



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:38 AM UTC

PDB ID : 4QXJ / pdb_00004qxj
Title : yCP beta5-M45A mutant in complex with the epoxyketone inhibitor ONX 0914
Authors : Huber, E.M.; Heinemeyer, W.; Groll, M.
Deposited on : 2014-07-21
Resolution : 2.80 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 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

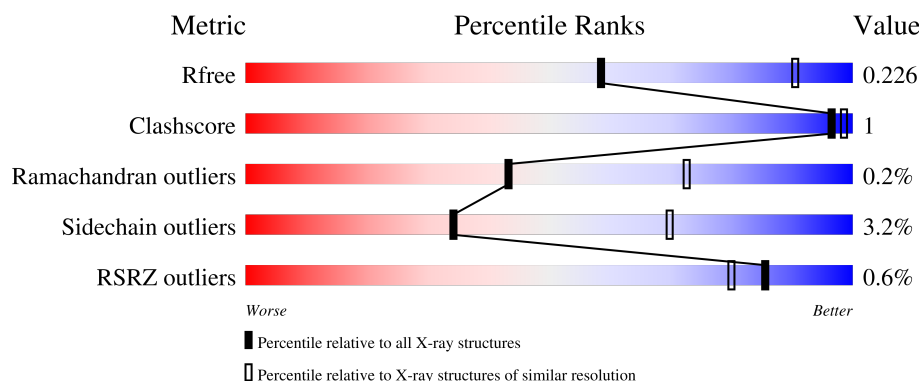
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

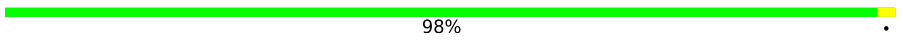
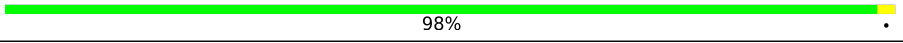
The reported resolution of this entry is 2.80 Å.

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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 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	250	 98% .
1	O	250	 98% .
2	B	258	 90% . . 5%
2	P	258	 90% . . 5%
3	C	254	 90% . . 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	 3% 90% 5% 6%
4	D	260	 85% 5% 10%
4	R	260	 85% 5% 10%
5	E	234	 94% 5%
5	S	234	 94% 5%
6	F	288	 81% 16%
6	T	288	 81% 16%
7	G	252	 90% 5%
7	U	252	 90% 6%
8	H	232	 93% 5%
8	V	232	 93% 5%
9	I	205	 95% 5%
9	W	205	 95% 5%
10	J	198	 93% 5%
10	X	198	 93% 5%
11	K	212	 94% 5%
11	Y	212	 94% 5%
12	L	222	 94% 5%
12	Z	222	 94% 5%
13	M	246	 89% 7%
13	a	246	 89% 8%
14	N	196	 96%
14	b	196	 95% 5%

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 49783 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 Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			
3	Q	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			
4	R	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			
5	S	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			

- Molecule 6 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			
6	T	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			
7	U	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			

- Molecule 8 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			
8	V	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
9	W	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	212	Total	C	N	O	S	0	0	0
			1641	1043	280	312	6			
11	Y	212	Total	C	N	O	S	0	0	0
			1641	1043	280	312	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	45	ALA	MET	engineered mutation	UNP P30656
Y	45	ALA	MET	engineered mutation	UNP P30656

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	228	Total	C	N	O	S	0	0	0
			1786	1131	305	343	7			
13	a	226	Total	C	N	O	S	0	0	0
			1770	1120	303	340	7			

- Molecule 14 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

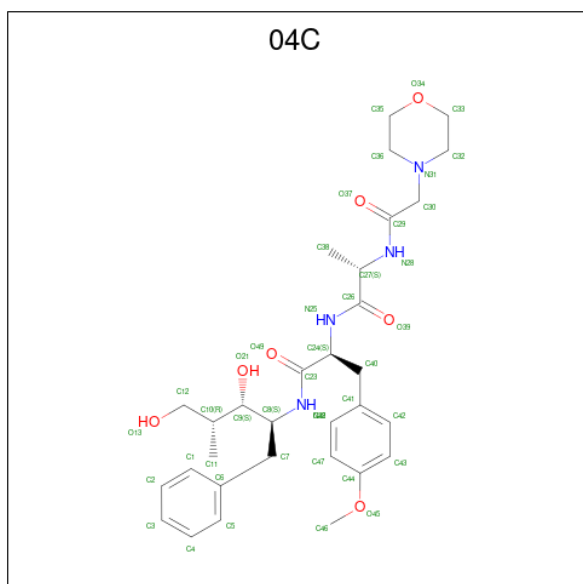
- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	G	1	Total Mg 1 1	0	0
15	I	1	Total Mg 1 1	0	0
15	K	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	V	1	Total Mg 1 1	0	0
15	Y	1	Total Mg 1 1	0	0

- Molecule 16 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0

- Molecule 17 is 1,2,4-trideoxy-4-methyl-2-{[N-(morpholin-4-ylacetyl)-L-alanyl-O-methyl-L-tyrosyl]amino}-1-phenyl-D-xylitol (CCD ID: 04C) (formula: $C_{31}H_{44}N_4O_7$).



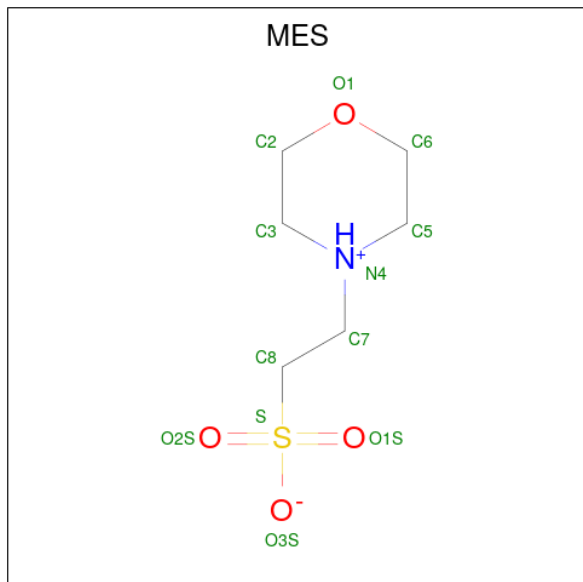
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
17	H	1	Total	C	N	O	0	0
			42	31	4	7		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
17	K	1	Total	C	N	O	0	0
			42	31	4	7		
17	N	1	Total	C	N	O	0	0
			42	31	4	7		
17	V	1	Total	C	N	O	0	0
			42	31	4	7		
17	Y	1	Total	C	N	O	0	0
			42	31	4	7		
17	b	1	Total	C	N	O	0	0
			42	31	4	7		

- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	H	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	K	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	V	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	Y	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 19 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	A	4	Total O 4 4	0	0
19	B	16	Total O 16 16	0	0
19	C	9	Total O 9 9	0	0
19	D	3	Total O 3 3	0	0
19	E	3	Total O 3 3	0	0
19	F	9	Total O 9 9	0	0
19	G	7	Total O 7 7	0	0
19	H	11	Total O 11 11	0	0
19	I	10	Total O 10 10	0	0
19	J	15	Total O 15 15	0	0
19	K	15	Total O 15 15	0	0
19	L	20	Total O 20 20	0	0
19	M	12	Total O 12 12	0	0
19	N	9	Total O 9 9	0	0
19	O	6	Total O 6 6	0	0
19	P	8	Total O 8 8	0	0
19	Q	7	Total O 7 7	0	0
19	R	7	Total O 7 7	0	0
19	S	3	Total O 3 3	0	0
19	T	5	Total O 5 5	0	0
19	U	9	Total O 9 9	0	0
19	V	9	Total O 9 9	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	W	5	Total 5	O 5	0	0
19	X	16	Total 16	O 16	0	0
19	Y	16	Total 16	O 16	0	0
19	Z	16	Total 16	O 16	0	0
19	a	15	Total 15	O 15	0	0
19	b	12	Total 12	O 12	0	0

3 Residue-property plots [i](#)

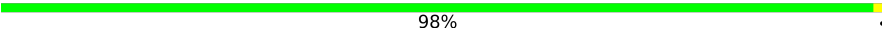
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Proteasome subunit alpha type-2

Chain A:  98%



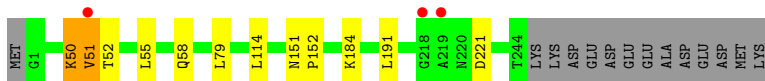
- Molecule 1: Proteasome subunit alpha type-2

Chain O:  98%



- Molecule 2: Proteasome subunit alpha type-3

Chain B:  90% 5%



- Molecule 2: Proteasome subunit alpha type-3

Chain P:  90% 5%

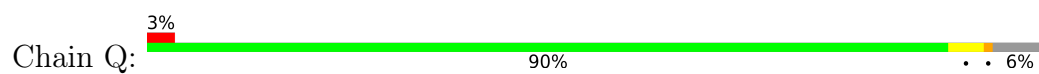


- Molecule 3: Proteasome subunit alpha type-4

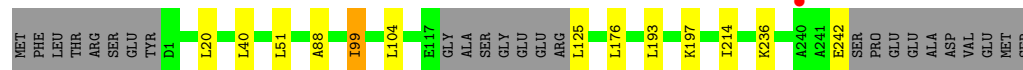
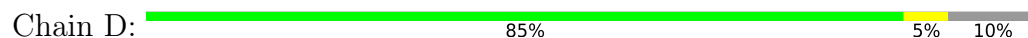
Chain C:  90% 6%



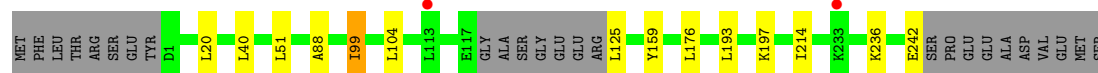
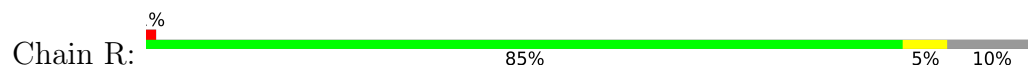
- Molecule 3: Proteasome subunit alpha type-4



- Molecule 4: Proteasome subunit alpha type-5



- Molecule 4: Proteasome subunit alpha type-5



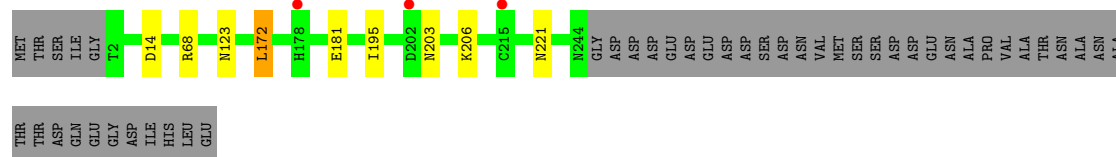
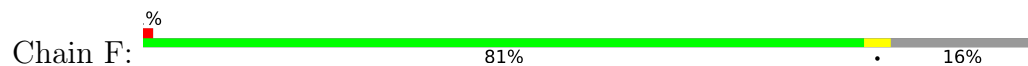
- Molecule 5: Proteasome subunit alpha type-6



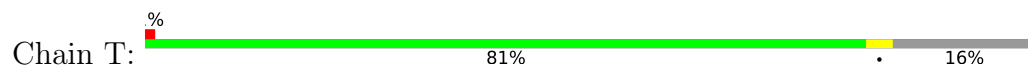
- Molecule 5: Proteasome subunit alpha type-6

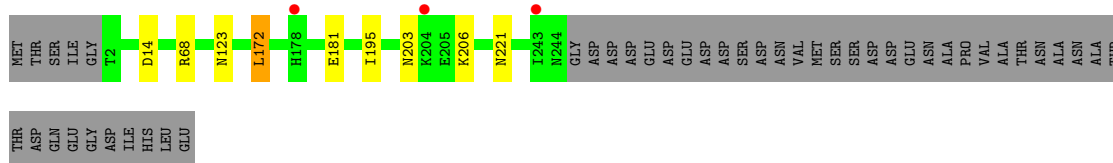


- Molecule 6: Probable proteasome subunit alpha type-7



- Molecule 6: Probable proteasome subunit alpha type-7





- Molecule 7: Proteasome subunit alpha type-1

Chain G: 90% 5% .



- Molecule 7: Proteasome subunit alpha type-1

Chain U: 90% 6% .



- Molecule 8: Proteasome subunit beta type-2

Chain H: 93% . .



- Molecule 8: Proteasome subunit beta type-2

Chain V: 93% . .



- Molecule 9: Proteasome subunit beta type-3

Chain I: 95% 5%

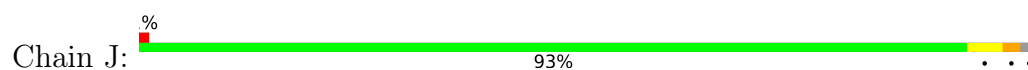


- Molecule 9: Proteasome subunit beta type-3

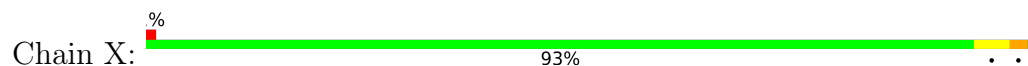
Chain W: 95% 5%



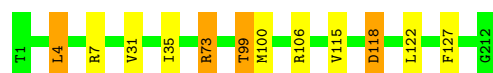
- Molecule 10: Proteasome subunit beta type-4



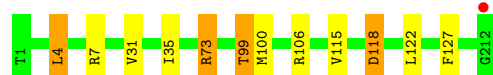
- Molecule 10: Proteasome subunit beta type-4



- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5



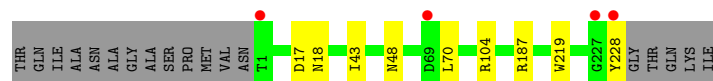
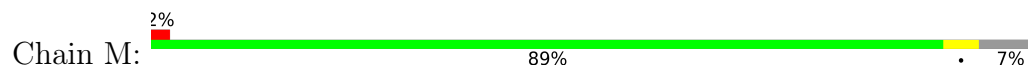
- Molecule 12: Proteasome subunit beta type-6



- Molecule 12: Proteasome subunit beta type-6



- Molecule 13: Proteasome subunit beta type-7



- Molecule 13: Proteasome subunit beta type-7

Chain a:

89%

8%



• Molecule 14: Proteasome subunit beta type-1

Chain N:

96%



• Molecule 14: Proteasome subunit beta type-1

Chain b:

95%

5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	137.49Å 299.73Å 145.61Å 90.00° 113.16° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.1 (15.00-2.80) 97.5 (15.00-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.81Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.188 , 0.222 0.192 , 0.226	Depositor DCC
R_{free} test set	12919 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	62.4	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 50.0	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	0.95	EDS
Total number of atoms	49783	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, MES, 04C, MG

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	0.41	0/1952	0.69	0/2642
1	O	0.41	0/1952	0.69	0/2642
2	B	0.41	0/1934	0.68	0/2618
2	P	0.41	0/1934	0.67	0/2618
3	C	0.41	0/1910	0.69	0/2586
3	Q	0.41	0/1910	0.70	0/2586
4	D	0.40	0/1837	0.66	0/2475
4	R	0.40	0/1837	0.66	0/2475
5	E	0.40	0/1800	0.66	0/2433
5	S	0.40	0/1800	0.66	0/2433
6	F	0.41	0/1932	0.69	0/2609
6	T	0.41	0/1932	0.70	0/2609
7	G	0.41	0/1945	0.67	0/2634
7	U	0.41	0/1945	0.67	0/2634
8	H	0.39	0/1715	0.66	1/2326 (0.0%)
8	V	0.39	0/1715	0.66	0/2326
9	I	0.40	0/1611	0.69	0/2174
9	W	0.39	0/1611	0.69	0/2174
10	J	0.41	0/1589	0.69	0/2142
10	X	0.41	0/1589	0.68	0/2142
11	K	0.37	0/1678	0.67	0/2271
11	Y	0.37	0/1678	0.67	0/2271
12	L	0.39	0/1795	0.66	0/2420
12	Z	0.39	0/1795	0.67	0/2420
13	M	0.41	0/1817	0.69	0/2465
13	a	0.41	0/1800	0.69	0/2442
14	N	0.38	0/1541	0.69	0/2087
14	b	0.38	0/1541	0.69	0/2087
All	All	0.40	0/50095	0.68	1/67741 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	1	THR	N-CA-C	5.00	125.00	111.00

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	1915	0	1929	1	0
1	O	1915	0	1929	2	0
2	B	1904	0	1904	2	0
2	P	1904	0	1904	3	0
3	C	1881	0	1895	4	0
3	Q	1881	0	1895	4	0
4	D	1813	0	1797	2	0
4	R	1813	0	1797	3	0
5	E	1773	0	1775	2	0
5	S	1773	0	1775	3	0
6	F	1892	0	1883	1	0
6	T	1892	0	1883	1	0
7	G	1907	0	1901	4	0
7	U	1907	0	1901	5	0
8	H	1684	0	1685	1	0
8	V	1684	0	1685	2	0
9	I	1581	0	1574	4	0
9	W	1581	0	1574	4	0
10	J	1561	0	1569	7	0
10	X	1561	0	1569	7	0
11	K	1641	0	1588	7	0
11	Y	1641	0	1588	7	0
12	L	1757	0	1711	4	0
12	Z	1757	0	1711	4	0
13	M	1786	0	1790	3	0
13	a	1770	0	1778	2	0
14	N	1512	0	1478	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	b	1512	0	1478	5	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	Y	1	0	0	0	0
16	G	1	0	0	0	0
16	U	1	0	0	0	0
17	H	42	0	42	4	0
17	K	42	0	42	1	0
17	N	42	0	42	4	0
17	V	42	0	42	4	0
17	Y	42	0	42	1	0
17	b	42	0	42	4	0
18	H	12	0	13	0	0
18	K	12	0	13	0	0
18	V	12	0	13	0	0
18	Y	12	0	13	0	0
19	A	4	0	0	0	0
19	B	16	0	0	0	0
19	C	9	0	0	0	0
19	D	3	0	0	0	0
19	E	3	0	0	0	0
19	F	9	0	0	0	0
19	G	7	0	0	0	0
19	H	11	0	0	0	0
19	I	10	0	0	0	0
19	J	15	0	0	0	0
19	K	15	0	0	0	0
19	L	20	0	0	0	0
19	M	12	0	0	0	0
19	N	9	0	0	0	0
19	O	6	0	0	0	0
19	P	8	0	0	0	0
19	Q	7	0	0	0	0
19	R	7	0	0	0	0
19	S	3	0	0	0	0
19	T	5	0	0	0	0
19	U	9	0	0	1	0
19	V	9	0	0	0	0
19	W	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	X	16	0	0	0	0
19	Y	16	0	0	0	0
19	Z	16	0	0	0	0
19	a	15	0	0	0	0
19	b	12	0	0	0	0
All	All	49783	0	49250	98	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 1.

All (98) 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)
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.72	0.71
17:V:301:04C:C35	17:V:301:04C:H25	2.21	0.70
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.72	0.69
10:J:1:MET:O	10:J:2:ASP:HB2	1.92	0.69
17:H:301:04C:H25	17:H:301:04C:C35	2.22	0.69
10:X:23:ARG:NH2	11:Y:118:ASP:OD1	2.26	0.68
10:X:1:MET:O	10:X:2:ASP:HB2	1.92	0.68
17:N:201:04C:H38	17:N:201:04C:H31	1.43	0.66
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.78	0.66
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.77	0.65
10:J:23:ARG:NH2	11:K:118:ASP:OD1	2.30	0.65
14:b:48:SER:HB2	17:b:201:04C:H25	1.80	0.64
14:N:48:SER:HB2	17:N:201:04C:H25	1.81	0.62
17:V:301:04C:H25	17:V:301:04C:H7	1.83	0.61
17:H:301:04C:H25	17:H:301:04C:H7	1.83	0.60
17:H:301:04C:H25	17:H:301:04C:H6	1.84	0.60
17:N:201:04C:H8	17:N:201:04C:H24	1.84	0.59
17:V:301:04C:H25	17:V:301:04C:H6	1.84	0.59
17:b:201:04C:H8	17:b:201:04C:H24	1.85	0.59
11:Y:73:ARG:HH11	11:Y:73:ARG:HG2	1.70	0.57
11:K:73:ARG:HG2	11:K:73:ARG:HH11	1.70	0.57
11:Y:99:THR:HG22	11:Y:115:VAL:HB	1.91	0.53
14:b:152:VAL:HA	14:b:175:MET:HE1	1.90	0.53
11:K:99:THR:HG22	11:K:115:VAL:HB	1.92	0.52
14:b:45:ARG:CZ	17:b:201:04C:H44	2.40	0.52
14:N:152:VAL:HA	14:N:175:MET:HE1	1.91	0.51
17:K:301:04C:O13	17:K:301:04C:H19	2.11	0.51
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.46	0.51
17:Y:301:04C:O13	17:Y:301:04C:H19	2.11	0.50
17:b:201:04C:H38	17:b:201:04C:H31	1.48	0.50
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.94	0.50
7:G:23:PHE:O	7:G:26:THR:HB	2.12	0.49
3:C:201:VAL:O	3:C:202:GLN:CB	2.60	0.49
7:U:23:PHE:O	7:U:26:THR:HB	2.13	0.49
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.60	0.49
14:N:45:ARG:CZ	17:N:201:04C:H44	2.42	0.49
9:I:98:ARG:O	9:I:126:ILE:HD11	2.13	0.49
10:J:174:MET:HA	10:X:174:MET:HA	1.93	0.49
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.94	0.48
9:I:36:SER:HB2	10:J:126:VAL:HG11	1.97	0.47
9:W:98:ARG:O	9:W:126:ILE:HD11	2.15	0.46
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.98	0.46
2:P:50:LYS:O	2:P:51:VAL:C	2.59	0.46
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.98	0.45
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.98	0.45
11:K:73:ARG:HH11	11:K:73:ARG:CG	2.30	0.45
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.98	0.45
11:Y:73:ARG:HH11	11:Y:73:ARG:CG	2.30	0.45
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.98	0.45
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	1.99	0.45
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.99	0.44
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.32	0.44
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.52	0.44
2:B:50:LYS:O	2:B:51:VAL:C	2.60	0.44
3:C:201:VAL:HG13	3:C:202:GLN:N	2.32	0.44
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.99	0.44
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.18	0.43
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.43
5:S:87:LEU:HD21	5:S:107:ALA:HB1	2.01	0.43
13:M:219:TRP:CH2	14:b:171:GLY:HA2	2.54	0.43
12:L:8:ASN:HA	12:L:30:ILE:O	2.18	0.42
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.85	0.42
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.34	0.42
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.55	0.42
12:L:147:MET:N	12:L:148:PRO:HD2	2.34	0.42
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.50	0.42
1:A:55:LEU:HD12	7:G:170:THR:HG23	2.01	0.42
11:K:4:LEU:HD22	11:K:4:LEU:C	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:171:GLY:HA2	13:a:219:TRP:CH2	2.55	0.42
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.42
10:J:21:VAL:HG11	11:K:122:LEU:HD11	2.01	0.41
7:U:122:ARG:HD2	19:U:404:HOH:O	2.20	0.41
12:L:125:PHE:CD2	12:L:131:TYR:HB3	2.55	0.41
3:Q:201:VAL:O	3:Q:202:GLN:HB2	2.20	0.41
5:S:77:ALA:N	5:S:78:PRO:CD	2.84	0.41
4:R:99:ILE:HD11	4:R:104:LEU:HB2	2.01	0.41
4:D:99:ILE:HD11	4:D:104:LEU:HB2	2.01	0.41
5:E:77:ALA:N	5:E:78:PRO:CD	2.84	0.41
17:V:301:04C:H36	17:V:301:04C:H19	2.01	0.41
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.50	0.41
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.02	0.41
4:D:88:ALA:HA	4:D:99:ILE:HG21	2.02	0.41
5:E:87:LEU:HD21	5:E:107:ALA:HB1	2.02	0.41
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.55	0.41
11:Y:4:LEU:C	11:Y:4:LEU:HD22	2.46	0.41
3:C:201:VAL:O	3:C:202:GLN:HB2	2.20	0.41
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.51	0.41
6:F:172:LEU:CD1	6:F:195:ILE:HD13	2.51	0.41
10:J:16:ALA:HB2	10:J:161:LEU:HD21	2.02	0.41
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.51	0.41
13:M:228:TYR:HA	8:V:121:VAL:HG23	2.03	0.40
14:b:38:HIS:O	14:b:39:ASP:C	2.63	0.40
13:M:17:ASP:OD1	13:M:18:ASN:N	2.54	0.40
6:T:172:LEU:CD1	6:T:195:ILE:HD13	2.52	0.40
10:X:16:ALA:HB2	10:X:161:LEU:HD21	2.02	0.40
13:a:17:ASP:OD1	13:a:18:ASN:N	2.54	0.40
17:H:301:04C:H19	17:H:301:04C:H36	2.03	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	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
1	O	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
2	B	242/258 (94%)	233 (96%)	7 (3%)	2 (1%)	16	44
2	P	242/258 (94%)	233 (96%)	7 (3%)	2 (1%)	16	44
3	C	238/254 (94%)	231 (97%)	5 (2%)	2 (1%)	16	44
3	Q	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	16	44
4	D	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
4	R	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
5	E	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
5	S	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
6	F	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
6	T	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
7	G	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
7	U	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
8	H	220/232 (95%)	216 (98%)	4 (2%)	0	100	100
8	V	220/232 (95%)	216 (98%)	4 (2%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
9	W	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	J	193/198 (98%)	190 (98%)	2 (1%)	1 (0%)	24	55
10	X	193/198 (98%)	190 (98%)	2 (1%)	1 (0%)	24	55
11	K	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
11	Y	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
12	L	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
12	Z	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
13	M	226/246 (92%)	218 (96%)	8 (4%)	0	100	100
13	a	224/246 (91%)	216 (96%)	8 (4%)	0	100	100
14	N	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
14	b	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
All	All	6264/6614 (95%)	6101 (97%)	153 (2%)	10 (0%)	43	72

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
10	J	2	ASP
2	P	51	VAL
3	Q	202	GLN
10	X	2	ASP
3	C	205	ALA
3	Q	205	ALA
2	B	221	ASP
2	P	221	ASP

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	209/209 (100%)	204 (98%)	5 (2%)	43	77
1	O	209/209 (100%)	204 (98%)	5 (2%)	43	77
2	B	203/216 (94%)	195 (96%)	8 (4%)	28	64
2	P	203/216 (94%)	195 (96%)	8 (4%)	28	64
3	C	212/226 (94%)	205 (97%)	7 (3%)	33	69
3	Q	212/226 (94%)	205 (97%)	7 (3%)	33	69
4	D	194/215 (90%)	183 (94%)	11 (6%)	18	49
4	R	194/215 (90%)	183 (94%)	11 (6%)	18	49
5	E	190/193 (98%)	184 (97%)	6 (3%)	34	70
5	S	190/193 (98%)	184 (97%)	6 (3%)	34	70
6	F	201/239 (84%)	193 (96%)	8 (4%)	28	63
6	T	201/239 (84%)	193 (96%)	8 (4%)	28	63
7	G	206/210 (98%)	200 (97%)	6 (3%)	37	73
7	U	206/210 (98%)	200 (97%)	6 (3%)	37	73
8	H	181/190 (95%)	177 (98%)	4 (2%)	45	78
8	V	181/190 (95%)	177 (98%)	4 (2%)	45	78
9	I	172/173 (99%)	169 (98%)	3 (2%)	53	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	W	172/173 (99%)	169 (98%)	3 (2%)	53	83
10	J	173/175 (99%)	169 (98%)	4 (2%)	44	78
10	X	173/175 (99%)	170 (98%)	3 (2%)	53	83
11	K	168/168 (100%)	160 (95%)	8 (5%)	23	56
11	Y	168/168 (100%)	160 (95%)	8 (5%)	23	56
12	L	185/185 (100%)	178 (96%)	7 (4%)	29	64
12	Z	185/185 (100%)	178 (96%)	7 (4%)	29	64
13	M	195/208 (94%)	190 (97%)	5 (3%)	40	75
13	a	194/208 (93%)	189 (97%)	5 (3%)	40	75
14	N	162/162 (100%)	160 (99%)	2 (1%)	63	87
14	b	162/162 (100%)	160 (99%)	2 (1%)	63	87
All	All	5301/5538 (96%)	5134 (97%)	167 (3%)	34	70

All (167) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	17	LYS
1	A	61	LEU
1	A	122	THR
1	A	157	PHE
2	B	50	LYS
2	B	52	THR
2	B	55	LEU
2	B	58	GLN
2	B	79	LEU
2	B	114	LEU
2	B	184	LYS
2	B	191	LEU
3	C	4	ARG
3	C	38	ASN
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	203	THR
4	D	20	LEU
4	D	40	LEU

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Mol	Chain	Res	Type
4	D	51	LEU
4	D	99	ILE
4	D	125	LEU
4	D	176	LEU
4	D	193	LEU
4	D	197	LYS
4	D	214	ILE
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	25	LEU
5	E	29	LYS
5	E	54	GLU
5	E	71	LEU
5	E	188	LEU
6	F	14	ASP
6	F	68	ARG
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	203	ASN
6	F	206	LYS
6	F	221	ASN
7	G	115	LEU
7	G	125	MET
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
7	G	236	LEU
8	H	56	THR
8	H	68	LEU
8	H	127	LEU
8	H	196	ARG
9	I	37	ASN
9	I	171	LEU
9	I	182	TRP
10	J	23	ARG
10	J	75	LEU
10	J	144	LEU
10	J	174	MET
11	K	4	LEU
11	K	7	ARG

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Mol	Chain	Res	Type
11	K	31	VAL
11	K	35	ILE
11	K	73	ARG
11	K	99	THR
11	K	106	ARG
11	K	118	ASP
12	L	1	GLN
12	L	13	LEU
12	L	23	LEU
12	L	49	ASN
12	L	136	CYS
12	L	150	LEU
12	L	167	LYS
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	187	ARG
14	N	9	LYS
14	N	119	VAL
1	O	1	MET
1	O	17	LYS
1	O	61	LEU
1	O	122	THR
1	O	157	PHE
2	P	50	LYS
2	P	52	THR
2	P	55	LEU
2	P	58	GLN
2	P	79	LEU
2	P	114	LEU
2	P	184	LYS
2	P	191	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	203	THR
4	R	20	LEU
4	R	40	LEU

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Mol	Chain	Res	Type
4	R	51	LEU
4	R	99	ILE
4	R	125	LEU
4	R	176	LEU
4	R	193	LEU
4	R	197	LYS
4	R	214	ILE
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	25	LEU
5	S	29	LYS
5	S	54	GLU
5	S	71	LEU
5	S	188	LEU
6	T	14	ASP
6	T	68	ARG
6	T	123	ASN
6	T	172	LEU
6	T	181	GLU
6	T	203	ASN
6	T	206	LYS
6	T	221	ASN
7	U	115	LEU
7	U	125	MET
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
7	U	236	LEU
8	V	56	THR
8	V	68	LEU
8	V	127	LEU
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU
9	W	182	TRP
10	X	75	LEU
10	X	144	LEU
10	X	174	MET
11	Y	4	LEU
11	Y	7	ARG
11	Y	31	VAL

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Mol	Chain	Res	Type
11	Y	35	ILE
11	Y	73	ARG
11	Y	99	THR
11	Y	106	ARG
11	Y	118	ASP
12	Z	1	GLN
12	Z	13	LEU
12	Z	23	LEU
12	Z	49	ASN
12	Z	136	CYS
12	Z	150	LEU
12	Z	167	LYS
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	187	ARG
14	b	9	LYS
14	b	119	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (113) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	119	GLN
2	B	123	GLN
2	B	124	HIS
2	B	176	GLN
2	B	232	GLN
3	C	38	ASN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
3	C	233	GLN
4	D	15	GLN
4	D	91	HIS
4	D	100	ASN
4	D	106	GLN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN

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Mol	Chain	Res	Type
5	E	118	ASN
5	E	120	GLN
5	E	147	GLN
5	E	151	ASN
5	E	165	GLN
5	E	184	ASN
6	F	86	ASN
6	F	123	ASN
7	G	30	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	175	ASN
8	H	30	ASN
8	H	86	HIS
8	H	189	ASN
9	I	88	GLN
9	I	168	GLN
9	I	172	ASN
10	J	55	GLN
10	J	63	ASN
10	J	146	HIS
10	J	147	HIS
11	K	9	GLN
11	K	85	ASN
11	K	143	ASN
11	K	176	ASN
11	K	208	ASN
12	L	79	HIS
12	L	197	GLN
13	M	102	GLN
13	M	149	HIS
13	M	194	ASN
13	M	213	GLN
14	N	38	HIS
14	N	69	GLN
14	N	141	ASN
1	O	30	GLN
1	O	94	HIS
2	P	93	HIS
2	P	119	GLN

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Mol	Chain	Res	Type
2	P	123	GLN
2	P	124	HIS
2	P	176	GLN
2	P	232	GLN
3	Q	38	ASN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
3	Q	233	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	225	ASN
5	S	68	HIS
5	S	99	ASN
5	S	116	GLN
5	S	120	GLN
5	S	151	ASN
5	S	165	GLN
5	S	184	ASN
6	T	86	ASN
6	T	123	ASN
7	U	30	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	175	ASN
8	V	30	ASN
8	V	189	ASN
8	V	194	ASN
9	W	88	GLN
9	W	168	GLN
9	W	172	ASN
10	X	55	GLN
10	X	63	ASN
10	X	86	GLN
10	X	146	HIS
11	Y	9	GLN
11	Y	85	ASN
11	Y	143	ASN

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Mol	Chain	Res	Type
11	Y	176	ASN
11	Y	208	ASN
12	Z	79	HIS
12	Z	197	GLN
13	a	102	GLN
13	a	194	ASN
13	a	213	GLN
14	b	38	HIS
14	b	69	GLN
14	b	141	ASN

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 ⓘ

Of 18 ligands modelled in this entry, 8 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	$\# Z > 2$
17	04C	b	201	14	44,44,44	1.35	3 (6%)	54,58,58	1.37	7 (12%)
17	04C	H	301	8	44,44,44	1.27	3 (6%)	54,58,58	1.15	5 (9%)
17	04C	Y	301	11	44,44,44	1.36	3 (6%)	54,58,58	1.28	9 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	MES	V	303	-	12,12,12	2.26	1 (8%)	15,16,16	1.19	2 (13%)
17	04C	V	301	8	44,44,44	1.24	3 (6%)	54,58,58	1.15	5 (9%)
17	04C	K	301	11	44,44,44	1.40	3 (6%)	54,58,58	1.24	8 (14%)
17	04C	N	201	14	44,44,44	1.36	3 (6%)	54,58,58	1.36	7 (12%)
18	MES	K	303	-	12,12,12	2.33	1 (8%)	15,16,16	1.17	2 (13%)
18	MES	Y	303	-	12,12,12	2.31	1 (8%)	15,16,16	1.36	2 (13%)
18	MES	H	302	-	12,12,12	2.21	1 (8%)	15,16,16	1.19	1 (6%)

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
17	04C	b	201	14	-	16/44/52/52	0/3/3/3
17	04C	H	301	8	-	13/44/52/52	0/3/3/3
17	04C	Y	301	11	-	10/44/52/52	0/3/3/3
18	MES	V	303	-	-	0/6/14/14	0/1/1/1
17	04C	V	301	8	-	13/44/52/52	0/3/3/3
17	04C	K	301	11	-	9/44/52/52	0/3/3/3
17	04C	N	201	14	-	16/44/52/52	0/3/3/3
18	MES	K	303	-	-	0/6/14/14	0/1/1/1
18	MES	Y	303	-	-	0/6/14/14	0/1/1/1
18	MES	H	302	-	-	3/6/14/14	0/1/1/1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	K	303	MES	C8-S	-7.71	1.66	1.77
18	Y	303	MES	C8-S	-7.63	1.66	1.77
18	V	303	MES	C8-S	-7.51	1.67	1.77
18	H	302	MES	C8-S	-7.38	1.67	1.77
17	K	301	04C	C10-C9	5.93	1.63	1.53
17	Y	301	04C	C10-C9	5.40	1.62	1.53
17	N	201	04C	C10-C9	4.96	1.61	1.53
17	H	301	04C	C40-C41	-4.81	1.40	1.51
17	K	301	04C	C40-C41	-4.75	1.40	1.51
17	b	201	04C	C10-C9	4.72	1.61	1.53
17	b	201	04C	C40-C41	-4.63	1.40	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	V	301	04C	C40-C41	-4.58	1.40	1.51
17	Y	301	04C	C40-C41	-4.54	1.40	1.51
17	N	201	04C	C40-C41	-4.46	1.40	1.51
17	H	301	04C	C10-C9	4.14	1.60	1.53
17	H	301	04C	C7-C6	-4.03	1.41	1.51
17	V	301	04C	C10-C9	4.02	1.60	1.53
17	V	301	04C	C7-C6	-4.02	1.41	1.51
17	N	201	04C	C7-C6	-3.87	1.42	1.51
17	b	201	04C	C7-C6	-3.86	1.42	1.51
17	Y	301	04C	C7-C6	-3.79	1.42	1.51
17	K	301	04C	C7-C6	-3.73	1.42	1.51

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	N	201	04C	C11-C10-C12	-5.15	103.20	109.76
17	b	201	04C	C11-C10-C12	-5.07	103.31	109.76
17	b	201	04C	C29-C30-N31	-3.82	104.53	113.41
17	N	201	04C	C29-C30-N31	-3.74	104.71	113.41
17	Y	301	04C	O13-C12-C10	-3.62	104.08	111.51
17	V	301	04C	O34-C33-C32	-3.57	104.09	111.77
17	H	301	04C	O34-C33-C32	-3.51	104.20	111.77
17	K	301	04C	O13-C12-C10	-3.37	104.59	111.51
17	V	301	04C	C29-C30-N31	-3.36	105.60	113.41
17	H	301	04C	C29-C30-N31	-3.35	105.63	113.41
18	Y	303	MES	O1S-S-C8	3.21	111.58	106.73
17	Y	301	04C	C11-C10-C12	-2.93	106.03	109.76
17	Y	301	04C	O34-C33-C32	-2.83	105.69	111.77
17	K	301	04C	O34-C33-C32	-2.77	105.80	111.77
18	K	303	MES	O1S-S-C8	2.77	110.92	106.73
17	K	301	04C	C11-C10-C12	-2.75	106.26	109.76
17	K	301	04C	C7-C6-C5	2.69	125.90	120.90
17	b	201	04C	C35-C36-N31	-2.67	106.06	110.12
17	N	201	04C	C35-C36-N31	-2.67	106.06	110.12
18	H	302	MES	O2S-S-C8	2.66	110.75	106.73
17	b	201	04C	C7-C6-C5	2.59	125.73	120.90
17	Y	301	04C	C7-C6-C5	2.59	125.72	120.90
17	H	301	04C	C7-C6-C1	-2.56	116.13	120.90
17	V	301	04C	C7-C6-C1	-2.56	116.14	120.90
17	b	201	04C	C41-C40-C24	-2.56	106.55	113.36
18	V	303	MES	O1S-S-C8	2.55	110.58	106.73
17	N	201	04C	C7-C6-C5	2.54	125.63	120.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	N	201	04C	O34-C33-C32	-2.54	106.30	111.77
17	b	201	04C	O34-C33-C32	-2.54	106.30	111.77
17	Y	301	04C	C30-N31-C36	-2.53	107.21	111.14
17	V	301	04C	C7-C6-C5	2.52	125.59	120.90
17	Y	301	04C	C41-C40-C24	-2.51	106.69	113.36
17	N	201	04C	C41-C40-C24	-2.50	106.71	113.36
17	H	301	04C	C7-C6-C5	2.49	125.54	120.90
17	K	301	04C	C7-C6-C1	-2.47	116.31	120.90
18	Y	303	MES	O2S-S-C8	2.46	110.44	106.73
17	N	201	04C	C7-C6-C1	-2.44	116.37	120.90
17	K	301	04C	C30-N31-C36	-2.43	107.37	111.14
17	b	201	04C	C7-C6-C1	-2.41	116.41	120.90
17	Y	301	04C	C7-C6-C1	-2.41	116.42	120.90
17	K	301	04C	C46-O45-C44	-2.41	112.33	117.50
17	K	301	04C	C41-C40-C24	-2.39	106.99	113.36
17	Y	301	04C	C46-O45-C44	-2.35	112.45	117.50
17	V	301	04C	C41-C40-C24	-2.17	107.59	113.36
17	H	301	04C	C41-C40-C24	-2.15	107.63	113.36
18	V	303	MES	O2S-S-C8	2.07	109.86	106.73
18	K	303	MES	O2S-S-C8	2.04	109.81	106.73
17	Y	301	04C	C29-C30-N31	-2.02	108.72	113.41

There are no chirality outliers.

All (80) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	H	301	04C	C11-C10-C9-C8
17	H	301	04C	C12-C10-C9-C8
17	H	301	04C	C11-C10-C12-O13
17	K	301	04C	C11-C10-C9-C8
17	K	301	04C	C12-C10-C9-C8
17	N	201	04C	C11-C10-C9-C8
17	N	201	04C	C12-C10-C9-C8
17	V	301	04C	C11-C10-C9-C8
17	V	301	04C	C12-C10-C9-C8
17	V	301	04C	C11-C10-C12-O13
17	Y	301	04C	C11-C10-C9-C8
17	Y	301	04C	C12-C10-C9-C8
17	b	201	04C	C11-C10-C9-C8
17	b	201	04C	C12-C10-C9-C8
18	H	302	MES	C7-C8-S-O1S
18	H	302	MES	C7-C8-S-O2S

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Mol	Chain	Res	Type	Atoms
17	K	301	04C	C47-C44-O45-C46
17	Y	301	04C	C47-C44-O45-C46
17	K	301	04C	C43-C44-O45-C46
17	Y	301	04C	C43-C44-O45-C46
17	N	201	04C	C47-C44-O45-C46
17	b	201	04C	C47-C44-O45-C46
17	N	201	04C	C43-C44-O45-C46
17	b	201	04C	C43-C44-O45-C46
17	N	201	04C	N25-C24-C40-C41
17	b	201	04C	N25-C24-C40-C41
18	H	302	MES	C7-C8-S-O3S
17	N	201	04C	C23-C24-C40-C41
17	b	201	04C	C23-C24-C40-C41
17	H	301	04C	C5-C6-C7-C8
17	V	301	04C	C5-C6-C7-C8
17	b	201	04C	C5-C6-C7-C8
17	N	201	04C	C5-C6-C7-C8
17	Y	301	04C	C5-C6-C7-C8
17	K	301	04C	C5-C6-C7-C8
17	b	201	04C	C1-C6-C7-C8
17	N	201	04C	C1-C6-C7-C8
17	H	301	04C	C1-C6-C7-C8
17	K	301	04C	C1-C6-C7-C8
17	V	301	04C	C1-C6-C7-C8
17	Y	301	04C	C1-C6-C7-C8
17	N	201	04C	N28-C29-C30-N31
17	b	201	04C	N28-C29-C30-N31
17	H	301	04C	C6-C7-C8-N22
17	V	301	04C	C6-C7-C8-N22
17	H	301	04C	C11-C10-C9-O21
17	K	301	04C	C11-C10-C9-O21
17	K	301	04C	C12-C10-C9-O21
17	N	201	04C	C11-C10-C9-O21
17	V	301	04C	C11-C10-C9-O21
17	Y	301	04C	C11-C10-C9-O21
17	Y	301	04C	C12-C10-C9-O21
17	b	201	04C	C11-C10-C9-O21
17	H	301	04C	N28-C29-C30-N31
17	V	301	04C	N28-C29-C30-N31
17	H	301	04C	O37-C29-C30-N31
17	N	201	04C	O37-C29-C30-N31
17	b	201	04C	O37-C29-C30-N31

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Mol	Chain	Res	Type	Atoms
17	V	301	04C	O37-C29-C30-N31
17	H	301	04C	N25-C24-C40-C41
17	N	201	04C	C6-C7-C8-N22
17	b	201	04C	C6-C7-C8-N22
17	N	201	04C	C29-C30-N31-C36
17	N	201	04C	C29-C30-N31-C32
17	b	201	04C	C29-C30-N31-C36
17	b	201	04C	C29-C30-N31-C32
17	V	301	04C	N25-C24-C40-C41
17	b	201	04C	C12-C10-C9-O21
17	H	301	04C	C12-C10-C9-O21
17	N	201	04C	C12-C10-C9-O21
17	V	301	04C	C12-C10-C9-O21
17	H	301	04C	C9-C10-C12-O13
17	V	301	04C	C9-C10-C12-O13
17	Y	301	04C	O49-C23-C24-N25
17	H	301	04C	C6-C7-C8-C9
17	N	201	04C	C6-C7-C8-C9
17	V	301	04C	C6-C7-C8-C9
17	b	201	04C	C6-C7-C8-C9
17	K	301	04C	O49-C23-C24-N25
17	Y	301	04C	N22-C23-C24-N25

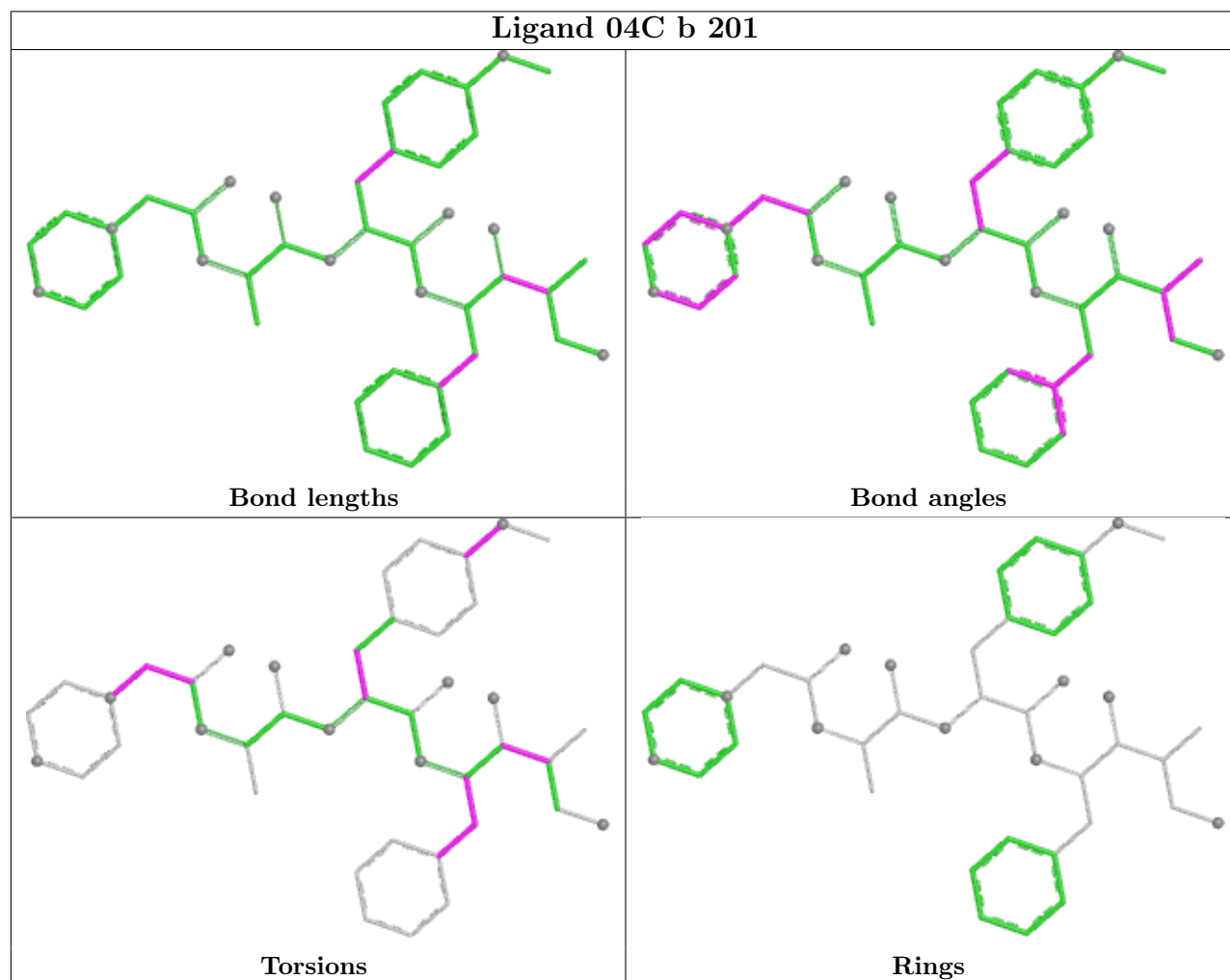
There are no ring outliers.

6 monomers are involved in 18 short contacts:

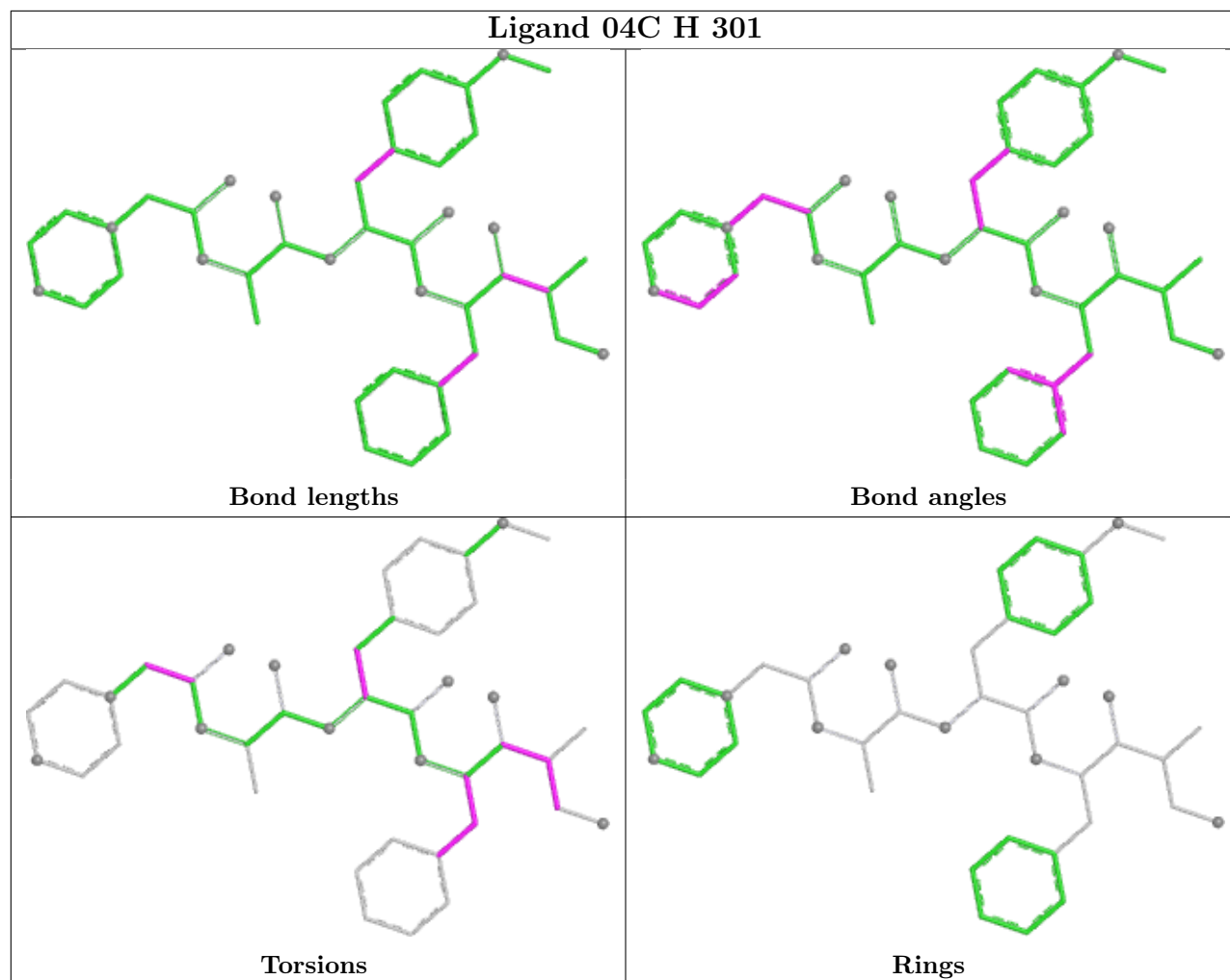
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	b	201	04C	4	0
17	H	301	04C	4	0
17	Y	301	04C	1	0
17	V	301	04C	4	0
17	K	301	04C	1	0
17	N	201	04C	4	0

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

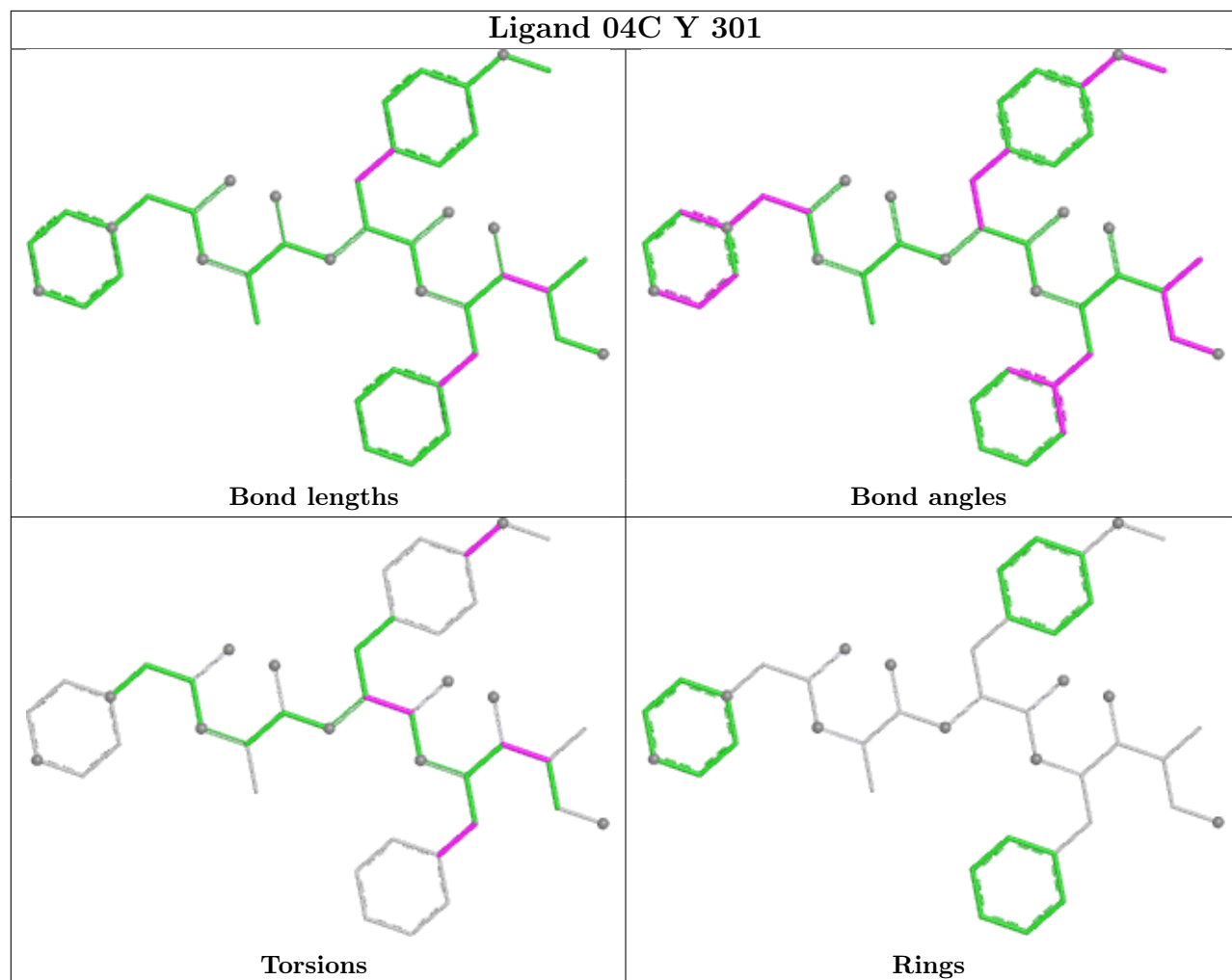
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents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



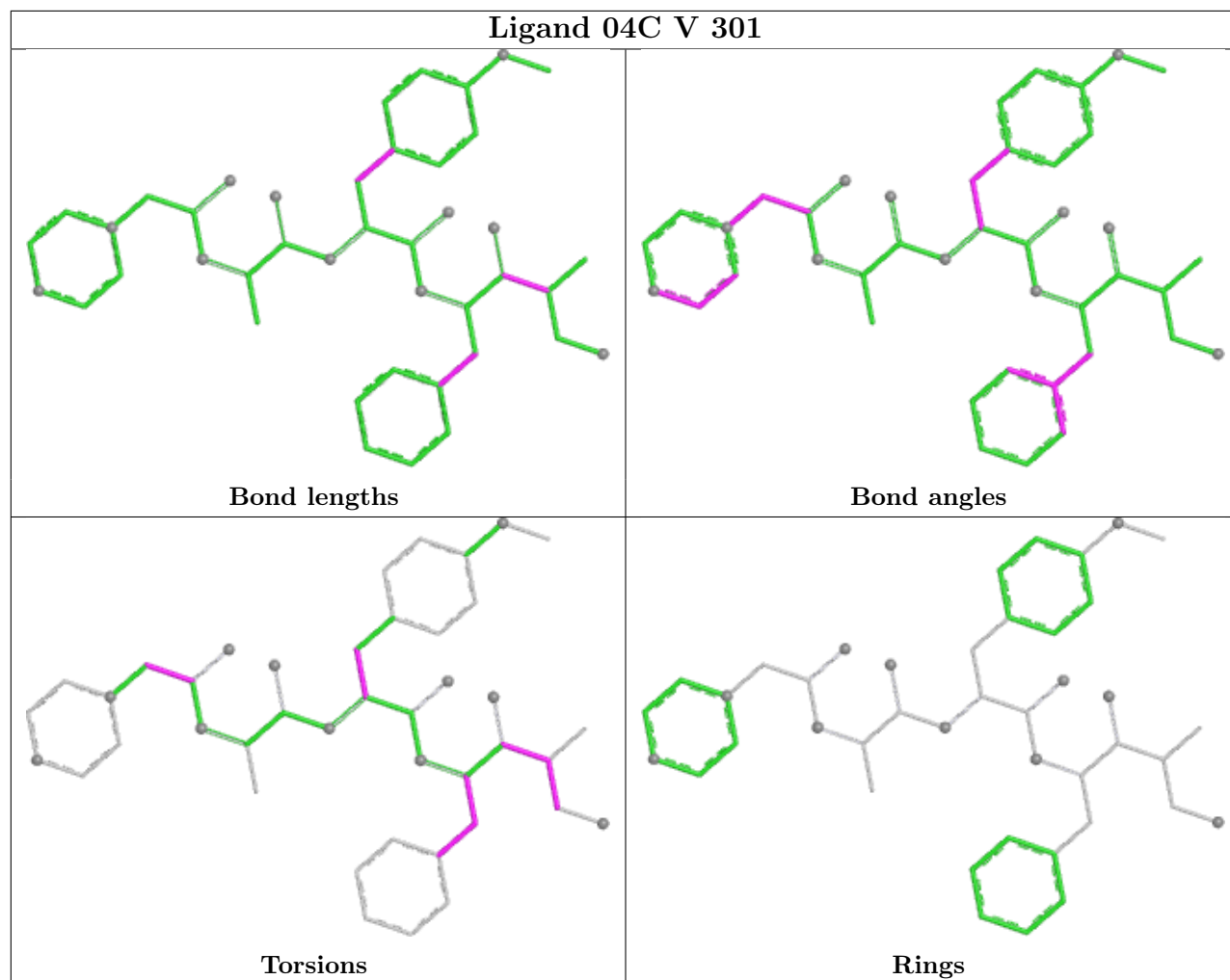
Ligand 04C H 301

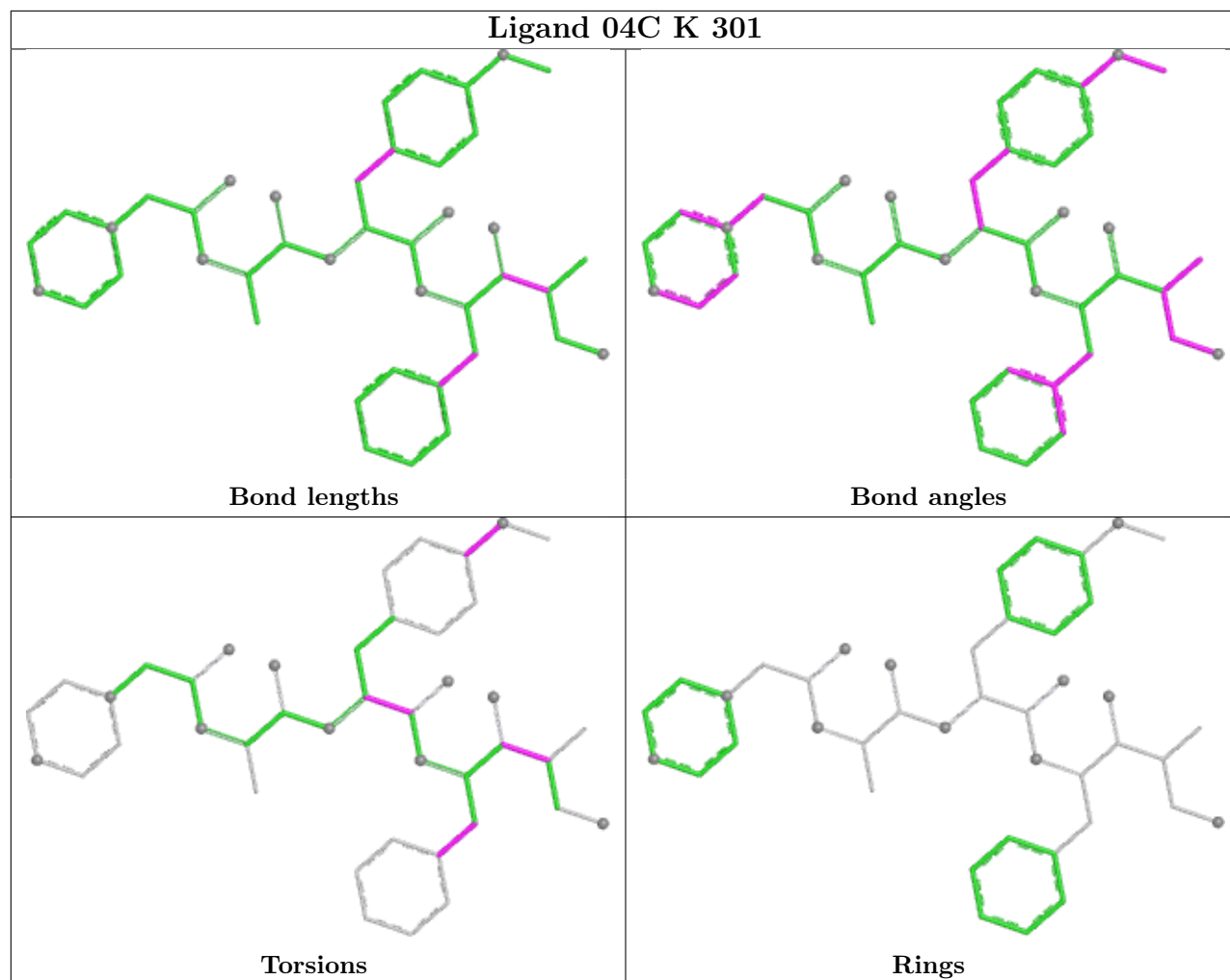


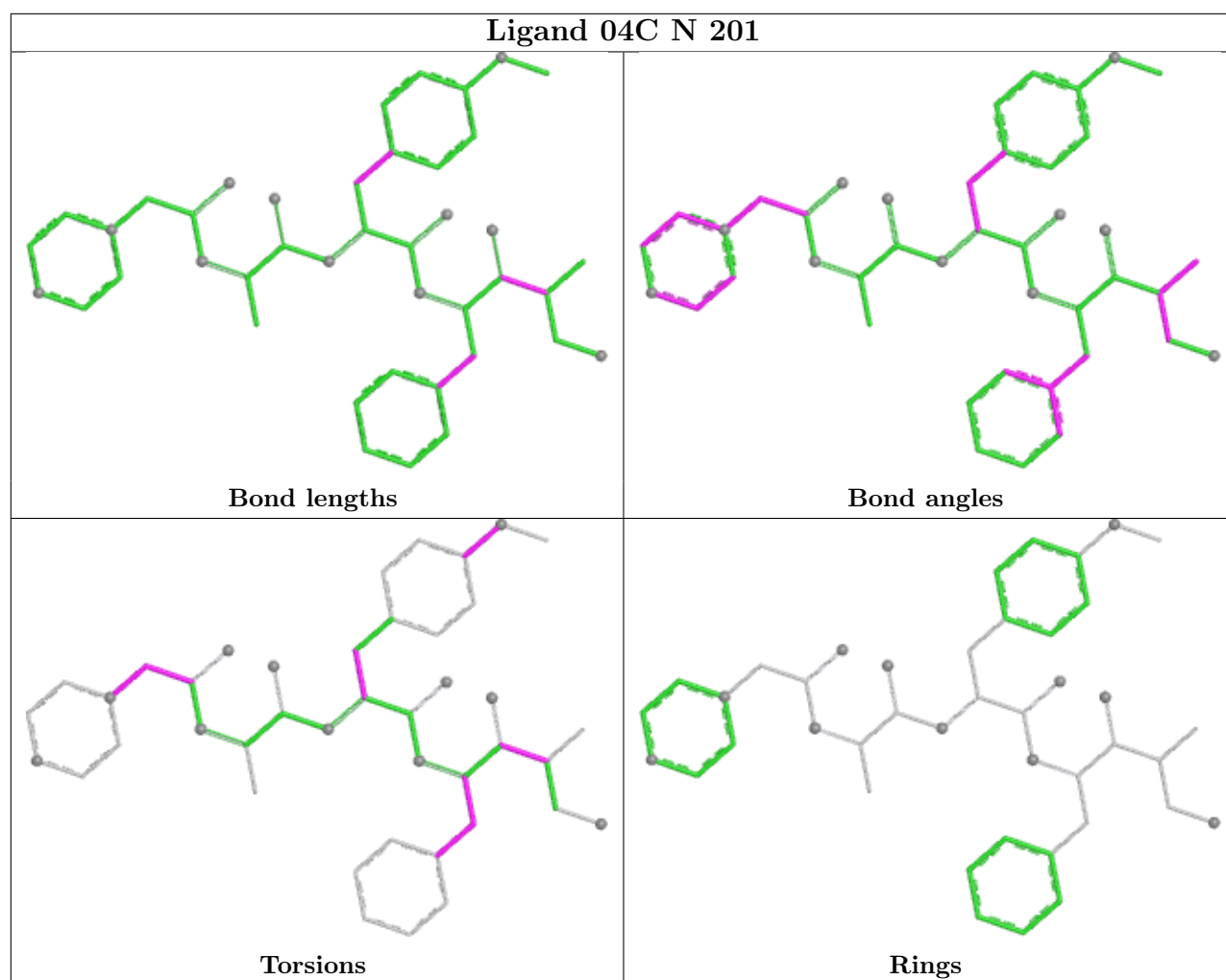
Ligand 04C Y 301



Ligand 04C V 301







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	250/250 (100%)	-0.45	1 (0%) 88 84	46, 61, 99, 151	0
1	O	250/250 (100%)	-0.38	1 (0%) 88 84	48, 69, 112, 154	0
2	B	244/258 (94%)	-0.27	3 (1%) 76 68	44, 66, 114, 165	0
2	P	244/258 (94%)	-0.22	3 (1%) 76 68	49, 72, 118, 162	0
3	C	240/254 (94%)	-0.28	3 (1%) 75 66	44, 70, 135, 163	0
3	Q	240/254 (94%)	-0.05	7 (2%) 53 43	57, 86, 173, 201	0
4	D	235/260 (90%)	-0.33	1 (0%) 88 84	51, 75, 107, 148	0
4	R	235/260 (90%)	-0.22	2 (0%) 81 74	54, 76, 118, 170	0
5	E	231/234 (98%)	-0.18	0 100 100	53, 79, 118, 160	0
5	S	231/234 (98%)	0.03	1 (0%) 88 84	58, 84, 136, 168	0
6	F	243/288 (84%)	-0.30	3 (1%) 76 68	48, 72, 122, 150	0
6	T	243/288 (84%)	-0.16	3 (1%) 76 68	48, 76, 136, 170	0
7	G	241/252 (95%)	-0.38	1 (0%) 88 84	43, 66, 109, 155	0
7	U	241/252 (95%)	-0.41	0 100 100	45, 65, 100, 130	0
8	H	222/232 (95%)	-0.45	0 100 100	44, 62, 93, 114	0
8	V	222/232 (95%)	-0.40	0 100 100	45, 64, 96, 122	0
9	I	204/205 (99%)	-0.60	1 (0%) 87 82	40, 55, 89, 112	0
9	W	204/205 (99%)	-0.58	0 100 100	41, 60, 91, 117	0
10	J	195/198 (98%)	-0.53	1 (0%) 87 82	42, 58, 88, 128	0
10	X	195/198 (98%)	-0.55	1 (0%) 87 82	46, 60, 93, 142	0
11	K	212/212 (100%)	-0.58	0 100 100	37, 60, 90, 109	0
11	Y	212/212 (100%)	-0.49	1 (0%) 87 82	31, 59, 88, 118	0
12	L	222/222 (100%)	-0.53	0 100 100	41, 62, 92, 109	0
12	Z	222/222 (100%)	-0.55	0 100 100	41, 59, 91, 111	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	228/246 (92%)	-0.45	4 (1%) 67 58	41, 63, 92, 110	0
13	a	226/246 (91%)	-0.54	1 (0%) 88 84	41, 60, 91, 114	0
14	N	196/196 (100%)	-0.50	0 100 100	40, 59, 93, 115	0
14	b	196/196 (100%)	-0.46	1 (0%) 87 82	42, 60, 93, 113	0
All	All	6324/6614 (95%)	-0.38	39 (0%) 85 80	31, 66, 115, 201	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	J	1	MET	5.6
10	X	1	MET	5.2
1	O	1	MET	4.2
3	Q	50	LEU	4.0
1	A	1	MET	3.8
6	T	178	HIS	3.3
2	B	219	ALA	3.2
11	Y	212	GLY	3.1
2	B	51	VAL	3.1
2	B	218	GLY	3.0
4	R	113	LEU	3.0
3	C	205	ALA	3.0
2	P	51	VAL	3.0
13	M	227	GLY	3.0
3	Q	51	LYS	2.9
3	Q	52	LEU	2.9
3	Q	49	THR	2.8
13	M	1	THR	2.8
5	S	52	ALA	2.7
14	b	103	ASP	2.7
3	Q	205	ALA	2.6
13	a	1	THR	2.6
3	C	204	GLY	2.6
6	F	215	CYS	2.5
6	T	204	LYS	2.4
3	Q	234	ILE	2.4
3	C	207	ASN	2.2
6	F	202	ASP	2.2
6	T	243	ILE	2.2
4	D	240	ALA	2.2
4	R	233	LYS	2.2
13	M	228	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
7	G	168	GLU	2.1
2	P	218	GLY	2.1
3	Q	204	GLY	2.1
9	I	1	SER	2.1
2	P	52	THR	2.1
6	F	178	HIS	2.0
13	M	69	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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(Å ²)	Q<0.9
17	04C	N	201	42/42	0.86	0.13	41,56,72,77	0
17	04C	b	201	42/42	0.86	0.12	42,61,78,81	0
17	04C	H	301	42/42	0.91	0.09	39,48,74,75	0
17	04C	V	301	42/42	0.92	0.10	41,50,80,81	0
18	MES	V	303	12/12	0.94	0.11	58,66,80,85	0
17	04C	K	301	42/42	0.95	0.08	34,46,61,63	0
17	04C	Y	301	42/42	0.95	0.07	28,42,62,64	0
15	MG	N	202	1/1	0.96	0.05	56,56,56,56	0
18	MES	H	302	12/12	0.96	0.08	61,64,77,77	0
15	MG	G	301	1/1	0.96	0.05	52,52,52,52	0
15	MG	I	301	1/1	0.97	0.09	51,51,51,51	0
18	MES	K	303	12/12	0.97	0.12	39,42,57,60	0
15	MG	V	302	1/1	0.97	0.06	70,70,70,70	0
15	MG	K	302	1/1	0.98	0.10	63,63,63,63	0
15	MG	Y	302	1/1	0.98	0.04	58,58,58,58	0
16	CL	G	302	1/1	0.98	0.06	48,48,48,48	0

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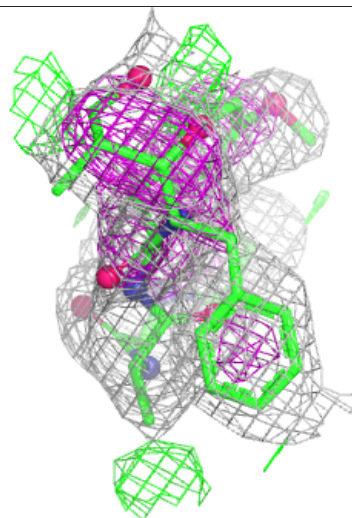
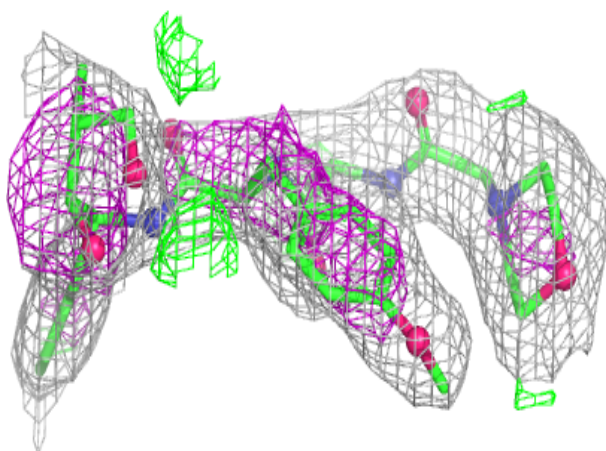
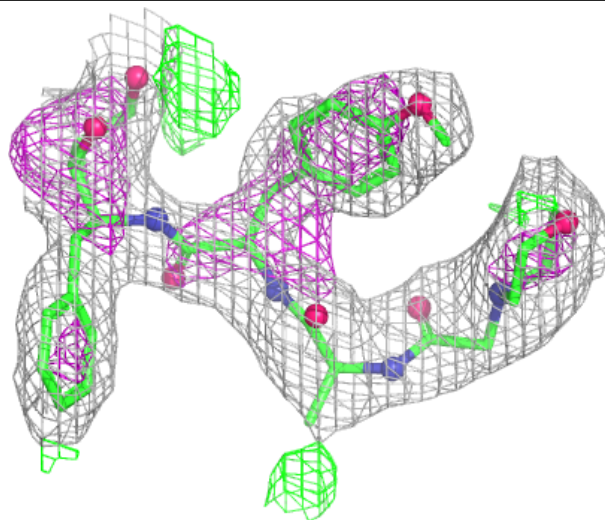
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
18	MES	Y	303	12/12	0.98	0.11	39,40,45,47	0
16	CL	U	301	1/1	0.99	0.10	47,47,47,47	0

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.

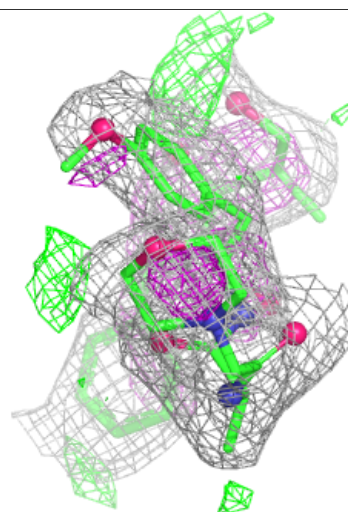
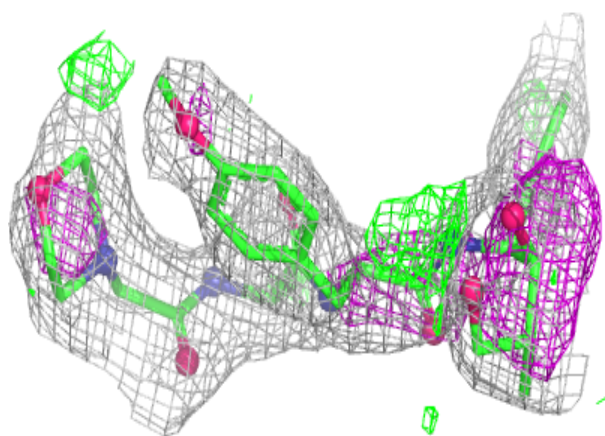
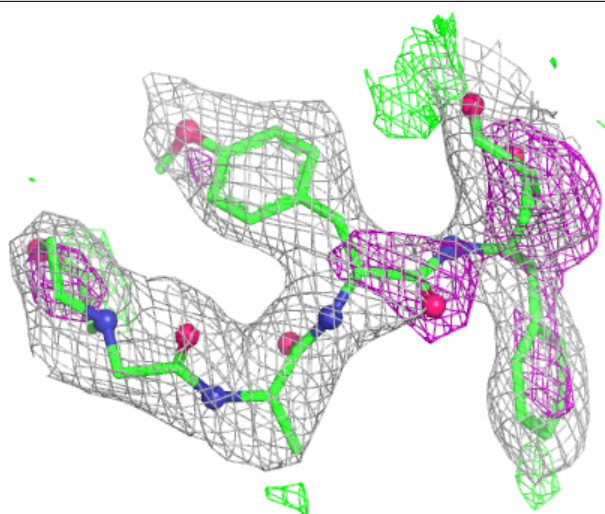
Electron density around 04C N 201:

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



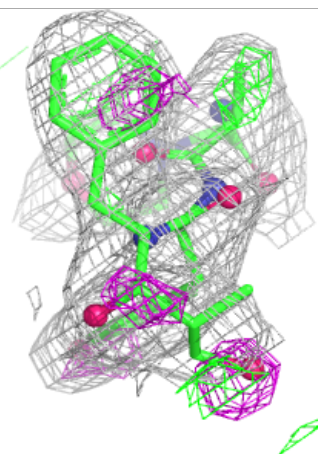
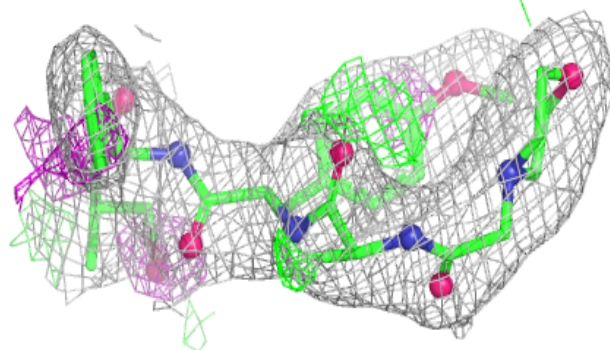
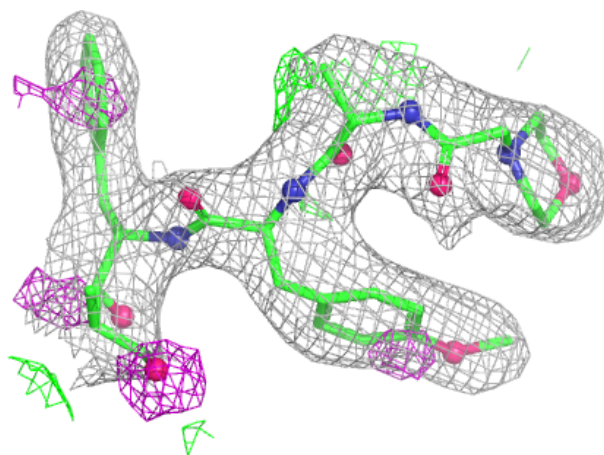
Electron density around 04C b 201:

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



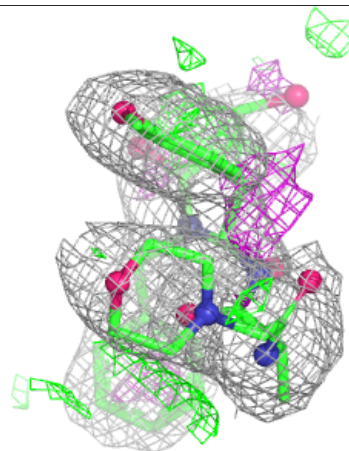
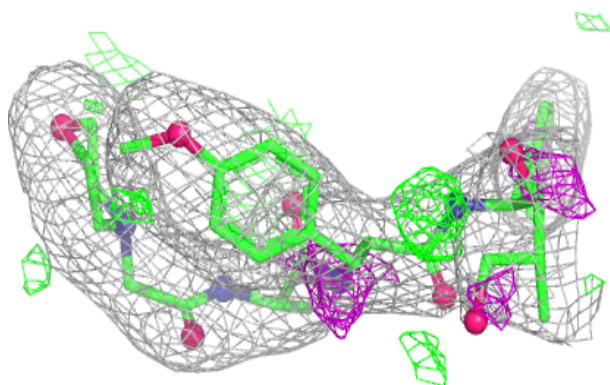
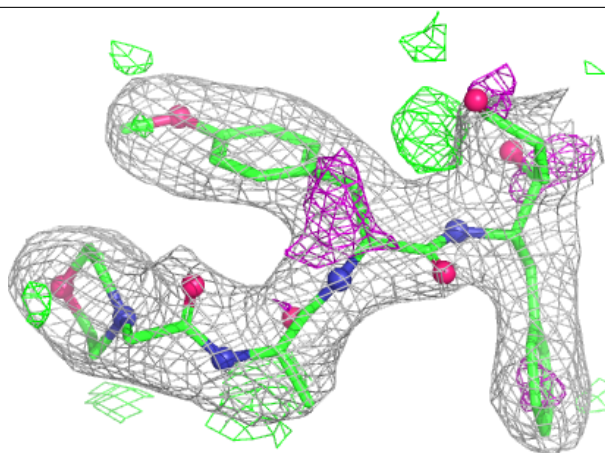
Electron density around 04C H 301:

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

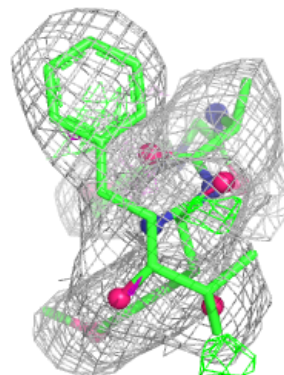
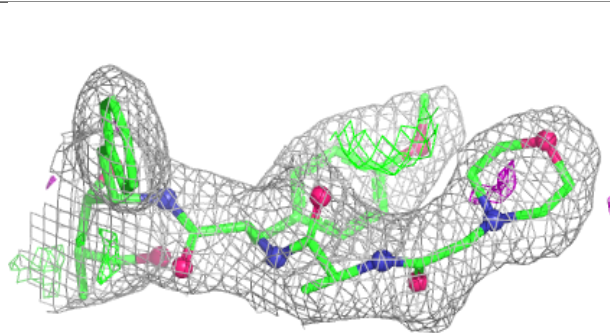
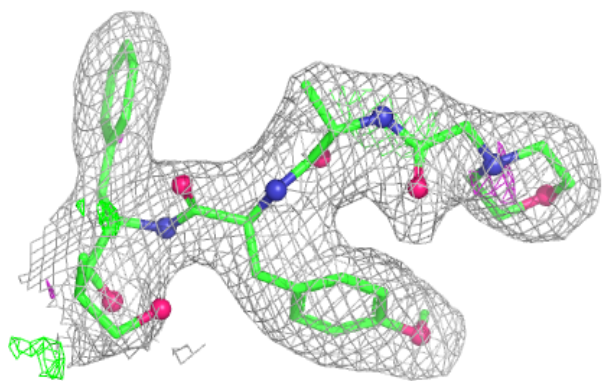


Electron density around 04C V 301:

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

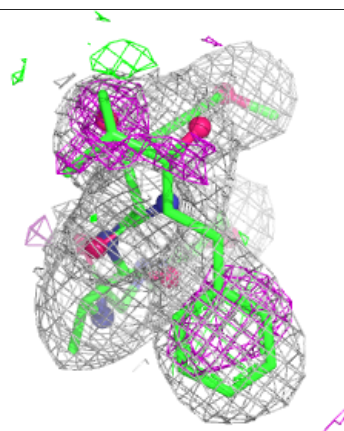
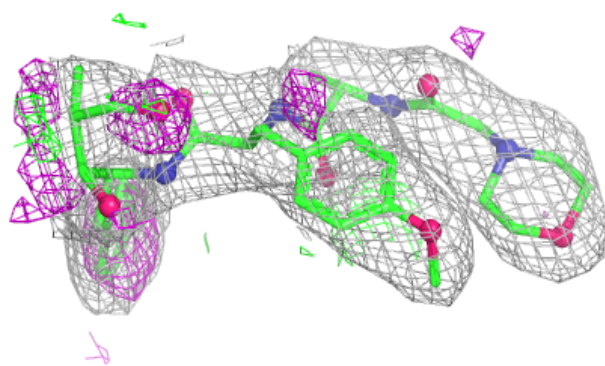
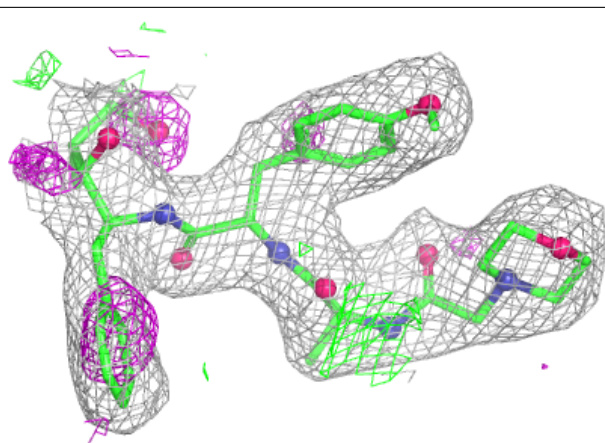
**Electron density around 04C K 301:**

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



Electron density around 04C Y 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.