



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 14, 2024 – 06:46 am GMT

PDB ID : 6HVR
Title : Yeast 20S proteasome with human beta2i (1-53) in complex with 16
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-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

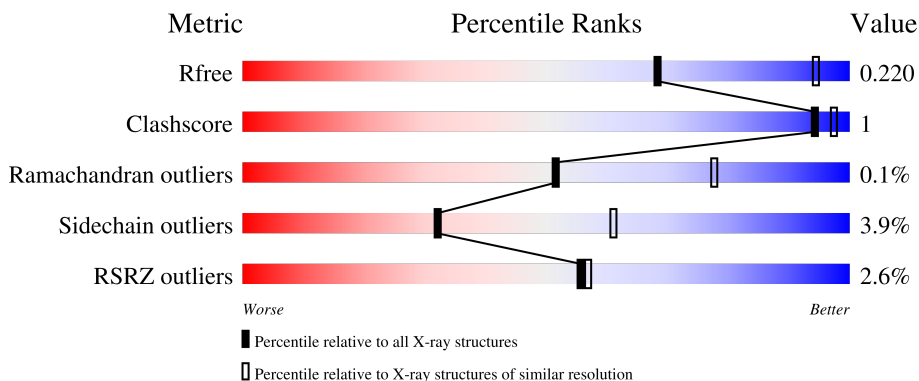
1 Overall quality at a glance i

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

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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	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 18 unique types of molecules in this entry. The entry contains 50153 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-10, Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	226	Total 1716	C 1081	N 291	O 336	S 8	0	0	0
8	V	223	Total 1688	C 1066	N 287	O 327	S 8	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	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	I	2	Total	Mg	0	0
			2	2		

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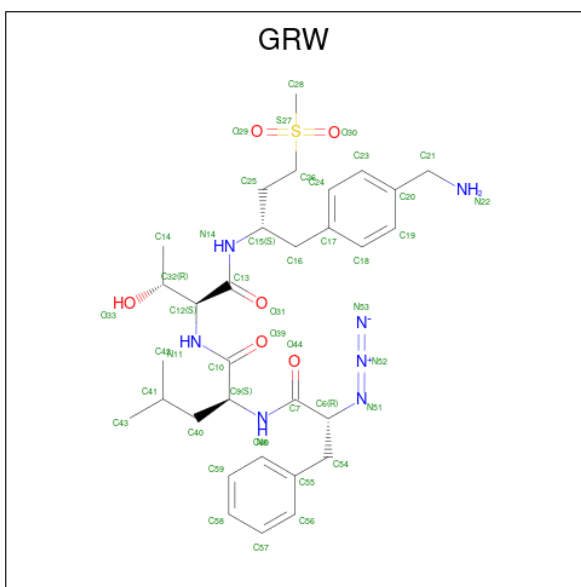
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	K	1	Total Mg 1 1	0	0
15	L	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	W	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0

- 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 (2 {S})- {N}-[(2 {S},3 {R})-1-[[2 {S})-1-[4-(aminomethyl)phenyl]-4-methylsulfonyl-butan-2-yl]amino]-3-oxidanyl-1-oxidanylidene-butan-2-yl]-2-[[2 {R})-2-azido-3-phenyl-propanoyl]amino]-4-methyl-pentanamide (three-letter code: GRW) (formula: C₃₁H₄₅N₇O₆S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	H	1	Total C N O S 45 31 7 6 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	K	1	Total	C	N	O	S	0	0
			45	31	7	6	1		
17	V	1	Total	C	N	O	S	0	0
			45	31	7	6	1		
17	Y	1	Total	C	N	O	S	0	0
			45	31	7	6	1		

- Molecule 18 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	A	20	Total	O	0	0
			20	20		
18	B	20	Total	O	0	0
			20	20		
18	C	20	Total	O	0	0
			20	20		
18	D	21	Total	O	0	0
			21	21		
18	E	11	Total	O	0	0
			11	11		
18	F	27	Total	O	0	0
			27	27		
18	G	24	Total	O	0	0
			24	24		
18	H	37	Total	O	0	0
			37	37		
18	I	22	Total	O	0	0
			22	22		
18	J	24	Total	O	0	0
			24	24		
18	K	32	Total	O	0	0
			32	32		
18	L	31	Total	O	0	0
			31	31		
18	M	31	Total	O	0	0
			31	31		
18	N	21	Total	O	0	0
			21	21		
18	O	13	Total	O	0	0
			13	13		
18	P	23	Total	O	0	0
			23	23		

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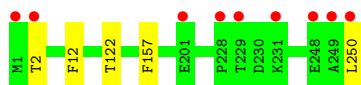
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	Q	12	Total 12	O 12	0	0
18	R	18	Total 18	O 18	0	0
18	S	10	Total 10	O 10	0	0
18	T	21	Total 21	O 21	0	0
18	U	29	Total 29	O 29	0	0
18	V	28	Total 28	O 28	0	0
18	W	16	Total 16	O 16	0	0
18	X	23	Total 23	O 23	0	0
18	Y	24	Total 24	O 24	0	0
18	Z	24	Total 24	O 24	0	0
18	a	27	Total 27	O 27	0	0
18	b	22	Total 22	O 22	0	0

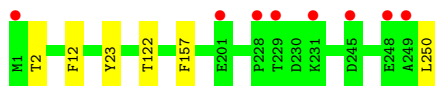
3 Residue-property plots [i](#)

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

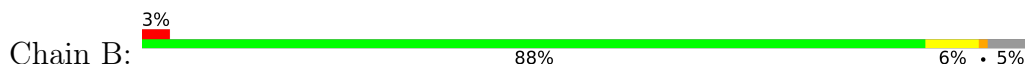
- Molecule 1: Proteasome subunit alpha type-2



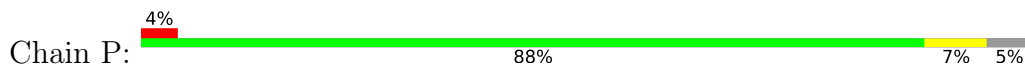
- Molecule 1: Proteasome subunit alpha type-2



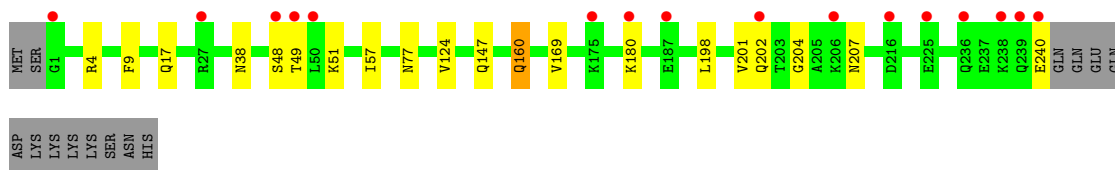
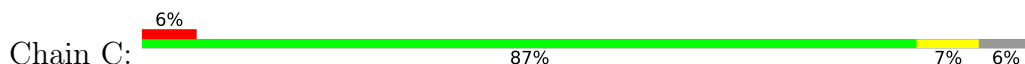
- Molecule 2: Proteasome subunit alpha type-3




- Molecule 2: Proteasome subunit alpha type-3




- Molecule 3: Proteasome subunit alpha type-4



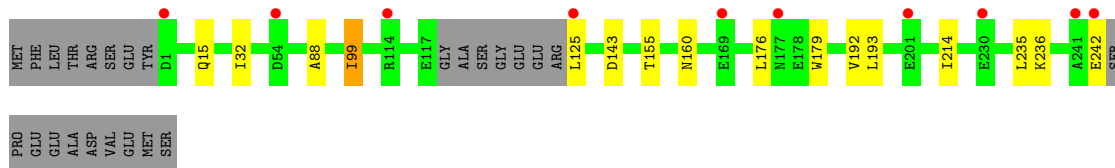

● Molecule 3: Proteasome subunit alpha type-4

Chain Q: 


● Molecule 4: Proteasome subunit alpha type-5

Chain D: 

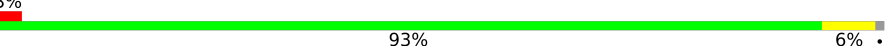
● Molecule 4: Proteasome subunit alpha type-5

Chain R: 


● Molecule 5: Proteasome subunit alpha type-6

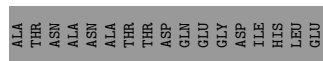
Chain E: 

● Molecule 5: Proteasome subunit alpha type-6

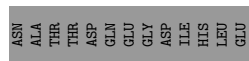
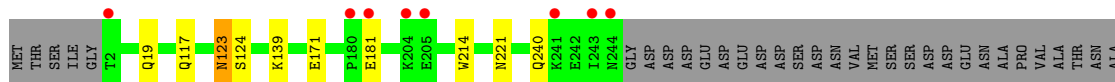
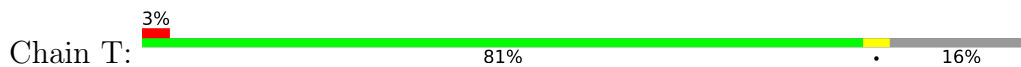
Chain S: 

● Molecule 6: Probable proteasome subunit alpha type-7

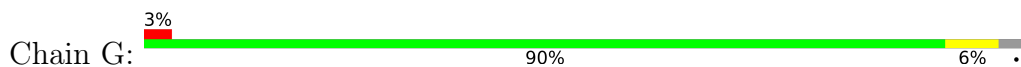
Chain F: 



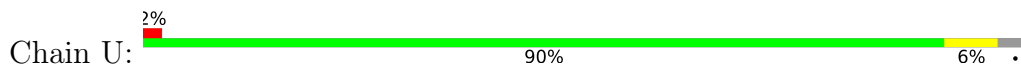
- Molecule 6: Probable proteasome subunit alpha type-7



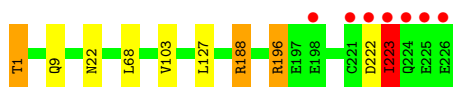
- Molecule 7: Proteasome subunit alpha type-1



- Molecule 7: Proteasome subunit alpha type-1



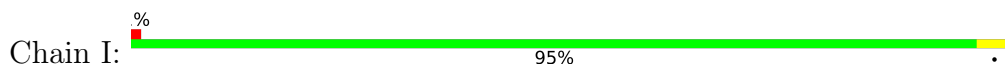
- Molecule 8: Proteasome subunit beta type-10, Proteasome subunit beta type-2



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



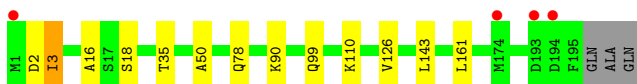
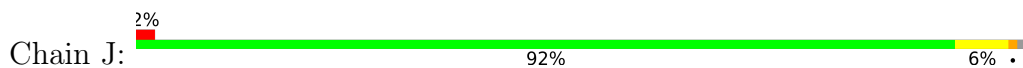
- Molecule 9: Proteasome subunit beta type-3



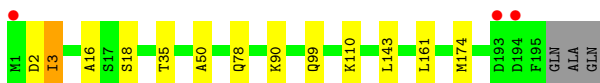
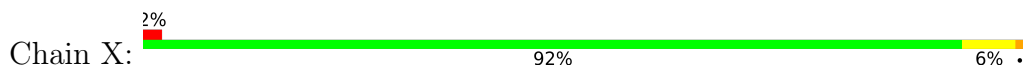
- Molecule 9: Proteasome subunit beta type-3



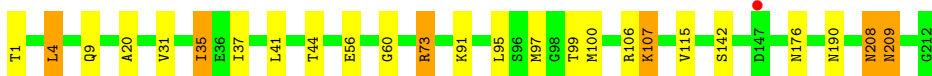
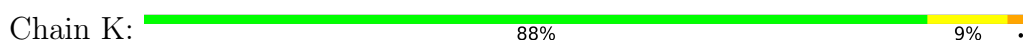
- Molecule 10: Proteasome subunit beta type-4



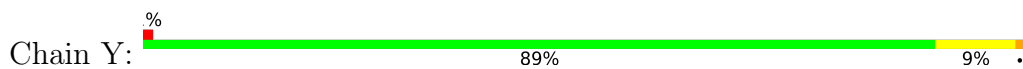
- Molecule 10: Proteasome subunit beta type-4



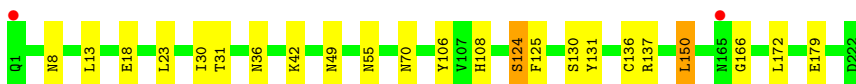
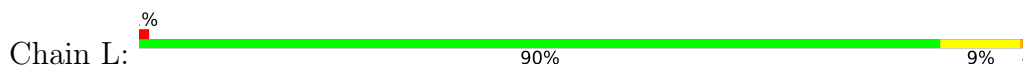
- Molecule 11: Proteasome subunit beta type-5



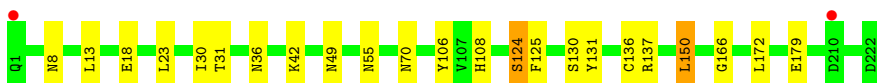
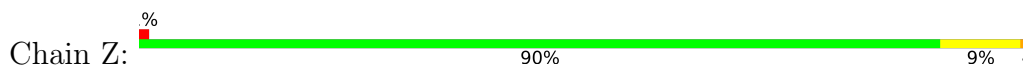
- Molecule 11: Proteasome subunit beta type-5



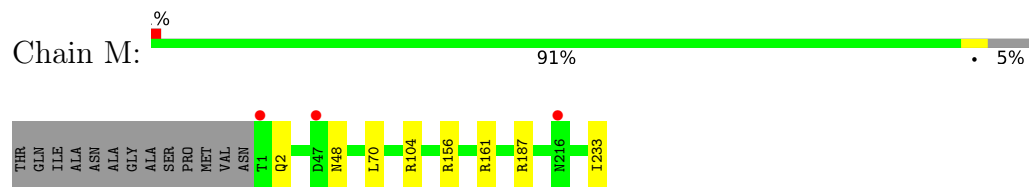
- Molecule 12: Proteasome subunit beta type-6



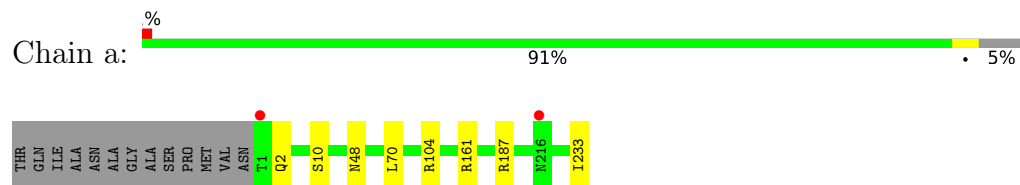
- Molecule 12: Proteasome subunit beta type-6



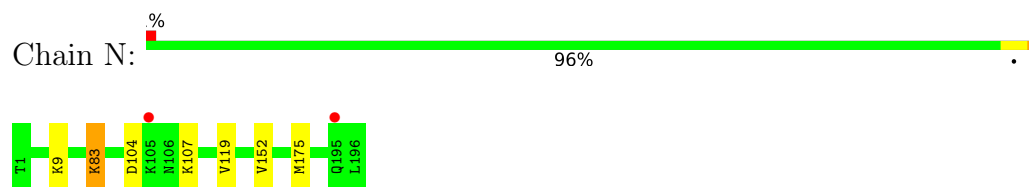
- Molecule 13: Proteasome subunit beta type-7



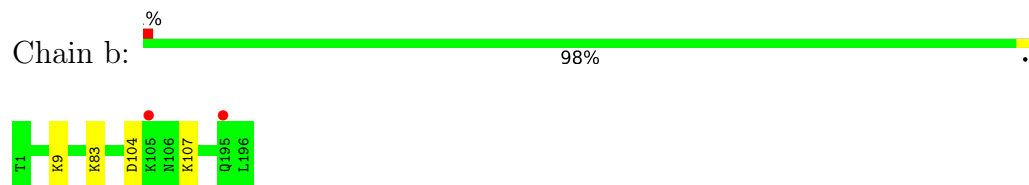
- Molecule 13: Proteasome subunit beta type-7



- 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, α , β , γ	135.77Å 299.59Å 144.64Å 90.00° 113.24° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 15.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.3 (15.00-2.70) 98.9 (15.00-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.191 , 0.219 0.196 , 0.220	Depositor DCC
R_{free} test set	14231 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	57.3	Xtrriage
Anisotropy	0.275	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 28.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	50153	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.36	0/1952	0.57	0/2642
1	O	0.36	0/1952	0.57	0/2642
2	B	0.38	0/1934	0.66	2/2618 (0.1%)
2	P	0.38	0/1934	0.66	2/2618 (0.1%)
3	C	0.38	0/1910	0.64	0/2586
3	Q	0.37	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	0.36	0/1800	0.58	0/2433
6	F	0.36	0/1932	0.57	0/2609
6	T	0.37	0/1932	0.57	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	0.33	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	0.62	0/2142
11	K	0.37	0/1681	0.88	5/2274 (0.2%)
11	Y	0.36	0/1681	0.89	5/2274 (0.2%)
12	L	0.37	0/1795	0.62	0/2420
12	Z	0.37	0/1795	0.61	0/2420
13	M	0.37	0/1855	0.64	0/2514
13	a	0.37	0/1855	0.64	0/2514
14	N	0.34	0/1541	0.58	0/2087
14	b	0.34	0/1541	0.58	0/2087
All	All	0.36	0/50228	0.64	23/67910 (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 (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	V	188	ARG	NE-CZ-NH2	-21.49	109.56	120.30
11	K	73	ARG	NE-CZ-NH2	-20.05	110.27	120.30
11	Y	73	ARG	NE-CZ-NH1	-19.51	110.55	120.30
8	H	188	ARG	NE-CZ-NH1	-18.23	111.18	120.30
11	Y	73	ARG	NE-CZ-NH2	16.31	128.46	120.30
8	H	188	ARG	NE-CZ-NH2	14.94	127.77	120.30
11	K	73	ARG	NE-CZ-NH1	14.53	127.57	120.30
8	V	188	ARG	NE-CZ-NH1	14.20	127.40	120.30
11	Y	4	LEU	CD1-CG-CD2	-11.90	74.81	110.50
11	K	4	LEU	CD1-CG-CD2	-11.62	75.64	110.50
8	V	188	ARG	CD-NE-CZ	10.30	138.02	123.60
11	K	73	ARG	CD-NE-CZ	10.26	137.97	123.60
11	Y	73	ARG	CD-NE-CZ	9.20	136.49	123.60
8	H	188	ARG	CD-NE-CZ	8.50	135.50	123.60
11	Y	4	LEU	CB-CG-CD1	8.21	124.95	111.00
11	K	4	LEU	CB-CG-CD2	7.81	124.27	111.00
2	P	224	VAL	CG1-CB-CG2	5.77	120.13	110.90
2	B	224	VAL	CG1-CB-CG2	5.45	119.62	110.90
2	B	51	VAL	CG1-CB-CG2	5.44	119.61	110.90
8	H	1	THR	CA-CB-OG1	5.42	120.39	109.00
2	P	51	VAL	CG1-CB-CG2	5.30	119.37	110.90
8	H	196	ARG	NE-CZ-NH1	5.23	122.91	120.30
8	V	196	ARG	NE-CZ-NH1	5.16	122.88	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
8	V	188	ARG	Sidechain
11	Y	73	ARG	Sidechain

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	1	0
1	O	1915	0	1929	2	0
2	B	1904	0	1904	9	0
2	P	1904	0	1904	7	0
3	C	1881	0	1895	8	0
3	Q	1881	0	1895	5	0
4	D	1813	0	1797	4	0
4	R	1813	0	1797	5	0
5	E	1773	0	1775	8	0
5	S	1773	0	1775	6	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	1716	0	1702	3	0
8	V	1688	0	1682	5	0
9	I	1581	0	1574	7	0
9	W	1581	0	1574	4	0
10	J	1561	0	1569	5	0
10	X	1561	0	1569	5	0
11	K	1644	0	1594	17	0
11	Y	1644	0	1594	14	0
12	L	1757	0	1711	10	0
12	Z	1757	0	1711	10	0
13	M	1824	0	1832	1	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	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	K	1	0	0	0	0
15	L	1	0	0	0	0
15	N	1	0	0	0	0
15	W	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	45	0	0	4	0
17	K	45	0	0	2	0
17	V	45	0	0	1	0
17	Y	45	0	0	2	0
18	A	20	0	0	0	0
18	B	20	0	0	2	0
18	C	20	0	0	0	0
18	D	21	0	0	0	0
18	E	11	0	0	1	0
18	F	27	0	0	0	0
18	G	24	0	0	0	0
18	H	37	0	0	0	0
18	I	22	0	0	0	0
18	J	24	0	0	0	0
18	K	32	0	0	1	0
18	L	31	0	0	0	0
18	M	31	0	0	0	0
18	N	21	0	0	0	0
18	O	13	0	0	0	0
18	P	23	0	0	0	0
18	Q	12	0	0	0	0
18	R	18	0	0	0	0
18	S	10	0	0	0	0
18	T	21	0	0	0	0
18	U	29	0	0	0	0
18	V	28	0	0	0	0
18	W	16	0	0	0	0
18	X	23	0	0	1	0
18	Y	24	0	0	0	0
18	Z	24	0	0	0	0
18	a	27	0	0	0	0
18	b	22	0	0	0	0
All	All	50153	0	49074	122	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (122) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:92:ASN:HD21	12:Z:70:ASN:HD21	1.25	0.82
5:E:92:ASN:HD21	12:L:70:ASN:HD21	1.26	0.81
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.53	0.73
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.54	0.72
11:K:142:SER:OG	10:X:143:LEU:HD21	1.92	0.68
5:E:12:PHE:H	6:F:19:GLN:HE22	1.42	0.66
10:J:143:LEU:HD21	11:Y:142:SER:OG	1.95	0.66
5:S:92:ASN:HD21	12:Z:70:ASN:ND2	1.94	0.65
2:B:93:HIS:HB3	18:B:301:HOH:O	1.96	0.65
2:B:145:TYR:OH	2:B:217:LYS:N	2.30	0.64
5:E:92:ASN:HD21	12:L:70:ASN:ND2	1.94	0.64
1:O:12:PHE:H	2:P:20:GLN:HE22	1.44	0.64
5:E:92:ASN:ND2	12:L:70:ASN:HD21	1.95	0.63
1:A:12:PHE:H	2:B:20:GLN:HE22	1.46	0.63
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.62	0.63
2:P:145:TYR:OH	2:P:217:LYS:N	2.31	0.63
2:B:12:PHE:H	3:C:17:GLN:HE22	1.48	0.62
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.64	0.62
5:S:12:PHE:H	6:T:19:GLN:HE22	1.45	0.62
5:S:92:ASN:ND2	12:Z:70:ASN:HD21	1.95	0.61
6:F:123:ASN:HD22	6:F:124:SER:N	2.01	0.58
2:P:225:TYR:CD1	8:V:223:ILE:HG13	2.39	0.57
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.53	0.57
6:T:123:ASN:HD22	6:T:124:SER:N	2.02	0.57
2:P:145:TYR:HH	2:P:217:LYS:N	2.02	0.57
7:U:23:PHE:O	7:U:26:THR:HB	2.06	0.55
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.90	0.54
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.90	0.54
11:K:176:ASN:ND2	11:K:190:ASN:HD22	2.06	0.53
2:B:145:TYR:HH	2:B:217:LYS:N	2.05	0.53
11:K:1:THR:HB	17:K:301:GRW:O30	2.09	0.53
7:G:23:PHE:O	7:G:26:THR:HB	2.09	0.52
11:Y:176:ASN:ND2	11:Y:190:ASN:HD22	2.08	0.52
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.57	0.52
12:Z:42:LYS:HD2	12:Z:55:ASN:HD22	1.75	0.52
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	1.94	0.50
3:C:198:LEU:HA	3:C:201:VAL:HG12	1.94	0.50
12:L:42:LYS:HD2	12:L:55:ASN:HD22	1.77	0.50
8:H:1:THR:HB	17:H:301:GRW:O30	2.12	0.49
2:P:95:GLN:HE22	9:W:71:ASN:HD22	1.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:123:ASN:HD22	6:F:123:ASN:C	2.16	0.49
11:K:208:ASN:HD22	11:K:208:ASN:N	2.12	0.48
3:Q:202:GLN:CG	3:Q:202:GLN:O	2.62	0.47
7:G:167:GLN:HE21	7:G:171:THR:HG23	1.79	0.47
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.95	0.47
3:C:202:GLN:O	3:C:202:GLN:CG	2.62	0.47
2:B:113:ARG:NE	18:B:301:HOH:O	2.42	0.47
10:X:50:ALA:O	11:Y:91:LYS:NZ	2.47	0.47
11:Y:208:ASN:HD22	11:Y:208:ASN:N	2.11	0.47
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.95	0.47
10:X:174:MET:HB2	18:X:215:HOH:O	2.14	0.47
11:Y:1:THR:HB	17:Y:301:GRW:O30	2.14	0.47
11:K:44:THR:HG21	11:K:100:MET:HE3	1.98	0.46
9:I:37:ASN:ND2	11:Y:209:ASN:O	2.46	0.46
11:K:37:ILE:HG23	11:K:60:GLY:HA2	1.97	0.46
11:Y:37:ILE:HG23	11:Y:60:GLY:HA2	1.98	0.46
12:Z:31:THR:CG2	12:Z:36:ASN:HD21	2.24	0.46
13:M:156:ARG:HH11	8:V:165:ASN:HD22	1.64	0.46
11:Y:37:ILE:HB	11:Y:41:LEU:HB3	1.98	0.46
3:C:9:PHE:H	4:D:15:GLN:HE22	1.63	0.46
11:K:209:ASN:O	9:W:37:ASN:ND2	2.47	0.46
8:V:223:ILE:HD13	8:V:223:ILE:N	2.31	0.46
6:T:123:ASN:HD22	6:T:123:ASN:C	2.19	0.46
17:H:301:GRW:C10	17:H:301:GRW:C14	2.94	0.45
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.46	0.45
17:V:301:GRW:C10	17:V:301:GRW:C14	2.93	0.45
10:J:50:ALA:O	11:K:91:LYS:NZ	2.49	0.45
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.47	0.45
8:V:223:ILE:HD13	8:V:223:ILE:H	1.82	0.45
8:H:223:ILE:N	8:H:223:ILE:HD13	2.32	0.45
11:K:37:ILE:HB	11:K:41:LEU:HB3	1.99	0.45
2:P:12:PHE:H	3:Q:17:GLN:HE22	1.65	0.45
7:U:167:GLN:HE21	7:U:171:THR:HG23	1.82	0.45
10:J:3:ILE:HG23	10:J:18:SER:HB3	1.98	0.45
11:Y:44:THR:HG21	11:Y:100:MET:HE3	1.99	0.44
12:L:31:THR:CG2	12:L:36:ASN:HD21	2.25	0.44
11:K:176:ASN:HD21	11:K:190:ASN:HD22	1.64	0.44
11:K:95:LEU:HD13	11:K:97:MET:CE	2.47	0.44
2:B:146:GLN:HG2	3:C:57:ILE:HG21	2.00	0.44
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.19	0.43
10:X:3:ILE:HG23	10:X:18:SER:HB3	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:18:LEU:HD21	6:F:126:ARG:HD2	2.00	0.43
8:H:223:ILE:HD13	8:H:223:ILE:H	1.83	0.43
11:Y:176:ASN:HD21	11:Y:190:ASN:HD22	1.67	0.43
3:C:48:SER:HB2	3:C:207:ASN:HD21	1.84	0.43
11:K:20:ALA:HB2	11:K:31:VAL:HG21	2.01	0.42
12:L:8:ASN:HA	12:L:30:ILE:O	2.18	0.42
17:H:301:GRW:C57	9:I:125:LEU:HD21	2.49	0.42
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	2.02	0.42
9:I:36:SER:HB2	10:J:126:VAL:HG11	2.01	0.42
11:K:107:LYS:NZ	18:K:401:HOH:O	2.40	0.42
11:Y:31:VAL:HG11	17:Y:301:GRW:C23	2.49	0.42
9:I:10:ILE:HG21	9:I:141:ALA:HB3	2.02	0.42
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.55	0.42
8:V:196:ARG:NH2	9:W:150:GLU:O	2.53	0.42
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.55	0.42
4:D:88:ALA:HA	4:D:99:ILE:HG21	2.01	0.41
11:K:31:VAL:HG11	17:K:301:GRW:C23	2.50	0.41
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.51	0.41
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.01	0.41
17:H:301:GRW:C56	9:I:125:LEU:HD21	2.50	0.41
12:Z:124:SER:HB2	12:Z:137:ARG:HG2	2.03	0.41
11:Y:95:LEU:HD13	11:Y:97:MET:CE	2.50	0.41
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.51	0.41
2:B:124:HIS:HB3	3:C:124:VAL:HG12	2.03	0.40
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.56	0.40
4:D:176:LEU:HD22	5:E:55:LEU:CD2	2.51	0.40
4:R:155:THR:HG23	5:S:59:GLN:HE22	1.86	0.40
11:Y:9:GLN:NE2	11:Y:148:LEU:O	2.54	0.40
2:P:47:ALA:HB1	2:P:64:LYS:HD2	2.04	0.40
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.57	0.40
11:K:99:THR:HG22	11:K:115:VAL:O	2.21	0.40
11:K:209:ASN:N	11:K:209:ASN:HD22	2.19	0.40
14:N:152:VAL:HA	14:N:175:MET:HE1	2.04	0.40
4:R:32:ILE:HD12	4:R:192:VAL:HG23	2.02	0.40
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.51	0.40
9:I:9:GLY:HA3	9:I:41:LYS:HE2	2.04	0.40
5:E:147:GLN:HG2	18:E:306:HOH:O	2.21	0.40
11:K:35:ILE:HG21	11:K:56:GLU:HB3	2.02	0.40
12:L:124:SER:HB2	12:L:137:ARG:HG2	2.02	0.40
12:L:125:PHE:CD2	12:L:131:TYR:HB3	2.57	0.40
9:W:10:ILE:HG21	9:W:141:ALA:HB3	2.03	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%)	243 (98%)	5 (2%)	0	100	100
1	O	248/250 (99%)	243 (98%)	5 (2%)	0	100	100
2	B	242/258 (94%)	232 (96%)	10 (4%)	0	100	100
2	P	242/258 (94%)	232 (96%)	10 (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%)	227 (98%)	4 (2%)	0	100	100
4	R	231/260 (89%)	226 (98%)	5 (2%)	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%)	239 (99%)	2 (1%)	0	100	100
6	T	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
7	G	239/252 (95%)	236 (99%)	3 (1%)	0	100	100
7	U	239/252 (95%)	236 (99%)	3 (1%)	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%)	193 (96%)	9 (4%)	0	100	100
9	W	202/205 (98%)	193 (96%)	9 (4%)	0	100	100
10	J	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
10	X	193/198 (98%)	188 (97%)	5 (3%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L	220/222 (99%)	214 (97%)	5 (2%)	1 (0%)	29	54
12	Z	220/222 (99%)	215 (98%)	4 (2%)	1 (0%)	29	54
13	M	231/246 (94%)	223 (96%)	8 (4%)	0	100	100
13	a	231/246 (94%)	224 (97%)	7 (3%)	0	100	100
14	N	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
14	b	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
All	All	6281/6602 (95%)	6126 (98%)	150 (2%)	5 (0%)	51	78

All (5) 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

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%)	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%)	186 (96%)	8 (4%)	30	59
4	R	194/215 (90%)	185 (95%)	9 (5%)	27	54
5	E	190/193 (98%)	181 (95%)	9 (5%)	26	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	176 (96%)	8 (4%)	29	57
8	V	181/184 (98%)	172 (95%)	9 (5%)	24	51
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%)	166 (96%)	7 (4%)	31	60
10	X	173/175 (99%)	166 (96%)	7 (4%)	31	60
11	K	169/169 (100%)	162 (96%)	7 (4%)	30	59
11	Y	169/169 (100%)	162 (96%)	7 (4%)	30	59
12	L	185/185 (100%)	174 (94%)	11 (6%)	19	43
12	Z	185/185 (100%)	174 (94%)	11 (6%)	19	43
13	M	199/208 (96%)	192 (96%)	7 (4%)	36	65
13	a	199/208 (96%)	191 (96%)	8 (4%)	31	60
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%)	5107 (96%)	208 (4%)	32	61

All (208) 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

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Mol	Chain	Res	Type
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	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	139	LYS
6	F	171	GLU
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

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Mol	Chain	Res	Type
7	G	208	GLU
7	G	235	ARG
7	G	236	LEU
8	H	9	GLN
8	H	22	ASN
8	H	68	LEU
8	H	103	VAL
8	H	127	LEU
8	H	196	ARG
8	H	222	ASP
8	H	223	ILE
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
10	J	110	LYS
11	K	4	LEU
11	K	9	GLN
11	K	35	ILE
11	K	106	ARG
11	K	107	LYS
11	K	208	ASN
11	K	209	ASN
12	L	18	GLU
12	L	23	LEU
12	L	49	ASN
12	L	106	TYR
12	L	108	HIS
12	L	124	SER
12	L	130	SER
12	L	136	CYS
12	L	150	LEU
12	L	172	LEU
12	L	179	GLU
13	M	2	GLN
13	M	48	ASN
13	M	70	LEU

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	139	LYS
6	T	171	GLU
6	T	181	GLU
6	T	214	TRP
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	68	LEU
8	V	103	VAL
8	V	118	SER
8	V	127	LEU
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
10	X	110	LYS
11	Y	9	GLN

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Mol	Chain	Res	Type
11	Y	35	ILE
11	Y	73	ARG
11	Y	106	ARG
11	Y	107	LYS
11	Y	208	ASN
11	Y	209	ASN
12	Z	18	GLU
12	Z	23	LEU
12	Z	49	ASN
12	Z	106	TYR
12	Z	108	HIS
12	Z	124	SER
12	Z	130	SER
12	Z	136	CYS
12	Z	150	LEU
12	Z	172	LEU
12	Z	179	GLU
13	a	2	GLN
13	a	10	SER
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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (124) 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

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Mol	Chain	Res	Type
3	C	38	ASN
3	C	77	ASN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	91	HIS
4	D	100	ASN
4	D	160	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
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
8	H	172	ASN
10	J	55	GLN
10	J	191	GLN
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
11	K	209	ASN
12	L	3	ASN
12	L	49	ASN
12	L	55	ASN
12	L	70	ASN

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Mol	Chain	Res	Type
12	L	79	HIS
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
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	100	ASN
4	R	146	GLN
4	R	160	ASN
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

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Mol	Chain	Res	Type
6	T	240	GLN
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	165	ASN
8	V	172	ASN
10	X	55	GLN
10	X	86	GLN
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
11	Y	209	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	55	ASN
12	Z	70	ASN
12	Z	79	HIS
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 ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 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	GRW	H	301	8	45,46,46	1.91	7 (15%)	58,62,62	8.10	17 (29%)
17	GRW	K	301	11	45,46,46	1.52	7 (15%)	58,62,62	7.97	12 (20%)
17	GRW	Y	301	11	45,46,46	1.61	8 (17%)	58,62,62	7.81	10 (17%)
17	GRW	V	301	8	45,46,46	2.17	7 (15%)	58,62,62	7.71	15 (25%)

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	GRW	H	301	8	-	7/51/51/51	0/2/2/2
17	GRW	K	301	11	-	9/51/51/51	0/2/2/2
17	GRW	Y	301	11	-	10/51/51/51	0/2/2/2
17	GRW	V	301	8	-	11/51/51/51	0/2/2/2

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	V	301	GRW	N52-N51	-9.30	0.98	1.23
17	H	301	GRW	C54-C55	-6.59	1.35	1.51
17	V	301	GRW	C54-C55	-6.07	1.36	1.51
17	H	301	GRW	C16-C17	-5.62	1.37	1.51
17	Y	301	GRW	C16-C17	-5.29	1.38	1.51
17	K	301	GRW	C16-C17	-5.26	1.38	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	V	301	GRW	C16-C17	-4.94	1.39	1.51
17	H	301	GRW	N52-N51	-4.86	1.10	1.23
17	H	301	GRW	C21-C20	-4.06	1.37	1.51
17	Y	301	GRW	O29-S27	4.04	1.53	1.44
17	K	301	GRW	O29-S27	3.89	1.52	1.44
17	V	301	GRW	C21-C20	-3.84	1.38	1.51
17	Y	301	GRW	O30-S27	3.75	1.52	1.44
17	K	301	GRW	O30-S27	3.66	1.52	1.44
17	K	301	GRW	C21-C20	-3.42	1.39	1.51
17	K	301	GRW	C54-C55	-3.37	1.43	1.51
17	Y	301	GRW	C21-C20	-3.33	1.39	1.51
17	Y	301	GRW	C54-C55	-3.28	1.43	1.51
17	Y	301	GRW	C26-S27	3.07	1.82	1.78
17	V	301	GRW	C6-N51	-3.05	1.44	1.48
17	Y	301	GRW	N52-N51	-2.91	1.15	1.23
17	K	301	GRW	N52-N51	-2.64	1.16	1.23
17	V	301	GRW	C6-C7	-2.52	1.47	1.52
17	H	301	GRW	C13-N14	-2.39	1.28	1.34
17	Y	301	GRW	C25-C26	2.36	1.55	1.52
17	H	301	GRW	C54-C6	-2.28	1.50	1.53
17	V	301	GRW	C54-C6	-2.22	1.50	1.53
17	H	301	GRW	C6-C7	-2.06	1.48	1.52
17	K	301	GRW	C26-S27	2.05	1.81	1.78

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	H	301	GRW	C6-N51-N52	60.06	178.41	115.24
17	K	301	GRW	C6-N51-N52	59.79	178.14	115.24
17	Y	301	GRW	C6-N51-N52	58.60	176.88	115.24
17	V	301	GRW	C6-N51-N52	56.63	174.82	115.24
17	V	301	GRW	O29-S27-C26	-7.21	103.30	108.34
17	V	301	GRW	O30-S27-C26	6.13	112.64	108.34
17	V	301	GRW	O30-S27-C28	4.92	113.85	108.91
17	H	301	GRW	C54-C6-C7	-4.88	99.17	109.55
17	H	301	GRW	O30-S27-C28	4.57	113.50	108.91
17	V	301	GRW	O29-S27-O30	-4.33	107.85	117.09
17	H	301	GRW	O29-S27-O30	-4.31	107.87	117.09
17	H	301	GRW	O29-S27-C26	-4.12	105.46	108.34
17	K	301	GRW	O29-S27-O30	-3.90	108.75	117.09
17	H	301	GRW	C40-C9-C10	-3.82	101.47	110.57
17	H	301	GRW	C54-C6-N51	3.78	115.53	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	Y	301	GRW	O29-S27-O30	-3.59	109.42	117.09
17	V	301	GRW	C54-C6-N51	3.41	114.93	109.30
17	V	301	GRW	C16-C15-N14	-3.25	104.14	110.39
17	K	301	GRW	O30-S27-C26	3.08	110.50	108.34
17	H	301	GRW	C16-C15-N14	-2.74	105.13	110.39
17	K	301	GRW	C16-C17-C18	-2.59	115.77	120.91
17	H	301	GRW	C10-C9-N8	-2.58	104.14	111.16
17	H	301	GRW	C25-C15-N14	-2.58	106.91	110.54
17	K	301	GRW	C16-C17-C24	2.57	126.00	120.91
17	Y	301	GRW	C16-C17-C18	-2.53	115.88	120.91
17	Y	301	GRW	C16-C17-C24	2.51	125.90	120.91
17	Y	301	GRW	C54-C6-C7	2.50	114.85	109.55
17	H	301	GRW	C15-N14-C13	2.48	127.15	123.20
17	V	301	GRW	C25-C15-C16	2.47	115.16	111.14
17	V	301	GRW	C15-N14-C13	2.47	127.13	123.20
17	V	301	GRW	O44-C7-C6	-2.46	116.48	120.30
17	H	301	GRW	O30-S27-C26	2.46	110.07	108.34
17	Y	301	GRW	C54-C55-C60	2.45	125.78	120.91
17	K	301	GRW	C54-C6-C7	2.45	114.74	109.55
17	Y	301	GRW	C25-C15-N14	-2.42	107.13	110.54
17	V	301	GRW	C9-N8-C7	-2.42	116.48	121.67
17	H	301	GRW	C9-N8-C7	-2.39	116.54	121.67
17	Y	301	GRW	C9-C10-N11	-2.39	111.47	116.70
17	K	301	GRW	C25-C15-N14	-2.37	107.20	110.54
17	V	301	GRW	C40-C9-C10	-2.37	104.92	110.57
17	V	301	GRW	C25-C15-N14	-2.36	107.22	110.54
17	V	301	GRW	C32-C12-C13	-2.35	106.10	111.28
17	K	301	GRW	C54-C55-C60	2.29	125.45	120.91
17	K	301	GRW	C9-C10-N11	-2.29	111.68	116.70
17	Y	301	GRW	C40-C9-C10	-2.24	105.24	110.57
17	H	301	GRW	C41-C40-C9	-2.22	109.33	115.43
17	H	301	GRW	C54-C55-C60	-2.19	116.55	120.91
17	V	301	GRW	C41-C40-C9	-2.11	109.64	115.43
17	K	301	GRW	O29-S27-C26	-2.09	106.88	108.34
17	H	301	GRW	O44-C7-C6	-2.07	117.09	120.30
17	K	301	GRW	C40-C9-C10	-2.04	105.70	110.57
17	H	301	GRW	C40-C9-N8	2.02	115.22	110.58
17	Y	301	GRW	C28-S27-C26	2.00	112.93	105.21
17	K	301	GRW	C28-S27-C26	2.00	112.92	105.21

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	H	301	GRW	N51-C6-C7-N8
17	K	301	GRW	N51-C6-C7-N8
17	V	301	GRW	N51-C6-C7-N8
17	V	301	GRW	N51-C6-C7-O44
17	Y	301	GRW	N51-C6-C7-N8
17	Y	301	GRW	N51-C6-C7-O44
17	V	301	GRW	C15-C16-C17-C18
17	Y	301	GRW	C6-C54-C55-C56
17	K	301	GRW	C6-C54-C55-C56
17	Y	301	GRW	C6-C54-C55-C60
17	V	301	GRW	C6-C54-C55-C56
17	K	301	GRW	C6-C54-C55-C60
17	V	301	GRW	C15-C16-C17-C24
17	H	301	GRW	C15-C16-C17-C18
17	H	301	GRW	C15-C16-C17-C24
17	K	301	GRW	C15-C16-C17-C24
17	Y	301	GRW	C15-C16-C17-C24
17	K	301	GRW	C15-C16-C17-C18
17	V	301	GRW	C6-C54-C55-C60
17	Y	301	GRW	C15-C16-C17-C18
17	Y	301	GRW	C54-C6-C7-O44
17	H	301	GRW	C54-C6-C7-N8
17	K	301	GRW	C54-C6-C7-N8
17	V	301	GRW	C54-C6-C7-N8
17	H	301	GRW	C54-C6-C7-O44
17	K	301	GRW	C54-C6-C7-O44
17	V	301	GRW	C54-C6-C7-O44
17	K	301	GRW	C54-C6-N51-N52
17	Y	301	GRW	C54-C6-C7-N8
17	V	301	GRW	C13-C12-N11-C10
17	V	301	GRW	C25-C26-S27-C28
17	V	301	GRW	C6-N51-N52-N53
17	H	301	GRW	C13-C12-N11-C10
17	K	301	GRW	C15-C25-C26-S27
17	Y	301	GRW	C15-C25-C26-S27
17	H	301	GRW	C25-C26-S27-C28
17	Y	301	GRW	C25-C26-S27-C28

There are no ring outliers.

4 monomers are involved in 9 short contacts:

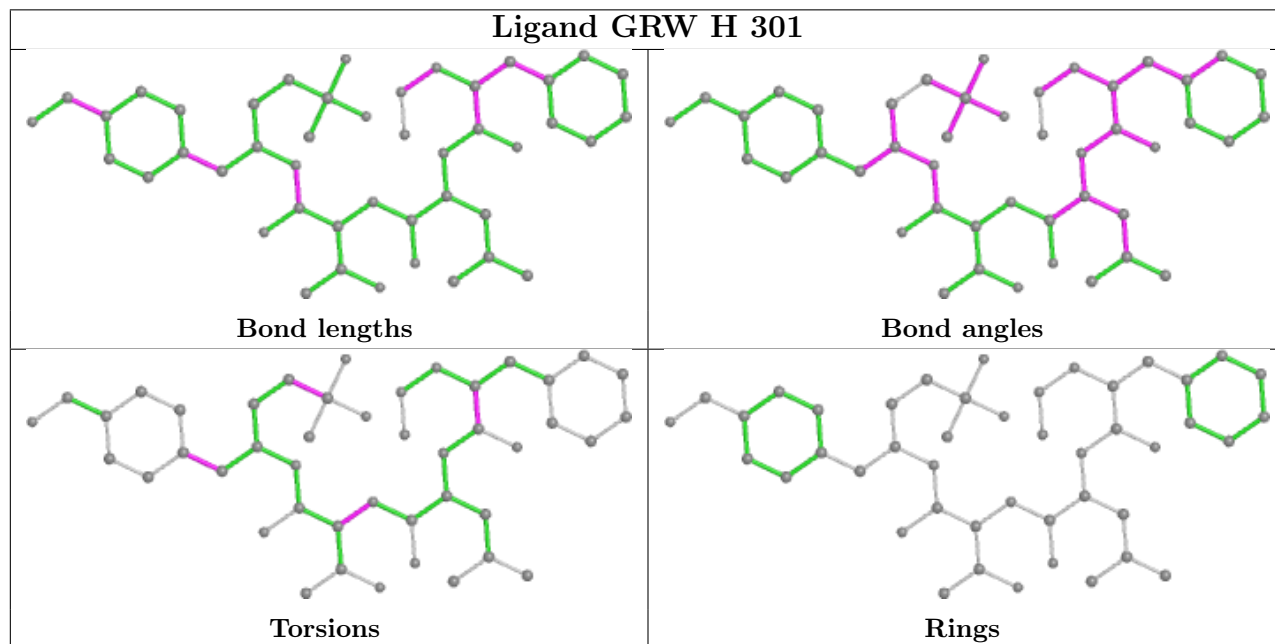
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	H	301	GRW	4	0

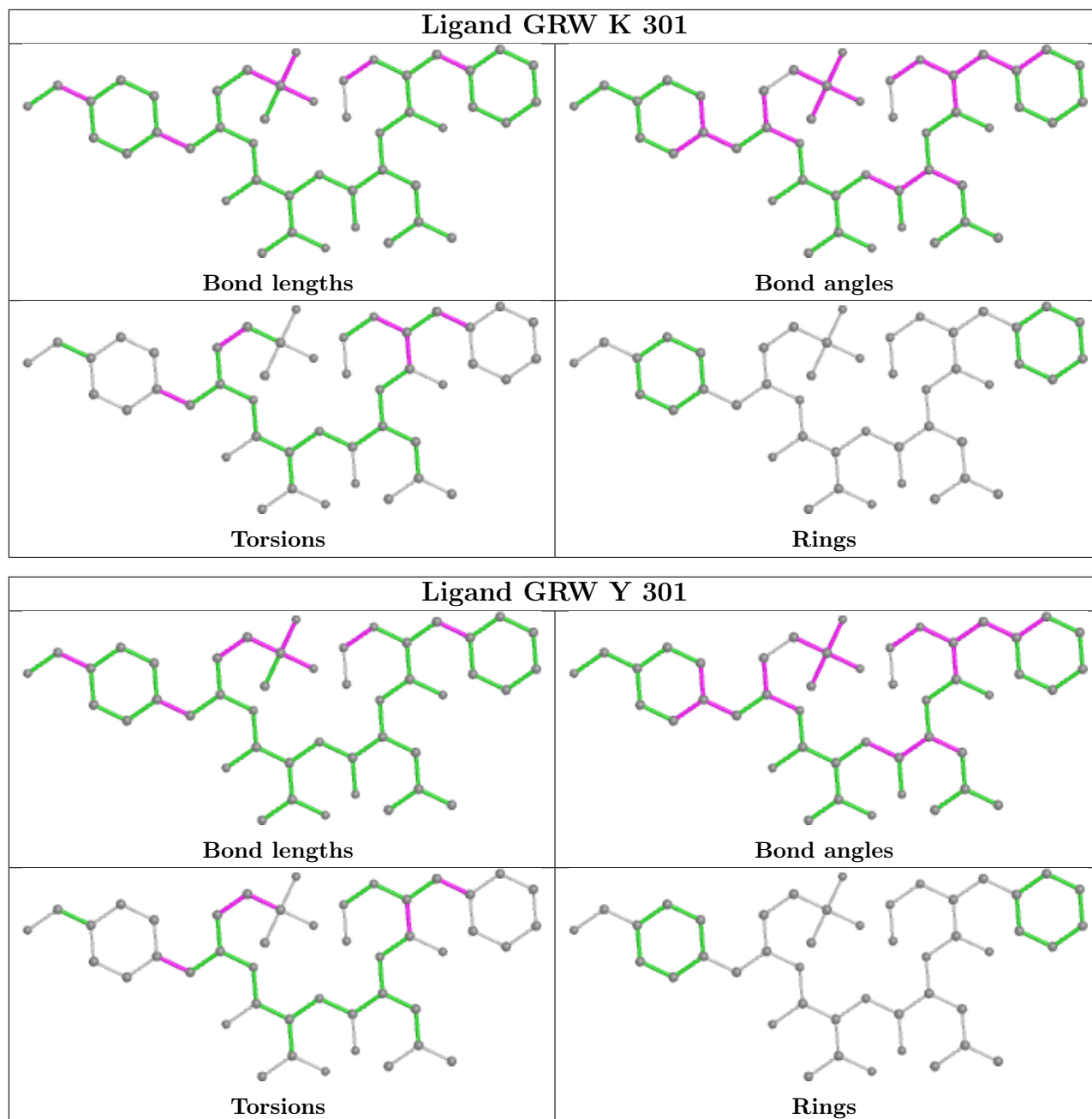
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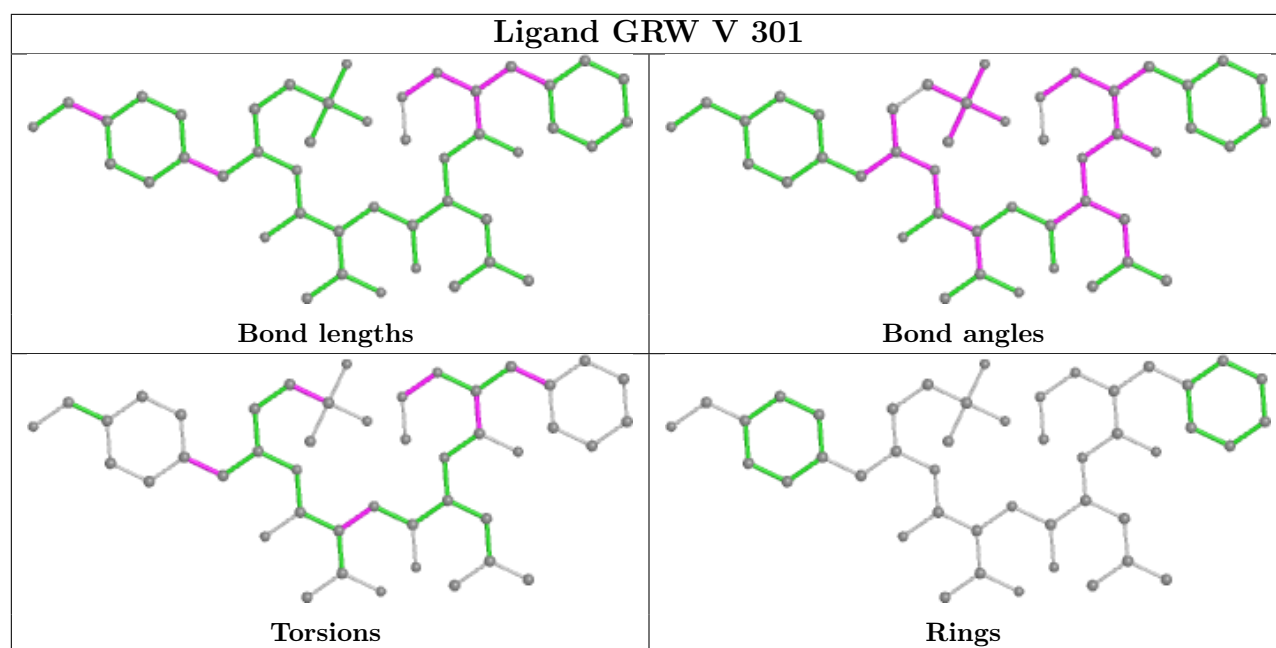
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	K	301	GRW	2	0
17	Y	301	GRW	2	0
17	V	301	GRW	1	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.25	9 (3%) 42 42	46, 62, 99, 122	0
1	O	250/250 (100%)	-0.18	8 (3%) 47 48	49, 71, 111, 137	0
2	B	244/258 (94%)	-0.13	8 (3%) 46 46	46, 67, 107, 131	0
2	P	244/258 (94%)	-0.08	11 (4%) 33 31	50, 70, 109, 135	0
3	C	240/254 (94%)	-0.07	16 (6%) 17 16	42, 69, 125, 160	0
3	Q	240/254 (94%)	0.14	18 (7%) 14 12	53, 83, 155, 196	0
4	D	235/260 (90%)	-0.28	4 (1%) 70 72	51, 69, 97, 135	0
4	R	235/260 (90%)	-0.11	10 (4%) 35 33	59, 77, 113, 149	0
5	E	231/234 (98%)	-0.13	6 (2%) 56 57	52, 72, 108, 132	0
5	S	231/234 (98%)	-0.00	8 (3%) 44 44	57, 79, 123, 145	0
6	F	243/288 (84%)	-0.29	9 (3%) 41 41	43, 67, 109, 130	0
6	T	243/288 (84%)	-0.19	8 (3%) 46 46	46, 72, 121, 150	0
7	G	241/252 (95%)	-0.34	8 (3%) 46 46	43, 61, 95, 136	0
7	U	241/252 (95%)	-0.32	4 (1%) 70 72	47, 63, 95, 130	0
8	H	226/226 (100%)	-0.29	7 (3%) 49 49	44, 56, 94, 155	0
8	V	223/226 (98%)	-0.37	5 (2%) 62 63	44, 61, 88, 135	0
9	I	204/205 (99%)	-0.52	3 (1%) 73 76	41, 58, 82, 100	0
9	W	204/205 (99%)	-0.54	3 (1%) 73 76	42, 59, 84, 102	0
10	J	195/198 (98%)	-0.30	4 (2%) 63 65	44, 61, 86, 106	0
10	X	195/198 (98%)	-0.31	3 (1%) 73 76	46, 62, 87, 112	0
11	K	212/212 (100%)	-0.50	1 (0%) 91 92	42, 57, 86, 102	0
11	Y	212/212 (100%)	-0.44	2 (0%) 84 85	46, 61, 90, 105	0
12	L	222/222 (100%)	-0.44	2 (0%) 84 85	45, 60, 92, 111	0
12	Z	222/222 (100%)	-0.43	2 (0%) 84 85	44, 61, 97, 113	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.43	3 (1%) 77 78	41, 58, 86, 101	0
13	a	233/246 (94%)	-0.43	2 (0%) 84 85	40, 58, 82, 97	0
14	N	196/196 (100%)	-0.50	2 (1%) 82 83	41, 54, 82, 99	0
14	b	196/196 (100%)	-0.47	2 (1%) 82 83	40, 55, 83, 99	0
All	All	6341/6602 (96%)	-0.29	168 (2%) 56 57	40, 64, 107, 196	0

All (168) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
8	H	224	GLN	9.9
2	P	220	ASN	9.2
8	H	225	GLU	8.9
3	Q	49	THR	8.3
2	P	219	ALA	7.3
2	B	221	ASP	7.2
1	A	228	PRO	6.4
10	J	1	MET	6.0
8	H	226	GLU	5.9
2	B	220	ASN	5.7
10	X	1	MET	5.4
1	A	229	THR	5.3
1	O	231	LYS	5.2
3	Q	240	GLU	5.0
8	V	223	ILE	5.0
3	Q	236	GLN	4.9
2	P	218	GLY	4.9
3	C	50	LEU	4.8
8	H	222	ASP	4.7
3	Q	50	LEU	4.7
9	W	1	SER	4.7
8	V	222	ASP	4.7
1	A	249	ALA	4.6
1	O	229	THR	4.6
3	C	202	GLN	4.6
2	P	221	ASP	4.6
5	E	202	ASP	4.6
3	Q	238	LYS	4.5
5	S	202	ASP	4.5
7	G	2	GLY	4.5
2	P	52	THR	4.4
13	M	1	THR	4.4

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Mol	Chain	Res	Type	RSRZ
3	C	238	LYS	4.2
1	A	231	LYS	4.2
2	B	218	GLY	4.1
6	T	244	ASN	4.1
1	O	228	PRO	4.1
3	Q	239	GLN	4.1
2	B	217	LYS	4.0
10	J	194	ASP	3.9
2	P	59	ASP	3.9
13	a	1	THR	3.9
1	O	249	ALA	3.8
3	C	49	THR	3.8
6	F	205	GLU	3.8
7	U	222	ASP	3.8
3	Q	202	GLN	3.8
7	U	242	GLN	3.7
7	G	240	ALA	3.6
8	H	221	CYS	3.6
3	Q	206	LYS	3.4
5	S	180	LYS	3.4
3	Q	237	GLU	3.4
5	S	54	GLU	3.4
10	X	194	ASP	3.3
5	S	203	GLU	3.3
8	V	221	CYS	3.3
2	P	51	VAL	3.3
3	Q	48	SER	3.2
8	H	223	ILE	3.2
2	P	225	TYR	3.2
4	D	242	GLU	3.1
6	F	243	ILE	3.1
3	C	48	SER	3.1
6	T	241	LYS	3.1
13	M	47	ASP	3.1
5	E	201	ARG	3.1
3	C	236	GLN	3.1
14	b	105	LYS	3.0
6	T	243	ILE	3.0
1	A	201	GLU	3.0
6	F	181	GLU	2.9
5	E	173	ARG	2.9
7	G	51	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
4	R	54	ASP	2.9
4	R	241	ALA	2.9
1	O	201	GLU	2.9
14	b	195	GLN	2.9
3	Q	225	GLU	2.9
11	Y	106	ARG	2.8
10	J	193	ASP	2.8
10	X	193	ASP	2.8
5	S	173	ARG	2.8
5	E	123	GLY	2.7
1	A	2	THR	2.7
14	N	195	GLN	2.7
4	R	177	ASN	2.6
4	R	242	GLU	2.6
2	B	59	ASP	2.6
2	B	51	VAL	2.6
6	F	2	THR	2.6
14	N	105	LYS	2.5
3	Q	204	GLY	2.5
6	F	241	LYS	2.5
7	G	241	GLU	2.5
1	A	1	MET	2.5
1	A	250	LEU	2.5
5	E	233	ILE	2.5
3	Q	223	SER	2.5
4	R	125	LEU	2.4
12	L	165	ASN	2.4
3	Q	235	GLU	2.4
4	D	1	ASP	2.4
3	C	239	GLN	2.4
2	B	60	THR	2.4
6	F	244	ASN	2.4
3	C	1	GLY	2.4
6	T	181	GLU	2.4
8	H	198	GLU	2.4
2	P	50	LYS	2.4
6	F	215	CYS	2.4
5	S	3	ASN	2.3
7	G	222	ASP	2.3
3	Q	180	LYS	2.3
6	T	180	PRO	2.3
6	T	2	THR	2.3

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Mol	Chain	Res	Type	RSRZ
4	R	169	GLU	2.3
12	Z	210	ASP	2.3
13	M	216	ASN	2.3
12	Z	1	GLN	2.3
6	T	205	GLU	2.3
3	C	216	ASP	2.3
3	C	225	GLU	2.3
9	W	192	ASP	2.3
7	G	242	GLN	2.2
9	W	160	GLU	2.2
3	C	240	GLU	2.2
3	C	206	LYS	2.2
4	R	1	ASP	2.2
4	R	201	GLU	2.2
13	a	216	ASN	2.2
1	O	245	ASP	2.2
8	V	9	GLN	2.2
3	Q	51	LYS	2.2
1	O	1	MET	2.2
4	R	230	GLU	2.2
9	I	192	ASP	2.2
9	I	1	SER	2.2
7	U	2	GLY	2.2
7	U	181	LYS	2.1
3	C	187	GLU	2.1
9	I	160	GLU	2.1
2	B	235	LYS	2.1
5	S	204	SER	2.1
5	E	180	LYS	2.1
12	L	1	GLN	2.1
3	C	180	LYS	2.1
4	D	238	LYS	2.1
10	J	174	MET	2.1
3	Q	233	GLN	2.1
2	P	217	LYS	2.1
3	C	27	ARG	2.1
3	C	175	LYS	2.1
4	R	114	ARG	2.1
1	O	248	GLU	2.1
11	K	147	ASP	2.1
7	G	179	LYS	2.0
3	Q	187	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
7	G	181	LYS	2.0
5	S	207	VAL	2.0
6	F	180	PRO	2.0
1	A	248	GLU	2.0
8	V	219	ASN	2.0
2	P	60	THR	2.0
11	Y	147	ASP	2.0
6	T	204	LYS	2.0
4	D	224	ASP	2.0
6	F	202	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

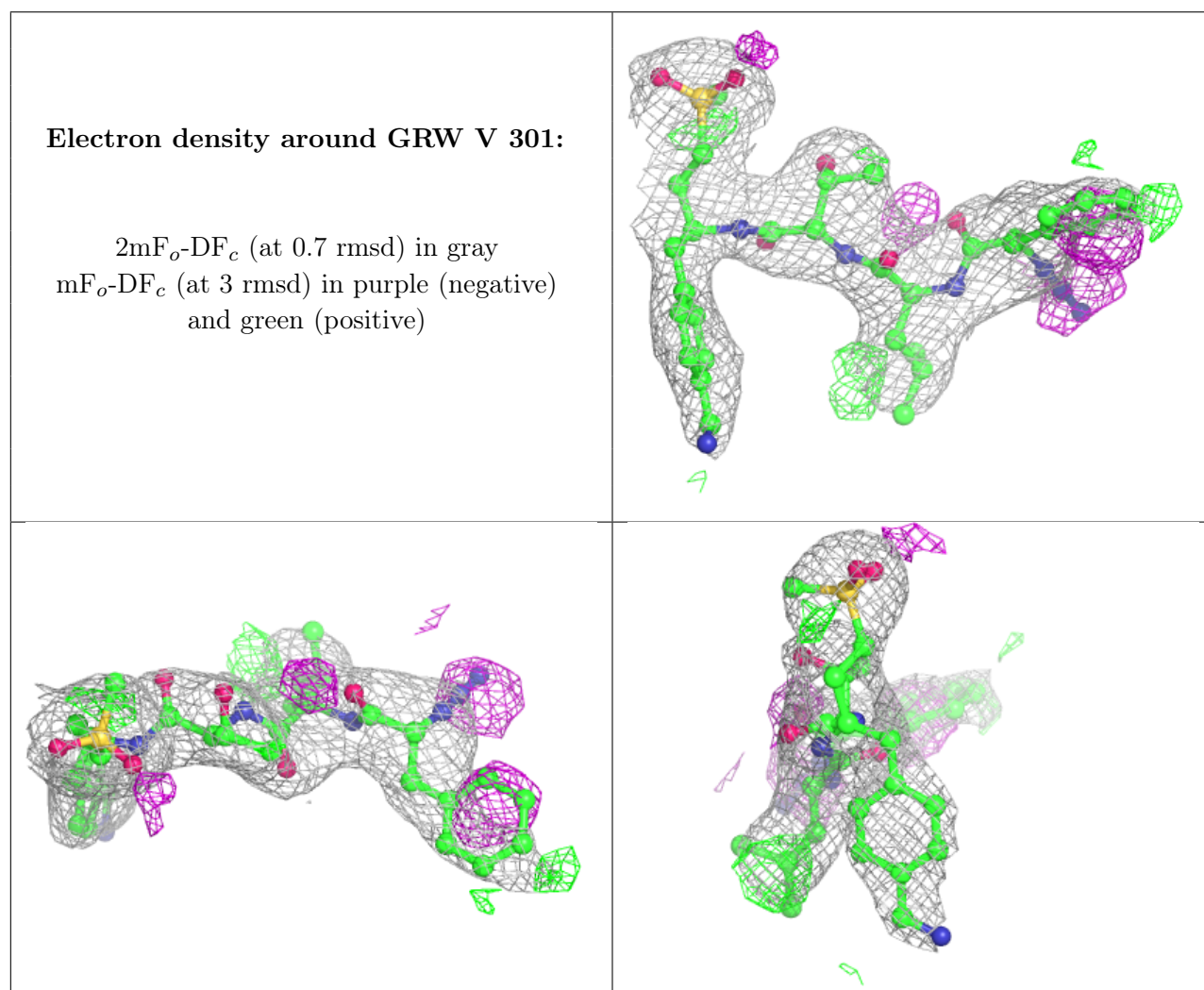
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	MG	I	302	1/1	0.90	0.14	72,72,72,72	0
17	GRW	V	301	45/45	0.91	0.20	56,70,100,104	0
17	GRW	K	301	45/45	0.92	0.18	47,52,77,92	0
17	GRW	H	301	45/45	0.92	0.18	58,64,96,99	0
17	GRW	Y	301	45/45	0.92	0.19	48,58,77,88	0
15	MG	Z	301	1/1	0.93	0.33	66,66,66,66	0
15	MG	I	301	1/1	0.94	0.39	77,77,77,77	0
15	MG	G	301	1/1	0.96	0.09	65,65,65,65	0
15	MG	W	301	1/1	0.97	0.30	62,62,62,62	0
15	MG	K	302	1/1	0.98	0.10	62,62,62,62	0
15	MG	L	301	1/1	0.99	0.06	73,73,73,73	0
15	MG	N	201	1/1	0.99	0.06	48,48,48,48	0
16	CL	G	302	1/1	0.99	0.12	47,47,47,47	0

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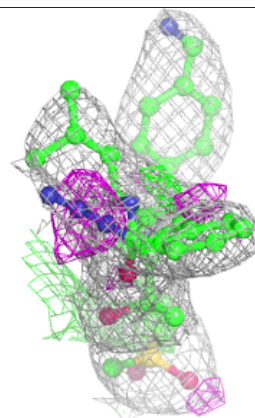
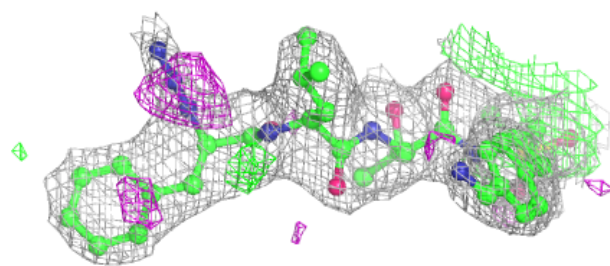
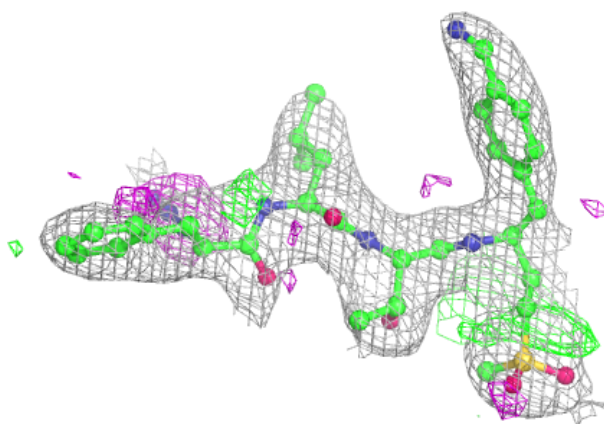
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
16	CL	U	301	1/1	0.99	0.15	54,54,54,54	0

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.



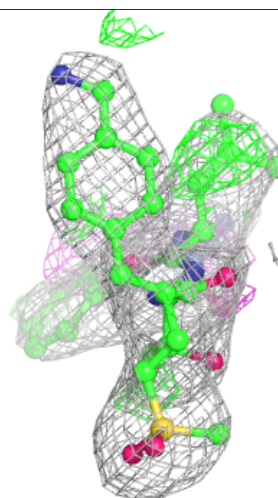
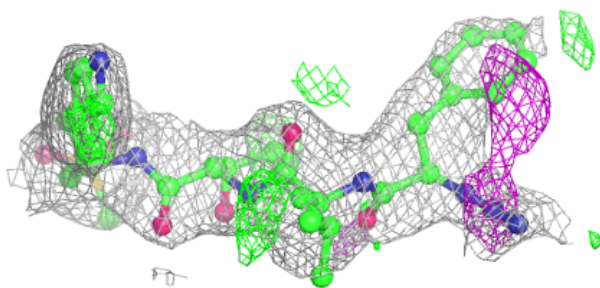
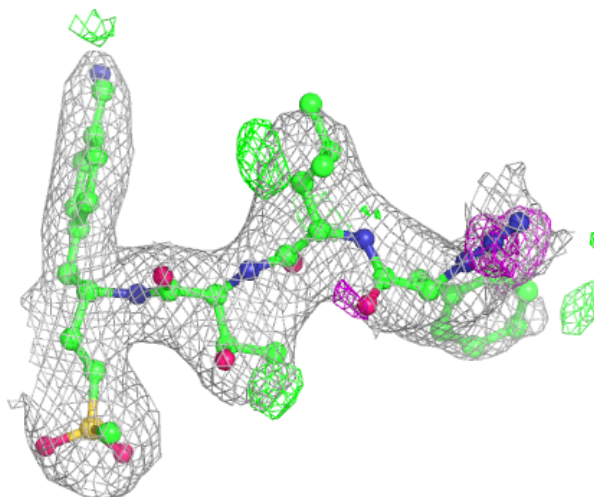
Electron density around GRW K 301:

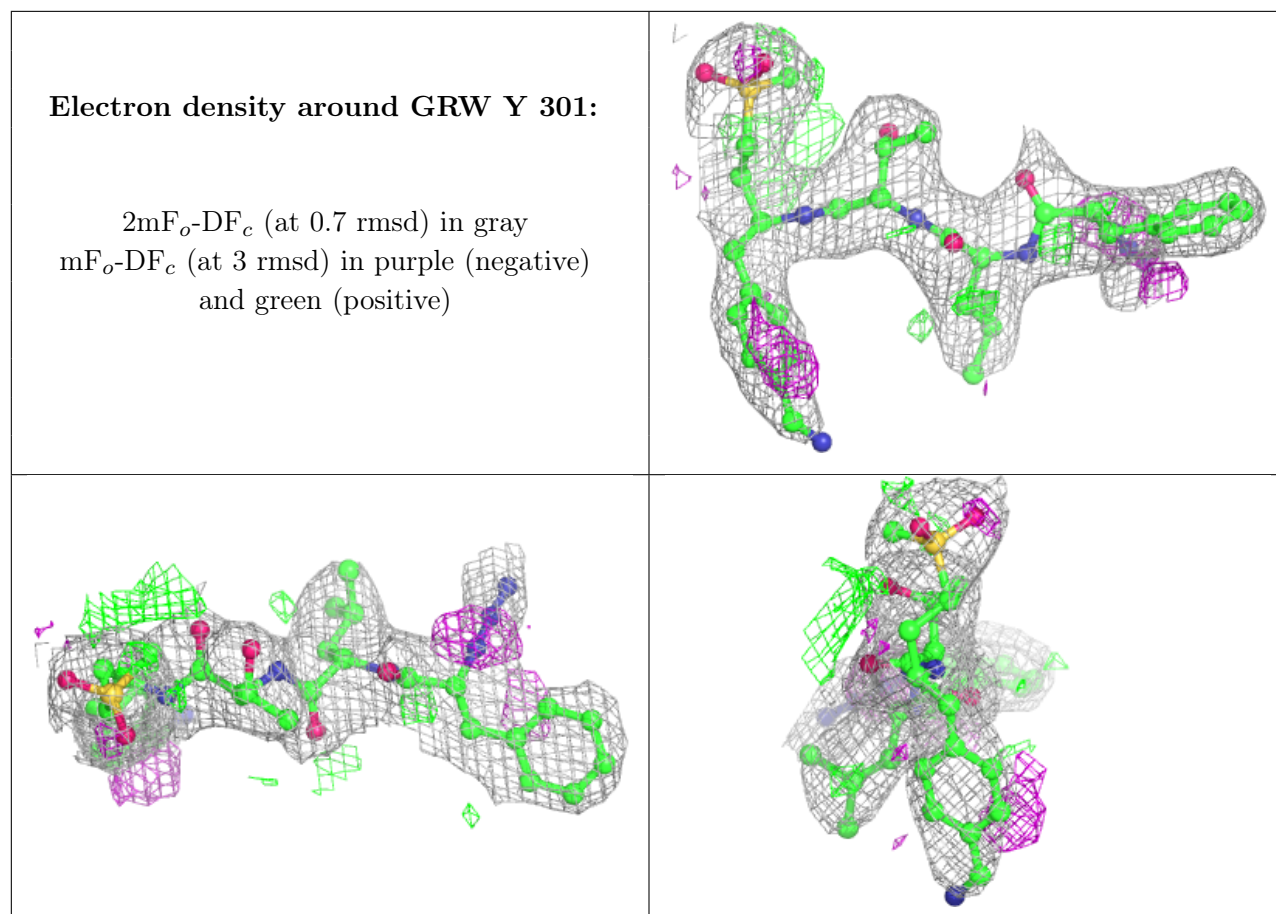
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GRW 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.