



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 05:16 am BST

PDB ID : 1JGU
Title : STRUCTURAL BASIS FOR DISFAVORED ELIMINATION REACTION IN CATALYTIC ANTIBODY 1D4
Authors : Larsen, N.A.; Heine, A.; Crane, L.; Cravatt, B.F.; Lerner, R.A.; Wilson, I.A.
Deposited on : 2001-06-26
Resolution : 1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

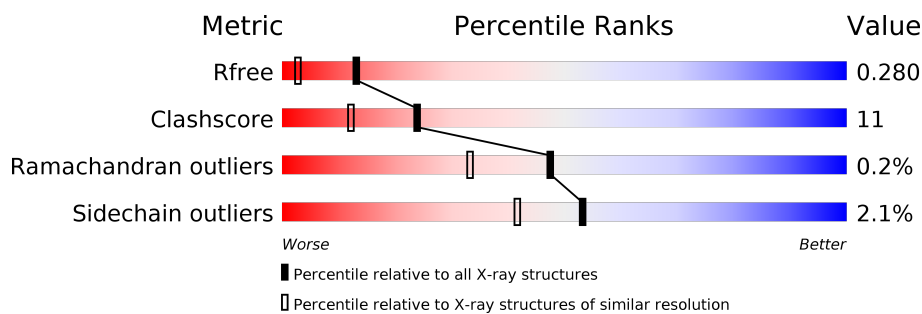
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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

Mol	Chain	Length	Quality of chain
1	L	220	 82% 16%
2	H	217	 78% 22%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3707 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 Antibody Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	L	220	1701	1061	290	343	7	0	0	0

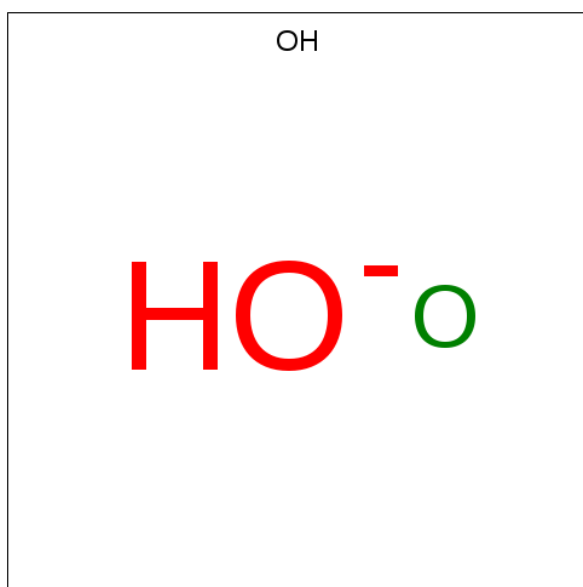
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	1	GLU	ASP	SEE REMARK 999	GB 522337
L	27B	LEU	ILE	SEE REMARK 999	GB 522337
L	34	HIS	GLU	SEE REMARK 999	GB 522337
L	87	PHE	TYR	SEE REMARK 999	GB 522337
L	89	SER	PHE	SEE REMARK 999	GB 522337
L	91	SER	GLY	SEE REMARK 999	GB 522337
L	97	THR	SER	SEE REMARK 999	GB 522337
L	96	LEU	-	SEE REMARK 999	GB 522337
L	100	ALA	GLY	SEE REMARK 999	GB 522337
L	103	LYS	ASN	SEE REMARK 999	GB 522337
L	106	LEU	ILE	SEE REMARK 999	GB 522337

- Molecule 2 is a protein called Antibody Heavy Chain.

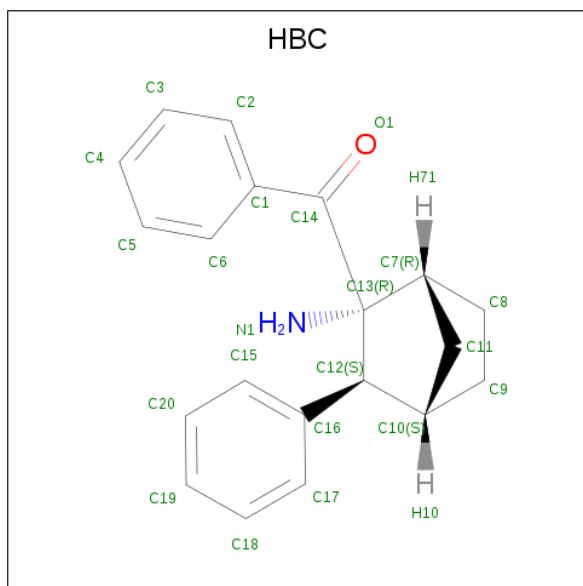
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	217	1653	1051	272	322	8	0	0	0

- Molecule 3 is HYDROXIDE ION (three-letter code: OH) (formula: HO).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total O 1 1	0	0

- Molecule 4 is (2-AMINO-3-PHENYL-BICYCLO[2.2.1]HEPT-2-YL)-PHENYL-METHANO NE (three-letter code: HBC) (formula: C₂₀H₂₁NO).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total C N O 22 20 1 1	0	0

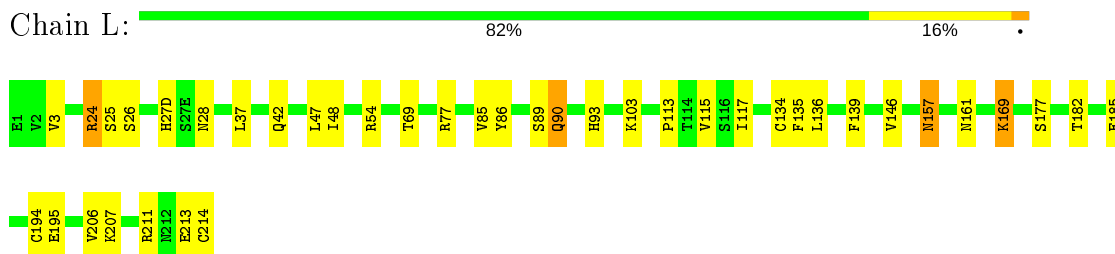
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	190	Total 190	O 190	0	0
5	H	140	Total 140	O 140	0	0

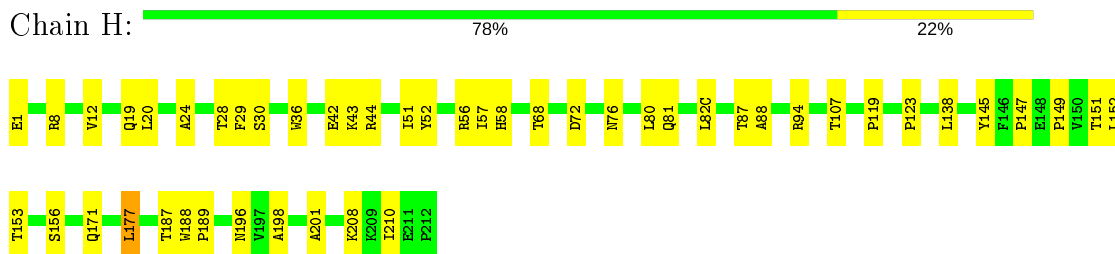
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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: Antibody Light Chain



- Molecule 2: Antibody Heavy Chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.37Å 48.63Å 69.37Å 90.00° 106.77° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80 39.24 – 1.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-1.80) 92.0 (39.24-1.85)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.45 (at 1.84Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.209 , 0.229 0.254 , 0.280	Depositor DCC
R_{free} test set	1804 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	19.0	Xtrriage
Anisotropy	0.313	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.022 for l,-k,h	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3707	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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: HBC, OH

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	L	0.32	0/1740	0.62	0/2361
2	H	0.32	0/1696	0.64	0/2312
All	All	0.32	0/3436	0.63	0/4673

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	L	1701	0	1646	37	0
2	H	1653	0	1617	35	0
3	H	1	0	0	1	0
4	H	22	0	21	2	0
5	H	140	0	0	3	0
5	L	190	0	0	9	0
All	All	3707	0	3284	74	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 11.

All (74) 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:L:134:CYS:HB2	5:L:280:HOH:O	1.69	0.92
2:H:12:VAL:HG11	2:H:82(C):LEU:HD13	1.55	0.85
1:L:194:CYS:HB2	5:L:263:HOH:O	1.76	0.83
2:H:156:SER:H	2:H:196:ASN:HD21	1.26	0.83
1:L:3:VAL:HG22	1:L:26:SER:HB3	1.63	0.80
2:H:28:THR:HG22	2:H:30:SER:H	1.45	0.79
1:L:117:ILE:HG13	5:L:280:HOH:O	1.86	0.75
1:L:24:ARG:HG2	1:L:24:ARG:HH11	1.57	0.69
2:H:156:SER:H	2:H:196:ASN:ND2	1.92	0.68
2:H:119:PRO:HB3	2:H:145:TYR:HB3	1.77	0.65
2:H:52:TYR:HB3	2:H:56:ARG:HB2	1.77	0.65
1:L:182:THR:OG1	1:L:185:GLU:HG3	1.98	0.62
1:L:85:VAL:HG22	1:L:103:LYS:HG2	1.81	0.62
1:L:77:ARG:HB2	1:L:77:ARG:NH1	2.15	0.61
1:L:24:ARG:HG2	1:L:24:ARG:NH1	2.17	0.59
3:H:4000:OH:O	4:H:3001:HBC:N1	2.36	0.59
1:L:27(D):HIS:HD2	1:L:28:ASN:H	1.51	0.58
1:L:213:GLU:O	1:L:214:CYS:HB2	2.02	0.58
2:H:12:VAL:HG11	2:H:82(C):LEU:CD1	2.29	0.58
2:H:188:TRP:CG	2:H:189:PRO:HA	2.39	0.57
1:L:195:GLU:HG2	1:L:206:VAL:HG22	1.86	0.57
2:H:210:ILE:HD11	5:H:4026:HOH:O	2.03	0.56
2:H:123:PRO:HD3	2:H:208:LYS:HG2	1.86	0.56
1:L:77:ARG:HB2	1:L:77:ARG:HH11	1.71	0.56
1:L:90:GLN:HE22	1:L:93:HIS:H	1.54	0.55
2:H:24:ALA:HB2	2:H:29:PHE:CE1	2.42	0.55
1:L:3:VAL:CG2	1:L:26:SER:HB3	2.35	0.54
1:L:27(D):HIS:CD2	1:L:28:ASN:H	2.28	0.52
2:H:171:GLN:O	2:H:171:GLN:HG3	2.10	0.52
1:L:157:ASN:N	1:L:157:ASN:HD22	2.06	0.52
1:L:115:VAL:HG12	1:L:207:LYS:HG3	1.92	0.51
2:H:19:GLN:HB2	2:H:81:GLN:HE22	1.76	0.51
1:L:134:CYS:SG	5:L:263:HOH:O	2.60	0.51
1:L:115:VAL:CG1	1:L:207:LYS:HG3	2.41	0.50
2:H:19:GLN:HB2	2:H:81:GLN:NE2	2.27	0.50
1:L:3:VAL:HG22	1:L:26:SER:CB	2.37	0.50
1:L:42:GLN:HG3	5:L:300:HOH:O	2.11	0.50
2:H:68:THR:OG1	2:H:81:GLN:HB3	2.11	0.49
1:L:25:SER:O	1:L:69:THR:HG23	2.12	0.48
2:H:188:TRP:CD1	2:H:189:PRO:HA	2.48	0.48
1:L:135:PHE:C	1:L:136:LEU:HD12	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:152:LEU:HD23	2:H:152:LEU:C	2.33	0.48
1:L:169:LYS:NZ	1:L:169:LYS:HA	2.29	0.48
1:L:213:GLU:O	1:L:214:CYS:CB	2.62	0.48
2:H:42:GLU:HB2	2:H:44:ARG:NH1	2.29	0.47
1:L:37:LEU:HB2	1:L:47:LEU:HD11	1.95	0.47
1:L:48:ILE:HD13	1:L:54:ARG:HA	1.95	0.47
2:H:51:ILE:O	2:H:51:ILE:HG23	2.14	0.47
2:H:36:TRP:CE2	2:H:80:LEU:HB2	2.49	0.47
2:H:151:THR:OG1	2:H:198:ALA:HB3	2.15	0.46
2:H:87:THR:O	2:H:88:ALA:HB2	2.16	0.46
4:H:3001:HBC:H61	4:H:3001:HBC:HN12	1.80	0.45
2:H:20:LEU:HD22	2:H:107:THR:HG21	1.98	0.45
1:L:89:SER:HB2	5:L:304:HOH:O	2.16	0.45
5:L:376:HOH:O	2:H:44:ARG:HG2	2.17	0.44
1:L:37:LEU:HD13	1:L:86:TYR:CZ	2.52	0.44
2:H:72:ASP:O	2:H:76:ASN:N	2.49	0.43
1:L:117:ILE:CG1	5:L:280:HOH:O	2.57	0.43
1:L:211:ARG:HH11	1:L:211:ARG:HG2	1.84	0.43
2:H:138:LEU:HD22	2:H:138:LEU:N	2.34	0.43
2:H:51:ILE:HG13	2:H:57:ILE:HG12	2.01	0.43
1:L:136:LEU:N	1:L:136:LEU:HD12	2.34	0.42
1:L:169:LYS:HZ3	1:L:169:LYS:HA	1.85	0.42
1:L:113:PRO:HB3	1:L:139:PHE:HB3	2.02	0.42
2:H:42:GLU:O	2:H:43:LYS:HB2	2.19	0.41
2:H:94:ARG:HG3	2:H:94:ARG:O	2.19	0.41
2:H:177:LEU:HD23	2:H:177:LEU:C	2.41	0.41
2:H:147:PRO:HD2	2:H:201:ALA:CB	2.50	0.41
2:H:58:HIS:HD2	5:H:4076:HOH:O	2.04	0.41
2:H:188:TRP:CE3	2:H:189:PRO:HG3	2.56	0.41
2:H:152:LEU:HD23	2:H:153:THR:N	2.36	0.40
2:H:12:VAL:HG23	5:H:4129:HOH:O	2.21	0.40
1:L:161:ASN:HD22	1:L:177:SER:HA	1.86	0.40
1:L:146:VAL:HG23	5:L:263:HOH:O	2.21	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	L	218/220 (99%)	214 (98%)	4 (2%)	0	100	100
2	H	215/217 (99%)	206 (96%)	8 (4%)	1 (0%)	29	15
All	All	433/437 (99%)	420 (97%)	12 (3%)	1 (0%)	47	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	187	THR

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	L	198/198 (100%)	194 (98%)	4 (2%)	55	44
2	H	185/185 (100%)	181 (98%)	4 (2%)	52	39
All	All	383/383 (100%)	375 (98%)	8 (2%)	53	42

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	24	ARG
1	L	90	GLN
1	L	157	ASN
1	L	169	LYS
2	H	1	GLU

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Mol	Chain	Res	Type
2	H	8	ARG
2	H	149	PRO
2	H	177	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	18	GLN
1	L	27(D)	HIS
1	L	42	GLN
1	L	90	GLN
1	L	157	ASN
1	L	161	ASN
2	H	19	GLN
2	H	58	HIS
2	H	81	GLN
2	H	164	HIS
2	H	196	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is modelled with single atom - leaving 1 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
4	HBC	H	3001	-	21,25,25	2.26	6 (28%)	25,37,37	1.44	2 (8%)

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
4	HBC	H	3001	-	-	2/12/39/39	0/5/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	3001	HBC	C16-C12	5.61	1.59	1.51
4	H	3001	HBC	C17-C16	3.51	1.44	1.39
4	H	3001	HBC	C1-C14	3.30	1.54	1.49
4	H	3001	HBC	C15-C16	2.98	1.43	1.39
4	H	3001	HBC	C2-C1	2.92	1.44	1.39
4	H	3001	HBC	C6-C1	2.81	1.44	1.39

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	3001	HBC	C9-C10-C12	6.05	116.40	107.88
4	H	3001	HBC	C11-C7-C8	-2.20	94.71	100.16

There are no chirality outliers.

All (2) torsion outliers are listed below:

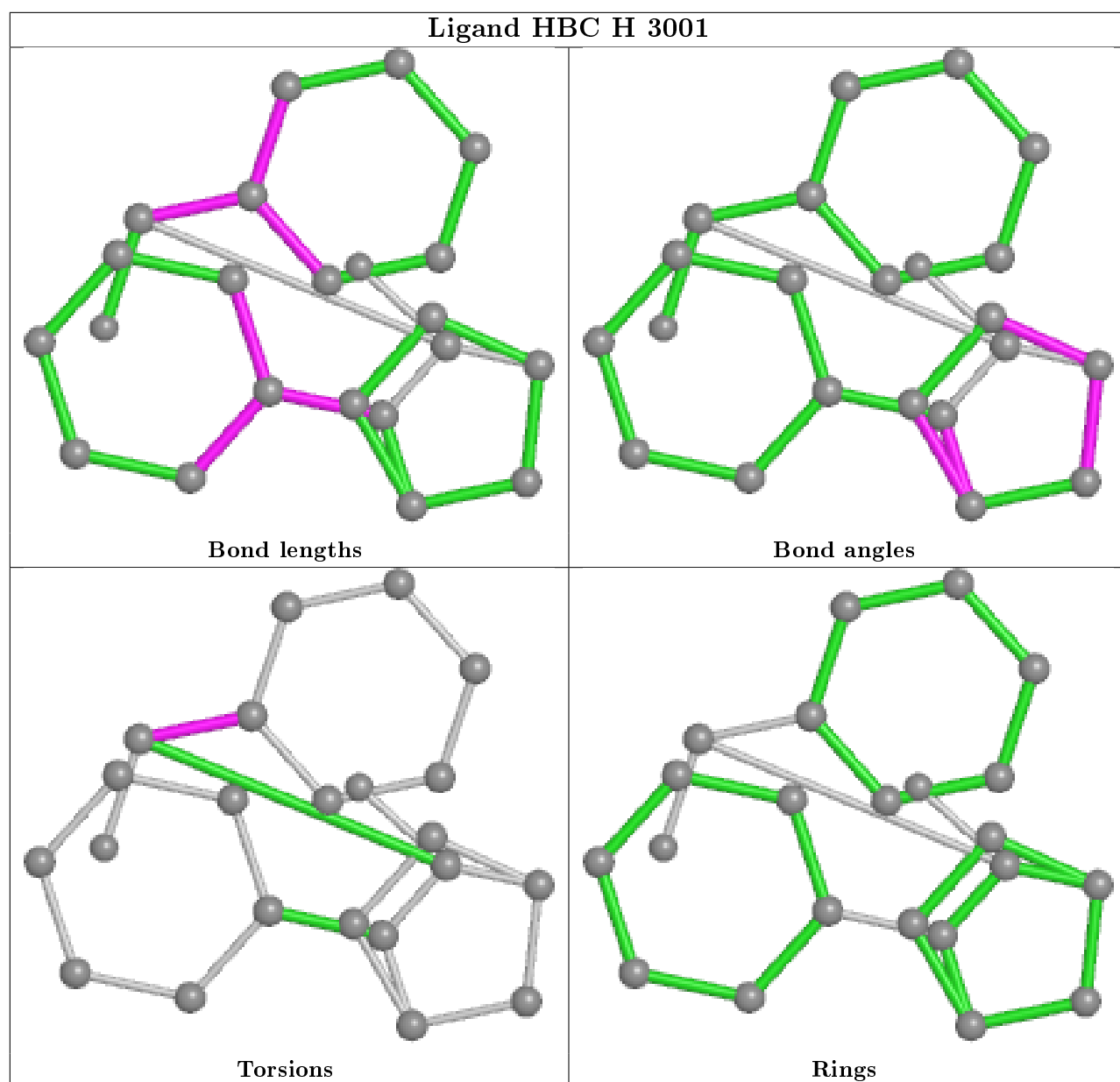
Mol	Chain	Res	Type	Atoms
4	H	3001	HBC	C2-C1-C14-C13
4	H	3001	HBC	C6-C1-C14-C13

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	3001	HBC	2	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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

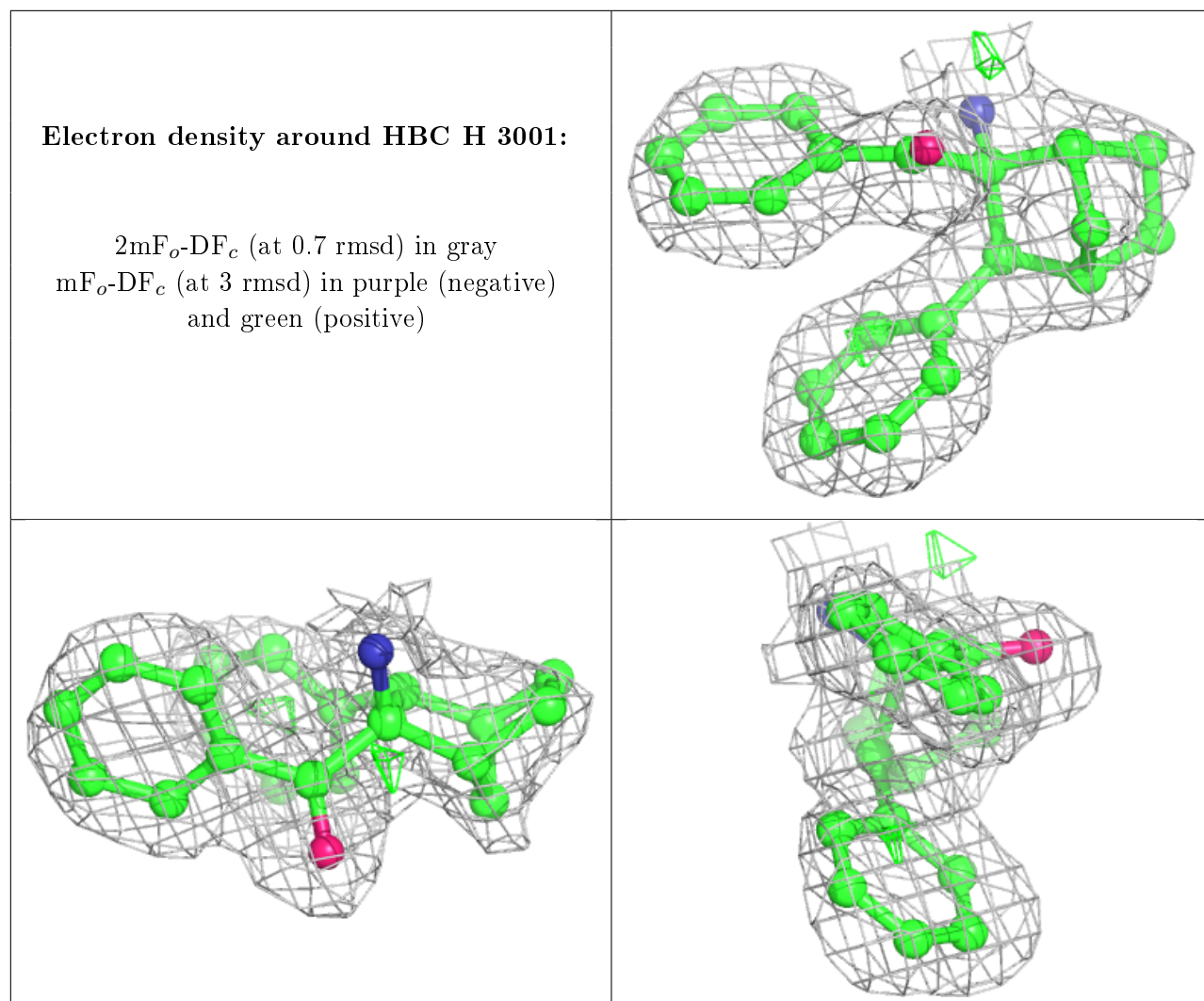
6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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.



6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.