



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 8, 2024 – 02:50 am GMT

PDB ID : 6G7F  
Title : Yeast 20S proteasome in complex with Cystargolide B  
Authors : Groll, M.; Tello-Aburto, R.  
Deposited on : 2018-04-05  
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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

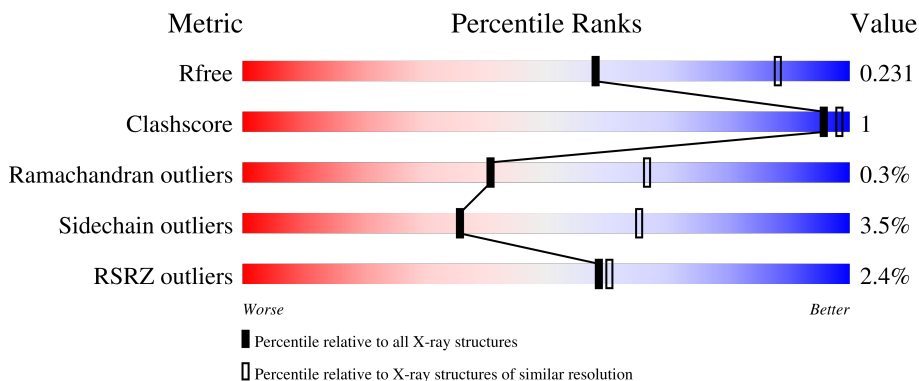
# 1 Overall quality at a glance i

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 of 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	 2% 97%
1	O	250	 3% 98%
2	B	258	 5% 88% 7% 5%
2	P	258	 5% 88% 6% 5%
3	C	254	 4% 87% 6% 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	6% 88% 6% • 6%
4	D	260	2% 85% • • 10%
4	R	260	3% 86% • 10%
5	E	234	3% 93% 6% •
5	S	234	4% 93% 6% •
6	F	288	2% 80% • 16%
6	T	288	% 81% • 16%
7	G	252	3% 90% 5% •
7	U	252	2% 90% 6% •
8	H	232	3% 90% 7% • •
8	V	232	3% 89% 8% • •
9	I	205	96% •
9	W	205	% 96% •
10	J	198	% 94% • • •
10	X	198	% 95% • • •
11	K	212	91% 9%
11	Y	212	94% 6%
12	L	222	% 94% 5% •
12	Z	222	93% 6%
13	M	246	2% 90% • 7%
13	a	246	2% 91% • 6%
14	N	196	% 94% 5% •
14	b	196	% 98% •

## 2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 49937 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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
5	E	231	Total 1773	C 1114	N 307	O 348	S 4	0	0	0
5	S	231	Total 1773	C 1114	N 307	O 348	S 4	0	0	0

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	226	Total 1719	C 1082	N 298	O 332	S 7	0	0	0
8	V	226	Total 1719	C 1082	N 298	O 332	S 7	0	0	0

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

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

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

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

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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	229	Total	C	N	O	S	0	0	0
			1790	1133	306	344	7			
13	a	232	Total	C	N	O	S	0	0	0
			1815	1148	311	349	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	I	1	Total	Mg	0	0
			1	1		

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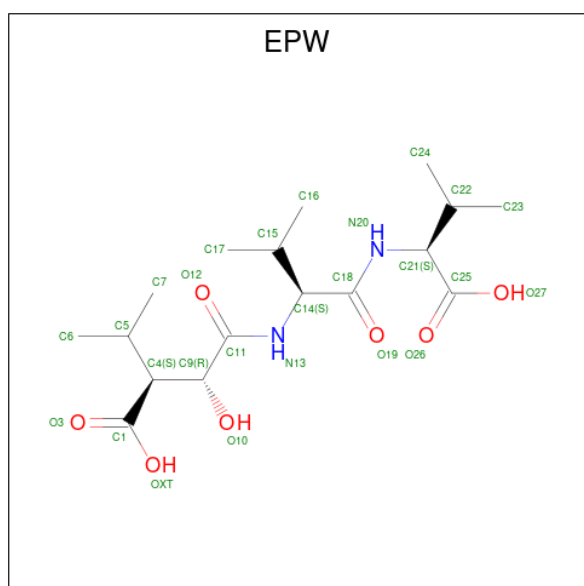
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	K	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	V	1	Total Mg 1 1	0	0
15	W	1	Total Mg 1 1	0	0
15	Y	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0

- 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 Cystargolide B- bound form (three-letter code: EPW) (formula: C<sub>17</sub>H<sub>30</sub>N<sub>2</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	H	1	Total C N O 25 17 2 6	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
17	K	1	25	17	2	6	0	0
17	N	1	25	17	2	6	0	0
17	V	1	25	17	2	6	0	0
17	Y	1	25	17	2	6	0	0
17	b	1	25	17	2	6	0	0

- Molecule 18 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	A	9	Total 9	O 9	0	0
18	B	13	Total 13	O 13	0	0
18	C	18	Total 18	O 18	0	0
18	D	10	Total 10	O 10	0	0
18	E	7	Total 7	O 7	0	0
18	F	12	Total 12	O 12	0	0
18	G	19	Total 19	O 19	0	0
18	H	16	Total 16	O 16	0	0
18	I	14	Total 14	O 14	0	0
18	J	18	Total 18	O 18	0	0
18	K	30	Total 30	O 30	0	0
18	L	24	Total 24	O 24	0	0
18	M	27	Total 27	O 27	0	0
18	N	18	Total 18	O 18	0	0

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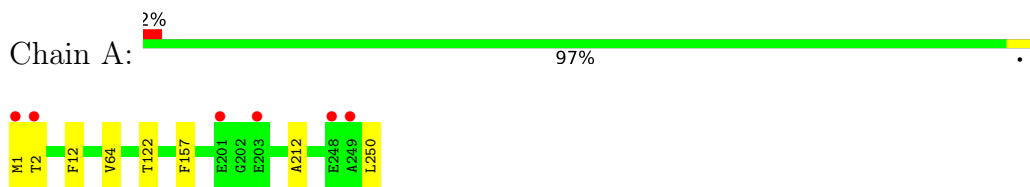
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
18	O	5	Total O 5 5	0	0
18	P	15	Total O 15 15	0	0
18	Q	16	Total O 16 16	0	0
18	R	8	Total O 8 8	0	0
18	S	7	Total O 7 7	0	0
18	T	14	Total O 14 14	0	0
18	U	15	Total O 15 15	0	0
18	V	17	Total O 17 17	0	0
18	W	11	Total O 11 11	0	0
18	X	17	Total O 17 17	0	0
18	Y	22	Total O 22 22	0	0
18	Z	25	Total O 25 25	0	0
18	a	27	Total O 27 27	0	0
18	b	20	Total O 20 20	0	0

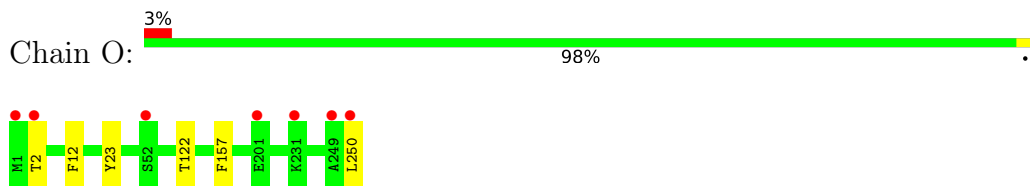
### 3 Residue-property plots

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.

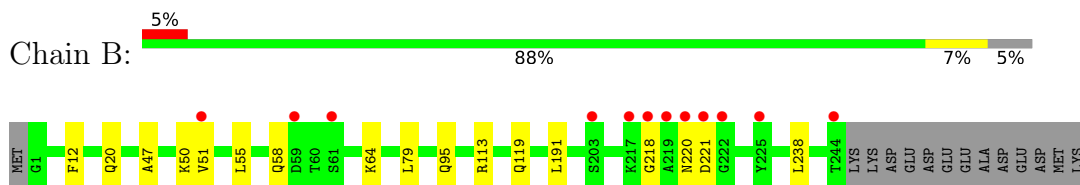
- Molecule 1: Proteasome subunit alpha type-2



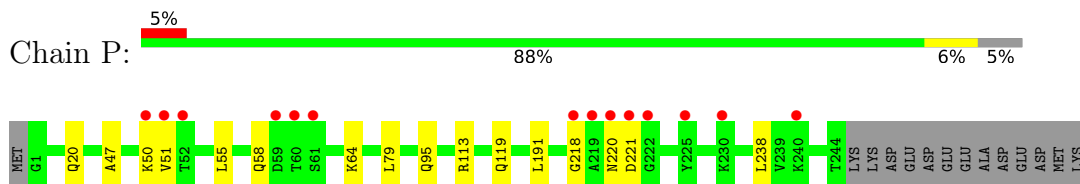
- Molecule 1: Proteasome subunit alpha type-2



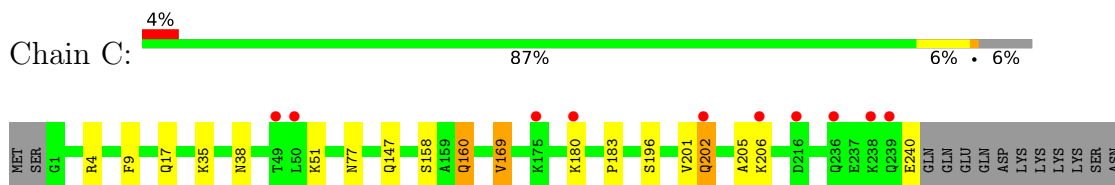
- Molecule 2: Proteasome subunit alpha type-3



- Molecule 2: Proteasome subunit alpha type-3




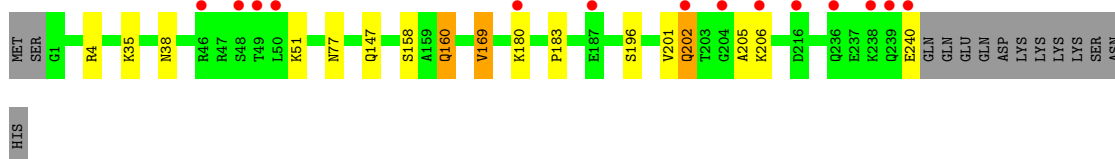
- Molecule 3: Proteasome subunit alpha type-4




HIS

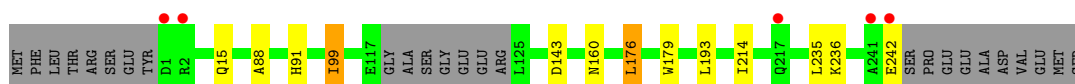
- Molecule 3: Proteasome subunit alpha type-4

Chain Q: 




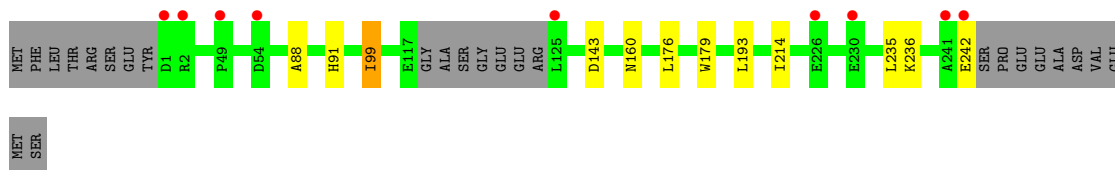
- Molecule 4: Proteasome subunit alpha type-5

Chain D: 



- Molecule 4: Proteasome subunit alpha type-5

Chain R: 

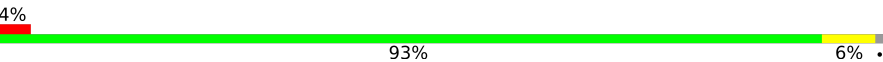


- Molecule 5: Proteasome subunit alpha type-6

Chain E: 




- Molecule 5: Proteasome subunit alpha type-6

Chain S: 



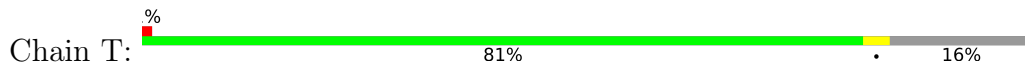
- Molecule 6: Probable proteasome subunit alpha type-7

Chain F: 



ALA  
ASN  
ALA  
THR  
THR  
ASP  
GLN  
GLU  
GLY  
ASP  
ASP  
ILE  
HIS  
LEU  
GLU

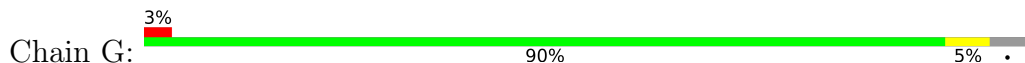
• Molecule 6: Probable proteasome subunit alpha type-7



MET THR THR SER ILE GLY T2 Q19 Q117 N123 S124 K139 L172 H178 E181 E201 D202 W214 Q240 W244 GLY ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP VAL MET SER SER ASP ASP ASP ASP ASN ALA ALA PRO VAL VAL ALA THR THR ASN ALA ALA ASN THR

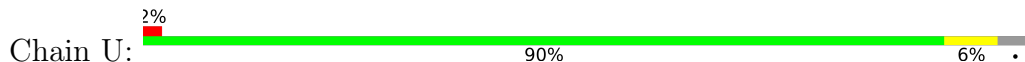
THR ASP GLN GLU GLY ILE HIS LEU GLU

• Molecule 7: Proteasome subunit alpha type-1



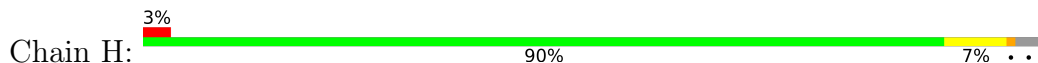
MET SER GLY ALA ALA ALA SER ALA ALA G2 Y3 F23 T26 R68 V73 N83 L115 L116 Q117 R122 M125 T133 Q167 T171 E188 E208 D222 R235 L236 A240 E241 Q242 ASP

• Molecule 7: Proteasome subunit alpha type-1



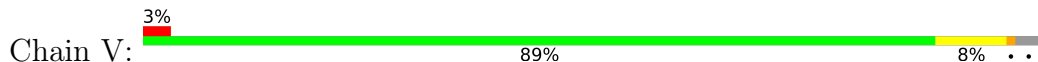
MET SER GLY ALA ALA ALA SER ALA ALA G2 P12 F23 T26 V73 N83 L115 S116 Q117 R122 M125 T133 Q167 T171 D183 E188 G206 T207 E208 D222 R235 L236 E243 Q242 ASP

• Molecule 8: Proteasome subunit beta type-2



T1 T2 I14 D17 S20 N30 L34 V55 L68 K84 L87 Y97 S112 I113 H114 L125 S169 R196 E197 E198 G221 D222 I223 Q224 E225 E226 VAL ASP ILE THR ALA

• Molecule 8: Proteasome subunit beta type-2



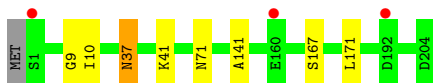
T1 T2 I14 D17 S20 N30 L34 V55 L68 L80 K84 L87 S112 I113 H114 T119 L125 S128 L127 D145 M165 R196 T210 G221 D222 I223 Q224 E225 E226 GLN VAL ASP ILE THR ALA

• Molecule 9: Proteasome subunit beta type-3

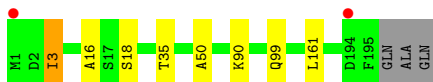


MET S1 G9 I10 N87 K41 N71 A141 L171 D177 D204

• Molecule 9: Proteasome subunit beta type-3



- Molecule 10: Proteasome subunit beta type-4



- Molecule 10: Proteasome subunit beta type-4



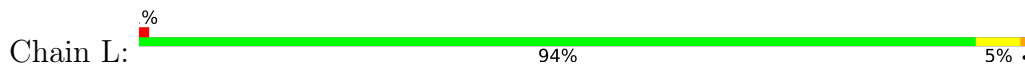
- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5



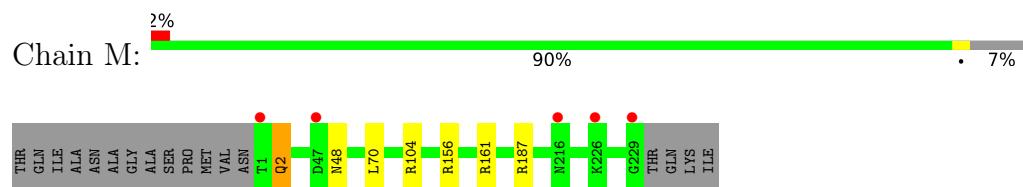
- Molecule 12: Proteasome subunit beta type-6



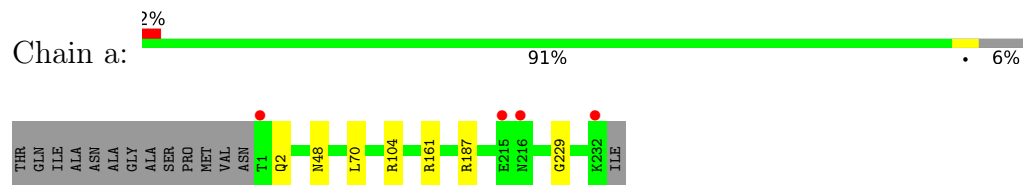
- Molecule 12: Proteasome subunit beta type-6



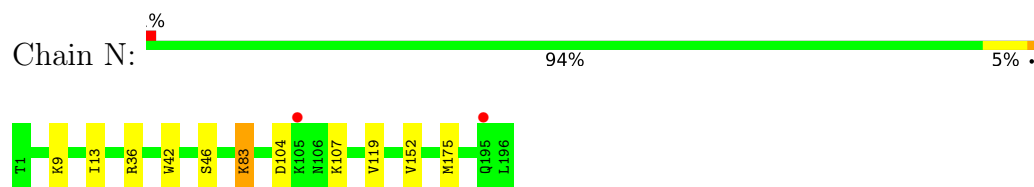
- Molecule 13: Proteasome subunit beta type-7



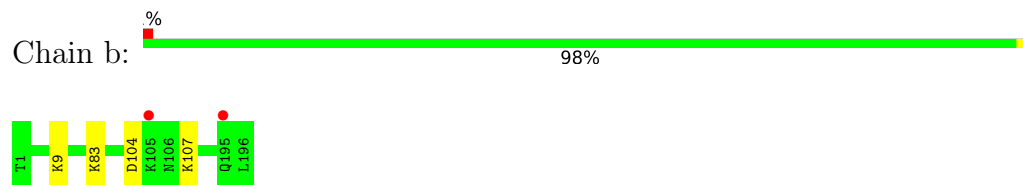
- Molecule 13: Proteasome subunit beta type-7



- 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, $\alpha$ , $\beta$ , $\gamma$	134.74Å 301.97Å 143.62Å 90.00° 112.95° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 15.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.2 (15.00-2.70) 96.8 (15.00-2.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.15 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.188 , 0.214 0.202 , 0.231	Depositor DCC
$R_{free}$ test set	13861 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	59.6	Xtrriage
Anisotropy	0.194	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 41.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	49937	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	78.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EPW, MG, 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	0.36	0/1952	0.58	0/2642
1	O	0.36	0/1952	0.57	0/2642
2	B	0.37	0/1934	0.61	0/2618
2	P	0.37	0/1934	0.61	0/2618
3	C	0.36	0/1910	0.63	0/2586
3	Q	0.36	0/1910	0.63	0/2586
4	D	0.35	0/1837	0.59	0/2475
4	R	0.35	0/1837	0.59	0/2475
5	E	0.36	0/1800	0.58	0/2433
5	S	0.35	0/1800	0.58	0/2433
6	F	0.36	0/1932	0.57	0/2609
6	T	0.36	0/1932	0.56	0/2609
7	G	0.37	0/1945	0.59	0/2634
7	U	0.37	0/1945	0.58	0/2634
8	H	0.35	0/1750	0.62	1/2373 (0.0%)
8	V	0.35	0/1750	0.62	1/2373 (0.0%)
9	I	0.36	0/1611	0.59	0/2174
9	W	0.35	0/1611	0.60	0/2174
10	J	0.35	0/1589	0.62	0/2142
10	X	0.36	0/1589	0.61	0/2142
11	K	0.37	0/1681	0.63	1/2274 (0.0%)
11	Y	0.36	0/1681	0.63	1/2274 (0.0%)
12	L	0.36	0/1795	0.60	0/2420
12	Z	0.36	0/1795	0.59	0/2420
13	M	0.37	0/1821	0.64	0/2470
13	a	0.37	0/1846	0.64	0/2503
14	N	0.36	0/1541	0.60	0/2087
14	b	0.36	0/1541	0.61	0/2087
All	All	0.36	0/50221	0.60	4/67907 (0.0%)

There are no bond length outliers.



All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	V	196	ARG	NE-CZ-NH1	5.72	123.16	120.30
8	H	196	ARG	NE-CZ-NH1	5.51	123.06	120.30
11	K	4	LEU	CA-CB-CG	5.47	127.88	115.30
11	Y	4	LEU	CA-CB-CG	5.34	127.58	115.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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	3	0
1	O	1915	0	1929	2	0
2	B	1904	0	1904	4	0
2	P	1904	0	1904	3	0
3	C	1881	0	1895	6	0
3	Q	1881	0	1895	4	0
4	D	1813	0	1797	5	0
4	R	1813	0	1797	3	0
5	E	1773	0	1775	4	0
5	S	1773	0	1775	4	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	4	0
8	H	1719	0	1718	6	0
8	V	1719	0	1718	7	0
9	I	1581	0	1574	5	0
9	W	1581	0	1574	5	0
10	J	1561	0	1569	3	0
10	X	1561	0	1569	2	0
11	K	1644	0	1594	6	0
11	Y	1644	0	1594	2	0
12	L	1757	0	1711	5	0
12	Z	1757	0	1711	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	1790	0	1793	2	0
13	a	1815	0	1821	0	0
14	N	1512	0	1480	6	0
14	b	1512	0	1480	0	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	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	25	0	0	1	0
17	K	25	0	0	0	0
17	N	25	0	0	2	0
17	V	25	0	0	0	0
17	Y	25	0	0	2	0
17	b	25	0	0	0	0
18	A	9	0	0	0	0
18	B	13	0	0	0	0
18	C	18	0	0	0	0
18	D	10	0	0	0	0
18	E	7	0	0	0	0
18	F	12	0	0	0	0
18	G	19	0	0	0	0
18	H	16	0	0	0	0
18	I	14	0	0	0	0
18	J	18	0	0	0	0
18	K	30	0	0	0	0
18	L	24	0	0	0	0
18	M	27	0	0	1	0
18	N	18	0	0	0	0
18	O	5	0	0	0	0
18	P	15	0	0	0	0
18	Q	16	0	0	0	0
18	R	8	0	0	0	0
18	S	7	0	0	1	0
18	T	14	0	0	0	0
18	U	15	0	0	0	0
18	V	17	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	W	11	0	0	0	0
18	X	17	0	0	0	0
18	Y	22	0	0	0	0
18	Z	25	0	0	0	0
18	a	27	0	0	0	0
18	b	20	0	0	0	0
All	All	49937	0	49074	94	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 (94) 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)
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.54	0.72
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.55	0.71
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.59	0.68
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.60	0.66
5:S:12:PHE:H	6:T:19:GLN:HE22	1.47	0.63
5:E:12:PHE:H	6:F:19:GLN:HE22	1.49	0.59
1:O:12:PHE:H	2:P:20:GLN:HE22	1.50	0.58
2:B:12:PHE:H	3:C:17:GLN:HE22	1.53	0.56
7:U:23:PHE:O	7:U:26:THR:HB	2.06	0.56
7:G:23:PHE:O	7:G:26:THR:HB	2.04	0.56
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.89	0.55
8:V:3:ILE:HD11	8:V:127:LEU:HB3	1.87	0.55
13:M:2:GLN:NE2	18:M:301:HOH:O	2.40	0.55
12:L:42:LYS:HD2	12:L:55:ASN:HD22	1.72	0.54
12:Z:42:LYS:HD2	12:Z:55:ASN:HD22	1.72	0.54
8:V:80:LEU:HD13	8:V:119:THR:HG21	1.90	0.54
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.90	0.54
6:F:123:ASN:HD22	6:F:124:SER:N	2.07	0.51
17:N:201:EPW:N20	17:N:201:EPW:C16	2.73	0.51
6:T:123:ASN:HD22	6:T:124:SER:N	2.07	0.51
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.93	0.49
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.59	0.49
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.94	0.49
7:G:73:VAL:HG12	7:G:133:THR:HB	1.95	0.48
8:H:87:LEU:HD12	8:H:113:ILE:HD13	1.95	0.48
12:L:3:ASN:HD22	12:L:4:PRO:HD2	1.79	0.48
11:K:176:ASN:ND2	11:K:190:ASN:HD22	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.94	0.48
8:V:87:LEU:HD12	8:V:113:ILE:HD13	1.95	0.48
6:T:123:ASN:HD22	6:T:123:ASN:C	2.17	0.48
12:Z:3:ASN:HD22	12:Z:4:PRO:HD2	1.78	0.48
1:A:12:PHE:H	2:B:20:GLN:HE22	1.61	0.48
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.95	0.47
6:F:123:ASN:HD22	6:F:123:ASN:C	2.18	0.47
7:U:73:VAL:HG12	7:U:133:THR:HB	1.96	0.47
11:K:3:THR:HG22	11:K:16:VAL:HG12	1.96	0.47
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.98	0.46
3:C:9:PHE:H	4:D:15:GLN:HE22	1.63	0.46
2:P:95:GLN:HE22	9:W:71:ASN:HD22	1.62	0.46
8:H:2:THR:OG1	8:H:169:SER:OG	2.32	0.45
8:V:84:LYS:HA	8:V:113:ILE:HD11	1.99	0.45
10:J:50:ALA:O	11:K:91:LYS:NZ	2.50	0.45
2:P:47:ALA:HB1	2:P:64:LYS:HD2	1.98	0.45
10:X:3:ILE:HG23	10:X:18:SER:HB3	1.99	0.45
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.97	0.45
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.52	0.45
11:Y:176:ASN:ND2	11:Y:190:ASN:HD22	2.15	0.45
8:H:84:LYS:HA	8:H:113:ILE:HD11	1.98	0.44
7:U:167:GLN:HE21	7:U:171:THR:HG23	1.83	0.44
10:J:3:ILE:HG23	10:J:18:SER:HB3	1.98	0.44
8:H:112:SER:HB3	8:H:125:LEU:HD13	2.00	0.44
13:M:156:ARG:HH11	8:V:165:ASN:HD22	1.64	0.44
14:N:152:VAL:HA	14:N:175:MET:HE1	2.00	0.44
8:V:112:SER:HB3	8:V:125:LEU:HD13	2.00	0.44
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.53	0.43
7:G:167:GLN:HE21	7:G:171:THR:HG23	1.82	0.43
17:Y:301:EPW:C18	17:Y:301:EPW:C24	2.96	0.43
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.00	0.43
8:H:1:THR:OG1	17:H:301:EPW:O10	2.37	0.43
14:N:13:ILE:HG21	14:N:175:MET:CE	2.49	0.43
9:W:37:ASN:C	9:W:37:ASN:HD22	2.22	0.42
3:C:201:VAL:O	3:C:202:GLN:CB	2.68	0.42
9:I:37:ASN:C	9:I:37:ASN:HD22	2.23	0.42
11:K:1:THR:O	11:K:130:GLY:HA3	2.19	0.42
9:W:10:ILE:HG21	9:W:141:ALA:HB3	2.02	0.42
5:S:92:ASN:HD21	12:Z:70:ASN:HD21	1.68	0.42
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.50	0.42
17:Y:301:EPW:C7	17:Y:301:EPW:C11	2.98	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:46:SER:HA	17:N:201:EPW:O3	2.20	0.41
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.49	0.41
11:K:128:CYS:HB2	11:K:137:TYR:CE2	2.55	0.41
5:E:92:ASN:HD21	12:L:70:ASN:HD21	1.67	0.41
12:Z:146:ILE:HG22	12:Z:150:LEU:HD22	2.02	0.41
9:I:10:ILE:HG21	9:I:141:ALA:HB3	2.02	0.41
12:L:146:ILE:HG22	12:L:150:LEU:HD22	2.02	0.41
14:N:36:ARG:HG3	14:N:42:TRP:CZ2	2.56	0.41
11:Y:38:ASN:HB2	11:Y:39:PRO:CD	2.51	0.41
12:Z:141:ALA:HB1	12:Z:195:HIS:NE2	2.35	0.41
9:I:141:ALA:HB2	9:I:177:ASP:HB2	2.02	0.41
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.54	0.41
1:A:1:MET:HG3	6:F:122:TYR:CZ	2.56	0.41
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	2.02	0.41
1:A:64:VAL:HG11	1:A:212:ALA:HB3	2.03	0.41
8:H:97:TYR:HE2	8:H:114:HIS:CE1	2.39	0.41
5:S:147:GLN:HG2	18:S:306:HOH:O	2.21	0.41
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.51	0.40
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.21	0.40
3:C:35:LYS:HG2	3:C:158:SER:O	2.21	0.40
4:D:176:LEU:HD22	5:E:55:LEU:CD2	2.51	0.40
8:V:210:THR:HG21	9:W:167:SER:HB3	2.02	0.40
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.69	0.40
11:K:12:ILE:HB	11:K:180:VAL:HB	2.04	0.40
3:C:169:VAL:HG23	3:C:196:SER:HB2	2.03	0.40
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.56	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%)	237 (96%)	10 (4%)	1 (0%)	34	60
1	O	248/250 (99%)	237 (96%)	10 (4%)	1 (0%)	34	60
2	B	242/258 (94%)	235 (97%)	3 (1%)	4 (2%)	9	23
2	P	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	9	23
3	C	238/254 (94%)	233 (98%)	2 (1%)	3 (1%)	12	30
3	Q	238/254 (94%)	233 (98%)	2 (1%)	3 (1%)	12	30
4	D	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
4	R	231/260 (89%)	228 (99%)	3 (1%)	0	100	100
5	E	229/234 (98%)	220 (96%)	9 (4%)	0	100	100
5	S	229/234 (98%)	220 (96%)	9 (4%)	0	100	100
6	F	241/288 (84%)	237 (98%)	4 (2%)	0	100	100
6	T	241/288 (84%)	237 (98%)	4 (2%)	0	100	100
7	G	239/252 (95%)	237 (99%)	2 (1%)	0	100	100
7	U	239/252 (95%)	237 (99%)	2 (1%)	0	100	100
8	H	224/232 (97%)	219 (98%)	5 (2%)	0	100	100
8	V	224/232 (97%)	219 (98%)	5 (2%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
9	W	202/205 (98%)	196 (97%)	6 (3%)	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%)	207 (99%)	3 (1%)	0	100	100
11	Y	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
12	L	220/222 (99%)	214 (97%)	6 (3%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	227/246 (92%)	219 (96%)	8 (4%)	0	100	100
13	a	230/246 (94%)	221 (96%)	8 (4%)	1 (0%)	34	60
14	N	194/196 (99%)	191 (98%)	3 (2%)	0	100	100
14	b	194/196 (99%)	191 (98%)	3 (2%)	0	100	100
All	All	6279/6614 (95%)	6122 (98%)	140 (2%)	17 (0%)	41	66

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
2	B	51	VAL
2	B	218	GLY
2	B	221	ASP
3	C	202	GLN
1	O	2	THR
2	P	51	VAL
2	P	221	ASP
3	Q	202	GLN
2	P	218	GLY
2	P	220	ASN
2	B	220	ASN
3	C	205	ALA
3	Q	205	ALA
13	a	229	GLY
3	Q	183	PRO
3	C	183	PRO

### 5.3.2 Protein sidechains [i](#)

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%)	206 (99%)	3 (1%)	67 86
1	O	209/209 (100%)	206 (99%)	3 (1%)	67 86
2	B	203/216 (94%)	195 (96%)	8 (4%)	32 61
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%)	186 (96%)	8 (4%)	30 59
4	R	194/215 (90%)	186 (96%)	8 (4%)	30 59
5	E	190/193 (98%)	182 (96%)	8 (4%)	30 58
5	S	190/193 (98%)	182 (96%)	8 (4%)	30 58
6	F	201/239 (84%)	192 (96%)	9 (4%)	27 55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	T	201/239 (84%)	192 (96%)	9 (4%)	27	55
7	G	206/210 (98%)	199 (97%)	7 (3%)	37	66
7	U	206/210 (98%)	198 (96%)	8 (4%)	32	61
8	H	185/190 (97%)	176 (95%)	9 (5%)	25	52
8	V	185/190 (97%)	175 (95%)	10 (5%)	22	47
9	I	172/173 (99%)	170 (99%)	2 (1%)	71	88
9	W	172/173 (99%)	170 (99%)	2 (1%)	71	88
10	J	173/175 (99%)	169 (98%)	4 (2%)	50	78
10	X	173/175 (99%)	169 (98%)	4 (2%)	50	78
11	K	169/169 (100%)	160 (95%)	9 (5%)	22	48
11	Y	169/169 (100%)	160 (95%)	9 (5%)	22	48
12	L	185/185 (100%)	179 (97%)	6 (3%)	39	68
12	Z	185/185 (100%)	180 (97%)	5 (3%)	44	74
13	M	195/208 (94%)	189 (97%)	6 (3%)	40	69
13	a	198/208 (95%)	192 (97%)	6 (3%)	41	70
14	N	162/162 (100%)	158 (98%)	4 (2%)	47	76
14	b	162/162 (100%)	158 (98%)	4 (2%)	47	76
All	All	5315/5540 (96%)	5128 (96%)	187 (4%)	36	65

All (187) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	50	LYS
2	B	55	LEU
2	B	58	GLN
2	B	79	LEU
2	B	113	ARG
2	B	119	GLN
2	B	191	LEU
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	51	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	206	LYS
3	C	240	GLU
4	D	99	ILE
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	71	LEU
5	E	116	GLN
5	E	184	ASN
5	E	188	LEU
5	E	202	ASP
5	E	231	LYS
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	172	LEU
6	F	181	GLU
6	F	201	GLU
6	F	202	ASP
6	F	214	TRP
6	F	240	GLN
7	G	83	ASN
7	G	115	LEU
7	G	122	ARG
7	G	125	MET
7	G	208	GLU
7	G	235	ARG
7	G	236	LEU
8	H	14	ILE
8	H	17	ASP
8	H	20	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
8	H	30	ASN
8	H	34	LEU
8	H	55	VAL
8	H	68	LEU
8	H	114	HIS
8	H	196	ARG
9	I	37	ASN
9	I	171	LEU
10	J	3	ILE
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
11	K	4	LEU
11	K	9	GLN
11	K	25	TRP
11	K	32	LYS
11	K	104	TYR
11	K	107	LYS
11	K	116	ASP
11	K	140	LEU
11	K	148	LEU
12	L	3	ASN
12	L	23	LEU
12	L	49	ASN
12	L	130	SER
12	L	136	CYS
12	L	150	LEU
13	M	2	GLN
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	161	ARG
13	M	187	ARG
14	N	9	LYS
14	N	83	LYS
14	N	104	ASP
14	N	107	LYS
1	O	122	THR
1	O	157	PHE
1	O	250	LEU
2	P	50	LYS
2	P	55	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	P	58	GLN
2	P	79	LEU
2	P	113	ARG
2	P	119	GLN
2	P	191	LEU
2	P	238	LEU
3	Q	4	ARG
3	Q	38	ASN
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	206	LYS
3	Q	240	GLU
4	R	99	ILE
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	71	LEU
5	S	116	GLN
5	S	184	ASN
5	S	188	LEU
5	S	202	ASP
5	S	231	LYS
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	172	LEU
6	T	181	GLU
6	T	201	GLU
6	T	202	ASP
6	T	214	TRP
6	T	240	GLN
7	U	83	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
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	14	ILE
8	V	17	ASP
8	V	20	SER
8	V	30	ASN
8	V	34	LEU
8	V	55	VAL
8	V	68	LEU
8	V	80	LEU
8	V	114	HIS
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU
10	X	3	ILE
10	X	35	THR
10	X	90	LYS
10	X	99	GLN
11	Y	4	LEU
11	Y	9	GLN
11	Y	25	TRP
11	Y	32	LYS
11	Y	104	TYR
11	Y	107	LYS
11	Y	116	ASP
11	Y	140	LEU
11	Y	148	LEU
12	Z	23	LEU
12	Z	49	ASN
12	Z	130	SER
12	Z	136	CYS
12	Z	150	LEU
13	a	2	GLN
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG

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Mol	Chain	Res	Type
13	a	187	ARG
14	b	9	LYS
14	b	83	LYS
14	b	104	ASP
14	b	107	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
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	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
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	30	ASN
7	G	83	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
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	22	GLN
8	H	30	ASN
8	H	165	ASN
8	H	189	ASN
9	I	37	ASN
10	J	55	GLN
10	J	63	ASN
11	K	85	ASN
11	K	176	ASN
11	K	208	ASN
12	L	3	ASN
12	L	49	ASN
12	L	55	ASN
12	L	70	ASN
12	L	79	HIS
12	L	158	ASN
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN
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
2	P	123	GLN
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

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
4	R	91	HIS
4	R	146	GLN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
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	22	GLN
8	V	30	ASN
8	V	165	ASN
8	V	189	ASN
9	W	37	ASN
10	X	55	GLN
11	Y	85	ASN
11	Y	176	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	55	ASN
12	Z	70	ASN
12	Z	80	ASN
12	Z	158	ASN
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN

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Mol	Chain	Res	Type
13	a	108	ASN
13	a	149	HIS
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 monosaccharides 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	EPW	V	301	8	24,24,25	1.13	1 (4%)	30,33,35	1.26	1 (3%)
17	EPW	Y	301	11	24,24,25	1.13	3 (12%)	30,33,35	1.62	7 (23%)
17	EPW	H	301	8	24,24,25	1.54	2 (8%)	30,33,35	1.39	3 (10%)
17	EPW	N	201	14	24,24,25	0.83	2 (8%)	30,33,35	1.85	11 (36%)
17	EPW	K	301	11	24,24,25	1.04	1 (4%)	30,33,35	1.65	7 (23%)
17	EPW	b	201	14	24,24,25	1.01	3 (12%)	30,33,35	1.65	9 (30%)



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	EPW	V	301	8	-	0/38/38/40	-
17	EPW	Y	301	11	-	3/38/38/40	-
17	EPW	H	301	8	-	0/38/38/40	-
17	EPW	N	201	14	-	8/38/38/40	-
17	EPW	K	301	11	-	5/38/38/40	-
17	EPW	b	201	14	-	7/38/38/40	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	H	301	EPW	C4-C5	-4.24	1.48	1.55
17	H	301	EPW	C4-C9	-3.95	1.50	1.54
17	V	301	EPW	C4-C5	-3.09	1.50	1.55
17	b	201	EPW	C4-C9	-2.77	1.51	1.54
17	b	201	EPW	C4-C5	-2.59	1.51	1.55
17	Y	301	EPW	C4-C9	-2.35	1.52	1.54
17	K	301	EPW	C4-C5	-2.25	1.51	1.55
17	N	201	EPW	C4-C9	-2.22	1.52	1.54
17	N	201	EPW	O27-C25	-2.20	1.23	1.30
17	Y	301	EPW	C9-C11	-2.18	1.48	1.52
17	Y	301	EPW	C4-C5	-2.17	1.52	1.55
17	b	201	EPW	O27-C25	-2.02	1.23	1.30

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	H	301	EPW	C6-C5-C4	-4.50	103.39	111.74
17	K	301	EPW	C15-C14-C18	-4.31	100.60	111.38
17	Y	301	EPW	C15-C14-C18	-4.11	101.10	111.38
17	N	201	EPW	C21-N20-C18	3.89	131.81	121.89
17	b	201	EPW	C21-N20-C18	3.59	131.03	121.89
17	V	301	EPW	C6-C5-C4	-3.44	105.35	111.74
17	Y	301	EPW	C9-C11-N13	-3.18	111.87	116.25
17	Y	301	EPW	C9-C4-C1	-3.10	104.23	110.65
17	K	301	EPW	C15-C14-N13	-3.09	103.79	111.43
17	N	201	EPW	C18-C14-N13	3.02	118.59	110.36
17	N	201	EPW	C9-C4-C1	-2.93	104.57	110.65
17	K	301	EPW	C9-C4-C1	-2.88	104.68	110.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	b	201	EPW	C9-C4-C1	-2.78	104.88	110.65
17	Y	301	EPW	C15-C14-N13	-2.78	104.56	111.43
17	K	301	EPW	C9-C11-N13	-2.75	112.46	116.25
17	b	201	EPW	C15-C14-N13	-2.66	104.85	111.43
17	N	201	EPW	C15-C14-C18	-2.52	105.07	111.38
17	N	201	EPW	C15-C14-N13	-2.50	105.25	111.43
17	N	201	EPW	C14-C18-N20	-2.49	111.11	116.48
17	b	201	EPW	C23-C22-C24	-2.30	104.16	110.59
17	N	201	EPW	C22-C21-N20	2.28	117.07	111.43
17	N	201	EPW	C6-C5-C4	-2.27	107.53	111.74
17	K	301	EPW	C6-C5-C4	-2.25	107.56	111.74
17	b	201	EPW	O3-C1-C4	-2.24	119.57	125.23
17	N	201	EPW	C22-C21-C25	2.21	116.09	111.05
17	b	201	EPW	C18-C14-N13	2.19	116.31	110.36
17	Y	301	EPW	O12-C11-N13	2.16	126.92	122.93
17	b	201	EPW	C22-C21-C25	2.14	115.92	111.05
17	K	301	EPW	C24-C22-C21	-2.13	105.14	111.16
17	H	301	EPW	C7-C5-C4	-2.08	107.88	111.74
17	Y	301	EPW	O3-C1-C4	-2.06	120.01	125.23
17	N	201	EPW	O19-C18-N20	2.04	126.70	122.93
17	H	301	EPW	C22-C21-C25	-2.04	106.41	111.05
17	N	201	EPW	C9-C11-N13	-2.03	113.46	116.25
17	b	201	EPW	C25-C21-N20	-2.03	105.85	110.28
17	Y	301	EPW	C6-C5-C4	-2.02	107.99	111.74
17	b	201	EPW	C6-C5-C4	-2.01	108.00	111.74
17	K	301	EPW	O3-C1-C4	-2.01	120.16	125.23

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	K	301	EPW	O12-C11-C9-O10
17	N	201	EPW	C22-C21-N20-C18
17	Y	301	EPW	O12-C11-C9-O10
17	b	201	EPW	C22-C21-N20-C18
17	N	201	EPW	O12-C11-C9-O10
17	b	201	EPW	O12-C11-C9-O10
17	K	301	EPW	N13-C11-C9-O10
17	N	201	EPW	N13-C11-C9-O10
17	Y	301	EPW	N13-C11-C9-O10
17	N	201	EPW	N20-C21-C25-O26
17	b	201	EPW	N20-C21-C25-O26

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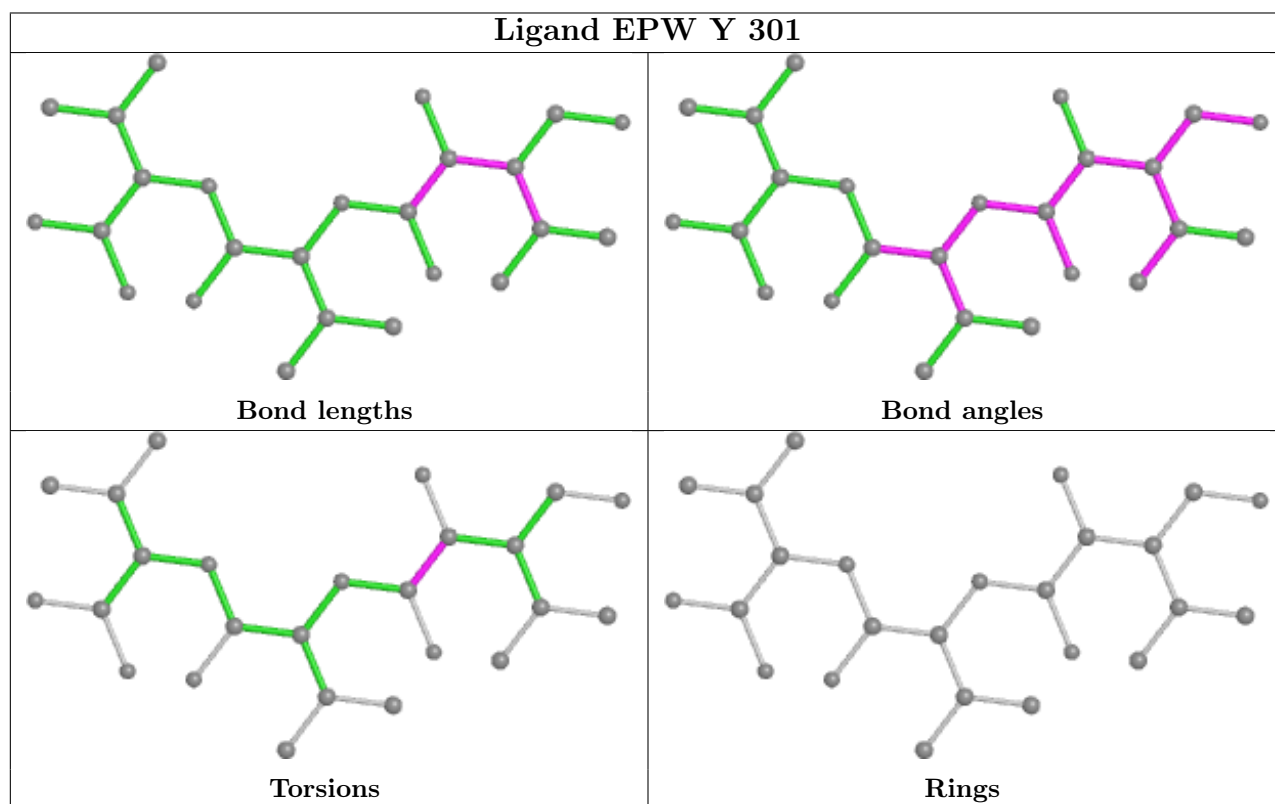
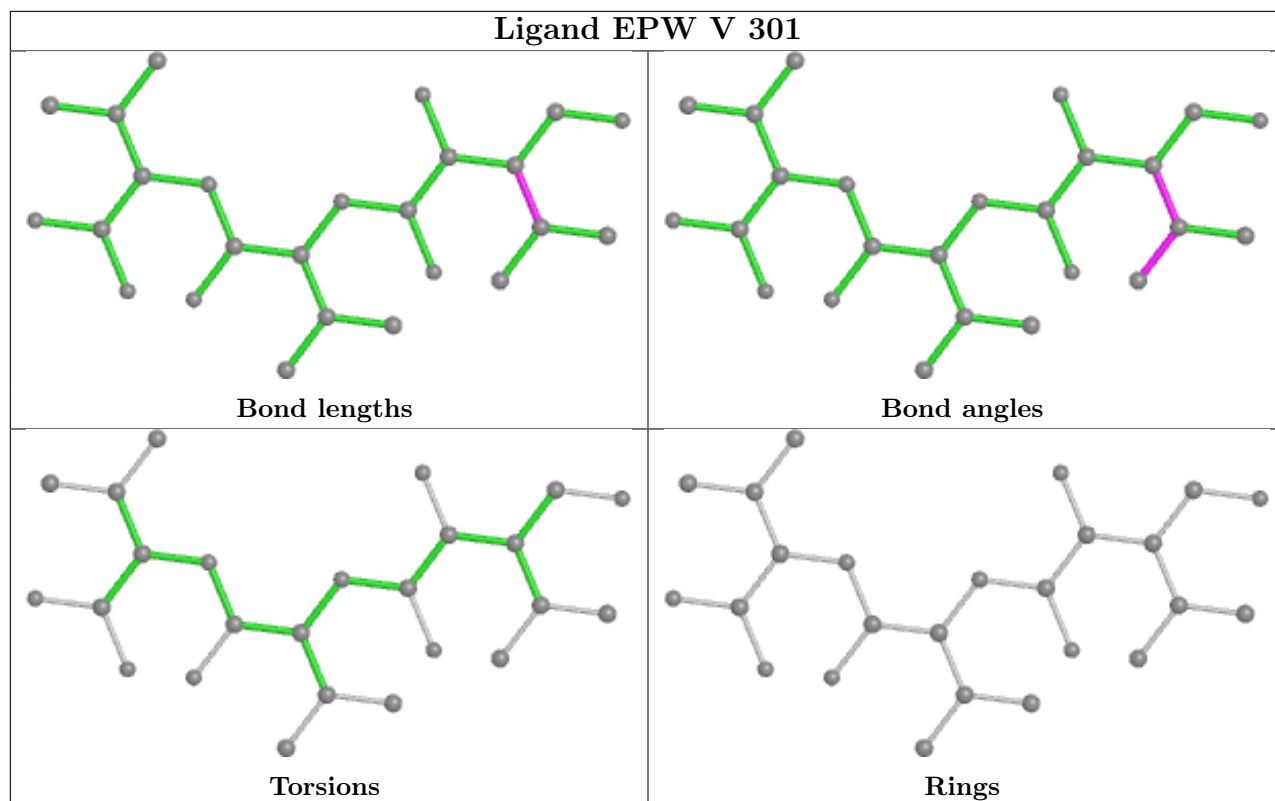
Mol	Chain	Res	Type	Atoms
17	b	201	EPW	C22-C21-C25-O26
17	b	201	EPW	C22-C21-C25-O27
17	N	201	EPW	N20-C21-C25-O27
17	b	201	EPW	N20-C21-C25-O27
17	K	301	EPW	C22-C21-C25-O26
17	K	301	EPW	C22-C21-C25-O27
17	N	201	EPW	C22-C21-C25-O26
17	N	201	EPW	C22-C21-C25-O27
17	b	201	EPW	N13-C11-C9-O10
17	N	201	EPW	O12-C11-C9-C4
17	Y	301	EPW	O12-C11-C9-C4
17	K	301	EPW	O12-C11-C9-C4

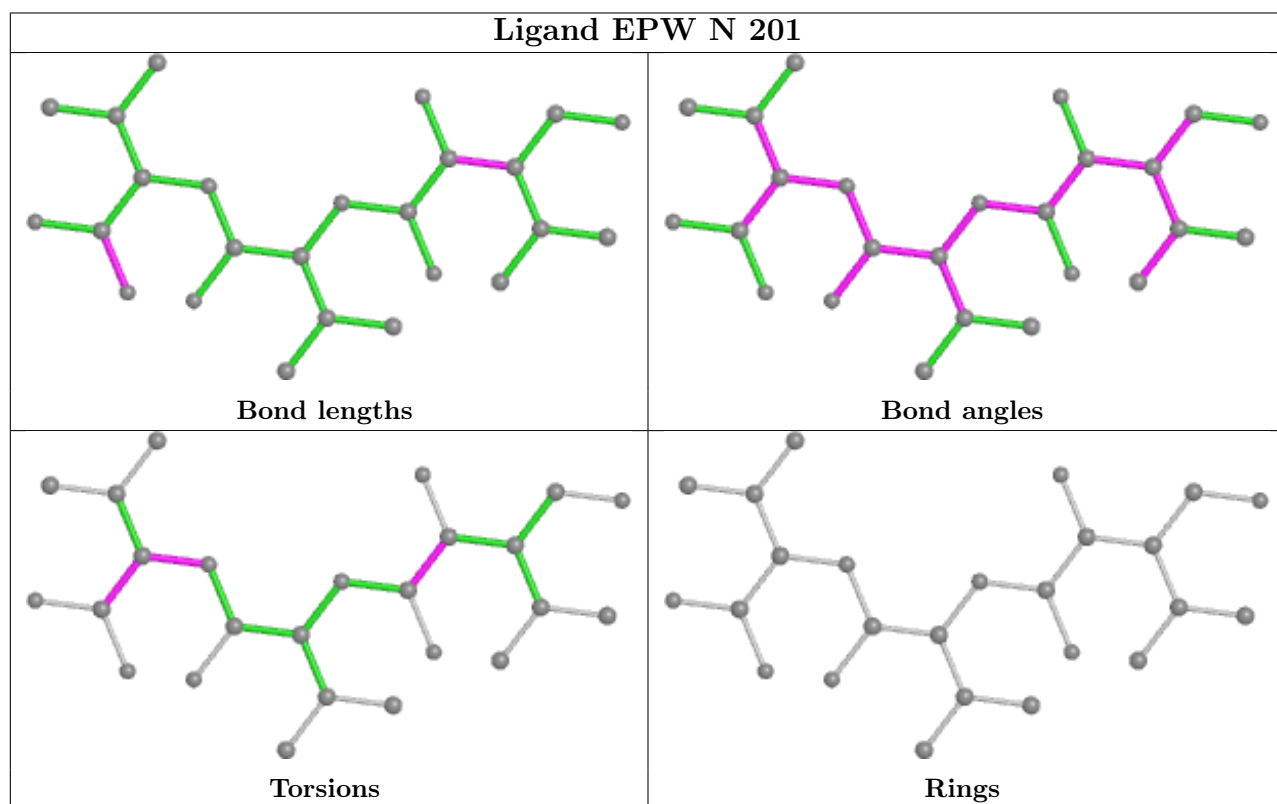
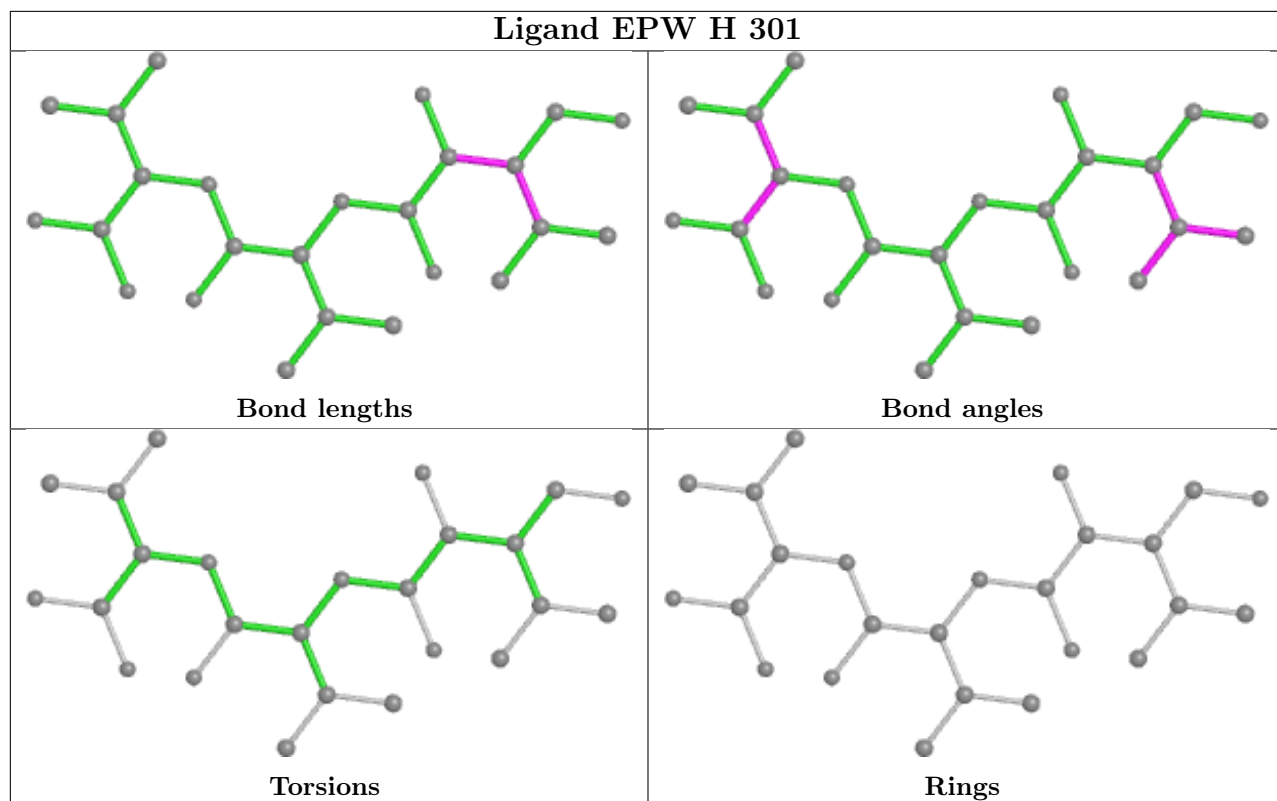
There are no ring outliers.

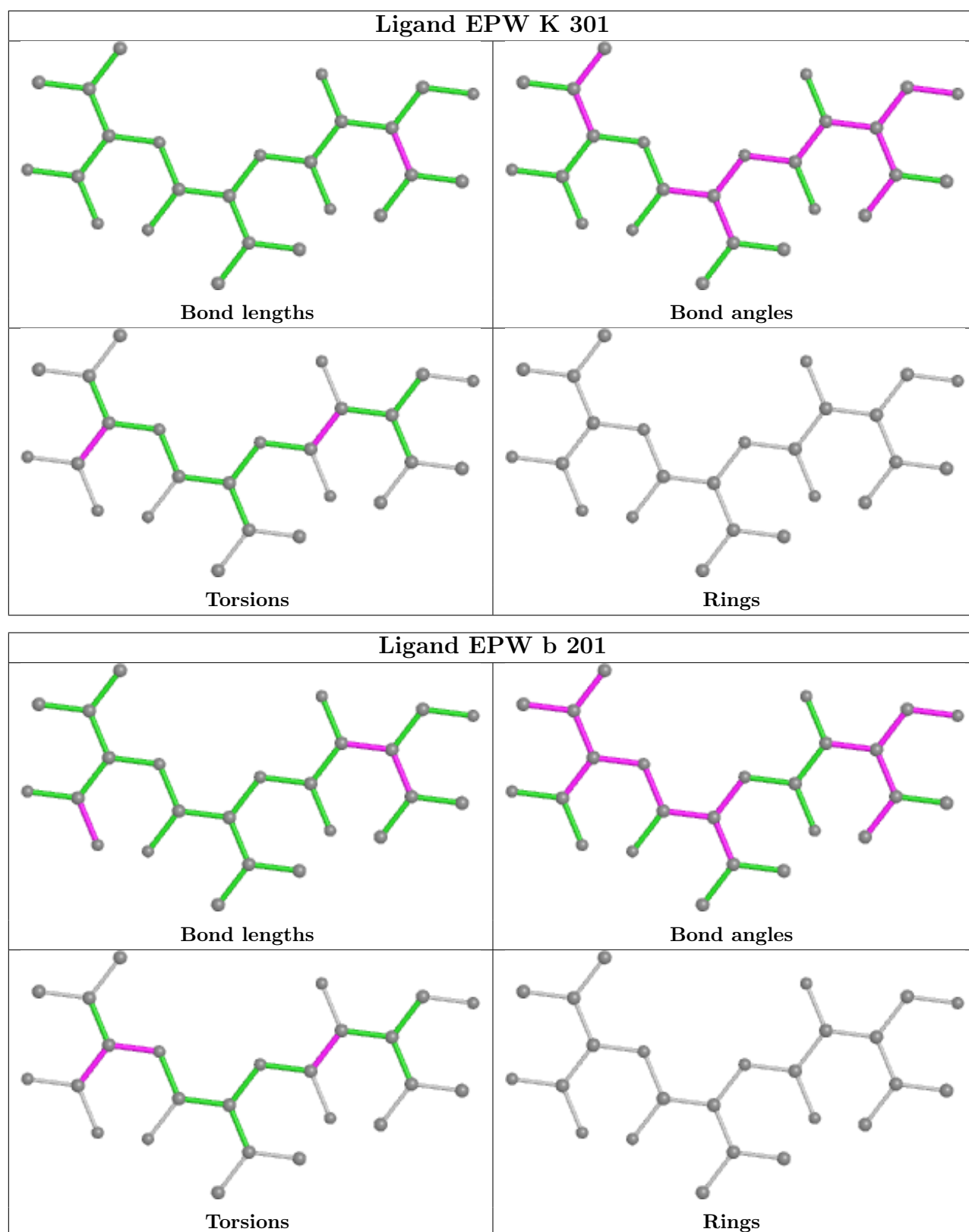
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	Y	301	EPW	2	0
17	H	301	EPW	1	0
17	N	201	EPW	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.







## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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%)	-0.28	6 (2%) 59 60	51, 68, 109, 148	0
1	O	250/250 (100%)	-0.16	7 (2%) 53 54	57, 77, 126, 152	0
2	B	244/258 (94%)	-0.08	12 (4%) 29 28	52, 78, 136, 193	0
2	P	244/258 (94%)	-0.08	14 (5%) 23 22	57, 78, 132, 185	0
3	C	240/254 (94%)	-0.11	10 (4%) 36 35	52, 79, 142, 167	0
3	Q	240/254 (94%)	0.07	14 (5%) 23 22	62, 93, 174, 195	0
4	D	235/260 (90%)	-0.26	5 (2%) 63 65	58, 80, 115, 157	0
4	R	235/260 (90%)	-0.16	9 (3%) 40 39	60, 86, 131, 169	0
5	E	231/234 (98%)	-0.15	6 (2%) 56 57	55, 81, 121, 160	0
5	S	231/234 (98%)	-0.09	9 (3%) 39 38	61, 91, 141, 168	0
6	F	243/288 (84%)	-0.32	5 (2%) 63 65	53, 75, 128, 153	0
6	T	243/288 (84%)	-0.32	4 (1%) 72 74	56, 83, 141, 172	0
7	G	241/252 (95%)	-0.41	8 (3%) 46 46	49, 68, 104, 149	0
7	U	241/252 (95%)	-0.33	6 (2%) 57 59	55, 73, 108, 162	0
8	H	226/232 (97%)	-0.29	7 (3%) 49 49	45, 64, 104, 180	0
8	V	226/232 (97%)	-0.21	7 (3%) 49 49	48, 68, 106, 195	0
9	I	204/205 (99%)	-0.55	0 100 100	47, 63, 93, 121	0
9	W	204/205 (99%)	-0.48	3 (1%) 73 76	49, 64, 95, 125	0
10	J	195/198 (98%)	-0.40	2 (1%) 82 83	49, 66, 93, 144	0
10	X	195/198 (98%)	-0.40	2 (1%) 82 83	52, 68, 94, 156	0
11	K	212/212 (100%)	-0.49	1 (0%) 91 92	39, 64, 89, 110	0
11	Y	212/212 (100%)	-0.48	1 (0%) 91 92	50, 67, 95, 115	0
12	L	222/222 (100%)	-0.47	2 (0%) 84 85	49, 67, 104, 138	0
12	Z	222/222 (100%)	-0.39	1 (0%) 91 92	47, 68, 103, 142	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
13	M	229/246 (93%)	-0.43	5 (2%) 62 63	46, 67, 100, 119	0
13	a	232/246 (94%)	-0.45	4 (1%) 70 72	45, 66, 93, 114	0
14	N	196/196 (100%)	-0.53	2 (1%) 82 83	47, 60, 91, 120	0
14	b	196/196 (100%)	-0.50	2 (1%) 82 83	45, 63, 97, 127	0
All	All	6339/6614 (95%)	-0.30	154 (2%) 59 60	39, 72, 123, 195	0

All (154) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	V	224	GLN	12.7
2	P	219	ALA	9.8
3	Q	50	LEU	7.8
8	H	223	ILE	7.7
8	H	224	GLN	7.7
2	B	221	ASP	7.6
8	V	226	GLU	7.3
8	V	222	ASP	7.1
8	V	225	GLU	7.1
10	X	1	MET	7.0
2	P	220	ASN	6.9
8	V	223	ILE	6.7
8	H	226	GLU	6.5
2	B	220	ASN	6.1
3	Q	49	THR	5.9
1	A	2	THR	5.9
1	O	2	THR	5.8
2	P	221	ASP	5.7
8	H	225	GLU	5.6
8	H	222	ASP	5.4
2	P	51	VAL	5.3
8	V	221	CYS	4.9
2	B	51	VAL	4.9
13	M	229	GLY	4.8
7	U	242	GLN	4.7
2	B	219	ALA	4.4
10	J	1	MET	4.3
5	E	202	ASP	4.3
3	Q	206	LYS	4.2
3	C	206	LYS	4.1
9	W	1	SER	4.1
4	R	241	ALA	4.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	C	238	LYS	3.9
2	P	59	ASP	3.8
1	O	249	ALA	3.8
3	Q	238	LYS	3.8
3	Q	204	GLY	3.7
3	Q	236	GLN	3.7
8	H	221	CYS	3.6
4	R	1	ASP	3.6
6	F	205	GLU	3.6
5	S	180	LYS	3.5
10	X	194	ASP	3.5
4	D	1	ASP	3.4
5	S	173	ARG	3.4
7	U	222	ASP	3.4
4	D	2	ARG	3.4
2	B	61	SER	3.4
5	S	202	ASP	3.4
12	Z	174	TYR	3.3
2	P	52	THR	3.3
2	B	218	GLY	3.3
3	C	50	LEU	3.3
12	L	174	TYR	3.3
2	P	225	TYR	3.3
13	a	232	LYS	3.2
14	N	195	GLN	3.2
4	R	125	LEU	3.2
1	O	1	MET	3.1
2	P	60	THR	3.1
3	Q	202	GLN	3.1
13	M	1	THR	3.0
13	M	216	ASN	3.0
7	G	68	ARG	3.0
13	a	1	THR	3.0
6	F	181	GLU	3.0
3	C	236	GLN	3.0
7	G	2	GLY	3.0
2	B	203	SER	2.9
7	U	188	GLU	2.9
2	P	222	GLY	2.9
3	C	49	THR	2.8
14	b	105	LYS	2.8
3	Q	187	GLU	2.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	1	MET	2.8
3	C	216	ASP	2.8
11	K	212	GLY	2.8
6	F	244	ASN	2.7
3	C	180	LYS	2.7
3	Q	240	GLU	2.7
5	S	29	LYS	2.7
2	P	240	LYS	2.6
5	E	217	LYS	2.6
7	G	188	GLU	2.6
1	O	201	GLU	2.6
4	D	241	ALA	2.6
6	F	229	GLY	2.6
8	H	198	GLU	2.6
1	A	249	ALA	2.6
3	C	202	GLN	2.6
5	E	54	GLU	2.6
7	G	222	ASP	2.5
5	E	233	ILE	2.5
10	J	194	ASP	2.5
4	D	242	GLU	2.5
5	S	203	GLU	2.5
6	T	201	GLU	2.5
6	F	215	CYS	2.5
13	M	226	LYS	2.5
3	Q	46	ARG	2.5
1	A	248	GLU	2.4
2	P	50	LYS	2.4
3	C	239	GLN	2.4
3	Q	216	ASP	2.4
4	R	242	GLU	2.4
13	M	47	ASP	2.4
1	O	250	LEU	2.4
4	R	54	ASP	2.4
4	D	217	GLN	2.4
1	O	52	SER	2.4
2	P	61	SER	2.4
14	N	105	LYS	2.4
2	B	217	LYS	2.3
5	S	54	GLU	2.3
1	O	231	LYS	2.3
2	B	59	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
7	U	241	GLU	2.3
6	T	2	THR	2.3
1	A	201	GLU	2.3
5	S	3	ASN	2.3
4	R	226	GLU	2.3
5	E	201	ARG	2.3
7	U	206	GLY	2.3
14	b	195	GLN	2.3
3	Q	239	GLN	2.2
11	Y	212	GLY	2.2
5	E	173	ARG	2.2
12	L	210	ASP	2.2
3	Q	180	LYS	2.2
2	B	244	THR	2.2
5	S	122	TYR	2.2
7	G	240	ALA	2.2
4	R	49	PRO	2.2
1	A	203	GLU	2.2
7	G	241	GLU	2.2
13	a	216	ASN	2.2
7	G	242	GLN	2.2
9	W	160	GLU	2.1
2	P	230	LYS	2.1
3	C	175	LYS	2.1
8	V	145	ASP	2.1
3	Q	48	SER	2.1
2	B	222	GLY	2.1
2	P	218	GLY	2.1
6	T	178	HIS	2.1
5	S	165	GLN	2.1
4	R	2	ARG	2.1
7	G	3	TYR	2.1
13	a	215	GLU	2.1
7	U	183	ASP	2.1
9	W	192	ASP	2.1
6	T	181	GLU	2.1
2	B	225	TYR	2.0
4	R	230	GLU	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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

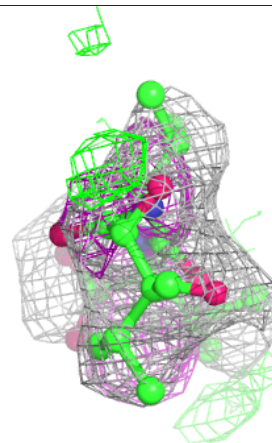
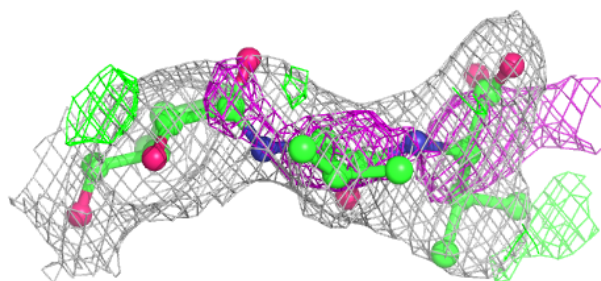
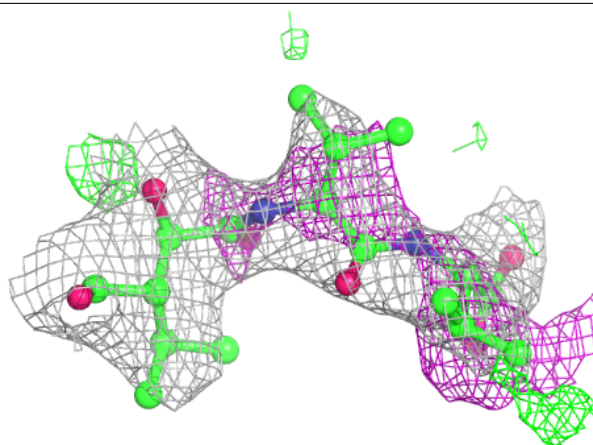
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
17	EPW	b	201	25/26	0.85	0.28	59,75,90,92	0
17	EPW	Y	301	25/26	0.86	0.23	61,73,88,99	0
17	EPW	N	201	25/26	0.88	0.24	59,73,80,85	0
17	EPW	K	301	25/26	0.89	0.22	58,73,86,96	0
15	MG	Z	301	1/1	0.90	0.45	79,79,79,79	0
15	MG	V	302	1/1	0.91	0.22	93,93,93,93	0
17	EPW	V	301	25/26	0.92	0.21	53,60,73,81	0
17	EPW	H	301	25/26	0.93	0.19	58,61,71,77	0
15	MG	G	301	1/1	0.94	0.07	62,62,62,62	0
15	MG	I	301	1/1	0.95	0.42	88,88,88,88	0
15	MG	W	301	1/1	0.97	0.40	76,76,76,76	0
15	MG	N	202	1/1	0.98	0.09	54,54,54,54	0
15	MG	Y	302	1/1	0.98	0.14	76,76,76,76	0
15	MG	K	302	1/1	0.98	0.09	59,59,59,59	0
16	CL	G	302	1/1	0.99	0.15	55,55,55,55	0
16	CL	U	301	1/1	0.99	0.14	62,62,62,62	0

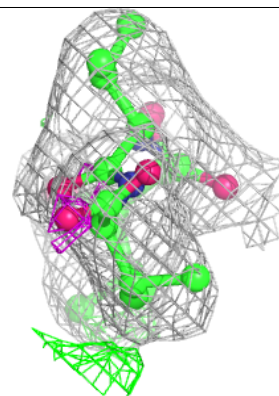
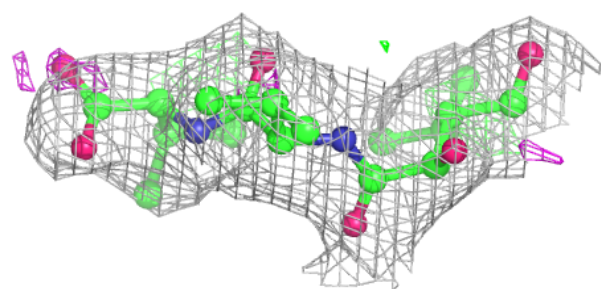
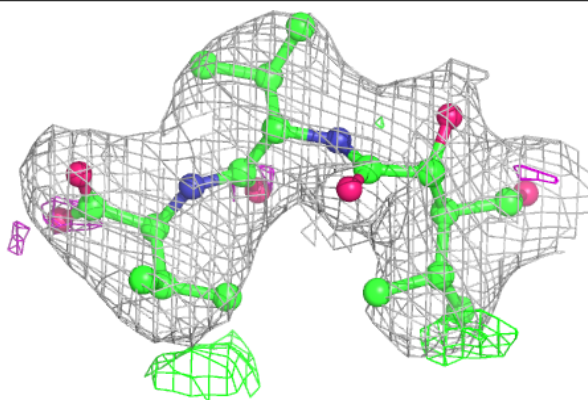
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around EPW b 201:**

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

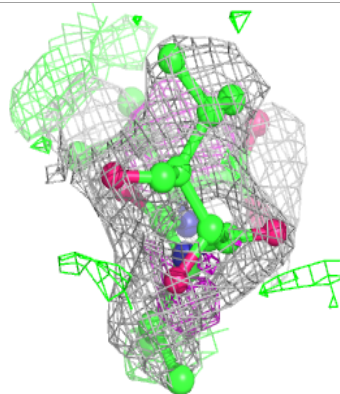
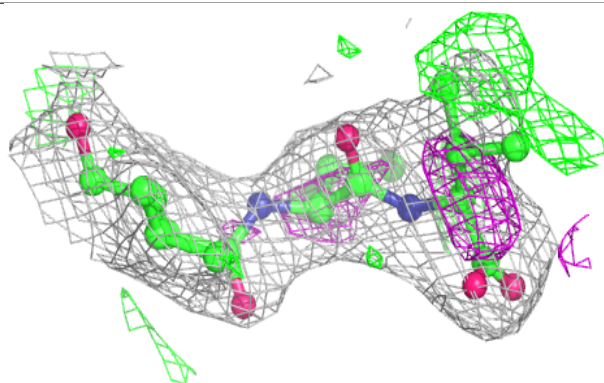
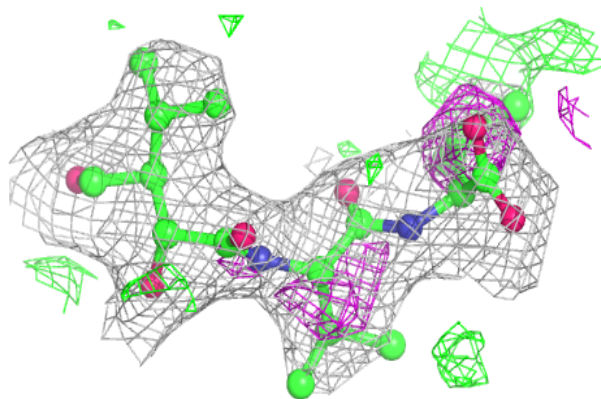
**Electron density around EPW Y 301:**

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

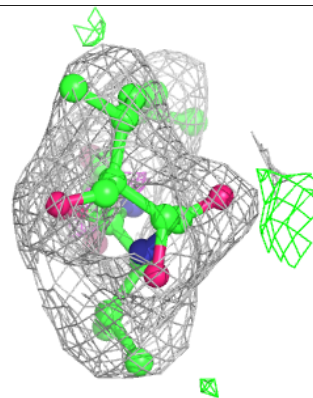
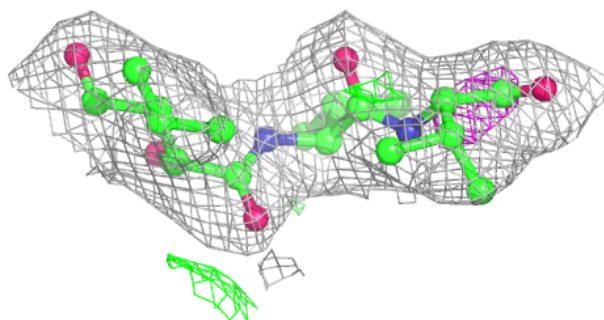
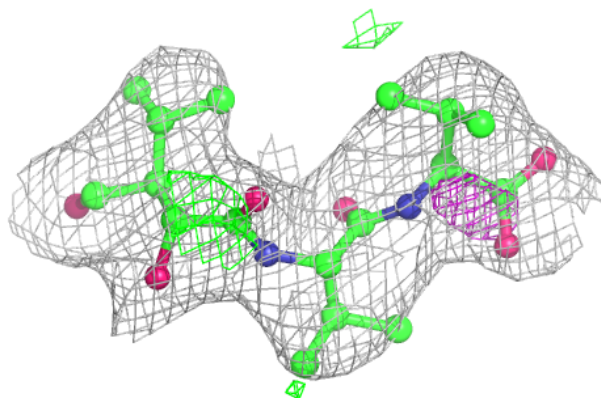


**Electron density around EPW N 201:**

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

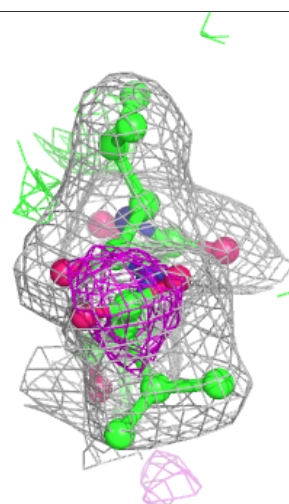
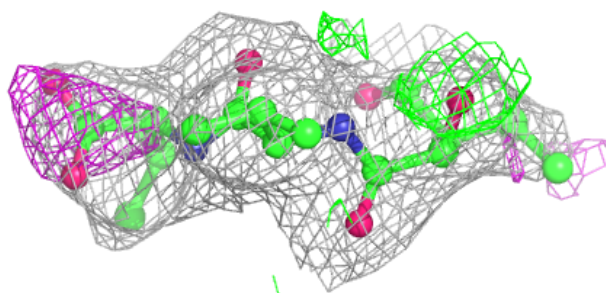
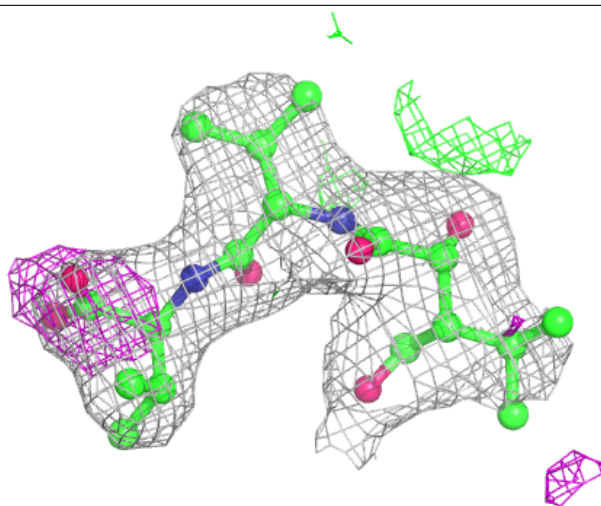
**Electron density around EPW K 301:**

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

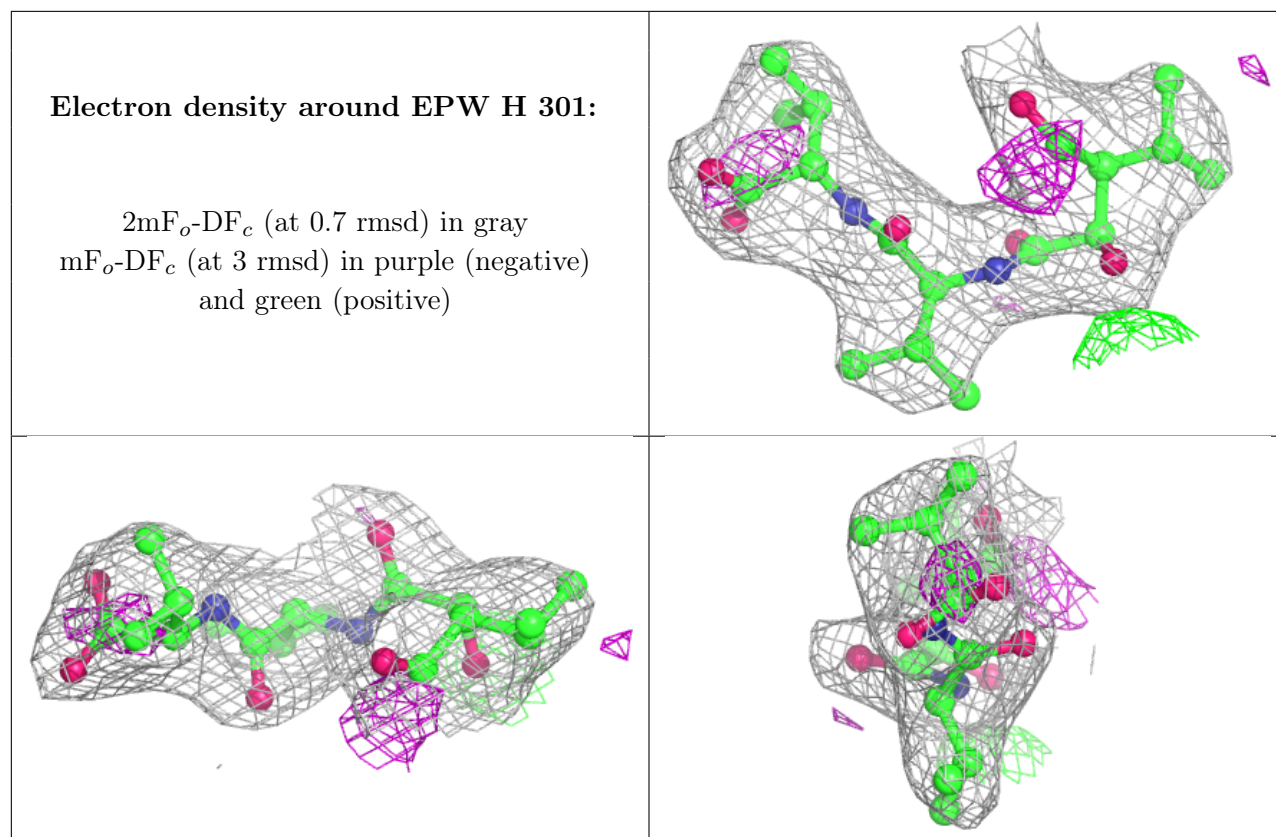


**Electron density around EPW V 301:**

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







## 6.5 Other polymers [i](#)

There are no such residues in this entry.