.24	0.45
1:A:259:ARG:O	1:A:263:GLU:HG3	2.17	0.45
1:B:205:ARG:H	1:B:206:PRO:HD2	1.80	0.45
1:D:236:ILE:O	1:D:240:SER:HB2	2.17	0.45
1:A:234:ILE:HD11	1:D:236:ILE:HG22	1.99	0.45
1:C:192:GLN:HG3	1:D:200:SER:CB	2.47	0.45
1:A:230:LEU:HD11	1:D:233:PHE:CE1	2.52	0.45
1:B:203:ILE:O	1:B:207:VAL:HG23	2.16	0.45
1:B:241:MET:CG	1:C:241:MET:CE	2.95	0.45
1:C:153:ILE:HD13	1:C:231:ASN:HB2	1.99	0.45
1:A:233[B]:PHE:CE2	1:A:237:ILE:HD12	2.52	0.44
1:A:268:LEU:CD1	1:A:272:ARG:CZ	2.94	0.44
1:A:258:GLN:O	1:A:259:ARG:C	2.54	0.44
1:B:272:ARG:NH2	1:B:272:ARG:CG	2.79	0.44
1:C:205:ARG:HB2	1:C:206:PRO:CD	2.47	0.44
1:C:277:LYS:HD3	1:D:279:ASP:HB3	1.98	0.44
1:B:153:ILE:HG22	1:B:228:THR:HG23	2.00	0.44
1:B:159:VAL:O	1:B:163:VAL:HG23	2.17	0.44
1:A:173:ALA:HB2	1:A:180:PHE:O	2.17	0.44
1:A:257:GLU:O	1:A:257:GLU:HG3	2.16	0.44
1:C:157:LEU:C	1:C:157:LEU:HD13	2.37	0.44
1:C:274:LEU:HD21	1:D:274:LEU:CD2	2.47	0.44
1:C:152:TRP:HA	1:C:152:TRP:CE3	2.52	0.44
1:A:265:LEU:HD12	1:A:265:LEU:HA	1.84	0.44
1:C:233:PHE:HD2	1:D:230:LEU:HD11	1.82	0.44
1:B:203:ILE:HD11	1:C:201:MET:HE2	2.00	0.44
1:A:284:ARG:NH1	1:B:282:GLU:CG	2.82	0.43
1:D:155:LEU:O	1:D:159:VAL:HG23	2.17	0.43
1:C:253:ARG:O	1:C:254:ILE:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:TRP:O	1:A:250:ASP:CB	2.66	0.43
1:B:153:ILE:O	1:B:156:LEU:HB3	2.18	0.43
1:C:270:LEU:N	1:C:270:LEU:HD23	2.33	0.43
1:D:153:ILE:HD11	1:D:232:LEU:HA	2.00	0.43
1:B:176:PHE:CZ	1:B:207:VAL:HA	2.54	0.43
1:B:205:ARG:N	1:B:206:PRO:CD	2.80	0.43
1:D:197:GLU:O	1:D:198:SER:HB2	2.17	0.43
1:B:150:ILE:O	1:B:153:ILE:N	2.46	0.43
1:B:233:PHE:HD1	1:C:230:LEU:CD1	2.32	0.43
1:B:253:ARG:HE	1:B:253:ARG:HB2	1.63	0.43
1:C:156:LEU:HD12	1:C:160:ILE:HG13	2.01	0.43
1:A:274:LEU:O	1:A:278:VAL:HG23	2.19	0.43
1:A:233[B]:PHE:CE2	1:A:237:ILE:HD11	2.53	0.43
1:A:284:ARG:HH11	1:B:282:GLU:HG2	1.84	0.43
1:B:284:ARG:HH21	1:C:282:GLU:HG2	1.84	0.43
1:D:173:ALA:HB1	1:D:181:GLY:HA2	2.01	0.42
1:A:234:ILE:O	1:A:237:ILE:N	2.52	0.42
1:C:156:LEU:CG	1:C:160:ILE:HD11	2.49	0.42
1:D:225:SER:O	1:D:229:VAL:HG23	2.19	0.42
1:B:234:ILE:HG22	1:B:235:GLY:N	2.34	0.42
1:B:213:TRP:HE3	1:B:213:TRP:O	2.02	0.42
1:B:269:GLN:O	1:B:272:ARG:N	2.52	0.42
1:D:203:ILE:O	1:D:207:VAL:HG23	2.19	0.42
1:B:150:ILE:HG21	1:B:236:ILE:HG13	2.02	0.42
1:D:208:ILE:O	1:D:208:ILE:HG22	2.19	0.42
1:D:258:GLN:OE1	1:D:258:GLN:HA	2.18	0.42
1:B:259:ARG:O	1:B:260:ALA:C	2.58	0.42
1:A:268:LEU:HD13	1:A:272:ARG:CZ	2.50	0.42
1:A:233[B]:PHE:CD1	1:B:230:LEU:CD1	2.97	0.42
1:A:255:GLU:HG2	1:A:256:GLN:N	2.34	0.42
1:A:229:VAL:O	1:A:233[A]:PHE:CE2	2.69	0.42
1:A:229:VAL:HG12	1:A:233[A]:PHE:CD2	2.38	0.41
1:C:193:VAL:HG13	1:C:199:TRP:HB2	2.02	0.41
1:D:279:ASP:HA	1:D:282:GLU:HB2	2.01	0.41
1:C:178:GLU:H	1:C:178:GLU:CD	2.24	0.41
1:D:153:ILE:O	1:D:154:ALA:C	2.57	0.41
1:D:150:ILE:O	1:D:153:ILE:N	2.52	0.41
1:B:216:ILE:O	1:B:220:SER:HB3	2.20	0.41
1:B:230:LEU:O	1:B:233:PHE:HB3	2.20	0.41
1:A:233[B]:PHE:CZ	1:B:233:PHE:CE2	2.99	0.41
1:B:168:GLY:O	1:B:172:PHE:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:205:ARG:HB2	1:C:206:PRO:HD3	2.03	0.41
1:D:150:ILE:C	1:D:152:TRP:N	2.74	0.41
1:C:198:SER:OG	1:D:201:MET:HG3	2.21	0.41
1:C:277:LYS:CD	1:D:279:ASP:HB3	2.51	0.41
1:A:215:TRP:CD2	3:A:302:VVA:O31	2.74	0.40
1:A:231:ASN:N	1:A:231:ASN:HD22	2.19	0.40
1:A:242:GLN:HA	1:A:246:TRP:HB2	2.02	0.40
1:A:256:GLN:CD	1:B:253:ARG:HH21	2.21	0.40
1:B:150:ILE:O	1:B:153:ILE:HG13	2.21	0.40
1:B:203:ILE:CG1	1:C:201:MET:CE	2.98	0.40
1:C:208:ILE:HD11	1:C:215:TRP:HA	2.02	0.40
1:C:197:GLU:OE2	1:C:198:SER:HB3	2.20	0.40
1:D:200:SER:O	1:D:205:ARG:HG3	2.21	0.40
1:D:268:LEU:HD23	1:D:268:LEU:HA	1.75	0.40
1:A:274:LEU:HD21	1:B:274:LEU:HG	2.03	0.40
1:B:270:LEU:N	1:B:270:LEU:CD2	2.84	0.40
1:D:183:LEU:O	1:D:187:MET:HG3	2.21	0.40
1:D:188:TYR:CD1	1:D:188:TYR:C	2.95	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	138/152 (91%)	131 (95%)	7 (5%)	0	100	100
1	B	137/152 (90%)	130 (95%)	6 (4%)	1 (1%)	22	56
1	C	136/152 (90%)	130 (96%)	6 (4%)	0	100	100
1	D	136/152 (90%)	130 (96%)	6 (4%)	0	100	100
All	All	547/608 (90%)	521 (95%)	25 (5%)	1 (0%)	47	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	238	ILE

### 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	118/131 (90%)	95 (80%)	23 (20%)	1	6
1	B	118/131 (90%)	90 (76%)	28 (24%)	1	2
1	C	118/131 (90%)	100 (85%)	18 (15%)	2	11
1	D	119/131 (91%)	99 (83%)	20 (17%)	2	9
All	All	473/524 (90%)	384 (81%)	89 (19%)	1	7

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	TRP
1	A	153	ILE
1	A	161	PHE
1	A	175	SER
1	A	178	GLU
1	A	182	THR
1	A	186	SER
1	A	197	GLU
1	A	201	MET
1	A	205	ARG
1	A	226	SER
1	A	232	LEU
1	A	240	SER
1	A	241	MET
1	A	247	GLU
1	A	249	GLU
1	A	254	ILE
1	A	255	GLU
1	A	258	GLN
1	A	268	LEU
1	A	269	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	277	LYS
1	A	282	GLU
1	B	150	ILE
1	B	152	TRP
1	B	153	ILE
1	B	158	LEU
1	B	161	PHE
1	B	167	MET
1	B	174	GLN
1	B	175	SER
1	B	178[A]	GLU
1	B	178[B]	GLU
1	B	182	THR
1	B	183	LEU
1	B	205	ARG
1	B	206	PRO
1	B	232	LEU
1	B	234	ILE
1	B	239	GLU
1	B	240	SER
1	B	242	GLN
1	B	243	SER
1	B	253	ARG
1	B	255	GLU
1	B	258	GLN
1	B	268	LEU
1	B	270	LEU
1	B	275	SER
1	B	283	ARG
1	B	284	ARG
1	C	152	TRP
1	C	161	PHE
1	C	182	THR
1	C	192	GLN
1	C	197	GLU
1	C	226	SER
1	C	227	PHE
1	C	232	LEU
1	C	233	PHE
1	C	237	ILE
1	C	240	SER
1	C	242	GLN

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Mol	Chain	Res	Type
1	C	249	GLU
1	C	253	ARG
1	C	259	ARG
1	C	268	LEU
1	C	275	SER
1	C	285	SER
1	D	150	ILE
1	D	152	TRP
1	D	155	LEU
1	D	158	LEU
1	D	162	TYR
1	D	174	GLN
1	D	175	SER
1	D	186	SER
1	D	200	SER
1	D	222	ILE
1	D	227	PHE
1	D	240	SER
1	D	252	LYS
1	D	253	ARG
1	D	254	ILE
1	D	256	GLN
1	D	265	LEU
1	D	275	SER
1	D	280	ARG
1	D	283	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	231	ASN
1	A	245	HIS
1	B	231	ASN
1	B	242	GLN
1	B	245	HIS
1	C	242	GLN
1	D	256	GLN

### 5.3.3 RNA

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 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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
3	VVA	B	303	-	16,16,28	0.41	0	15,15,31	0.61	0
3	VVA	C	301	-	20,20,28	1.63	2 (10%)	22,23,31	2.17	4 (18%)
3	VVA	C	302	-	9,9,28	0.66	0	8,8,31	0.49	0
3	VVA	C	304	-	10,10,28	0.51	0	9,9,31	0.28	0
3	VVA	D	301	-	9,9,28	0.49	0	8,8,31	0.63	0
3	VVA	A	303	-	12,12,28	0.46	0	11,11,31	0.37	0
3	VVA	A	302	-	20,20,28	1.77	2 (10%)	22,23,31	1.64	3 (13%)
3	VVA	B	301	-	20,20,28	1.57	1 (5%)	22,23,31	1.73	5 (22%)
3	VVA	C	303	-	5,5,28	0.56	0	4,4,31	0.38	0
3	VVA	B	302	-	20,20,28	1.51	1 (5%)	22,23,31	1.55	3 (13%)

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
3	VVA	B	303	-	-	11/14/14/29	-
3	VVA	C	301	-	-	11/21/21/29	-
3	VVA	C	302	-	-	2/7/7/29	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	VVA	C	304	-	-	7/8/8/29	-
3	VVA	D	301	-	-	4/7/7/29	-
3	VVA	A	303	-	-	5/10/10/29	-
3	VVA	A	302	-	-	10/21/21/29	-
3	VVA	B	301	-	-	10/21/21/29	-
3	VVA	C	303	-	-	2/3/3/29	-
3	VVA	B	302	-	-	8/21/21/29	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	VVA	O2-C31	6.41	1.52	1.33
3	B	301	VVA	O2-C31	6.08	1.51	1.33
3	C	301	VVA	O2-C31	5.90	1.50	1.33
3	B	302	VVA	O2-C31	5.64	1.49	1.33
3	A	302	VVA	C32-C31	2.57	1.58	1.50
3	C	301	VVA	C32-C31	2.14	1.57	1.50

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	301	VVA	O2-C31-C32	5.54	129.30	111.91
3	C	301	VVA	C2-O2-C31	4.84	132.56	116.92
3	C	301	VVA	O2-C31-O31	-4.62	111.94	123.59
3	A	302	VVA	O2-C31-C32	4.52	126.09	111.91
3	B	301	VVA	O2-C31-C32	4.43	125.82	111.91
3	B	301	VVA	C2-O2-C31	4.26	130.69	116.92
3	B	302	VVA	O2-C31-C32	4.00	124.47	111.91
3	B	302	VVA	C2-O2-C31	3.98	129.77	116.92
3	A	302	VVA	O2-C31-O31	-3.29	115.28	123.59
3	A	302	VVA	C2-O2-C31	2.76	125.84	116.92
3	B	301	VVA	O2-C31-O31	-2.51	117.25	123.59
3	B	302	VVA	O2-C31-O31	-2.50	117.28	123.59
3	B	301	VVA	O3P-C1-C2	2.44	118.45	109.50
3	C	301	VVA	O3P-C1-C2	2.38	118.20	109.50
3	B	301	VVA	O2-C2-C1	2.34	115.54	108.61

There are no chirality outliers.

All (70) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
3	A	302	VVA	C4-O4P-P-O1P
3	A	302	VVA	C4-O4P-P-O2P
3	A	302	VVA	C4-O4P-P-O3P
3	A	302	VVA	C1-O3P-P-O2P
3	A	302	VVA	C2-C1-O3P-P
3	A	302	VVA	O3P-C1-C2-O2
3	B	301	VVA	O3P-C1-C2-O2
3	B	301	VVA	C1-C2-O2-C31
3	B	302	VVA	O3P-C1-C2-O2
3	C	301	VVA	O3P-C1-C2-O2
3	C	301	VVA	C1-C2-O2-C31
3	C	301	VVA	C32-C31-O2-C2
3	C	301	VVA	O31-C31-O2-C2
3	D	301	VVA	C35-C36-C37-C38
3	A	302	VVA	C1-O3P-P-O4P
3	B	302	VVA	C1-O3P-P-O4P
3	B	303	VVA	C40-C41-C42-C43
3	C	304	VVA	C35-C36-C37-C38
3	A	302	VVA	C34-C35-C36-C37
3	A	303	VVA	C35-C36-C37-C38
3	B	303	VVA	C43-C44-C45-C46
3	A	303	VVA	C36-C37-C38-C39
3	B	301	VVA	O4P-C4-C5-N6
3	B	302	VVA	C34-C35-C36-C37
3	B	303	VVA	C33-C34-C35-C36
3	B	301	VVA	C32-C31-O2-C2
3	B	303	VVA	C41-C42-C43-C44
3	C	301	VVA	C33-C34-C35-C36
3	B	301	VVA	O31-C31-O2-C2
3	C	303	VVA	C33-C34-C35-C36
3	A	302	VVA	C35-C36-C37-C38
3	B	303	VVA	C32-C33-C34-C35
3	C	304	VVA	C37-C38-C39-C40
3	C	304	VVA	C32-C33-C34-C35
3	D	301	VVA	C34-C35-C36-C37
3	C	302	VVA	C32-C33-C34-C35
3	B	303	VVA	C36-C37-C38-C39
3	B	303	VVA	C44-C45-C46-C47
3	A	302	VVA	C36-C37-C38-C39
3	D	301	VVA	C36-C37-C38-C39
3	C	301	VVA	O4P-C4-C5-N6
3	B	302	VVA	C36-C37-C38-C39
3	C	304	VVA	C31-C32-C33-C34

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Mol	Chain	Res	Type	Atoms
3	C	303	VVA	C32-C33-C34-C35
3	C	301	VVA	C36-C37-C38-C39
3	C	304	VVA	C33-C34-C35-C36
3	A	303	VVA	C38-C39-C40-C41
3	C	304	VVA	C38-C39-C40-C41
3	C	304	VVA	C34-C35-C36-C37
3	B	302	VVA	C1-O3P-P-O1P
3	B	303	VVA	C35-C36-C37-C38
3	B	302	VVA	C35-C36-C37-C38
3	B	301	VVA	C4-O4P-P-O3P
3	B	301	VVA	C1-O3P-P-O4P
3	B	302	VVA	C4-O4P-P-O3P
3	C	301	VVA	C4-O4P-P-O3P
3	C	301	VVA	C1-O3P-P-O4P
3	B	303	VVA	C37-C38-C39-C40
3	A	303	VVA	C31-C32-C33-C34
3	D	301	VVA	C37-C38-C39-C40
3	B	301	VVA	C35-C36-C37-C38
3	A	303	VVA	C33-C34-C35-C36
3	C	301	VVA	C32-C33-C34-C35
3	B	302	VVA	O4P-C4-C5-N6
3	B	303	VVA	C34-C35-C36-C37
3	C	302	VVA	C34-C35-C36-C37
3	B	303	VVA	C39-C40-C41-C42
3	B	301	VVA	C36-C37-C38-C39
3	B	301	VVA	C4-O4P-P-O1P
3	C	301	VVA	C4-O4P-P-O1P

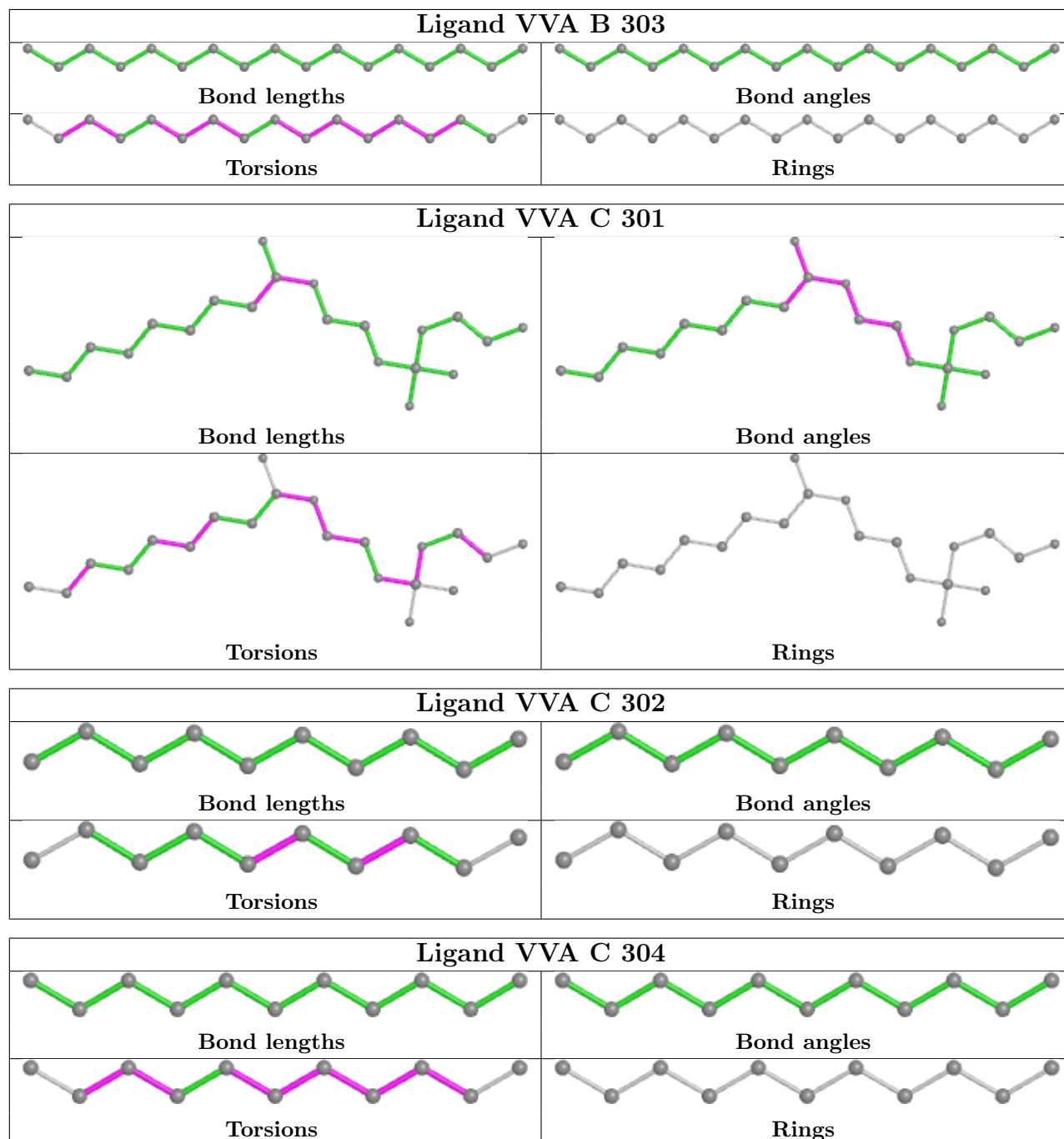
There are no ring outliers.

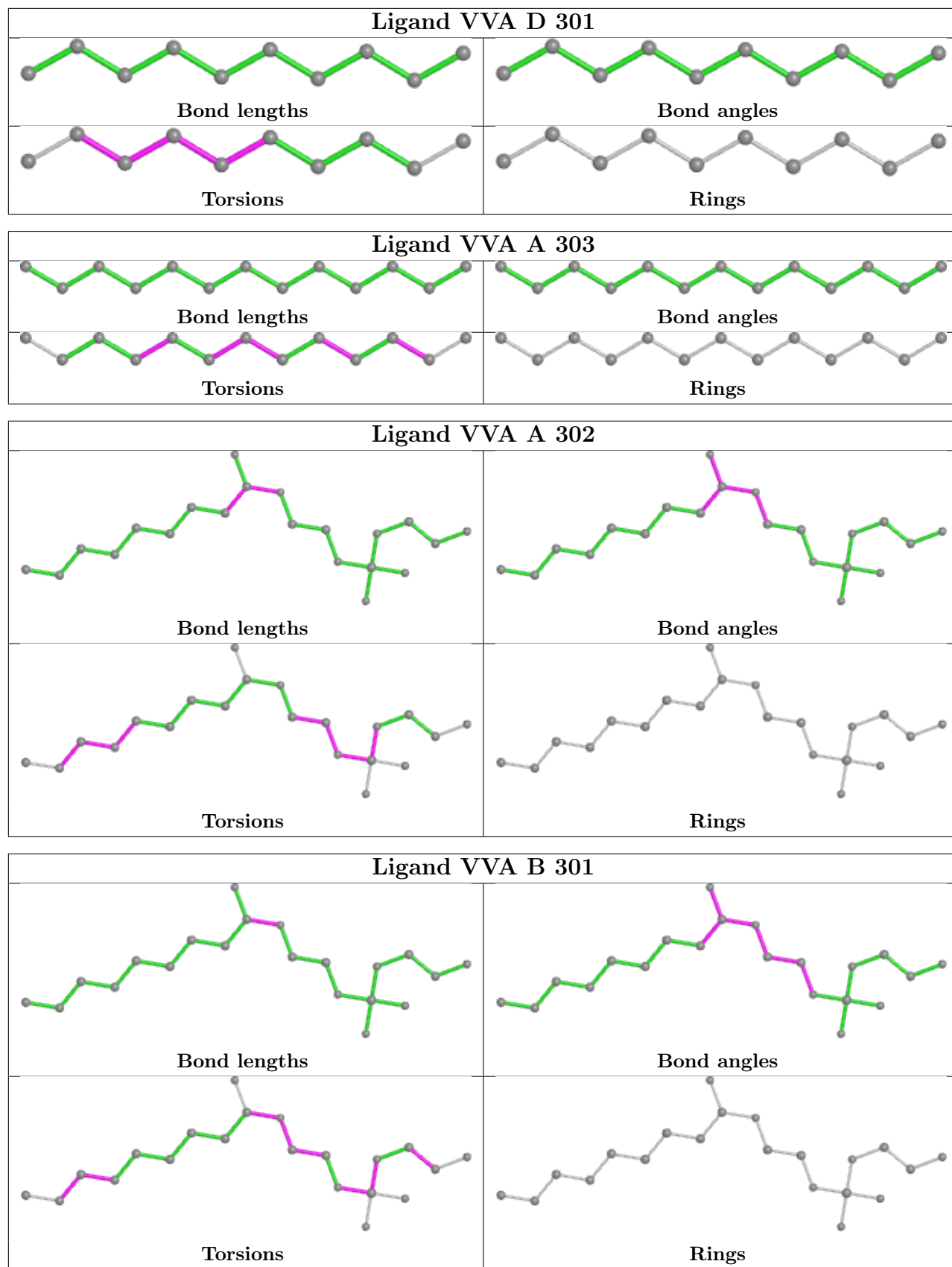
2 monomers are involved in 2 short contacts:

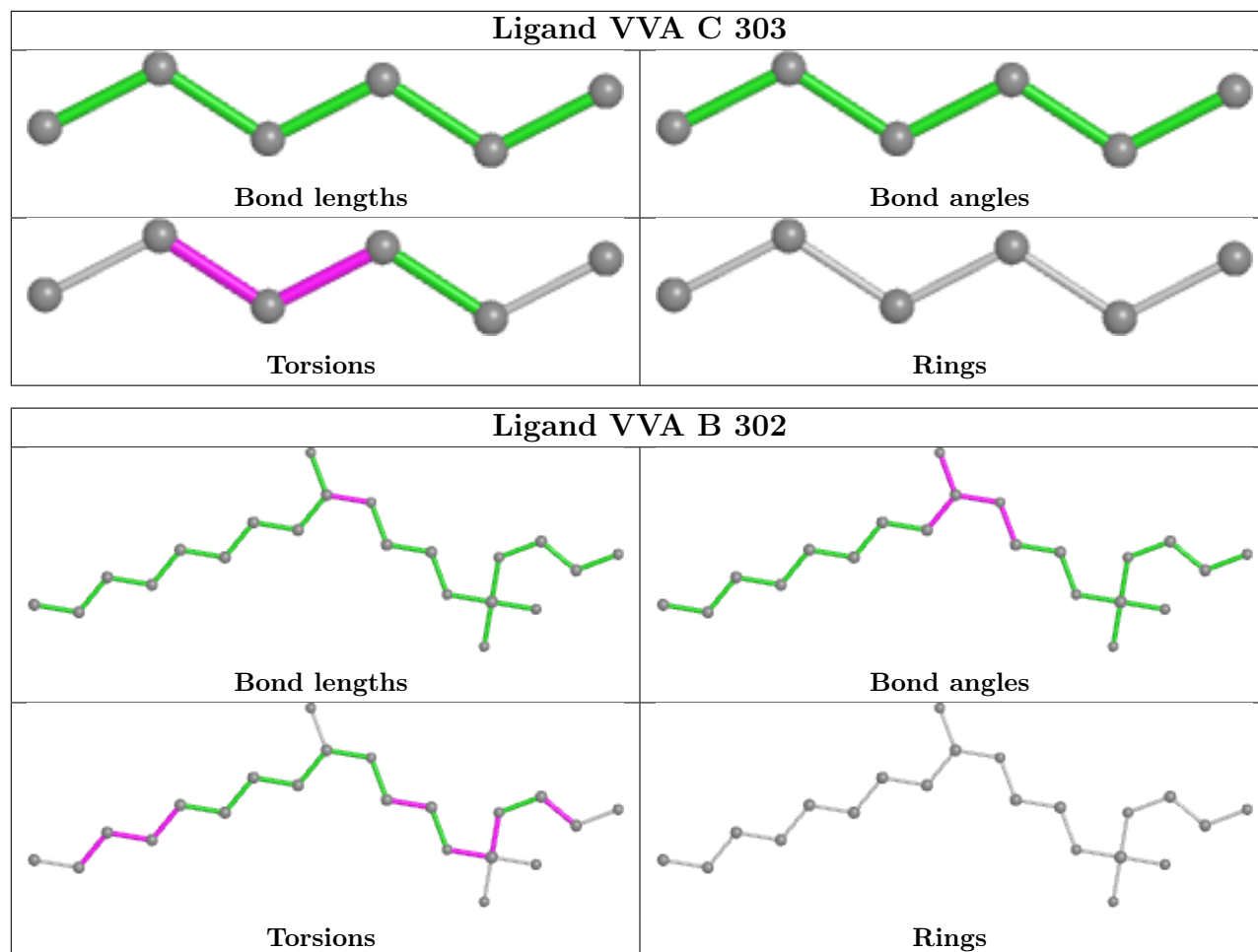
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	VVA	1	0
3	A	302	VVA	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	139/152 (91%)	-0.53	1 (0%) 87 76	60, 87, 127, 165	0
1	B	138/152 (90%)	-0.53	1 (0%) 87 76	61, 93, 131, 168	1 (0%)
1	C	138/152 (90%)	-0.56	1 (0%) 87 76	56, 87, 135, 168	0
1	D	138/152 (90%)	-0.64	1 (0%) 87 76	53, 82, 125, 145	1 (0%)
All	All	553/608 (90%)	-0.56	4 (0%) 87 76	53, 88, 131, 168	2 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	286	GLY	4.3
1	D	284	ARG	2.9
1	C	148	PRO	2.6
1	B	149	GLY	2.3

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

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

### 6.3 Carbohydrates [i](#)

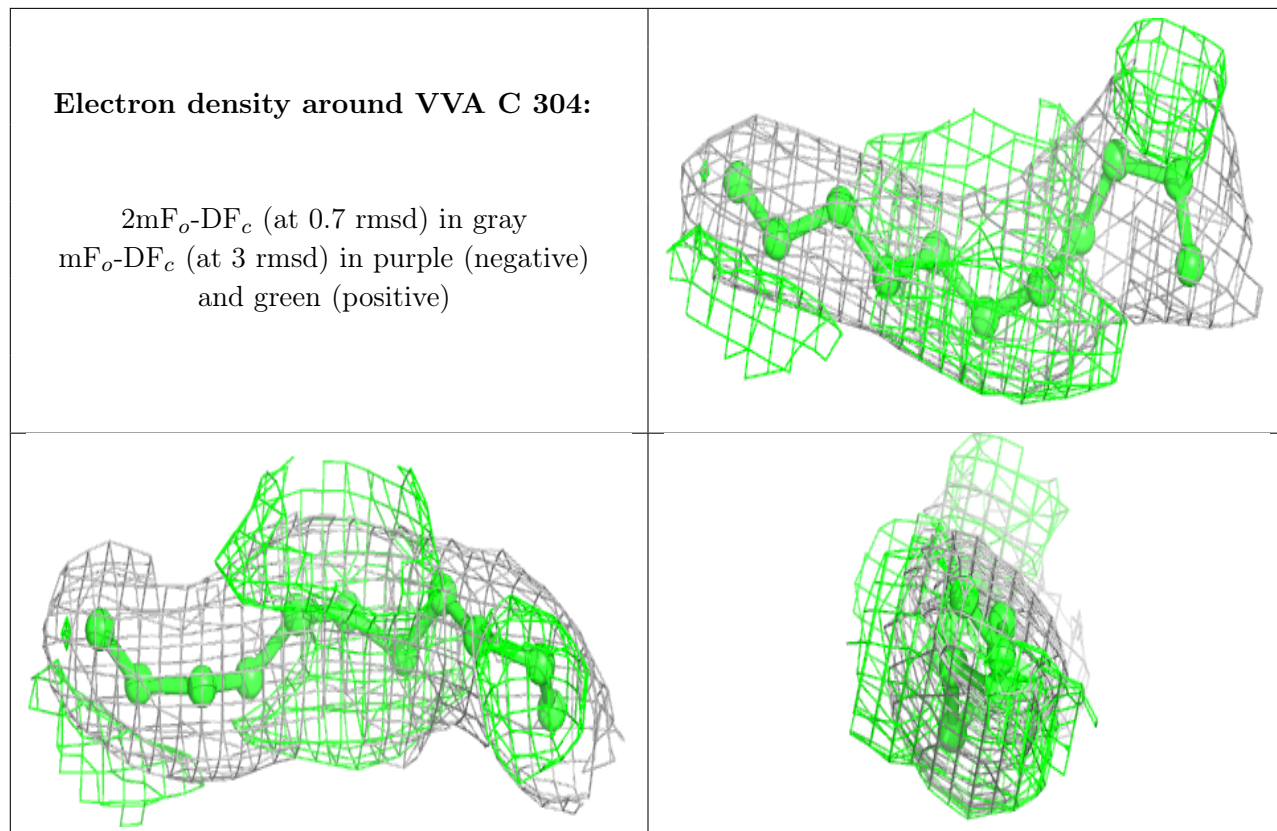
There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

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

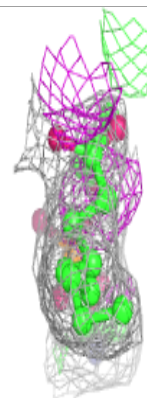
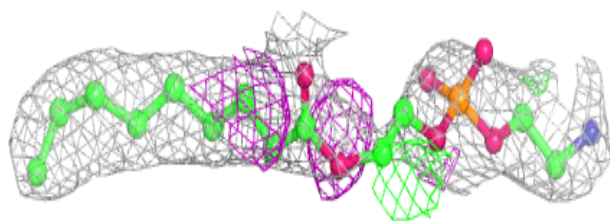
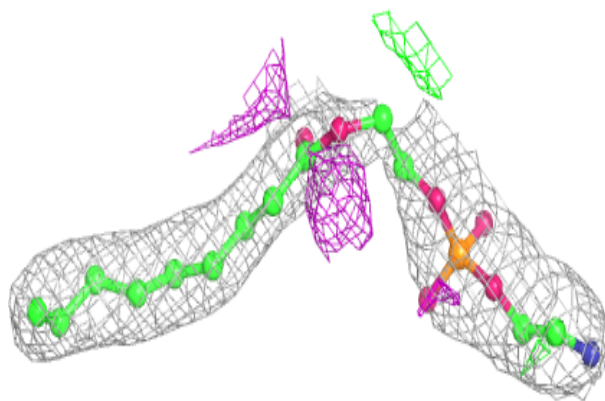
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NA	C	305	1/1	0.48	1.19	105,105,105,105	0
3	VVA	C	304	11/29	0.84	0.19	77,112,125,131	0
3	VVA	B	301	21/29	0.86	0.29	68,85,135,197	0
3	VVA	B	303	17/29	0.86	0.22	99,108,130,131	0
4	NA	B	304	1/1	0.87	0.64	81,81,81,81	0
3	VVA	D	301	10/29	0.88	0.21	78,97,108,111	0
3	VVA	A	302	21/29	0.90	0.17	59,91,139,194	0
3	VVA	C	302	10/29	0.91	0.31	69,86,95,100	0
3	VVA	C	303	6/29	0.91	0.53	79,104,110,113	0
3	VVA	A	303	13/29	0.91	0.18	94,108,143,150	0
3	VVA	B	302	21/29	0.92	0.19	67,90,161,187	0
3	VVA	C	301	21/29	0.92	0.23	63,97,146,166	0
2	CL	A	301	1/1	0.98	0.05	72,72,72,72	0
2	CL	A	304	1/1	0.98	0.78	108,108,108,108	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.

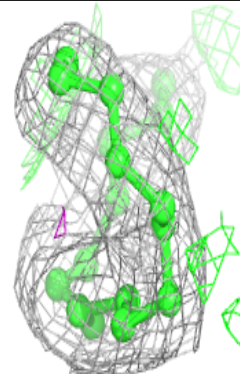
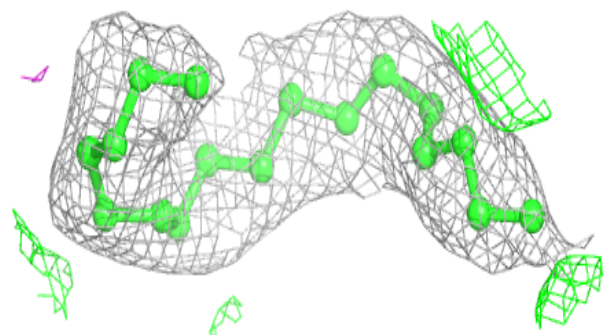
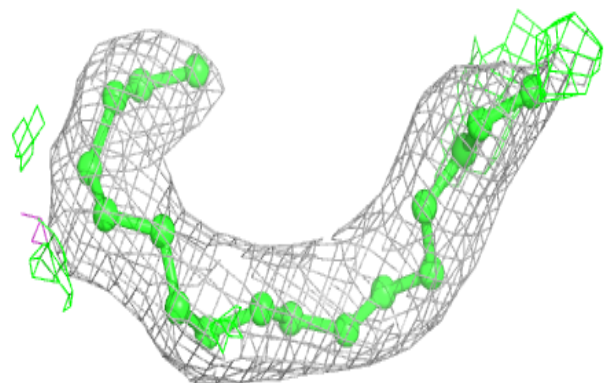


**Electron density around VVA B 301:**

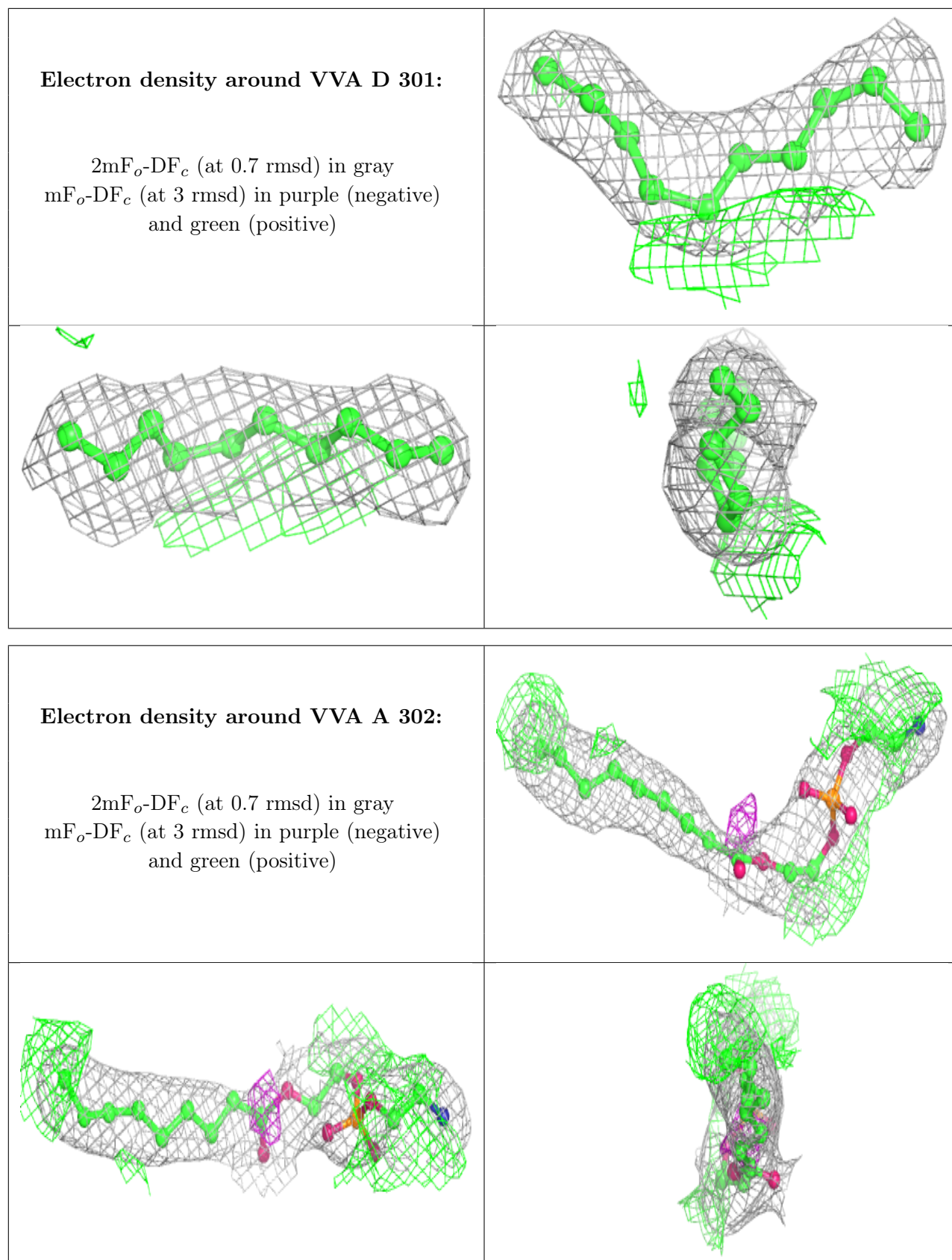
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

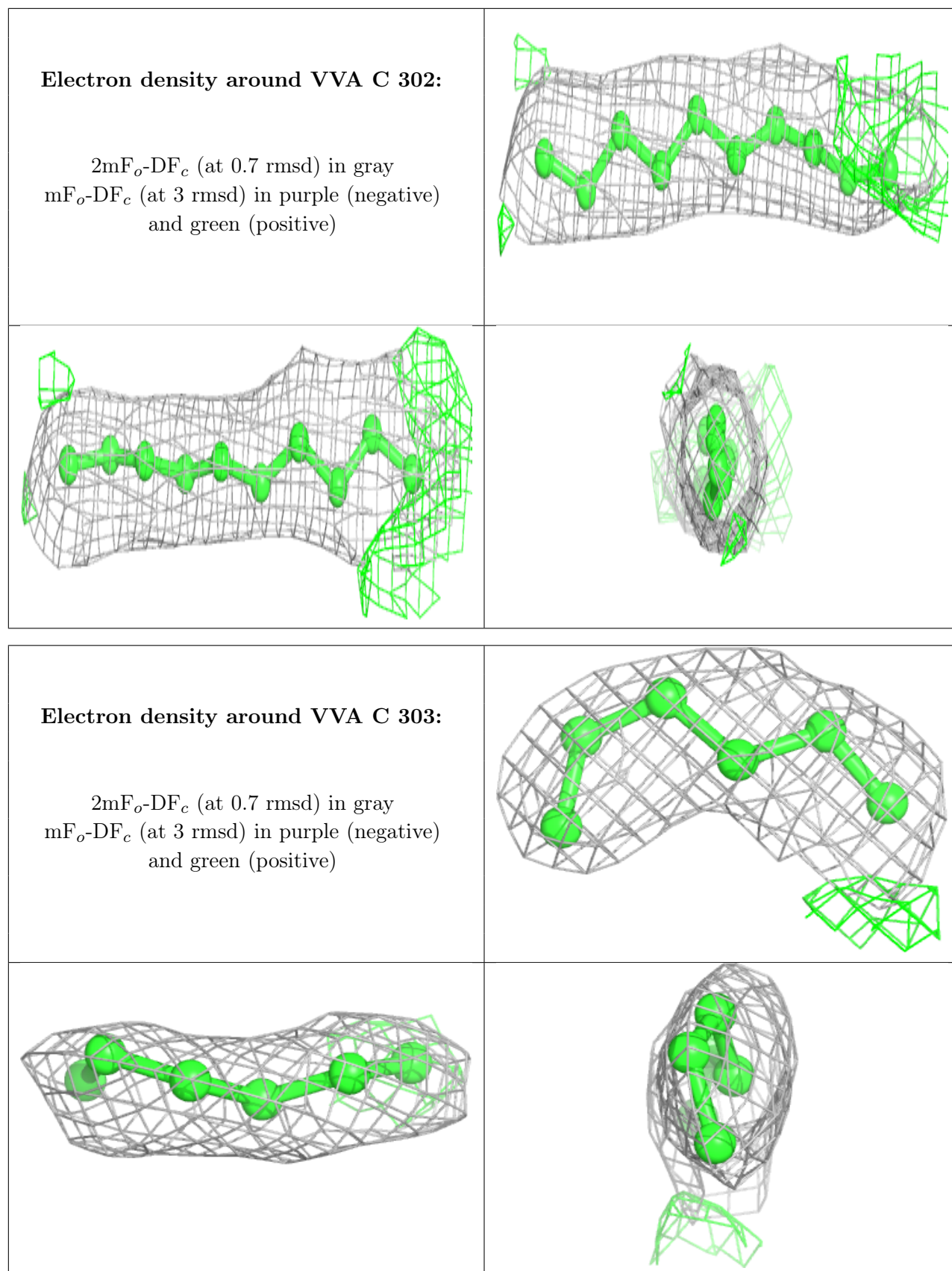
**Electron density around VVA B 303:**

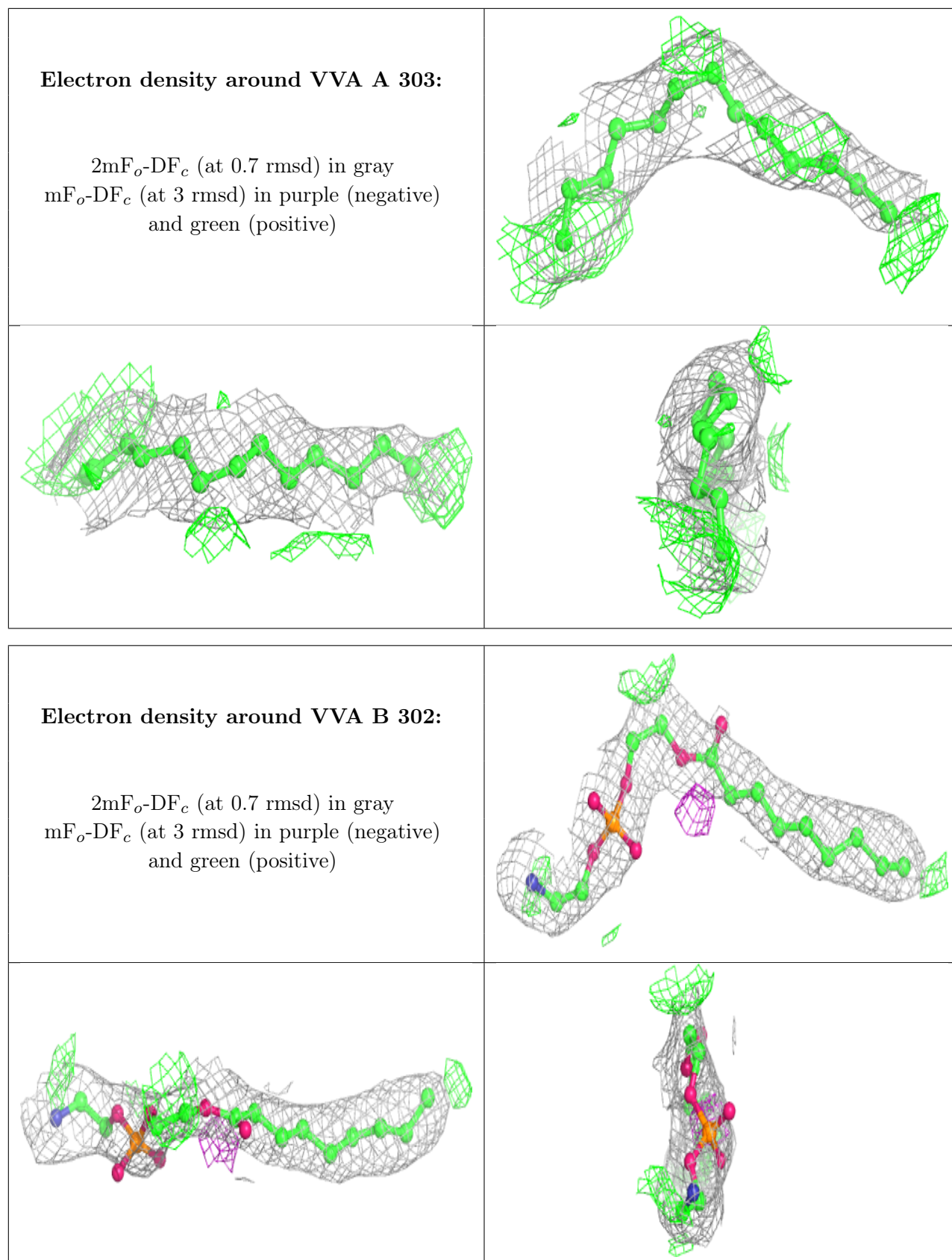
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

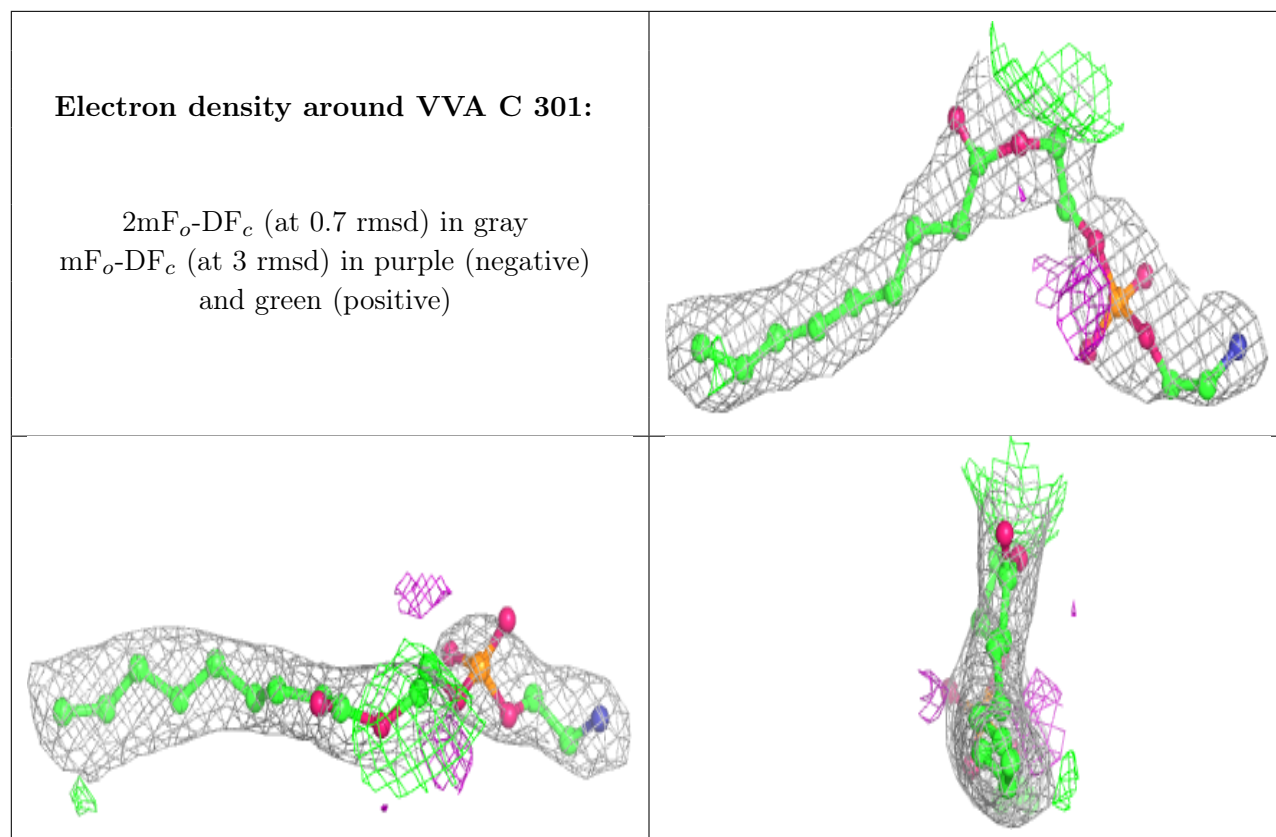












## 6.5 Other polymers [i](#)

There are no such residues in this entry.