



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 03:41 PM UTC

PDB ID : 2WHO / pdb_00002who
Title : CRYSTAL STRUCTURE OF HEPATITIS C VIRUS NS5B POLYMERASE
FROM 1B GENOTYPE IN COMPLEX WITH A NON-NUCLEOSIDE IN-
HIBITOR
Authors : Di Marco, S.
Deposited on : 2009-05-05
Resolution : 2.00 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

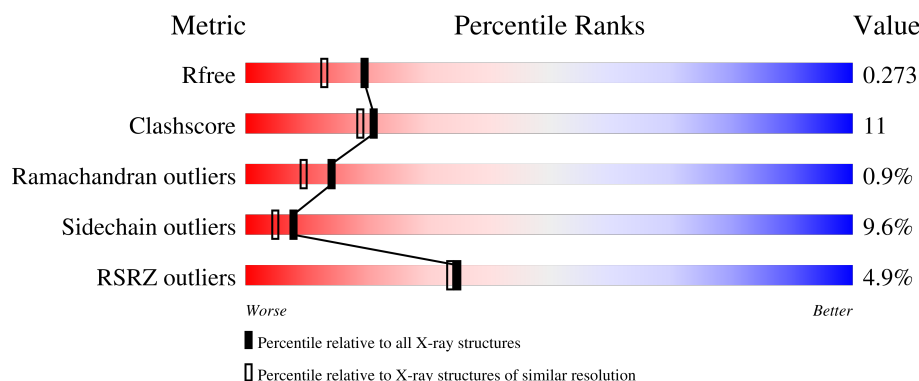
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	536	6% 76% 19% ..
1	B	536	4% 76% 18% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8817 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.

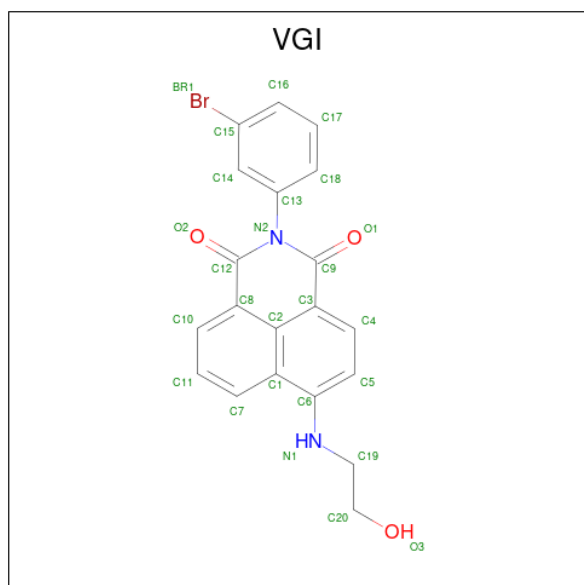
- Molecule 1 is a protein called RNA-DIRECTED RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	531	Total	C	N	O	S	0	0	0
			4121	2595	727	768	31			
1	B	531	Total	C	N	O	S	0	0	0
			4121	2595	727	768	31			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		
2	B	2	Total	Mn	0	0
			2	2		

- Molecule 3 is 2-(3-bromophenyl)-6-[(2-hydroxyethyl)amino]-1h-benzo[de]isoquinoline-1,3(2h)-dione (CCD ID: VGI) (formula: C₂₀H₁₅BrN₂O₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	Br	C	N	O	0	0
			26	1	20	2	3		
3	B	1	Total	Br	C	N	O	0	0
			26	1	20	2	3		

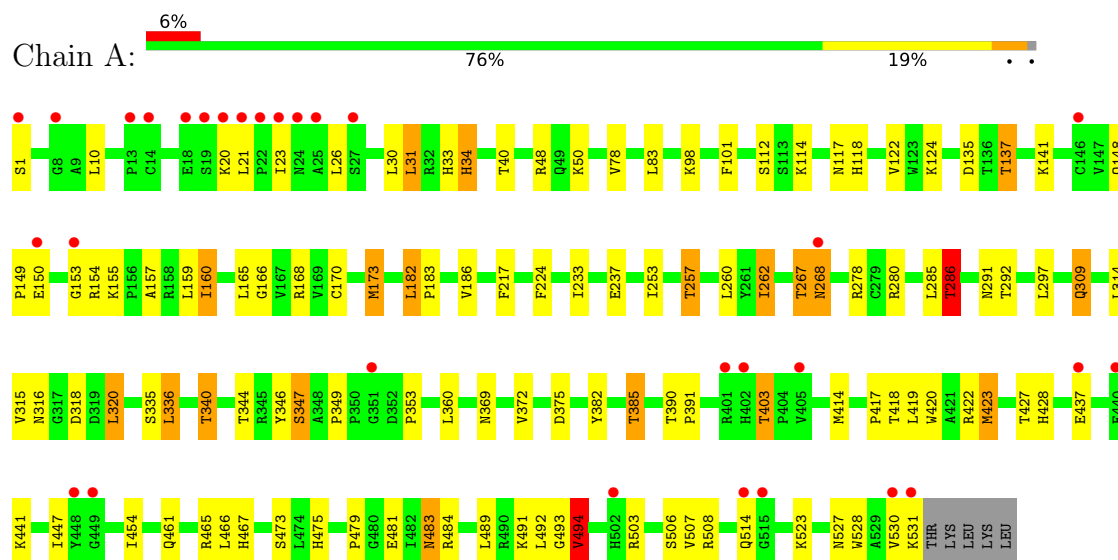
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	259	Total	O	0	0
			259	259		
4	B	260	Total	O	0	0
			260	260		

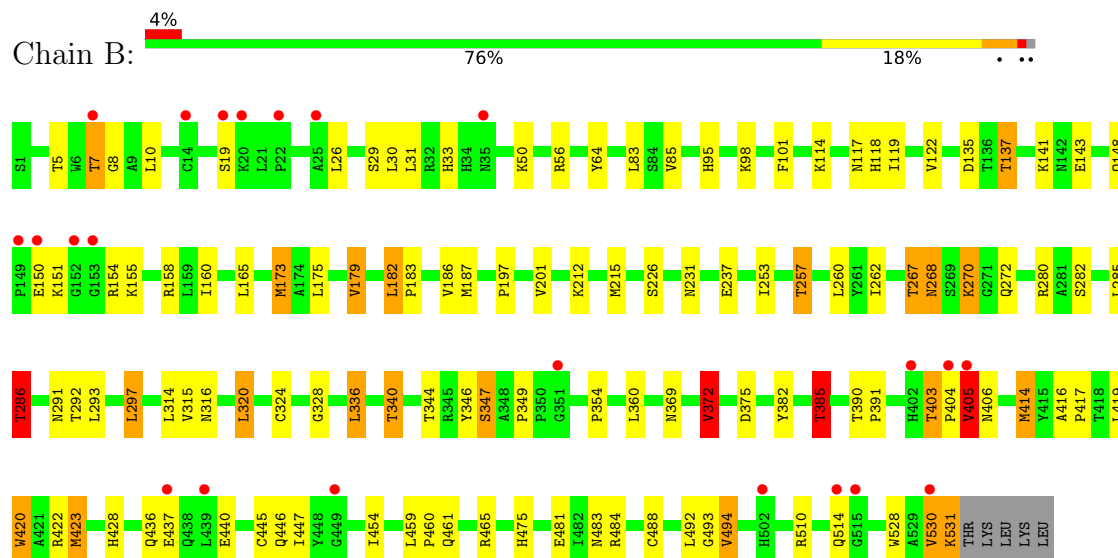
3 Residue-property plots [i](#)

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: RNA-DIRECTED RNA POLYMERASE



• Molecule 1: RNA-DIRECTED RNA POLYMERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.21Å 97.00Å 193.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	95.35 – 2.00 95.35 – 2.00	Depositor EDS
% Data completeness (in resolution range)	74.3 (95.35-2.00) 74.3 (95.35-2.00)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.211 , 0.266 0.221 , 0.273	Depositor DCC
R_{free} test set	3282 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8817	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.96 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1880e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

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

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	0.93	3/4209 (0.1%)	1.00	2/5712 (0.0%)
1	B	0.91	4/4209 (0.1%)	1.00	6/5712 (0.1%)
All	All	0.92	7/8418 (0.1%)	1.00	8/11424 (0.1%)

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	B	0	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	173	MET	SD-CE	-19.89	1.29	1.79
1	B	173	MET	SD-CE	-13.17	1.46	1.79
1	B	423	MET	SD-CE	-10.96	1.52	1.79
1	A	423	MET	SD-CE	-9.32	1.56	1.79
1	A	494	VAL	CA-CB	6.42	1.62	1.54
1	B	405	VAL	CA-CB	6.38	1.61	1.54
1	B	414	MET	SD-CE	6.30	1.95	1.79

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	385	THR	CB-CA-C	-7.10	98.87	112.43
1	B	372	VAL	CB-CA-C	-6.23	101.34	110.62
1	B	436	GLN	N-CA-C	-6.05	102.51	110.43
1	A	286	THR	N-CA-CB	-5.75	101.64	110.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	420	TRP	N-CA-C	5.61	117.48	111.36
1	B	328	GLY	CA-C-O	-5.47	118.45	122.23
1	A	353	PRO	O-C-N	5.47	123.83	121.31
1	B	286	THR	N-CA-CB	-5.26	102.39	110.44

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	7	THR	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4121	0	4134	94	0
1	B	4121	0	4134	91	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	26	0	15	3	0
3	B	26	0	15	3	0
4	A	259	0	0	18	0
4	B	260	0	0	18	0
All	All	8817	0	8298	183	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 (183) 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:423:MET:HE2	3:A:1534:VGI:H14	1.08	1.07
1:B:423:MET:CE	3:B:1534:VGI:H14	1.90	1.02
1:B:423:MET:HE2	3:B:1534:VGI:C14	1.91	0.98
1:A:1:SER:HA	4:A:2003:HOH:O	1.62	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:423:MET:HE2	3:B:1534:VGI:H14	0.97	0.97
1:B:85:VAL:HA	1:B:173:MET:HE2	1.46	0.95
1:A:423:MET:CE	3:A:1534:VGI:H14	1.98	0.93
1:A:369:ASN:HD21	1:A:484:ARG:HH22	1.14	0.92
1:A:423:MET:HE2	3:A:1534:VGI:C14	2.00	0.87
1:B:369:ASN:HD21	1:B:484:ARG:HH22	1.25	0.85
1:B:340:THR:O	1:B:344:THR:HG23	1.81	0.80
1:A:344:THR:HG21	4:A:2179:HOH:O	1.85	0.77
1:B:344:THR:HG21	4:B:2058:HOH:O	1.84	0.77
1:B:280:ARG:HE	1:B:291:ASN:ND2	1.83	0.76
1:A:346:TYR:O	1:A:347:SER:HB3	1.86	0.76
1:A:33:HIS:CD2	1:A:493:GLY:HA3	2.21	0.76
1:A:280:ARG:HE	1:A:291:ASN:ND2	1.84	0.75
1:B:385:THR:HG21	1:B:481:GLU:OE2	1.86	0.75
1:A:340:THR:O	1:A:344:THR:HG23	1.86	0.75
1:A:309:GLN:HG3	4:A:2161:HOH:O	1.87	0.74
1:A:30:LEU:O	1:A:494:VAL:HB	1.87	0.74
1:B:101:PHE:CD1	1:B:118:HIS:HE1	2.05	0.74
1:A:33:HIS:HD2	1:A:493:GLY:HA3	1.54	0.73
1:A:414:MET:HG2	4:A:2218:HOH:O	1.90	0.71
1:A:385:THR:HG21	1:A:481:GLU:OE2	1.90	0.70
1:A:101:PHE:CD1	1:A:118:HIS:HE1	2.11	0.69
1:B:30:LEU:O	1:B:494:VAL:HB	1.94	0.68
1:A:170:CYS:HA	1:A:173:MET:CE	2.24	0.68
1:A:369:ASN:ND2	1:A:484:ARG:HH22	1.91	0.66
1:A:280:ARG:HE	1:A:291:ASN:HD21	1.43	0.65
1:B:414:MET:HG2	4:B:2223:HOH:O	1.95	0.65
1:B:280:ARG:HE	1:B:291:ASN:HD21	1.45	0.65
1:B:253:ILE:O	1:B:257:THR:HG23	1.96	0.65
1:A:375:ASP:O	1:A:475:HIS:HE1	1.80	0.64
1:A:170:CYS:HA	1:A:173:MET:HE2	1.81	0.62
1:A:257:THR:O	1:A:262:ILE:HB	2.00	0.62
1:A:135:ASP:OD1	1:A:267:THR:CG2	2.48	0.61
1:B:101:PHE:CG	1:B:118:HIS:HE1	2.17	0.61
1:B:143:GLU:CD	4:B:2072:HOH:O	2.43	0.61
1:B:385:THR:HG22	1:B:420:TRP:HE1	1.64	0.61
1:B:119:ILE:CG2	1:B:173:MET:HE1	2.31	0.60
1:B:406:ASN:N	4:B:2208:HOH:O	2.35	0.59
1:B:488:CYS:HB2	4:B:2202:HOH:O	2.03	0.58
1:B:148:GLN:NE2	4:B:2075:HOH:O	2.37	0.58
1:B:483:ASN:HB2	4:B:2243:HOH:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:419:LEU:CD2	1:B:423:MET:HE3	2.34	0.58
1:B:315:VAL:HG22	1:B:320:LEU:HD23	1.86	0.58
1:A:148:GLN:O	1:A:153:GLY:HA2	2.04	0.57
1:A:372:VAL:CG1	1:A:382:TYR:CE2	2.88	0.56
1:A:168:ARG:NH2	4:A:2082:HOH:O	2.39	0.56
1:A:118:HIS:CD2	1:A:122:VAL:HG23	2.41	0.55
1:A:101:PHE:CG	1:A:118:HIS:HE1	2.23	0.55
1:B:369:ASN:ND2	1:B:484:ARG:HH22	2.02	0.55
1:A:419:LEU:CD2	1:A:423:MET:HE3	2.37	0.55
1:B:118:HIS:CD2	1:B:122:VAL:HG23	2.41	0.55
1:A:182:LEU:HD22	1:A:186:VAL:HG23	1.90	0.54
1:A:166:GLY:HA3	4:A:2057:HOH:O	2.07	0.54
1:B:344:THR:HG22	1:B:349:PRO:HB3	1.90	0.54
1:A:118:HIS:O	1:A:118:HIS:HD2	1.91	0.54
1:A:346:TYR:O	1:A:347:SER:CB	2.55	0.53
1:B:215:MET:HE3	1:B:324:CYS:SG	2.49	0.53
1:A:83:LEU:HB2	1:A:173:MET:HA	1.91	0.53
1:B:118:HIS:O	1:B:118:HIS:HD2	1.92	0.53
1:B:372:VAL:HG13	1:B:382:TYR:CE2	2.44	0.53
1:B:336:LEU:HD12	1:B:354:PRO:HG2	1.89	0.52
1:A:170:CYS:HA	1:A:173:MET:HE3	1.91	0.52
1:B:101:PHE:CG	1:B:118:HIS:CE1	2.98	0.52
1:A:253:ILE:O	1:A:257:THR:HG23	2.10	0.51
1:A:233:ILE:CG2	1:A:262:ILE:HD12	2.41	0.51
1:A:118:HIS:CE1	4:A:2057:HOH:O	2.64	0.51
1:A:286:THR:CG2	4:A:2152:HOH:O	2.59	0.51
1:A:315:VAL:HG22	1:A:320:LEU:HD23	1.93	0.51
1:A:390:THR:HB	1:A:391:PRO:HD3	1.93	0.51
1:A:419:LEU:HD23	1:A:423:MET:HE3	1.93	0.51
1:A:422:ARG:HD3	4:A:2231:HOH:O	2.11	0.51
1:B:445:CYS:HB3	1:B:454:ILE:HD12	1.92	0.50
1:A:267:THR:HG22	4:A:2146:HOH:O	2.10	0.50
1:B:85:VAL:HG22	1:B:173:MET:HE1	1.93	0.50
1:B:422:ARG:HD2	4:B:2215:HOH:O	2.12	0.50
1:B:64:TYR:CE1	1:B:297:LEU:HD13	2.47	0.50
1:A:101:PHE:CG	1:A:118:HIS:CE1	2.99	0.50
1:B:182:LEU:HD22	1:B:186:VAL:HG23	1.94	0.50
1:B:385:THR:HG21	1:B:481:GLU:CD	2.37	0.50
1:B:531:LYS:C	1:B:531:LYS:HZ3	2.20	0.50
1:B:95:HIS:CD2	4:B:2050:HOH:O	2.64	0.49
1:A:372:VAL:HG12	1:A:382:TYR:CD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:THR:HG22	1:A:349:PRO:HA	1.94	0.49
1:A:21:LEU:HD23	1:A:34:HIS:HB2	1.95	0.49
1:A:237:GLU:HG3	1:A:257:THR:HG21	1.94	0.49
1:A:427:THR:HG22	4:A:2213:HOH:O	2.12	0.49
1:A:466:LEU:HB3	1:A:467:HIS:HD2	1.78	0.49
1:A:503:ARG:O	1:A:507:VAL:HG23	2.13	0.49
1:B:237:GLU:HG3	1:B:257:THR:HG21	1.94	0.49
1:A:118:HIS:CD2	1:A:118:HIS:O	2.65	0.48
1:A:479:PRO:O	1:A:483:ASN:HB2	2.13	0.48
1:A:417:PRO:HD3	1:A:467:HIS:CE1	2.49	0.48
1:B:33:HIS:CD2	1:B:493:GLY:HA3	2.49	0.48
1:A:182:LEU:HB3	1:A:183:PRO:HD3	1.96	0.47
1:B:253:ILE:O	1:B:257:THR:CG2	2.62	0.47
1:B:10:LEU:O	1:B:268:ASN:ND2	2.47	0.47
1:A:372:VAL:HG12	1:A:382:TYR:CE2	2.50	0.47
1:A:428:HIS:HD2	4:A:2246:HOH:O	1.96	0.47
1:B:137:THR:HG23	4:B:2078:HOH:O	2.15	0.47
1:A:78:VAL:HG21	1:A:182:LEU:HD23	1.97	0.47
1:B:280:ARG:HH21	1:B:291:ASN:HD22	1.61	0.47
1:A:385:THR:HG23	1:A:418:THR:HG22	1.97	0.47
1:B:118:HIS:CD2	1:B:118:HIS:C	2.92	0.47
1:A:33:HIS:CD2	1:A:493:GLY:CA	2.96	0.46
1:B:268:ASN:HB2	1:B:272:GLN:H	1.79	0.46
1:B:286:THR:CG2	4:B:2143:HOH:O	2.63	0.46
1:B:530:VAL:HG12	1:B:530:VAL:O	2.16	0.46
1:B:137:THR:CG2	4:B:2078:HOH:O	2.63	0.46
1:B:405:VAL:HG22	4:B:2208:HOH:O	2.15	0.46
1:A:40:THR:HB	1:A:157:ALA:HB2	1.97	0.46
1:B:175:LEU:O	1:B:179:VAL:HB	2.15	0.46
1:A:137:THR:HA	1:A:267:THR:O	2.16	0.46
1:A:508:ARG:HD3	1:A:530:VAL:HG23	1.98	0.46
1:B:416:ALA:N	1:B:417:PRO:CD	2.79	0.46
1:B:182:LEU:HD22	1:B:186:VAL:CG2	2.46	0.45
1:A:141:LYS:HG3	1:A:160:ILE:HG23	1.98	0.45
1:B:446:GLN:NE2	4:B:2222:HOH:O	2.49	0.45
1:B:390:THR:HB	1:B:391:PRO:HD3	1.98	0.45
1:B:375:ASP:O	1:B:475:HIS:HE1	1.99	0.45
1:B:428:HIS:HD2	4:B:2011:HOH:O	1.99	0.45
1:B:344:THR:HG22	1:B:349:PRO:HA	1.98	0.45
1:B:56:ARG:HD2	1:B:226:SER:O	2.17	0.44
1:A:118:HIS:CD2	1:A:118:HIS:C	2.94	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:GLU:CG	1:A:257:THR:HG21	2.47	0.44
1:B:419:LEU:HD23	1:B:423:MET:HE3	1.99	0.44
1:A:422:ARG:HD2	4:A:2253:HOH:O	2.17	0.44
1:B:336:LEU:O	1:B:340:THR:HG23	2.18	0.44
1:B:119:ILE:HG21	1:B:173:MET:HE1	1.99	0.44
1:B:292:THR:OG1	1:B:316:ASN:O	2.27	0.44
1:B:135:ASP:OD2	1:B:267:THR:CG2	2.66	0.43
1:A:10:LEU:O	1:A:268:ASN:OD1	2.36	0.43
1:B:118:HIS:HD2	1:B:122:VAL:HG23	1.83	0.43
1:A:489:LEU:HA	1:A:494:VAL:HG13	2.00	0.43
1:B:340:THR:HG21	1:B:354:PRO:HD2	2.00	0.43
1:A:369:ASN:HD21	1:A:484:ARG:NH2	1.98	0.43
1:B:160:ILE:HG22	4:B:2144:HOH:O	2.18	0.43
1:A:117:ASN:OD1	1:B:465:ARG:NH1	2.52	0.43
1:B:182:LEU:HB3	1:B:183:PRO:HD3	2.01	0.43
1:B:83:LEU:HB2	1:B:173:MET:HA	2.00	0.43
1:B:187:MET:HE2	1:B:293:LEU:HD23	2.01	0.43
1:B:340:THR:HG21	4:B:2173:HOH:O	2.19	0.43
1:A:135:ASP:OD1	1:A:267:THR:HG23	2.17	0.42
1:A:137:THR:HG23	4:A:2078:HOH:O	2.18	0.42
1:A:523:LYS:O	1:A:527:ASN:HB2	2.19	0.42
1:A:31:LEU:HD13	1:A:492:LEU:O	2.19	0.42
1:A:48:ARG:HG2	1:A:159:LEU:HG	2.00	0.42
1:A:101:PHE:CD1	1:A:118:HIS:CE1	3.01	0.42
1:B:85:VAL:HG22	1:B:173:MET:CE	2.49	0.42
1:B:237:GLU:CG	1:B:257:THR:HG21	2.50	0.42
1:A:465:ARG:NH1	1:B:117:ASN:OD1	2.53	0.42
1:A:491:LYS:HG2	1:A:492:LEU:HD23	2.02	0.42
1:B:346:TYR:O	1:B:347:SER:CB	2.67	0.42
1:A:118:HIS:CD2	4:A:2057:HOH:O	2.72	0.42
1:A:385:THR:HG22	1:A:420:TRP:HE1	1.85	0.42
1:B:197:PRO:O	1:B:201:VAL:HG23	2.20	0.42
1:A:292:THR:OG1	1:A:316:ASN:O	2.32	0.42
1:A:385:THR:HG21	1:A:481:GLU:CD	2.45	0.42
1:A:423:MET:HG2	1:A:528:TRP:CH2	2.55	0.42
1:B:423:MET:HA	1:B:528:TRP:CZ2	2.54	0.42
1:A:124:LYS:HE2	4:A:2065:HOH:O	2.20	0.41
1:B:141:LYS:NZ	1:B:158:ARG:HH21	2.18	0.41
1:B:182:LEU:CD2	1:B:186:VAL:HG23	2.50	0.41
1:B:336:LEU:HA	1:B:336:LEU:HD13	1.82	0.41
1:B:344:THR:HG22	1:B:349:PRO:CB	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:ILE:HG22	1:B:173:MET:HE1	2.01	0.41
1:B:118:HIS:CD2	1:B:118:HIS:O	2.73	0.41
1:A:118:HIS:CG	4:A:2057:HOH:O	2.74	0.41
1:A:217:PHE:CD1	1:A:336:LEU:HD11	2.55	0.41
1:A:372:VAL:CG1	1:A:382:TYR:CD2	3.04	0.41
1:B:160:ILE:HA	1:B:282:SER:OG	2.21	0.41
1:B:268:ASN:HB3	1:B:270:LYS:H	1.85	0.41
1:A:224:PHE:CG	1:A:318:ASP:HB3	2.56	0.41
1:A:278:ARG:NE	4:A:2150:HOH:O	2.34	0.41
1:A:217:PHE:CG	1:A:336:LEU:HD11	2.56	0.40
1:A:237:GLU:HG3	1:A:257:THR:CG2	2.51	0.40
1:B:423:MET:HG2	1:B:528:TRP:CH2	2.56	0.40
1:B:459:LEU:N	1:B:460:PRO:CD	2.84	0.40
1:B:510:ARG:CB	4:B:2254:HOH:O	2.69	0.40
1:A:417:PRO:CG	1:A:467:HIS:ND1	2.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	529/536 (99%)	510 (96%)	15 (3%)	4 (1%)	16	11
1	B	529/536 (99%)	506 (96%)	17 (3%)	6 (1%)	11	7
All	All	1058/1072 (99%)	1016 (96%)	32 (3%)	10 (1%)	14	9

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	ASN
1	B	268	ASN
1	A	149	PRO

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Mol	Chain	Res	Type
1	A	347	SER
1	A	403	THR
1	B	154	ARG
1	B	347	SER
1	B	403	THR
1	B	404	PRO
1	B	8	GLY

5.3.2 Protein sidechains ⓘ

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	452/459 (98%)	409 (90%)	43 (10%)	8	5
1	B	452/459 (98%)	408 (90%)	44 (10%)	8	5
All	All	904/918 (98%)	817 (90%)	87 (10%)	8	5

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LYS
1	A	23	ILE
1	A	26	LEU
1	A	31	LEU
1	A	34	HIS
1	A	50	LYS
1	A	98	LYS
1	A	112	SER
1	A	114	LYS
1	A	137	THR
1	A	150	GLU
1	A	154	ARG
1	A	155	LYS
1	A	160	ILE
1	A	165	LEU
1	A	182	LEU

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Mol	Chain	Res	Type
1	A	257	THR
1	A	260	LEU
1	A	262	ILE
1	A	267	THR
1	A	285	LEU
1	A	286	THR
1	A	297	LEU
1	A	309	GLN
1	A	314	LEU
1	A	320	LEU
1	A	335	SER
1	A	336	LEU
1	A	340	THR
1	A	360	LEU
1	A	385	THR
1	A	403	THR
1	A	437	GLU
1	A	441	LYS
1	A	447	ILE
1	A	454	ILE
1	A	461	GLN
1	A	473	SER
1	A	483	ASN
1	A	494	VAL
1	A	506	SER
1	A	514	GLN
1	A	531	LYS
1	B	5	THR
1	B	7	THR
1	B	19	SER
1	B	26	LEU
1	B	29	SER
1	B	31	LEU
1	B	50	LYS
1	B	98	LYS
1	B	114	LYS
1	B	137	THR
1	B	150	GLU
1	B	151	LYS
1	B	155	LYS
1	B	165	LEU
1	B	179	VAL

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Mol	Chain	Res	Type
1	B	182	LEU
1	B	212	LYS
1	B	231	ASN
1	B	257	THR
1	B	260	LEU
1	B	262	ILE
1	B	267	THR
1	B	270	LYS
1	B	285	LEU
1	B	286	THR
1	B	297	LEU
1	B	314	LEU
1	B	320	LEU
1	B	336	LEU
1	B	340	THR
1	B	360	LEU
1	B	372	VAL
1	B	385	THR
1	B	403	THR
1	B	405	VAL
1	B	437	GLU
1	B	440	GLU
1	B	447	ILE
1	B	461	GLN
1	B	492	LEU
1	B	494	VAL
1	B	514	GLN
1	B	530	VAL
1	B	531	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	HIS
1	A	49	GLN
1	A	58	GLN
1	A	118	HIS
1	A	120	HIS
1	A	194	GLN
1	A	206	ASN
1	A	291	ASN
1	A	355	GLN

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Mol	Chain	Res	Type
1	A	369	ASN
1	A	428	HIS
1	A	438	GLN
1	A	461	GLN
1	A	475	HIS
1	A	514	GLN
1	B	28	ASN
1	B	33	HIS
1	B	95	HIS
1	B	118	HIS
1	B	194	GLN
1	B	206	ASN
1	B	273	ASN
1	B	291	ASN
1	B	369	ASN
1	B	406	ASN
1	B	428	HIS
1	B	438	GLN
1	B	446	GLN
1	B	461	GLN
1	B	475	HIS
1	B	483	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	VGI	A	1534	-	29,29,29	1.25	3 (10%)	42,42,42	1.58	10 (23%)
3	VGI	B	1534	-	29,29,29	1.38	3 (10%)	42,42,42	1.63	9 (21%)

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	VGI	A	1534	-	-	4/8/8/8	0/4/4/4
3	VGI	B	1534	-	-	4/8/8/8	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1534	VGI	C3-C9	-3.92	1.38	1.48
3	B	1534	VGI	C3-C9	-3.64	1.39	1.48
3	B	1534	VGI	C8-C12	-3.20	1.40	1.48
3	A	1534	VGI	C8-C12	-3.00	1.40	1.48
3	B	1534	VGI	C13-N2	-2.66	1.40	1.44
3	A	1534	VGI	C6-N1	-2.14	1.32	1.36

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1534	VGI	C13-N2-C12	4.36	123.80	117.24
3	B	1534	VGI	C12-N2-C9	-4.16	119.52	125.31
3	A	1534	VGI	C5-C6-N1	-3.94	117.91	122.29
3	A	1534	VGI	C12-N2-C9	-3.73	120.11	125.31
3	B	1534	VGI	C3-C9-N2	3.12	120.51	116.47
3	B	1534	VGI	C18-C13-N2	3.10	123.36	119.65
3	B	1534	VGI	C5-C6-N1	-3.09	118.85	122.29
3	A	1534	VGI	C18-C13-N2	2.89	123.12	119.65
3	A	1534	VGI	C13-C14-C15	2.63	121.89	118.49
3	A	1534	VGI	C8-C12-N2	2.56	119.79	116.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1534	VGI	C13-N2-C9	2.55	121.08	117.24
3	B	1534	VGI	C13-C14-C15	2.49	121.72	118.49
3	A	1534	VGI	C16-C15-C14	-2.37	118.12	121.53
3	A	1534	VGI	C3-C9-N2	2.32	119.47	116.47
3	A	1534	VGI	O1-C9-C3	-2.27	118.60	122.65
3	B	1534	VGI	BR1-C15-C16	2.27	122.39	119.30
3	B	1534	VGI	C16-C15-C14	-2.22	118.33	121.53
3	B	1534	VGI	C8-C12-N2	2.10	119.19	116.47
3	A	1534	VGI	C1-C6-N1	2.01	121.94	119.71

There are no chirality outliers.

All (8) torsion outliers are listed below:

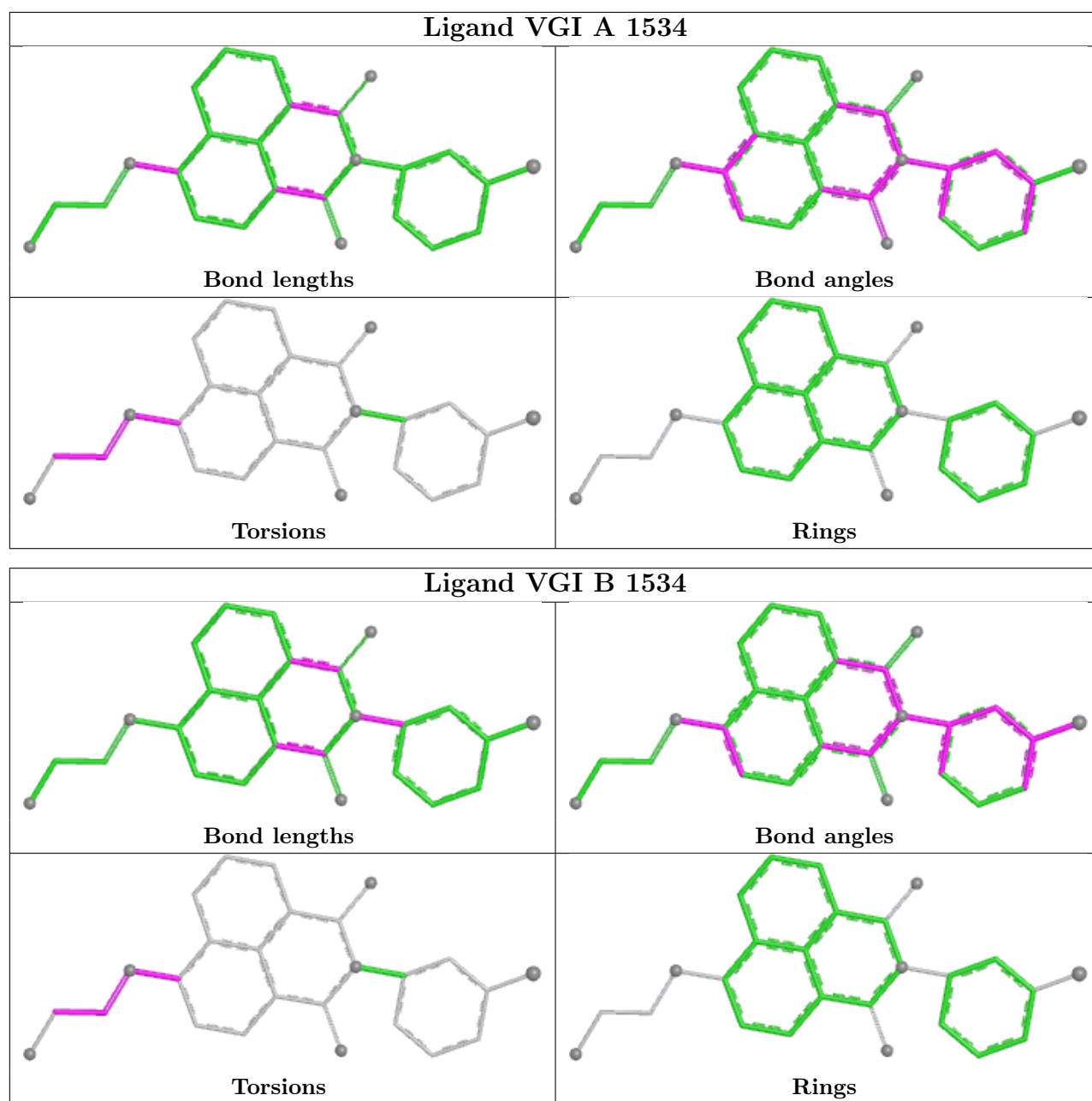
Mol	Chain	Res	Type	Atoms
3	A	1534	VGI	C1-C6-N1-C19
3	A	1534	VGI	C5-C6-N1-C19
3	B	1534	VGI	C1-C6-N1-C19
3	B	1534	VGI	C5-C6-N1-C19
3	B	1534	VGI	N1-C19-C20-O3
3	A	1534	VGI	C20-C19-N1-C6
3	B	1534	VGI	C20-C19-N1-C6
3	A	1534	VGI	N1-C19-C20-O3

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1534	VGI	3	0
3	B	1534	VGI	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	531/536 (99%)	0.33	30 (5%) 30 29	19, 31, 56, 71	0
1	B	531/536 (99%)	0.29	22 (4%) 41 40	20, 31, 51, 71	0
All	All	1062/1072 (99%)	0.31	52 (4%) 35 34	19, 31, 54, 71	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	153	GLY	6.9
1	A	23	ILE	5.2
1	B	7	THR	4.7
1	A	153	GLY	4.0
1	A	22	PRO	3.7
1	A	27	SER	3.4
1	A	21	LEU	3.2
1	A	437	GLU	3.1
1	B	14	CYS	3.1
1	A	530	VAL	3.1
1	B	405	VAL	3.0
1	B	150	GLU	3.0
1	A	14	CYS	2.9
1	B	152	GLY	2.9
1	A	502	HIS	2.9
1	A	150	GLU	2.8
1	B	437	GLU	2.8
1	A	351	GLY	2.8
1	B	22	PRO	2.7
1	A	402	HIS	2.7
1	A	440	GLU	2.7
1	A	18	GLU	2.7
1	A	449	GLY	2.7
1	B	402	HIS	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	530	VAL	2.7
1	B	515	GLY	2.6
1	A	24	ASN	2.6
1	A	19	SER	2.6
1	B	502	HIS	2.5
1	A	1	SER	2.5
1	B	404	PRO	2.5
1	B	149	PRO	2.4
1	A	514	GLN	2.4
1	B	514	GLN	2.3
1	A	268	ASN	2.3
1	B	449	GLY	2.3
1	A	20	LYS	2.3
1	B	20	LYS	2.3
1	A	25	ALA	2.2
1	A	8	GLY	2.2
1	A	146	CYS	2.2
1	A	401	ARG	2.2
1	A	13	PRO	2.1
1	B	439	LEU	2.1
1	A	405	VAL	2.1
1	B	35	ASN	2.1
1	A	515	GLY	2.1
1	B	19	SER	2.1
1	B	25	ALA	2.1
1	A	448	TYR	2.0
1	B	351	GLY	2.0
1	A	531	LYS	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 oligosaccharides in this entry.

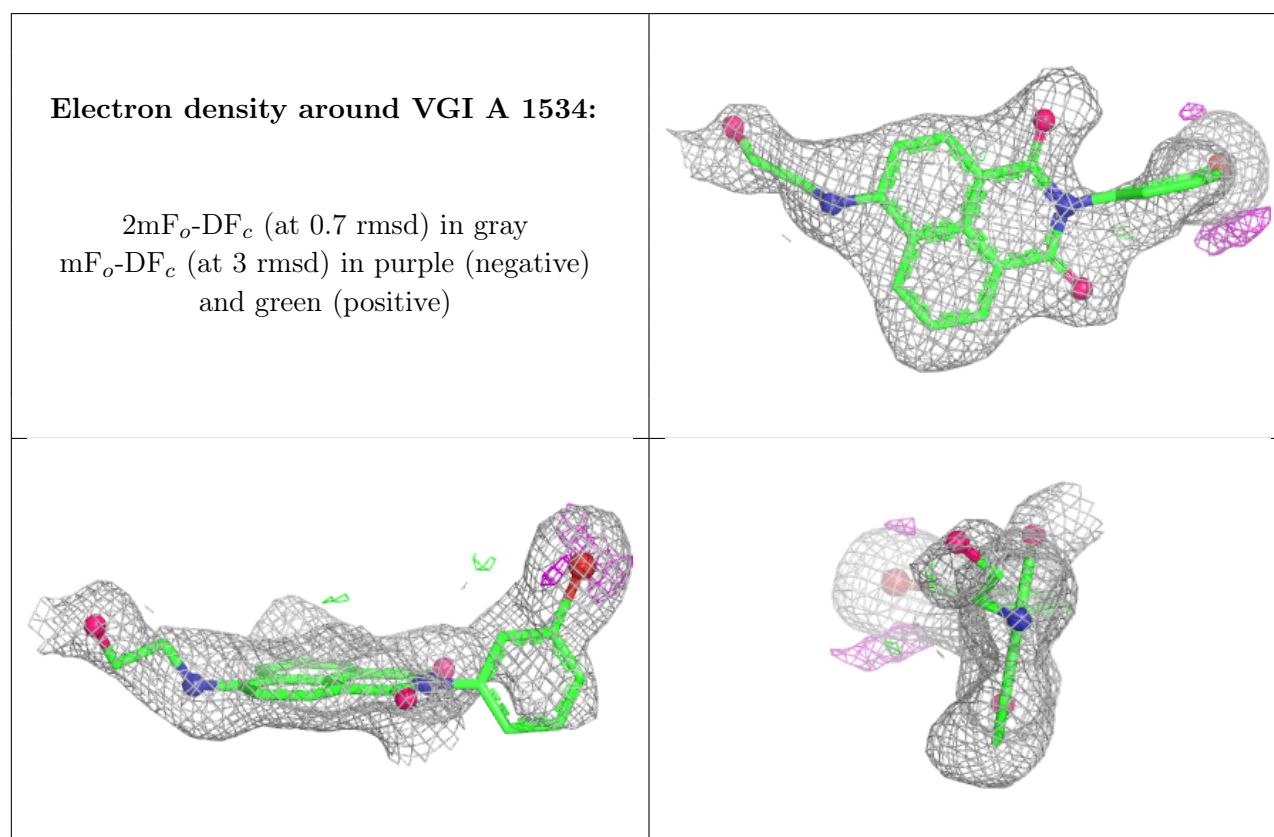
6.4 Ligands [i](#)

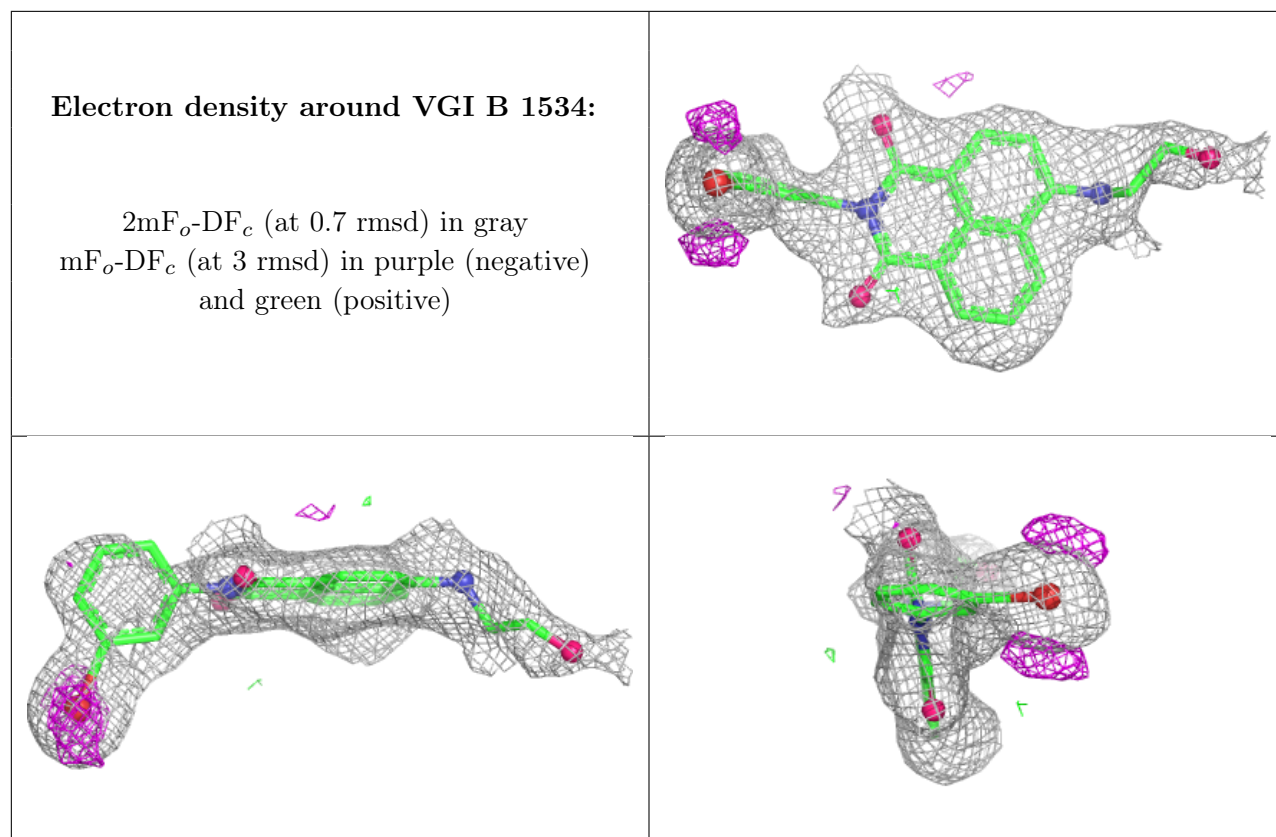
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	VGI	A	1534	26/26	0.96	0.10	43,48,51,52	0
3	VGI	B	1534	26/26	0.96	0.09	41,46,49,50	0
2	MN	B	1532	1/1	0.99	0.03	28,28,28,28	0
2	MN	B	1533	1/1	0.99	0.03	28,28,28,28	0
2	MN	A	1532	1/1	0.99	0.03	26,26,26,26	0
2	MN	A	1533	1/1	0.99	0.02	29,29,29,29	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.