



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:17 AM UTC

PDB ID : 4LCW / pdb_00004lcw
Title : The structure of human MAIT TCR in complex with MR1-K43A-RL-6-Me-7OH
Authors : Patel, O.; Rossjohn, J.
Deposited on : 2013-06-24
Resolution : 2.40 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

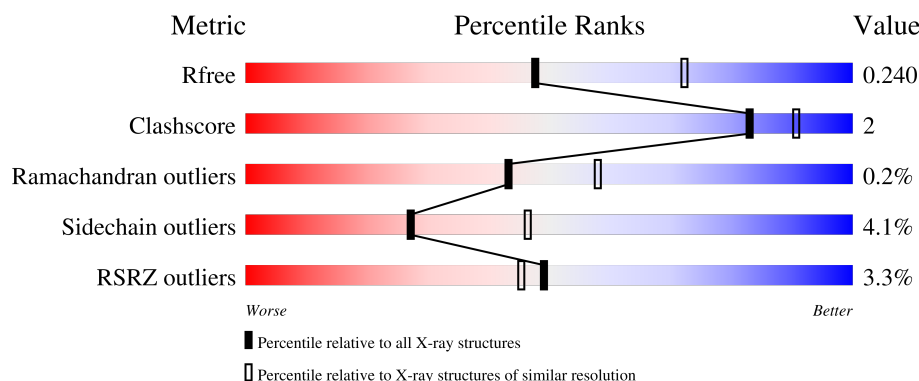
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	271	2% 84% 12% ..
1	C	271	4% 85% 9% 6%
2	B	99	% 88% 7% ..
2	F	99	3% 86% 11% .
3	D	203	% 89% 9% ..

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Mol	Chain	Length	Quality of chain
3	G	203	8% 79% 12% 7%
4	E	245	2% 93% 7%
4	H	245	3% 87% 9%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 12797 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 Major histocompatibility complex class I-related gene protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	0	0
			2150	1379	370	390	11			
1	C	256	Total	C	N	O	S	0	0	0
			2064	1321	359	373	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q95460
A	43	ALA	LYS	engineered mutation	UNP Q95460
A	261	SER	CYS	engineered mutation	UNP Q95460
C	0	MET	-	expression tag	UNP Q95460
C	43	ALA	LYS	engineered mutation	UNP Q95460
C	261	SER	CYS	engineered mutation	UNP Q95460

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	96	Total	C	N	O	S	0	0	0
			769	494	131	142	2			
2	F	96	Total	C	N	O	S	0	0	0
			755	486	126	141	2			

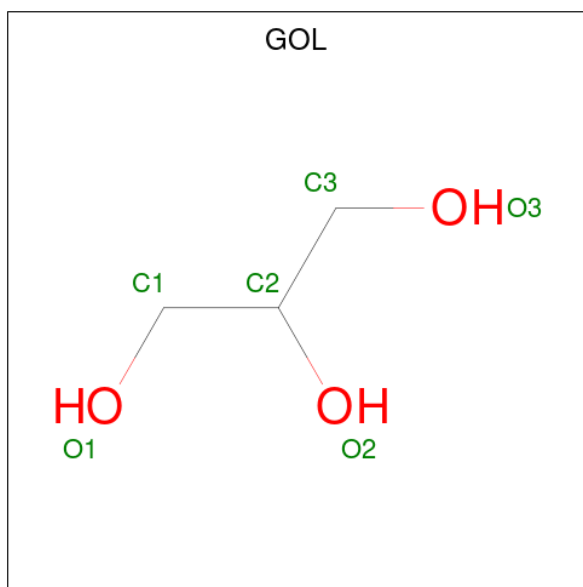
- Molecule 3 is a protein called MAIT T cell receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	200	Total	C	N	O	S	0	0	0
			1532	968	248	307	9			
3	G	188	Total	C	N	O	S	0	2	0
			1426	917	225	275	9			

- Molecule 4 is a protein called MAIT T cell receptor beta chain.

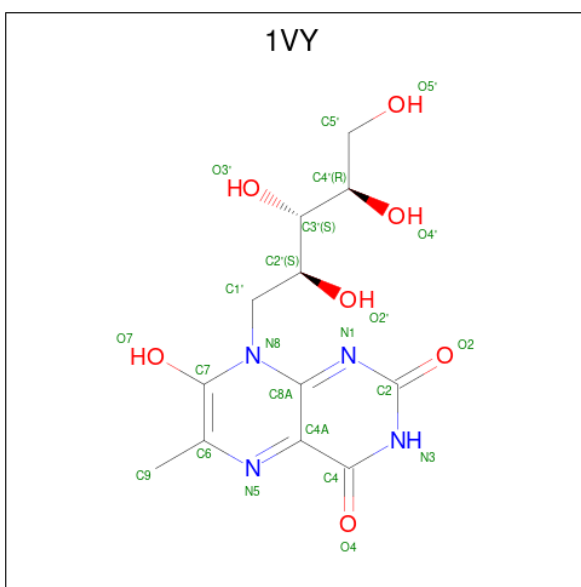
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	243	Total	C	N	O	S	0	1	0
			1893	1193	329	362	9			
4	H	240	Total	C	N	O	S	0	0	0
			1822	1153	310	350	9			

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is 1-deoxy-1-(7-hydroxy-6-methyl-2,4-dioxo-3,4-dihydropteridin-8(2H)-yl)-D-ribitol (CCD ID: 1VY) (formula: $C_{12}H_{16}N_4O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			23	12	4	7		
6	C	1	Total	C	N	O	0	0
			23	12	4	7		

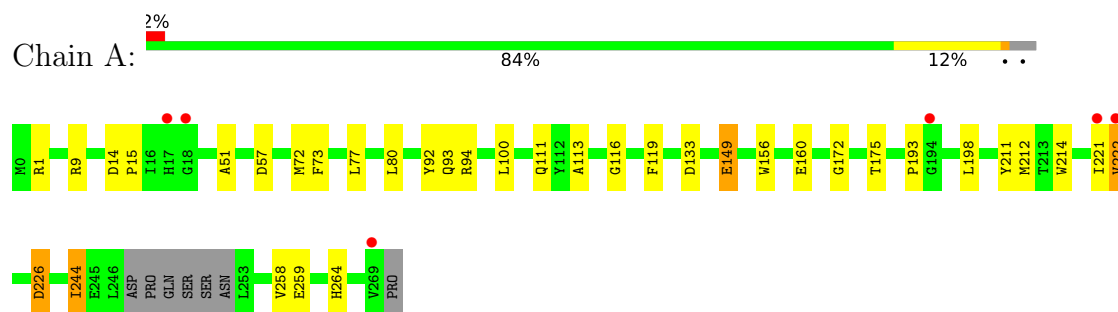
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	65	Total	O	0	0
			65	65		
7	B	32	Total	O	0	0
			32	32		
7	C	51	Total	O	0	0
			51	51		
7	D	60	Total	O	0	0
			60	60		
7	E	59	Total	O	0	0
			59	59		
7	F	16	Total	O	0	0
			16	16		
7	G	32	Total	O	0	0
			32	32		
7	H	19	Total	O	0	0
			19	19		

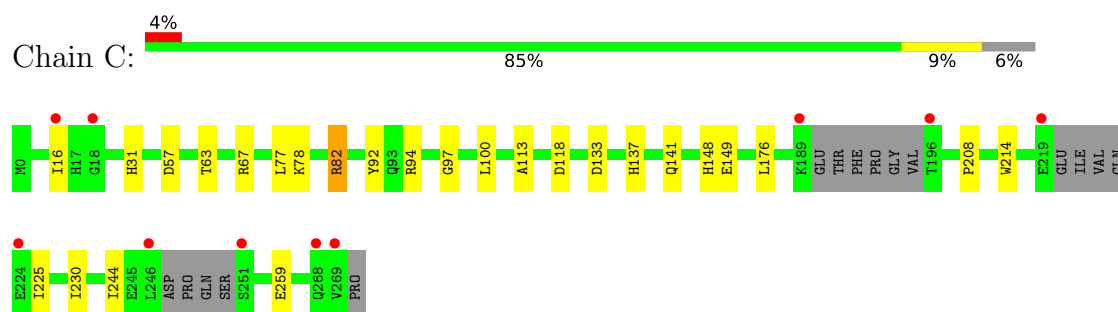
3 Residue-property plots [i](#)

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.

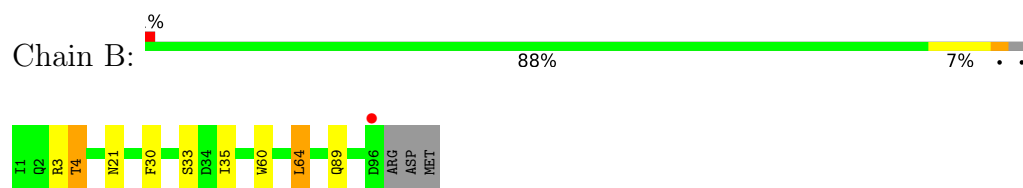
- Molecule 1: Major histocompatibility complex class I-related gene protein



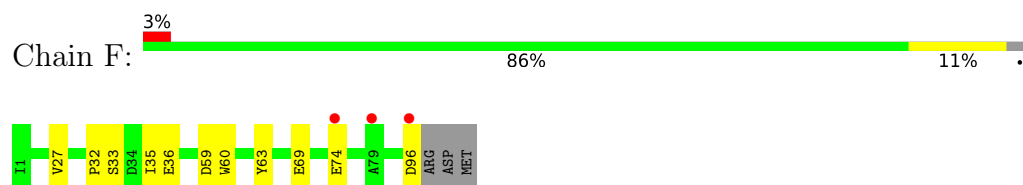
- Molecule 1: Major histocompatibility complex class I-related gene protein



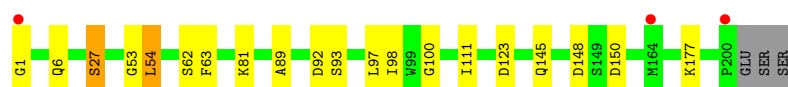
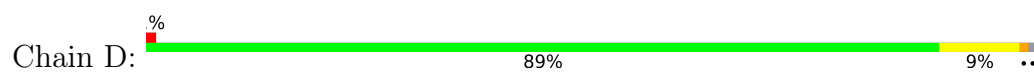
- Molecule 2: Beta-2-microglobulin



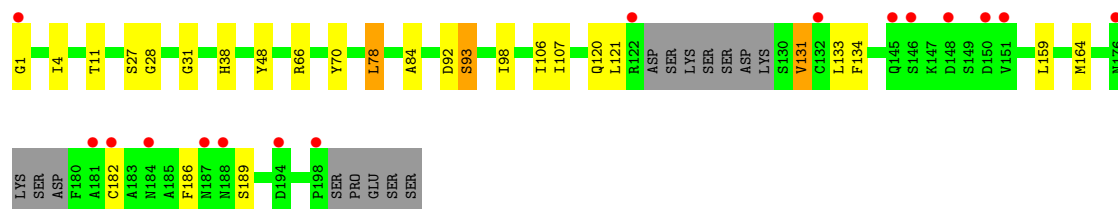
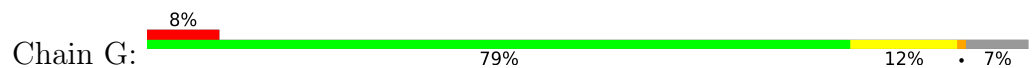
- Molecule 2: Beta-2-microglobulin



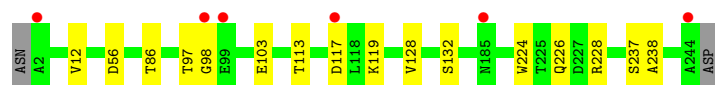
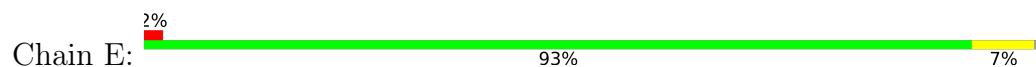
- Molecule 3: MAIT T cell receptor alpha chain



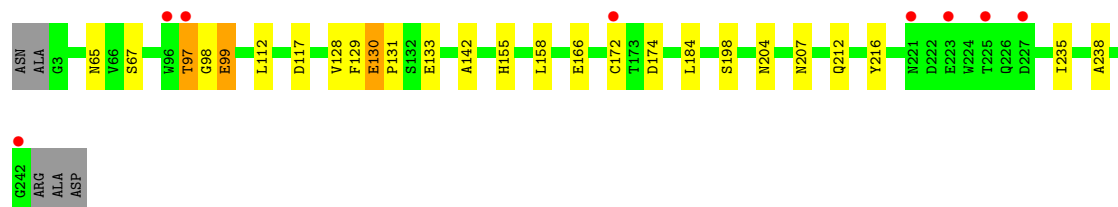
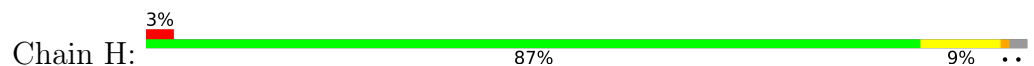
• Molecule 3: MAIT T cell receptor alpha chain



• Molecule 4: MAIT T cell receptor beta chain



• Molecule 4: MAIT T cell receptor beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	215.91Å 69.36Å 142.83Å 90.00° 104.30° 90.00°	Depositor
Resolution (Å)	35.14 – 2.40 35.14 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (35.14-2.40) 99.7 (35.14-2.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.40Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.179 , 0.227 0.191 , 0.240	Depositor DCC
R_{free} test set	4021 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.548	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12797	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 1VY, GOL

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	0.87	1/2215 (0.0%)	1.22	10/3014 (0.3%)
1	C	0.89	0/2124	1.21	5/2888 (0.2%)
2	B	0.78	0/792	1.15	3/1080 (0.3%)
2	F	0.82	0/778	1.17	4/1064 (0.4%)
3	D	0.89	0/1567	1.21	7/2130 (0.3%)
3	G	0.87	0/1464	1.14	1/1989 (0.1%)
4	E	0.84	0/1948	1.16	7/2656 (0.3%)
4	H	0.81	0/1873	1.18	8/2562 (0.3%)
All	All	0.85	1/12761 (0.0%)	1.19	45/17383 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	14	ASP	CA-CB	5.35	1.56	1.52

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	92	ASP	CA-CB-CG	8.23	120.83	112.60
3	D	92	ASP	CA-CB-CG	6.82	119.42	112.60
1	C	118	ASP	CA-CB-CG	6.57	119.17	112.60
4	H	117	ASP	CA-CB-CG	6.11	118.71	112.60
4	H	65	ASN	CA-CB-CG	6.06	118.66	112.60
4	E	56	ASP	CA-C-N	6.05	129.31	120.71
4	E	56	ASP	C-N-CA	6.05	129.31	120.71
3	D	123	ASP	CA-CB-CG	5.97	118.57	112.60
3	D	148	ASP	CA-C-N	5.95	128.53	120.38
3	D	148	ASP	C-N-CA	5.95	128.53	120.38
2	F	33	SER	N-CA-C	5.91	118.67	111.82
2	F	59	ASP	CA-CB-CG	5.89	118.49	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	133	ASP	CA-CB-CG	5.78	118.38	112.60
4	H	98	GLY	CA-C-N	5.77	131.63	122.74
4	H	98	GLY	C-N-CA	5.77	131.63	122.74
2	F	32	PRO	CA-C-N	5.75	129.04	120.31
2	F	32	PRO	C-N-CA	5.75	129.04	120.31
3	D	53	GLY	N-CA-C	5.71	119.92	111.76
1	C	148	HIS	CA-C-N	5.60	128.06	120.44
1	C	148	HIS	C-N-CA	5.60	128.06	120.44
1	C	97	GLY	N-CA-C	5.54	118.06	110.69
1	A	15	PRO	CA-C-N	5.52	128.02	120.35
1	A	15	PRO	C-N-CA	5.52	128.02	120.35
1	A	133	ASP	CA-CB-CG	5.43	118.03	112.60
4	H	174	ASP	CA-CB-CG	5.41	118.01	112.60
1	A	14	ASP	CA-CB-CG	5.38	117.98	112.60
4	E	117	ASP	CA-CB-CG	5.28	117.88	112.60
4	E	98	GLY	CA-C-N	5.27	130.20	122.77
4	E	98	GLY	C-N-CA	5.27	130.20	122.77
4	H	97	THR	N-CA-C	-5.27	102.40	110.14
2	B	21	ASN	CA-CB-CG	5.26	117.86	112.60
2	B	4	THR	CB-CA-C	5.22	116.24	108.87
2	B	33	SER	N-CA-C	5.22	117.88	111.82
1	A	175	THR	CA-C-N	5.17	127.63	120.29
1	A	175	THR	C-N-CA	5.17	127.63	120.29
1	A	172	GLY	CA-C-N	5.13	128.51	120.82
1	A	172	GLY	C-N-CA	5.13	128.51	120.82
4	E	132	SER	CA-C-N	5.07	127.08	120.28
4	E	132	SER	C-N-CA	5.07	127.08	120.28
4	H	133	GLU	CA-C-N	5.06	127.06	120.28
4	H	133	GLU	C-N-CA	5.06	127.06	120.28
1	A	51	ALA	CA-C-N	5.05	127.98	120.31
1	A	51	ALA	C-N-CA	5.05	127.98	120.31
3	D	111	ILE	CA-C-N	5.04	126.99	120.44
3	D	111	ILE	C-N-CA	5.04	126.99	120.44

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2150	0	2030	18	0
1	C	2064	0	1932	10	0
2	B	769	0	715	3	0
2	F	755	0	687	2	0
3	D	1532	0	1426	5	0
3	G	1426	0	1336	12	0
4	E	1893	0	1766	4	0
4	H	1822	0	1664	11	0
5	A	6	0	8	0	0
6	A	23	0	16	1	0
6	C	23	0	16	1	0
7	A	65	0	0	1	0
7	B	32	0	0	0	0
7	C	51	0	0	0	0
7	D	60	0	0	0	0
7	E	59	0	0	0	0
7	F	16	0	0	0	0
7	G	32	0	0	0	0
7	H	19	0	0	0	0
All	All	12797	0	11596	57	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 (57) 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:C:94:ARG:HH22	6:C:301:1VY:H14	1.53	0.74
1:A:94:ARG:HH22	6:A:302:1VY:H14	1.57	0.70
3:D:1:GLY:HA2	3:D:27:SER:H	1.60	0.66
1:A:77:LEU:HD13	1:A:92:TYR:HB2	1.80	0.63
3:D:150:ASP:HB2	3:D:177:LYS:HD2	1.82	0.62
4:H:155:HIS:HB3	4:H:216:TYR:HB2	1.83	0.59
1:C:214:TRP:HB2	1:C:225:ILE:HG12	1.84	0.58
1:A:259:GLU:HG2	1:A:264:HIS:CD2	2.39	0.57
1:A:259:GLU:HG2	1:A:264:HIS:HD2	1.69	0.57
1:A:226:ASP:HB2	1:C:82:ARG:HH12	1.70	0.56
1:C:77:LEU:HD13	1:C:92:TYR:HB2	1.87	0.55
3:D:54:LEU:HD13	3:D:63:PHE:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:63:THR:O	1:C:67:ARG:HG3	2.07	0.55
4:H:131:PRO:HG2	4:H:142:ALA:HB1	1.88	0.54
3:G:1:GLY:HA2	3:G:27:SER:H	1.71	0.54
4:E:86:THR:HG23	4:E:113:THR:HA	1.90	0.53
1:A:221:ILE:O	1:A:221:ILE:HG23	2.08	0.53
3:G:159:LEU:HB3	4:H:172:CYS:HB2	1.91	0.53
3:G:78:LEU:HG	3:G:107:ILE:HD12	1.92	0.51
1:A:212:MET:HG2	1:A:258:VAL:HG22	1.91	0.51
1:A:80:LEU:HD21	1:A:119:PHE:CZ	2.46	0.50
3:G:121:LEU:HB3	4:H:129:PHE:HB3	1.93	0.50
4:H:128:VAL:HG23	4:H:238:ALA:HB3	1.94	0.49
1:A:214:TRP:O	1:A:221:ILE:HG22	2.12	0.49
1:C:113:ALA:HB2	2:F:60:TRP:CE2	2.47	0.49
4:E:128:VAL:HG23	4:E:238:ALA:HB3	1.94	0.49
4:E:224:TRP:CZ2	4:E:226:GLN:HB2	2.48	0.48
4:E:119:LYS:O	4:E:228:ARG:NH2	2.45	0.48
1:A:156:TRP:HA	1:A:160:GLU:HB2	1.95	0.47
1:C:31:HIS:CD2	1:C:176:LEU:HD23	2.50	0.47
1:A:113:ALA:HB2	2:B:60:TRP:CE2	2.50	0.46
2:B:30:PHE:HZ	2:B:64:LEU:HD12	1.81	0.46
3:G:11:THR:HA	3:G:106:ILE:O	2.16	0.45
3:G:121:LEU:HB2	3:G:131:VAL:HG12	1.97	0.45
1:C:208:PRO:O	1:C:230:ILE:HD13	2.16	0.45
1:A:72:MET:HE1	7:A:461:HOH:O	2.16	0.45
4:H:130:GLU:H	4:H:130:GLU:HG2	1.53	0.45
2:F:27:VAL:O	2:F:63:TYR:HA	2.17	0.45
3:G:28:GLY:HA3	3:G:93[B]:SER:HB3	1.99	0.45
4:H:131:PRO:CG	4:H:142:ALA:HB1	2.47	0.45
3:G:164:MET:HE1	4:H:198:SER:HB3	2.00	0.44
3:G:134:PHE:HB2	3:G:186:PHE:CE1	2.53	0.44
1:A:211:TYR:HB2	1:A:259:GLU:HB2	1.99	0.44
3:G:31:GLY:HA3	3:G:48:TYR:CE1	2.53	0.44
4:H:204:ASN:HB3	4:H:207:ASN:HD22	1.82	0.43
1:A:198:LEU:HD12	1:A:244:ILE:HD11	2.00	0.43
3:G:4:ILE:HD12	3:G:98:ILE:O	2.18	0.43
1:A:116:GLY:O	2:B:3:ARG:NH2	2.52	0.43
3:D:89:ALA:HB1	3:D:97:LEU:HD22	2.00	0.43
3:D:6:GLN:HE21	3:D:100:GLY:HA3	1.84	0.42
3:G:38:HIS:CD2	3:G:84:ALA:HB2	2.55	0.42
1:C:208:PRO:O	1:C:230:ILE:HG21	2.19	0.42
1:C:137:HIS:O	1:C:141:GLN:HG2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:GLU:HG2	4:H:99:GLU:OE2	2.21	0.41
4:H:212:GLN:HG3	4:H:235:ILE:HG23	2.02	0.41
1:A:9:ARG:O	1:A:93:GLN:HA	2.21	0.40
1:A:80:LEU:HD23	1:A:80:LEU:HA	1.83	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	260/271 (96%)	251 (96%)	7 (3%)	2 (1%)	16	25
1	C	248/271 (92%)	243 (98%)	5 (2%)	0	100	100
2	B	94/99 (95%)	94 (100%)	0	0	100	100
2	F	94/99 (95%)	92 (98%)	1 (1%)	1 (1%)	11	18
3	D	198/203 (98%)	194 (98%)	4 (2%)	0	100	100
3	G	184/203 (91%)	178 (97%)	6 (3%)	0	100	100
4	E	242/245 (99%)	237 (98%)	5 (2%)	0	100	100
4	H	238/245 (97%)	232 (98%)	6 (2%)	0	100	100
All	All	1558/1636 (95%)	1521 (98%)	34 (2%)	3 (0%)	43	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	74	GLU
1	A	193	PRO
1	A	222	VAL

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	225/240 (94%)	216 (96%)	9 (4%)	28	47
1	C	213/240 (89%)	205 (96%)	8 (4%)	29	49
2	B	83/94 (88%)	79 (95%)	4 (5%)	23	40
2	F	80/94 (85%)	76 (95%)	4 (5%)	22	38
3	D	167/180 (93%)	160 (96%)	7 (4%)	26	45
3	G	150/180 (83%)	140 (93%)	10 (7%)	15	26
4	E	201/211 (95%)	197 (98%)	4 (2%)	48	70
4	H	189/211 (90%)	181 (96%)	8 (4%)	26	45
All	All	1308/1450 (90%)	1254 (96%)	54 (4%)	27	46

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ARG
1	A	57	ASP
1	A	73	PHE
1	A	100	LEU
1	A	111	GLN
1	A	149	GLU
1	A	222	VAL
1	A	226	ASP
1	A	244	ILE
2	B	4	THR
2	B	35	ILE
2	B	64	LEU
2	B	89	GLN
1	C	16	ILE
1	C	57	ASP
1	C	78	LYS
1	C	82	ARG
1	C	100	LEU
1	C	149	GLU

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Mol	Chain	Res	Type
1	C	244	ILE
1	C	259	GLU
3	D	27	SER
3	D	54	LEU
3	D	62	SER
3	D	81	LYS
3	D	93	SER
3	D	98	ILE
3	D	145	GLN
4	E	12	VAL
4	E	97	THR
4	E	103	GLU
4	E	237	SER
2	F	35	ILE
2	F	36	GLU
2	F	69	GLU
2	F	96	ASP
3	G	66	ARG
3	G	70	TYR
3	G	78	LEU
3	G	93[A]	SER
3	G	93[B]	SER
3	G	120	GLN
3	G	131	VAL
3	G	133	LEU
3	G	182	CYS
3	G	189	SER
4	H	67	SER
4	H	97	THR
4	H	99	GLU
4	H	112	LEU
4	H	130	GLU
4	H	158	LEU
4	H	166	GLU
4	H	184	LEU

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	83	HIS
1	A	93	GLN
1	A	123	ASN

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Mol	Chain	Res	Type
1	A	141	GLN
1	A	147	GLN
1	A	203	HIS
1	A	217	ASN
1	A	264	HIS
2	B	13	HIS
2	B	17	ASN
1	C	146	ASN
1	C	203	HIS
1	C	239	GLN
1	C	264	HIS
3	D	3	ASN
3	D	6	GLN
3	D	37	GLN
3	D	120	GLN
4	E	22	GLN
4	E	37	GLN
4	E	208	HIS
4	E	214	GLN
2	F	8	GLN
2	F	31	HIS
3	G	3	ASN
3	G	19	GLN
3	G	21	ASN
3	G	37	GLN
4	H	11	GLN
4	H	30	ASN
4	H	37	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
6	1VY	C	301	-	24,24,24	1.48	3 (12%)	31,35,35	2.02	12 (38%)
5	GOL	A	301	-	5,5,5	0.15	0	5,5,5	0.50	0
6	1VY	A	302	-	24,24,24	1.41	3 (12%)	31,35,35	2.12	14 (45%)

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
6	1VY	C	301	-	-	3/14/14/14	0/2/2/2
5	GOL	A	301	-	-	0/4/4/4	-
6	1VY	A	302	-	-	2/14/14/14	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	301	1VY	C9-C6	-4.46	1.41	1.49
6	A	302	1VY	C9-C6	-4.07	1.42	1.49
6	A	302	1VY	O7-C7	2.57	1.38	1.31
6	C	301	1VY	C6-C7	2.41	1.41	1.39
6	A	302	1VY	C6-C7	2.28	1.41	1.39
6	C	301	1VY	O7-C7	2.15	1.37	1.31

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	301	1VY	C9-C6-N5	5.29	120.35	112.45
6	A	302	1VY	C9-C6-N5	5.18	120.18	112.45
6	A	302	1VY	O7-C7-C6	-4.38	116.50	124.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	301	1VY	O7-C7-C6	-3.89	117.47	124.98
6	A	302	1VY	O7-C7-N8	3.75	122.54	114.94
6	C	301	1VY	C7-N8-C8A	-3.41	118.85	121.98
6	C	301	1VY	O7-C7-N8	3.07	121.15	114.94
6	A	302	1VY	O2'-C2'-C3'	2.84	115.89	109.25
6	A	302	1VY	C8A-N1-C2	2.63	122.54	116.85
6	A	302	1VY	C4A-C4-N3	2.62	119.93	113.25
6	C	301	1VY	C4A-C4-N3	2.61	119.89	113.25
6	C	301	1VY	C8A-N1-C2	2.60	122.47	116.85
6	A	302	1VY	C4-N3-C2	-2.58	121.07	125.64
6	A	302	1VY	C4A-C8A-N1	-2.56	118.30	124.59
6	A	302	1VY	C4-C4A-N5	2.49	121.62	118.18
6	A	302	1VY	C7-N8-C8A	-2.48	119.70	121.98
6	C	301	1VY	C4-C4A-N5	2.39	121.48	118.18
6	A	302	1VY	O4-C4-C4A	-2.37	120.27	126.53
6	A	302	1VY	C8A-C4A-N5	-2.37	120.04	124.80
6	C	301	1VY	C4A-C8A-N1	-2.35	118.82	124.59
6	A	302	1VY	C2'-C1'-N8	2.30	121.05	110.20
6	C	301	1VY	C4A-C8A-N8	2.29	119.78	116.53
6	C	301	1VY	O2'-C2'-C3'	2.25	114.53	109.25
6	A	302	1VY	C4A-C8A-N8	2.16	119.59	116.53
6	C	301	1VY	C4-N3-C2	-2.12	121.88	125.64
6	C	301	1VY	O4-C4-C4A	-2.11	120.97	126.53

There are no chirality outliers.

All (5) torsion outliers are listed below:

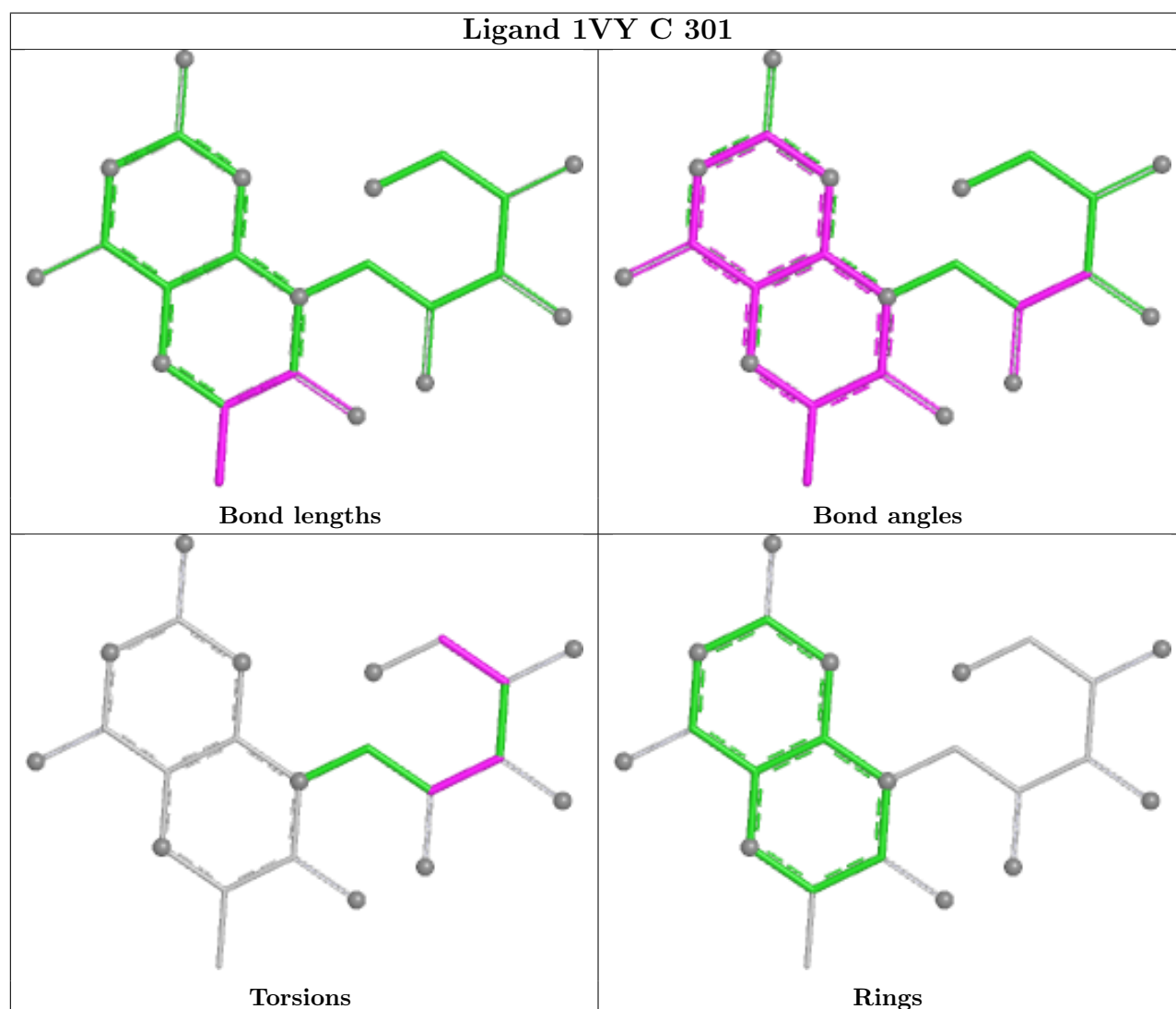
Mol	Chain	Res	Type	Atoms
6	A	302	1VY	O4'-C4'-C5'-O5'
6	C	301	1VY	C3'-C4'-C5'-O5'
6	C	301	1VY	O4'-C4'-C5'-O5'
6	A	302	1VY	C3'-C4'-C5'-O5'
6	C	301	1VY	C1'-C2'-C3'-O3'

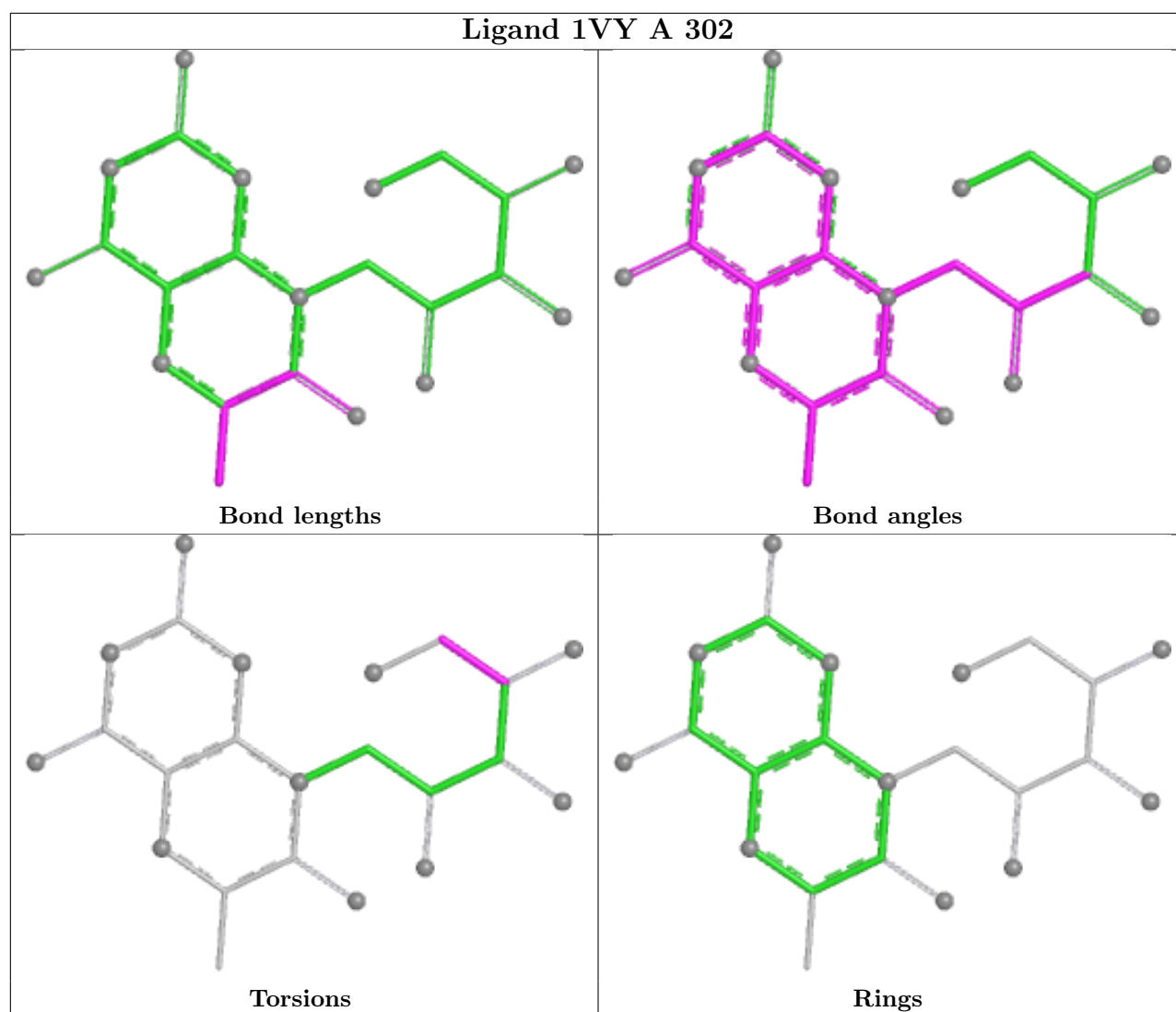
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	301	1VY	1	0
6	A	302	1VY	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 ⓘ

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	264/271 (97%)	-0.26	6 (2%) 61 57	17, 30, 53, 70	1 (0%)
1	C	256/271 (94%)	-0.13	10 (3%) 43 39	16, 32, 58, 75	0
2	B	96/99 (96%)	-0.25	1 (1%) 79 76	16, 33, 55, 70	0
2	F	96/99 (96%)	0.38	3 (3%) 51 47	23, 47, 64, 85	0
3	D	200/203 (98%)	-0.27	3 (1%) 72 68	12, 28, 54, 64	0
3	G	188/203 (92%)	0.29	16 (8%) 16 13	17, 39, 69, 84	2 (1%)
4	E	243/245 (99%)	-0.30	6 (2%) 58 54	18, 29, 48, 69	2 (0%)
4	H	240/245 (97%)	0.12	8 (3%) 49 45	19, 41, 63, 79	0
All	All	1583/1636 (96%)	-0.08	53 (3%) 49 45	12, 33, 61, 85	5 (0%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	176	ASN	5.5
4	H	96	TRP	4.5
1	A	221	ILE	4.3
3	D	1	GLY	3.8
4	E	2	ALA	3.5
3	G	194	ASP	3.4
3	G	122	ARG	3.4
1	C	219	GLU	3.3
4	H	242	GLY	3.1
4	H	221	ASN	3.1
2	F	96	ASP	3.0
3	G	150	ASP	3.0
3	G	132	CYS	3.0
3	G	148	ASP	3.0
1	C	246	LEU	2.9
4	E	117	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
4	E	244	ALA	2.8
3	D	164	MET	2.8
1	C	269	VAL	2.8
3	G	188	ASN	2.7
4	H	227	ASP	2.7
4	H	97	THR	2.6
3	G	198	PRO	2.6
1	C	251	SER	2.6
1	C	189	LYS	2.5
4	E	99	GLU	2.5
1	C	224	GLU	2.5
3	G	145	GLN	2.4
4	H	223	GLU	2.4
3	G	1	GLY	2.3
2	B	96	ASP	2.3
3	G	182	CYS	2.3
3	G	187	ASN	2.3
2	F	74	GLU	2.3
4	H	172	CYS	2.3
2	F	79	ALA	2.3
1	C	196	THR	2.3
1	C	16	ILE	2.3
1	A	17	HIS	2.2
1	A	222	VAL	2.2
3	G	184	ASN	2.2
4	E	185	ASN	2.2
1	A	194	GLY	2.2
3	G	146	SER	2.2
1	C	268	GLN	2.2
3	G	151	VAL	2.1
4	E	98	GLY	2.1
3	D	200	PRO	2.1
1	A	269	VAL	2.1
1	C	18	GLY	2.1
3	G	181	ALA	2.0
4	H	225	THR	2.0
1	A	18	GLY	2.0

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

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](#)

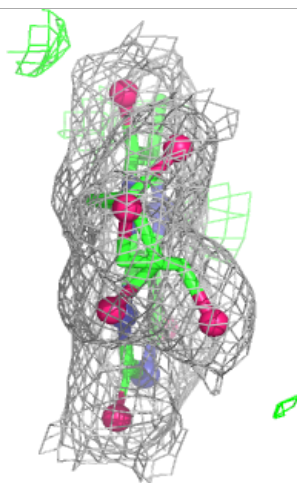
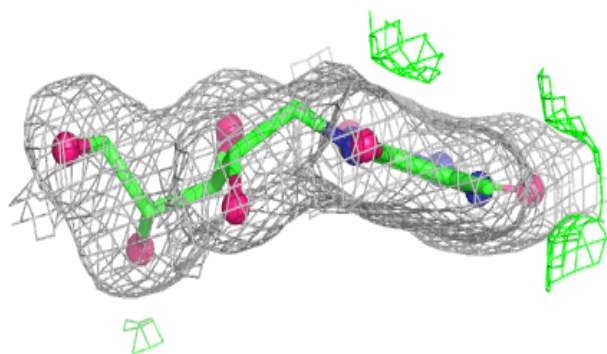
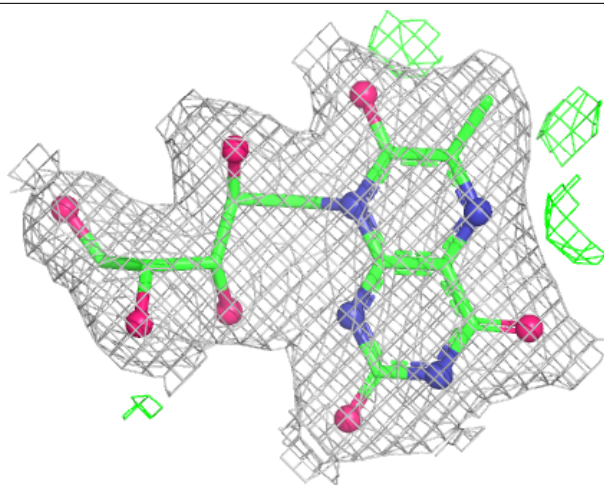
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
5	GOL	A	301	6/6	0.88	0.13	37,45,49,50	0
6	1VY	A	302	23/23	0.95	0.07	25,33,38,40	0
6	1VY	C	301	23/23	0.96	0.07	19,26,37,43	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.

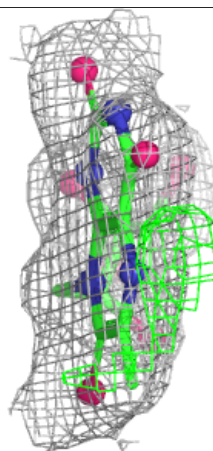
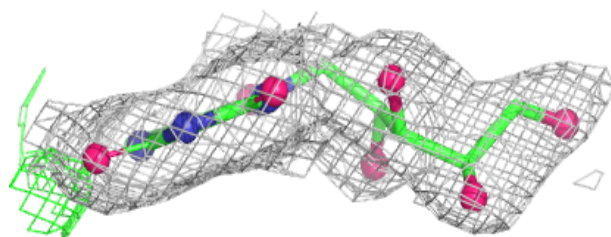
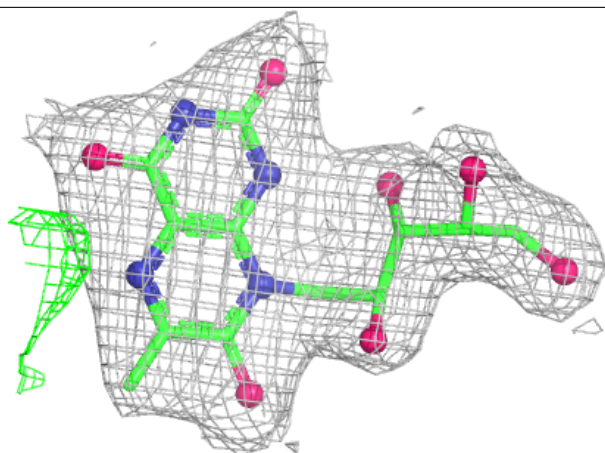
Electron density around 1VY A 302:

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



Electron density around 1VY C 301:

$2mF_o-DF_c$ (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.