



# Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2020 – 11:18 am BST

PDB ID : 6HVV  
Title : Yeast 20S proteasome with human beta2i (1-53) in complex with 39  
Authors : Huber, E.M.; Groll, M.  
Deposited on : 2018-10-11  
Resolution : 2.70 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](mailto: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.

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

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

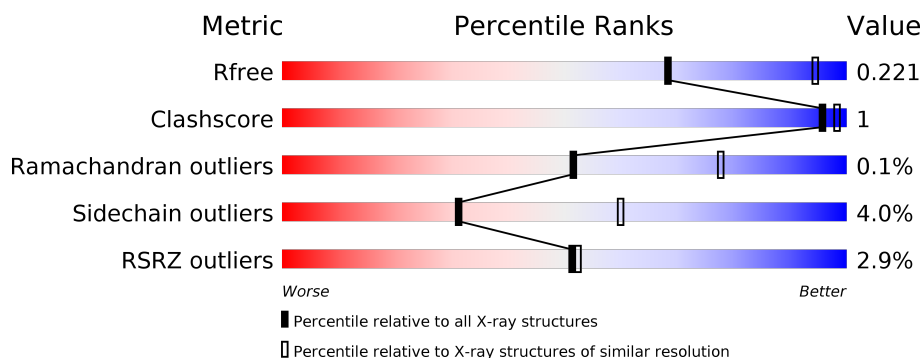
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	<div> <div>4%</div> <div>98%</div> <div>•</div> </div>
1	O	250	<div> <div>5%</div> <div>98%</div> <div>•</div> </div>
2	B	258	<div> <div>4%</div> <div>88%</div> <div>6% • 5%</div> </div>
2	P	258	<div> <div>5%</div> <div>88%</div> <div>6% 5%</div> </div>
3	C	254	<div> <div>5%</div> <div>87%</div> <div>7% 6%</div> </div>
3	Q	254	<div> <div>10%</div> <div>87%</div> <div>7% 6%</div> </div>

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Mol	Chain	Length	Quality of chain
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	226	
8	V	226	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
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 50087 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-10, Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	226	Total	C	N	O	S	0	0	0
			1716	1081	291	336	8			
8	V	223	Total	C	N	O	S	0	0	0
			1688	1066	287	327	8			

- 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
			1644	1045	280	312	7			
11	Y	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			

- 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 (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	K	1	Total	Mg	0	0
			1	1		

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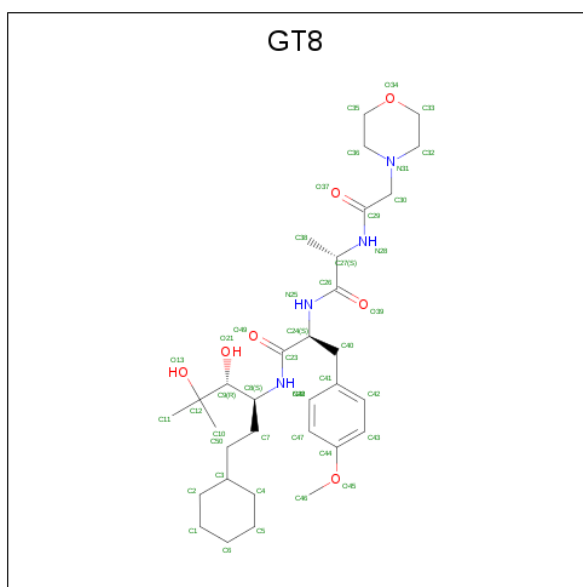
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	I	1	Total Mg 1 1	0	0
15	V	1	Total Mg 1 1	0	0
15	W	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	Y	1	Total Mg 1 1	0	0

- Molecule 16 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

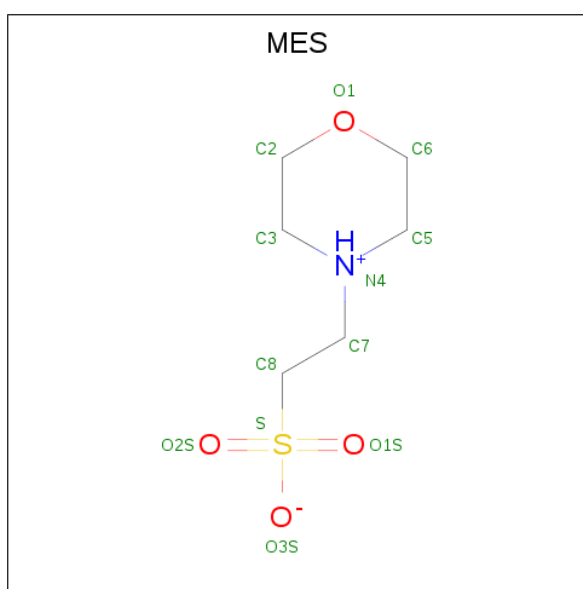
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0

- Molecule 17 is (2 {S})- {N}-[(3 {S},4 {R})-1-cyclohexyl-5-methyl-4,5-bis(oxidanyl)hexan-3-yl]-3-(4-methoxyphenyl)-2-[[2 {S})-2-(2-morpholin-4-ylethanoylamino)propanoyl]amino]propanamide (three-letter code: GT8) (formula: C<sub>32</sub>H<sub>52</sub>N<sub>4</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
17	H	1	Total	C	N	O	0	0
			43	32	4	7		
17	K	1	Total	C	N	O	0	0
			43	32	4	7		
17	V	1	Total	C	N	O	0	0
			43	32	4	7		
17	Y	1	Total	C	N	O	0	0
			43	32	4	7		

- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



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	16	Total	O	0	0
			16	16		
19	B	18	Total	O	0	0
			18	18		
19	C	18	Total	O	0	0
			18	18		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	D	10	Total O 10 10	0	0
19	E	3	Total O 3 3	0	0
19	F	16	Total O 16 16	0	0
19	G	22	Total O 22 22	0	0
19	H	33	Total O 33 33	0	0
19	I	22	Total O 22 22	0	0
19	J	18	Total O 18 18	0	0
19	K	33	Total O 33 33	0	0
19	L	36	Total O 36 36	0	0
19	M	25	Total O 25 25	0	0
19	N	13	Total O 13 13	0	0
19	O	13	Total O 13 13	0	0
19	P	18	Total O 18 18	0	0
19	Q	11	Total O 11 11	0	0
19	R	11	Total O 11 11	0	0
19	S	12	Total O 12 12	0	0
19	T	14	Total O 14 14	0	0
19	U	24	Total O 24 24	0	0
19	V	22	Total O 22 22	0	0
19	W	23	Total O 23 23	0	0
19	X	18	Total O 18 18	0	0

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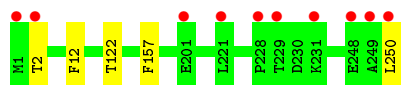
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	Y	32	Total 32	O 32	0	0
19	Z	29	Total 29	O 29	0	0
19	a	27	Total 27	O 27	0	0
19	b	12	Total 12	O 12	0	0

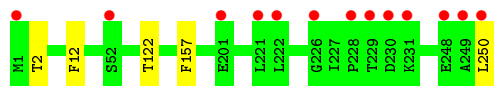
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

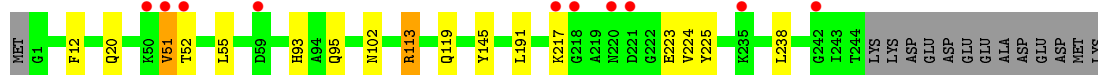
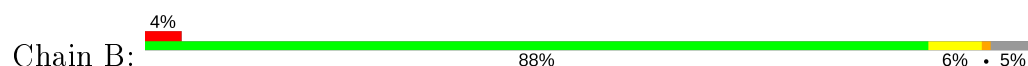
- Molecule 1: Proteasome subunit alpha type-2



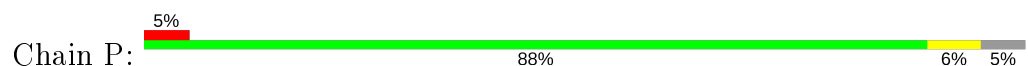
- Molecule 1: Proteasome subunit alpha type-2



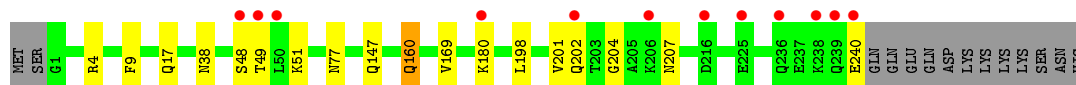
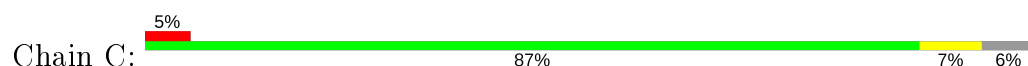
- Molecule 2: Proteasome subunit alpha type-3



- Molecule 2: Proteasome subunit alpha type-3

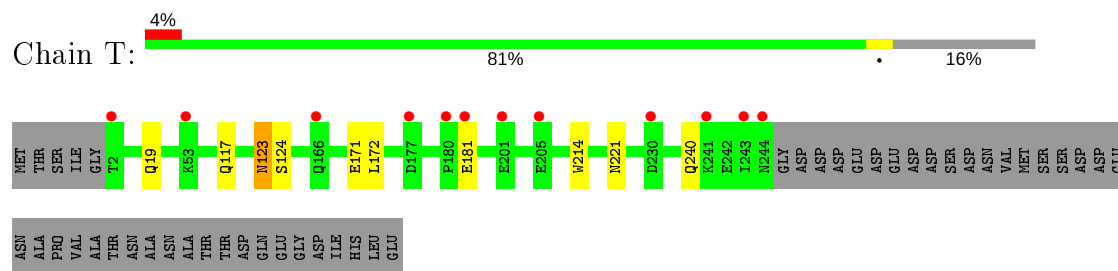


- Molecule 3: Proteasome subunit alpha type-4

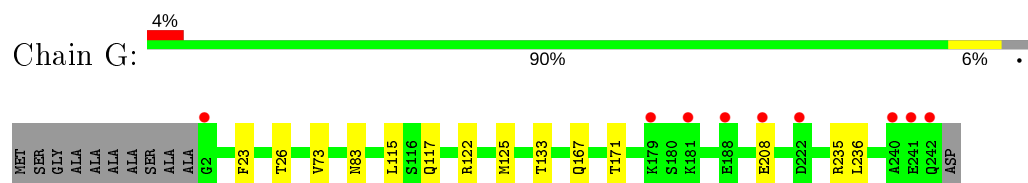


- Molecule 3: Proteasome subunit alpha type-4

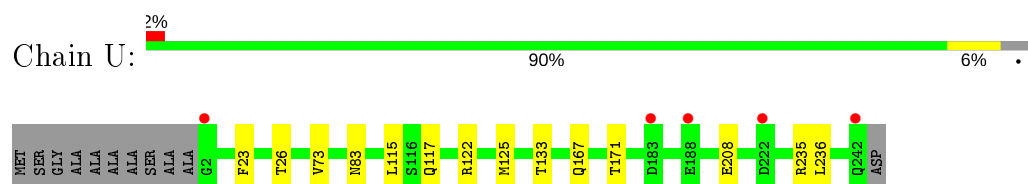




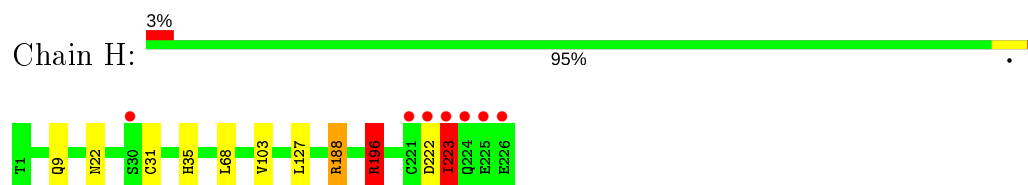
- Molecule 7: Proteasome subunit alpha type-1



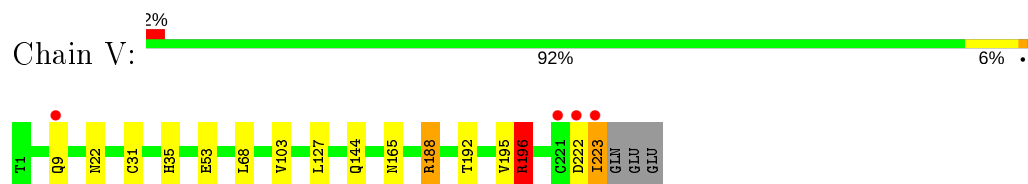
- Molecule 7: Proteasome subunit alpha type-1



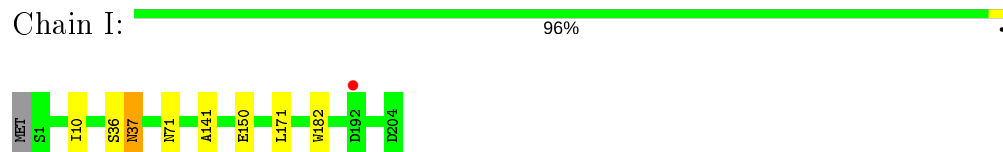
- Molecule 8: Proteasome subunit beta type-10, Proteasome subunit beta type-2



- Molecule 8: Proteasome subunit beta type-10, Proteasome subunit beta type-2



- Molecule 9: Proteasome subunit beta type-3

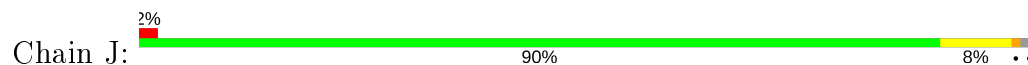


- Molecule 9: Proteasome subunit beta type-3

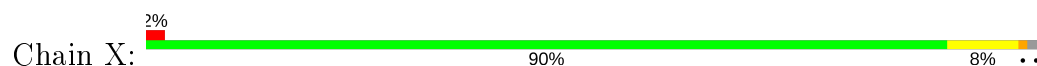




- Molecule 10: Proteasome subunit beta type-4



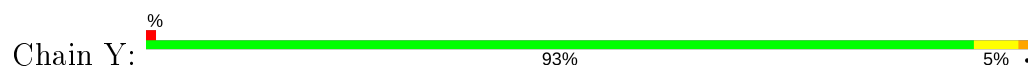
- Molecule 10: Proteasome subunit beta type-4



- Molecule 11: Proteasome subunit beta type-5



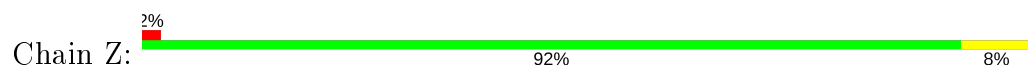
- Molecule 11: Proteasome subunit beta type-5



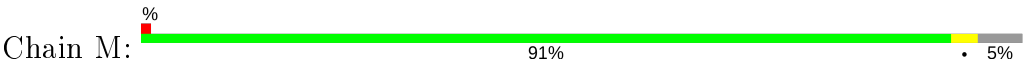
- Molecule 12: Proteasome subunit beta type-6



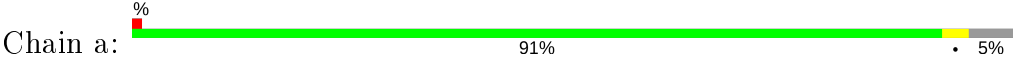
- Molecule 12: Proteasome subunit beta type-6



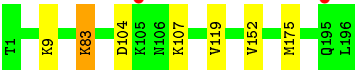
- Molecule 13: Proteasome subunit beta type-7



• 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, $\alpha$ , $\beta$ , $\gamma$	136.14Å 299.37Å 144.45Å 90.00° 113.09° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 15.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.3 (15.00-2.70) 97.9 (15.00-2.70)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.97 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.184 , 0.219 0.189 , 0.221	Depositor DCC
$R_{free}$ test set	14118 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	53.2	Xtriage
Anisotropy	0.643	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 30.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	50087	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GT8, MG, MES, 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	0.38	0/1952	0.57	0/2642
1	O	0.37	0/1952	0.57	0/2642
2	B	0.38	0/1934	0.65	2/2618 (0.1%)
2	P	0.38	0/1934	0.66	2/2618 (0.1%)
3	C	0.37	0/1910	0.64	0/2586
3	Q	0.37	0/1910	0.63	0/2586
4	D	0.36	0/1837	0.59	0/2475
4	R	0.36	0/1837	0.59	0/2475
5	E	0.37	0/1800	0.59	0/2433
5	S	0.36	0/1800	0.59	0/2433
6	F	0.37	0/1932	0.56	0/2609
6	T	0.36	0/1932	0.56	0/2609
7	G	0.37	0/1945	0.58	0/2634
7	U	0.37	0/1945	0.58	0/2634
8	H	0.33	0/1746	0.81	5/2365 (0.2%)
8	V	0.35	0/1718	0.84	4/2329 (0.2%)
9	I	0.36	0/1611	0.59	0/2174
9	W	0.35	0/1611	0.59	0/2174
10	J	0.36	0/1589	0.63	0/2142
10	X	0.36	0/1589	0.63	0/2142
11	K	0.35	0/1681	0.84	4/2274 (0.2%)
11	Y	0.35	0/1681	0.86	4/2274 (0.2%)
12	L	0.38	0/1795	0.62	0/2420
12	Z	0.38	0/1795	0.62	0/2420
13	M	0.37	0/1855	0.65	0/2514
13	a	0.37	0/1855	0.65	0/2514
14	N	0.34	0/1541	0.58	0/2087
14	b	0.34	0/1541	0.59	0/2087
All	All	0.37	0/50228	0.64	21/67910 (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
8	H	0	1
8	V	0	1
11	K	0	1
11	Y	0	1
All	All	0	4

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	V	188	ARG	NE-CZ-NH2	-21.23	109.69	120.30
11	Y	73	ARG	NE-CZ-NH1	-19.69	110.45	120.30
11	K	73	ARG	NE-CZ-NH2	-19.64	110.48	120.30
8	H	188	ARG	NE-CZ-NH1	-18.35	111.13	120.30
11	Y	73	ARG	NE-CZ-NH2	16.27	128.44	120.30
8	H	188	ARG	NE-CZ-NH2	15.22	127.91	120.30
11	K	73	ARG	NE-CZ-NH1	14.79	127.70	120.30
8	V	188	ARG	NE-CZ-NH1	14.78	127.69	120.30
8	V	188	ARG	CD-NE-CZ	10.30	138.02	123.60
11	K	73	ARG	CD-NE-CZ	9.94	137.51	123.60
11	Y	73	ARG	CD-NE-CZ	9.41	136.78	123.60
8	H	188	ARG	CD-NE-CZ	8.61	135.66	123.60
2	P	224	VAL	CG1-CB-CG2	5.85	120.26	110.90
11	Y	4	LEU	CA-CB-CG	5.53	128.03	115.30
2	B	224	VAL	CG1-CB-CG2	5.45	119.62	110.90
11	K	4	LEU	CA-CB-CG	5.40	127.71	115.30
2	P	51	VAL	CG1-CB-CG2	5.38	119.51	110.90
2	B	51	VAL	CG1-CB-CG2	5.38	119.50	110.90
8	H	196	ARG	NE-CZ-NH1	5.29	122.94	120.30
8	H	223	ILE	CB-CA-C	-5.01	101.57	111.60
8	V	196	ARG	NE-CZ-NH1	5.00	122.80	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	188	ARG	Sidechain
11	K	73	ARG	Sidechain

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Mol	Chain	Res	Type	Group
8	V	188	ARG	Sidechain
11	Y	73	ARG	Sidechain

## 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	1	0
2	B	1904	0	1904	10	0
2	P	1904	0	1904	10	0
3	C	1881	0	1895	6	0
3	Q	1881	0	1895	6	0
4	D	1813	0	1797	3	0
4	R	1813	0	1797	2	0
5	E	1773	0	1775	6	0
5	S	1773	0	1775	5	0
6	F	1892	0	1883	4	0
6	T	1892	0	1883	3	0
7	G	1907	0	1901	3	0
7	U	1907	0	1901	3	0
8	H	1716	0	1700	4	0
8	V	1688	0	1680	8	0
9	I	1581	0	1574	6	0
9	W	1581	0	1574	6	0
10	J	1561	0	1569	9	0
10	X	1561	0	1569	9	0
11	K	1644	0	1593	7	0
11	Y	1644	0	1593	7	0
12	L	1757	0	1711	9	0
12	Z	1757	0	1711	9	0
13	M	1824	0	1832	2	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	2	0
14	b	1512	0	1481	0	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	W	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	1	0	0	0	0
16	U	1	0	0	0	0
17	H	43	0	0	0	0
17	K	43	0	0	0	0
17	V	43	0	0	0	0
17	Y	43	0	0	0	0
18	H	12	0	13	0	0
18	V	12	0	13	0	0
19	A	16	0	0	0	0
19	B	18	0	0	2	0
19	C	18	0	0	0	0
19	D	10	0	0	0	0
19	E	3	0	0	0	0
19	F	16	0	0	0	0
19	G	22	0	0	0	0
19	H	33	0	0	0	0
19	I	22	0	0	0	0
19	J	18	0	0	0	0
19	K	33	0	0	0	0
19	L	36	0	0	0	0
19	M	25	0	0	1	0
19	N	13	0	0	0	0
19	O	13	0	0	0	0
19	P	18	0	0	1	0
19	Q	11	0	0	0	0
19	R	11	0	0	0	0
19	S	12	0	0	0	0
19	T	14	0	0	0	0
19	U	24	0	0	0	0
19	V	22	0	0	0	0
19	W	23	0	0	0	0
19	X	18	0	0	0	0
19	Y	32	0	0	0	0
19	Z	29	0	0	0	0
19	a	27	0	0	0	0
19	b	12	0	0	0	0
All	All	50087	0	49094	105	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 (105) 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)
8:V:35:HIS:CE1	8:V:53:GLU:OE1	2.04	1.10
8:V:35:HIS:NE2	8:V:53:GLU:OE1	2.04	0.90
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.54	0.73
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.54	0.71
11:K:142:SER:OG	10:X:143:LEU:HD21	1.90	0.71
5:E:92:ASN:HD21	12:L:70:ASN:HD21	1.38	0.70
10:J:143:LEU:HD21	11:Y:142:SER:OG	1.92	0.69
5:S:92:ASN:HD21	12:Z:70:ASN:HD21	1.41	0.68
2:B:145:TYR:OH	2:B:217:LYS:N	2.28	0.67
2:P:145:TYR:OH	2:P:217:LYS:N	2.29	0.66
2:B:12:PHE:H	3:C:17:GLN:HE22	1.46	0.64
2:P:225:TYR:CD1	8:V:223:ILE:HG13	2.32	0.64
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.45	0.64
5:S:12:PHE:H	6:T:19:GLN:HE22	1.46	0.64
2:P:95:GLN:HE22	9:W:71:ASN:HD22	1.46	0.63
5:E:92:ASN:HD21	12:L:70:ASN:ND2	1.99	0.60
6:F:123:ASN:HD22	6:F:124:SER:N	1.99	0.60
5:E:12:PHE:H	6:F:19:GLN:HE22	1.48	0.60
12:L:42:LYS:HD2	12:L:55:ASN:HD22	1.67	0.60
6:T:123:ASN:HD22	6:T:124:SER:N	1.99	0.60
5:S:92:ASN:HD21	12:Z:70:ASN:ND2	1.98	0.60
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.67	0.59
7:U:23:PHE:O	7:U:26:THR:HB	2.03	0.58
3:C:160:GLN:HA	3:C:160:GLN:HE21	1.67	0.58
12:Z:42:LYS:HD2	12:Z:55:ASN:HD22	1.69	0.58
5:S:92:ASN:ND2	12:Z:70:ASN:HD21	2.02	0.57
7:G:23:PHE:O	7:G:26:THR:HB	2.05	0.57
5:E:92:ASN:ND2	12:L:70:ASN:HD21	2.02	0.56
6:F:123:ASN:C	6:F:123:ASN:HD22	2.09	0.56
11:K:176:ASN:HD21	11:K:190:ASN:HD22	1.54	0.56
11:K:176:ASN:ND2	11:K:190:ASN:HD22	2.04	0.56
1:O:12:PHE:H	2:P:20:GLN:HE22	1.55	0.55
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.89	0.54
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.55	0.54
9:I:37:ASN:ND2	11:Y:209:ASN:O	2.42	0.53
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.90	0.53
3:C:9:PHE:H	4:D:15:GLN:HE22	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:T:123:ASN:C	6:T:123:ASN:HD22	2.12	0.52
10:J:50:ALA:O	11:K:91:LYS:NZ	2.42	0.52
2:P:95:GLN:NE2	9:W:71:ASN:HD22	2.07	0.52
10:X:50:ALA:O	11:Y:91:LYS:NZ	2.42	0.52
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.92	0.52
3:Q:202:GLN:O	3:Q:202:GLN:CG	2.58	0.51
13:M:2:GLN:NE2	19:M:301:HOH:O	2.43	0.51
11:Y:176:ASN:ND2	11:Y:190:ASN:HD22	2.07	0.51
3:C:202:GLN:CG	3:C:202:GLN:O	2.59	0.51
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.41	0.51
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.92	0.51
8:H:196:ARG:NH2	9:I:150:GLU:O	2.44	0.51
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.40	0.51
1:A:12:PHE:H	2:B:20:GLN:HE22	1.57	0.50
12:L:31:THR:CG2	12:L:36:ASN:HD21	2.24	0.50
11:Y:176:ASN:HD21	11:Y:190:ASN:HD22	1.58	0.50
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	1.94	0.50
11:K:208:ASN:HD22	11:K:208:ASN:N	2.10	0.50
3:C:198:LEU:HA	3:C:201:VAL:HG12	1.94	0.49
8:V:223:ILE:H	8:V:223:ILE:HD13	1.78	0.49
11:K:209:ASN:O	9:W:37:ASN:ND2	2.46	0.49
11:Y:208:ASN:HD22	11:Y:208:ASN:N	2.11	0.48
2:P:145:TYR:HH	2:P:217:LYS:N	2.11	0.48
2:B:113:ARG:NE	19:B:301:HOH:O	2.43	0.47
2:B:95:GLN:NE2	9:I:71:ASN:HD22	2.12	0.47
11:K:18:SER:OG	11:K:29:GLN:O	2.32	0.47
8:H:223:ILE:H	8:H:223:ILE:HD13	1.78	0.47
12:Z:31:THR:CG2	12:Z:36:ASN:HD21	2.23	0.46
2:P:113:ARG:NE	19:P:301:HOH:O	2.44	0.46
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.97	0.46
8:V:223:ILE:HD13	8:V:223:ILE:N	2.31	0.45
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.98	0.45
11:Y:18:SER:OG	11:Y:29:GLN:O	2.35	0.45
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.17	0.45
7:G:167:GLN:HE21	7:G:171:THR:HG23	1.82	0.44
12:L:8:ASN:HA	12:L:30:ILE:O	2.17	0.44
2:B:145:TYR:HH	2:B:217:LYS:N	2.14	0.44
8:H:223:ILE:N	8:H:223:ILE:HD13	2.32	0.44
2:P:12:PHE:H	3:Q:17:GLN:HE22	1.65	0.44
3:C:48:SER:HB2	3:C:207:ASN:HD21	1.83	0.43
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:36:SER:HB2	10:J:126:VAL:HG11	2.00	0.43
13:M:156:ARG:HH11	8:V:165:ASN:HD22	1.67	0.43
3:Q:48:SER:HB2	3:Q:207:ASN:HD21	1.83	0.43
2:B:93:HIS:HB3	19:B:301:HOH:O	2.18	0.43
10:X:3:ILE:HG23	10:X:18:SER:HB3	2.01	0.43
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.00	0.42
10:J:25:ILE:O	10:X:139:TYR:OH	2.38	0.42
8:V:196:ARG:NH2	9:W:150:GLU:O	2.52	0.42
10:J:139:TYR:OH	10:X:25:ILE:O	2.38	0.41
9:I:10:ILE:HG21	9:I:141:ALA:HB3	2.02	0.41
10:J:169:GLU:O	10:X:177:LYS:NZ	2.54	0.41
10:J:177:LYS:NZ	10:X:169:GLU:O	2.53	0.41
5:E:18:LEU:HD21	6:F:126:ARG:HD2	2.03	0.41
2:P:145:TYR:OH	2:P:217:LYS:HB2	2.20	0.41
2:B:225:TYR:CD1	8:H:223:ILE:HG13	2.56	0.41
9:W:36:SER:HB2	10:X:126:VAL:HG11	2.03	0.41
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.51	0.41
8:V:192:THR:HG22	8:V:195:VAL:HG13	2.03	0.41
9:W:9:GLY:HA3	9:W:41:LYS:HE2	2.02	0.40
7:G:73:VAL:HG12	7:G:133:THR:HB	2.03	0.40
14:N:152:VAL:HA	14:N:175:MET:HE1	2.03	0.40
7:U:167:GLN:HE21	7:U:171:THR:HG23	1.86	0.40
4:D:32:ILE:HD12	4:D:192:VAL:HG23	2.03	0.40
10:J:3:ILE:HG23	10:J:18:SER:HB3	2.02	0.40
2:P:42:GLY:HA2	2:P:145:TYR:CZ	2.57	0.40
7:U:73:VAL:HG12	7:U:133:THR:HB	2.03	0.40
2:B:145:TYR:OH	2:B:217:LYS:HB2	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	242 (98%)	6 (2%)	0	100	100
1	O	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
2	B	242/258 (94%)	231 (96%)	11 (4%)	0	100	100
2	P	242/258 (94%)	231 (96%)	11 (4%)	0	100	100
3	C	238/254 (94%)	235 (99%)	2 (1%)	1 (0%)	34	60
3	Q	238/254 (94%)	235 (99%)	2 (1%)	1 (0%)	34	60
4	D	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
4	R	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
5	E	229/234 (98%)	221 (96%)	8 (4%)	0	100	100
5	S	229/234 (98%)	221 (96%)	8 (4%)	0	100	100
6	F	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
6	T	241/288 (84%)	240 (100%)	1 (0%)	0	100	100
7	G	239/252 (95%)	237 (99%)	2 (1%)	0	100	100
7	U	239/252 (95%)	238 (100%)	1 (0%)	0	100	100
8	H	224/226 (99%)	217 (97%)	6 (3%)	1 (0%)	34	60
8	V	221/226 (98%)	216 (98%)	5 (2%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (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	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%)	214 (97%)	5 (2%)	1 (0%)	29	54
12	Z	220/222 (99%)	214 (97%)	5 (2%)	1 (0%)	29	54
13	M	231/246 (94%)	224 (97%)	6 (3%)	1 (0%)	34	60
13	a	231/246 (94%)	224 (97%)	6 (3%)	1 (0%)	34	60
14	N	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
14	b	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
All	All	6281/6602 (95%)	6129 (98%)	145 (2%)	7 (0%)	51	78

All (7) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
8	H	223	ILE
3	C	204	GLY
3	Q	204	GLY
12	L	166	GLY
12	Z	166	GLY
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%)	57	82
1	O	209/209 (100%)	205 (98%)	4 (2%)	57	82
2	B	203/216 (94%)	194 (96%)	9 (4%)	28	56
2	P	203/216 (94%)	195 (96%)	8 (4%)	32	61
3	C	212/226 (94%)	202 (95%)	10 (5%)	26	54
3	Q	212/226 (94%)	202 (95%)	10 (5%)	26	54
4	D	194/215 (90%)	185 (95%)	9 (5%)	27	54
4	R	194/215 (90%)	185 (95%)	9 (5%)	27	54
5	E	190/193 (98%)	181 (95%)	9 (5%)	26	54
5	S	190/193 (98%)	181 (95%)	9 (5%)	26	54
6	F	201/239 (84%)	193 (96%)	8 (4%)	31	60
6	T	201/239 (84%)	193 (96%)	8 (4%)	31	60
7	G	206/210 (98%)	198 (96%)	8 (4%)	32	61
7	U	206/210 (98%)	198 (96%)	8 (4%)	32	61
8	H	184/184 (100%)	174 (95%)	10 (5%)	22	47
8	V	181/184 (98%)	171 (94%)	10 (6%)	21	46
9	I	172/173 (99%)	169 (98%)	3 (2%)	60	84
9	W	172/173 (99%)	169 (98%)	3 (2%)	60	84
10	J	173/175 (99%)	167 (96%)	6 (4%)	36	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	X	173/175 (99%)	167 (96%)	6 (4%)	36	65
11	K	169/169 (100%)	160 (95%)	9 (5%)	22	48
11	Y	169/169 (100%)	159 (94%)	10 (6%)	19	43
12	L	185/185 (100%)	176 (95%)	9 (5%)	25	52
12	Z	185/185 (100%)	176 (95%)	9 (5%)	25	52
13	M	199/208 (96%)	192 (96%)	7 (4%)	36	65
13	a	199/208 (96%)	192 (96%)	7 (4%)	36	65
14	N	162/162 (100%)	158 (98%)	4 (2%)	47	76
14	b	162/162 (100%)	158 (98%)	4 (2%)	47	76
All	All	5315/5528 (96%)	5105 (96%)	210 (4%)	31	60

All (210) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	51	VAL
2	B	52	THR
2	B	55	LEU
2	B	102	ASN
2	B	113	ARG
2	B	119	GLN
2	B	191	LEU
2	B	223	GLU
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	49	THR
3	C	51	LYS
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	240	GLU
4	D	99	ILE
4	D	125	LEU

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Mol	Chain	Res	Type
4	D	143	ASP
4	D	176	LEU
4	D	193	LEU
4	D	214	ILE
4	D	235	LEU
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	29	LYS
5	E	55	LEU
5	E	71	LEU
5	E	99	ASN
5	E	116	GLN
5	E	184	ASN
5	E	188	LEU
5	E	202	ASP
6	F	117	GLN
6	F	123	ASN
6	F	171	GLU
6	F	172	LEU
6	F	181	GLU
6	F	214	TRP
6	F	221	ASN
6	F	240	GLN
7	G	83	ASN
7	G	115	LEU
7	G	117	GLN
7	G	122	ARG
7	G	125	MET
7	G	208	GLU
7	G	235	ARG
7	G	236	LEU
8	H	9	GLN
8	H	22	ASN
8	H	31	CYS
8	H	35	HIS
8	H	68	LEU
8	H	103	VAL
8	H	127	LEU
8	H	196	ARG
8	H	222	ASP
8	H	223	ILE

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Mol	Chain	Res	Type
9	I	37	ASN
9	I	171	LEU
9	I	182	TRP
10	J	2	ASP
10	J	3	ILE
10	J	35	THR
10	J	78	GLN
10	J	90	LYS
10	J	99	GLN
11	K	4	LEU
11	K	9	GLN
11	K	18	SER
11	K	35	ILE
11	K	106	ARG
11	K	107	LYS
11	K	118	ASP
11	K	208	ASN
11	K	209	ASN
12	L	18	GLU
12	L	23	LEU
12	L	49	ASN
12	L	108	HIS
12	L	136	CYS
12	L	144	SER
12	L	150	LEU
12	L	172	LEU
12	L	179	GLU
13	M	2	GLN
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	161	ARG
13	M	187	ARG
13	M	233	ILE
14	N	9	LYS
14	N	83	LYS
14	N	104	ASP
14	N	107	LYS
1	O	2	THR
1	O	122	THR
1	O	157	PHE
1	O	250	LEU

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Mol	Chain	Res	Type
2	P	52	THR
2	P	55	LEU
2	P	102	ASN
2	P	113	ARG
2	P	119	GLN
2	P	191	LEU
2	P	223	GLU
2	P	238	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	49	THR
3	Q	51	LYS
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	240	GLU
4	R	99	ILE
4	R	125	LEU
4	R	143	ASP
4	R	176	LEU
4	R	193	LEU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	55	LEU
5	S	71	LEU
5	S	99	ASN
5	S	116	GLN
5	S	184	ASN
5	S	188	LEU
5	S	202	ASP
6	T	117	GLN
6	T	123	ASN
6	T	171	GLU
6	T	172	LEU
6	T	181	GLU
6	T	214	TRP

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Mol	Chain	Res	Type
6	T	221	ASN
6	T	240	GLN
7	U	83	ASN
7	U	115	LEU
7	U	117	GLN
7	U	122	ARG
7	U	125	MET
7	U	208	GLU
7	U	235	ARG
7	U	236	LEU
8	V	9	GLN
8	V	22	ASN
8	V	31	CYS
8	V	68	LEU
8	V	103	VAL
8	V	127	LEU
8	V	144	GLN
8	V	196	ARG
8	V	222	ASP
8	V	223	ILE
9	W	37	ASN
9	W	171	LEU
9	W	182	TRP
10	X	2	ASP
10	X	3	ILE
10	X	35	THR
10	X	78	GLN
10	X	90	LYS
10	X	99	GLN
11	Y	4	LEU
11	Y	9	GLN
11	Y	18	SER
11	Y	35	ILE
11	Y	73	ARG
11	Y	106	ARG
11	Y	107	LYS
11	Y	118	ASP
11	Y	208	ASN
11	Y	209	ASN
12	Z	18	GLU
12	Z	23	LEU
12	Z	49	ASN

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Mol	Chain	Res	Type
12	Z	108	HIS
12	Z	136	CYS
12	Z	144	SER
12	Z	150	LEU
12	Z	172	LEU
12	Z	179	GLU
13	a	2	GLN
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
13	a	233	ILE
14	b	9	LYS
14	b	83	LYS
14	b	104	ASP
14	b	107	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (121) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	20	GLN
2	B	58	GLN
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN
3	C	17	GLN
3	C	38	ASN
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	91	HIS
4	D	100	ASN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN

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Mol	Chain	Res	Type
5	E	151	ASN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	191	GLN
6	F	240	GLN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	167	GLN
7	G	175	ASN
8	H	165	ASN
10	J	55	GLN
10	J	118	GLN
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
11	K	209	ASN
12	L	3	ASN
12	L	29	ASN
12	L	36	ASN
12	L	49	ASN
12	L	55	ASN
12	L	70	ASN
12	L	152	ASN
12	L	153	GLN
12	L	158	ASN
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	161	GLN
2	P	20	GLN
2	P	58	GLN
2	P	95	GLN
2	P	119	GLN

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Mol	Chain	Res	Type
2	P	123	GLN
2	P	155	ASN
2	P	176	GLN
3	Q	17	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	91	HIS
4	R	225	ASN
5	S	59	GLN
5	S	68	HIS
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	151	ASN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	191	GLN
6	T	240	GLN
7	U	30	ASN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	167	GLN
7	U	175	ASN
8	V	35	HIS
8	V	165	ASN
10	X	55	GLN
10	X	86	GLN
10	X	118	GLN
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
11	Y	209	ASN

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Mol	Chain	Res	Type
12	Z	3	ASN
12	Z	29	ASN
12	Z	36	ASN
12	Z	49	ASN
12	Z	55	ASN
12	Z	70	ASN
12	Z	152	ASN
12	Z	153	GLN
12	Z	158	ASN
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	179	ASN
13	a	194	ASN
13	a	213	GLN
14	b	161	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 10 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	GT8	V	301	8	45,45,45	1.24	3 (6%)	59,61,61	1.54	6 (10%)
17	GT8	K	301	11	45,45,45	1.38	5 (11%)	59,61,61	1.80	12 (20%)
17	GT8	H	301	8	45,45,45	1.28	4 (8%)	59,61,61	1.56	8 (13%)
18	MES	H	302	-	12,12,12	2.26	1 (8%)	14,16,16	1.66	2 (14%)
18	MES	V	303	-	12,12,12	2.22	1 (8%)	14,16,16	1.84	2 (14%)
17	GT8	Y	301	11	45,45,45	1.44	5 (11%)	59,61,61	1.77	12 (20%)

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	GT8	V	301	8	-	11/45/61/61	0/3/3/3
17	GT8	K	301	11	-	8/45/61/61	0/3/3/3
17	GT8	H	301	8	-	11/45/61/61	0/3/3/3
18	MES	H	302	-	-	0/6/14/14	0/1/1/1
18	MES	V	303	-	-	5/6/14/14	0/1/1/1
17	GT8	Y	301	11	-	6/45/61/61	0/3/3/3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	H	302	MES	C8-S	-7.65	1.66	1.77
18	V	303	MES	C8-S	-7.51	1.66	1.77
17	K	301	GT8	C40-C41	-5.49	1.38	1.51
17	H	301	GT8	C40-C41	-5.30	1.38	1.51
17	Y	301	GT8	C40-C41	-5.27	1.38	1.51
17	V	301	GT8	C40-C41	-4.96	1.39	1.51
17	Y	301	GT8	C11-C12	4.47	1.60	1.52
17	K	301	GT8	C11-C12	4.08	1.59	1.52
17	V	301	GT8	C11-C12	3.90	1.59	1.52
17	Y	301	GT8	C12-C9	3.83	1.62	1.54
17	H	301	GT8	C11-C12	3.68	1.58	1.52
17	H	301	GT8	C12-C9	3.43	1.61	1.54
17	K	301	GT8	C12-C9	3.28	1.61	1.54
17	V	301	GT8	C12-C9	3.26	1.61	1.54
17	Y	301	GT8	C9-C8	3.21	1.57	1.53
17	K	301	GT8	C9-C8	2.63	1.56	1.53
17	K	301	GT8	C10-C12	2.25	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Y	301	GT8	C10-C12	2.18	1.56	1.52
17	H	301	GT8	C10-C12	2.01	1.55	1.52

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	H	301	GT8	C11-C12-C10	-6.57	101.16	110.56
17	V	301	GT8	C11-C12-C10	-6.44	101.35	110.56
17	K	301	GT8	C11-C12-C9	6.23	122.94	111.28
17	Y	301	GT8	C11-C12-C9	6.20	122.88	111.28
17	K	301	GT8	C11-C12-C10	-5.79	102.27	110.56
17	K	301	GT8	C33-C32-N31	5.34	118.20	110.10
17	Y	301	GT8	C33-C32-N31	5.21	118.00	110.10
17	Y	301	GT8	C11-C12-C10	-5.06	103.33	110.56
18	V	303	MES	O1S-S-C8	4.62	112.47	106.92
18	H	302	MES	O2S-S-C8	4.26	112.04	106.92
18	V	303	MES	O3S-S-C8	3.71	111.77	105.77
17	K	301	GT8	C46-O45-C44	3.20	124.46	117.51
17	Y	301	GT8	C46-O45-C44	3.14	124.32	117.51
17	Y	301	GT8	C12-C9-C8	-3.04	108.63	115.71
17	V	301	GT8	C30-N31-C36	2.97	115.70	111.09
18	H	302	MES	O3S-S-C8	2.87	110.42	105.77
17	V	301	GT8	C11-C12-C9	2.86	116.63	111.28
17	K	301	GT8	C12-C9-C8	-2.84	109.09	115.71
17	K	301	GT8	C7-C8-N22	-2.81	106.64	110.33
17	H	301	GT8	C46-O45-C44	2.81	123.60	117.51
17	H	301	GT8	C11-C12-C9	2.80	116.52	111.28
17	H	301	GT8	C30-N31-C36	2.78	115.40	111.09
17	Y	301	GT8	C7-C8-N22	-2.77	106.69	110.33
17	V	301	GT8	C46-O45-C44	2.68	123.33	117.51
17	Y	301	GT8	C35-C36-N31	-2.57	106.20	110.10
17	K	301	GT8	C6-C1-C2	-2.45	106.43	111.42
17	K	301	GT8	C35-C36-N31	-2.44	106.40	110.10
17	V	301	GT8	C10-C12-C9	2.40	115.77	111.28
17	Y	301	GT8	C6-C1-C2	-2.37	106.58	111.42
17	V	301	GT8	C6-C1-C2	-2.34	106.64	111.42
17	Y	301	GT8	C50-C3-C2	-2.31	106.60	112.11
17	H	301	GT8	C10-C12-C9	2.30	115.58	111.28
17	Y	301	GT8	C41-C40-C24	-2.27	107.12	113.39
17	K	301	GT8	C41-C40-C24	-2.26	107.16	113.39
17	H	301	GT8	O34-C33-C32	-2.23	106.87	111.80
17	H	301	GT8	C6-C1-C2	-2.20	106.93	111.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	K	301	GT8	C50-C3-C2	-2.19	106.87	112.11
17	Y	301	GT8	C5-C4-C3	-2.19	108.01	112.15
17	K	301	GT8	O34-C35-C36	-2.18	106.99	111.80
17	K	301	GT8	C5-C4-C3	-2.14	108.10	112.15
17	Y	301	GT8	O34-C35-C36	-2.14	107.09	111.80
17	H	301	GT8	C7-C8-N22	-2.14	107.52	110.33

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	V	301	GT8	C10-C12-C9-C8
17	V	301	GT8	C11-C12-C9-C8
17	V	301	GT8	O13-C12-C9-C8
17	V	301	GT8	C10-C12-C9-O21
17	V	301	GT8	C11-C12-C9-O21
17	V	301	GT8	O13-C12-C9-O21
17	V	301	GT8	C29-C30-N31-C36
17	H	301	GT8	C10-C12-C9-C8
17	H	301	GT8	C11-C12-C9-C8
17	H	301	GT8	O13-C12-C9-C8
17	H	301	GT8	C10-C12-C9-O21
17	H	301	GT8	C11-C12-C9-O21
17	H	301	GT8	O13-C12-C9-O21
17	H	301	GT8	C29-C30-N31-C36
18	V	303	MES	C7-C8-S-O1S
18	V	303	MES	C7-C8-S-O3S
17	K	301	GT8	N28-C29-C30-N31
17	Y	301	GT8	N28-C29-C30-N31
17	V	301	GT8	O37-C29-C30-N31
17	K	301	GT8	O37-C29-C30-N31
17	H	301	GT8	O37-C29-C30-N31
17	Y	301	GT8	O37-C29-C30-N31
17	V	301	GT8	N28-C29-C30-N31
17	H	301	GT8	N28-C29-C30-N31
18	V	303	MES	C8-C7-N4-C3
18	V	303	MES	C8-C7-N4-C5
17	K	301	GT8	C11-C12-C9-O21
17	K	301	GT8	C29-C30-N31-C36
17	Y	301	GT8	C29-C30-N31-C36
18	V	303	MES	C7-C8-S-O2S
17	K	301	GT8	O49-C23-C24-N25

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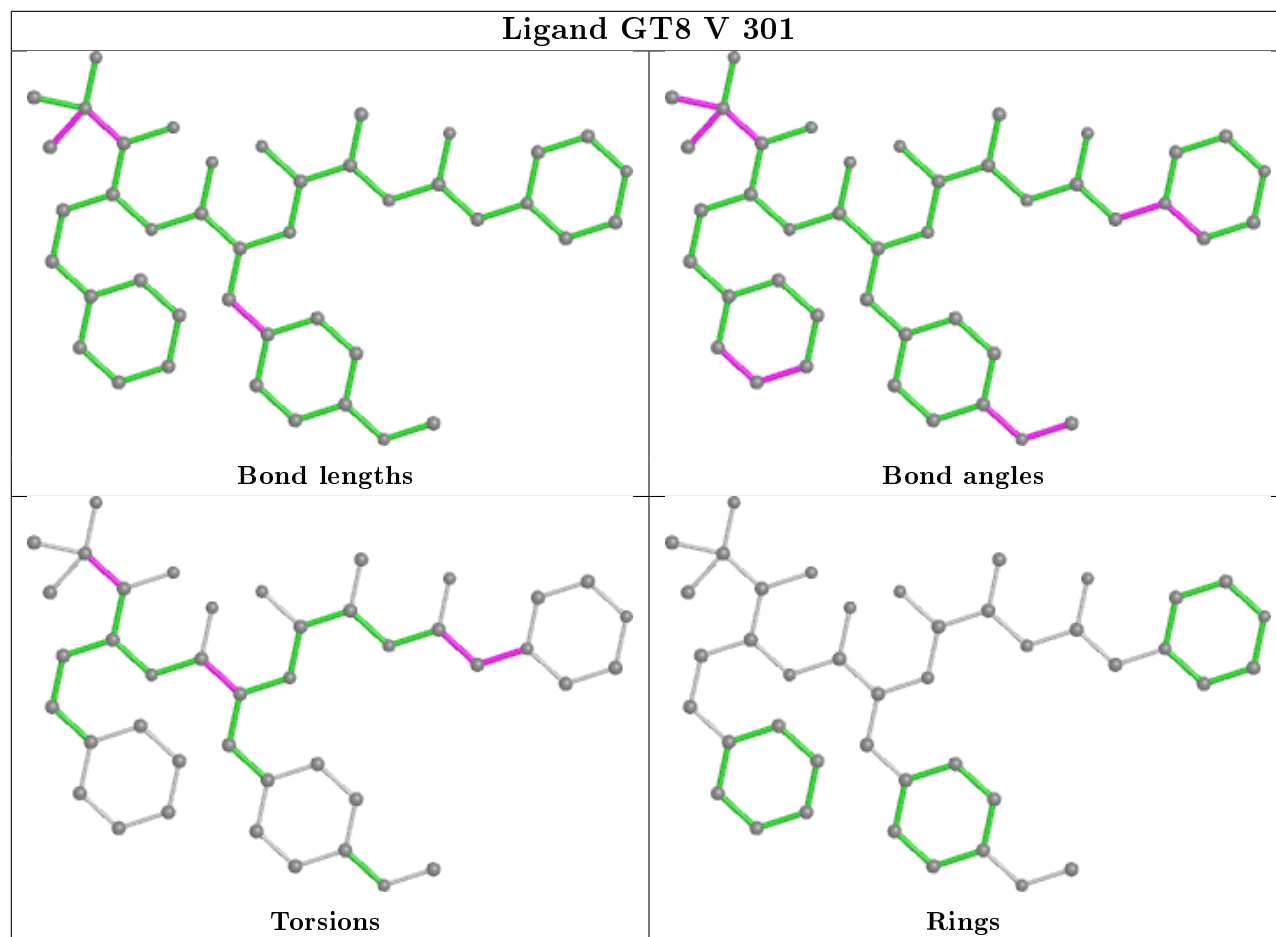
Mol	Chain	Res	Type	Atoms
17	Y	301	GT8	O49-C23-C24-N25
17	K	301	GT8	C10-C12-C9-C8
17	Y	301	GT8	C10-C12-C9-C8
17	V	301	GT8	O49-C23-C24-N25
17	V	301	GT8	N22-C23-C24-N25
17	H	301	GT8	C4-C3-C50-C7
17	K	301	GT8	O13-C12-C9-O21
17	H	301	GT8	N22-C23-C24-N25
17	K	301	GT8	N22-C23-C24-N25
17	Y	301	GT8	N22-C23-C24-N25

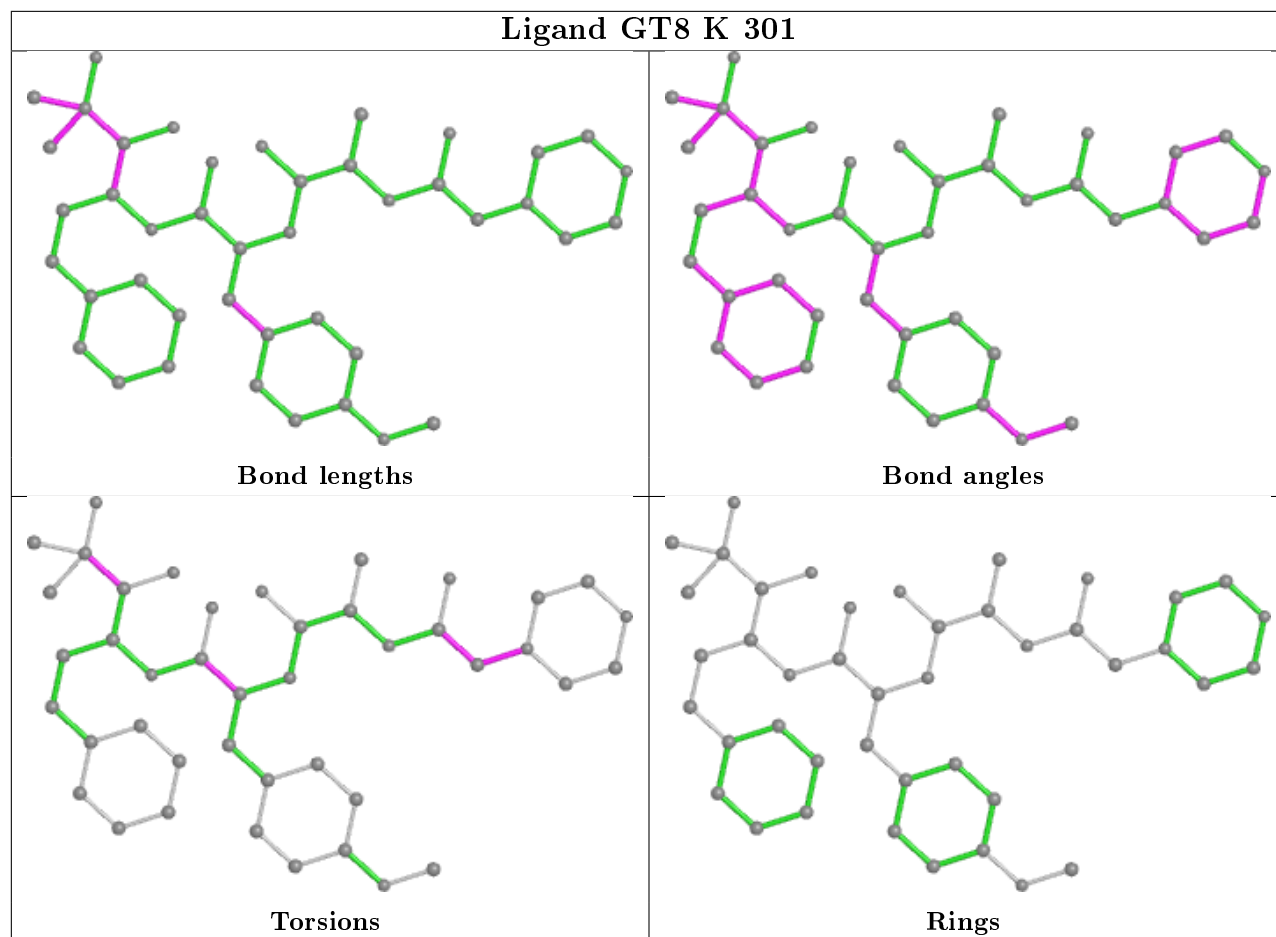
There are no ring outliers.

No monomer is involved in short contacts.

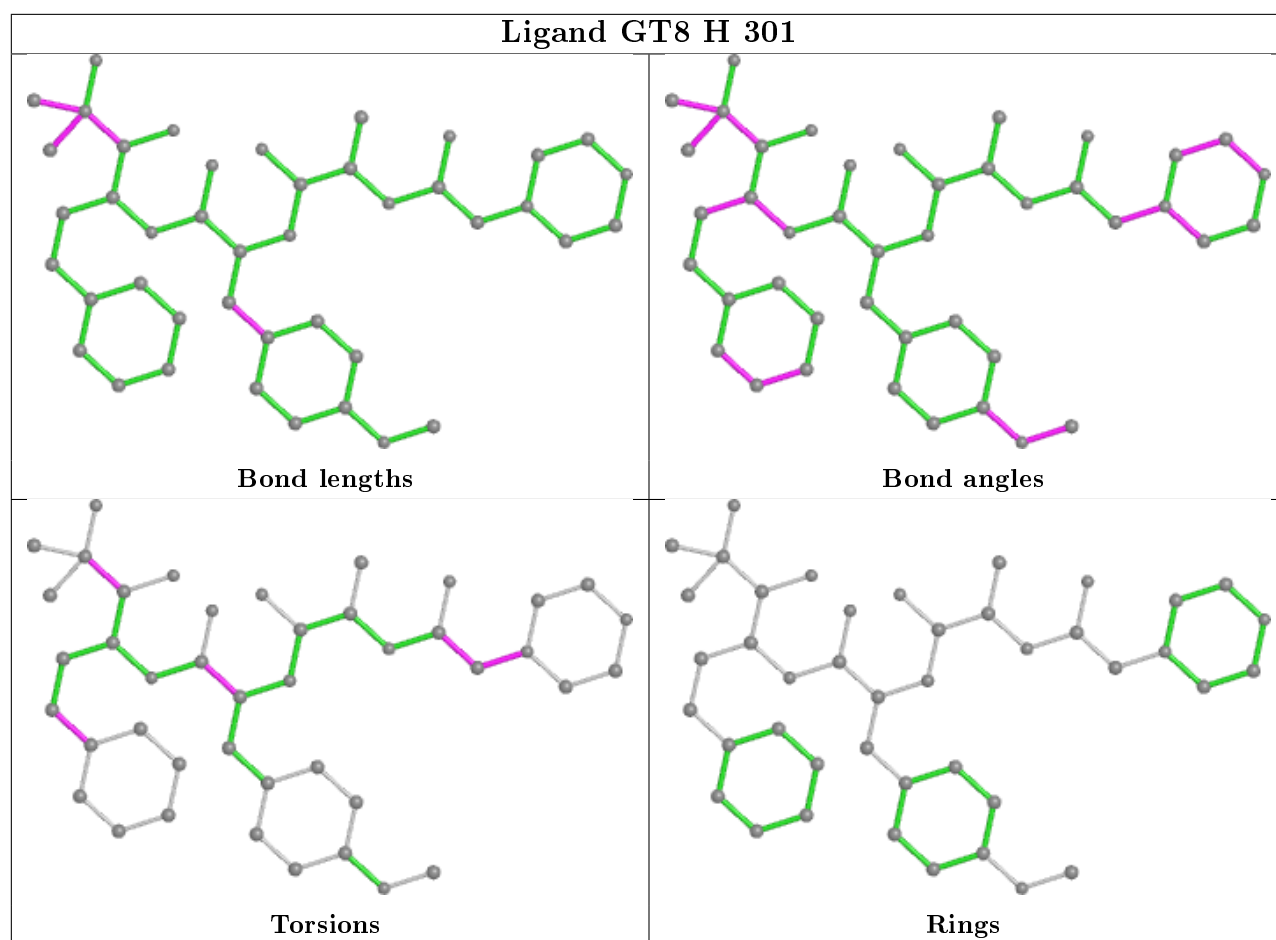
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

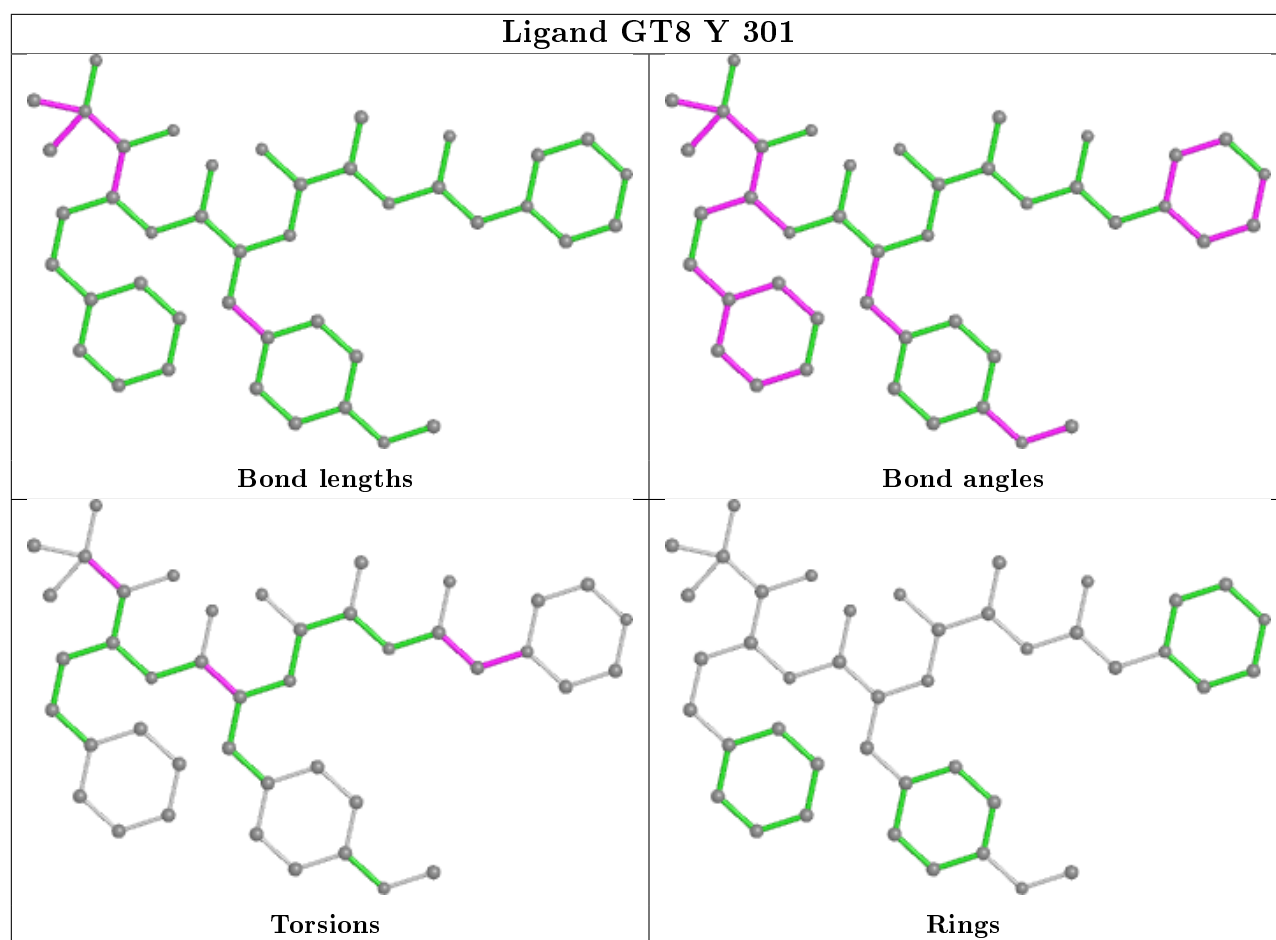
## Ligand GT8 V 301











## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	250/250 (100%)	-0.19	10 (4%) 38 37	43, 59, 95, 118	0
1	O	250/250 (100%)	-0.12	13 (5%) 27 25	46, 66, 106, 130	0
2	B	244/258 (94%)	-0.18	10 (4%) 37 36	44, 62, 101, 115	0
2	P	244/258 (94%)	-0.16	12 (4%) 29 28	47, 66, 101, 123	0
3	C	240/254 (94%)	-0.07	12 (5%) 28 27	41, 66, 118, 156	0
3	Q	240/254 (94%)	0.18	26 (10%) 5 4	49, 80, 143, 185	0
4	D	235/260 (90%)	-0.31	4 (1%) 70 72	46, 66, 93, 127	0
4	R	235/260 (90%)	-0.16	9 (3%) 40 39	52, 70, 101, 135	0
5	E	231/234 (98%)	-0.11	7 (3%) 50 51	52, 69, 107, 125	0
5	S	231/234 (98%)	-0.03	10 (4%) 35 33	53, 76, 118, 140	0
6	F	243/288 (84%)	-0.32	9 (3%) 41 41	43, 65, 103, 125	0
6	T	243/288 (84%)	-0.20	12 (4%) 29 28	39, 69, 112, 142	0
7	G	241/252 (95%)	-0.35	9 (3%) 41 41	43, 59, 91, 131	0
7	U	241/252 (95%)	-0.31	5 (2%) 63 65	45, 60, 90, 125	0
8	H	226/226 (100%)	-0.32	7 (3%) 49 49	42, 54, 80, 133	0
8	V	223/226 (98%)	-0.37	4 (1%) 68 70	41, 56, 81, 119	0
9	I	204/205 (99%)	-0.61	1 (0%) 91 92	37, 51, 72, 86	0
9	W	204/205 (99%)	-0.63	2 (0%) 82 83	36, 53, 73, 89	0
10	J	195/198 (98%)	-0.32	4 (2%) 63 65	40, 56, 79, 97	0
10	X	195/198 (98%)	-0.33	4 (2%) 63 65	43, 58, 80, 102	0
11	K	212/212 (100%)	-0.47	1 (0%) 91 92	41, 54, 78, 90	0
11	Y	212/212 (100%)	-0.50	2 (0%) 84 85	42, 55, 79, 94	0
12	L	222/222 (100%)	-0.50	0 100 100	42, 55, 78, 94	0
12	Z	222/222 (100%)	-0.46	4 (1%) 68 70	41, 55, 82, 97	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
13	M	233/246 (94%)	-0.48	3 (1%)	77	78	40, 55, 79, 91	0
13	a	233/246 (94%)	-0.45	3 (1%)	77	78	38, 55, 77, 89	0
14	N	196/196 (100%)	-0.49	2 (1%)	82	83	39, 53, 78, 91	0
14	b	196/196 (100%)	-0.48	2 (1%)	82	83	40, 54, 80, 95	0
All	All	6341/6602 (96%)	-0.30	187 (2%)	51	52	36, 60, 101, 185	0

All (187) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	H	224	GLN	10.2
3	Q	49	THR	8.3
8	H	225	GLU	8.2
2	P	220	ASN	7.6
1	A	229	THR	7.5
1	A	228	PRO	7.4
1	O	228	PRO	7.3
3	Q	50	LEU	7.2
2	B	221	ASP	6.3
3	Q	48	SER	6.3
8	V	223	ILE	6.2
10	X	1	MET	6.1
1	O	249	ALA	6.0
8	H	226	GLU	6.0
2	B	220	ASN	5.7
10	J	1	MET	5.6
1	O	229	THR	5.6
5	E	202	ASP	5.3
5	S	202	ASP	5.3
2	P	219	ALA	5.3
3	Q	206	LYS	5.3
8	H	222	ASP	5.2
1	A	249	ALA	5.1
8	V	222	ASP	5.0
3	C	202	GLN	4.8
2	P	52	THR	4.6
3	Q	236	GLN	4.5
2	P	221	ASP	4.3
8	H	223	ILE	4.3
3	Q	202	GLN	4.3
1	O	231	LYS	4.2
3	Q	240	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
3	C	49	THR	4.2
3	Q	239	GLN	4.2
2	P	59	ASP	4.2
3	Q	238	LYS	4.1
4	R	241	ALA	4.1
10	J	194	ASP	4.1
2	B	52	THR	4.0
5	S	173	ARG	4.0
7	G	2	GLY	3.9
2	B	51	VAL	3.9
3	C	48	SER	3.8
3	C	238	LYS	3.8
5	E	201	ARG	3.8
1	A	201	GLU	3.7
6	T	244	ASN	3.6
3	C	216	ASP	3.6
8	V	221	CYS	3.6
5	S	54	GLU	3.6
3	C	240	GLU	3.5
6	T	241	LYS	3.5
2	P	51	VAL	3.4
13	M	1	THR	3.4
4	R	242	GLU	3.4
12	Z	1	GLN	3.4
6	T	2	THR	3.3
7	U	242	GLN	3.3
7	G	242	GLN	3.3
6	T	181	GLU	3.3
10	X	194	ASP	3.2
1	O	1	MET	3.2
5	S	180	LYS	3.2
5	S	203	GLU	3.2
3	C	180	LYS	3.2
3	Q	205	ALA	3.2
4	D	242	GLU	3.2
3	C	236	GLN	3.2
7	G	240	ALA	3.2
6	F	181	GLU	3.1
10	X	193	ASP	3.1
1	O	201	GLU	3.1
3	C	50	LEU	3.1
3	Q	180	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
9	I	192	ASP	3.0
14	N	105	LYS	3.0
1	O	52	SER	3.0
3	Q	204	GLY	3.0
13	M	47	ASP	3.0
1	A	221	LEU	3.0
2	B	217	LYS	3.0
3	Q	223	SER	3.0
13	a	1	THR	3.0
3	C	225	GLU	2.9
5	E	233	ILE	2.9
6	T	243	ILE	2.9
6	T	205	GLU	2.9
3	C	239	GLN	2.9
11	K	212	GLY	2.9
14	b	195	GLN	2.9
6	F	2	THR	2.9
3	Q	216	ASP	2.8
3	C	206	LYS	2.8
5	E	173	ARG	2.8
11	Y	106	ARG	2.8
1	A	250	LEU	2.8
3	Q	55	THR	2.8
14	N	195	GLN	2.8
6	F	205	GLU	2.8
3	Q	59	PRO	2.8
7	U	2	GLY	2.8
7	G	179	LYS	2.8
3	Q	187	GLU	2.8
1	A	231	LYS	2.8
5	S	225	ASP	2.7
7	U	222	ASP	2.7
1	O	250	LEU	2.7
8	V	9	GLN	2.7
2	P	218	GLY	2.6
8	H	221	CYS	2.6
4	D	1	ASP	2.6
7	G	222	ASP	2.6
5	S	204	SER	2.6
10	J	174	MET	2.6
1	A	1	MET	2.5
1	O	222	LEU	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	P	225	TYR	2.5
3	Q	141	ASP	2.5
10	X	149	ARG	2.5
1	O	230	ASP	2.5
7	G	208	GLU	2.5
13	a	216	ASN	2.5
3	Q	237	GLU	2.4
9	W	1	SER	2.4
5	E	217	LYS	2.4
1	O	221	LEU	2.4
4	R	1	ASP	2.4
7	G	241	GLU	2.4
2	B	59	ASP	2.4
1	A	248	GLU	2.4
7	G	188	GLU	2.4
4	R	54	ASP	2.4
6	F	244	ASN	2.4
2	P	50	LYS	2.4
3	Q	52	LEU	2.3
4	R	112	ALA	2.3
5	E	123	GLY	2.3
4	D	2	ARG	2.3
6	F	202	ASP	2.3
5	E	194	GLU	2.3
1	A	2	THR	2.3
3	Q	229	GLN	2.3
12	Z	116	GLU	2.3
2	B	242	GLY	2.3
7	G	181	LYS	2.3
6	F	241	LYS	2.3
6	T	180	PRO	2.3
11	Y	212	GLY	2.2
3	Q	225	GLU	2.2
5	S	201	ARG	2.2
6	T	53	LYS	2.2
6	F	229	GLY	2.2
6	F	243	ILE	2.2
5	S	227	GLU	2.2
6	T	177	ASP	2.2
2	B	218	GLY	2.2
7	U	183	ASP	2.2
3	Q	181	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
4	R	49	PRO	2.2
4	R	125	LEU	2.2
2	B	50	LYS	2.2
9	W	192	ASP	2.2
2	B	235	LYS	2.2
4	R	201	GLU	2.2
14	b	105	LYS	2.2
13	M	216	ASN	2.1
6	T	230	ASP	2.1
12	Z	165	ASN	2.1
2	P	240	LYS	2.1
3	Q	171	GLU	2.1
4	D	241	ALA	2.1
2	P	230	LYS	2.1
6	F	180	PRO	2.1
3	Q	235	GLU	2.1
2	P	222	GLY	2.1
13	a	47	ASP	2.1
6	T	201	GLU	2.1
7	U	188	GLU	2.1
8	H	30	SER	2.1
1	O	226	GLY	2.1
10	J	193	ASP	2.1
12	Z	210	ASP	2.1
1	O	248	GLU	2.0
5	S	30	GLN	2.0
3	Q	51	LYS	2.0
6	T	166	GLN	2.0
4	R	169	GLU	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.



## 6.4 Ligands

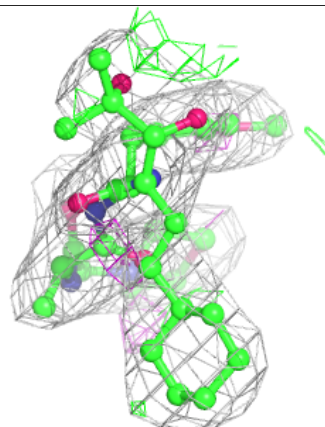
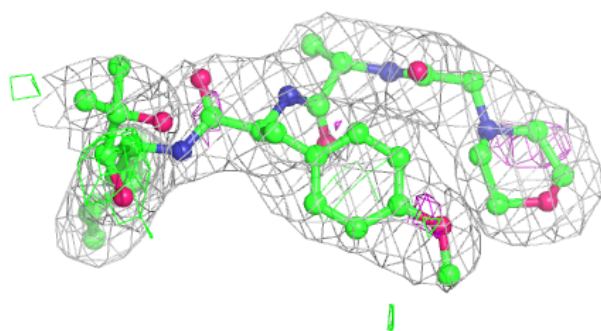
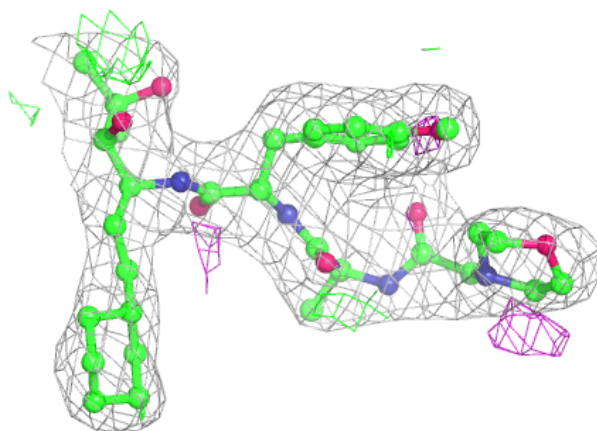
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
15	MG	I	301	1/1	0.88	0.27	80,80,80,80	0
18	MES	V	303	12/12	0.91	0.29	56,102,111,113	12
18	MES	H	302	12/12	0.91	0.30	50,100,110,112	12
15	MG	Y	302	1/1	0.92	0.21	96,96,96,96	0
15	MG	K	302	1/1	0.93	0.17	81,81,81,81	0
17	GT8	K	301	43/43	0.94	0.15	38,46,54,56	0
17	GT8	H	301	43/43	0.94	0.15	40,48,58,62	0
17	GT8	Y	301	43/43	0.95	0.15	42,49,55,56	0
15	MG	V	302	1/1	0.95	0.17	91,91,91,91	0
15	MG	W	301	1/1	0.95	0.43	77,77,77,77	0
15	MG	G	301	1/1	0.96	0.10	75,75,75,75	0
15	MG	N	201	1/1	0.96	0.17	65,65,65,65	0
17	GT8	V	301	43/43	0.96	0.14	42,48,58,58	0
15	MG	Z	301	1/1	0.97	0.26	87,87,87,87	0
16	CL	G	302	1/1	0.98	0.08	55,55,55,55	0
16	CL	U	301	1/1	0.99	0.14	56,56,56,56	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.

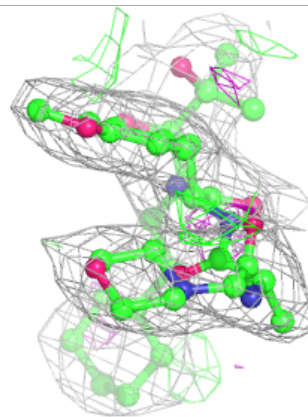
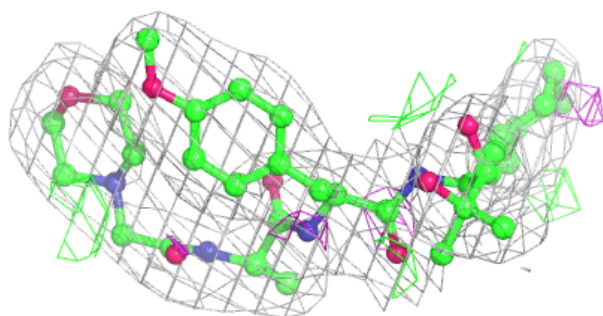
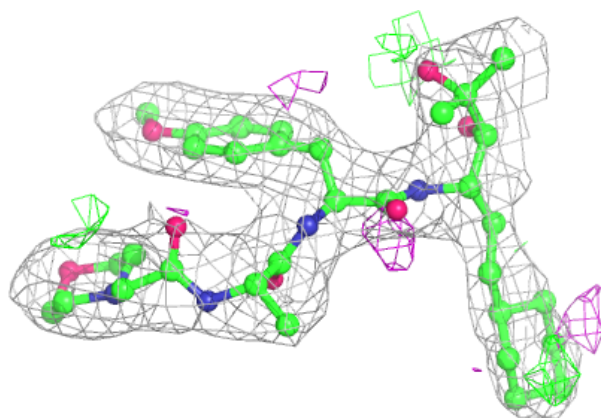
**Electron density around GT8 K 301:**

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



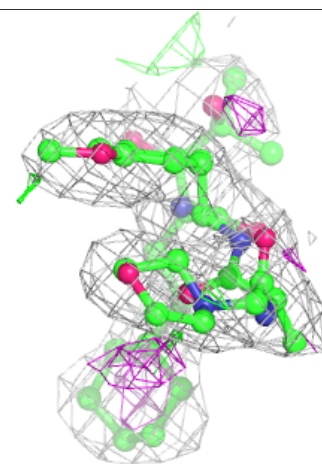
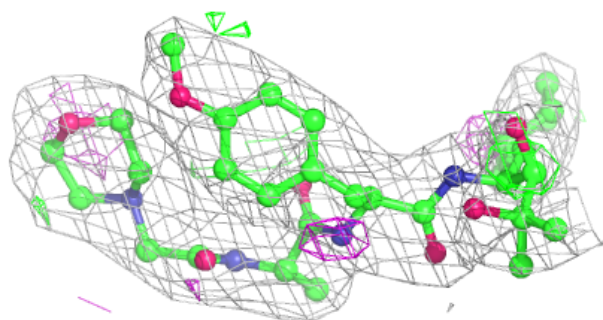
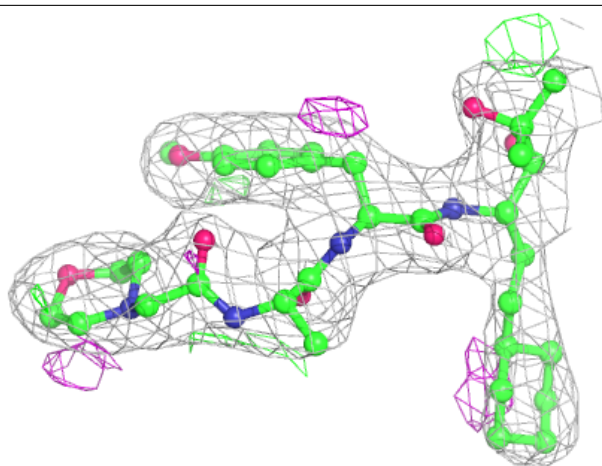
**Electron density around GT8 H 301:**

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



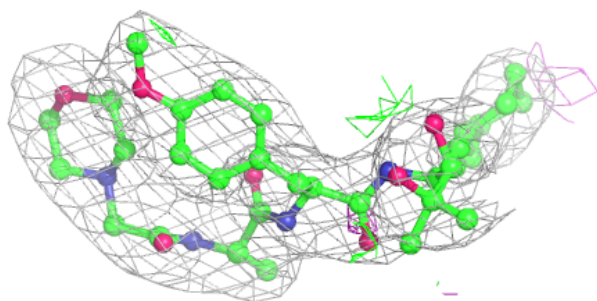
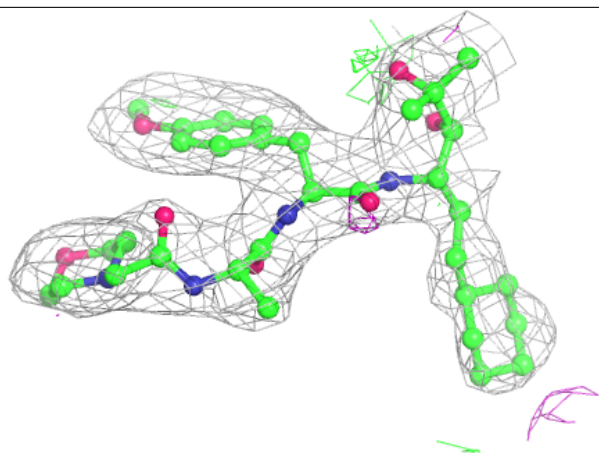
**Electron density around GT8 Y 301:**

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



**Electron density around GT8 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)



## 6.5 Other polymers ⓘ

There are no such residues in this entry.