



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:31 PM UTC

PDB ID : 5BOU / pdb_00005bou
Title : Yeast 20S proteasome in complex with a beta1 / beta2 specific non-peptidic sulfonamide Ligand
Authors : Beck, P.; Groll, M.
Deposited on : 2015-05-27
Resolution : 2.60 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

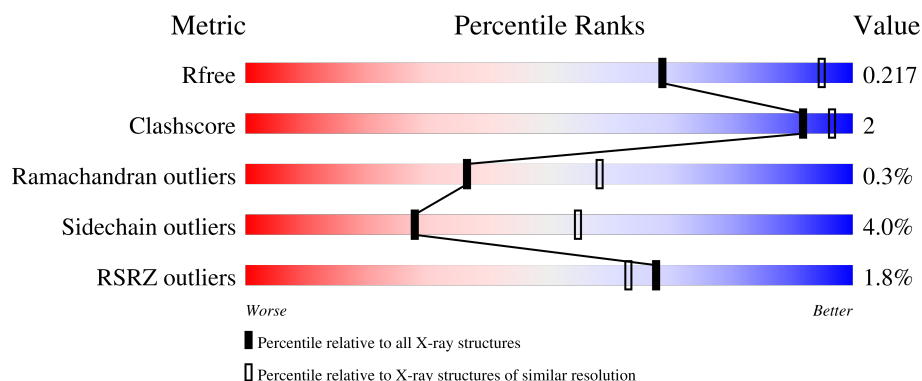
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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% 86% 8% • 5%
2	P	258	5% 86% 8% • 5%
3	C	254	4% 85% 7% • 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	 5% 86% 7% • 6%
4	D	260	 2% 84% 5% • 10%
4	R	260	 % 83% 7% • 10%
5	E	234	 % 93% 5% •
5	S	234	 2% 92% 6% •
6	F	288	 % 81% • 16%
6	T	288	 4% 81% • 16%
7	G	252	 % 90% 5% •
7	U	252	 2% 90% 5% •
8	H	232	 % 87% 9% • •
8	V	232	 % 88% 8% • •
9	I	205	 % 94% 6%
9	W	205	 93% 7%
10	J	198	 % 92% 6% • •
10	X	198	 % 92% 6% • •
11	K	212	 % 92% 6% •
11	Y	212	 92% 6% •
12	L	222	 % 95% • •
12	Z	222	 95% 5%
13	M	246	 % 87% 6% 7%
13	a	246	 88% 6% • 6%
14	N	196	 91% 8% •
14	b	196	 % 91% 7% •

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 50207 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	229	Total	C	N	O	S	0	0	0
			1790	1133	306	344	7			
13	a	232	Total	C	N	O	S	0	0	0
			1815	1148	311	349	7			

- Molecule 14 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Mg	0	0
			1	1		
15	I	2	Total	Mg	0	0
			2	2		

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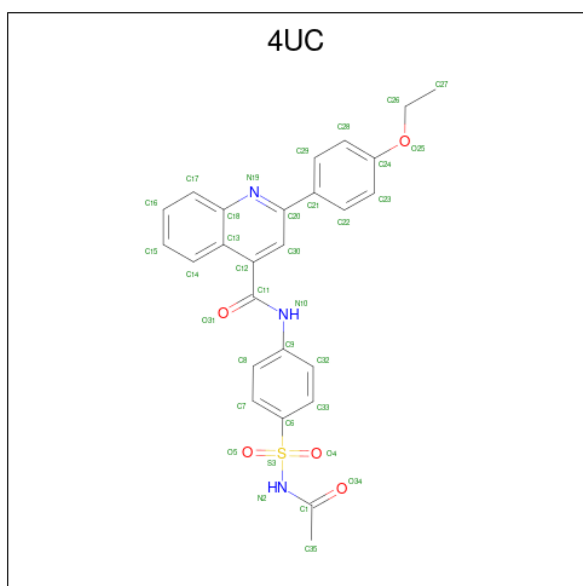
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	K	1	Total	Mg	0	0
			1	1		
15	L	1	Total	Mg	0	0
			1	1		
15	N	1	Total	Mg	0	0
			1	1		
15	W	1	Total	Mg	0	0
			1	1		
15	Z	1	Total	Mg	0	0
			1	1		

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

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

- Molecule 17 is N-[4-(acetylsulfamoyl)phenyl]-2-(4-ethoxyphenyl)quinoline-4-carboxamide (CCD ID: 4UC) (formula: C₂₆H₂₃N₃O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	H	1	Total	C	N	O	S	0	0
			35	26	3	5	1		
17	V	1	Total	C	N	O	S	0	0
			35	26	3	5	1		

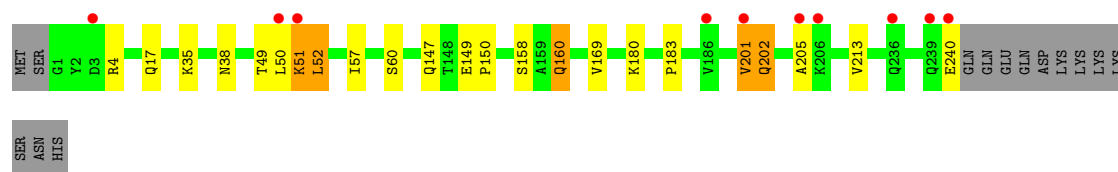
- Molecule 18 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
18	A	33	Total O 33 33	0	0
18	B	32	Total O 32 32	0	0
18	C	30	Total O 30 30	0	0
18	D	16	Total O 16 16	0	0
18	E	12	Total O 12 12	0	0
18	F	26	Total O 26 26	0	0
18	G	27	Total O 27 27	0	0
18	H	36	Total O 36 36	0	0
18	I	37	Total O 37 37	0	0
18	J	31	Total O 31 31	0	0
18	K	38	Total O 38 38	0	0
18	L	34	Total O 34 34	0	0
18	M	43	Total O 43 43	0	0
18	N	29	Total O 29 29	0	0
18	O	17	Total O 17 17	0	0
18	P	19	Total O 19 19	0	0
18	Q	20	Total O 20 20	0	0
18	R	14	Total O 14 14	0	0
18	S	9	Total O 9 9	0	0
18	T	26	Total O 26 26	0	0
18	U	40	Total O 40 40	0	0

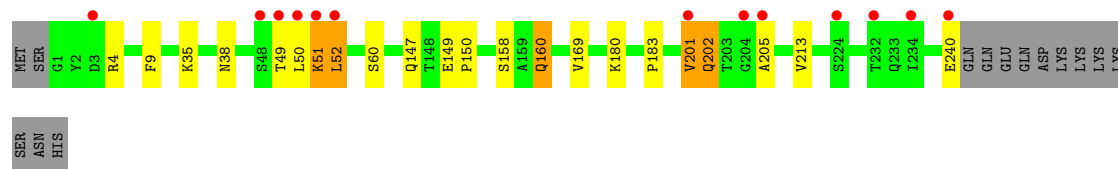
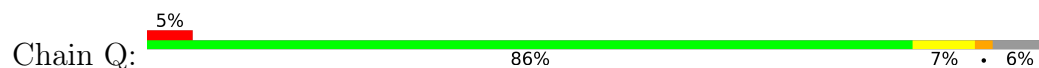
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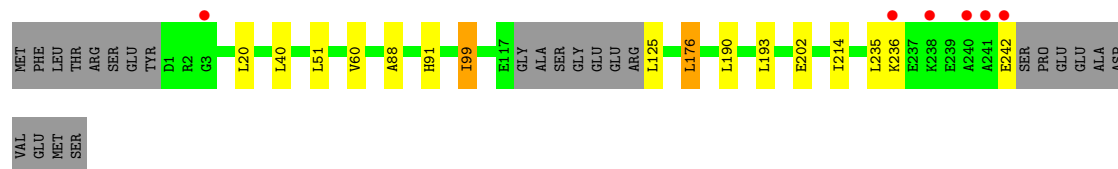
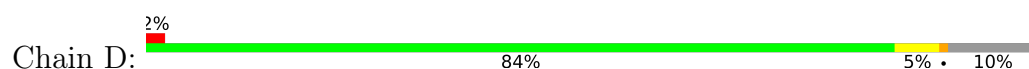
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	V	22	Total 22	O 22	0	0
18	W	28	Total 28	O 28	0	0
18	X	31	Total 31	O 31	0	0
18	Y	36	Total 36	O 36	0	0
18	Z	40	Total 40	O 40	0	0
18	a	41	Total 41	O 41	0	0
18	b	37	Total 37	O 37	0	0



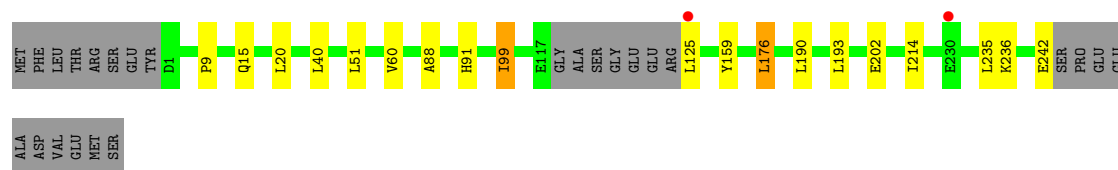
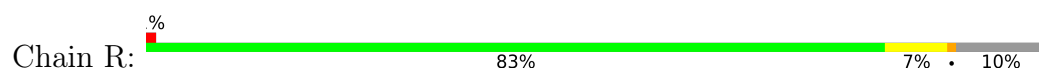
• Molecule 3: Proteasome subunit alpha type-4



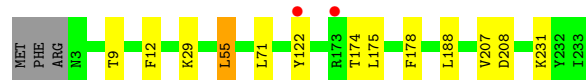
• Molecule 4: Proteasome subunit alpha type-5



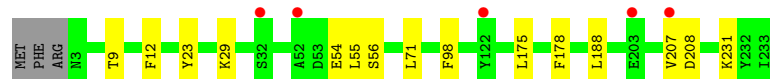
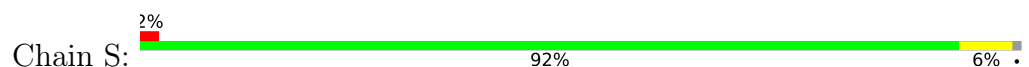
• Molecule 4: Proteasome subunit alpha type-5



• Molecule 5: Proteasome subunit alpha type-6



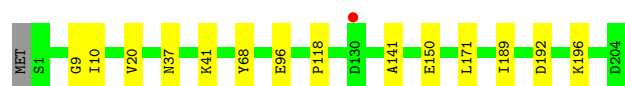
• Molecule 5: Proteasome subunit alpha type-6



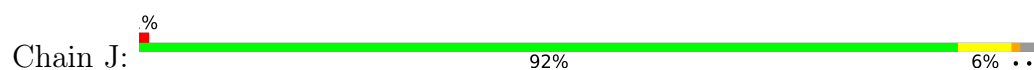
- Molecule 9: Proteasome subunit beta type-3



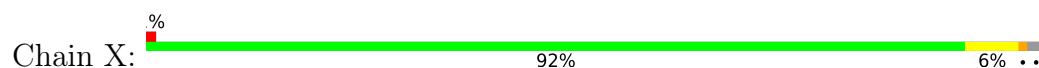
- Molecule 9: Proteasome subunit beta type-3



- Molecule 10: Proteasome subunit beta type-4



- Molecule 10: Proteasome subunit beta type-4



- Molecule 11: Proteasome subunit beta type-5



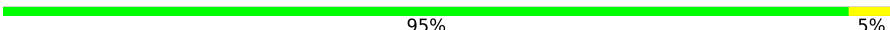
- Molecule 11: Proteasome subunit beta type-5

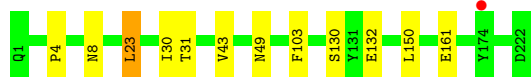


- Molecule 12: Proteasome subunit beta type-6



- Molecule 12: Proteasome subunit beta type-6

Chain Z:  95% 5%



- Molecule 13: Proteasome subunit beta type-7

Chain M:  87% 6% 7%



- Molecule 13: Proteasome subunit beta type-7

Chain a:  88% 6% 6%



- Molecule 14: Proteasome subunit beta type-1

Chain N:  91% 8% .



- Molecule 14: Proteasome subunit beta type-1

Chain b:  91% 7% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.84Å 301.00Å 146.30Å 90.00° 113.27° 90.00°	Depositor
Resolution (Å)	15.00 – 2.60 15.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.5 (15.00-2.60) 95.1 (15.00-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.42 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.192 , 0.214 0.197 , 0.217	Depositor DCC
R_{free} test set	15663 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	52.6	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.4	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	0.95	EDS
Total number of atoms	50207	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 4UC, CL

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.40	0/1952	0.67	0/2642
1	O	0.39	0/1952	0.67	0/2642
2	B	0.41	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	0.38	0/1837	0.66	0/2475
4	R	0.38	0/1837	0.66	0/2475
5	E	0.39	0/1800	0.65	0/2433
5	S	0.39	0/1800	0.65	0/2433
6	F	0.40	0/1932	0.68	0/2609
6	T	0.40	0/1932	0.68	0/2609
7	G	0.39	0/1945	0.67	0/2634
7	U	0.39	0/1945	0.67	0/2634
8	H	0.47	1/1750 (0.1%)	0.70	0/2373
8	V	0.43	1/1750 (0.1%)	0.69	0/2373
9	I	0.34	0/1611	0.71	0/2174
9	W	0.34	0/1611	0.71	0/2174
10	J	0.35	0/1589	0.68	0/2142
10	X	0.34	0/1589	0.68	0/2142
11	K	0.32	0/1681	0.68	0/2274
11	Y	0.32	0/1681	0.68	0/2274
12	L	0.34	0/1795	0.71	2/2420 (0.1%)
12	Z	0.33	0/1795	0.71	2/2420 (0.1%)
13	M	0.34	0/1821	0.70	1/2470 (0.0%)
13	a	0.34	0/1846	0.69	1/2503 (0.0%)
14	N	0.33	0/1541	0.69	1/2087 (0.0%)
14	b	0.33	0/1541	0.69	1/2087 (0.0%)
All	All	0.38	2/50221 (0.0%)	0.68	10/67907 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	113	ILE	C-O	-6.30	1.17	1.24
8	V	3	ILE	C-O	-5.02	1.19	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	201	VAL	N-CA-C	6.33	116.47	110.53
3	C	201	VAL	N-CA-C	6.29	116.44	110.53
12	Z	103	PHE	CA-C-N	5.48	125.42	119.78
12	Z	103	PHE	C-N-CA	5.48	125.42	119.78
12	L	103	PHE	CA-C-N	5.26	125.20	119.78
12	L	103	PHE	C-N-CA	5.26	125.20	119.78
13	a	10	SER	N-CA-C	5.20	117.57	110.24
14	b	115	LEU	N-CA-C	5.14	117.28	111.11
13	M	10	SER	N-CA-C	5.09	117.42	110.24
14	N	115	LEU	N-CA-C	5.06	117.18	111.11

There are no chirality outliers.

There are no planarity outliers.

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	6	0
2	B	1904	0	1904	12	0
2	P	1904	0	1904	11	0
3	C	1881	0	1895	8	0
3	Q	1881	0	1895	6	0
4	D	1813	0	1797	5	0
4	R	1813	0	1797	8	0
5	E	1773	0	1775	5	0
5	S	1773	0	1775	6	0
6	F	1892	0	1883	3	0
6	T	1892	0	1883	2	0
7	G	1907	0	1901	3	0
7	U	1907	0	1901	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1719	0	1719	19	0
8	V	1719	0	1719	15	0
9	I	1581	0	1574	6	0
9	W	1581	0	1574	7	0
10	J	1561	0	1569	5	0
10	X	1561	0	1569	5	0
11	K	1644	0	1595	8	0
11	Y	1644	0	1595	8	0
12	L	1757	0	1711	4	0
12	Z	1757	0	1711	4	0
13	M	1790	0	1793	5	0
13	a	1815	0	1821	7	0
14	N	1512	0	1481	10	0
14	b	1512	0	1481	10	0
15	G	1	0	0	0	0
15	I	2	0	0	0	0
15	K	1	0	0	0	0
15	L	1	0	0	0	0
15	N	1	0	0	0	0
15	W	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	1	0	0	0	0
16	U	1	0	0	0	0
17	H	35	0	23	3	0
17	V	35	0	23	4	0
18	A	33	0	0	0	0
18	B	32	0	0	1	0
18	C	30	0	0	0	0
18	D	16	0	0	0	0
18	E	12	0	0	1	0
18	F	26	0	0	0	0
18	G	27	0	0	0	0
18	H	36	0	0	0	0
18	I	37	0	0	0	0
18	J	31	0	0	0	0
18	K	38	0	0	0	0
18	L	34	0	0	0	0
18	M	43	0	0	0	0
18	N	29	0	0	0	0
18	O	17	0	0	0	0
18	P	19	0	0	1	0
18	Q	20	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	R	14	0	0	0	0
18	S	9	0	0	0	0
18	T	26	0	0	0	0
18	U	40	0	0	0	0
18	V	22	0	0	0	0
18	W	28	0	0	0	0
18	X	31	0	0	0	0
18	Y	36	0	0	0	0
18	Z	40	0	0	0	0
18	a	41	0	0	0	0
18	b	37	0	0	0	0
All	All	50207	0	49126	161	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 2.

All (161) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:126:SER:O	8:H:127:LEU:HD12	1.62	1.00
8:H:126:SER:O	8:H:127:LEU:CD1	2.27	0.82
8:H:80:LEU:HD12	8:H:113:ILE:CD1	2.18	0.73
8:H:80:LEU:HD12	8:H:113:ILE:HD11	1.78	0.64
7:G:68:ARG:HH12	14:N:36:ARG:HH22	1.47	0.61
14:b:152:VAL:HA	14:b:175:MET:HE1	1.84	0.60
14:N:152:VAL:HA	14:N:175:MET:HE1	1.84	0.59
8:H:43:CYS:SG	8:H:56:THR:HG21	2.43	0.59
11:K:31:VAL:HA	12:L:132:GLU:OE1	2.03	0.58
14:b:35:THR:HG21	14:b:45:ARG:HE	1.68	0.58
8:V:43:CYS:SG	8:V:56:THR:HG21	2.44	0.58
11:Y:31:VAL:HA	12:Z:132:GLU:OE1	2.04	0.58
2:P:217:LYS:C	2:P:219:ALA:H	2.12	0.57
14:N:35:THR:HG21	14:N:45:ARG:HE	1.68	0.57
8:H:43:CYS:SG	8:H:56:THR:CG2	2.93	0.57
8:V:43:CYS:SG	8:V:56:THR:CG2	2.94	0.56
2:B:217:LYS:C	2:B:219:ALA:H	2.12	0.56
10:J:3:ILE:HG23	10:J:18:SER:HB3	1.88	0.56
10:X:3:ILE:HG23	10:X:18:SER:HB3	1.89	0.55
10:X:126:VAL:HG12	10:X:128:LEU:HG	1.89	0.55
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.41	0.55
11:K:145:LYS:HB2	11:K:148:LEU:HD13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:H:301:4UC:O31	17:H:301:4UC:H16	2.07	0.55
10:J:126:VAL:HG12	10:J:128:LEU:HG	1.88	0.54
14:b:83:LYS:HG3	14:b:119:VAL:CG2	2.38	0.54
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.38	0.54
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	1.88	0.54
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.91	0.53
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.90	0.53
11:Y:107:LYS:HG3	11:Y:108:GLU:HG3	1.91	0.53
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.08	0.53
2:B:3:ARG:HB3	5:E:122:TYR:OH	2.09	0.52
3:C:51:LYS:O	3:C:52:LEU:HB2	2.08	0.52
8:H:80:LEU:HD12	8:H:113:ILE:HD13	1.91	0.52
3:C:201:VAL:O	3:C:202:GLN:CB	2.57	0.52
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.57	0.52
17:V:301:4UC:H16	17:V:301:4UC:O31	2.08	0.52
8:V:1:THR:N	17:V:301:4UC:H22	2.25	0.52
11:K:107:LYS:HG3	11:K:108:GLU:HG3	1.91	0.51
8:H:196:ARG:NH2	9:I:150:GLU:HG3	2.26	0.51
8:V:218:VAL:CG2	9:W:196:LYS:HB2	2.41	0.51
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.77	0.50
8:H:3:ILE:HG13	8:H:99:ILE:HD12	1.93	0.50
13:M:96:LEU:O	13:M:100:MET:HG2	2.12	0.50
2:B:12:PHE:H	3:C:17:GLN:HE22	1.58	0.50
12:L:23:LEU:HD13	12:L:43:VAL:HG13	1.93	0.50
7:G:23:PHE:O	7:G:26:THR:HB	2.12	0.50
8:V:99:ILE:HG13	8:V:127:LEU:HD22	1.93	0.50
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.94	0.50
10:X:168:LEU:O	10:X:172:MET:HB2	2.13	0.49
13:M:187:ARG:HG3	14:b:25:TYR:CE1	2.47	0.49
12:Z:23:LEU:HD13	12:Z:43:VAL:HG13	1.93	0.49
1:O:1:MET:HG3	6:T:122:TYR:CZ	2.47	0.49
8:V:126:SER:O	8:V:127:LEU:CD1	2.61	0.49
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.77	0.48
5:E:12:PHE:H	6:F:19:GLN:HE22	1.59	0.48
7:U:68:ARG:HH12	14:b:36:ARG:HH22	1.61	0.48
10:J:168:LEU:O	10:J:172:MET:HB2	2.12	0.48
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.49	0.48
7:U:23:PHE:O	7:U:26:THR:HB	2.13	0.48
13:a:96:LEU:O	13:a:100:MET:HG2	2.12	0.48
8:V:126:SER:O	8:V:127:LEU:HD12	2.13	0.48
8:V:196:ARG:NH2	9:W:150:GLU:HG3	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:20:VAL:HG23	9:W:189:ILE:HB	1.96	0.48
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.95	0.48
8:H:113:ILE:HG23	8:H:119:THR:HG22	1.95	0.48
2:B:93:HIS:HB3	18:B:301:HOH:O	2.12	0.48
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.95	0.48
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.96	0.47
9:I:20:VAL:HG23	9:I:189:ILE:HB	1.96	0.47
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.97	0.47
14:N:35:THR:CG2	14:N:45:ARG:HE	2.28	0.47
8:H:196:ARG:NH2	9:I:150:GLU:O	2.47	0.47
11:K:46:ALA:HB3	11:K:98:GLY:O	2.15	0.47
11:Y:46:ALA:HB3	11:Y:98:GLY:O	2.14	0.47
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.78	0.47
2:P:47:ALA:HB1	2:P:64:LYS:HD2	1.97	0.47
4:R:91:HIS:HB3	4:R:99:ILE:HG22	1.97	0.47
12:Z:4:PRO:O	13:a:104:ARG:NH1	2.42	0.47
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.96	0.47
8:V:1:THR:HB	17:V:301:4UC:O5	2.14	0.46
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.96	0.46
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.97	0.46
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.81	0.46
8:V:112:SER:HB3	8:V:125:LEU:HD13	1.98	0.46
4:D:91:HIS:HB3	4:D:99:ILE:HG22	1.98	0.46
8:H:139:GLU:OE1	13:a:187:ARG:NH1	2.42	0.46
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	1.96	0.46
14:b:35:THR:CG2	14:b:45:ARG:HE	2.28	0.46
14:N:133:PHE:HA	14:b:132:THR:O	2.16	0.46
14:N:176:VAL:HG12	14:N:178:LEU:HD13	1.98	0.46
2:B:146:GLN:HG2	3:C:57:ILE:HG21	1.98	0.46
4:D:176:LEU:HD22	5:E:55:LEU:CD2	2.46	0.46
11:Y:128:CYS:HB2	11:Y:137:TYR:CZ	2.51	0.45
1:O:14:PRO:HA	2:P:23:TYR:CD1	2.51	0.45
2:P:50:LYS:O	2:P:51:VAL:C	2.59	0.45
5:S:12:PHE:H	6:T:19:GLN:HE22	1.63	0.45
8:H:104:ASP:HB2	8:H:105:PRO:CD	2.46	0.45
8:H:46:ALA:HB1	17:H:301:4UC:H19	1.98	0.45
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.99	0.45
11:K:128:CYS:HB2	11:K:137:TYR:CZ	2.52	0.45
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.47	0.45
2:B:50:LYS:O	2:B:51:VAL:C	2.59	0.45
14:b:176:VAL:HG12	14:b:178:LEU:HD13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:1:THR:H1	17:V:301:4UC:H22	1.81	0.45
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.17	0.45
8:V:104:ASP:HB2	8:V:105:PRO:CD	2.47	0.45
3:C:35:LYS:HG2	3:C:158:SER:O	2.17	0.44
8:H:112:SER:HB3	8:H:125:LEU:HD13	1.98	0.44
2:P:93:HIS:HB3	18:P:301:HOH:O	2.17	0.44
14:b:35:THR:OG1	14:b:43:CYS:SG	2.74	0.44
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.47	0.44
14:N:35:THR:OG1	14:N:43:CYS:SG	2.75	0.44
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.99	0.44
1:O:99:ARG:HE	8:V:61:SER:HG	1.65	0.44
3:C:149:GLU:HB2	3:C:150:PRO:HD2	2.00	0.44
5:E:174:THR:HG21	18:E:306:HOH:O	2.18	0.43
3:Q:149:GLU:HB2	3:Q:150:PRO:HD2	2.00	0.43
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.48	0.43
2:P:217:LYS:C	2:P:219:ALA:N	2.75	0.43
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.48	0.43
13:M:127:LEU:HG	13:M:142:LEU:HD12	2.01	0.43
5:S:98:PHE:O	13:a:91:TYR:HA	2.18	0.43
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.43
7:U:78:ILE:N	7:U:79:PRO:CD	2.82	0.42
14:b:36:ARG:HG3	14:b:42:TRP:CE2	2.54	0.42
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.19	0.42
13:a:27:LEU:HD21	13:a:34:LEU:HD22	2.02	0.42
8:H:1:THR:HB	17:H:301:4UC:O5	2.20	0.42
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.54	0.42
2:P:95:GLN:HB3	9:W:68:TYR:CD2	2.55	0.42
4:D:88:ALA:HA	4:D:99:ILE:HG21	2.02	0.42
12:L:8:ASN:HA	12:L:30:ILE:O	2.20	0.42
2:B:148:TYR:OH	3:C:57:ILE:HB	2.20	0.42
4:R:91:HIS:CD2	4:R:99:ILE:HG22	2.55	0.42
13:M:27:LEU:HD21	13:M:34:LEU:HD22	2.01	0.42
10:J:25:ILE:O	10:X:139:TYR:OH	2.38	0.41
11:Y:86:LEU:HD13	11:Y:86:LEU:C	2.46	0.41
8:H:126:SER:C	8:H:127:LEU:CD1	2.93	0.41
4:D:91:HIS:CD2	4:D:99:ILE:HG22	2.56	0.41
4:R:9:PRO:HA	5:S:23:TYR:CD1	2.55	0.41
8:H:165:ASN:HD22	13:a:156:ARG:HH11	1.69	0.41
11:Y:12:ILE:HB	11:Y:180:VAL:HB	2.03	0.41
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.68	0.41
8:V:84:LYS:HA	8:V:113:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:12:PHE:H	2:P:20:GLN:HE22	1.69	0.41
2:P:151:ASN:HB2	2:P:152:PRO:HD2	2.03	0.41
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.03	0.41
2:B:217:LYS:C	2:B:219:ALA:N	2.75	0.41
13:a:127:LEU:HG	13:a:142:LEU:HD12	2.01	0.41
14:N:163:ILE:HG23	14:N:170:GLY:HA2	2.03	0.40
11:K:12:ILE:HB	11:K:180:VAL:HB	2.03	0.40
4:R:176:LEU:HD11	5:S:54:GLU:HB2	2.02	0.40
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.57	0.40
6:F:198:LEU:HD12	6:F:243:ILE:HG22	2.03	0.40
1:A:1:MET:HG3	6:F:122:TYR:CZ	2.56	0.40
2:B:151:ASN:HB2	2:B:152:PRO:HD2	2.03	0.40
11:K:86:LEU:C	11:K:86:LEU:HD13	2.46	0.40
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.86	0.40
13:M:165:ILE:HB	13:M:166:PRO:HD3	2.04	0.40
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	51
1	O	248/250 (99%)	238 (96%)	9 (4%)	1 (0%)	30	51
2	B	242/258 (94%)	235 (97%)	3 (1%)	4 (2%)	7	15
2	P	242/258 (94%)	236 (98%)	2 (1%)	4 (2%)	7	15
3	C	238/254 (94%)	232 (98%)	3 (1%)	3 (1%)	9	21
3	Q	238/254 (94%)	232 (98%)	3 (1%)	3 (1%)	9	21
4	D	231/260 (89%)	229 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	R	231/260 (89%)	229 (99%)	2 (1%)	0	100	100
5	E	229/234 (98%)	225 (98%)	4 (2%)	0	100	100
5	S	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
6	F	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
6	T	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
7	G	239/252 (95%)	238 (100%)	1 (0%)	0	100	100
7	U	239/252 (95%)	239 (100%)	0	0	100	100
8	H	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
8	V	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
10	J	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
10	X	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
11	K	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
11	Y	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
12	L	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
12	Z	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
13	M	227/246 (92%)	220 (97%)	7 (3%)	0	100	100
13	a	230/246 (94%)	222 (96%)	8 (4%)	0	100	100
14	N	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
14	b	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
All	All	6279/6614 (95%)	6137 (98%)	126 (2%)	16 (0%)	36	58

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
2	B	221	ASP
3	C	202	GLN
2	P	51	VAL
2	P	221	ASP
3	Q	202	GLN
1	A	2	THR
2	B	218	GLY
2	B	220	ASN

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Mol	Chain	Res	Type
1	O	2	THR
2	P	218	GLY
2	P	220	ASN
3	C	205	ALA
3	Q	205	ALA
3	C	183	PRO
3	Q	183	PRO

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%)	203 (97%)	6 (3%)	37	65
1	O	209/209 (100%)	203 (97%)	6 (3%)	37	65
2	B	203/216 (94%)	196 (97%)	7 (3%)	32	60
2	P	203/216 (94%)	196 (97%)	7 (3%)	32	60
3	C	212/226 (94%)	199 (94%)	13 (6%)	17	37
3	Q	212/226 (94%)	199 (94%)	13 (6%)	17	37
4	D	194/215 (90%)	180 (93%)	14 (7%)	13	30
4	R	194/215 (90%)	180 (93%)	14 (7%)	13	30
5	E	190/193 (98%)	182 (96%)	8 (4%)	26	52
5	S	190/193 (98%)	182 (96%)	8 (4%)	26	52
6	F	201/239 (84%)	194 (96%)	7 (4%)	32	59
6	T	201/239 (84%)	194 (96%)	7 (4%)	32	59
7	G	206/210 (98%)	197 (96%)	9 (4%)	25	50
7	U	206/210 (98%)	197 (96%)	9 (4%)	25	50
8	H	185/190 (97%)	175 (95%)	10 (5%)	20	42
8	V	185/190 (97%)	176 (95%)	9 (5%)	22	47
9	I	172/173 (99%)	168 (98%)	4 (2%)	44	71
9	W	172/173 (99%)	168 (98%)	4 (2%)	44	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	173/175 (99%)	169 (98%)	4 (2%)	44	71
10	X	173/175 (99%)	169 (98%)	4 (2%)	44	71
11	K	169/169 (100%)	163 (96%)	6 (4%)	31	58
11	Y	169/169 (100%)	163 (96%)	6 (4%)	31	58
12	L	185/185 (100%)	180 (97%)	5 (3%)	39	67
12	Z	185/185 (100%)	179 (97%)	6 (3%)	34	62
13	M	195/208 (94%)	188 (96%)	7 (4%)	31	58
13	a	198/208 (95%)	191 (96%)	7 (4%)	32	59
14	N	162/162 (100%)	156 (96%)	6 (4%)	30	57
14	b	162/162 (100%)	156 (96%)	6 (4%)	30	57
All	All	5315/5540 (96%)	5103 (96%)	212 (4%)	28	55

All (212) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	59	GLU
1	A	62	SER
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	50	LYS
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	49	THR
3	C	50	LEU
3	C	51	LYS
3	C	52	LEU
3	C	60	SER
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL

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Mol	Chain	Res	Type
3	C	180	LYS
3	C	213	VAL
3	C	240	GLU
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU
4	D	60	VAL
4	D	99	ILE
4	D	125	LEU
4	D	176	LEU
4	D	190	LEU
4	D	193	LEU
4	D	202	GLU
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	207	VAL
5	E	208	ASP
5	E	231	LYS
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	201	GLU
6	F	207	ASP
6	F	221	ASN
6	F	240	GLN
7	G	13	GLU
7	G	26	THR
7	G	75	ASN
7	G	83	ASN
7	G	115	LEU
7	G	122	ARG
7	G	125	MET
7	G	235	ARG
7	G	236	LEU
8	H	3	ILE

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Mol	Chain	Res	Type
8	H	30	ASN
8	H	34	LEU
8	H	53	GLU
8	H	55	VAL
8	H	56	THR
8	H	68	LEU
8	H	113	ILE
8	H	144	GLN
8	H	196	ARG
9	I	37	ASN
9	I	96	GLU
9	I	171	LEU
9	I	192	ASP
10	J	3	ILE
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
11	K	4	LEU
11	K	107	LYS
11	K	116	ASP
11	K	128	CYS
11	K	140	LEU
11	K	148	LEU
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	150	LEU
12	L	161	GLU
13	M	2	GLN
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	161	ARG
13	M	187	ARG
13	M	212	LEU
14	N	9	LYS
14	N	104	ASP
14	N	107	LYS
14	N	115	LEU
14	N	119	VAL
14	N	178	LEU
1	O	1	MET

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Mol	Chain	Res	Type
1	O	59	GLU
1	O	62	SER
1	O	122	THR
1	O	157	PHE
1	O	250	LEU
2	P	50	LYS
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	49	THR
3	Q	50	LEU
3	Q	51	LYS
3	Q	52	LEU
3	Q	60	SER
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	213	VAL
3	Q	240	GLU
4	R	20	LEU
4	R	40	LEU
4	R	51	LEU
4	R	60	VAL
4	R	99	ILE
4	R	125	LEU
4	R	176	LEU
4	R	190	LEU
4	R	193	LEU
4	R	202	GLU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	55	LEU

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Mol	Chain	Res	Type
5	S	71	LEU
5	S	188	LEU
5	S	207	VAL
5	S	208	ASP
5	S	231	LYS
6	T	123	ASN
6	T	172	LEU
6	T	181	GLU
6	T	201	GLU
6	T	207	ASP
6	T	221	ASN
6	T	240	GLN
7	U	13	GLU
7	U	26	THR
7	U	75	ASN
7	U	83	ASN
7	U	115	LEU
7	U	122	ARG
7	U	125	MET
7	U	235	ARG
7	U	236	LEU
8	V	30	ASN
8	V	34	LEU
8	V	53	GLU
8	V	55	VAL
8	V	56	THR
8	V	68	LEU
8	V	127	LEU
8	V	144	GLN
8	V	196	ARG
9	W	37	ASN
9	W	96	GLU
9	W	171	LEU
9	W	192	ASP
10	X	3	ILE
10	X	35	THR
10	X	90	LYS
10	X	99	GLN
11	Y	4	LEU
11	Y	107	LYS
11	Y	116	ASP
11	Y	128	CYS

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Mol	Chain	Res	Type
11	Y	140	LEU
11	Y	148	LEU
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	130	SER
12	Z	150	LEU
12	Z	161	GLU
13	a	2	GLN
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
13	a	212	LEU
14	b	9	LYS
14	b	104	ASP
14	b	107	LYS
14	b	115	LEU
14	b	119	VAL
14	b	178	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (148) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	93	HIS
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	124	HIS
2	B	146	GLN
2	B	176	GLN
2	B	232	GLN
3	C	17	GLN
3	C	115	GLN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	100	ASN
4	D	146	GLN
4	D	225	ASN

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Mol	Chain	Res	Type
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	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	167	GLN
7	G	175	ASN
8	H	22	GLN
8	H	30	ASN
8	H	35	HIS
8	H	57	GLN
8	H	66	HIS
8	H	165	ASN
8	H	189	ASN
9	I	37	ASN
9	I	63	ASN
9	I	88	GLN
9	I	203	GLN
10	J	10	GLN
10	J	55	GLN
10	J	63	ASN
10	J	146	HIS
10	J	147	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	49	ASN

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Mol	Chain	Res	Type
12	L	70	ASN
12	L	79	HIS
12	L	80	ASN
12	L	153	GLN
12	L	155	ASN
12	L	158	ASN
12	L	165	ASN
12	L	197	GLN
13	M	48	ASN
13	M	102	GLN
13	M	194	ASN
13	M	213	GLN
14	N	38	HIS
14	N	62	HIS
14	N	141	ASN
14	N	161	GLN
1	O	94	HIS
2	P	20	GLN
2	P	93	HIS
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	124	HIS
2	P	176	GLN
2	P	232	GLN
3	Q	17	GLN
3	Q	115	GLN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	118	ASN
5	S	120	GLN
5	S	184	ASN
6	T	19	GLN

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Mol	Chain	Res	Type
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
7	U	30	ASN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	172	ASN
7	U	175	ASN
8	V	22	GLN
8	V	30	ASN
8	V	35	HIS
8	V	57	GLN
8	V	116	HIS
8	V	189	ASN
9	W	37	ASN
9	W	44	HIS
9	W	63	ASN
9	W	88	GLN
10	X	10	GLN
10	X	55	GLN
10	X	63	ASN
10	X	147	HIS
11	Y	9	GLN
11	Y	85	ASN
11	Y	143	ASN
11	Y	176	ASN
11	Y	208	ASN
11	Y	209	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	153	GLN
12	Z	155	ASN
12	Z	158	ASN
12	Z	165	ASN
12	Z	197	GLN
13	a	48	ASN
13	a	62	HIS
13	a	102	GLN

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Mol	Chain	Res	Type
13	a	149	HIS
13	a	194	ASN
13	a	213	GLN
14	b	38	HIS
14	b	141	ASN

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 12 ligands modelled in this entry, 10 are monoatomic - leaving 2 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	4UC	H	301	-	38,38,38	2.73	12 (31%)	54,54,54	2.23	9 (16%)
17	4UC	V	301	-	38,38,38	2.82	11 (28%)	54,54,54	2.21	9 (16%)

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	4UC	H	301	-	-	11/26/26/26	0/4/4/4
17	4UC	V	301	-	-	12/26/26/26	0/4/4/4

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	V	301	4UC	S3-N2	-8.49	1.43	1.64
17	V	301	4UC	C12-C11	-7.89	1.38	1.50
17	H	301	4UC	S3-N2	-7.62	1.45	1.64
17	V	301	4UC	C21-C20	-6.98	1.38	1.49
17	H	301	4UC	C12-C11	-6.86	1.40	1.50
17	H	301	4UC	C21-C20	-6.42	1.39	1.49
17	H	301	4UC	C6-S3	-6.35	1.66	1.76
17	V	301	4UC	C6-S3	-5.18	1.68	1.76
17	V	301	4UC	C9-N10	-5.03	1.31	1.41
17	H	301	4UC	C9-N10	-4.26	1.33	1.41
17	H	301	4UC	O4-S3	3.93	1.48	1.43
17	H	301	4UC	C1-N2	-3.62	1.34	1.38
17	V	301	4UC	O4-S3	3.53	1.47	1.43
17	H	301	4UC	C18-N19	-3.22	1.32	1.37
17	V	301	4UC	C18-N19	-3.21	1.32	1.37
17	H	301	4UC	C13-C18	-3.00	1.37	1.42
17	V	301	4UC	C13-C18	-2.85	1.38	1.42
17	V	301	4UC	C1-N2	-2.75	1.35	1.38
17	H	301	4UC	O5-S3	2.73	1.46	1.43
17	V	301	4UC	C12-C13	-2.30	1.38	1.42
17	H	301	4UC	C17-C18	-2.10	1.38	1.41
17	V	301	4UC	C17-C18	-2.10	1.38	1.41
17	H	301	4UC	C12-C13	-2.08	1.39	1.42

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	H	301	4UC	O5-S3-O4	-10.15	107.19	119.52
17	V	301	4UC	O5-S3-O4	-9.30	108.22	119.52
17	H	301	4UC	C35-C1-N2	7.94	121.33	114.79
17	V	301	4UC	C35-C1-N2	7.90	121.30	114.79
17	H	301	4UC	C20-N19-C18	4.98	122.03	118.12
17	V	301	4UC	C6-S3-N2	4.93	113.91	106.06
17	V	301	4UC	C20-N19-C18	4.25	121.45	118.12
17	H	301	4UC	O4-S3-C6	3.71	112.66	107.98
17	V	301	4UC	O4-S3-C6	3.35	112.20	107.98
17	H	301	4UC	C30-C20-N19	-3.03	119.41	122.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	V	301	4UC	O34-C1-C35	-2.58	117.46	122.05
17	H	301	4UC	O34-C1-C35	-2.45	117.68	122.05
17	H	301	4UC	C9-N10-C11	-2.43	120.21	126.61
17	V	301	4UC	C21-C20-N19	2.40	120.24	117.05
17	V	301	4UC	C30-C20-N19	-2.39	119.99	122.17
17	H	301	4UC	C6-S3-N2	2.38	109.86	106.06
17	V	301	4UC	C9-N10-C11	-2.26	120.67	126.61
17	H	301	4UC	C12-C13-C18	2.14	119.41	117.08

There are no chirality outliers.

All (23) torsion outliers are listed below:

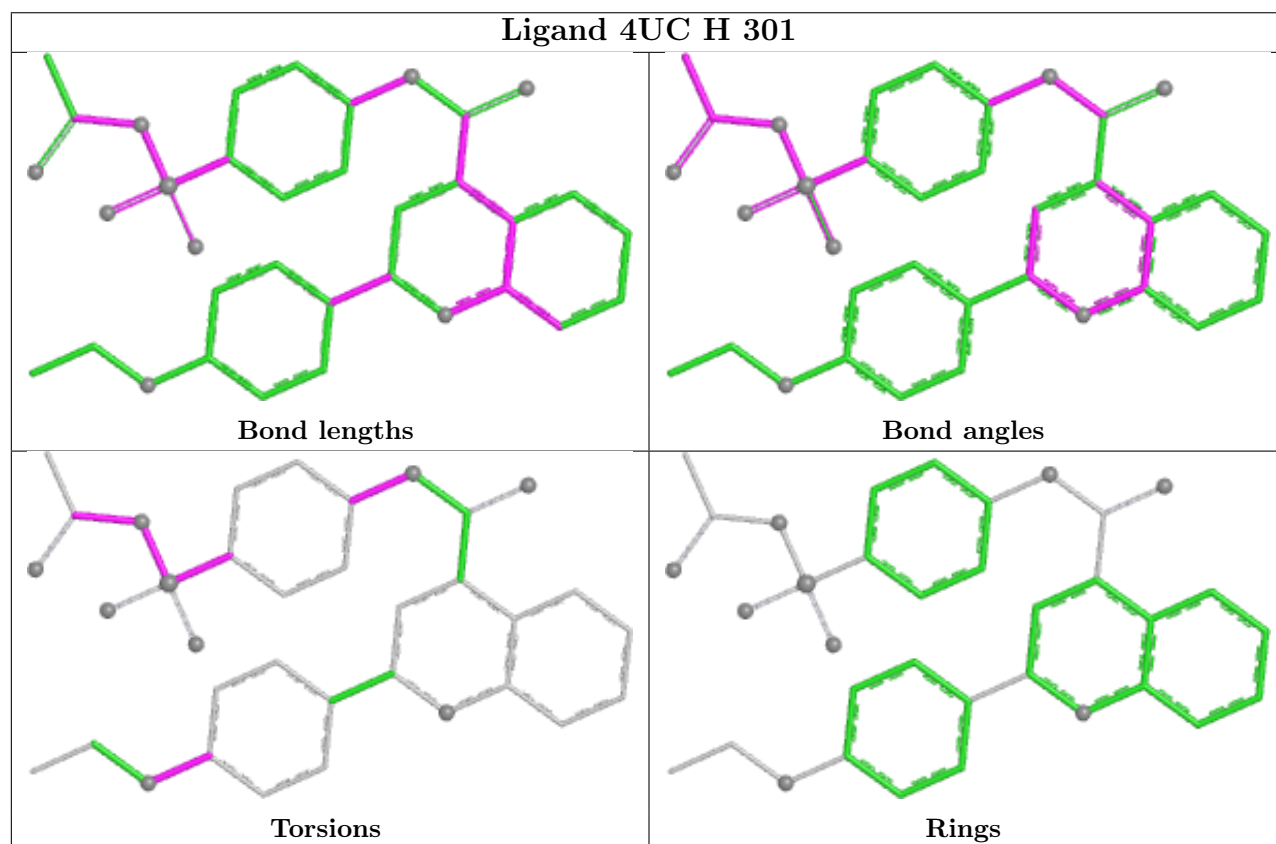
Mol	Chain	Res	Type	Atoms
17	H	301	4UC	O34-C1-N2-S3
17	H	301	4UC	C35-C1-N2-S3
17	V	301	4UC	O34-C1-N2-S3
17	V	301	4UC	C35-C1-N2-S3
17	H	301	4UC	C7-C6-S3-N2
17	H	301	4UC	C1-N2-S3-C6
17	V	301	4UC	C1-N2-S3-C6
17	H	301	4UC	C33-C6-S3-N2
17	V	301	4UC	C27-C26-O25-C24
17	V	301	4UC	C7-C6-S3-N2
17	V	301	4UC	C33-C6-S3-N2
17	V	301	4UC	C8-C9-N10-C11
17	V	301	4UC	C32-C9-N10-C11
17	H	301	4UC	C23-C24-O25-C26
17	V	301	4UC	C7-C6-S3-O5
17	H	301	4UC	C28-C24-O25-C26
17	V	301	4UC	C33-C6-S3-O5
17	H	301	4UC	C7-C6-S3-O5
17	H	301	4UC	C33-C6-S3-O5
17	H	301	4UC	C8-C9-N10-C11
17	V	301	4UC	C23-C24-O25-C26
17	V	301	4UC	C28-C24-O25-C26
17	H	301	4UC	C32-C9-N10-C11

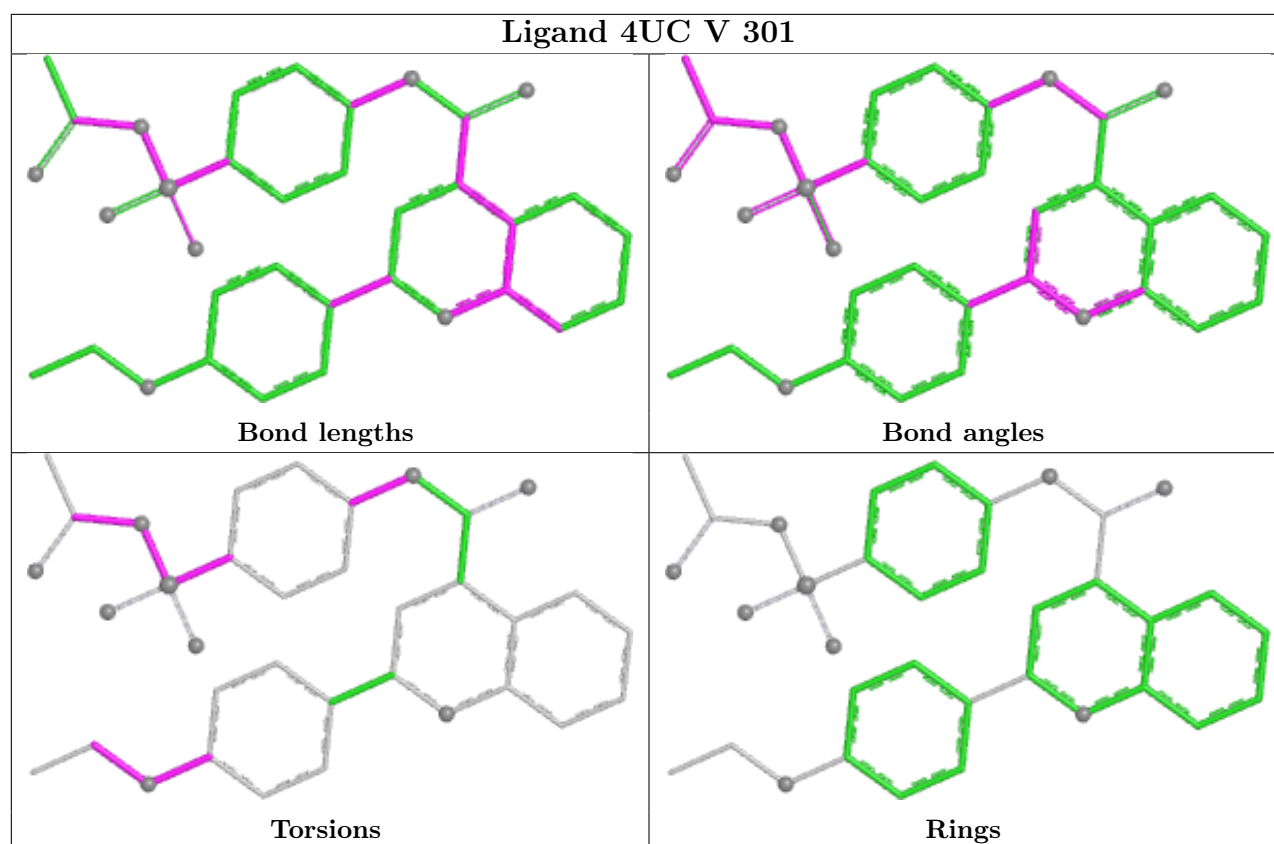
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	H	301	4UC	3	0
17	V	301	4UC	4	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%)	-0.29	3 (1%) 76 73	36, 49, 82, 120	0
1	O	250/250 (100%)	-0.15	4 (1%) 70 66	41, 57, 100, 130	0
2	B	244/258 (94%)	-0.10	9 (3%) 45 39	36, 54, 95, 142	0
2	P	244/258 (94%)	0.04	14 (5%) 29 24	42, 58, 102, 147	0
3	C	240/254 (94%)	0.06	10 (4%) 40 35	36, 60, 123, 153	0
3	Q	240/254 (94%)	0.24	13 (5%) 31 26	43, 70, 152, 183	0
4	D	235/260 (90%)	-0.10	6 (2%) 57 51	41, 61, 94, 137	0
4	R	235/260 (90%)	-0.06	2 (0%) 81 78	43, 64, 103, 138	0
5	E	231/234 (98%)	-0.05	2 (0%) 81 78	45, 63, 101, 145	0
5	S	231/234 (98%)	0.19	5 (2%) 62 57	48, 72, 110, 155	0
6	F	243/288 (84%)	-0.19	4 (1%) 70 66	38, 55, 105, 137	0
6	T	243/288 (84%)	0.14	11 (4%) 38 32	41, 66, 123, 156	0
7	G	241/252 (95%)	-0.25	2 (0%) 82 80	31, 51, 85, 135	0
7	U	241/252 (95%)	-0.12	4 (1%) 69 64	40, 55, 87, 131	0
8	H	226/232 (97%)	-0.22	2 (0%) 81 78	33, 49, 81, 143	0
8	V	226/232 (97%)	-0.19	3 (1%) 75 71	40, 52, 84, 159	0
9	I	204/205 (99%)	-0.46	2 (0%) 79 76	34, 45, 74, 95	0
9	W	204/205 (99%)	-0.43	1 (0%) 87 85	37, 48, 78, 102	0
10	J	195/198 (98%)	-0.41	1 (0%) 87 85	34, 49, 74, 127	0
10	X	195/198 (98%)	-0.39	2 (1%) 79 76	35, 50, 73, 135	0
11	K	212/212 (100%)	-0.43	2 (0%) 81 78	32, 48, 69, 89	0
11	Y	212/212 (100%)	-0.47	1 (0%) 87 85	36, 48, 71, 92	0
12	L	222/222 (100%)	-0.38	3 (1%) 73 69	36, 51, 81, 114	0
12	Z	222/222 (100%)	-0.29	1 (0%) 87 85	37, 50, 82, 117	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	229/246 (93%)	-0.37	3 (1%) 75 71	34, 51, 74, 90	0
13	a	232/246 (94%)	-0.45	1 (0%) 88 86	33, 49, 70, 89	0
14	N	196/196 (100%)	-0.47	0 100 100	34, 45, 72, 100	0
14	b	196/196 (100%)	-0.45	1 (0%) 87 85	35, 47, 74, 105	0
All	All	6339/6614 (95%)	-0.21	112 (1%) 67 63	31, 54, 98, 183	0

All (112) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	X	1	MET	6.5
10	J	1	MET	5.4
3	Q	50	LEU	4.8
2	B	218	GLY	4.7
2	B	219	ALA	4.6
6	T	178	HIS	4.6
2	P	51	VAL	4.5
3	C	50	LEU	4.3
8	V	223	ILE	4.0
2	P	52	THR	3.9
3	C	205	ALA	3.7
13	a	1	THR	3.7
2	P	218	GLY	3.6
3	C	236	GLN	3.5
4	D	240	ALA	3.4
5	E	122	TYR	3.3
3	Q	51	LYS	3.3
1	O	53	SER	3.2
4	D	241	ALA	3.2
2	P	219	ALA	3.2
8	H	223	ILE	3.2
2	P	59	ASP	3.1
2	P	53	SER	3.1
14	b	103	ASP	3.0
3	Q	201	VAL	3.0
2	P	220	ASN	3.0
5	S	122	TYR	2.9
3	Q	48	SER	2.8
3	Q	204	GLY	2.8
4	D	238	LYS	2.8
3	C	3	ASP	2.8
3	Q	49	THR	2.8

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Mol	Chain	Res	Type	RSRZ
6	T	215	CYS	2.8
1	A	1	MET	2.8
9	I	1	SER	2.7
3	Q	205	ALA	2.7
6	T	14	ASP	2.7
6	T	53	LYS	2.7
12	L	174	TYR	2.7
2	B	51	VAL	2.6
2	B	93	HIS	2.6
13	M	47	ASP	2.6
1	O	1	MET	2.6
7	G	3	TYR	2.6
5	S	207	VAL	2.6
2	B	52	THR	2.5
2	P	54	THR	2.5
7	U	40	ASP	2.5
3	C	206	LYS	2.5
3	Q	240	GLU	2.5
7	G	242	GLN	2.5
3	Q	232	THR	2.5
12	Z	174	TYR	2.5
2	P	93	HIS	2.4
2	P	222	GLY	2.4
6	T	182	GLY	2.4
4	D	236	LYS	2.4
7	U	242	GLN	2.4
8	H	224	GLN	2.4
3	Q	224	SER	2.4
6	F	215	CYS	2.4
13	M	1	THR	2.4
3	C	51	LYS	2.4
2	B	222	GLY	2.4
3	Q	3	ASP	2.4
2	P	55	LEU	2.3
6	F	178	HIS	2.3
2	B	221	ASP	2.3
1	O	231	LYS	2.3
9	W	130	ASP	2.3
3	C	186	VAL	2.3
1	A	249	ALA	2.3
6	T	179	HIS	2.3
6	T	244	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
10	X	11	ASP	2.3
7	U	14	GLY	2.3
8	V	224	GLN	2.3
6	F	179	HIS	2.3
5	S	52	ALA	2.2
3	C	240	GLU	2.2
5	S	32	SER	2.2
2	P	1	GLY	2.2
13	M	38	GLY	2.2
6	F	176	VAL	2.2
4	R	230	GLU	2.2
11	K	24	ASN	2.2
2	P	56	LEU	2.2
6	T	183	LEU	2.2
5	S	203	GLU	2.2
6	T	204	LYS	2.2
8	V	145	ASP	2.2
12	L	163	GLY	2.2
1	A	167	GLY	2.2
4	D	3	GLY	2.2
2	B	201	ASP	2.2
12	L	166	GLY	2.1
3	Q	234	ILE	2.1
3	Q	52	LEU	2.1
2	B	59	ASP	2.1
1	O	54	PRO	2.1
4	R	125	LEU	2.1
6	T	203	ASN	2.1
4	D	242	GLU	2.1
5	E	173	ARG	2.1
3	C	239	GLN	2.1
11	Y	212	GLY	2.1
3	C	201	VAL	2.1
7	U	68	ARG	2.0
11	K	118	ASP	2.0
6	T	39	ASN	2.0
9	I	130	ASP	2.0
2	P	209	ARG	2.0

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

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

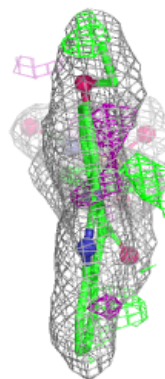
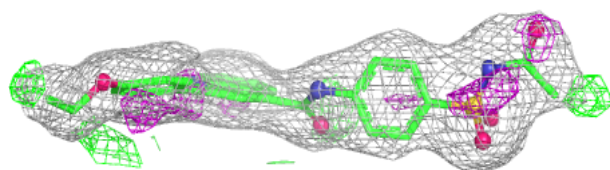
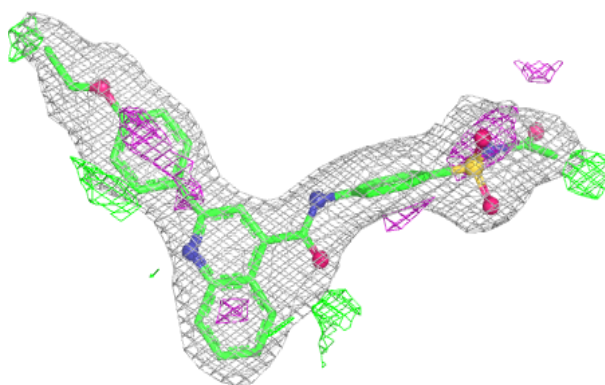
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
17	4UC	H	301	35/35	0.89	0.11	60,68,74,74	0
17	4UC	V	301	35/35	0.89	0.10	61,69,73,76	0
15	MG	I	301	1/1	0.90	0.09	54,54,54,54	0
15	MG	Z	301	1/1	0.95	0.05	55,55,55,55	0
15	MG	I	302	1/1	0.95	0.15	44,44,44,44	0
15	MG	W	301	1/1	0.95	0.05	56,56,56,56	0
15	MG	G	301	1/1	0.96	0.06	47,47,47,47	0
15	MG	N	201	1/1	0.96	0.05	50,50,50,50	0
15	MG	L	301	1/1	0.98	0.10	59,59,59,59	0
15	MG	K	301	1/1	0.98	0.13	44,44,44,44	0
16	CL	G	302	1/1	0.99	0.05	43,43,43,43	0
16	CL	U	301	1/1	0.99	0.11	44,44,44,44	0

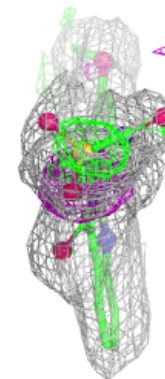
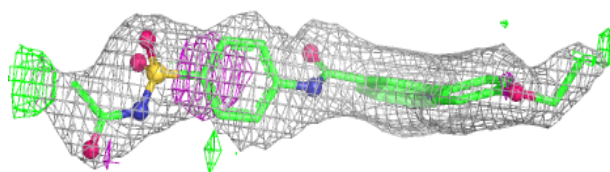
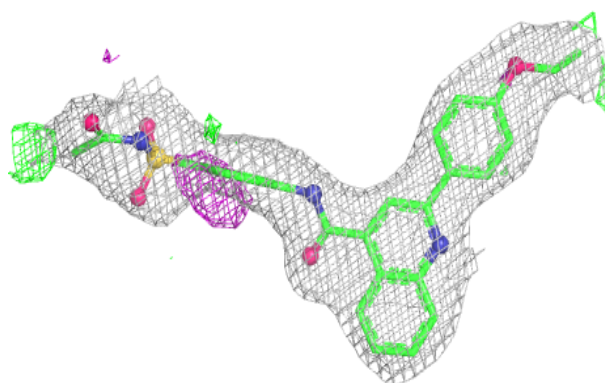
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 4UC 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 4UC V 301:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.