



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:17 PM UTC

PDB ID : 5DKI / pdb_00005dki
Title : Yeast 20S proteasome in complex with alkyne-PI
Authors : Beck, P.; Cui, H.; Groll, M.
Deposited on : 2015-09-03
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

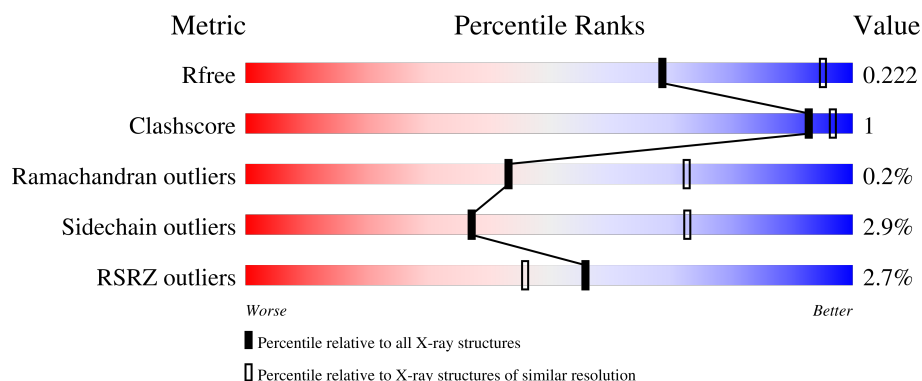
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	250	0% 97% •
1	O	250	2% 96% •
2	B	258	3% 87% 7% 5%
2	P	258	4% 88% 6% • 5%
3	C	254	4% 87% 6% • 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	5% 88% 5% • 6%
4	D	260	2% 85% • • 10%
4	R	260	2% 85% 5% • 10%
5	E	234	% 95% • •
5	S	234	% 94% • •
6	F	288	2% 82% • 16%
6	T	288	3% 82% • 16%
7	G	252	2% 90% • • •
7	U	252	90% 5% •
8	H	232	% 93% • •
8	V	232	2% 92% 5% • •
9	I	205	94% 5%
9	W	205	94% 5%
10	J	198	4% 91% 7% • •
10	X	198	6% 91% 6% • • •
11	K	212	7% 91% 8% •
11	Y	212	6% 91% 8% •
12	L	222	7% 96% •
12	Z	222	6% 95% 5%
13	M	246	% 88% 7% 5%
13	a	246	% 90% • 5%
14	N	196	93% 6% •
14	b	196	% 94% 6% •

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 49870 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			
3	Q	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			
4	R	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			
5	S	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	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 (CCD ID: MG) (formula: Mg).

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

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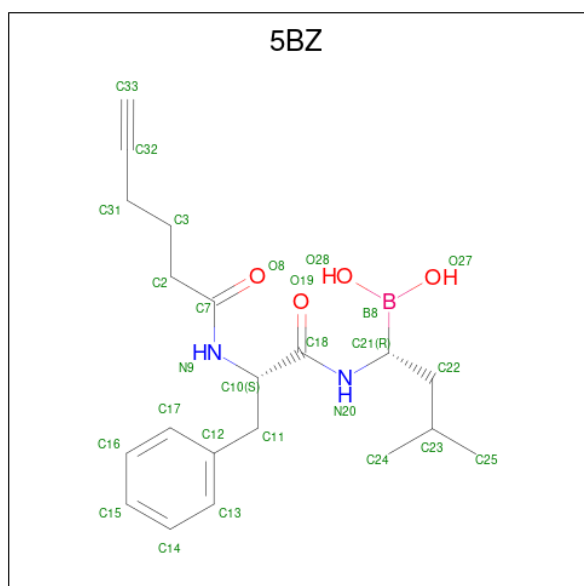
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	J	1	Total	Mg	0	0
			1	1		
15	K	1	Total	Mg	0	0
			1	1		
15	N	1	Total	Mg	0	0
			1	1		
15	V	1	Total	Mg	0	0
			1	1		
15	Y	1	Total	Mg	0	0
			1	1		
15	Z	1	Total	Mg	0	0
			1	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	G	2	Total	Cl	0	0
			2	2		
16	N	1	Total	Cl	0	0
			1	1		
16	U	1	Total	Cl	0	0
			1	1		
16	b	1	Total	Cl	0	0
			1	1		

- Molecule 17 is [(1 {R})-1-[(2 {S})-2-(hex-5-ynoylamino)-3-phenyl-propanoyl]amino]-3-methyl-butyl]boronic acid (CCD ID: 5BZ) (formula: C₂₀H₂₉BN₂O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	H	1	Total	B	C	N	O	0	0
			27	1	20	2	4		
17	K	1	Total	B	C	N	O	0	0
			27	1	20	2	4		
17	N	1	Total	B	C	N	O	0	0
			27	1	20	2	4		
17	V	1	Total	B	C	N	O	0	0
			27	1	20	2	4		
17	Y	1	Total	B	C	N	O	0	0
			27	1	20	2	4		
17	b	1	Total	B	C	N	O	0	0
			27	1	20	2	4		

- Molecule 18 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	A	7	Total	O	0	0
			7	7		
18	B	15	Total	O	0	0
			15	15		
18	C	9	Total	O	0	0
			9	9		
18	D	6	Total	O	0	0
			6	6		
18	E	12	Total	O	0	0
			12	12		
18	F	11	Total	O	0	0
			11	11		
18	G	17	Total	O	0	0
			17	17		
18	H	11	Total	O	0	0
			11	11		
18	I	13	Total	O	0	0
			13	13		
18	J	11	Total	O	0	0
			11	11		
18	K	10	Total	O	0	0
			10	10		
18	L	18	Total	O	0	0
			18	18		
18	M	17	Total	O	0	0
			17	17		
18	N	10	Total	O	0	0
			10	10		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
18	O	8	Total O 8 8	0	0
18	P	12	Total O 12 12	0	0
18	Q	8	Total O 8 8	0	0
18	R	9	Total O 9 9	0	0
18	S	15	Total O 15 15	0	0
18	T	11	Total O 11 11	0	0
18	U	9	Total O 9 9	0	0
18	V	8	Total O 8 8	0	0
18	W	13	Total O 13 13	0	0
18	X	13	Total O 13 13	0	0
18	Y	9	Total O 9 9	0	0
18	Z	18	Total O 18 18	0	0
18	a	20	Total O 20 20	0	0
18	b	9	Total O 9 9	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.

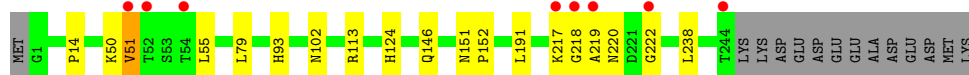
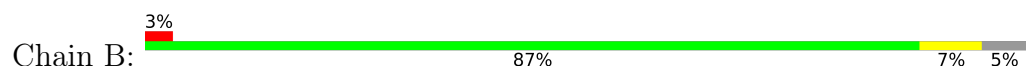
- Molecule 1: Proteasome subunit alpha type-2



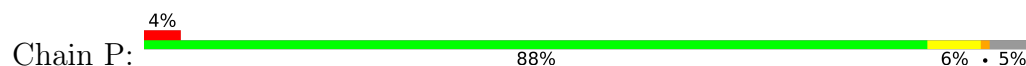
- Molecule 1: Proteasome subunit alpha type-2



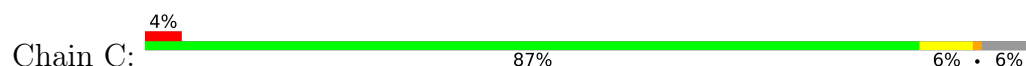
- Molecule 2: Proteasome subunit alpha type-3



- Molecule 2: Proteasome subunit alpha type-3



- Molecule 3: Proteasome subunit alpha type-4



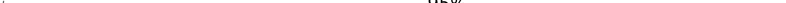
- Molecule 3: Proteasome subunit alpha type-4

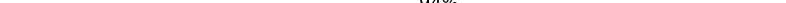
MET	SR	G1	Y2	D3	R4	K36	N38	S48	T49	L50	K51	L52	V124	Q147	S158	A159	Q160	V169	K180	V201	T202	T203	G204	A205	K206	E225	T234	E235	T236	E240	GLN	GLN	GLU	GLN	ASP	LVS	LVS	LVS	LVS	SR	ASN	HIS
-----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	-----	-----

Chain D:  2% 85% 10%

Chain R: 

SER.

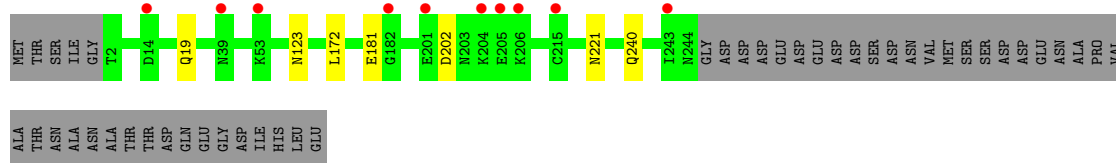
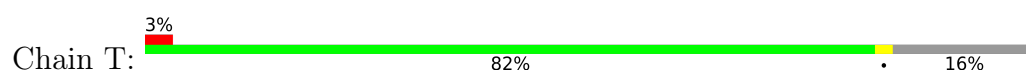
Chain E:  95%

Chain S:  94%

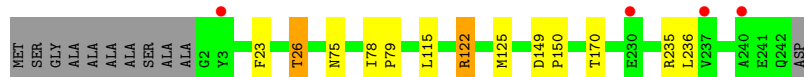
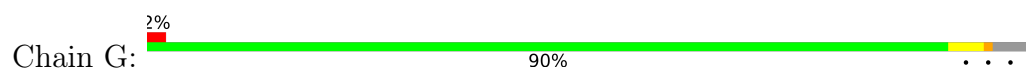
Chain F: 

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

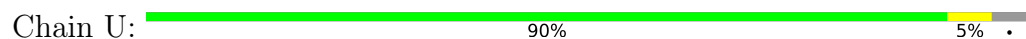




- Molecule 7: Proteasome subunit alpha type-1



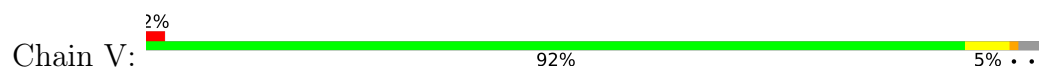
- Molecule 7: Proteasome subunit alpha type-1



- Molecule 8: Proteasome subunit beta type-2



- Molecule 8: Proteasome subunit beta type-2



- Molecule 9: Proteasome subunit beta type-3

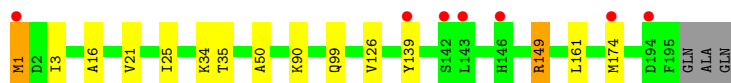
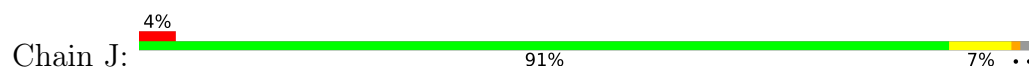


- Molecule 9: Proteasome subunit beta type-3

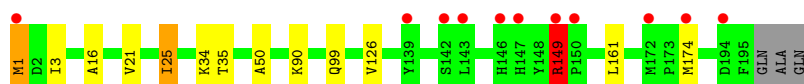




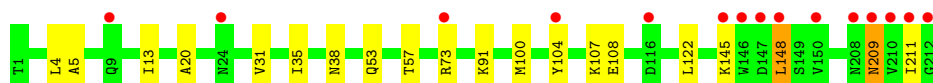
- Molecule 10: Proteasome subunit beta type-4



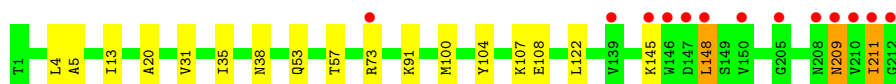
- Molecule 10: Proteasome subunit beta type-4



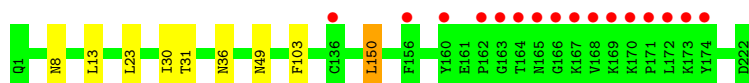
- Molecule 11: Proteasome subunit beta type-5



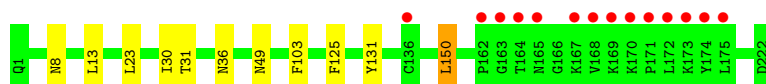
- Molecule 11: Proteasome subunit beta type-5



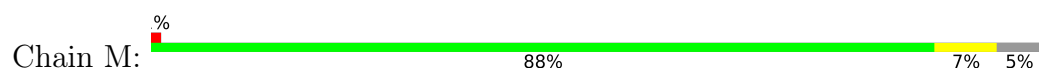
- Molecule 12: Proteasome subunit beta type-6



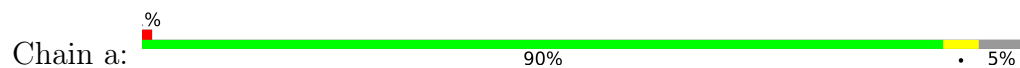
- Molecule 12: Proteasome subunit beta type-6



- Molecule 13: Proteasome subunit beta type-7



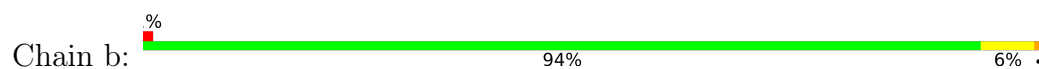
• Molecule 13: Proteasome subunit beta type-7



• 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	137.16Å 298.09Å 145.96Å 90.00° 113.11° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.4 (15.00-2.80) 97.7 (15.00-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.199 , 0.219 0.203 , 0.222	Depositor DCC
R_{free} test set	12885 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	56.7	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 49.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	49870	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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: 5BZ, 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	0.41	0/1952	0.68	0/2642
1	O	0.41	0/1952	0.69	0/2642
2	B	0.42	0/1934	0.68	0/2618
2	P	0.41	0/1934	0.68	0/2618
3	C	0.41	0/1910	0.69	1/2586 (0.0%)
3	Q	0.41	0/1910	0.69	1/2586 (0.0%)
4	D	0.40	0/1837	0.66	0/2475
4	R	0.40	0/1837	0.66	0/2475
5	E	0.41	0/1800	0.65	0/2433
5	S	0.40	0/1800	0.65	0/2433
6	F	0.41	0/1932	0.67	0/2609
6	T	0.40	0/1932	0.68	0/2609
7	G	0.39	0/1945	0.67	0/2634
7	U	0.40	0/1945	0.67	0/2634
8	H	0.38	0/1750	0.69	0/2373
8	V	0.38	0/1750	0.69	0/2373
9	I	0.34	0/1611	0.71	0/2174
9	W	0.35	0/1611	0.71	0/2174
10	J	0.43	0/1589	0.73	3/2142 (0.1%)
10	X	0.43	0/1589	0.74	2/2142 (0.1%)
11	K	0.36	0/1681	0.69	0/2274
11	Y	0.38	0/1681	0.69	0/2274
12	L	0.34	0/1795	0.71	2/2420 (0.1%)
12	Z	0.39	0/1795	0.72	2/2420 (0.1%)
13	M	0.35	0/1855	0.73	2/2514 (0.1%)
13	a	0.35	0/1855	0.70	1/2514 (0.0%)
14	N	0.60	0/1541	0.73	0/2087
14	b	0.35	0/1541	0.70	0/2087
All	All	0.40	0/50264	0.69	14/67962 (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
10	X	0	1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	X	149	ARG	CD-NE-CZ	12.28	141.60	124.40
13	M	35	ARG	N-CA-C	9.68	122.72	111.11
10	J	149	ARG	NE-CZ-NH2	8.11	126.50	119.20
10	J	149	ARG	NE-CZ-NH1	-7.85	113.65	121.50
3	Q	201	VAL	N-CA-C	6.64	116.80	110.42
10	X	149	ARG	NE-CZ-NH2	-6.60	113.26	119.20
3	C	201	VAL	N-CA-C	6.53	116.69	110.42
12	Z	103	PHE	CA-C-N	5.81	125.76	119.78
12	Z	103	PHE	C-N-CA	5.81	125.76	119.78
10	J	149	ARG	CD-NE-CZ	5.78	132.49	124.40
12	L	103	PHE	CA-C-N	5.64	125.59	119.78
12	L	103	PHE	C-N-CA	5.64	125.59	119.78
13	a	10	SER	N-CA-C	5.26	117.71	110.35
13	M	10	SER	N-CA-C	5.23	117.67	110.35

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	X	149	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	2	0
1	O	1915	0	1929	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1904	0	1904	7	0
2	P	1904	0	1904	9	0
3	C	1881	0	1895	8	0
3	Q	1881	0	1895	6	0
4	D	1813	0	1797	3	0
4	R	1813	0	1797	4	0
5	E	1773	0	1775	3	0
5	S	1773	0	1775	4	0
6	F	1892	0	1883	3	0
6	T	1892	0	1883	2	0
7	G	1907	0	1901	5	0
7	U	1907	0	1901	4	0
8	H	1719	0	1718	9	0
8	V	1719	0	1718	12	0
9	I	1581	0	1574	7	0
9	W	1581	0	1574	8	0
10	J	1561	0	1569	7	0
10	X	1561	0	1569	7	0
11	K	1644	0	1594	11	0
11	Y	1644	0	1594	12	0
12	L	1757	0	1711	4	0
12	Z	1757	0	1711	5	0
13	M	1824	0	1832	8	0
13	a	1824	0	1832	4	0
14	N	1512	0	1480	6	0
14	b	1512	0	1480	6	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	J	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	2	0	0	0	0
16	N	1	0	0	0	0
16	U	1	0	0	0	0
16	b	1	0	0	0	0
17	H	27	0	29	0	0
17	K	27	0	29	0	0
17	N	27	0	29	1	0
17	V	27	0	29	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Y	27	0	29	1	0
17	b	27	0	29	1	0
18	A	7	0	0	0	0
18	B	15	0	0	1	0
18	C	9	0	0	0	0
18	D	6	0	0	0	0
18	E	12	0	0	0	0
18	F	11	0	0	0	0
18	G	17	0	0	1	0
18	H	11	0	0	0	0
18	I	13	0	0	0	0
18	J	11	0	0	1	0
18	K	10	0	0	0	0
18	L	18	0	0	0	0
18	M	17	0	0	1	0
18	N	10	0	0	0	0
18	O	8	0	0	0	0
18	P	12	0	0	1	0
18	Q	8	0	0	1	0
18	R	9	0	0	0	0
18	S	15	0	0	0	0
18	T	11	0	0	0	0
18	U	9	0	0	0	0
18	V	8	0	0	0	0
18	W	13	0	0	1	0
18	X	13	0	0	1	0
18	Y	9	0	0	0	0
18	Z	18	0	0	1	0
18	a	20	0	0	1	0
18	b	9	0	0	0	0
All	All	49870	0	49298	145	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 (145) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:209:ASN:O	9:W:38:LYS:NZ	2.21	0.73
11:K:73:ARG:NH2	11:K:104:TYR:O	2.24	0.70
11:Y:73:ARG:NH2	11:Y:104:TYR:O	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:38:LYS:NZ	11:Y:209:ASN:O	2.28	0.67
13:M:35:ARG:HG2	13:M:36:PHE:CE2	2.30	0.66
2:B:93:HIS:HB3	18:B:301:HOH:O	2.02	0.60
17:Y:302:5BZ:C32	18:Z:415:HOH:O	2.50	0.59
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.71	0.55
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.71	0.55
8:H:35:HIS:HB3	8:H:56:THR:HG21	1.89	0.53
8:V:35:HIS:HB3	8:V:56:THR:HG21	1.89	0.53
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	1.91	0.52
11:K:145:LYS:HB2	11:K:148:LEU:HD13	1.92	0.52
8:V:22:GLN:HE21	17:V:302:5BZ:H28	1.75	0.52
10:X:174:MET:HB2	18:X:206:HOH:O	2.08	0.52
10:X:50:ALA:O	11:Y:91:LYS:NZ	2.43	0.52
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.58	0.51
8:V:35:HIS:CB	8:V:56:THR:HG21	2.41	0.51
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.47	0.50
3:C:201:VAL:O	3:C:202:GLN:CB	2.58	0.50
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.94	0.50
14:b:152:VAL:HA	14:b:175:MET:HE1	1.92	0.50
8:H:35:HIS:CB	8:H:56:THR:HG21	2.41	0.50
7:G:23:PHE:O	7:G:26:THR:HB	2.12	0.49
14:N:152:VAL:HA	14:N:175:MET:HE1	1.94	0.49
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.94	0.49
8:V:113:ILE:HG12	8:V:119:THR:HG22	1.94	0.49
17:V:302:5BZ:C33	18:W:312:HOH:O	2.61	0.49
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	1.94	0.49
8:V:196:ARG:NH2	9:W:150:GLU:O	2.45	0.49
7:U:23:PHE:O	7:U:26:THR:HB	2.12	0.49
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.94	0.49
8:H:113:ILE:HG12	8:H:119:THR:HG22	1.94	0.48
10:J:174:MET:HB2	18:J:304:HOH:O	2.13	0.48
8:H:196:ARG:NH2	9:I:150:GLU:O	2.46	0.48
2:P:93:HIS:HB3	18:P:301:HOH:O	2.12	0.48
3:Q:1:GLY:N	18:Q:301:HOH:O	2.41	0.48
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.94	0.48
14:b:36:ARG:HG3	14:b:42:TRP:CE2	2.48	0.48
10:J:50:ALA:O	11:K:91:LYS:NZ	2.47	0.47
2:B:50:LYS:O	2:B:51:VAL:C	2.57	0.47
2:P:50:LYS:O	2:P:51:VAL:C	2.57	0.47
10:J:21:VAL:HG11	11:K:122:LEU:HD11	1.96	0.47
13:M:35:ARG:NH1	18:M:301:HOH:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.49	0.47
8:V:80:LEU:HD12	8:V:113:ILE:HD11	1.96	0.47
8:H:80:LEU:HD12	8:H:113:ILE:HD11	1.96	0.47
13:M:228:TYR:HE2	14:b:35:THR:HG21	1.80	0.47
8:V:84:LYS:HE2	8:V:119:THR:HG23	1.97	0.47
2:B:217:LYS:C	2:B:219:ALA:H	2.23	0.46
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.98	0.46
10:J:1:MET:HG2	10:J:34:LYS:HE3	1.96	0.46
4:R:176:LEU:HA	5:S:55:LEU:HD21	1.97	0.46
11:K:209:ASN:OD1	11:K:209:ASN:C	2.59	0.46
10:X:1:MET:HG2	10:X:34:LYS:HE3	1.96	0.46
1:A:55:LEU:HD12	7:G:170:THR:HG23	1.98	0.46
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.98	0.45
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.97	0.45
8:H:84:LYS:HE2	8:H:119:THR:HG23	1.98	0.45
12:L:13:LEU:HD11	12:L:150:LEU:HD21	1.98	0.45
8:H:196:ARG:NH2	9:I:150:GLU:HG3	2.31	0.45
17:V:302:5BZ:H7	17:V:302:5BZ:O27	2.15	0.45
12:Z:13:LEU:HD11	12:Z:150:LEU:HD21	1.98	0.45
6:F:164:GLY:HA2	6:F:202:ASP:OD2	2.17	0.45
2:P:217:LYS:C	2:P:219:ALA:H	2.24	0.45
13:M:35:ARG:HG2	13:M:36:PHE:CZ	2.51	0.45
1:O:160:LYS:HD2	2:P:55:LEU:HA	1.98	0.45
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.47	0.44
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	1.99	0.44
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.48	0.44
14:b:176:VAL:HG12	14:b:178:LEU:HD13	1.98	0.44
3:C:35:LYS:HG2	3:C:158:SER:O	2.16	0.44
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.82	0.44
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.99	0.44
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.99	0.44
11:Y:209:ASN:OD1	11:Y:209:ASN:C	2.60	0.44
9:I:125:LEU:HG	9:I:126:ILE:HG22	1.99	0.44
9:W:125:LEU:HG	9:W:126:ILE:HG22	1.99	0.44
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.18	0.44
2:B:124:HIS:HB3	3:C:124:VAL:HG12	2.01	0.43
9:I:36:SER:HB2	10:J:126:VAL:HG11	2.00	0.43
11:Y:53:GLN:O	11:Y:57:THR:HG23	2.18	0.43
9:W:20:VAL:HG13	9:W:118:PRO:HB3	2.00	0.43
11:K:5:ALA:HA	11:K:13:ILE:O	2.19	0.43
13:a:27:LEU:HD21	13:a:34:LEU:HD22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Y:5:ALA:HA	11:Y:13:ILE:O	2.19	0.43
11:Y:211:ILE:H	11:Y:211:ILE:HG13	1.72	0.43
13:a:96:LEU:O	13:a:100:MET:HG2	2.18	0.43
14:b:83:LYS:HG3	14:b:119:VAL:CG2	2.49	0.43
9:I:20:VAL:HG13	9:I:118:PRO:HB3	2.00	0.43
11:K:53:GLN:O	11:K:57:THR:HG23	2.18	0.43
2:P:50:LYS:HD3	2:P:50:LYS:HA	1.87	0.42
4:R:9:PRO:HA	5:S:23:TYR:CD1	2.54	0.42
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.42
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	2.01	0.42
7:U:78:ILE:N	7:U:79:PRO:CD	2.82	0.42
13:a:2:GLN:NE2	18:a:301:HOH:O	2.52	0.42
4:D:91:HIS:CD2	4:D:99:ILE:HG22	2.54	0.42
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.49	0.42
13:M:27:LEU:HD21	13:M:34:LEU:HD22	2.01	0.42
7:G:122:ARG:HD2	18:G:415:HOH:O	2.19	0.42
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.85	0.42
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.84	0.42
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.50	0.42
17:V:302:5BZ:H29	9:W:130:ASP:HB2	2.02	0.42
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.50	0.42
10:J:139:TYR:OH	10:X:25:ILE:O	2.38	0.42
11:Y:107:LYS:HG3	11:Y:108:GLU:HG3	2.02	0.42
3:Q:201:VAL:O	3:Q:202:GLN:HB3	2.20	0.42
3:C:201:VAL:O	3:C:202:GLN:HB3	2.20	0.41
13:M:96:LEU:O	13:M:100:MET:HG2	2.20	0.41
12:L:8:ASN:HA	12:L:30:ILE:O	2.19	0.41
4:R:91:HIS:CD2	4:R:99:ILE:HG22	2.55	0.41
5:E:12:PHE:H	6:F:19:GLN:HE22	1.66	0.41
5:S:77:ALA:N	5:S:78:PRO:CD	2.84	0.41
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.50	0.41
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.50	0.41
1:O:115:ALA:HB1	1:O:154:GLY:O	2.20	0.41
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.20	0.41
8:H:104:ASP:HB2	8:H:105:PRO:CD	2.50	0.41
2:B:146:GLN:HG2	3:C:57:ILE:HG21	2.02	0.41
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.56	0.41
5:S:12:PHE:H	6:T:19:GLN:HE22	1.67	0.41
6:T:202:ASP:OD1	6:T:202:ASP:N	2.54	0.41
2:B:14:PRO:HA	3:C:20:TYR:CD1	2.56	0.41
6:F:202:ASP:OD1	6:F:202:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:107:LYS:HG3	11:K:108:GLU:HG3	2.02	0.41
8:V:1:THR:CB	17:V:302:5BZ:O27	2.69	0.41
8:V:104:ASP:HB2	8:V:105:PRO:CD	2.51	0.41
11:Y:38:ASN:OD1	11:Y:38:ASN:C	2.64	0.41
13:a:227:GLY:HA3	13:a:231:GLN:HB3	2.03	0.41
5:E:77:ALA:N	5:E:78:PRO:CD	2.84	0.41
11:K:38:ASN:OD1	11:K:38:ASN:C	2.64	0.41
14:N:1:THR:CB	17:N:201:5BZ:O27	2.69	0.41
8:V:196:ARG:NH2	9:W:150:GLU:HG3	2.36	0.41
13:M:187:ARG:NH1	8:V:139:GLU:OE1	2.48	0.40
13:M:227:GLY:HA3	13:M:231:GLN:HB3	2.03	0.40
2:P:151:ASN:HB2	2:P:152:PRO:HD2	2.04	0.40
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.56	0.40
1:A:115:ALA:HB1	1:A:154:GLY:O	2.22	0.40
14:N:3:ILE:HG22	14:N:16:ALA:CB	2.51	0.40
14:b:1:THR:CB	17:b:201:5BZ:O27	2.70	0.40
4:D:176:LEU:HD22	5:E:55:LEU:CD2	2.51	0.40
3:C:149:GLU:HB2	3:C:150:PRO:HD2	2.04	0.40
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	30 60
1	O	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	30 60
2	B	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	7 25
2	P	242/258 (94%)	233 (96%)	5 (2%)	4 (2%)	7 25
3	C	238/254 (94%)	233 (98%)	3 (1%)	2 (1%)	16 44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Q	238/254 (94%)	233 (98%)	3 (1%)	2 (1%)	16	44
4	D	231/260 (89%)	229 (99%)	2 (1%)	0	100	100
4	R	231/260 (89%)	229 (99%)	2 (1%)	0	100	100
5	E	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
5	S	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
6	F	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
6	T	241/288 (84%)	239 (99%)	2 (1%)	0	100	100
7	G	239/252 (95%)	237 (99%)	2 (1%)	0	100	100
7	U	239/252 (95%)	237 (99%)	2 (1%)	0	100	100
8	H	224/232 (97%)	217 (97%)	7 (3%)	0	100	100
8	V	224/232 (97%)	217 (97%)	7 (3%)	0	100	100
9	I	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
10	X	193/198 (98%)	190 (98%)	3 (2%)	0	100	100
11	K	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
11	Y	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
12	L	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	231/246 (94%)	222 (96%)	8 (4%)	1 (0%)	30	60
13	a	231/246 (94%)	222 (96%)	9 (4%)	0	100	100
14	N	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
14	b	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
All	All	6284/6614 (95%)	6132 (98%)	137 (2%)	15 (0%)	43	72

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
2	P	51	VAL
3	Q	202	GLN
1	A	2	THR
2	B	218	GLY

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Mol	Chain	Res	Type
2	B	222	GLY
1	O	2	THR
2	P	218	GLY
2	P	222	GLY
2	B	220	ASN
2	P	220	ASN
3	C	205	ALA
3	Q	205	ALA
13	M	83	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	205 (98%)	4 (2%)	50	81
1	O	209/209 (100%)	205 (98%)	4 (2%)	50	81
2	B	203/216 (94%)	197 (97%)	6 (3%)	36	72
2	P	203/216 (94%)	197 (97%)	6 (3%)	36	72
3	C	212/226 (94%)	203 (96%)	9 (4%)	26	61
3	Q	212/226 (94%)	203 (96%)	9 (4%)	26	61
4	D	194/215 (90%)	184 (95%)	10 (5%)	21	53
4	R	194/215 (90%)	184 (95%)	10 (5%)	21	53
5	E	190/193 (98%)	184 (97%)	6 (3%)	34	70
5	S	190/193 (98%)	184 (97%)	6 (3%)	34	70
6	F	201/239 (84%)	196 (98%)	5 (2%)	42	76
6	T	201/239 (84%)	196 (98%)	5 (2%)	42	76
7	G	206/210 (98%)	199 (97%)	7 (3%)	32	68
7	U	206/210 (98%)	199 (97%)	7 (3%)	32	68
8	H	185/190 (97%)	183 (99%)	2 (1%)	65	87
8	V	185/190 (97%)	182 (98%)	3 (2%)	55	83
9	I	172/173 (99%)	169 (98%)	3 (2%)	53	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	W	172/173 (99%)	169 (98%)	3 (2%)	53	83
10	J	173/175 (99%)	166 (96%)	7 (4%)	28	63
10	X	173/175 (99%)	166 (96%)	7 (4%)	28	63
11	K	169/169 (100%)	163 (96%)	6 (4%)	31	66
11	Y	169/169 (100%)	163 (96%)	6 (4%)	31	66
12	L	185/185 (100%)	182 (98%)	3 (2%)	55	83
12	Z	185/185 (100%)	182 (98%)	3 (2%)	55	83
13	M	199/208 (96%)	193 (97%)	6 (3%)	36	72
13	a	199/208 (96%)	194 (98%)	5 (2%)	42	76
14	N	162/162 (100%)	158 (98%)	4 (2%)	42	76
14	b	162/162 (100%)	159 (98%)	3 (2%)	50	81
All	All	5320/5540 (96%)	5165 (97%)	155 (3%)	37	73

All (155) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	55	LEU
2	B	79	LEU
2	B	102	ASN
2	B	113	ARG
2	B	191	LEU
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	51	LYS
3	C	52	LEU
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	240	GLU
4	D	40	LEU
4	D	51	LEU
4	D	99	ILE

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Mol	Chain	Res	Type
4	D	125	LEU
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	188	LEU
5	E	231	LYS
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	221	ASN
6	F	240	GLN
7	G	26	THR
7	G	75	ASN
7	G	115	LEU
7	G	122	ARG
7	G	125	MET
7	G	235	ARG
7	G	236	LEU
8	H	68	LEU
8	H	196	ARG
9	I	37	ASN
9	I	126	ILE
9	I	171	LEU
10	J	1	MET
10	J	3	ILE
10	J	25	ILE
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
10	J	149	ARG
11	K	4	LEU
11	K	35	ILE
11	K	100	MET
11	K	148	LEU
11	K	209	ASN

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Mol	Chain	Res	Type
11	K	211	ILE
12	L	23	LEU
12	L	49	ASN
12	L	150	LEU
13	M	2	GLN
13	M	35	ARG
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	190	ARG
14	N	3	ILE
14	N	9	LYS
14	N	104	ASP
14	N	119	VAL
1	O	1	MET
1	O	122	THR
1	O	157	PHE
1	O	250	LEU
2	P	55	LEU
2	P	79	LEU
2	P	102	ASN
2	P	113	ARG
2	P	191	LEU
2	P	238	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	51	LYS
3	Q	52	LEU
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	240	GLU
4	R	40	LEU
4	R	51	LEU
4	R	99	ILE
4	R	125	LEU
4	R	176	LEU
4	R	193	LEU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS

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Mol	Chain	Res	Type
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	55	LEU
5	S	71	LEU
5	S	188	LEU
5	S	231	LYS
6	T	123	ASN
6	T	172	LEU
6	T	181	GLU
6	T	221	ASN
6	T	240	GLN
7	U	26	THR
7	U	75	ASN
7	U	115	LEU
7	U	122	ARG
7	U	125	MET
7	U	235	ARG
7	U	236	LEU
8	V	22	GLN
8	V	68	LEU
8	V	196	ARG
9	W	37	ASN
9	W	126	ILE
9	W	171	LEU
10	X	1	MET
10	X	3	ILE
10	X	25	ILE
10	X	35	THR
10	X	90	LYS
10	X	99	GLN
10	X	149	ARG
11	Y	4	LEU
11	Y	35	ILE
11	Y	100	MET
11	Y	148	LEU
11	Y	209	ASN
11	Y	211	ILE
12	Z	23	LEU
12	Z	49	ASN
12	Z	150	LEU
13	a	2	GLN

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Mol	Chain	Res	Type
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	190	ARG
14	b	9	LYS
14	b	104	ASP
14	b	119	VAL

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

Mol	Chain	Res	Type
2	B	119	GLN
2	B	123	GLN
2	B	124	HIS
3	C	17	GLN
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	225	ASN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	151	ASN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	143	HIS
7	G	30	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	175	ASN
7	G	212	ASN

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Mol	Chain	Res	Type
8	H	30	ASN
8	H	189	ASN
8	H	194	ASN
9	I	37	ASN
9	I	88	GLN
9	I	203	GLN
10	J	55	GLN
10	J	63	ASN
10	J	146	HIS
11	K	9	GLN
11	K	85	ASN
11	K	143	ASN
11	K	176	ASN
11	K	208	ASN
12	L	3	ASN
12	L	29	ASN
12	L	36	ASN
12	L	49	ASN
12	L	70	ASN
12	L	155	ASN
12	L	158	ASN
12	L	159	GLN
12	L	197	GLN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN
13	M	149	HIS
13	M	194	ASN
13	M	213	GLN
14	N	38	HIS
14	N	141	ASN
14	N	161	GLN
2	P	93	HIS
2	P	119	GLN
2	P	123	GLN
2	P	124	HIS
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
4	R	91	HIS
4	R	100	ASN

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Mol	Chain	Res	Type
4	R	225	ASN
5	S	68	HIS
5	S	99	ASN
5	S	116	GLN
5	S	120	GLN
5	S	151	ASN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
7	U	30	ASN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	175	ASN
8	V	22	GLN
8	V	30	ASN
8	V	165	ASN
8	V	189	ASN
9	W	37	ASN
9	W	88	GLN
9	W	203	GLN
10	X	55	GLN
10	X	63	ASN
10	X	78	GLN
10	X	146	HIS
11	Y	9	GLN
11	Y	85	ASN
11	Y	133	GLN
11	Y	143	ASN
11	Y	176	ASN
11	Y	208	ASN
12	Z	3	ASN
12	Z	29	ASN
12	Z	36	ASN
12	Z	49	ASN
12	Z	79	HIS
12	Z	80	ASN
12	Z	155	ASN
12	Z	158	ASN
12	Z	159	GLN

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Mol	Chain	Res	Type
12	Z	197	GLN
13	a	48	ASN
13	a	108	ASN
13	a	194	ASN
13	a	213	GLN
14	b	38	HIS
14	b	141	ASN
14	b	161	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 13 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
17	5BZ	V	302	-	23,27,27	1.51	1 (4%)	29,34,34	1.03	1 (3%)
17	5BZ	H	301	-	23,27,27	1.55	1 (4%)	29,34,34	1.18	3 (10%)
17	5BZ	K	301	-	23,27,27	1.76	2 (8%)	29,34,34	1.34	3 (10%)
17	5BZ	N	201	-	23,27,27	1.53	2 (8%)	29,34,34	1.19	3 (10%)
17	5BZ	Y	302	-	23,27,27	1.70	2 (8%)	29,34,34	1.29	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	5BZ	b	201	-	23,27,27	1.57	1 (4%)	29,34,34	1.23	3 (10%)

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	5BZ	V	302	-	-	8/23/29/29	0/1/1/1
17	5BZ	H	301	-	-	4/23/29/29	0/1/1/1
17	5BZ	K	301	-	-	1/23/29/29	0/1/1/1
17	5BZ	N	201	-	-	1/23/29/29	0/1/1/1
17	5BZ	Y	302	-	-	0/23/29/29	0/1/1/1
17	5BZ	b	201	-	-	2/23/29/29	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	K	301	5BZ	C11-C12	-6.70	1.35	1.51
17	b	201	5BZ	C11-C12	-6.42	1.36	1.51
17	H	301	5BZ	C11-C12	-6.29	1.36	1.51
17	V	302	5BZ	C11-C12	-6.13	1.36	1.51
17	Y	302	5BZ	C11-C12	-5.96	1.37	1.51
17	N	201	5BZ	C11-C12	-5.51	1.38	1.51
17	Y	302	5BZ	C32-C33	-3.57	1.07	1.18
17	N	201	5BZ	C32-C33	-3.51	1.07	1.18
17	K	301	5BZ	C32-C33	-2.88	1.09	1.18

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	K	301	5BZ	C11-C10-N9	-4.87	100.75	110.83
17	Y	302	5BZ	C11-C10-N9	-3.73	103.11	110.83
17	V	302	5BZ	B8-C21-C22	-3.59	105.53	112.31
17	H	301	5BZ	C21-C22-C23	-3.48	110.88	115.32
17	Y	302	5BZ	C21-C22-C23	-3.07	111.40	115.32
17	K	301	5BZ	B8-C21-C22	-3.03	106.59	112.31
17	H	301	5BZ	B8-C21-C22	-2.93	106.77	112.31
17	Y	302	5BZ	B8-C21-C22	-2.85	106.93	112.31
17	b	201	5BZ	C12-C11-C10	-2.82	105.85	113.36
17	N	201	5BZ	C31-C3-C2	-2.75	107.74	112.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	N	201	5BZ	C21-C22-C23	-2.73	111.83	115.32
17	b	201	5BZ	C31-C3-C2	-2.60	108.03	112.76
17	K	301	5BZ	C21-C22-C23	-2.38	112.29	115.32
17	N	201	5BZ	B8-C21-C22	-2.05	108.44	112.31
17	b	201	5BZ	B8-C21-C22	-2.05	108.45	112.31
17	H	301	5BZ	C11-C10-N9	-2.01	106.67	110.83

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	V	302	5BZ	C21-C22-C23-C25
17	b	201	5BZ	C2-C3-C31-C32
17	V	302	5BZ	N20-C21-C22-C23
17	N	201	5BZ	C2-C3-C31-C32
17	V	302	5BZ	C7-C2-C3-C31
17	H	301	5BZ	C7-C2-C3-C31
17	V	302	5BZ	C21-C22-C23-C24
17	b	201	5BZ	N20-C21-C22-C23
17	V	302	5BZ	N9-C10-C18-O19
17	H	301	5BZ	C3-C2-C7-O8
17	V	302	5BZ	C3-C2-C7-O8
17	H	301	5BZ	C3-C2-C7-N9
17	H	301	5BZ	N9-C10-C18-O19
17	V	302	5BZ	C3-C2-C7-N9
17	V	302	5BZ	N9-C10-C18-N20
17	K	301	5BZ	C7-C2-C3-C31

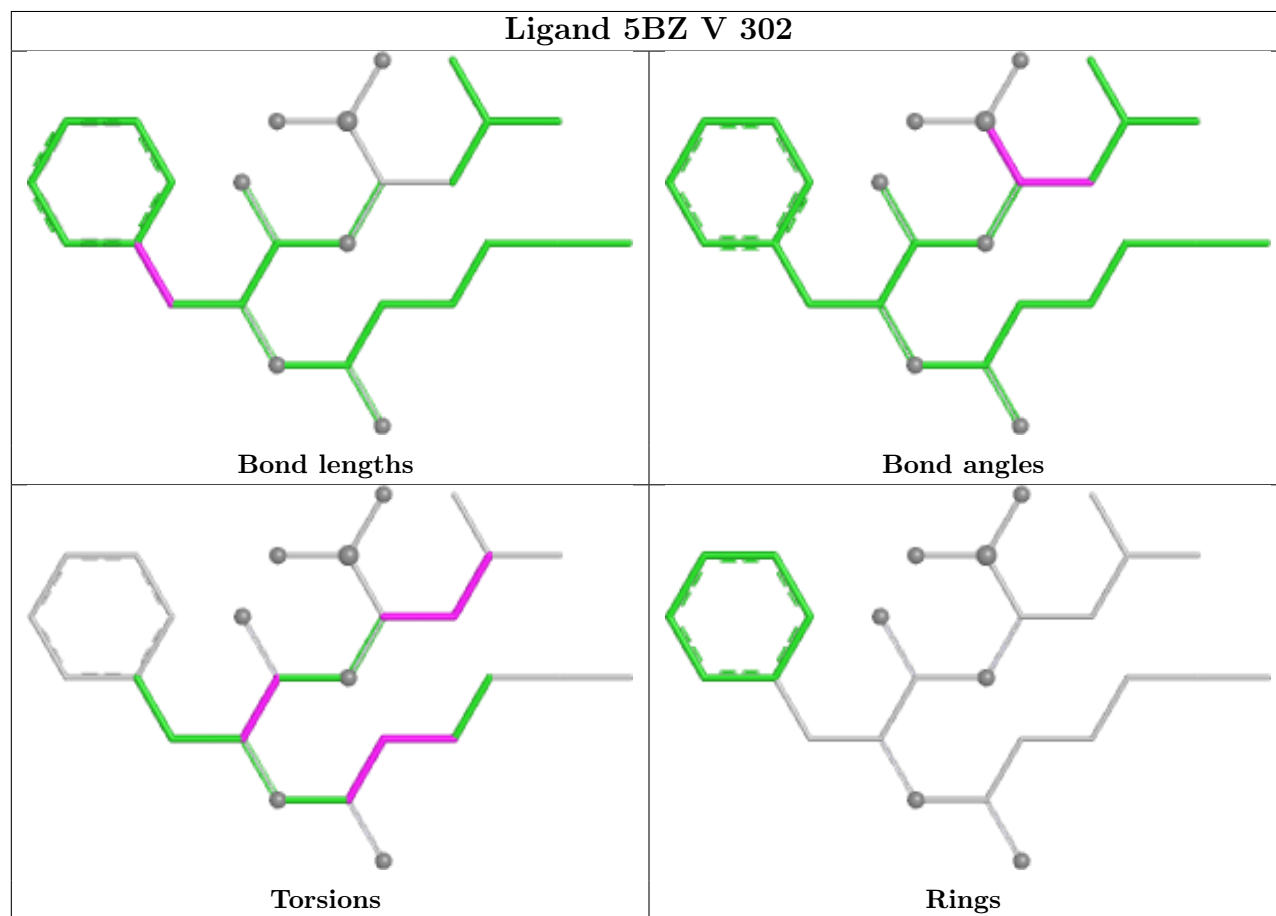
There are no ring outliers.

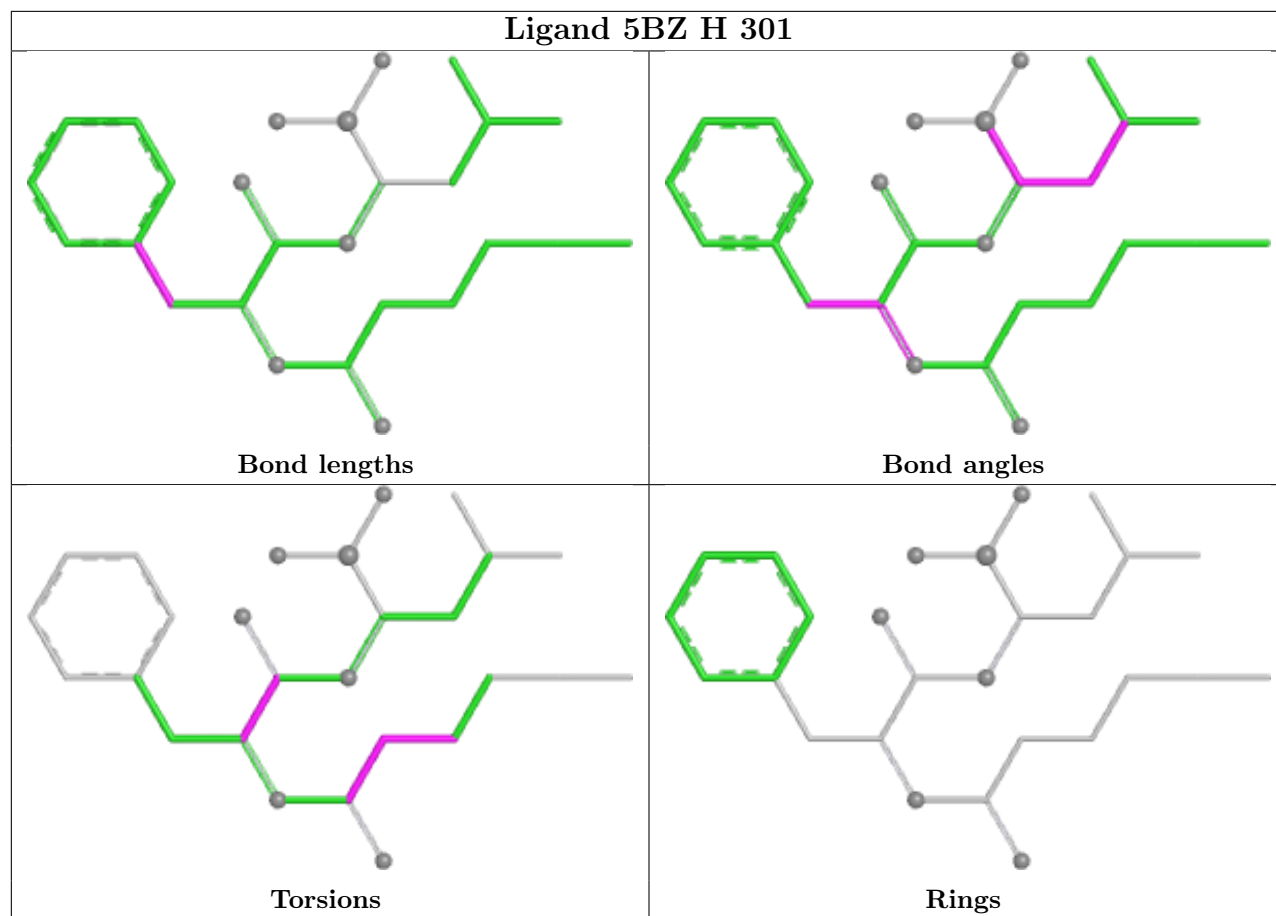
4 monomers are involved in 8 short contacts:

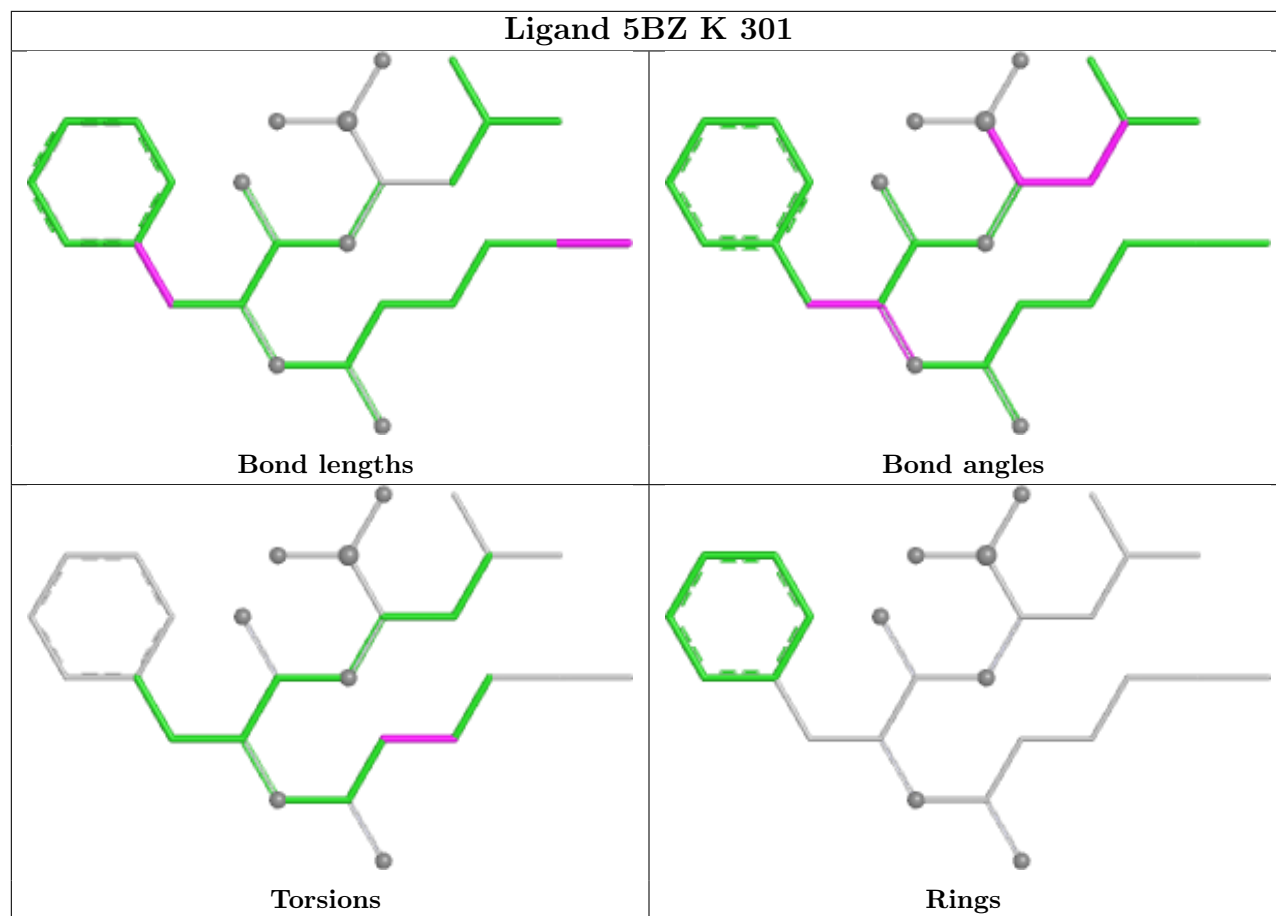
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	V	302	5BZ	5	0
17	N	201	5BZ	1	0
17	Y	302	5BZ	1	0
17	b	201	5BZ	1	0

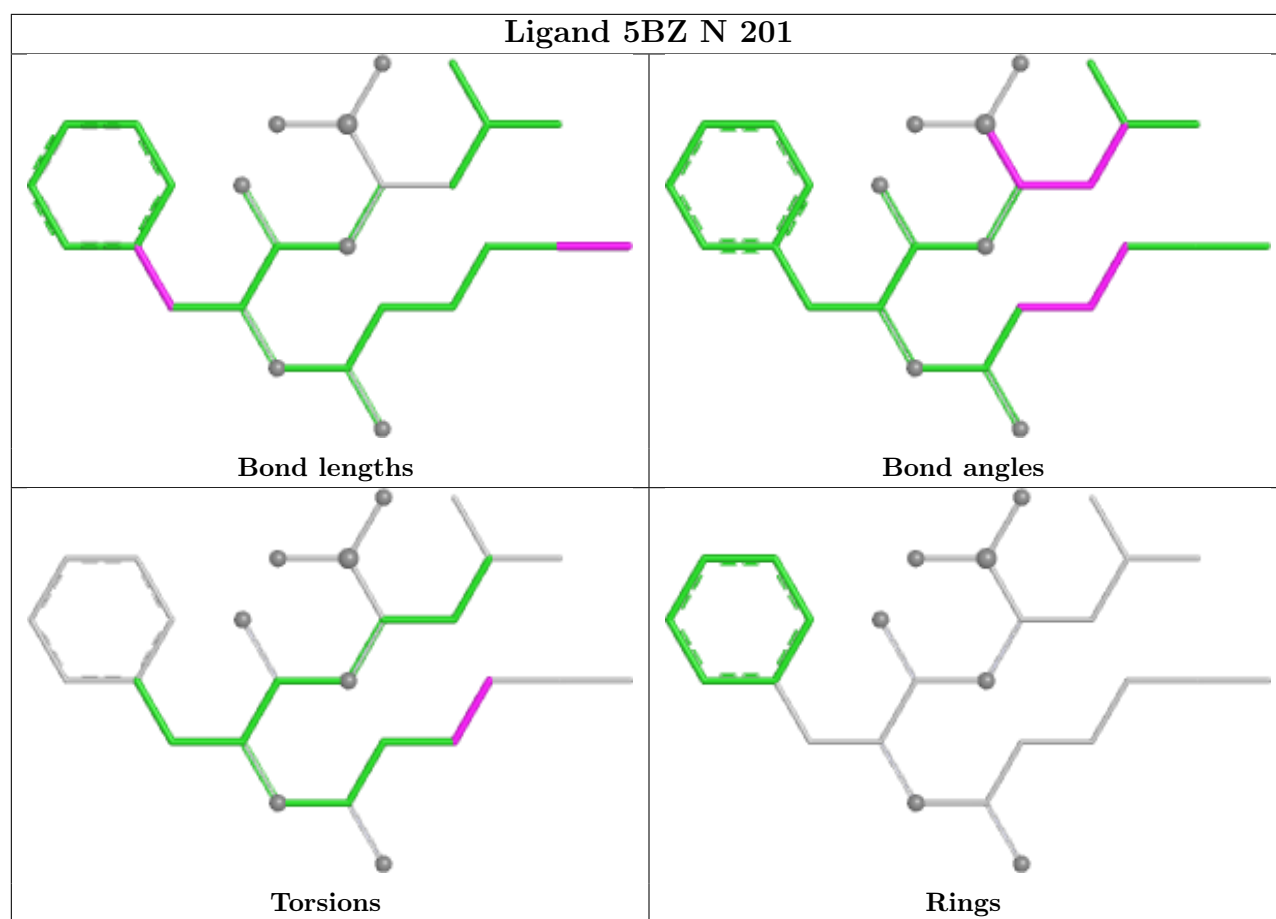
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

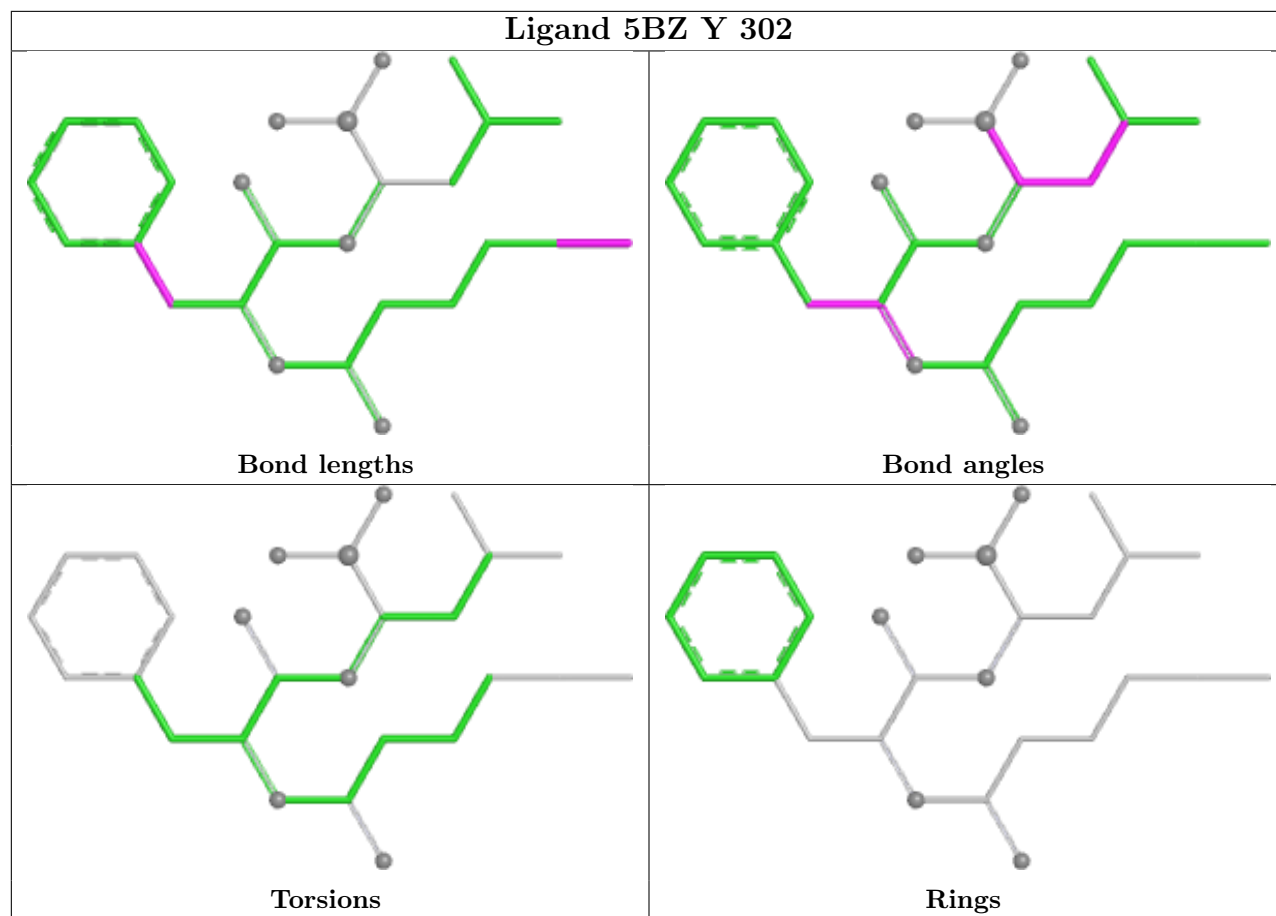
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD 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.

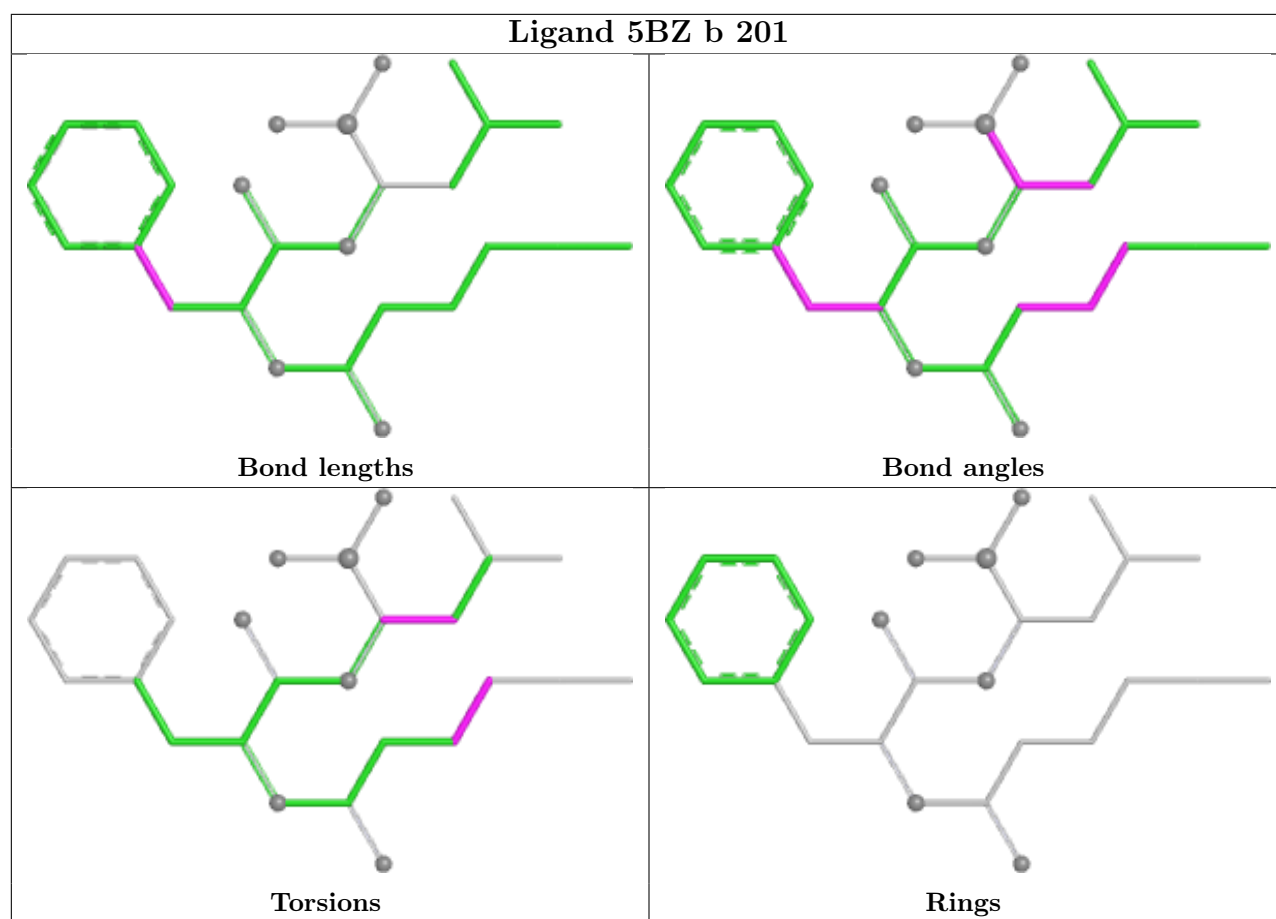












5.7 Other polymers [i](#)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.21	3 (1%) 76 68	35, 50, 91, 128	0
1	O	250/250 (100%)	-0.12	4 (1%) 70 61	39, 60, 104, 137	0
2	B	244/258 (94%)	0.02	8 (3%) 49 39	36, 58, 103, 157	0
2	P	244/258 (94%)	0.06	11 (4%) 38 30	41, 62, 107, 158	0
3	C	240/254 (94%)	-0.01	9 (3%) 44 35	37, 62, 127, 161	0
3	Q	240/254 (94%)	0.28	13 (5%) 31 24	45, 75, 159, 181	0
4	D	235/260 (90%)	-0.04	6 (2%) 57 47	40, 62, 95, 142	0
4	R	235/260 (90%)	0.16	6 (2%) 57 47	52, 71, 112, 145	0
5	E	231/234 (98%)	0.00	2 (0%) 81 74	43, 65, 103, 143	0
5	S	231/234 (98%)	0.11	3 (1%) 75 66	47, 69, 109, 147	0
6	F	243/288 (84%)	-0.07	5 (2%) 63 54	38, 59, 105, 135	0
6	T	243/288 (84%)	0.09	10 (4%) 41 33	37, 64, 120, 151	0
7	G	241/252 (95%)	-0.12	4 (1%) 69 60	35, 56, 97, 152	0
7	U	241/252 (95%)	-0.22	0 100 100	39, 55, 92, 135	0
8	H	226/232 (97%)	-0.26	2 (0%) 81 74	35, 49, 88, 156	0
8	V	226/232 (97%)	-0.16	4 (1%) 67 58	38, 53, 94, 175	0
9	I	204/205 (99%)	-0.39	1 (0%) 87 82	32, 48, 79, 106	0
9	W	204/205 (99%)	-0.35	1 (0%) 87 82	33, 51, 79, 108	0
10	J	195/198 (98%)	-0.12	7 (3%) 46 37	34, 52, 82, 123	0
10	X	195/198 (98%)	-0.09	11 (5%) 30 23	38, 55, 85, 134	0
11	K	212/212 (100%)	0.09	15 (7%) 22 16	35, 54, 90, 106	0
11	Y	212/212 (100%)	0.19	13 (6%) 27 20	35, 52, 93, 117	0
12	L	222/222 (100%)	0.08	16 (7%) 21 16	35, 54, 110, 148	0
12	Z	222/222 (100%)	0.02	14 (6%) 26 19	29, 52, 103, 135	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.32	3 (1%) 75 66	33, 52, 79, 99	0
13	a	233/246 (94%)	-0.29	2 (0%) 81 74	33, 50, 74, 92	0
14	N	196/196 (100%)	-0.47	0 100 100	32, 46, 77, 103	0
14	b	196/196 (100%)	-0.38	1 (0%) 87 82	33, 48, 80, 110	0
All	All	6344/6614 (95%)	-0.08	174 (2%) 56 46	29, 57, 104, 181	0

All (174) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
12	Z	174	TYR	7.5
12	L	174	TYR	7.2
10	J	1	MET	6.5
3	Q	50	LEU	5.7
11	Y	211	ILE	5.4
12	Z	168	VAL	5.2
2	B	218	GLY	5.2
12	L	163	GLY	5.1
12	L	165	ASN	5.1
12	L	169	LYS	4.9
12	L	170	LYS	4.9
12	L	172	LEU	4.7
11	Y	148	LEU	4.6
10	X	1	MET	4.5
12	L	168	VAL	4.3
12	Z	169	LYS	4.2
11	Y	208	ASN	4.2
11	K	208	ASN	4.2
6	F	202	ASP	4.0
12	Z	165	ASN	4.0
12	Z	173	LYS	4.0
11	K	212	GLY	3.9
6	T	243	ILE	3.9
12	Z	172	LEU	3.9
8	V	223	ILE	3.8
3	Q	205	ALA	3.8
12	Z	170	LYS	3.8
2	P	55	LEU	3.8
4	D	241	ALA	3.7
11	K	147	ASP	3.7
12	Z	163	GLY	3.7
11	Y	147	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
3	Q	234	ILE	3.5
11	K	211	ILE	3.5
11	Y	146	TRP	3.5
12	L	162	PRO	3.5
13	a	1	THR	3.5
12	L	136	CYS	3.5
3	Q	51	LYS	3.5
6	T	204	LYS	3.5
10	X	194	ASP	3.5
11	K	148	LEU	3.5
12	Z	162	PRO	3.5
6	F	215	CYS	3.4
10	X	143	LEU	3.4
9	I	4	SER	3.4
1	O	53	SER	3.3
1	A	249	ALA	3.2
6	T	201	GLU	3.2
12	L	167	LYS	3.2
12	L	173	LYS	3.2
6	T	14	ASP	3.1
2	B	217	LYS	3.1
11	Y	150	VAL	3.1
4	D	242	GLU	3.1
2	P	56	LEU	3.1
11	K	73	ARG	3.1
8	V	224	GLN	3.1
2	B	219	ALA	3.0
2	P	218	GLY	3.0
1	O	1	MET	3.0
3	Q	49	THR	3.0
12	L	156	PHE	3.0
11	K	209	ASN	3.0
12	L	171	PRO	3.0
1	O	249	ALA	3.0
11	K	104	TYR	3.0
5	S	207	VAL	3.0
13	M	233	ILE	2.9
4	R	125	LEU	2.9
11	Y	212	GLY	2.9
4	D	240	ALA	2.9
2	B	52	THR	2.9
12	Z	171	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
12	Z	167	LYS	2.9
11	K	150	VAL	2.9
2	P	53	SER	2.9
10	X	142	SER	2.9
3	Q	206	LYS	2.8
3	Q	48	SER	2.8
3	C	205	ALA	2.8
10	J	143	LEU	2.8
4	D	238	LYS	2.8
3	Q	236	GLN	2.7
4	R	113	LEU	2.7
11	Y	209	ASN	2.7
12	L	164	THR	2.7
14	b	103	ASP	2.7
3	C	50	LEU	2.7
2	P	52	THR	2.7
12	L	166	GLY	2.7
4	R	114	ARG	2.7
6	T	182	GLY	2.7
3	C	206	LYS	2.7
11	Y	73	ARG	2.7
2	B	222	GLY	2.7
11	Y	205	GLY	2.7
3	Q	240	GLU	2.7
3	Q	52	LEU	2.6
6	T	205	GLU	2.6
4	R	238	LYS	2.6
6	F	242	GLU	2.6
10	X	149	ARG	2.6
6	T	215	CYS	2.6
3	C	240	GLU	2.6
10	X	146	HIS	2.6
5	E	117	LYS	2.6
8	H	223	ILE	2.5
2	P	222	GLY	2.5
10	J	174	MET	2.5
3	Q	204	GLY	2.5
3	C	186	VAL	2.5
13	M	1	THR	2.5
5	S	173	ARG	2.5
11	Y	145	LYS	2.5
10	J	146	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
11	Y	139	VAL	2.5
2	P	54	THR	2.5
10	X	174	MET	2.4
10	J	142	SER	2.4
8	H	9	ASN	2.4
2	B	51	VAL	2.4
2	P	57	GLU	2.4
2	P	219	ALA	2.4
11	K	146	TRP	2.4
6	T	53	LYS	2.4
2	B	244	THR	2.4
3	C	49	THR	2.4
3	C	236	GLN	2.4
3	Q	3	ASP	2.3
10	J	194	ASP	2.3
3	C	203	THR	2.3
3	C	201	VAL	2.3
11	Y	210	VAL	2.3
3	Q	225	GLU	2.3
10	X	150	PRO	2.3
2	B	54	THR	2.3
9	W	1	SER	2.3
7	G	237	VAL	2.3
4	R	239	GLU	2.2
2	P	58	GLN	2.2
13	a	47	ASP	2.2
11	K	210	VAL	2.2
6	F	204	LYS	2.2
6	T	39	ASN	2.2
12	Z	164	THR	2.2
6	F	4	TYR	2.2
12	L	160	TYR	2.2
11	K	9	GLN	2.2
1	A	1	MET	2.2
11	K	145	LYS	2.1
12	Z	175	LEU	2.1
10	X	139	TYR	2.1
8	V	225	GLU	2.1
11	K	24	ASN	2.1
8	V	212	VAL	2.1
1	A	231	LYS	2.1
12	Z	136	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
10	X	147	HIS	2.1
4	D	224	ASP	2.1
7	G	3	TYR	2.1
1	O	231	LYS	2.1
4	D	167	GLY	2.1
13	M	47	ASP	2.1
7	G	230	GLU	2.1
10	J	139	TYR	2.1
2	P	1	GLY	2.0
7	G	240	ALA	2.0
5	E	122	TYR	2.0
5	S	122	TYR	2.0
6	T	206	LYS	2.0
10	X	172	MET	2.0
4	R	112	ALA	2.0
11	K	116	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
17	5BZ	V	302	27/27	0.85	0.12	24,46,57,62	0
17	5BZ	b	201	27/27	0.85	0.13	28,47,53,54	0
17	5BZ	N	201	27/27	0.86	0.12	22,45,51,52	0
17	5BZ	K	301	27/27	0.87	0.10	24,47,56,64	0
17	5BZ	H	301	27/27	0.87	0.12	21,46,56,58	0
17	5BZ	Y	302	27/27	0.88	0.10	29,46,53,59	0
15	MG	Z	301	1/1	0.89	0.09	67,67,67,67	0

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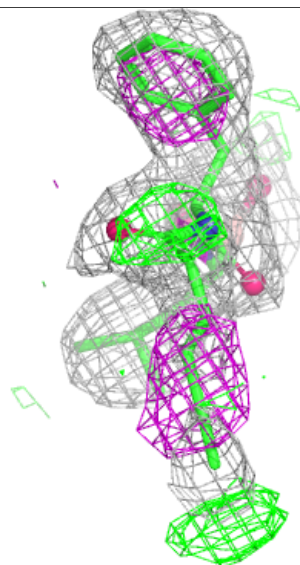
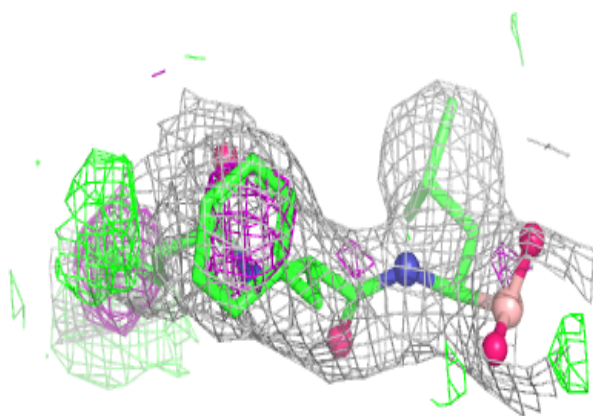
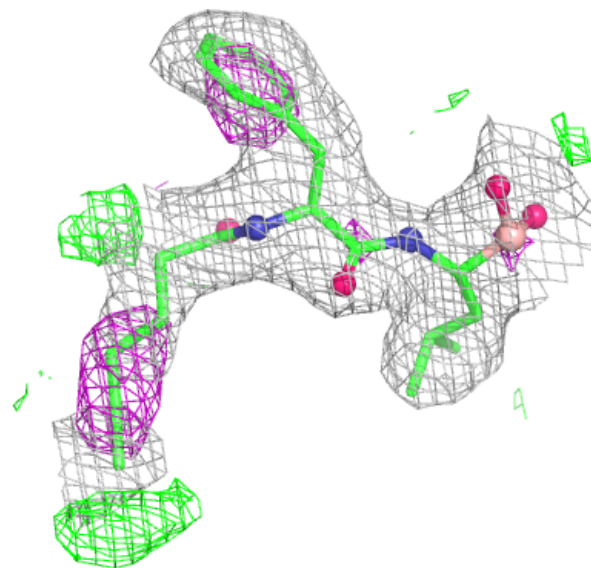
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
15	MG	I	301	1/1	0.95	0.05	56,56,56,56	0
16	CL	G	303	1/1	0.96	0.13	30,30,30,30	0
15	MG	K	302	1/1	0.97	0.08	49,49,49,49	0
16	CL	N	203	1/1	0.98	0.06	44,44,44,44	0
16	CL	b	202	1/1	0.98	0.16	56,56,56,56	0
15	MG	J	201	1/1	0.98	0.10	43,43,43,43	0
15	MG	V	301	1/1	0.98	0.08	59,59,59,59	0
15	MG	G	301	1/1	0.99	0.03	50,50,50,50	0
15	MG	Y	301	1/1	0.99	0.03	53,53,53,53	0
16	CL	U	301	1/1	0.99	0.13	39,39,39,39	0
15	MG	N	202	1/1	0.99	0.04	45,45,45,45	0
16	CL	G	302	1/1	0.99	0.08	40,40,40,40	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.

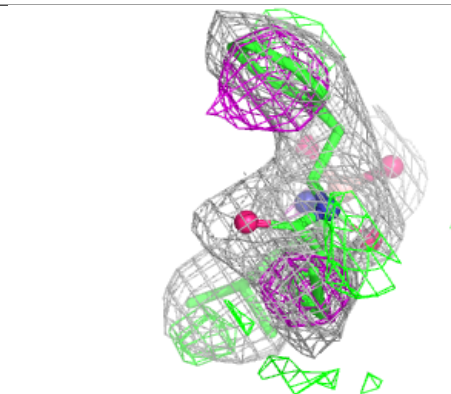
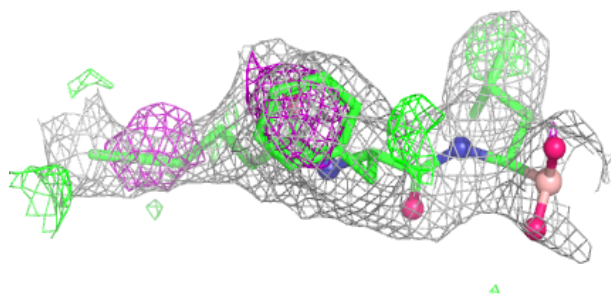
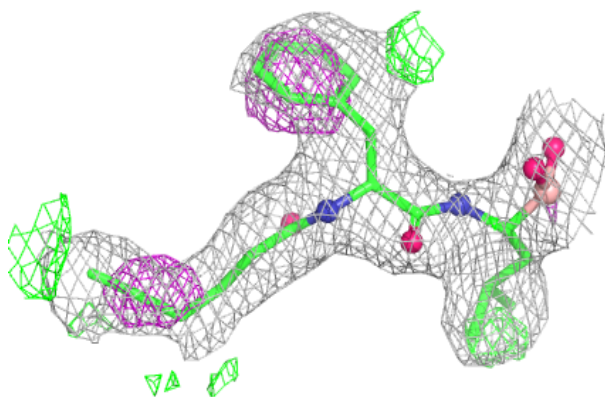
Electron density around 5BZ V 302:

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

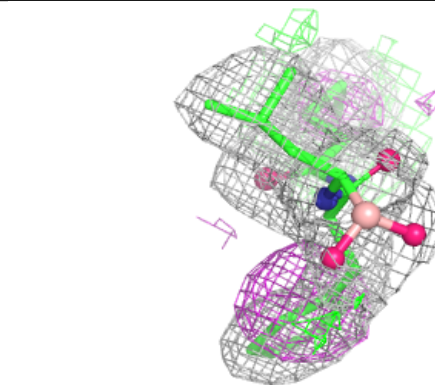
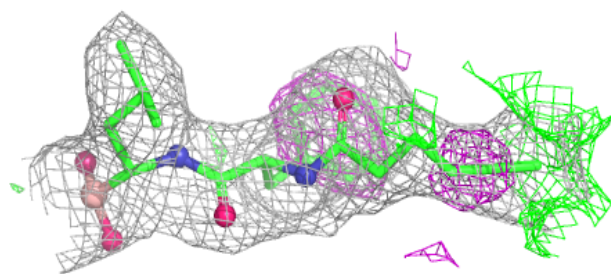
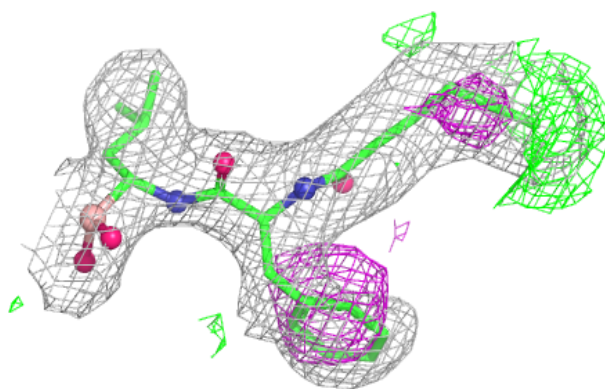


Electron density around 5BZ b 201:

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

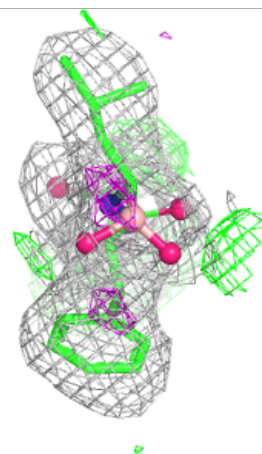
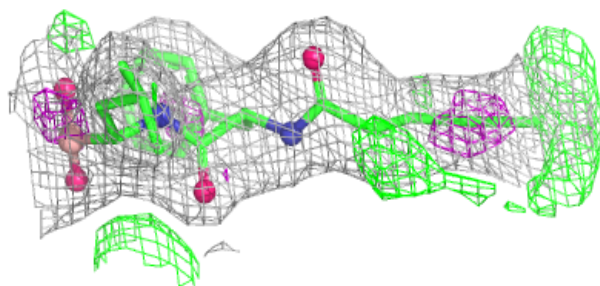
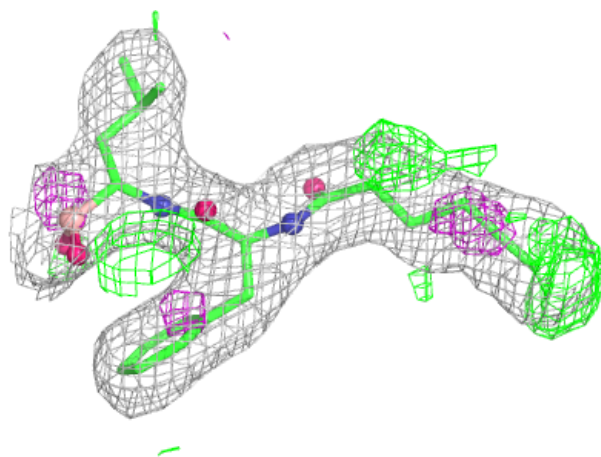
**Electron density around 5BZ N 201:**

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



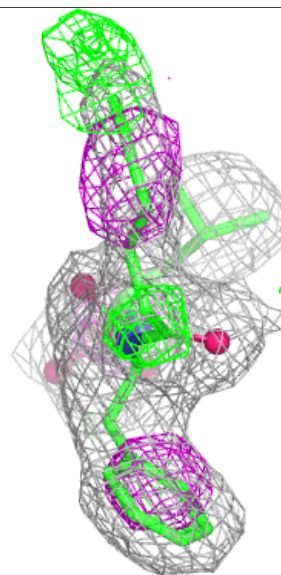
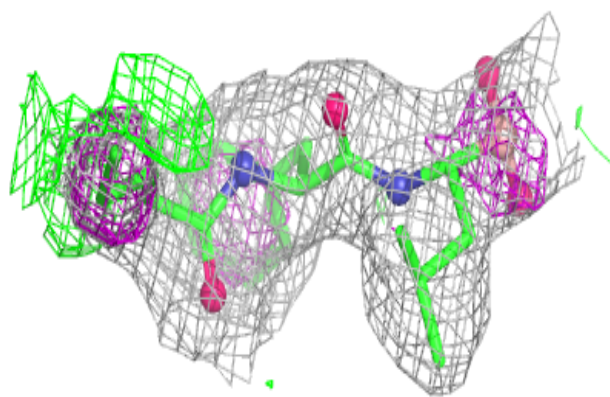
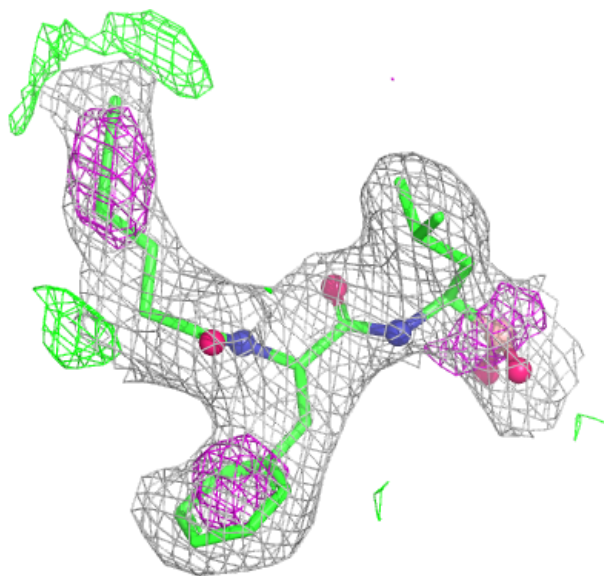
Electron density around 5BZ K 301:

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



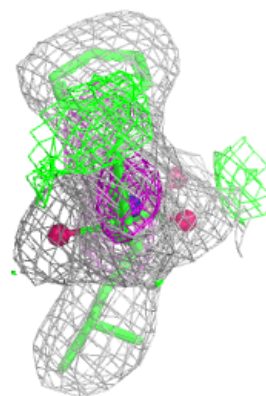
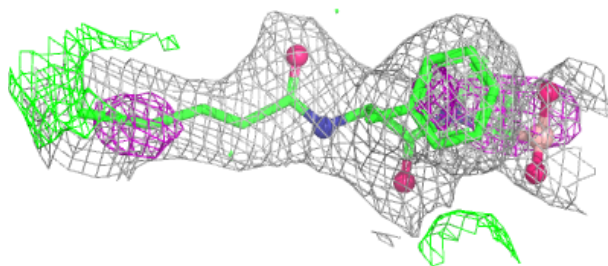
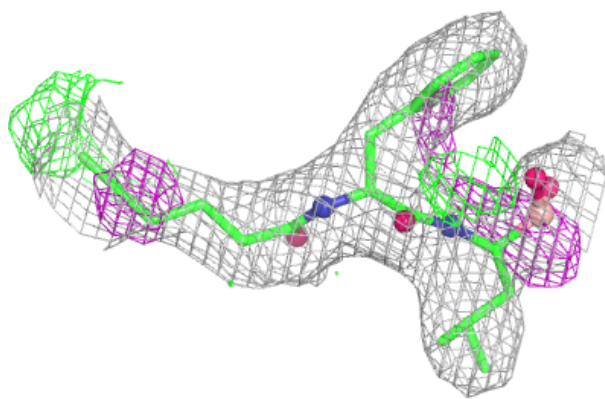
Electron density around 5BZ H 301:

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



Electron density around 5BZ Y 302:

$2mF_o-DF_c$ (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.