



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 24, 2020 – 02:54 PM BST

PDB ID : 5LF7
Title : Human 20S proteasome complex with Ixazomib at 2.0 Angstrom
Authors : Schrader, J.; Henneberg, F.; Mata, R.; Tittmann, K.; Schneider, T.R.; Stark, H.; Bourenkov, G.; Chari, A.
Deposited on : 2016-06-30
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
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) : 2.13

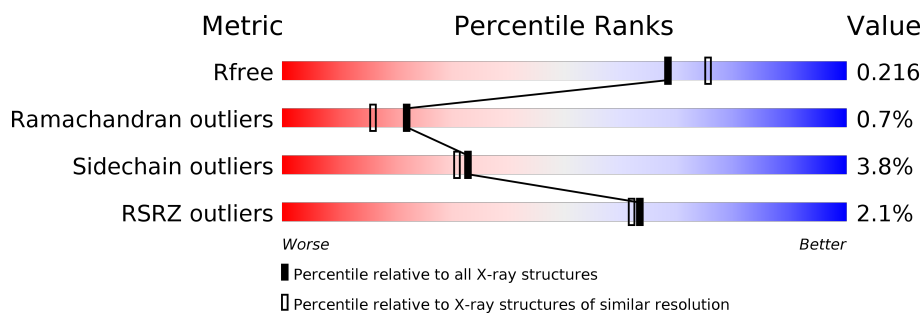
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	234	<div> <div></div> <div>92% 5% ..</div> </div>
1	O	234	<div> <div>6%</div> <div>91% 6% ..</div> </div>
2	B	261	<div> <div>2%</div> <div>90% 5% 5%</div> </div>
2	P	261	<div> <div>5%</div> <div>87% 6% • 5%</div> </div>
3	C	248	<div> <div>6%</div> <div>87% 8% •</div> </div>
3	Q	248	<div> <div>7%</div> <div>85% 10% • •</div> </div>
4	D	241	<div> <div>2%</div> <div>92% 5% •</div> </div>

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Mol	Chain	Length	Quality of chain
4	R	241	
5	E	263	
5	S	263	
6	F	255	
6	T	255	
7	G	246	
7	U	246	
8	H	234	
8	V	234	
9	I	205	
9	W	205	
10	J	201	
10	X	201	
11	K	204	
11	Y	204	
12	L	213	
12	Z	213	
13	M	219	
13	a	219	
14	N	205	
14	b	205	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	6V1	U	47	X	-	-	-

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 52085 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	3	0
			1788	1145	301	336	6			
1	O	230	Total	C	N	O	S	0	0	0
			1741	1111	293	331	6			

- Molecule 2 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	248	Total	C	N	O	S	0	2	0
			1926	1220	332	363	11			
2	P	247	Total	C	N	O	S	0	2	0
			1898	1200	321	366	11			

- Molecule 3 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	237	Total	C	N	O	S	0	2	0
			1798	1121	320	352	5			
3	Q	239	Total	C	N	O	S	0	0	0
			1820	1136	320	359	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	233	Total	C	N	O	S	0	1	0
			1762	1105	290	356	11			
4	R	233	Total	C	N	O	S	0	1	0
			1753	1103	293	346	11			

- Molecule 5 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	234	Total	C	N	O	S	0	1	0
			1822	1144	325	342	11			
5	S	238	Total	C	N	O	S	0	3	0
			1875	1175	340	349	11			

- Molecule 6 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	239	Total	C	N	O	S	0	4	0
			1888	1198	325	353	12			
6	T	240	Total	C	N	O	S	0	1	0
			1856	1178	315	351	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	244	Total	C	N	O	S	0	2	0
			1912	1214	321	364	13			
7	U	238	Total	C	N	O	S	0	1	0
			1815	1147	304	350	14			

- Molecule 8 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	220	Total	C	N	O	S	0	2	0
			1664	1047	284	320	13			
8	V	220	Total	C	N	O	S	0	2	0
			1622	1023	269	318	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	3	0
			1613	1028	270	295	20			
9	W	204	Total	C	N	O	S	0	2	0
			1599	1018	267	295	19			

- Molecule 10 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	196	Total	C	N	O	S	0	3	0
			1590	1021	271	288	10			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	196	Total	C	N	O	S	0	2	0
			1576	1012	267	287	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	200	Total	C	N	O	S	0	0	0
			1545	974	269	293	9			
11	Y	201	Total	C	N	O	S	0	3	0
			1580	996	280	294	10			

- Molecule 12 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	213	Total	C	N	O	S	0	2	0
			1636	1038	277	310	11			
12	Z	213	Total	C	N	O	S	0	1	0
			1642	1041	280	310	11			

- Molecule 13 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	216	Total	C	N	O	S	0	1	0
			1692	1067	291	322	12			
13	a	216	Total	C	N	O	S	0	2	0
			1688	1064	291	321	12			

- Molecule 14 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	202	Total	C	N	O	S	0	1	0
			1516	950	258	295	13			
14	b	203	Total	C	N	O	S	0	1	0
			1524	956	259	296	13			

- Molecule 15 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	P	1	Total	Cl	0	0
			1	1		
15	K	3	Total	Cl	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	B	2	Total 2	Cl 2	0	0
15	W	1	Total 1	Cl 1	0	0
15	N	2	Total 2	Cl 2	0	0
15	S	3	Total 3	Cl 3	0	0
15	E	3	Total 3	Cl 3	0	0
15	b	1	Total 1	Cl 1	0	0
15	V	1	Total 1	Cl 1	0	0
15	A	4	Total 4	Cl 4	0	0
15	R	2	Total 2	Cl 2	0	0
15	M	4	Total 4	Cl 4	0	0
15	D	2	Total 2	Cl 2	0	0
15	I	1	Total 1	Cl 1	0	0
15	a	4	Total 4	Cl 4	0	0
15	U	1	Total 1	Cl 1	0	0
15	G	2	Total 2	Cl 2	0	0
15	Q	2	Total 2	Cl 2	0	0
15	H	1	Total 1	Cl 1	0	0
15	C	2	Total 2	Cl 2	0	0
15	O	4	Total 4	Cl 4	0	0
15	Y	4	Total 4	Cl 4	0	0
15	F	1	Total 1	Cl 1	0	0

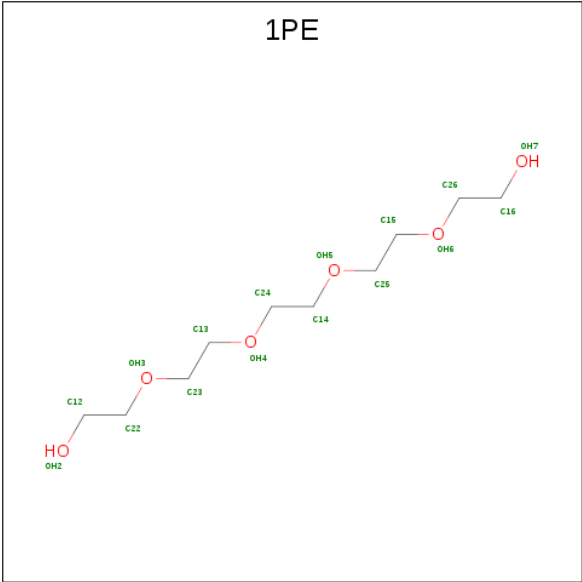
- Molecule 16 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total K 1 1	0	0
16	b	1	Total K 1 1	0	0
16	Z	1	Total K 1 1	0	0
16	N	1	Total K 1 1	0	0
16	U	1	Total K 1 1	0	0
16	L	1	Total K 1 1	0	0

- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

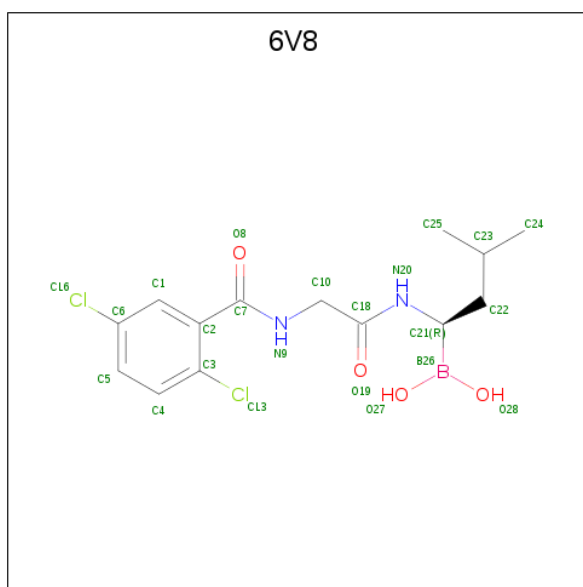
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	J	1	Total Mg 1 1	0	0
17	K	1	Total Mg 1 1	0	0
17	H	2	Total Mg 2 2	0	0
17	I	2	Total Mg 2 2	0	0
17	V	1	Total Mg 1 1	0	0
17	W	1	Total Mg 1 1	0	0
17	X	1	Total Mg 1 1	0	0
17	L	1	Total Mg 1 1	0	0

- Molecule 18 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	H	1	Total	C	O	0	0
			16	10	6		
18	I	1	Total	C	O	0	0
			16	10	6		
18	I	1	Total	C	O	0	0
			16	10	6		
18	L	1	Total	C	O	0	0
			16	10	6		
18	M	1	Total	C	O	0	0
			16	10	6		
18	N	1	Total	C	O	0	0
			16	10	6		
18	W	1	Total	C	O	0	0
			16	10	6		
18	Y	1	Total	C	O	0	0
			16	10	6		
18	b	1	Total	C	O	0	0
			16	10	6		

- Molecule 19 is [(1 {R})-1-[2-[[2,5-bis(chloranyl)phenyl]carbonylamino]ethanoylamino]-3-methyl-butyl]boronic acid (three-letter code: 6V8) (formula: C₁₄H₁₉BCl₂N₂O₄).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
19	H	1	Total	B	C	Cl	N	O	0	0
			23	1	14	2	2	4		
19	K	1	Total	B	C	Cl	N	O	0	0
			23	1	14	2	2	4		
19	N	1	Total	B	C	Cl	N	O	0	0
			23	1	14	2	2	4		
19	V	1	Total	B	C	Cl	N	O	0	0
			23	1	14	2	2	4		
19	Y	1	Total	B	C	Cl	N	O	0	0
			23	1	14	2	2	4		
19	b	1	Total	B	C	Cl	N	O	0	0
			23	1	14	2	2	4		

- Molecule 20 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	A	110	Total	O	0	0
			110	110		
20	B	124	Total	O	0	0
			124	124		
20	C	76	Total	O	0	0
			76	76		
20	D	88	Total	O	0	0
			88	88		
20	E	143	Total	O	0	0
			143	143		
20	F	189	Total	O	0	0
			189	189		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	G	190	Total 190	O 190	0	0
20	H	158	Total 158	O 158	0	0
20	I	153	Total 153	O 153	0	0
20	J	137	Total 137	O 137	0	0
20	K	100	Total 100	O 100	0	0
20	L	131	Total 131	O 131	0	0
20	M	146	Total 146	O 146	0	0
20	N	158	Total 158	O 158	0	0
20	O	92	Total 92	O 92	0	0
20	P	117	Total 117	O 117	0	0
20	Q	73	Total 73	O 73	0	0
20	R	124	Total 124	O 124	0	0
20	S	122	Total 122	O 122	0	0
20	T	89	Total 89	O 89	0	0
20	U	106	Total 106	O 106	0	0
20	V	114	Total 114	O 114	0	0
20	W	114	Total 114	O 114	0	0
20	X	128	Total 128	O 128	0	0
20	Y	150	Total 150	O 150	0	0
20	Z	169	Total 169	O 169	0	0
20	a	173	Total 173	O 173	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	b	121	Total	O	0	0
			121	121		

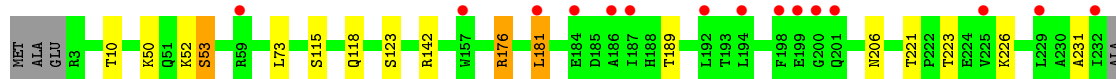
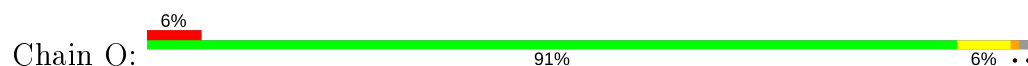
3 Residue-property plots [i](#)

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.

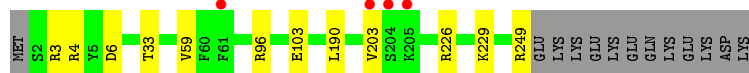
- Molecule 1: Proteasome subunit alpha type-2



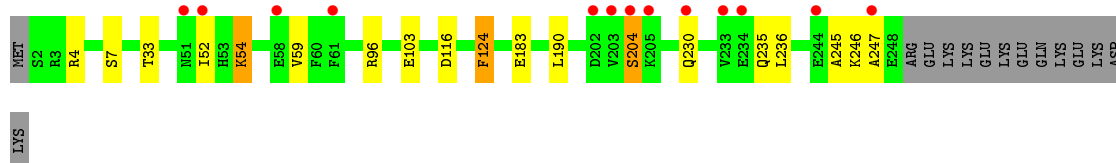
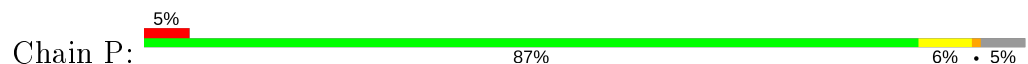
- Molecule 1: Proteasome subunit alpha type-2



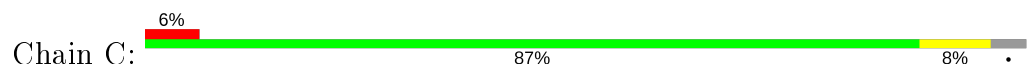
- Molecule 2: Proteasome subunit alpha type-4



- Molecule 2: Proteasome subunit alpha type-4




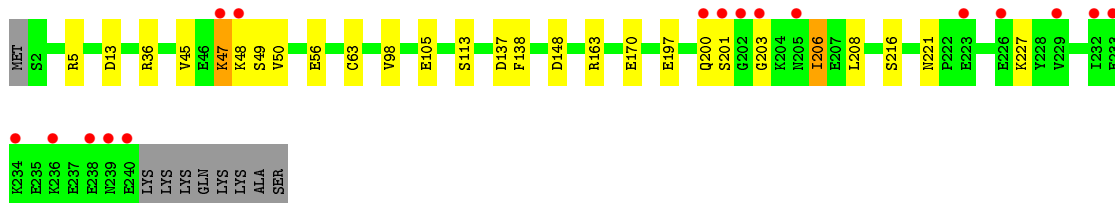
- Molecule 3: Proteasome subunit alpha type-7



LYS
GLN
LYS
LYS
ALA
SER

• Molecule 3: Proteasome subunit alpha type-7

Chain Q: 

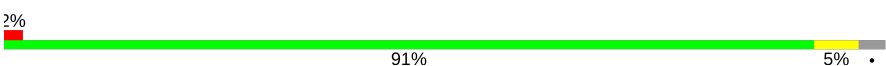


• Molecule 4: Proteasome subunit alpha type-5

Chain D: 




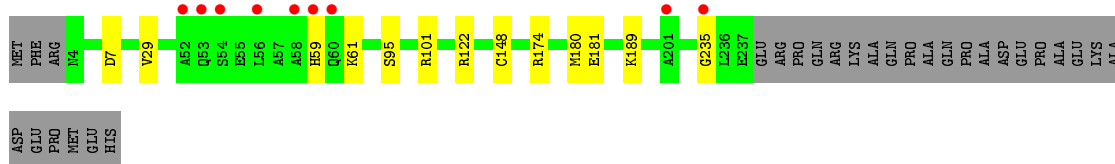
• Molecule 4: Proteasome subunit alpha type-5

Chain R: 




• Molecule 5: Proteasome subunit alpha type-1

Chain E: 




• Molecule 5: Proteasome subunit alpha type-1

Chain S: 

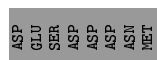
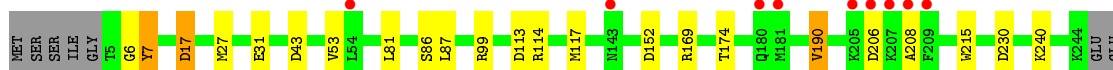
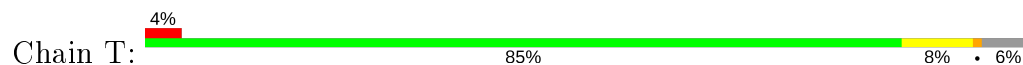


• Molecule 6: Proteasome subunit alpha type-3

Chain F: 



• Molecule 6: Proteasome subunit alpha type-3



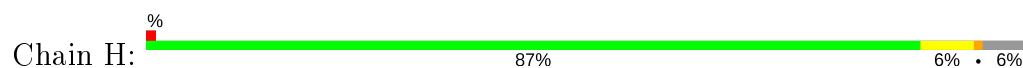
• Molecule 7: Proteasome subunit alpha type-6



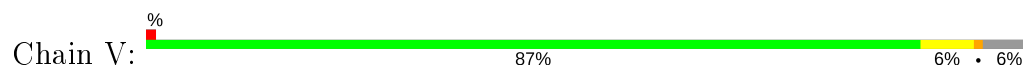
• Molecule 7: Proteasome subunit alpha type-6



• Molecule 8: Proteasome subunit beta type-7



• Molecule 8: Proteasome subunit beta type-7



• Molecule 9: Proteasome subunit beta type-3



- Molecule 9: Proteasome subunit beta type-3

Chain W:  94% 5%



- Molecule 10: Proteasome subunit beta type-2

Chain J:  91% 6% •



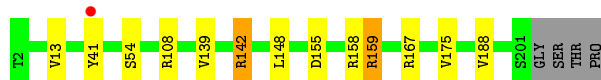
- Molecule 10: Proteasome subunit beta type-2

Chain X:  91% 6% •



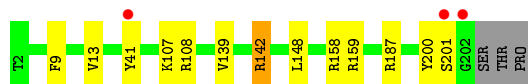
- Molecule 11: Proteasome subunit beta type-5

Chain K:  92% 5% ••



- Molecule 11: Proteasome subunit beta type-5

Chain Y:  92% 6% •



- Molecule 12: Proteasome subunit beta type-1

Chain L:  95% ••



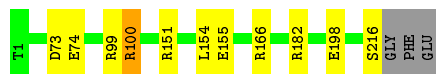
- Molecule 12: Proteasome subunit beta type-1

Chain Z:  94% 5% •



- Molecule 13: Proteasome subunit beta type-4

Chain M:  94% 5% •



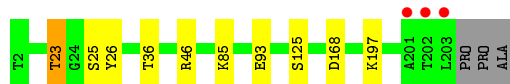
- Molecule 13: Proteasome subunit beta type-4

Chain a:  94% 5% •



- Molecule 14: Proteasome subunit beta type-6

Chain N:  94% • •



- Molecule 14: Proteasome subunit beta type-6

Chain b:  96% • • •



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.41Å 202.61Å 314.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	170.33 – 2.00 106.69 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (170.33-2.00) 99.4 (106.69-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.175 , 0.213 0.181 , 0.216	Depositor DCC
R_{free} test set	24030 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	40.1	Xtriage
Anisotropy	0.156	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	52085	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 6V8, K, CL, 6V1, 1PE, YCM

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	0.95	2/1833 (0.1%)	0.94	2/2489 (0.1%)
1	O	0.81	2/1778 (0.1%)	0.87	2/2419 (0.1%)
2	B	0.90	2/1962 (0.1%)	0.94	6/2649 (0.2%)
2	P	0.92	2/1934 (0.1%)	0.96	6/2617 (0.2%)
3	C	0.84	1/1818 (0.1%)	0.98	5/2469 (0.2%)
3	Q	0.87	2/1834 (0.1%)	0.96	5/2490 (0.2%)
4	D	0.87	1/1789 (0.1%)	0.91	3/2424 (0.1%)
4	R	0.98	3/1780 (0.2%)	0.98	5/2408 (0.2%)
5	E	0.94	1/1842 (0.1%)	0.98	2/2493 (0.1%)
5	S	0.85	0/1901	0.93	4/2571 (0.2%)
6	F	1.08	1/1935 (0.1%)	1.09	9/2605 (0.3%)
6	T	0.82	1/1894 (0.1%)	1.02	15/2556 (0.6%)
7	G	1.07	5/1909 (0.3%)	0.96	6/2579 (0.2%)
7	U	0.79	2/1804 (0.1%)	0.88	6/2441 (0.2%)
8	H	1.09	4/1697 (0.2%)	1.14	12/2299 (0.5%)
8	V	0.94	2/1655 (0.1%)	1.02	11/2251 (0.5%)
9	I	1.05	4/1648 (0.2%)	1.16	11/2219 (0.5%)
9	W	0.96	0/1630	1.10	11/2197 (0.5%)
10	J	0.94	1/1613 (0.1%)	1.14	10/2180 (0.5%)
10	X	0.99	2/1599 (0.1%)	1.14	8/2163 (0.4%)
11	K	1.04	3/1576 (0.2%)	1.04	6/2131 (0.3%)
11	Y	1.09	1/1620 (0.1%)	1.08	7/2185 (0.3%)
12	L	1.02	1/1672 (0.1%)	1.04	5/2257 (0.2%)
12	Z	1.11	3/1675 (0.2%)	1.09	7/2257 (0.3%)
13	M	1.01	1/1728 (0.1%)	1.04	7/2339 (0.3%)
13	a	1.01	3/1724 (0.2%)	1.01	3/2336 (0.1%)
14	N	1.06	5/1545 (0.3%)	0.98	4/2091 (0.2%)
14	b	0.92	1/1554 (0.1%)	0.99	4/2104 (0.2%)
All	All	0.96	56/48949 (0.1%)	1.01	182/66219 (0.3%)

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
2	P	0	2
3	C	0	2
3	Q	0	2
4	D	0	4
4	R	0	2
5	E	0	1
7	U	1	0
9	I	0	1
9	W	0	1
10	J	0	2
10	X	0	1
11	Y	0	1
13	a	0	1
All	All	1	20

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	108	GLU	CD-OE1	10.94	1.37	1.25
8	H	32	CYS	CB-SG	-9.11	1.66	1.82
12	Z	3	SER	CB-OG	9.01	1.53	1.42
2	P	103	GLU	CD-OE2	8.79	1.35	1.25
12	Z	142	SER	CB-OG	-7.82	1.32	1.42

The worst 5 of 182 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	X	86	ARG	NE-CZ-NH2	-18.15	111.23	120.30
10	J	86	ARG	NE-CZ-NH2	-17.76	111.42	120.30
9	I	69	ARG	NE-CZ-NH1	15.65	128.12	120.30
9	W	69	ARG	NE-CZ-NH1	13.79	127.20	120.30
10	J	86	ARG	NE-CZ-NH1	13.19	126.89	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	203	GLY	Peptide
3	C	237	GLU	Peptide
4	D	127	ASP	Peptide
4	D	175[A]	GLU	Peptide
4	D	175[B]	GLU	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	231/234 (99%)	220 (95%)	7 (3%)	4 (2%)	9	4
1	O	228/234 (97%)	215 (94%)	8 (4%)	5 (2%)	6	2
2	B	248/261 (95%)	239 (96%)	8 (3%)	1 (0%)	34	30
2	P	247/261 (95%)	233 (94%)	10 (4%)	4 (2%)	9	4
3	C	236/248 (95%)	222 (94%)	7 (3%)	7 (3%)	4	1
3	Q	236/248 (95%)	219 (93%)	7 (3%)	10 (4%)	3	1
4	D	232/241 (96%)	224 (97%)	5 (2%)	3 (1%)	12	6
4	R	232/241 (96%)	225 (97%)	4 (2%)	3 (1%)	12	6
5	E	232/263 (88%)	228 (98%)	3 (1%)	1 (0%)	34	30
5	S	238/263 (90%)	232 (98%)	5 (2%)	1 (0%)	34	30
6	F	241/255 (94%)	237 (98%)	4 (2%)	0	100	100
6	T	239/255 (94%)	234 (98%)	2 (1%)	3 (1%)	12	6
7	G	241/246 (98%)	237 (98%)	4 (2%)	0	100	100
7	U	232/246 (94%)	228 (98%)	4 (2%)	0	100	100
8	H	220/234 (94%)	217 (99%)	2 (1%)	1 (0%)	29	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	V	220/234 (94%)	216 (98%)	3 (1%)	1 (0%)	29	23
9	I	205/205 (100%)	200 (98%)	5 (2%)	0	100	100
9	W	204/205 (100%)	200 (98%)	4 (2%)	0	100	100
10	J	195/201 (97%)	193 (99%)	2 (1%)	0	100	100
10	X	195/201 (97%)	193 (99%)	2 (1%)	0	100	100
11	K	198/204 (97%)	195 (98%)	3 (2%)	0	100	100
11	Y	202/204 (99%)	198 (98%)	3 (2%)	1 (0%)	29	23
12	L	213/213 (100%)	210 (99%)	3 (1%)	0	100	100
12	Z	212/213 (100%)	209 (99%)	3 (1%)	0	100	100
13	M	215/219 (98%)	210 (98%)	5 (2%)	0	100	100
13	a	216/219 (99%)	210 (97%)	6 (3%)	0	100	100
14	N	201/205 (98%)	198 (98%)	3 (2%)	0	100	100
14	b	202/205 (98%)	201 (100%)	1 (0%)	0	100	100
All	All	6211/6458 (96%)	6043 (97%)	123 (2%)	45 (1%)	22	16

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	LYS
1	A	53	SER
5	E	59	HIS
1	O	52	LYS
1	O	53	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	185/191 (97%)	175 (95%)	10 (5%)	22	18
1	O	176/191 (92%)	165 (94%)	11 (6%)	18	13
2	B	200/221 (90%)	195 (98%)	5 (2%)	47	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	196/221 (89%)	184 (94%)	12 (6%)	18	14
3	C	179/210 (85%)	169 (94%)	10 (6%)	21	17
3	Q	184/210 (88%)	173 (94%)	11 (6%)	19	14
4	D	189/203 (93%)	183 (97%)	6 (3%)	39	38
4	R	187/203 (92%)	183 (98%)	4 (2%)	53	57
5	E	192/223 (86%)	184 (96%)	8 (4%)	30	27
5	S	197/223 (88%)	192 (98%)	5 (2%)	47	49
6	F	199/212 (94%)	188 (94%)	11 (6%)	21	17
6	T	192/212 (91%)	182 (95%)	10 (5%)	23	19
7	G	202/207 (98%)	195 (96%)	7 (4%)	36	35
7	U	186/207 (90%)	181 (97%)	5 (3%)	44	46
8	H	181/195 (93%)	175 (97%)	6 (3%)	38	37
8	V	172/195 (88%)	162 (94%)	10 (6%)	20	15
9	I	176/174 (101%)	174 (99%)	2 (1%)	73	78
9	W	173/174 (99%)	171 (99%)	2 (1%)	71	76
10	J	166/170 (98%)	158 (95%)	8 (5%)	25	22
10	X	165/170 (97%)	158 (96%)	7 (4%)	30	27
11	K	154/159 (97%)	147 (96%)	7 (4%)	27	24
11	Y	159/159 (100%)	150 (94%)	9 (6%)	20	16
12	L	175/178 (98%)	167 (95%)	8 (5%)	27	23
12	Z	175/178 (98%)	169 (97%)	6 (3%)	37	36
13	M	180/181 (99%)	175 (97%)	5 (3%)	43	44
13	a	178/181 (98%)	174 (98%)	4 (2%)	52	55
14	N	157/159 (99%)	153 (98%)	4 (2%)	47	49
14	b	158/159 (99%)	153 (97%)	5 (3%)	39	38
All	All	5033/5366 (94%)	4835 (96%)	198 (4%)	33	30

5 of 198 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	154	LEU
2	P	33	THR
11	Y	187[B]	ARG

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Mol	Chain	Res	Type
13	M	216	SER
1	O	142	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	62	HIS
2	P	146	GLN
13	a	89	HIS
1	O	118	GLN
1	O	206	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 non-standard protein/DNA/RNA residues are modelled in this entry.

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
3	YCM	Q	63	3	7,9,10	1.07	1 (14%)	4,10,12	3.08	3 (75%)
7	6V1	G	47	7	12,15,16	2.62	4 (33%)	9,20,22	1.48	1 (11%)
5	6V1	E	148	5	12,15,16	1.57	3 (25%)	9,20,22	3.19	4 (44%)
10	6V1	J	91	10	12,15,16	2.23	4 (33%)	9,20,22	5.54	6 (66%)
3	YCM	C	63	3	7,9,10	0.90	0	4,10,12	0.74	0
7	6V1	G	161	7	12,15,16	1.58	4 (33%)	9,20,22	3.15	6 (66%)
7	6V1	U	47	7	12,15,16	2.01	2 (16%)	9,20,22	2.04	3 (33%)
7	YCM	U	137	7	7,9,10	0.97	0	4,10,12	2.18	1 (25%)
7	YCM	G	137	7	7,9,10	2.21	3 (42%)	4,10,12	2.99	2 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	6V1	S	148	5	12,15,16	1.51	4 (33%)	9,20,22	2.89	3 (33%)
7	6V1	U	161	7	12,15,16	1.84	3 (25%)	9,20,22	2.87	4 (44%)
10	6V1	X	91	10	12,15,16	1.79	4 (33%)	9,20,22	5.90	6 (66%)

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
3	YCM	Q	63	3	-	3/6/8/10	-
7	6V1	G	47	7	-	0/6/25/27	0/1/1/1
5	6V1	E	148	5	-	2/6/25/27	0/1/1/1
7	6V1	G	161	7	-	2/6/25/27	0/1/1/1
3	YCM	C	63	3	-	1/6/8/10	-
10	6V1	J	91	10	-	2/6/25/27	0/1/1/1
7	6V1	U	47	7	1/1/5/6	0/6/25/27	0/1/1/1
7	YCM	U	137	7	-	1/6/8/10	-
7	YCM	G	137	7	-	3/6/8/10	-
5	6V1	S	148	5	-	2/6/25/27	0/1/1/1
7	6V1	U	161	7	-	1/6/25/27	0/1/1/1
10	6V1	X	91	10	-	2/6/25/27	0/1/1/1

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	47	6V1	CB-SG	-6.71	1.74	1.82
7	U	47	6V1	CB-SG	-5.67	1.76	1.82
10	J	91	6V1	CB-SG	-5.40	1.76	1.82
10	X	91	6V1	CB-SG	-4.42	1.77	1.82
7	U	161	6V1	CB-SG	-4.07	1.77	1.82

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	X	91	6V1	C5-C4-N3	9.28	113.60	108.13
10	J	91	6V1	C5-C4-N3	8.48	113.13	108.13
10	X	91	6V1	O7-C2-N3	8.14	134.10	124.14
10	X	91	6V1	C2-N3-C4	-8.14	108.21	113.04
10	J	91	6V1	O7-C2-N3	7.85	133.75	124.14

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	Q	63	YCM	CE-CD-SG-CB
3	Q	63	YCM	SG-CD-CE-OZ1
3	Q	63	YCM	SG-CD-CE-NZ2
5	E	148	6V1	C3-C6-N3-C4
10	J	91	6V1	C3-C6-N3-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 82 ligands modelled in this entry, 67 are monoatomic - leaving 15 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	$\# Z > 2$
18	1PE	I	303	-	15,15,15	0.56	0	14,14,14	0.90	0
18	1PE	L	301	-	15,15,15	0.60	0	14,14,14	0.76	0
18	1PE	Y	305	-	15,15,15	0.56	0	14,14,14	0.55	0
19	6V8	Y	306	11	19,23,23	1.70	5 (26%)	24,31,31	2.81	9 (37%)
18	1PE	N	303	-	15,15,15	0.51	0	14,14,14	0.78	0
19	6V8	b	304	14	19,23,23	1.73	1 (5%)	24,31,31	1.60	5 (20%)
18	1PE	b	302	-	15,15,15	0.63	0	14,14,14	1.07	1 (7%)
19	6V8	V	303	8	19,23,23	2.79	3 (15%)	24,31,31	3.00	10 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	1PE	M	305	-	15,15,15	0.51	0	14,14,14	0.43	0
18	1PE	W	303	-	15,15,15	0.58	0	14,14,14	0.47	0
19	6V8	N	305	14	19,23,23	1.34	2 (10%)	24,31,31	2.11	8 (33%)
19	6V8	H	305	8	19,23,23	2.45	3 (15%)	24,31,31	2.93	10 (41%)
18	1PE	H	304	-	15,15,15	0.43	0	14,14,14	0.47	0
19	6V8	K	305	11	19,23,23	1.65	3 (15%)	24,31,31	2.20	8 (33%)
18	1PE	I	304	-	15,15,15	0.50	0	14,14,14	0.78	0

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
18	1PE	I	303	-	-	7/13/13/13	-
18	1PE	L	301	-	-	6/13/13/13	-
18	1PE	Y	305	-	-	7/13/13/13	-
19	6V8	Y	306	11	-	0/15/21/21	0/1/1/1
18	1PE	N	303	-	-	5/13/13/13	-
19	6V8	b	304	14	-	1/15/21/21	0/1/1/1
18	1PE	b	302	-	-	7/13/13/13	-
19	6V8	V	303	8	-	2/15/21/21	0/1/1/1
18	1PE	M	305	-	-	6/13/13/13	-
18	1PE	W	303	-	-	8/13/13/13	-
19	6V8	N	305	14	-	1/15/21/21	0/1/1/1
19	6V8	H	305	8	-	3/15/21/21	0/1/1/1
18	1PE	H	304	-	-	5/13/13/13	-
19	6V8	K	305	11	-	0/15/21/21	0/1/1/1
18	1PE	I	304	-	-	8/13/13/13	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	V	303	6V8	C2-C3	10.73	1.54	1.39
19	H	305	6V8	C2-C3	9.05	1.52	1.39
19	b	304	6V8	C2-C3	6.77	1.48	1.39
19	K	305	6V8	C2-C3	5.34	1.46	1.39
19	Y	306	6V8	C1-C2	-4.96	1.32	1.39

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	V	303	6V8	C2-C3-CL3	7.74	132.44	121.00
19	V	303	6V8	C3-C2-C7	7.22	134.08	122.58
19	H	305	6V8	C2-C3-CL3	7.06	131.44	121.00
19	Y	306	6V8	C2-C3-CL3	-6.72	111.06	121.00
19	H	305	6V8	C3-C2-C7	6.20	132.45	122.58

There are no chirality outliers.

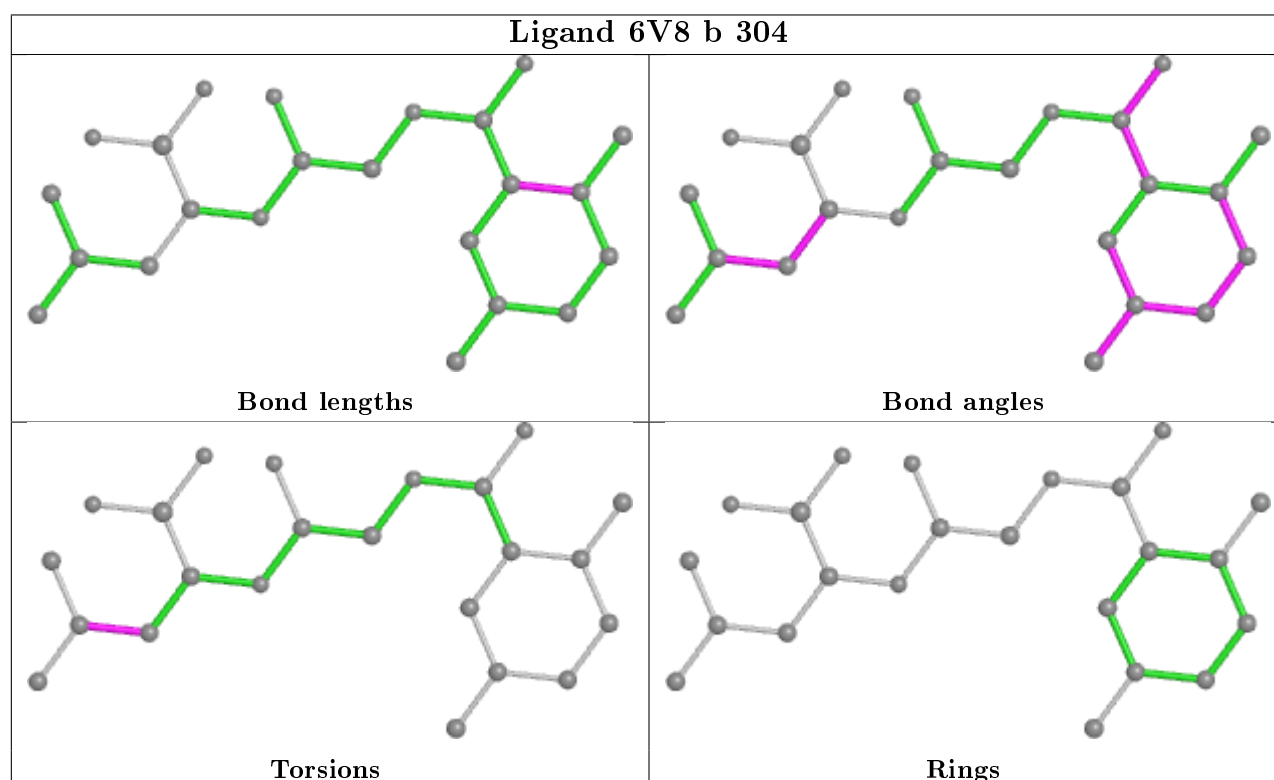
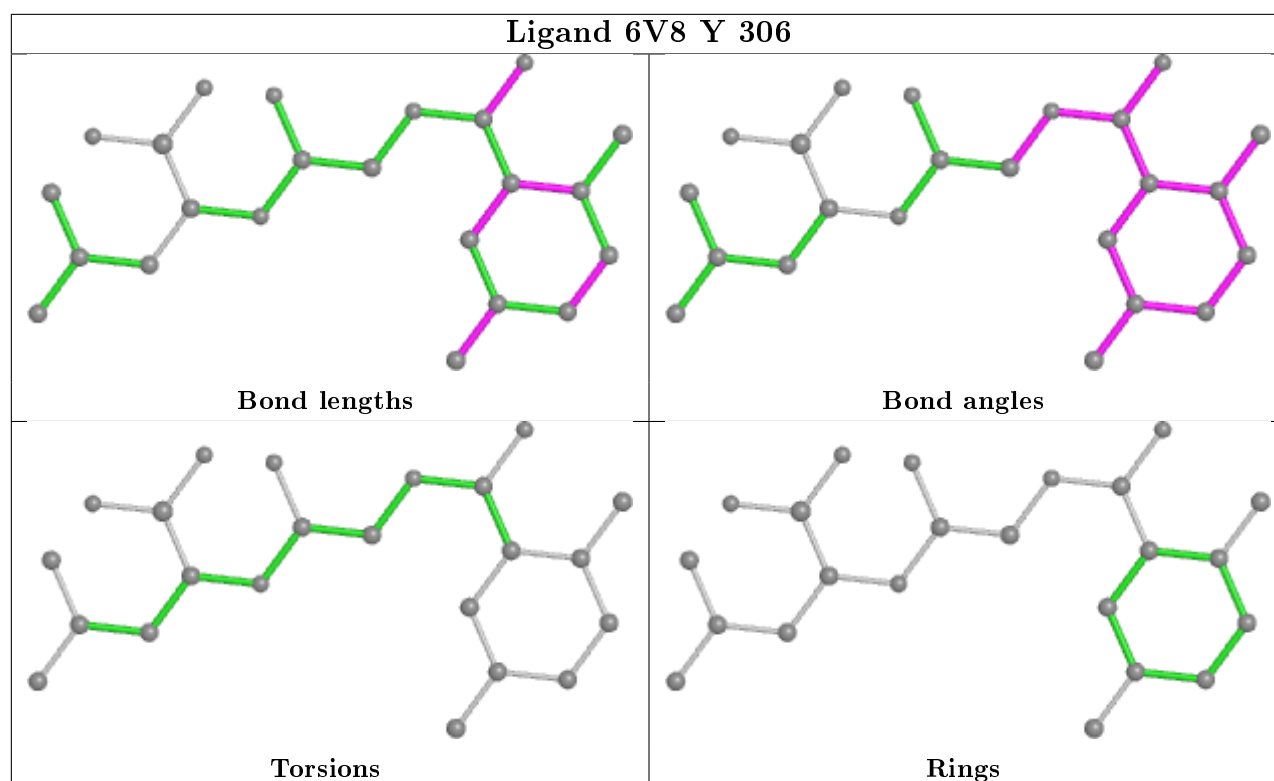
5 of 66 torsion outliers are listed below:

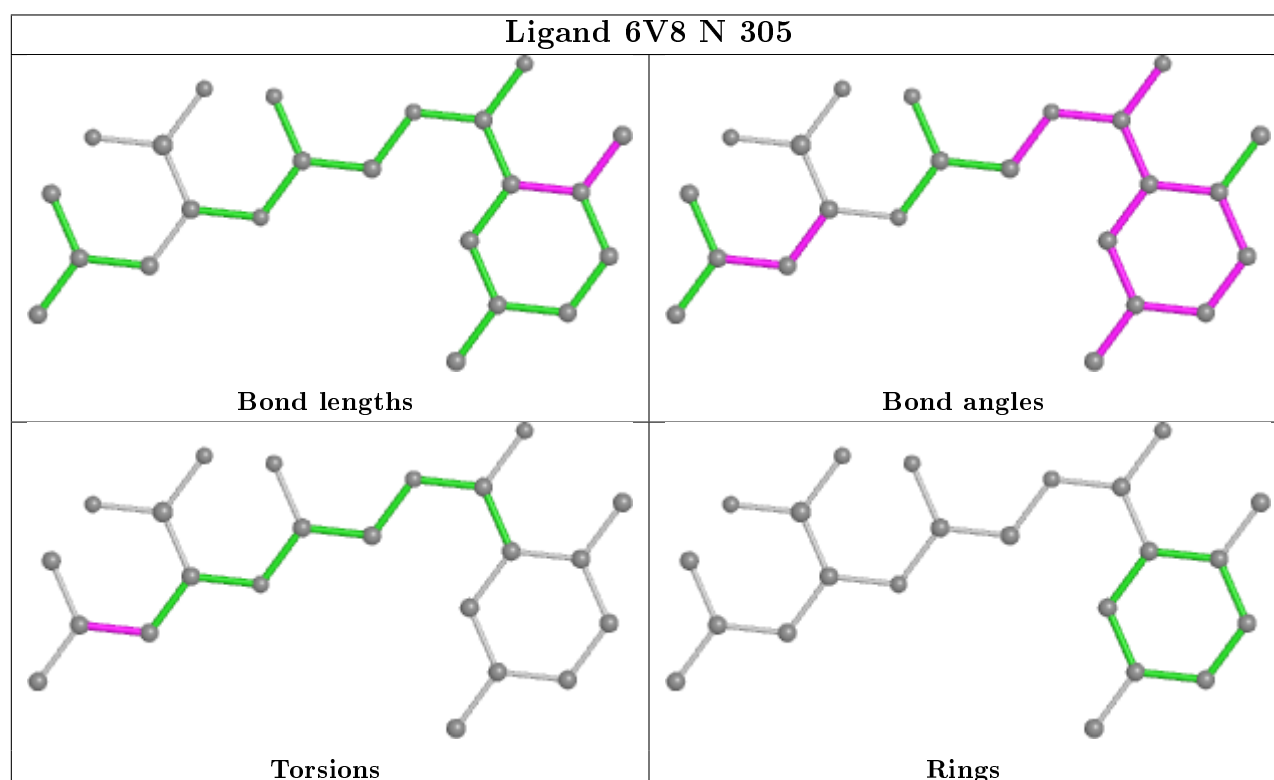
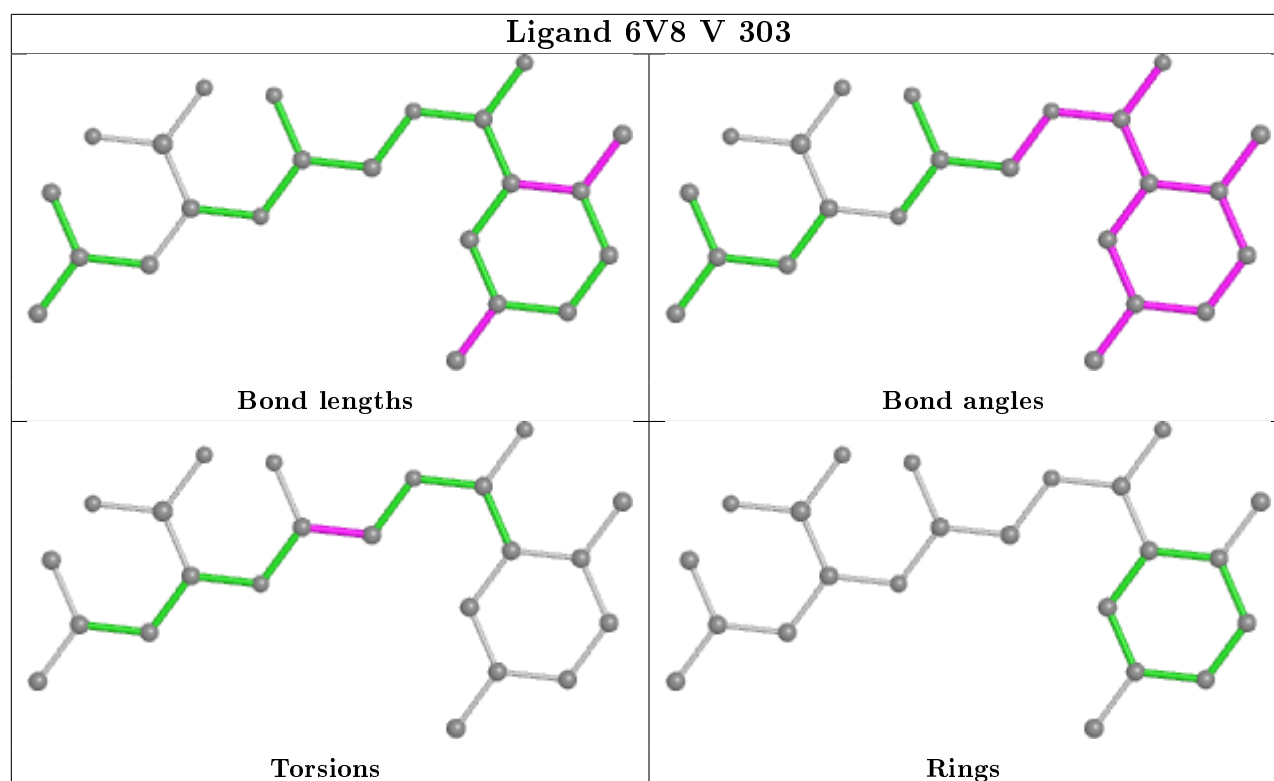
Mol	Chain	Res	Type	Atoms
18	b	302	1PE	C25-C15-OH6-C26
18	L	301	1PE	C16-C26-OH6-C15
18	N	303	1PE	C13-C23-OH3-C22
18	I	304	1PE	C24-C14-OH5-C25
18	M	305	1PE	OH5-C14-C24-OH4

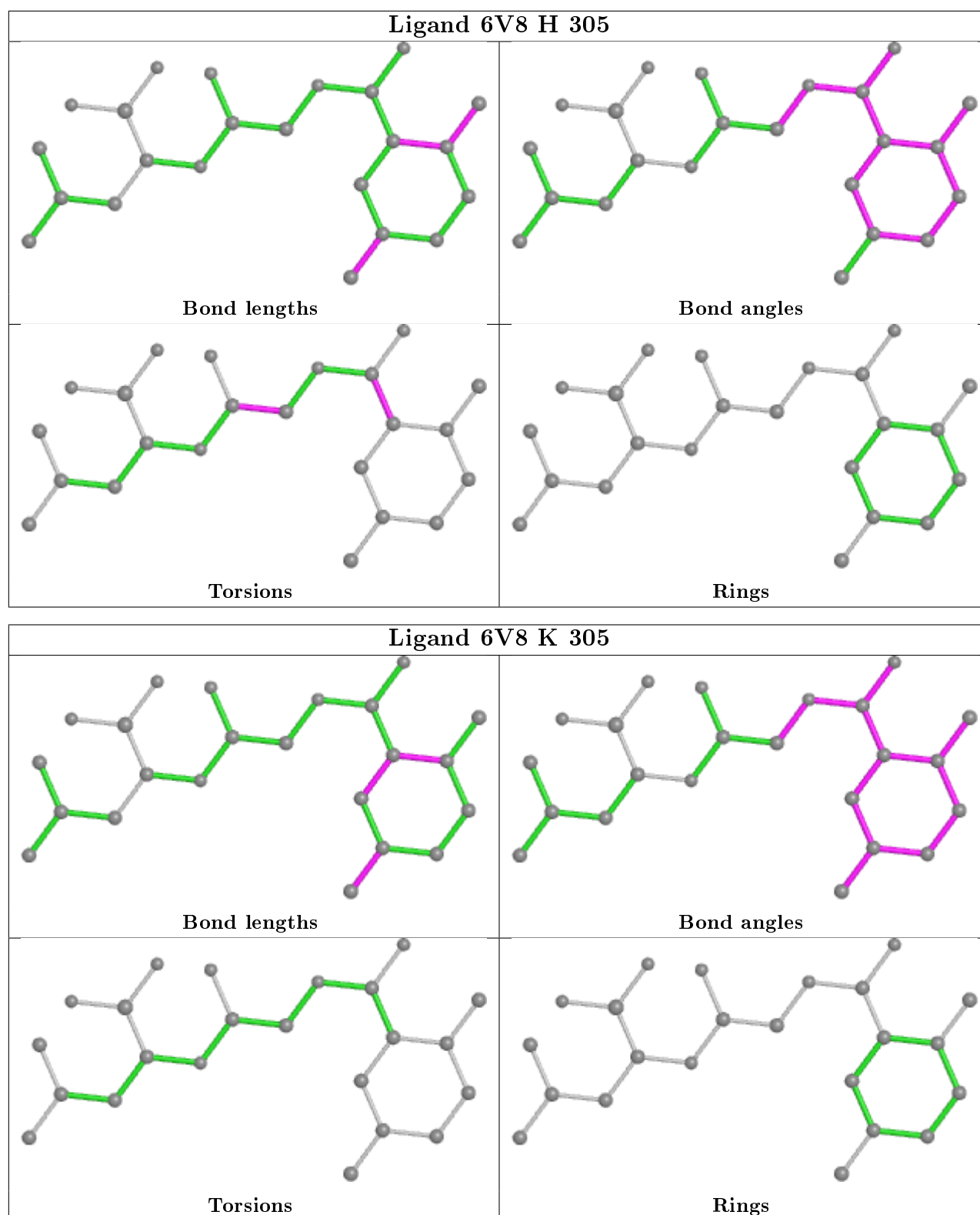
There are no ring outliers.

No monomer is involved in short contacts.

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







5.7 Other polymers ⓘ

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	230/234 (98%)	-0.14	2 (0%) 84 83	31, 45, 86, 98	0
1	O	230/234 (98%)	0.29	15 (6%) 18 18	43, 67, 110, 149	0
2	B	248/261 (95%)	-0.00	4 (1%) 72 70	34, 54, 98, 137	0
2	P	247/261 (94%)	0.22	13 (5%) 26 25	39, 60, 107, 154	0
3	C	236/248 (95%)	0.24	14 (5%) 22 21	37, 65, 106, 136	0
3	Q	238/248 (95%)	0.33	17 (7%) 16 15	37, 66, 126, 160	0
4	D	233/241 (96%)	0.06	4 (1%) 70 68	38, 61, 91, 135	0
4	R	233/241 (96%)	-0.11	4 (1%) 70 68	32, 48, 76, 116	0
5	E	233/263 (88%)	-0.03	9 (3%) 39 38	27, 43, 91, 112	0
5	S	237/263 (90%)	0.02	8 (3%) 45 44	37, 53, 88, 113	0
6	F	239/255 (93%)	-0.18	0 100 100	26, 36, 60, 82	0
6	T	240/255 (94%)	0.17	9 (3%) 40 39	41, 61, 96, 135	0
7	G	241/246 (97%)	-0.14	3 (1%) 79 78	28, 40, 72, 110	0
7	U	235/246 (95%)	0.22	11 (4%) 31 30	48, 70, 106, 140	0
8	H	220/234 (94%)	-0.11	3 (1%) 75 74	27, 38, 75, 126	0
8	V	220/234 (94%)	-0.10	3 (1%) 75 74	39, 52, 83, 120	0
9	I	204/205 (99%)	-0.21	0 100 100	29, 38, 60, 77	0
9	W	204/205 (99%)	-0.12	0 100 100	33, 50, 78, 88	0
10	J	195/201 (97%)	-0.21	1 (0%) 91 90	33, 44, 62, 78	0
10	X	195/201 (97%)	-0.26	0 100 100	33, 44, 60, 81	0
11	K	200/204 (98%)	-0.20	1 (0%) 91 90	33, 47, 76, 88	0
11	Y	201/204 (98%)	-0.22	3 (1%) 73 72	29, 39, 64, 84	0
12	L	213/213 (100%)	-0.12	0 100 100	32, 48, 71, 91	0
12	Z	213/213 (100%)	-0.20	0 100 100	28, 39, 65, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	216/219 (98%)	-0.15	0 100 100	28, 42, 67, 96	0
13	a	216/219 (98%)	-0.18	1 (0%) 91 90	31, 44, 64, 86	0
14	N	202/205 (98%)	-0.15	3 (1%) 73 72	28, 38, 60, 101	0
14	b	203/205 (99%)	-0.13	3 (1%) 73 72	36, 47, 72, 111	0
All	All	6222/6458 (96%)	-0.04	131 (2%) 63 62	26, 49, 91, 160	0

The worst 5 of 131 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	232	ILE	12.8
2	P	204	SER	12.2
4	D	241	ILE	8.7
3	Q	234	LYS	6.6
13	a	216	SER	6.5

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

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
7	6V1	U	47	15/16	0.79	0.29	85,120,126,126	0
7	YCM	U	137	10/11	0.86	0.19	59,67,78,79	0
7	YCM	G	137	10/11	0.89	0.15	32,40,55,61	0
3	YCM	C	63	10/11	0.90	0.11	58,60,68,69	0
5	6V1	S	148	15/16	0.91	0.19	45,78,85,86	0
10	6V1	X	91	15/16	0.91	0.19	37,67,74,80	0
7	6V1	U	161	15/16	0.92	0.14	66,88,97,97	0
3	YCM	Q	63	10/11	0.92	0.12	56,59,73,73	0
10	6V1	J	91	15/16	0.93	0.17	35,59,70,71	0
7	6V1	G	47	15/16	0.94	0.18	37,63,69,70	0
5	6V1	E	148	15/16	0.94	0.13	32,66,78,78	0
7	6V1	G	161	15/16	0.94	0.15	33,53,59,61	0

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	CL	O	303	1/1	0.69	0.17	103,103,103,103	0
17	MG	V	301	1/1	0.74	0.18	75,75,75,75	0
15	CL	Q	301	1/1	0.79	0.19	92,92,92,92	0
19	6V8	H	305	23/23	0.82	0.22	47,57,91,103	0
19	6V8	V	303	23/23	0.83	0.25	60,69,96,114	0
15	CL	A	302	1/1	0.84	0.10	72,72,72,72	0
18	1PE	I	304	16/16	0.84	0.23	60,79,98,99	0
18	1PE	L	301	16/16	0.85	0.20	59,76,84,85	0
18	1PE	M	305	16/16	0.86	0.19	68,77,95,97	0
15	CL	O	304	1/1	0.88	0.17	77,77,77,77	0
18	1PE	H	304	16/16	0.88	0.17	59,66,97,97	0
15	CL	K	303	1/1	0.88	0.18	78,78,78,78	0
18	1PE	Y	305	16/16	0.88	0.14	56,74,81,83	0
16	K	b	303	1/1	0.88	0.08	54,54,54,54	0
18	1PE	I	303	16/16	0.89	0.14	54,61,77,87	0
18	1PE	W	303	16/16	0.89	0.13	62,71,82,82	0
18	1PE	b	302	16/16	0.89	0.15	50,59,91,96	0
15	CL	C	302	1/1	0.90	0.17	76,76,76,76	0
16	K	L	302	1/1	0.92	0.08	57,57,57,57	0
19	6V8	K	305	23/23	0.92	0.14	41,45,60,77	0
15	CL	D	302	1/1	0.92	0.13	71,71,71,71	0
18	1PE	N	303	16/16	0.92	0.13	43,48,66,68	0
15	CL	a	302	1/1	0.92	0.11	67,67,67,67	0
15	CL	Q	302	1/1	0.92	0.16	72,72,72,72	0
15	CL	C	301	1/1	0.93	0.12	72,72,72,72	0
17	MG	K	301	1/1	0.93	0.08	37,37,37,37	0
15	CL	U	301	1/1	0.93	0.08	68,68,68,68	0
15	CL	R	302	1/1	0.93	0.27	69,69,69,69	0
19	6V8	Y	306	23/23	0.93	0.12	35,37,53,63	0
15	CL	V	302	1/1	0.93	0.09	66,66,66,66	0
15	CL	M	302	1/1	0.94	0.20	62,62,62,62	0
15	CL	K	304	1/1	0.94	0.22	70,70,70,70	0
17	MG	L	303	1/1	0.94	0.12	42,42,42,42	0
15	CL	O	302	1/1	0.94	0.11	67,67,67,67	0
15	CL	A	304	1/1	0.94	0.09	68,68,68,68	0
15	CL	S	301	1/1	0.94	0.29	77,77,77,77	0
17	MG	W	301	1/1	0.94	0.07	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
19	6V8	b	304	23/23	0.94	0.12	39,41,48,54	0
15	CL	M	304	1/1	0.94	0.08	59,59,59,59	0
15	CL	Y	304	1/1	0.94	0.18	77,77,77,77	0
19	6V8	N	305	23/23	0.94	0.10	32,34,37,43	0
15	CL	O	301	1/1	0.95	0.06	64,64,64,64	0
15	CL	D	301	1/1	0.95	0.25	84,84,84,84	0
15	CL	Y	303	1/1	0.95	0.08	60,60,60,60	0
15	CL	S	303	1/1	0.95	0.08	63,63,63,63	0
15	CL	N	302	1/1	0.96	0.14	58,58,58,58	0
17	MG	H	302	1/1	0.96	0.10	34,34,34,34	0
15	CL	B	302	1/1	0.96	0.20	64,64,64,64	0
17	MG	I	301	1/1	0.96	0.07	34,34,34,34	0
15	CL	A	301	1/1	0.96	0.09	50,50,50,50	0
15	CL	R	301	1/1	0.96	0.10	64,64,64,64	0
15	CL	a	303	1/1	0.96	0.09	49,49,49,49	0
17	MG	H	301	1/1	0.96	0.12	69,69,69,69	0
15	CL	a	301	1/1	0.96	0.11	73,73,73,73	0
16	K	N	304	1/1	0.96	0.06	49,49,49,49	0
17	MG	J	301	1/1	0.96	0.08	48,48,48,48	0
15	CL	E	301	1/1	0.96	0.10	69,69,69,69	0
15	CL	a	304	1/1	0.96	0.09	68,68,68,68	0
15	CL	E	303	1/1	0.97	0.09	62,62,62,62	0
15	CL	S	302	1/1	0.97	0.14	75,75,75,75	0
15	CL	W	302	1/1	0.97	0.07	55,55,55,55	0
15	CL	b	301	1/1	0.97	0.18	61,61,61,61	0
17	MG	I	305	1/1	0.97	0.08	33,33,33,33	0
15	CL	K	302	1/1	0.97	0.10	80,80,80,80	0
15	CL	E	302	1/1	0.97	0.07	57,57,57,57	0
16	K	Z	301	1/1	0.97	0.07	48,48,48,48	0
15	CL	F	301	1/1	0.97	0.12	58,58,58,58	0
15	CL	P	301	1/1	0.97	0.10	57,57,57,57	0
16	K	U	302	1/1	0.97	0.09	53,53,53,53	0
15	CL	Y	302	1/1	0.97	0.12	76,76,76,76	0
15	CL	Y	301	1/1	0.98	0.16	65,65,65,65	0
15	CL	G	301	1/1	0.98	0.11	58,58,58,58	0
15	CL	I	302	1/1	0.98	0.10	46,46,46,46	0
17	MG	X	301	1/1	0.98	0.07	49,49,49,49	0
15	CL	B	301	1/1	0.98	0.07	44,44,44,44	0
15	CL	M	303	1/1	0.98	0.06	45,45,45,45	0
15	CL	N	301	1/1	0.98	0.09	40,40,40,40	0
16	K	G	303	1/1	0.98	0.06	41,41,41,41	0
15	CL	M	301	1/1	0.98	0.27	70,70,70,70	0

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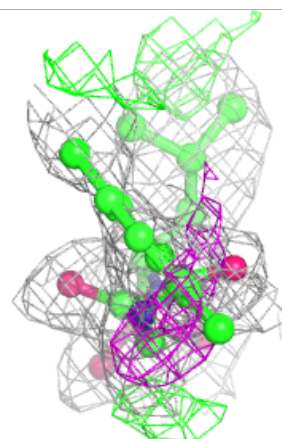
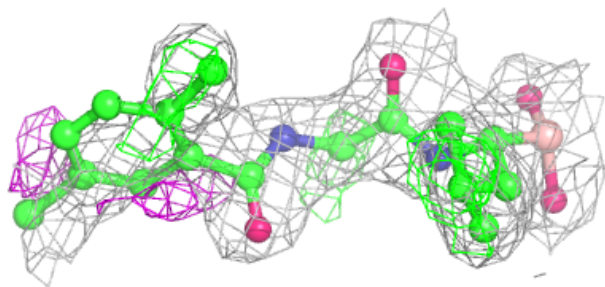
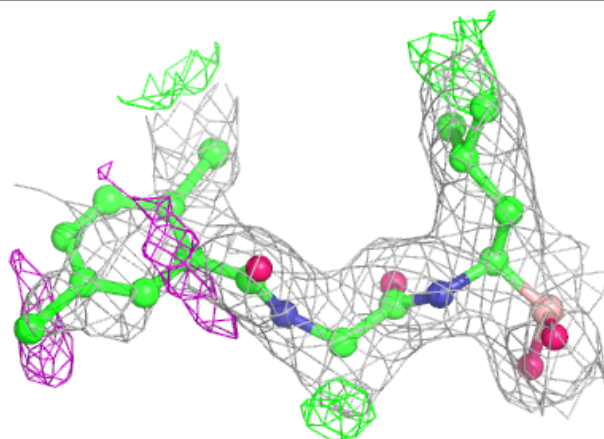
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
15	CL	A	303	1/1	0.99	0.08	56,56,56,56	0
15	CL	G	302	1/1	0.99	0.07	64,64,64,64	0
15	CL	H	303	1/1	0.99	0.09	50,50,50,50	0

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.

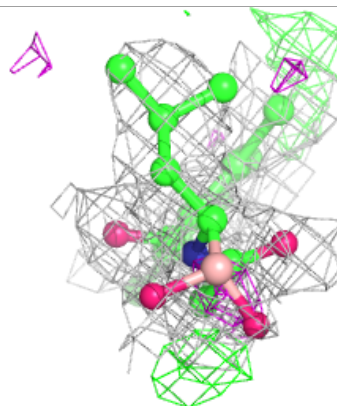
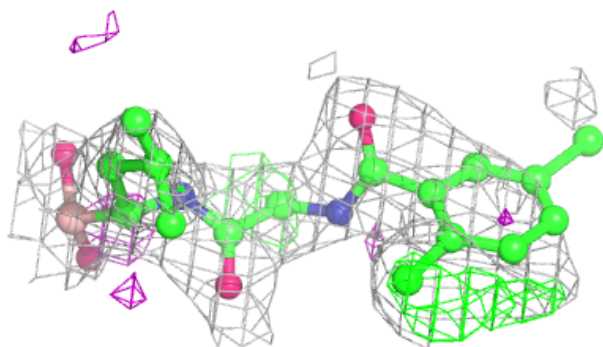
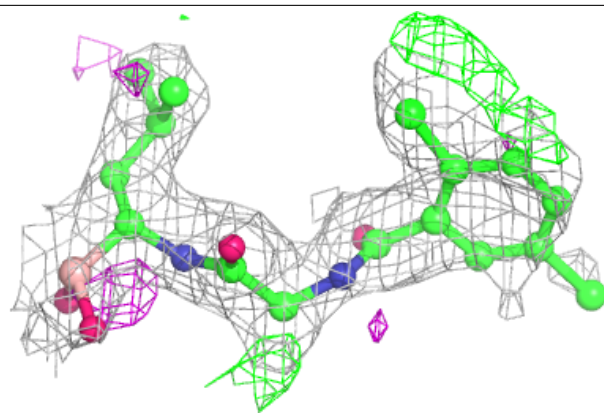
Electron density around 6V8 H 305:

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

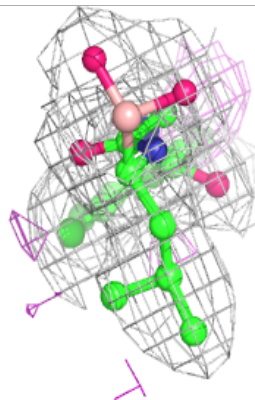
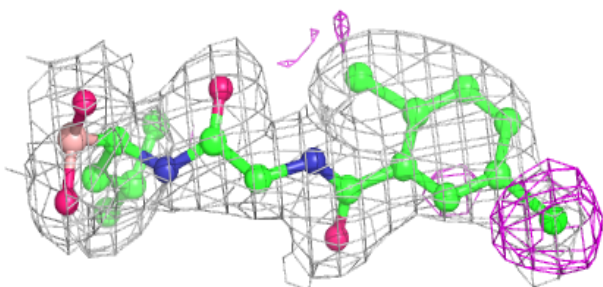
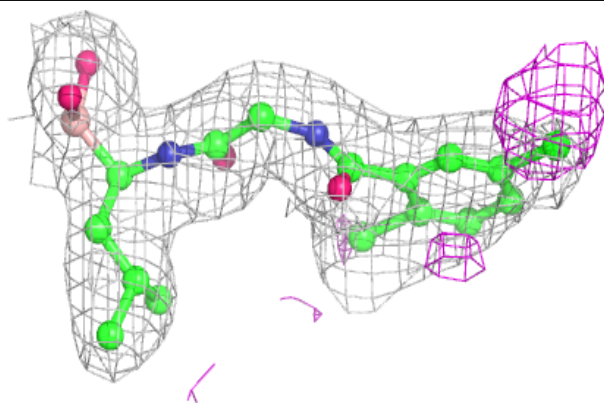


Electron density around 6V8 V 303:

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

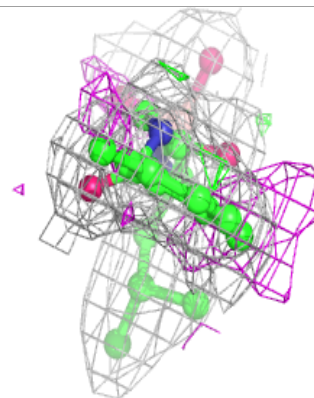
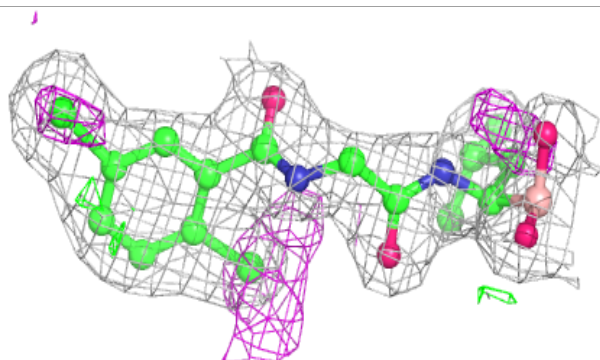
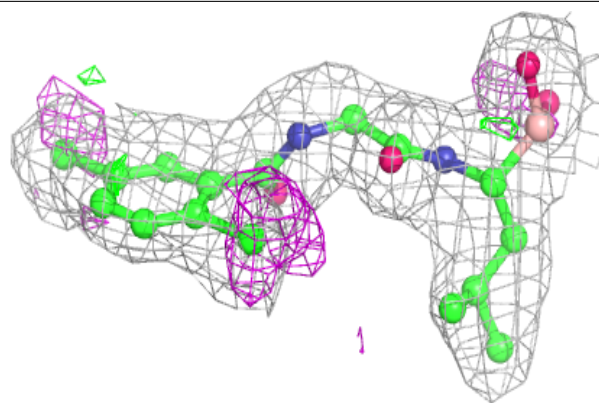
**Electron density around 6V8 K 305:**

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

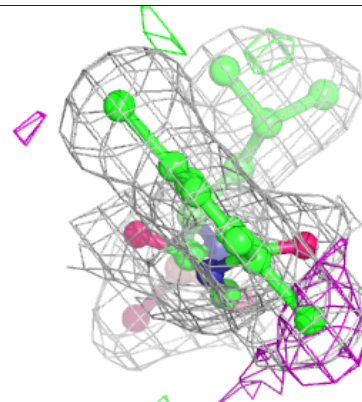
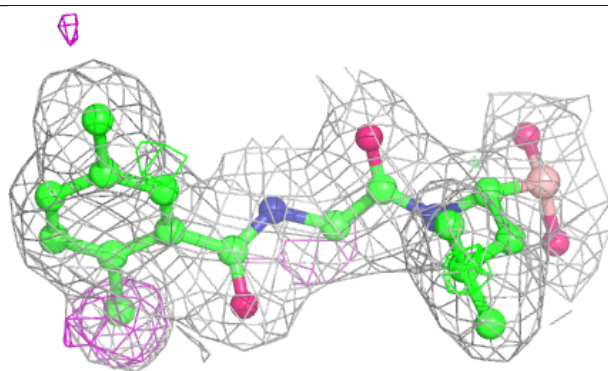
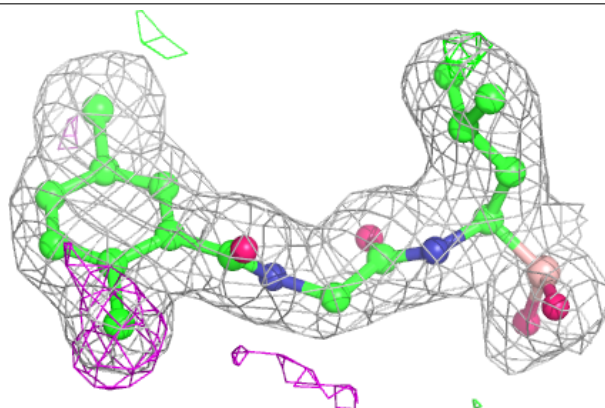


Electron density around 6V8 Y 306:

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

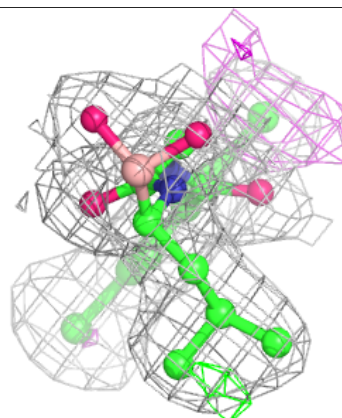
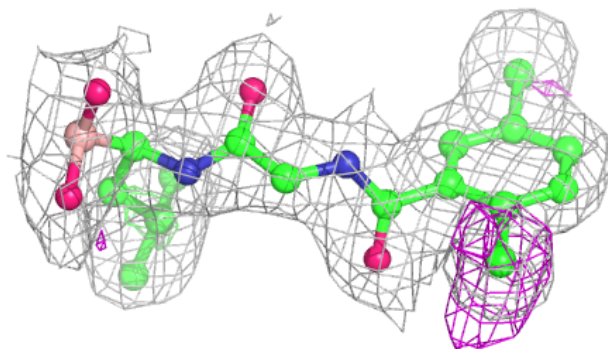
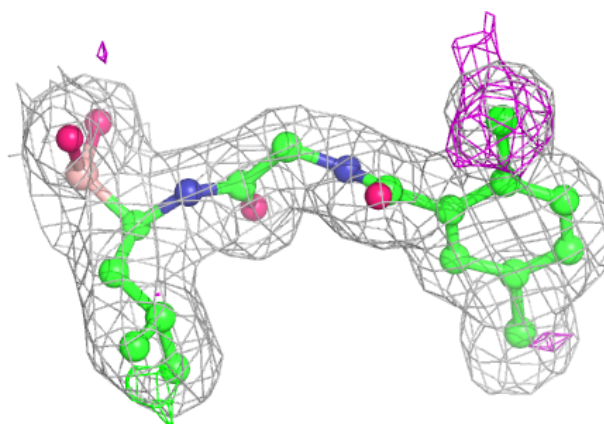
**Electron density around 6V8 b 304:**

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



Electron density around 6V8 N 305:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.