



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:01 PM UTC

PDB ID : 5CZ8 / pdb_00005cz8
Title : Yeast 20S proteasome beta5-L(-49)S-K33A mutant in complex with Carfilzomib
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-07-31
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

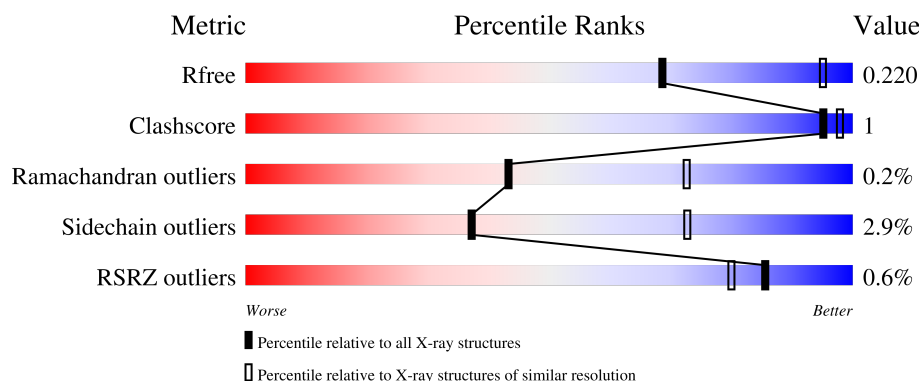
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

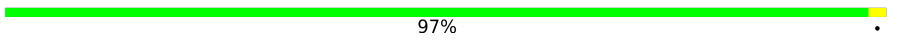
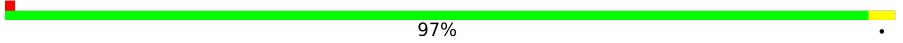
The reported resolution of this entry is 2.80 Å.

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	 97%
1	O	250	 97%
2	B	258	 90% 5% 5%
2	P	258	 89% 5% 5%
3	C	254	 90% 5% 5%

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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	221	
11	Y	221	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 49869 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	220	Total	C	N	O	S	0	0	0
			1699	1080	291	320	8			
11	Y	221	Total	C	N	O	S	0	0	0
			1707	1084	292	323	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	33	ALA	LYS	engineered mutation	UNP P30656
Y	33	ALA	LYS	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	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	a	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	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			

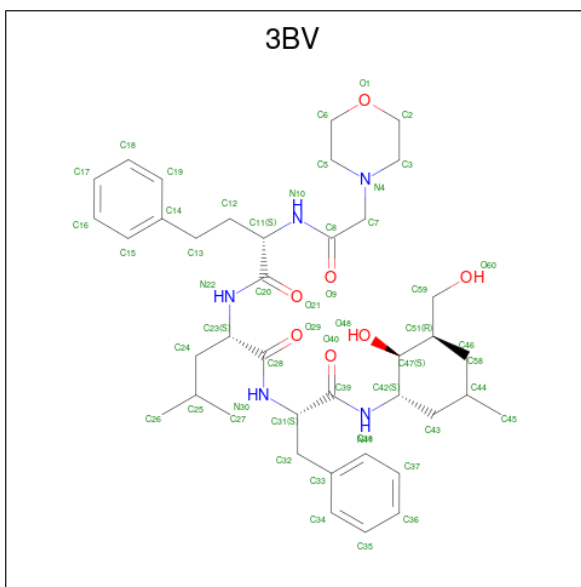
- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	G	2	Total Mg 2 2	0	0
15	I	1	Total Mg 1 1	0	0
15	K	1	Total Mg 1 1	0	0
15	L	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	U	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0

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

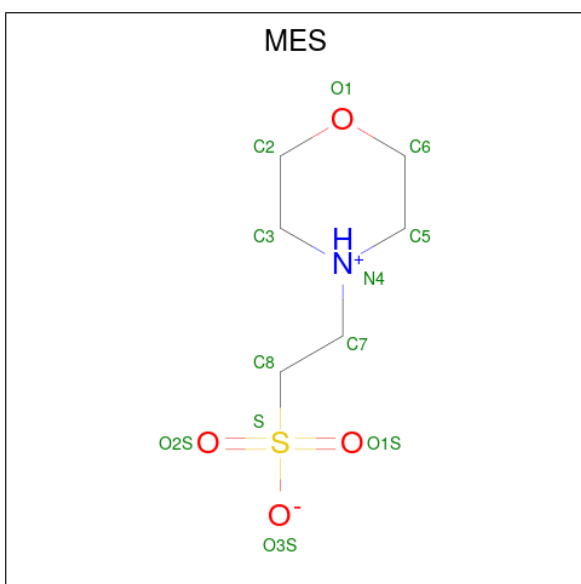
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	N	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0
16	b	1	Total Cl 1 1	0	0

- Molecule 17 is N-{(2S)-2-[(morpholin-4-ylacetyl)amino]-4-phenylbutanoyl}-L-leucyl-N-[(2R,3S,4S)-1,3-dihydroxy-2,6-dimethylheptan-4-yl]-L-phenylalaninamide (CCD ID: 3BV) (formula: C₄₀H₆₁N₅O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
17	H	1	Total	C	N	O	0	0
			52	40	5	7		
17	N	1	Total	C	N	O	0	0
			52	40	5	7		
17	V	1	Total	C	N	O	0	0
			52	40	5	7		
17	b	1	Total	C	N	O	0	0
			52	40	5	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	V	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	5	Total	O	0	0
			5	5		
19	B	12	Total	O	0	0
			12	12		
19	C	8	Total	O	0	0
			8	8		
19	D	1	Total	O	0	0
			1	1		
19	E	3	Total	O	0	0
			3	3		
19	F	5	Total	O	0	0
			5	5		
19	G	6	Total	O	0	0
			6	6		
19	H	9	Total	O	0	0
			9	9		
19	I	6	Total	O	0	0
			6	6		
19	J	10	Total	O	0	0
			10	10		
19	K	8	Total	O	0	0
			8	8		
19	L	8	Total	O	0	0
			8	8		
19	M	15	Total	O	0	0
			15	15		
19	N	7	Total	O	0	0
			7	7		
19	O	4	Total	O	0	0
			4	4		
19	P	9	Total	O	0	0
			9	9		
19	Q	6	Total	O	0	0
			6	6		
19	R	6	Total	O	0	0
			6	6		

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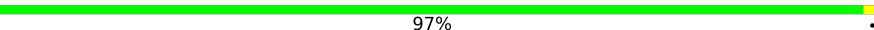
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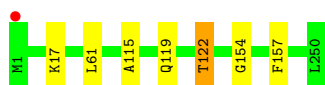
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	S	5	Total 5	O 5	0	0
19	T	7	Total 7	O 7	0	0
19	U	9	Total 9	O 9	0	0
19	V	8	Total 8	O 8	0	0
19	W	6	Total 6	O 6	0	0
19	X	10	Total 10	O 10	0	0
19	Y	6	Total 6	O 6	0	0
19	Z	11	Total 11	O 11	0	0
19	a	9	Total 9	O 9	0	0
19	b	12	Total 12	O 12	0	0

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:  97%



- Molecule 1: Proteasome subunit alpha type-2

Chain O:  97%



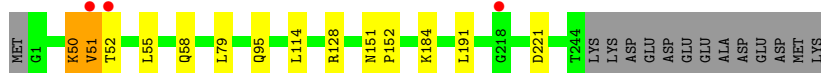
- Molecule 2: Proteasome subunit alpha type-3

Chain B:  90% 5%



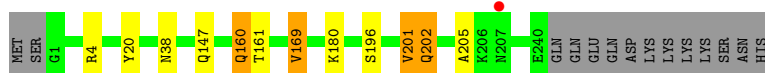
- Molecule 2: Proteasome subunit alpha type-3

Chain P:  89% 5% 5%

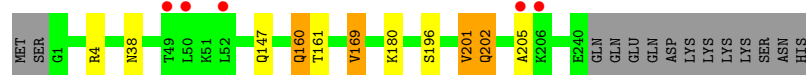
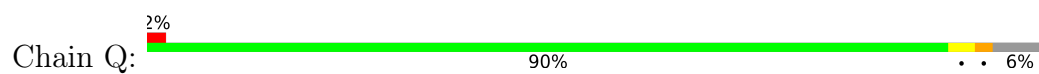


- Molecule 3: Proteasome subunit alpha type-4

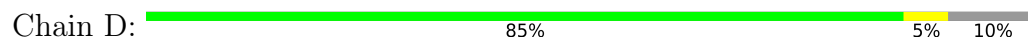
Chain C:  90% 6%



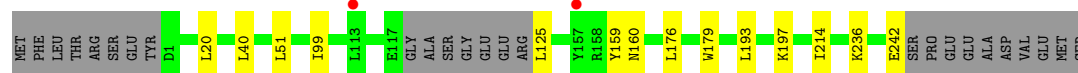
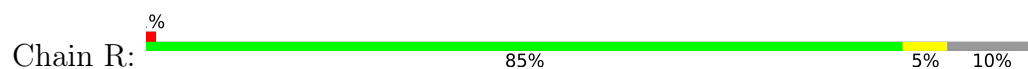
- Molecule 3: Proteasome subunit alpha type-4



- Molecule 4: Proteasome subunit alpha type-5



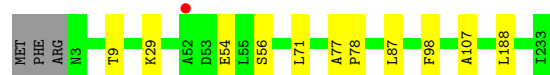
- Molecule 4: Proteasome subunit alpha type-5



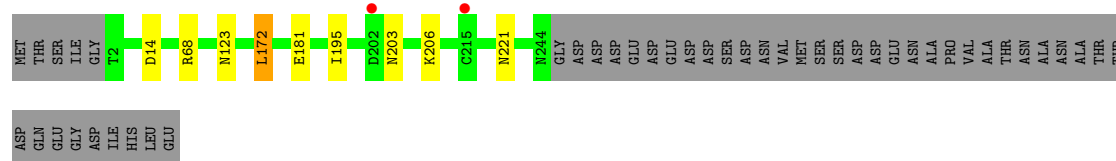
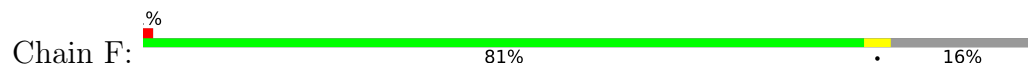
- Molecule 5: Proteasome subunit alpha type-6



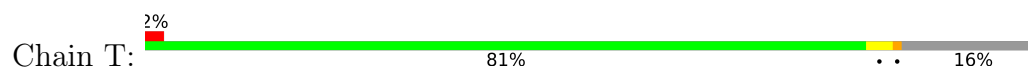
- Molecule 5: Proteasome subunit alpha type-6

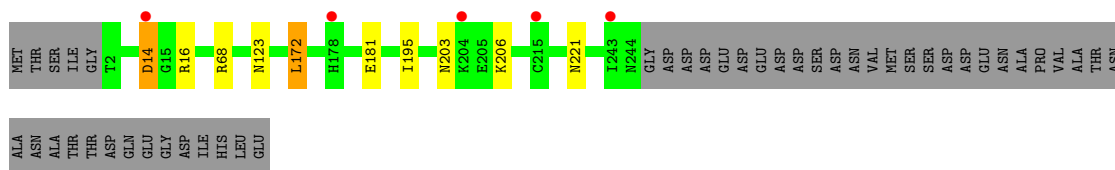


- Molecule 6: Probable proteasome subunit alpha type-7



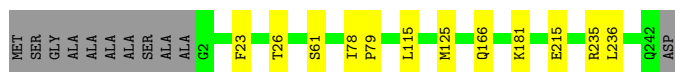
- Molecule 6: Probable proteasome subunit alpha type-7





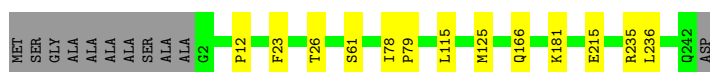
- Molecule 7: Proteasome subunit alpha type-1

Chain G: 91% 5% .



- Molecule 7: Proteasome subunit alpha type-1

Chain U: 90% 5% .



- Molecule 8: Proteasome subunit beta type-2

Chain H: 93% . .



- Molecule 8: Proteasome subunit beta type-2

Chain V: 93% . .



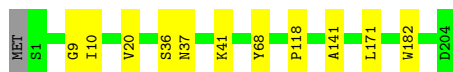
- Molecule 9: Proteasome subunit beta type-3

Chain I: 95% 5%

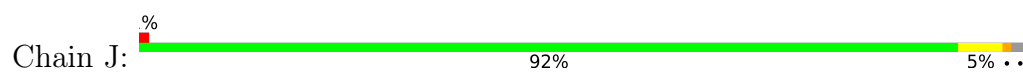


- Molecule 9: Proteasome subunit beta type-3

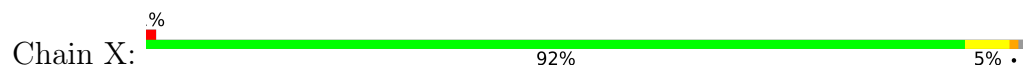
Chain W: 94% 5%



- Molecule 10: Proteasome subunit beta type-4



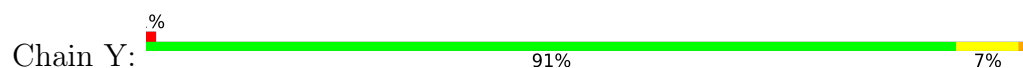
- Molecule 10: Proteasome subunit beta type-4



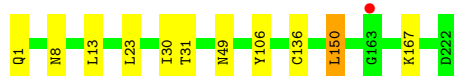
- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5



- Molecule 12: Proteasome subunit beta type-6



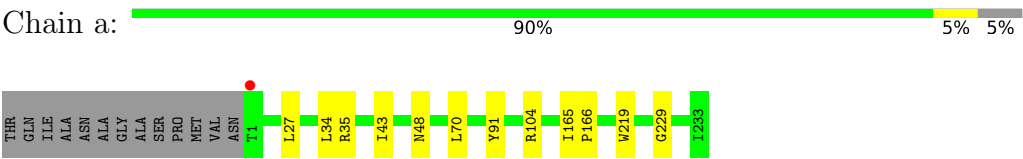
- Molecule 12: Proteasome subunit beta type-6



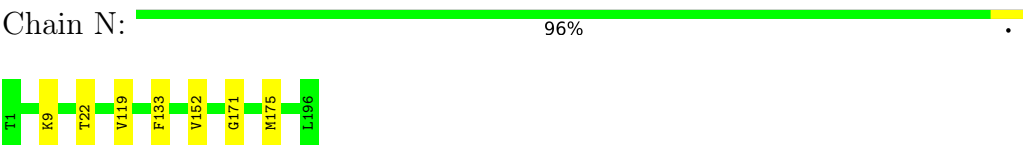
- Molecule 13: Proteasome subunit beta type-7



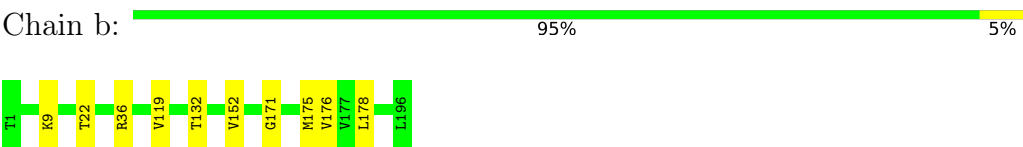
● Molecule 13: Proteasome subunit beta type-7



● Molecule 14: Proteasome subunit beta type-1



● Molecule 14: Proteasome subunit beta type-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.44Å 299.27Å 144.46Å 90.00° 113.12° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.4 (15.00-2.80) 95.8 (15.00-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.191 , 0.215 0.196 , 0.220	Depositor DCC
R_{free} test set	12481 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	67.7	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	49869	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% 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: MG, MES, 3BV, CL

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	0.39	0/1952	0.69	0/2642
1	O	0.39	0/1952	0.68	0/2642
2	B	0.39	0/1934	0.66	0/2618
2	P	0.38	0/1934	0.66	0/2618
3	C	0.39	0/1910	0.69	1/2586 (0.0%)
3	Q	0.39	0/1910	0.69	1/2586 (0.0%)
4	D	0.38	0/1837	0.65	0/2475
4	R	0.38	0/1837	0.65	0/2475
5	E	0.39	0/1800	0.65	0/2433
5	S	0.38	0/1800	0.65	0/2433
6	F	0.39	0/1932	0.69	0/2609
6	T	0.39	0/1932	0.69	0/2609
7	G	0.38	0/1945	0.66	0/2634
7	U	0.38	0/1945	0.66	0/2634
8	H	0.38	0/1715	0.63	0/2326
8	V	0.39	0/1715	0.64	0/2326
9	I	0.37	0/1611	0.68	0/2174
9	W	0.37	0/1611	0.67	0/2174
10	J	0.37	0/1589	0.66	0/2142
10	X	0.37	0/1589	0.66	0/2142
11	K	0.47	0/1737	0.70	1/2349 (0.0%)
11	Y	0.47	0/1745	0.67	1/2360 (0.0%)
12	L	0.37	0/1795	0.65	0/2420
12	Z	0.37	0/1795	0.66	0/2420
13	M	0.40	0/1855	0.70	1/2514 (0.0%)
13	a	0.40	0/1855	0.70	1/2514 (0.0%)
14	N	0.37	0/1541	0.67	0/2087
14	b	0.37	0/1541	0.68	0/2087
All	All	0.39	0/50314	0.67	6/68029 (0.0%)

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
11	Y	0	1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	0	GLY	N-CA-C	11.06	126.75	110.60
13	a	35	ARG	N-CA-C	9.04	120.91	111.14
13	M	35	ARG	N-CA-C	8.29	120.10	111.14
3	Q	201	VAL	N-CA-C	5.67	116.13	110.23
3	C	201	VAL	N-CA-C	5.57	116.03	110.23
11	Y	-5	ILE	CB-CA-C	-5.37	103.86	111.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	Y	0	GLY	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	1915	0	1929	2	0
1	O	1915	0	1929	4	0
2	B	1904	0	1904	3	0
2	P	1904	0	1904	4	0
3	C	1881	0	1895	6	0
3	Q	1881	0	1895	5	0
4	D	1813	0	1797	1	0
4	R	1813	0	1797	2	0
5	E	1773	0	1775	2	0
5	S	1773	0	1775	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	1892	0	1883	1	0
6	T	1892	0	1883	2	0
7	G	1907	0	1901	3	0
7	U	1907	0	1901	4	0
8	H	1684	0	1685	2	0
8	V	1684	0	1685	2	0
9	I	1581	0	1574	4	0
9	W	1581	0	1574	5	0
10	J	1561	0	1569	7	0
10	X	1561	0	1569	7	0
11	K	1699	0	1655	22	0
11	Y	1707	0	1659	16	0
12	L	1757	0	1711	6	0
12	Z	1757	0	1711	7	0
13	M	1824	0	1832	3	0
13	a	1824	0	1832	4	0
14	N	1512	0	1478	3	0
14	b	1512	0	1478	5	0
15	G	2	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	L	1	0	0	0	0
15	N	1	0	0	0	0
15	U	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	1	0	0	0	0
16	N	1	0	0	0	0
16	U	1	0	0	0	0
16	b	1	0	0	0	0
17	H	52	0	59	5	0
17	N	52	0	59	0	0
17	V	52	0	58	3	0
17	b	52	0	59	2	0
18	H	12	0	13	2	0
18	V	12	0	13	0	0
19	A	5	0	0	0	0
19	B	12	0	0	0	0
19	C	8	0	0	0	0
19	D	1	0	0	0	0
19	E	3	0	0	0	0
19	F	5	0	0	0	0
19	G	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	H	9	0	0	0	0
19	I	6	0	0	0	0
19	J	10	0	0	0	0
19	K	8	0	0	0	0
19	L	8	0	0	0	0
19	M	15	0	0	0	0
19	N	7	0	0	0	0
19	O	4	0	0	0	0
19	P	9	0	0	0	0
19	Q	6	0	0	0	0
19	R	6	0	0	0	0
19	S	5	0	0	0	0
19	T	7	0	0	0	0
19	U	9	0	0	0	0
19	V	8	0	0	0	0
19	W	6	0	0	0	0
19	X	10	0	0	0	0
19	Y	6	0	0	0	0
19	Z	11	0	0	0	0
19	a	9	0	0	0	0
19	b	12	0	0	2	0
All	All	49869	0	49441	122	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 (122) 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:-5:ILE:HG12	12:L:106:TYR:CZ	2.07	0.89
11:Y:-8:ASP:OD2	11:Y:-4:LYS:NZ	2.04	0.89
11:K:4:LEU:HD13	11:K:15:ALA:O	1.78	0.83
17:H:301:3BV:O60	18:H:302:MES:O1S	2.04	0.76
11:K:1:THR:HG21	11:K:33:ALA:CB	2.15	0.76
11:K:4:LEU:CD1	11:K:161:ILE:HD11	2.17	0.75
11:K:4:LEU:HD12	11:K:161:ILE:HD11	1.68	0.75
11:Y:-7:CYS:O	11:Y:-6:LYS:HB2	1.88	0.73
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.71	0.72
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.71	0.70
11:Y:-5:ILE:HG23	12:Z:106:TYR:CE2	2.26	0.69
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.77	0.67
17:V:301:3BV:O48	17:V:301:3BV:O60	2.15	0.65
11:K:-5:ILE:HG12	12:L:106:TYR:CE1	2.31	0.65
11:K:4:LEU:HD12	11:K:161:ILE:CD1	2.30	0.60
17:b:201:3BV:O60	17:b:201:3BV:O48	2.12	0.59
17:H:301:3BV:O60	17:H:301:3BV:O48	2.15	0.59
8:V:168:GLY:O	17:V:301:3BV:H57	2.05	0.56
14:b:152:VAL:HA	14:b:175:MET:HE1	1.87	0.56
11:K:0:GLY:O	11:K:1:THR:HB	2.05	0.56
14:N:152:VAL:HA	14:N:175:MET:HE1	1.88	0.55
11:Y:1:THR:HG23	11:Y:17:ASP:OD1	2.08	0.54
11:Y:-5:ILE:HG23	12:Z:106:TYR:CZ	2.44	0.52
10:J:174:MET:HA	10:X:174:MET:HA	1.91	0.52
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.45	0.52
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.93	0.51
11:K:4:LEU:CD1	11:K:161:ILE:CD1	2.86	0.51
11:Y:4:LEU:C	11:Y:4:LEU:HD22	2.35	0.51
11:K:4:LEU:HD11	11:K:161:ILE:HG12	1.91	0.51
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.92	0.51
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.59	0.51
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.46	0.51
9:I:36:SER:HB2	10:J:126:VAL:HG11	1.92	0.51
11:K:4:LEU:HD11	11:K:15:ALA:HB3	1.92	0.51
11:Y:-5:ILE:HG23	12:Z:106:TYR:CD2	2.45	0.51
3:C:201:VAL:O	3:C:202:GLN:CB	2.59	0.51
11:Y:0:GLY:O	11:Y:46:ALA:HA	2.11	0.50
11:K:1:THR:HG21	11:K:33:ALA:HB1	1.93	0.50
7:G:23:PHE:O	7:G:26:THR:HB	2.12	0.50
7:U:23:PHE:O	7:U:26:THR:HB	2.12	0.49
11:Y:4:LEU:C	11:Y:4:LEU:CD2	2.85	0.49
11:Y:-5:ILE:HD13	12:Z:106:TYR:CE1	2.48	0.48
8:H:168:GLY:O	17:H:301:3BV:H57	2.14	0.47
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.97	0.47
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.97	0.47
11:K:4:LEU:HD13	11:K:4:LEU:N	2.29	0.47
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.50	0.47
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.96	0.47
11:K:-5:ILE:CD1	12:L:106:TYR:CE1	2.98	0.47
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.96	0.47
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	1.97	0.46
11:Y:1:THR:HG21	11:Y:33:ALA:CB	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.97	0.46
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.97	0.46
11:K:4:LEU:HD13	11:K:4:LEU:H	1.81	0.46
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.16	0.46
13:a:27:LEU:HD21	13:a:34:LEU:HD22	1.98	0.46
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.97	0.46
12:L:8:ASN:HA	12:L:30:ILE:O	2.15	0.46
6:F:172:LEU:CD1	6:F:195:ILE:HD13	2.46	0.45
6:T:172:LEU:CD1	6:T:195:ILE:HD13	2.47	0.45
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.99	0.45
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.99	0.45
14:N:171:GLY:HA2	13:a:219:TRP:CH2	2.52	0.45
13:M:27:LEU:HD21	13:M:34:LEU:HD22	1.98	0.45
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.99	0.45
7:U:61:SER:OG	7:U:215:GLU:OE2	2.32	0.45
2:B:50:LYS:O	2:B:51:VAL:C	2.61	0.44
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.52	0.44
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.99	0.44
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.99	0.44
17:b:201:3BV:O60	19:b:301:HOH:O	1.80	0.44
5:S:98:PHE:O	13:a:91:TYR:HA	2.18	0.44
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	2.00	0.44
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.47	0.43
13:M:219:TRP:CH2	14:b:171:GLY:HA2	2.53	0.43
17:V:301:3BV:H53	17:V:301:3BV:O40	2.18	0.43
2:P:50:LYS:O	2:P:51:VAL:C	2.60	0.43
10:X:3:ILE:HD12	10:X:176:PHE:CG	2.54	0.43
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.34	0.43
11:K:5:ALA:HB3	11:K:100:MET:CE	2.49	0.43
11:Y:1:THR:HG22	11:Y:2:THR:N	2.33	0.43
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.42
14:N:133:PHE:HA	14:b:132:THR:O	2.19	0.42
3:C:201:VAL:HG13	3:C:202:GLN:N	2.34	0.42
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.83	0.42
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.84	0.42
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.54	0.42
11:Y:5:ALA:HB3	11:Y:100:MET:CE	2.49	0.42
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.47	0.42
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.55	0.42
1:A:119:GLN:O	1:A:122:THR:HB	2.19	0.42
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:14:PRO:HA	3:C:20:TYR:CE1	2.54	0.42
9:I:9:GLY:HA3	9:I:41:LYS:HE2	2.02	0.42
11:K:1:THR:HG21	11:K:33:ALA:HB2	2.00	0.42
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.85	0.41
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.50	0.41
1:A:115:ALA:HB1	1:A:154:GLY:O	2.21	0.41
17:H:301:3BV:H53	17:H:301:3BV:O40	2.20	0.41
13:M:165:ILE:HB	13:M:166:PRO:HD3	2.02	0.41
13:a:165:ILE:HB	13:a:166:PRO:HD3	2.03	0.41
14:b:176:VAL:HG12	14:b:178:LEU:HD13	2.02	0.41
14:b:36:ARG:NH1	19:b:303:HOH:O	2.51	0.41
10:J:3:ILE:HD12	10:J:176:PHE:CG	2.55	0.41
2:P:95:GLN:HB3	9:W:68:TYR:CD2	2.55	0.41
3:Q:161:THR:HG21	3:Q:169:VAL:HG13	2.02	0.41
9:W:9:GLY:HA3	9:W:41:LYS:HE2	2.02	0.41
17:H:301:3BV:O60	18:H:302:MES:S	2.78	0.41
1:O:119:GLN:O	1:O:122:THR:HB	2.21	0.41
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.50	0.41
3:C:161:THR:HG21	3:C:169:VAL:HG13	2.02	0.41
11:K:0:GLY:O	11:K:1:THR:CB	2.68	0.41
5:S:77:ALA:N	5:S:78:PRO:CD	2.84	0.41
5:E:77:ALA:N	5:E:78:PRO:CD	2.84	0.41
7:G:61:SER:OG	7:G:215:GLU:OE2	2.33	0.41
11:K:4:LEU:HD22	11:K:4:LEU:C	2.46	0.40
10:J:21:VAL:HG11	11:K:122:LEU:HD11	2.03	0.40
1:O:115:ALA:HB1	1:O:154:GLY:O	2.21	0.40
6:T:14:ASP:HB2	6:T:16:ARG:HD3	2.04	0.40
10:J:177:LYS:NZ	10:X:169:GLU:O	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	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%)	234 (97%)	6 (2%)	2 (1%)	16	44
2	P	242/258 (94%)	234 (97%)	6 (2%)	2 (1%)	16	44
3	C	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	16	44
3	Q	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	16	44
4	D	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
4	R	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
5	E	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
5	S	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
6	F	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
6	T	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
7	G	239/252 (95%)	234 (98%)	5 (2%)	0	100	100
7	U	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
8	H	220/232 (95%)	215 (98%)	5 (2%)	0	100	100
8	V	220/232 (95%)	215 (98%)	5 (2%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
10	X	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
11	K	218/221 (99%)	212 (97%)	5 (2%)	1 (0%)	24	55
11	Y	219/221 (99%)	212 (97%)	6 (3%)	1 (0%)	24	55
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	231/246 (94%)	218 (94%)	12 (5%)	1 (0%)	30	60
13	a	231/246 (94%)	219 (95%)	11 (5%)	1 (0%)	30	60
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	6293/6632 (95%)	6113 (97%)	168 (3%)	12 (0%)	43	72

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
2	P	51	VAL
3	Q	202	GLN
11	K	1	THR
3	C	205	ALA
3	Q	205	ALA
11	Y	1	THR
2	B	221	ASP
2	P	221	ASP
13	M	229	GLY
13	a	229	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	209/209 (100%)	205 (98%)	4 (2%)	50	81
1	O	209/209 (100%)	205 (98%)	4 (2%)	50	81
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%)	206 (97%)	6 (3%)	38	73
3	Q	212/226 (94%)	206 (97%)	6 (3%)	38	73
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%)	185 (97%)	5 (3%)	40	75
5	S	190/193 (98%)	185 (97%)	5 (3%)	40	75
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	V	181/190 (95%)	177 (98%)	4 (2%)	45	78
9	I	172/173 (99%)	169 (98%)	3 (2%)	53	83
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%)	169 (98%)	4 (2%)	44	78
11	K	174/175 (99%)	170 (98%)	4 (2%)	44	78
11	Y	175/175 (100%)	171 (98%)	4 (2%)	44	78
12	L	185/185 (100%)	178 (96%)	7 (4%)	29	64
12	Z	185/185 (100%)	178 (96%)	7 (4%)	29	64
13	M	199/208 (96%)	195 (98%)	4 (2%)	48	80
13	a	199/208 (96%)	195 (98%)	4 (2%)	48	80
14	N	162/162 (100%)	159 (98%)	3 (2%)	50	81
14	b	162/162 (100%)	159 (98%)	3 (2%)	50	81
All	All	5323/5552 (96%)	5169 (97%)	154 (3%)	37	73

All (154) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
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
4	D	20	LEU

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Mol	Chain	Res	Type
4	D	40	LEU
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	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	-5	ILE
11	K	4	LEU

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Mol	Chain	Res	Type
11	K	35	ILE
11	K	106	ARG
12	L	1	GLN
12	L	23	LEU
12	L	31	THR
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
14	N	9	LYS
14	N	22	THR
14	N	119	VAL
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
4	R	20	LEU
4	R	40	LEU
4	R	51	LEU
4	R	99	ILE
4	R	125	LEU
4	R	176	LEU
4	R	193	LEU
4	R	197	LYS

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Mol	Chain	Res	Type
4	R	214	ILE
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
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	23	ARG
10	X	75	LEU
10	X	144	LEU
10	X	174	MET
11	Y	-4	LYS
11	Y	4	LEU
11	Y	35	ILE
11	Y	106	ARG
12	Z	1	GLN
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	136	CYS

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Mol	Chain	Res	Type
12	Z	150	LEU
12	Z	167	LYS
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
14	b	9	LYS
14	b	22	THR
14	b	119	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (98) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	93	HIS
2	B	119	GLN
2	B	123	GLN
2	B	124	HIS
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
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	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	117	GLN
7	G	121	GLN
7	G	166	GLN

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Mol	Chain	Res	Type
7	G	175	ASN
8	H	30	ASN
8	H	66	HIS
8	H	189	ASN
9	I	63	ASN
10	J	37	GLN
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	70	ASN
12	L	79	HIS
12	L	158	ASN
13	M	213	GLN
14	N	38	HIS
14	N	141	ASN
2	P	93	HIS
2	P	119	GLN
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
5	S	68	HIS
5	S	99	ASN
5	S	116	GLN
5	S	120	GLN
5	S	151	ASN
5	S	165	GLN

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Mol	Chain	Res	Type
5	S	184	ASN
6	T	86	ASN
6	T	123	ASN
7	U	30	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	175	ASN
8	V	30	ASN
8	V	86	HIS
8	V	189	ASN
8	V	200	GLN
9	W	37	ASN
9	W	63	ASN
10	X	37	GLN
10	X	55	GLN
10	X	63	ASN
10	X	146	HIS
10	X	147	HIS
11	Y	9	GLN
11	Y	85	ASN
11	Y	143	ASN
11	Y	176	ASN
11	Y	208	ASN
13	a	213	GLN
14	b	38	HIS
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, 12 are monoatomic - leaving 6 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	3BV	N	201	14	54,54,54	1.34	3 (5%)	68,71,71	1.54	11 (16%)
18	MES	V	302	-	12,12,12	2.24	1 (8%)	15,16,16	1.17	1 (6%)
17	3BV	H	301	8	54,54,54	1.37	3 (5%)	68,71,71	1.50	6 (8%)
17	3BV	V	301	8	54,54,54	1.34	4 (7%)	68,71,71	1.67	13 (19%)
17	3BV	b	201	14	54,54,54	1.38	4 (7%)	68,71,71	1.38	7 (10%)
18	MES	H	302	-	12,12,12	2.19	1 (8%)	15,16,16	1.21	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	3BV	N	201	14	-	9/59/67/67	0/3/3/3
18	MES	V	302	-	-	2/6/14/14	0/1/1/1
17	3BV	H	301	8	-	11/59/67/67	0/3/3/3
17	3BV	V	301	8	-	15/59/67/67	0/3/3/3
17	3BV	b	201	14	-	19/59/67/67	0/3/3/3
18	MES	H	302	-	-	5/6/14/14	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	V	302	MES	C8-S	-7.41	1.67	1.77
18	H	302	MES	C8-S	-7.21	1.67	1.77
17	H	301	3BV	C32-C33	-6.80	1.35	1.51
17	b	201	3BV	C32-C33	-6.48	1.36	1.51
17	N	201	3BV	C51-C47	6.15	1.63	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	V	301	3BV	C32-C33	-5.92	1.37	1.51
17	N	201	3BV	C32-C33	-4.63	1.40	1.51
17	b	201	3BV	C13-C14	-4.38	1.39	1.51
17	V	301	3BV	C13-C14	-4.22	1.39	1.51
17	H	301	3BV	C13-C14	-4.20	1.39	1.51
17	N	201	3BV	C13-C14	-3.57	1.41	1.51
17	V	301	3BV	O48-C47	-2.57	1.36	1.43
17	b	201	3BV	C59-C51	2.47	1.55	1.52
17	H	301	3BV	O48-C47	-2.36	1.37	1.43
17	V	301	3BV	C11-C20	-2.12	1.47	1.52
17	b	201	3BV	C51-C47	2.08	1.57	1.53

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	V	301	3BV	C43-C42-N41	-8.24	99.63	110.20
17	H	301	3BV	C43-C42-N41	-7.99	99.95	110.20
17	b	201	3BV	C43-C42-N41	-5.54	103.08	110.20
17	N	201	3BV	C43-C42-N41	-5.46	103.18	110.20
17	N	201	3BV	C58-C51-C59	-5.18	103.17	109.76
17	V	301	3BV	C3-N4-C5	3.97	117.39	108.84
17	V	301	3BV	C58-C51-C59	-3.88	104.82	109.76
17	b	201	3BV	C58-C51-C59	-3.55	105.24	109.76
17	N	201	3BV	C33-C32-C31	-3.33	104.50	113.36
17	b	201	3BV	C43-C42-C47	-3.31	106.88	112.18
17	N	201	3BV	O1-C6-C5	-3.24	104.79	111.77
17	H	301	3BV	C12-C11-N10	-3.23	104.52	110.91
17	N	201	3BV	O1-C2-C3	-3.15	104.98	111.77
17	V	301	3BV	C7-N4-C3	3.13	116.02	111.14
17	H	301	3BV	C3-N4-C5	3.11	115.53	108.84
17	V	301	3BV	C43-C42-C47	-2.85	107.61	112.18
17	N	201	3BV	C12-C13-C14	-2.82	103.95	113.22
18	H	302	MES	O2S-S-C8	2.81	110.97	106.73
17	H	301	3BV	C43-C42-C47	-2.79	107.72	112.18
17	V	301	3BV	C20-C11-N10	-2.78	103.58	111.11
17	N	201	3BV	C24-C23-N22	2.73	116.75	110.58
18	V	302	MES	O1S-S-C8	2.69	110.79	106.73
17	V	301	3BV	C25-C24-C23	-2.65	108.28	115.40
17	H	301	3BV	C33-C32-C31	-2.58	106.51	113.36
17	N	201	3BV	C12-C11-C20	-2.56	103.85	110.11
17	N	201	3BV	O60-C59-C51	-2.55	106.27	111.51
17	N	201	3BV	C43-C42-C47	-2.48	108.21	112.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	b	201	3BV	C20-C11-N10	-2.46	104.46	111.11
17	V	301	3BV	C24-C23-N22	-2.42	105.12	110.58
17	b	201	3BV	C7-N4-C3	-2.40	107.41	111.14
17	b	201	3BV	C33-C32-C31	-2.37	107.05	113.36
17	b	201	3BV	C7-N4-C5	-2.37	107.46	111.14
17	H	301	3BV	C25-C24-C23	-2.35	109.09	115.40
17	V	301	3BV	O48-C47-C42	-2.34	103.68	109.28
17	V	301	3BV	C12-C11-N10	-2.29	106.36	110.91
17	V	301	3BV	C33-C32-C31	-2.13	107.68	113.36
17	V	301	3BV	O1-C6-C5	-2.08	107.29	111.77
17	V	301	3BV	C2-C3-N4	2.06	113.25	110.12
18	H	302	MES	O1S-S-C8	2.01	109.77	106.73
17	N	201	3BV	C13-C12-C11	-2.01	109.15	113.21

There are no chirality outliers.

All (61) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	H	301	3BV	C47-C42-C43-C44
17	N	201	3BV	C47-C42-C43-C44
17	N	201	3BV	C42-C47-C51-C58
17	N	201	3BV	C42-C47-C51-C59
17	V	301	3BV	C8-C7-N4-C3
17	V	301	3BV	N10-C11-C12-C13
17	V	301	3BV	C47-C42-C43-C44
17	b	201	3BV	N10-C11-C12-C13
17	b	201	3BV	N41-C42-C43-C44
17	b	201	3BV	C42-C47-C51-C58
17	b	201	3BV	C42-C47-C51-C59
17	b	201	3BV	C47-C51-C59-O60
18	H	302	MES	C7-C8-S-O1S
18	H	302	MES	C7-C8-S-O2S
18	H	302	MES	C7-C8-S-O3S
17	H	301	3BV	N10-C11-C12-C13
17	H	301	3BV	C20-C11-C12-C13
17	b	201	3BV	C20-C11-C12-C13
17	N	201	3BV	O48-C47-C51-C58
17	H	301	3BV	C42-C47-C51-C58
17	V	301	3BV	C23-C24-C25-C27
17	H	301	3BV	O48-C47-C51-C58
17	N	201	3BV	O48-C47-C51-C59
17	V	301	3BV	O48-C47-C51-C58

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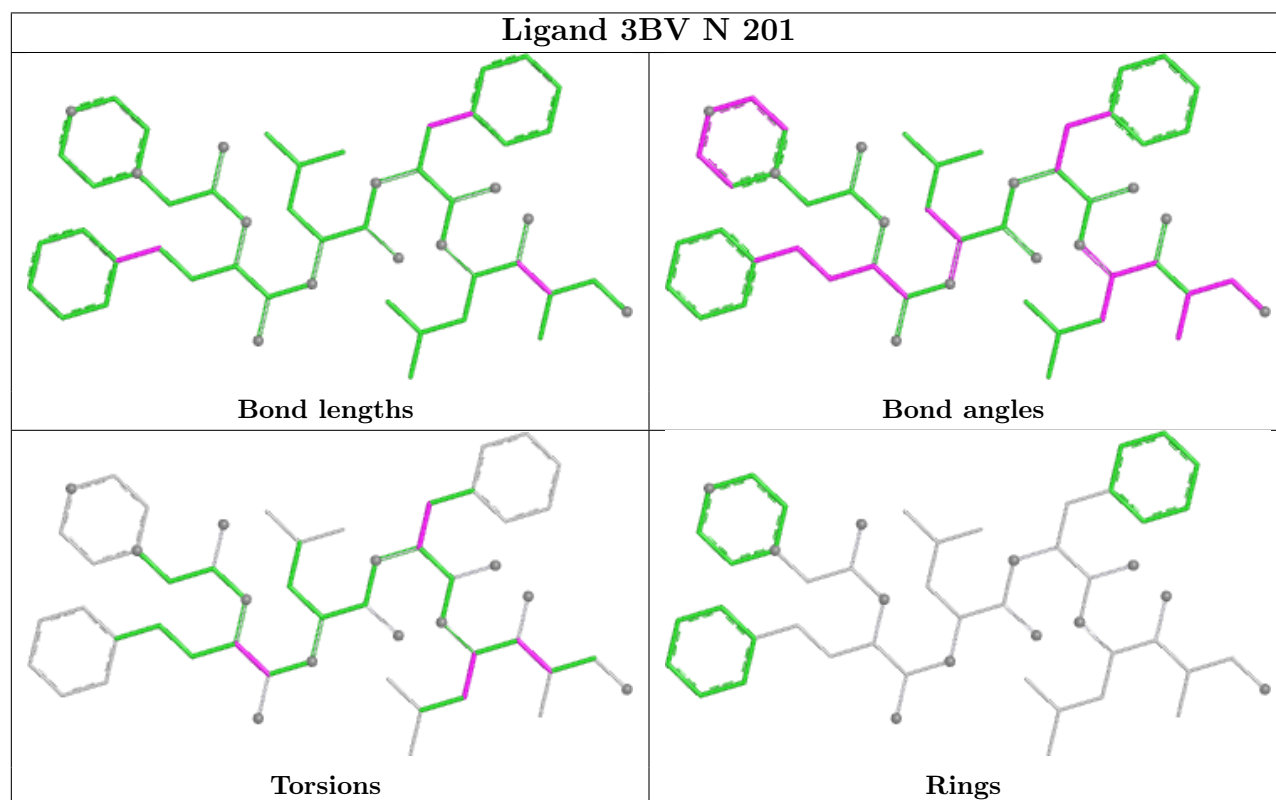
Mol	Chain	Res	Type	Atoms
17	b	201	3BV	O48-C47-C51-C58
17	b	201	3BV	O48-C47-C51-C59
18	H	302	MES	C8-C7-N4-C3
18	H	302	MES	C8-C7-N4-C5
18	V	302	MES	C8-C7-N4-C5
17	V	301	3BV	N30-C31-C39-O40
17	b	201	3BV	C42-C43-C44-C46
17	H	301	3BV	N41-C42-C43-C44
17	N	201	3BV	N41-C42-C43-C44
17	V	301	3BV	N41-C42-C43-C44
17	b	201	3BV	C58-C51-C59-O60
17	H	301	3BV	N30-C31-C39-O40
17	H	301	3BV	C8-C7-N4-C3
17	V	301	3BV	N30-C31-C39-N41
17	H	301	3BV	N30-C31-C39-N41
17	b	201	3BV	C8-C7-N4-C5
17	b	201	3BV	C47-C42-C43-C44
18	V	302	MES	C8-C7-N4-C3
17	V	301	3BV	C23-C24-C25-C26
17	b	201	3BV	C8-C7-N4-C3
17	H	301	3BV	C12-C13-C14-C19
17	V	301	3BV	C20-C11-C12-C13
17	b	201	3BV	N10-C11-C20-O21
17	b	201	3BV	N10-C11-C20-N22
17	H	301	3BV	C12-C13-C14-C15
17	V	301	3BV	C12-C13-C14-C19
17	b	201	3BV	N30-C31-C39-O40
17	V	301	3BV	C12-C13-C14-C15
17	b	201	3BV	N30-C31-C39-N41
17	N	201	3BV	N30-C31-C32-C33
17	V	301	3BV	C8-C7-N4-C5
17	N	201	3BV	N10-C11-C20-N22
17	N	201	3BV	N10-C11-C20-O21
17	V	301	3BV	C32-C31-C39-O40
17	V	301	3BV	N4-C7-C8-N10
17	b	201	3BV	C12-C13-C14-C19
17	b	201	3BV	N4-C7-C8-O9

There are no ring outliers.

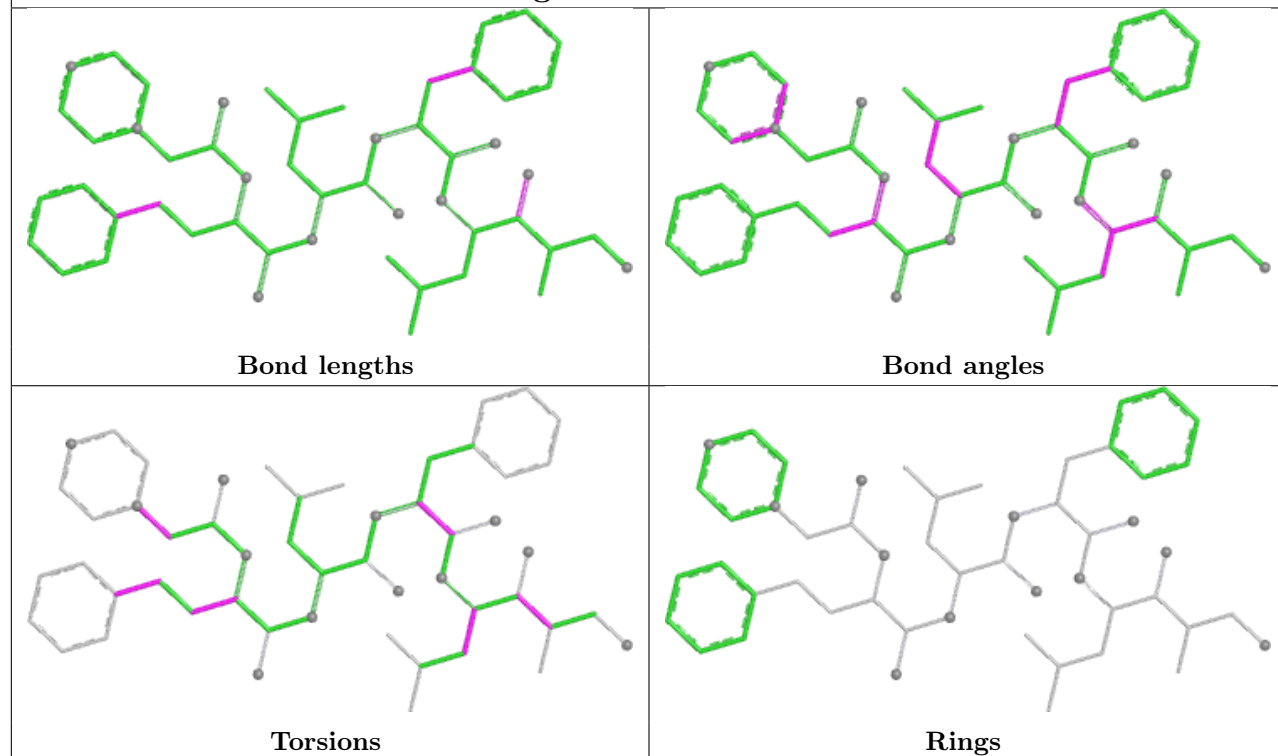
4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	H	301	3BV	5	0
17	V	301	3BV	3	0
17	b	201	3BV	2	0
18	H	302	MES	2	0

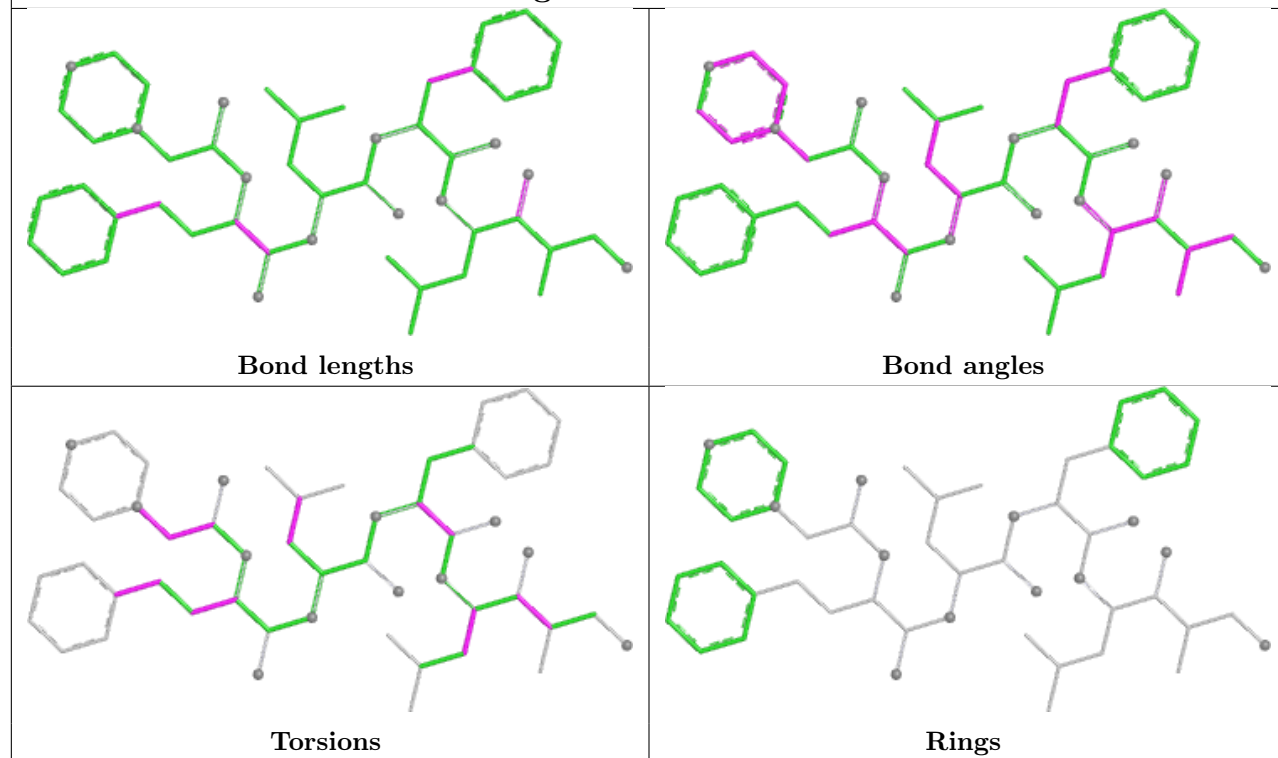
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

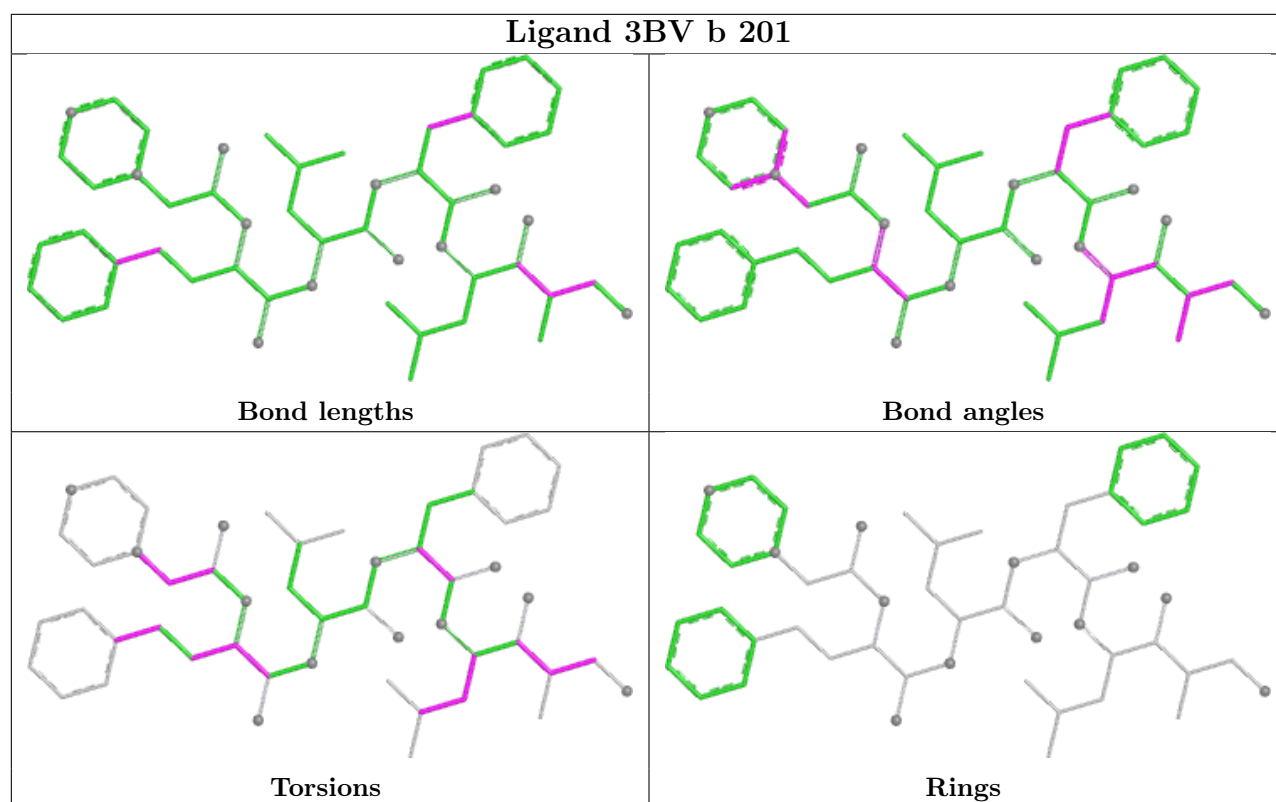


Ligand 3BV H 301



Ligand 3BV 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%)	-0.43	1 (0%) 88 84	48, 66, 103, 157	0
1	O	250/250 (100%)	-0.34	2 (0%) 82 75	54, 74, 118, 156	0
2	B	244/258 (94%)	-0.24	5 (2%) 65 56	48, 71, 120, 175	0
2	P	244/258 (94%)	-0.19	3 (1%) 76 68	53, 79, 127, 167	0
3	C	240/254 (94%)	-0.23	1 (0%) 88 84	50, 77, 147, 180	0
3	Q	240/254 (94%)	0.06	5 (2%) 63 54	64, 93, 176, 204	0
4	D	235/260 (90%)	-0.27	1 (0%) 88 84	60, 81, 114, 154	0
4	R	235/260 (90%)	-0.05	2 (0%) 81 74	65, 84, 132, 181	0
5	E	231/234 (98%)	-0.19	0 100 100	57, 83, 122, 163	0
5	S	231/234 (98%)	0.00	1 (0%) 88 84	61, 89, 142, 176	0
6	F	243/288 (84%)	-0.34	2 (0%) 82 75	52, 74, 122, 150	0
6	T	243/288 (84%)	-0.17	5 (2%) 63 54	54, 81, 138, 182	0
7	G	241/252 (95%)	-0.37	0 100 100	47, 68, 110, 161	0
7	U	241/252 (95%)	-0.40	0 100 100	43, 68, 105, 144	0
8	H	222/232 (95%)	-0.42	0 100 100	46, 64, 101, 127	0
8	V	222/232 (95%)	-0.41	0 100 100	48, 67, 103, 137	0
9	I	204/205 (99%)	-0.56	0 100 100	45, 63, 91, 124	0
9	W	204/205 (99%)	-0.55	0 100 100	47, 65, 95, 128	0
10	J	195/198 (98%)	-0.46	1 (0%) 87 82	48, 67, 95, 134	0
10	X	195/198 (98%)	-0.45	1 (0%) 87 82	51, 69, 99, 149	0
11	K	220/221 (99%)	-0.36	2 (0%) 81 74	26, 69, 102, 120	0
11	Y	221/221 (100%)	-0.29	2 (0%) 81 74	55, 72, 104, 126	0
12	L	222/222 (100%)	-0.44	1 (0%) 87 82	47, 67, 103, 136	0
12	Z	222/222 (100%)	-0.45	0 100 100	52, 68, 103, 130	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.50	1 (0%) 88 84	45, 64, 91, 101	0
13	a	233/246 (94%)	-0.54	1 (0%) 88 84	45, 62, 87, 95	0
14	N	196/196 (100%)	-0.50	0 100 100	44, 61, 94, 121	0
14	b	196/196 (100%)	-0.54	0 100 100	47, 61, 91, 119	0
All	All	6353/6632 (95%)	-0.34	37 (0%) 85 80	26, 71, 120, 204	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
11	K	-7	CYS	8.8
10	J	1	MET	5.0
10	X	1	MET	4.7
11	Y	-7	CYS	4.5
3	Q	50	LEU	4.0
1	A	1	MET	3.9
3	Q	205	ALA	3.8
1	O	1	MET	3.5
6	T	243	ILE	3.3
6	F	215	CYS	3.2
11	K	1	THR	3.2
13	a	1	THR	3.1
2	B	218	GLY	3.0
2	P	52	THR	3.0
4	D	240	ALA	3.0
3	Q	49	THR	2.9
11	Y	-8	ASP	2.7
4	R	157	TYR	2.7
1	O	249	ALA	2.6
2	P	51	VAL	2.6
2	B	93	HIS	2.5
3	Q	206	LYS	2.5
12	L	163	GLY	2.4
6	T	14	ASP	2.4
13	M	1	THR	2.4
5	S	52	ALA	2.4
2	B	51	VAL	2.3
6	F	202	ASP	2.3
4	R	113	LEU	2.3
6	T	215	CYS	2.2
2	P	218	GLY	2.2
2	B	219	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
3	Q	52	LEU	2.2
3	C	207	ASN	2.1
6	T	204	LYS	2.1
6	T	178	HIS	2.1
2	B	52	THR	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](#)

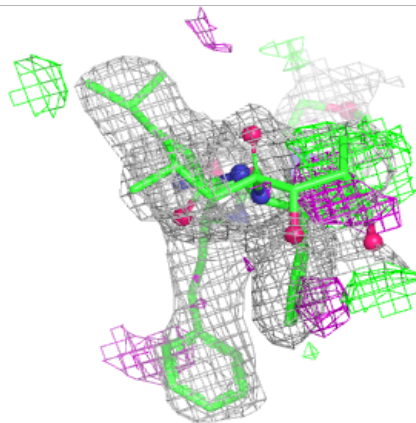
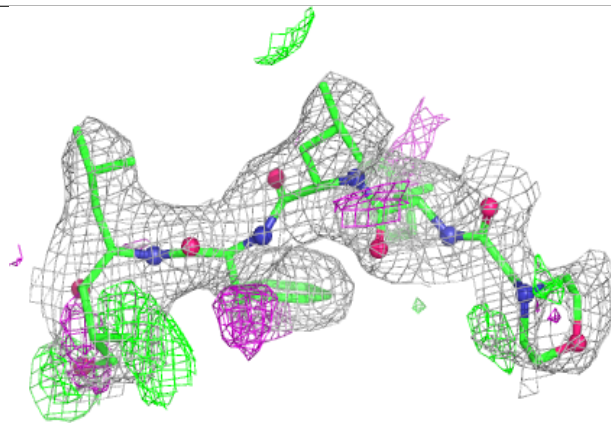
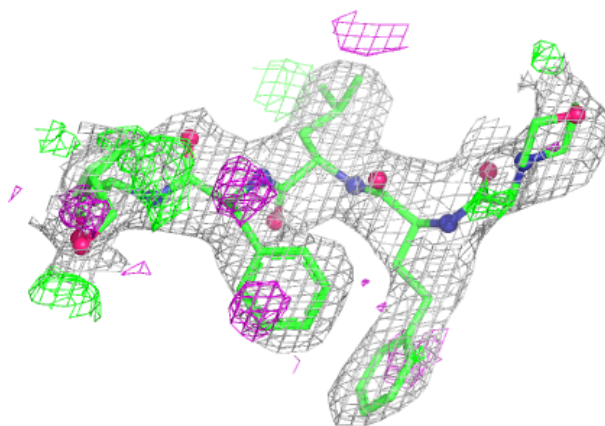
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
18	MES	V	302	12/12	0.80	0.14	79,88,110,125	0
17	3BV	N	201	52/52	0.89	0.13	48,59,144,146	0
18	MES	H	302	12/12	0.91	0.13	74,83,100,102	0
17	3BV	V	301	52/52	0.91	0.11	59,66,113,119	0
17	3BV	b	201	52/52	0.92	0.11	50,63,139,144	0
15	MG	U	301	1/1	0.92	0.05	30,30,30,30	0
17	3BV	H	301	52/52	0.92	0.10	55,64,112,116	0
15	MG	L	301	1/1	0.95	0.11	76,76,76,76	0
15	MG	G	301	1/1	0.96	0.04	58,58,58,58	0
15	MG	Z	301	1/1	0.96	0.07	72,72,72,72	0
16	CL	N	203	1/1	0.98	0.05	61,61,61,61	0
16	CL	b	202	1/1	0.98	0.07	58,58,58,58	0
15	MG	I	301	1/1	0.98	0.04	66,66,66,66	0
15	MG	N	202	1/1	0.98	0.09	67,67,67,67	0
16	CL	U	302	1/1	0.99	0.12	53,53,53,53	0
15	MG	K	301	1/1	0.99	0.05	70,70,70,70	0
16	CL	G	303	1/1	0.99	0.08	57,57,57,57	0
15	MG	G	302	1/1	0.99	0.06	30,30,30,30	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.

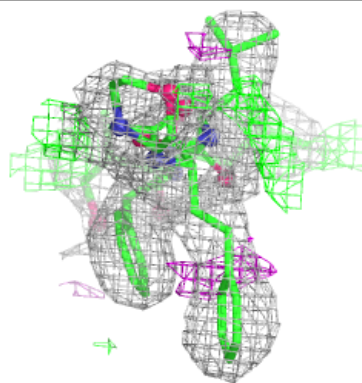
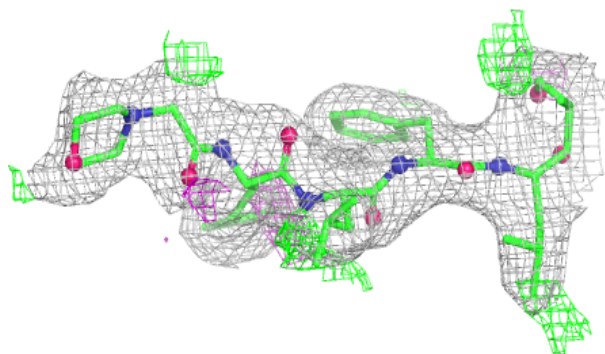
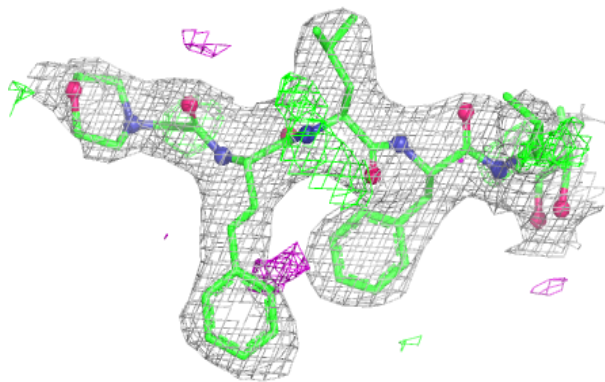
Electron density around 3BV N 201:

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



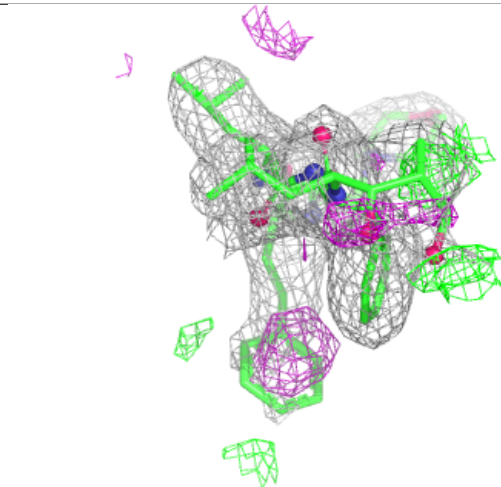
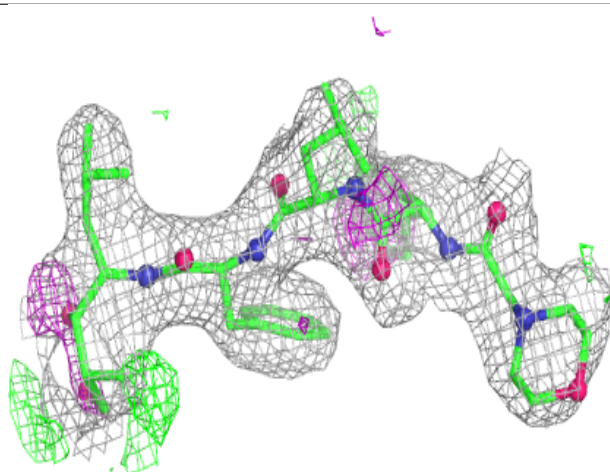
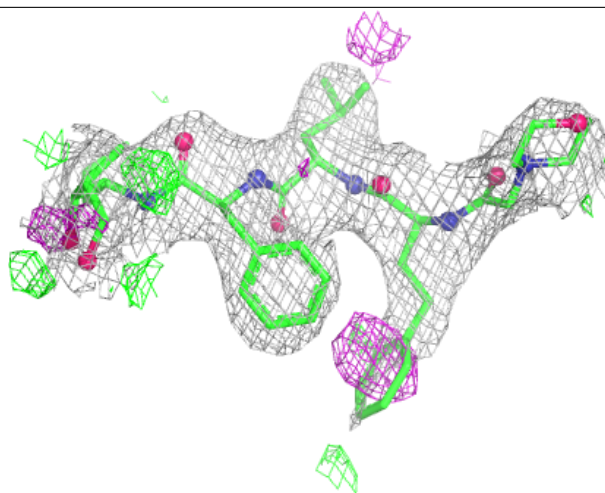
Electron density around 3BV V 301:

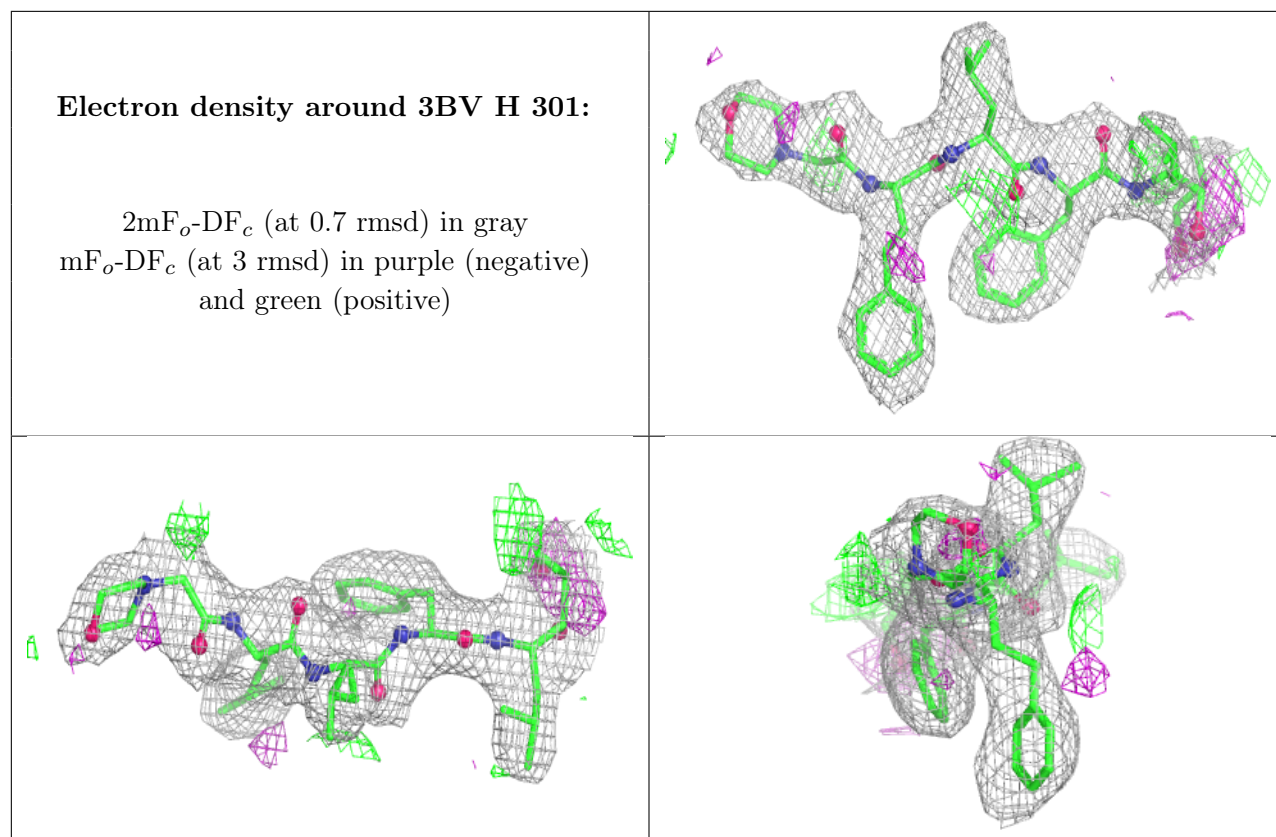
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 3BV 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.