



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:46 PM UTC

PDB ID : 4QZ5 / pdb_00004qz5
Title : yCP beta5-A49T-mutant in complex with ONX 0914
Authors : Huber, E.M.; Heinemeyer, W.; Groll, M.
Deposited on : 2014-07-27
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

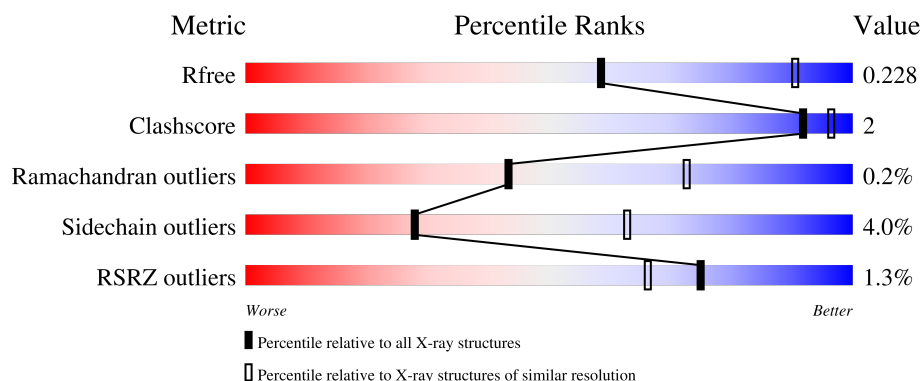
1 Overall quality at a glance

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	96%
1	O	250	96%
2	B	258	88% 6% • 5%
2	P	258	87% 7% • 5%
3	C	254	88% 6% • 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	2% 88% 5% • 6%
4	D	260	% 83% 7% 10%
4	R	260	83% 7% 10%
5	E	234	91% 7% •
5	S	234	89% 9% •
6	F	288	3% 82% • 16%
6	T	288	% 81% • 16%
7	G	252	2% 89% 6% •
7	U	252	90% 6% •
8	H	232	5% 89% 6% •
8	V	232	5% 89% 6% •
9	I	205	% 91% 8%
9	W	205	% 90% 9%
10	J	198	% 92% • • •
10	X	198	% 92% 5% • •
11	K	212	92% 8%
11	Y	212	92% 8%
12	L	222	94% 5% •
12	Z	222	93% 6% •
13	M	246	% 83% 8% 9%
13	a	246	84% 8% 9%
14	N	196	96% •
14	b	196	% 95% 5%

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 49654 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	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			
8	V	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	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
			1646	1046	280	313	7			
11	Y	212	Total	C	N	O	S	0	0	0
			1646	1046	280	313	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	49	THR	ALA	engineered mutation	UNP P30656
Y	49	THR	ALA	engineered mutation	UNP P30656

- 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	225	Total	C	N	O	S	0	0	0
			1761	1114	301	339	7			
13	a	225	Total	C	N	O	S	0	0	0
			1761	1114	301	339	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			

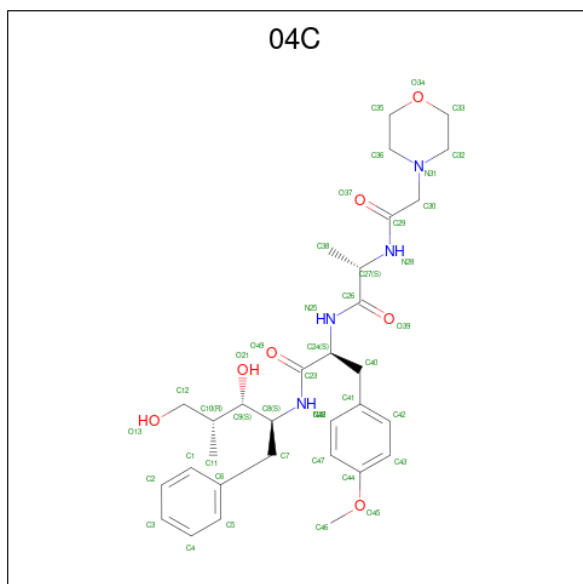
- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

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

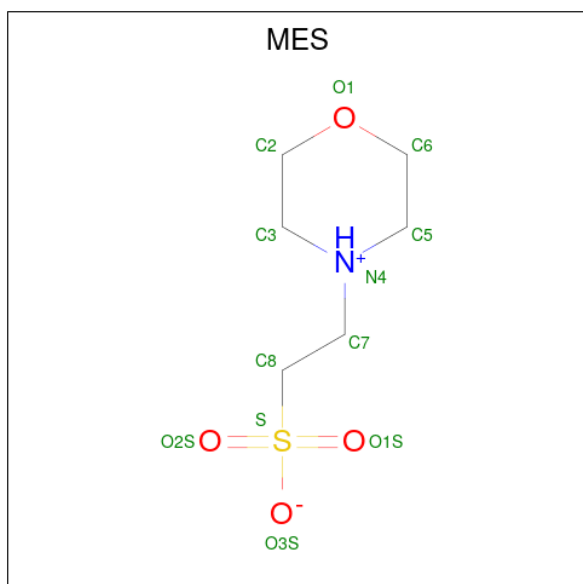
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0

- Molecule 17 is 1,2,4-trideoxy-4-methyl-2-{[N-(morpholin-4-ylacetyl)-L-alanyl-O-methyl-L-tyrosyl]amino}-1-phenyl-D-xylitol (CCD ID: 04C) (formula: C₃₁H₄₄N₄O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
17	H	1	Total	C	N	O	0	0
			42	31	4	7		
17	K	1	Total	C	N	O	0	0
			42	31	4	7		
17	N	1	Total	C	N	O	0	0
			42	31	4	7		
17	V	1	Total	C	N	O	0	0
			42	31	4	7		
17	Y	1	Total	C	N	O	0	0
			42	31	4	7		
17	b	1	Total	C	N	O	0	0
			42	31	4	7		

- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	K	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	Y	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 19 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	A	5	Total	O	0	0
			5	5		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	B	9	Total O 9 9	0	0
19	C	4	Total O 4 4	0	0
19	D	4	Total O 4 4	0	0
19	E	6	Total O 6 6	0	0
19	F	10	Total O 10 10	0	0
19	G	5	Total O 5 5	0	0
19	H	14	Total O 14 14	0	0
19	I	5	Total O 5 5	0	0
19	J	10	Total O 10 10	0	0
19	K	9	Total O 9 9	0	0
19	L	8	Total O 8 8	0	0
19	M	9	Total O 9 9	0	0
19	N	5	Total O 5 5	0	0
19	P	6	Total O 6 6	0	0
19	Q	5	Total O 5 5	0	0
19	R	2	Total O 2 2	0	0
19	S	1	Total O 1 1	0	0
19	T	7	Total O 7 7	0	0
19	U	5	Total O 5 5	0	0
19	V	9	Total O 9 9	0	0
19	W	4	Total O 4 4	0	0

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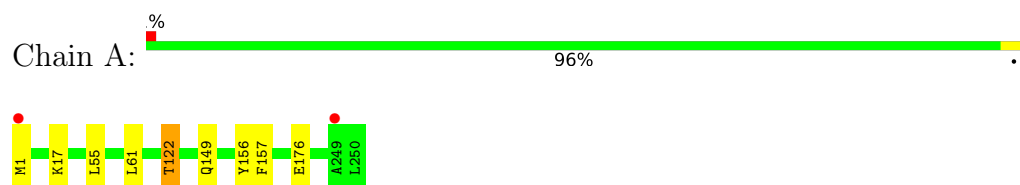
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	X	18	Total 18	O 18	0	0
19	Y	9	Total 9	O 9	0	0
19	Z	8	Total 8	O 8	0	0
19	a	11	Total 11	O 11	0	0
19	b	7	Total 7	O 7	0	0

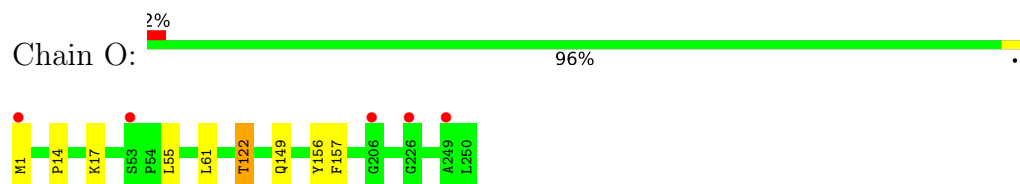
3 Residue-property plots [i](#)

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.

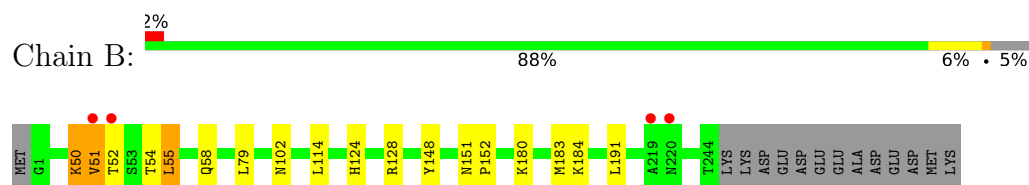
- Molecule 1: Proteasome subunit alpha type-2



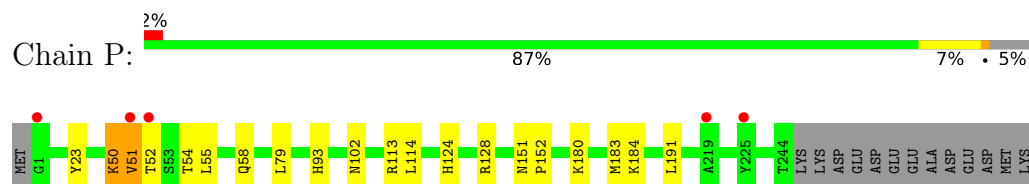
- Molecule 1: Proteasome subunit alpha type-2



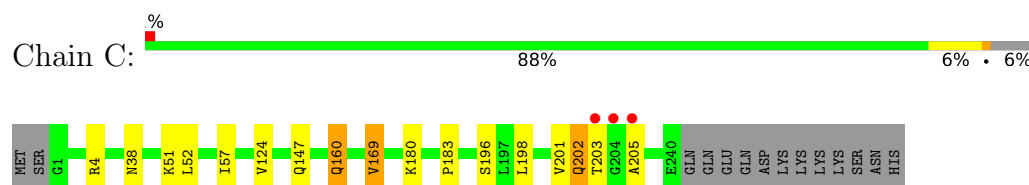
- Molecule 2: Proteasome subunit alpha type-3



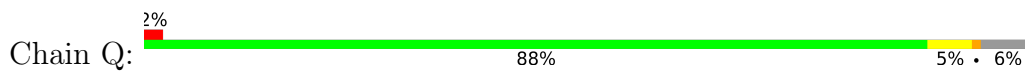
- Molecule 2: Proteasome subunit alpha type-3



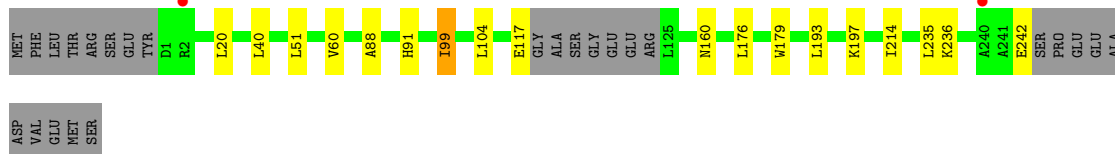
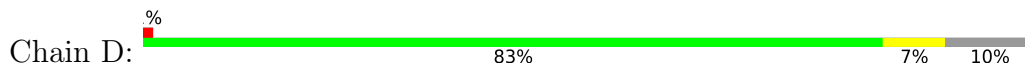
- Molecule 3: Proteasome subunit alpha type-4



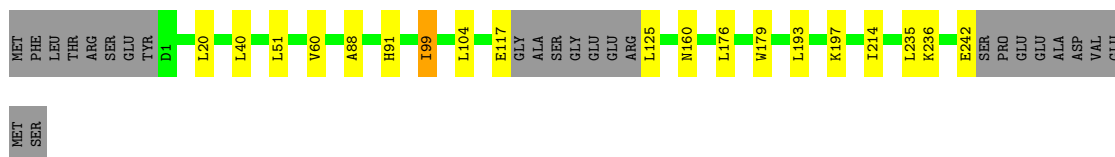
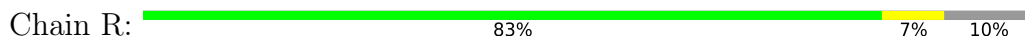
- Molecule 3: Proteasome subunit alpha type-4



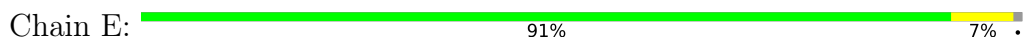
- Molecule 4: Proteasome subunit alpha type-5



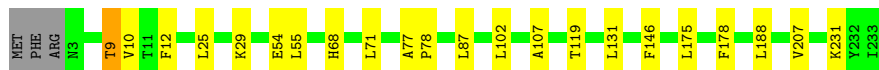
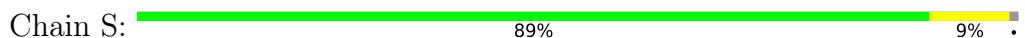
- Molecule 4: Proteasome subunit alpha type-5



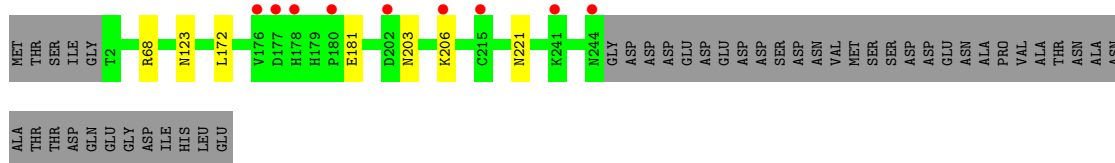
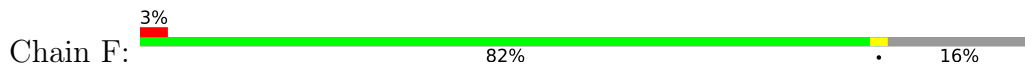
- Molecule 5: Proteasome subunit alpha type-6



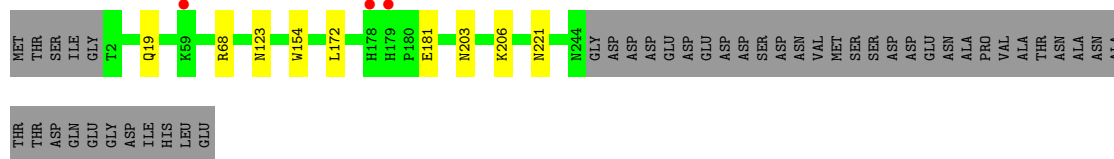
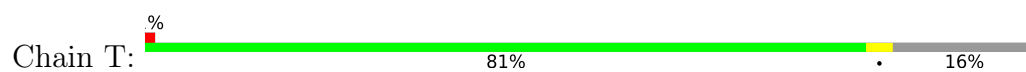
- Molecule 5: Proteasome subunit alpha type-6



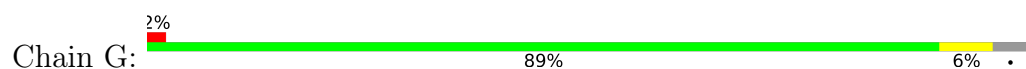
- Molecule 6: Probable proteasome subunit alpha type-7



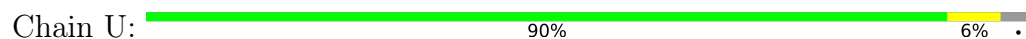
- Molecule 6: Probable proteasome subunit alpha type-7



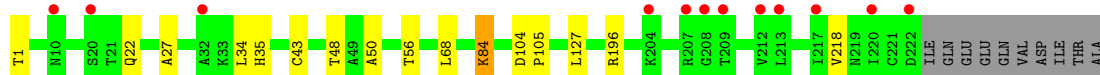
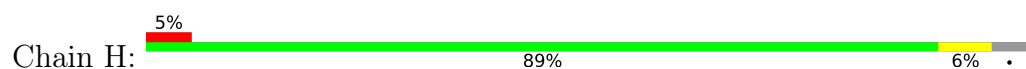
- Molecule 7: Proteasome subunit alpha type-1



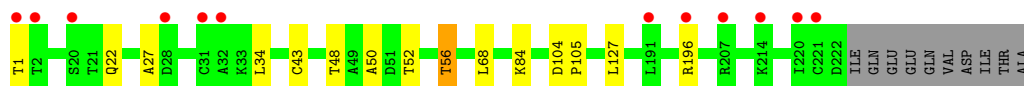
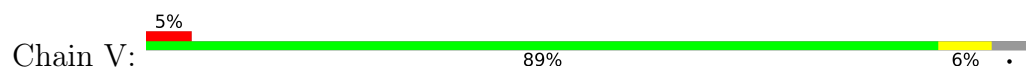
- Molecule 7: Proteasome subunit alpha type-1



- Molecule 8: Proteasome subunit beta type-2



- Molecule 8: Proteasome subunit beta type-2

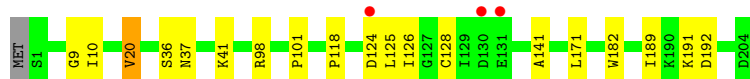


- Molecule 9: Proteasome subunit beta type-3

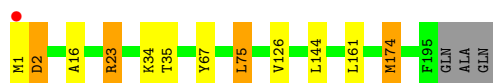
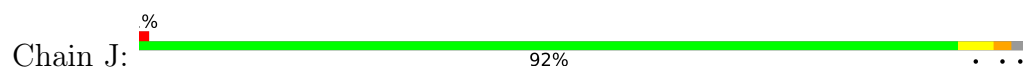


- Molecule 9: Proteasome subunit beta type-3

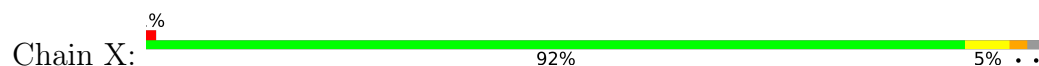




- Molecule 10: Proteasome subunit beta type-4



- Molecule 10: Proteasome subunit beta type-4



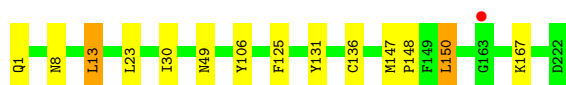
- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5



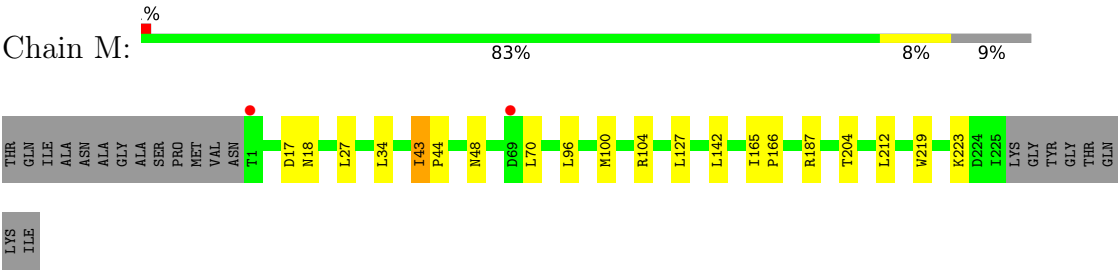
- Molecule 12: Proteasome subunit beta type-6



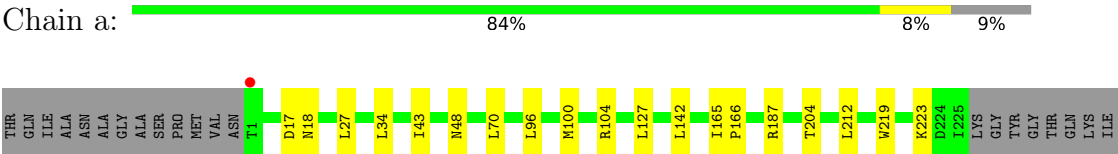
- Molecule 12: Proteasome subunit beta type-6



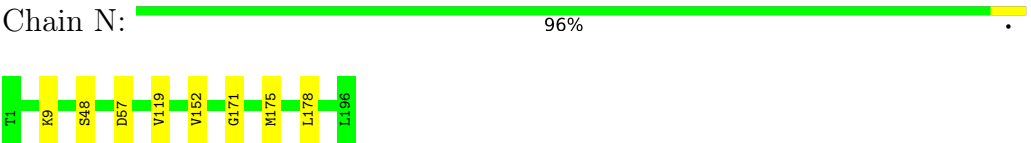
- Molecule 13: Proteasome subunit beta type-7



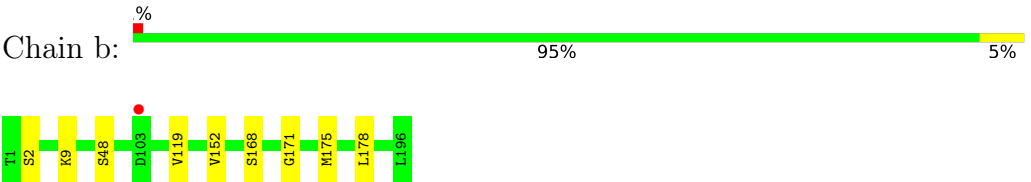
• Molecule 13: Proteasome subunit beta type-7



• 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	135.56Å 299.58Å 144.91Å 90.00° 112.81° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (15.00-2.80) 98.4 (15.00-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.81Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.195 , 0.224 0.199 , 0.228	Depositor DCC
R_{free} test set	12821 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	55.9	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	49654	wwPDB-VP
Average B, all atoms (Å ²)	64.0	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: MES, CL, 04C, 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	0.39	0/1952	0.70	0/2642
1	O	0.39	0/1952	0.70	0/2642
2	B	0.39	0/1934	0.68	0/2618
2	P	0.39	0/1934	0.68	0/2618
3	C	0.39	0/1910	0.70	0/2586
3	Q	0.39	0/1910	0.70	0/2586
4	D	0.39	0/1837	0.66	0/2475
4	R	0.39	0/1837	0.65	0/2475
5	E	0.39	0/1800	0.67	0/2433
5	S	0.39	0/1800	0.67	0/2433
6	F	0.39	0/1932	0.70	0/2609
6	T	0.39	0/1932	0.69	0/2609
7	G	0.40	0/1945	0.69	0/2634
7	U	0.40	0/1945	0.69	0/2634
8	H	0.39	0/1715	0.67	1/2326 (0.0%)
8	V	0.39	0/1715	0.67	1/2326 (0.0%)
9	I	0.37	0/1611	0.67	0/2174
9	W	0.37	0/1611	0.67	0/2174
10	J	0.40	0/1589	0.67	0/2142
10	X	0.40	0/1589	0.67	0/2142
11	K	0.37	0/1683	0.67	0/2277
11	Y	0.37	0/1683	0.67	0/2277
12	L	0.37	0/1795	0.66	0/2420
12	Z	0.38	0/1795	0.66	0/2420
13	M	0.39	0/1791	0.68	0/2431
13	a	0.39	0/1791	0.68	0/2431
14	N	0.37	0/1541	0.70	0/2087
14	b	0.36	0/1541	0.70	0/2087
All	All	0.39	0/50070	0.68	2/67708 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	1	THR	N-CA-C	5.52	126.45	111.00
8	V	1	THR	N-CA-C	5.49	126.36	111.00

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	4	0
1	O	1915	0	1929	4	0
2	B	1904	0	1904	8	0
2	P	1904	0	1904	8	0
3	C	1881	0	1895	9	0
3	Q	1881	0	1895	8	0
4	D	1813	0	1797	4	0
4	R	1813	0	1797	4	0
5	E	1773	0	1775	4	0
5	S	1773	0	1775	7	0
6	F	1892	0	1883	0	0
6	T	1892	0	1883	2	0
7	G	1907	0	1901	6	0
7	U	1907	0	1901	6	0
8	H	1684	0	1685	7	0
8	V	1684	0	1685	5	0
9	I	1581	0	1574	9	0
9	W	1581	0	1574	10	0
10	J	1561	0	1569	9	0
10	X	1561	0	1569	8	0
11	K	1646	0	1594	11	0
11	Y	1646	0	1594	11	0
12	L	1757	0	1711	4	0
12	Z	1757	0	1711	5	0
13	M	1761	0	1765	7	0
13	a	1761	0	1765	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	N	1512	0	1478	4	0
14	b	1512	0	1478	4	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	1	0	0	0	0
16	U	1	0	0	0	0
17	H	42	0	42	3	0
17	K	42	0	42	5	0
17	N	42	0	42	3	0
17	V	42	0	42	4	0
17	Y	42	0	42	6	0
17	b	42	0	42	4	0
18	K	12	0	13	0	0
18	Y	12	0	13	0	0
19	A	5	0	0	0	0
19	B	9	0	0	0	0
19	C	4	0	0	0	0
19	D	4	0	0	0	0
19	E	6	0	0	0	0
19	F	10	0	0	0	0
19	G	5	0	0	0	0
19	H	14	0	0	1	0
19	I	5	0	0	0	0
19	J	10	0	0	0	0
19	K	9	0	0	0	0
19	L	8	0	0	0	0
19	M	9	0	0	0	0
19	N	5	0	0	0	0
19	P	6	0	0	0	0
19	Q	5	0	0	0	0
19	R	2	0	0	0	0
19	S	1	0	0	0	0
19	T	7	0	0	0	0
19	U	5	0	0	0	0
19	V	9	0	0	0	0
19	W	4	0	0	0	0
19	X	18	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	Y	9	0	0	0	0
19	Z	8	0	0	0	0
19	a	11	0	0	0	0
19	b	7	0	0	0	0
All	All	49654	0	49198	160	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 (160) 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:100:MET:HE3	11:K:127:PHE:HB2	1.62	0.80
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.62	0.80
11:Y:31:VAL:HG11	17:Y:301:04C:C4	2.14	0.78
11:K:31:VAL:HG11	17:K:301:04C:C4	2.15	0.77
10:X:1:MET:O	10:X:2:ASP:HB2	1.87	0.75
10:J:1:MET:O	10:J:2:ASP:HB2	1.86	0.73
11:Y:31:VAL:HG11	17:Y:301:04C:H42	1.73	0.70
11:K:31:VAL:HG11	17:K:301:04C:H42	1.74	0.70
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.74	0.70
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.74	0.68
14:b:152:VAL:HA	14:b:175:MET:HE1	1.81	0.62
14:N:152:VAL:HA	14:N:175:MET:HE1	1.82	0.61
4:R:99:ILE:HD11	4:R:104:LEU:HB2	1.84	0.60
17:N:201:04C:H8	17:N:201:04C:H24	1.83	0.59
17:b:201:04C:H8	17:b:201:04C:H24	1.83	0.59
4:D:99:ILE:HD11	4:D:104:LEU:HB2	1.85	0.59
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.05	0.57
3:C:51:LYS:O	3:C:52:LEU:HB2	2.05	0.57
8:H:50:ALA:HB2	9:I:128:CYS:HB2	1.87	0.56
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.72	0.55
10:J:174:MET:HA	10:X:174:MET:HA	1.89	0.54
17:b:201:04C:O21	17:b:201:04C:O13	2.23	0.53
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.72	0.53
11:K:49:THR:HG22	17:K:301:04C:C4	2.38	0.53
11:Y:49:THR:HG22	17:Y:301:04C:C4	2.39	0.52
8:H:35:HIS:ND1	19:H:413:HOH:O	2.34	0.52
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.92	0.52
7:G:23:PHE:O	7:G:26:THR:HB	2.09	0.52
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:23:PHE:O	7:U:26:THR:HB	2.10	0.51
11:K:170:TYR:O	17:K:301:04C:H33	2.10	0.51
11:Y:170:TYR:O	17:Y:301:04C:H33	2.10	0.51
8:V:22:GLN:HG3	8:V:27:ALA:HB2	1.93	0.51
10:X:1:MET:O	10:X:2:ASP:CB	2.59	0.51
8:H:22:GLN:HG3	8:H:27:ALA:HB2	1.93	0.50
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.77	0.50
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.93	0.50
3:C:201:VAL:O	3:C:202:GLN:CB	2.60	0.50
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.94	0.49
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.60	0.49
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.94	0.49
3:C:201:VAL:HG13	3:C:202:GLN:N	2.28	0.49
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.28	0.48
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.94	0.48
10:J:1:MET:O	10:J:2:ASP:CB	2.58	0.48
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.96	0.48
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.96	0.48
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.96	0.47
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.80	0.47
7:G:34:LEU:C	7:G:34:LEU:HD23	2.39	0.47
8:H:218:VAL:CG2	9:I:196:LYS:HB2	2.45	0.47
3:Q:201:VAL:O	3:Q:202:GLN:HB2	2.14	0.47
5:S:12:PHE:H	6:T:19:GLN:HE22	1.62	0.47
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.97	0.47
14:N:48:SER:HB2	17:N:201:04C:H25	1.97	0.47
5:E:9:THR:HG21	5:E:119:THR:HA	1.97	0.47
13:M:219:TRP:CH2	14:b:171:GLY:HA2	2.50	0.47
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.97	0.46
11:K:49:THR:HG22	17:K:301:04C:C5	2.45	0.46
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.96	0.46
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.96	0.46
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.97	0.46
13:a:27:LEU:HD21	13:a:34:LEU:HD22	1.98	0.46
10:J:1:MET:HA	10:J:34:LYS:CE	2.45	0.46
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.97	0.46
4:R:88:ALA:HA	4:R:99:ILE:HG21	1.97	0.46
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.97	0.46
3:C:201:VAL:O	3:C:202:GLN:HB2	2.14	0.46
12:L:8:ASN:HA	12:L:30:ILE:O	2.15	0.46
13:M:27:LEU:HD21	13:M:34:LEU:HD22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:9:THR:HG21	5:S:119:THR:HA	1.98	0.46
7:U:34:LEU:HD23	7:U:34:LEU:C	2.40	0.46
11:Y:49:THR:HG22	17:Y:301:04C:C5	2.46	0.46
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.51	0.45
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.51	0.45
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.51	0.45
10:X:1:MET:HA	10:X:34:LYS:CE	2.46	0.45
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.17	0.45
3:C:198:LEU:HA	3:C:201:VAL:HG12	1.99	0.45
17:N:201:04C:O13	17:N:201:04C:O21	2.25	0.45
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.52	0.45
11:K:1:THR:CG2	11:K:3:THR:HG23	2.47	0.45
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.98	0.45
14:b:48:SER:HB2	17:b:201:04C:H25	1.98	0.45
11:K:100:MET:CE	11:K:127:PHE:HB2	2.40	0.45
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	1.99	0.45
7:U:26:THR:HG21	7:U:131:ILE:HD12	1.99	0.45
8:V:50:ALA:HB2	9:W:128:CYS:HB2	1.99	0.45
2:B:124:HIS:HB3	3:C:124:VAL:HG12	1.98	0.45
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.52	0.45
9:W:98:ARG:O	9:W:126:ILE:HD11	2.17	0.45
10:J:1:MET:HA	10:J:34:LYS:HE3	1.99	0.44
9:I:98:ARG:O	9:I:126:ILE:HD11	2.18	0.44
2:P:50:LYS:O	2:P:51:VAL:C	2.60	0.44
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.47	0.44
17:V:301:04C:H36	17:V:301:04C:H19	1.99	0.44
7:G:26:THR:HG21	7:G:131:ILE:HD12	1.99	0.44
11:K:37:ILE:HG23	11:K:60:GLY:HA2	1.99	0.44
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.48	0.44
11:Y:37:ILE:HG23	11:Y:60:GLY:HA2	1.99	0.44
1:A:55:LEU:HD12	7:G:170:THR:HG23	1.99	0.44
9:W:20:VAL:HG23	9:W:189:ILE:HB	2.00	0.44
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.52	0.44
8:H:84:LYS:HE3	14:N:57:ASP:OD2	2.18	0.44
2:B:180:LYS:O	2:B:183:MET:HB2	2.18	0.43
17:H:301:04C:H19	17:H:301:04C:H36	1.99	0.43
9:I:36:SER:HB2	10:J:126:VAL:HG11	1.99	0.43
11:Y:1:THR:CG2	11:Y:3:THR:HG23	2.47	0.43
6:T:154:TRP:CZ3	7:U:60:VAL:HA	2.53	0.43
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.33	0.43
14:N:171:GLY:HA2	13:a:219:TRP:CH2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:48:THR:OG1	17:H:301:04C:H24	2.18	0.43
10:J:23:ARG:NH2	11:K:120:THR:OG1	2.51	0.43
2:B:50:LYS:O	2:B:51:VAL:C	2.61	0.43
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.48	0.43
1:O:149:GLN:O	1:O:156:TYR:HA	2.19	0.43
13:a:17:ASP:OD1	13:a:18:ASN:N	2.52	0.43
9:I:20:VAL:HG23	9:I:189:ILE:HB	2.00	0.43
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.43
13:M:96:LEU:O	13:M:100:MET:HG2	2.19	0.43
13:a:165:ILE:HB	13:a:166:PRO:HD3	2.01	0.43
12:L:147:MET:N	12:L:148:PRO:HD2	2.33	0.42
13:a:96:LEU:O	13:a:100:MET:HG2	2.19	0.42
13:M:165:ILE:HB	13:M:166:PRO:HD3	2.01	0.42
2:P:180:LYS:O	2:P:183:MET:HB2	2.19	0.42
1:A:149:GLN:O	1:A:156:TYR:HA	2.18	0.42
13:M:17:ASP:OD1	13:M:18:ASN:N	2.52	0.42
9:I:101:PRO:HB3	9:I:126:ILE:HD12	2.02	0.42
17:V:301:04C:H1	9:W:124:ASP:HB2	2.02	0.42
9:W:101:PRO:HB3	9:W:126:ILE:HD12	2.02	0.42
10:X:1:MET:HA	10:X:34:LYS:HE3	2.00	0.42
1:A:176:GLU:HG2	2:B:55:LEU:HD13	2.01	0.42
17:H:301:04C:H41	17:H:301:04C:H29	1.86	0.42
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.49	0.42
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.42
13:M:43:ILE:HA	13:M:44:PRO:HD3	1.95	0.42
8:V:48:THR:OG1	17:V:301:04C:H24	2.20	0.42
17:V:301:04C:H5	9:W:125:LEU:HD22	2.02	0.41
2:B:151:ASN:HB2	2:B:152:PRO:HD2	2.02	0.41
11:Y:5:ALA:HB3	11:Y:100:MET:CE	2.50	0.41
12:L:125:PHE:CD2	12:L:131:TYR:HB3	2.56	0.41
11:K:5:ALA:HB3	11:K:100:MET:CE	2.51	0.41
11:Y:100:MET:CE	11:Y:127:PHE:HB2	2.40	0.41
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.56	0.41
13:a:127:LEU:HG	13:a:142:LEU:HD12	2.03	0.41
2:B:148:TYR:OH	3:C:57:ILE:HB	2.21	0.41
2:P:151:ASN:HB2	2:P:152:PRO:HD2	2.03	0.41
5:S:77:ALA:N	5:S:78:PRO:CD	2.84	0.41
11:Y:31:VAL:HG11	17:Y:301:04C:C3	2.51	0.41
7:G:187:GLU:HG2	7:G:192:LYS:HB2	2.03	0.41
13:M:127:LEU:HG	13:M:142:LEU:HD12	2.03	0.40
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:52:THR:O	8:V:56:THR:HB	2.21	0.40
12:Z:100:LYS:HD3	12:Z:105:TYR:CZ	2.56	0.40
14:b:168:SER:O	17:b:201:04C:H33	2.21	0.40
1:O:55:LEU:HB3	7:U:159:ALA:O	2.21	0.40
5:S:68:HIS:HE1	5:S:102:LEU:O	2.05	0.40
5:E:68:HIS:HE1	5:E:102:LEU:O	2.05	0.40
1:O:14:PRO:HA	2:P:23:TYR:CD1	2.57	0.40
5:S:131:LEU:HB2	5:S:146:PHE:HB3	2.03	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%)	241 (97%)	7 (3%)	0	100	100
1	O	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
2	B	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	30	60
2	P	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	30	60
3	C	238/254 (94%)	230 (97%)	5 (2%)	3 (1%)	9	31
3	Q	238/254 (94%)	230 (97%)	5 (2%)	3 (1%)	9	31
4	D	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
4	R	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
5	E	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
5	S	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
6	F	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
6	T	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
7	G	239/252 (95%)	236 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	U	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
8	H	220/232 (95%)	215 (98%)	5 (2%)	0	100	100
8	V	220/232 (95%)	215 (98%)	5 (2%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	24	55
10	X	193/198 (98%)	188 (97%)	4 (2%)	1 (0%)	24	55
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%)	216 (98%)	4 (2%)	0	100	100
12	Z	220/222 (99%)	217 (99%)	3 (1%)	0	100	100
13	M	223/246 (91%)	217 (97%)	6 (3%)	0	100	100
13	a	223/246 (91%)	217 (97%)	6 (3%)	0	100	100
14	N	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
14	b	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
All	All	6260/6614 (95%)	6102 (98%)	148 (2%)	10 (0%)	43	72

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
10	J	2	ASP
2	P	51	VAL
3	Q	202	GLN
10	X	2	ASP
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%)	204 (98%)	5 (2%)	43	77
1	O	209/209 (100%)	204 (98%)	5 (2%)	43	77
2	B	203/216 (94%)	193 (95%)	10 (5%)	22	55
2	P	203/216 (94%)	193 (95%)	10 (5%)	22	55
3	C	212/226 (94%)	205 (97%)	7 (3%)	33	69
3	Q	212/226 (94%)	205 (97%)	7 (3%)	33	69
4	D	194/215 (90%)	181 (93%)	13 (7%)	15	42
4	R	194/215 (90%)	180 (93%)	14 (7%)	13	39
5	E	190/193 (98%)	180 (95%)	10 (5%)	20	52
5	S	190/193 (98%)	180 (95%)	10 (5%)	20	52
6	F	201/239 (84%)	194 (96%)	7 (4%)	32	67
6	T	201/239 (84%)	194 (96%)	7 (4%)	32	67
7	G	206/210 (98%)	198 (96%)	8 (4%)	28	64
7	U	206/210 (98%)	198 (96%)	8 (4%)	28	64
8	H	181/190 (95%)	174 (96%)	7 (4%)	28	64
8	V	181/190 (95%)	174 (96%)	7 (4%)	28	64
9	I	172/173 (99%)	166 (96%)	6 (4%)	32	67
9	W	172/173 (99%)	166 (96%)	6 (4%)	32	67
10	J	173/175 (99%)	168 (97%)	5 (3%)	37	73
10	X	173/175 (99%)	168 (97%)	5 (3%)	37	73
11	K	170/170 (100%)	163 (96%)	7 (4%)	27	62
11	Y	170/170 (100%)	163 (96%)	7 (4%)	27	62
12	L	185/185 (100%)	177 (96%)	8 (4%)	26	60
12	Z	185/185 (100%)	177 (96%)	8 (4%)	26	60
13	M	193/208 (93%)	185 (96%)	8 (4%)	27	62
13	a	193/208 (93%)	185 (96%)	8 (4%)	27	62
14	N	162/162 (100%)	159 (98%)	3 (2%)	50	81
14	b	162/162 (100%)	158 (98%)	4 (2%)	42	76
All	All	5302/5542 (96%)	5092 (96%)	210 (4%)	28	63

All (210) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	17	LYS
1	A	61	LEU
1	A	122	THR
1	A	157	PHE
2	B	50	LYS
2	B	52	THR
2	B	54	THR
2	B	55	LEU
2	B	58	GLN
2	B	79	LEU
2	B	102	ASN
2	B	114	LEU
2	B	184	LYS
2	B	191	LEU
3	C	4	ARG
3	C	38	ASN
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	203	THR
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU
4	D	60	VAL
4	D	99	ILE
4	D	117	GLU
4	D	176	LEU
4	D	193	LEU
4	D	197	LYS
4	D	214	ILE
4	D	235	LEU
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	10	VAL
5	E	25	LEU
5	E	29	LYS
5	E	54	GLU
5	E	55	LEU
5	E	71	LEU
5	E	188	LEU

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Mol	Chain	Res	Type
5	E	207	VAL
5	E	231	LYS
6	F	68	ARG
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	203	ASN
6	F	206	LYS
6	F	221	ASN
7	G	13	GLU
7	G	26	THR
7	G	115	LEU
7	G	125	MET
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
7	G	236	LEU
8	H	34	LEU
8	H	43	CYS
8	H	56	THR
8	H	68	LEU
8	H	84	LYS
8	H	127	LEU
8	H	196	ARG
9	I	20	VAL
9	I	37	ASN
9	I	171	LEU
9	I	182	TRP
9	I	191	LYS
9	I	192	ASP
10	J	23	ARG
10	J	35	THR
10	J	75	LEU
10	J	144	LEU
10	J	174	MET
11	K	4	LEU
11	K	7	ARG
11	K	9	GLN
11	K	35	ILE
11	K	57	THR
11	K	106	ARG
11	K	118	ASP

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Mol	Chain	Res	Type
12	L	1	GLN
12	L	13	LEU
12	L	23	LEU
12	L	49	ASN
12	L	106	TYR
12	L	136	CYS
12	L	150	LEU
12	L	167	LYS
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	187	ARG
13	M	204	THR
13	M	212	LEU
13	M	223	LYS
14	N	9	LYS
14	N	119	VAL
14	N	178	LEU
1	O	1	MET
1	O	17	LYS
1	O	61	LEU
1	O	122	THR
1	O	157	PHE
2	P	50	LYS
2	P	52	THR
2	P	54	THR
2	P	55	LEU
2	P	58	GLN
2	P	79	LEU
2	P	102	ASN
2	P	114	LEU
2	P	184	LYS
2	P	191	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	203	THR
4	R	20	LEU

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Mol	Chain	Res	Type
4	R	40	LEU
4	R	51	LEU
4	R	60	VAL
4	R	99	ILE
4	R	117	GLU
4	R	125	LEU
4	R	176	LEU
4	R	193	LEU
4	R	197	LYS
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	10	VAL
5	S	25	LEU
5	S	29	LYS
5	S	54	GLU
5	S	55	LEU
5	S	71	LEU
5	S	188	LEU
5	S	207	VAL
5	S	231	LYS
6	T	68	ARG
6	T	123	ASN
6	T	172	LEU
6	T	181	GLU
6	T	203	ASN
6	T	206	LYS
6	T	221	ASN
7	U	13	GLU
7	U	26	THR
7	U	115	LEU
7	U	125	MET
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
7	U	236	LEU
8	V	34	LEU
8	V	43	CYS
8	V	56	THR
8	V	68	LEU

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Mol	Chain	Res	Type
8	V	84	LYS
8	V	127	LEU
8	V	196	ARG
9	W	20	VAL
9	W	37	ASN
9	W	171	LEU
9	W	182	TRP
9	W	191	LYS
9	W	192	ASP
10	X	23	ARG
10	X	35	THR
10	X	75	LEU
10	X	144	LEU
10	X	174	MET
11	Y	4	LEU
11	Y	7	ARG
11	Y	9	GLN
11	Y	35	ILE
11	Y	57	THR
11	Y	106	ARG
11	Y	118	ASP
12	Z	1	GLN
12	Z	13	LEU
12	Z	23	LEU
12	Z	49	ASN
12	Z	106	TYR
12	Z	136	CYS
12	Z	150	LEU
12	Z	167	LYS
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	187	ARG
13	a	204	THR
13	a	212	LEU
13	a	223	LYS
14	b	2	SER
14	b	9	LYS
14	b	119	VAL
14	b	178	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (125)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	149	GLN
2	B	58	GLN
2	B	119	GLN
2	B	123	GLN
2	B	124	HIS
2	B	176	GLN
2	B	232	GLN
3	C	38	ASN
3	C	77	ASN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
3	C	233	GLN
4	D	15	GLN
4	D	91	HIS
4	D	106	GLN
4	D	225	ASN
5	E	68	HIS
5	E	85	ASN
5	E	92	ASN
5	E	99	ASN
5	E	118	ASN
5	E	120	GLN
5	E	147	GLN
5	E	151	ASN
5	E	165	GLN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	123	ASN
7	G	30	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	30	ASN
8	H	66	HIS
8	H	86	HIS

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Mol	Chain	Res	Type
8	H	172	ASN
8	H	189	ASN
8	H	194	ASN
9	I	37	ASN
10	J	37	GLN
10	J	55	GLN
10	J	61	GLN
10	J	63	ASN
10	J	146	HIS
10	J	147	HIS
11	K	9	GLN
11	K	85	ASN
11	K	133	GLN
11	K	143	ASN
11	K	208	ASN
12	L	3	ASN
12	L	36	ASN
12	L	70	ASN
12	L	158	ASN
12	L	165	ASN
12	L	197	GLN
13	M	102	GLN
14	N	38	HIS
14	N	141	ASN
1	O	30	GLN
2	P	20	GLN
2	P	58	GLN
2	P	119	GLN
2	P	123	GLN
2	P	124	HIS
2	P	176	GLN
2	P	232	GLN
3	Q	38	ASN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
3	Q	233	GLN
4	R	15	GLN
4	R	106	GLN
4	R	217	GLN
4	R	225	ASN

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Mol	Chain	Res	Type
5	S	68	HIS
5	S	85	ASN
5	S	90	GLN
5	S	99	ASN
5	S	116	GLN
5	S	120	GLN
5	S	147	GLN
5	S	151	ASN
5	S	165	GLN
6	T	19	GLN
6	T	86	ASN
6	T	123	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	167	GLN
7	U	175	ASN
8	V	86	HIS
8	V	165	ASN
8	V	194	ASN
10	X	37	GLN
10	X	55	GLN
10	X	63	ASN
10	X	146	HIS
10	X	147	HIS
11	Y	9	GLN
11	Y	62	GLN
11	Y	85	ASN
11	Y	143	ASN
11	Y	208	ASN
12	Z	3	ASN
12	Z	70	ASN
12	Z	79	HIS
12	Z	158	ASN
12	Z	165	ASN
12	Z	197	GLN
13	a	102	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 17 ligands modelled in this entry, 9 are monoatomic - leaving 8 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	04C	K	301	11	44,44,44	1.35	3 (6%)	54,58,58	1.31	8 (14%)
18	MES	Y	303	-	12,12,12	2.22	1 (8%)	15,16,16	1.15	1 (6%)
18	MES	K	303	-	12,12,12	2.25	1 (8%)	15,16,16	1.19	1 (6%)
17	04C	b	201	14	44,44,44	1.29	3 (6%)	54,58,58	1.28	7 (12%)
17	04C	H	301	8	44,44,44	1.37	4 (9%)	54,58,58	1.15	6 (11%)
17	04C	N	201	14	44,44,44	1.30	3 (6%)	54,58,58	1.31	7 (12%)
17	04C	Y	301	11	44,44,44	1.38	3 (6%)	54,58,58	1.34	9 (16%)
17	04C	V	301	8	44,44,44	1.35	4 (9%)	54,58,58	1.14	7 (12%)

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	04C	K	301	11	-	11/44/52/52	0/3/3/3
18	MES	Y	303	-	-	0/6/14/14	0/1/1/1
18	MES	K	303	-	-	0/6/14/14	0/1/1/1
17	04C	b	201	14	-	17/44/52/52	0/3/3/3
17	04C	H	301	8	-	10/44/52/52	0/3/3/3
17	04C	N	201	14	-	17/44/52/52	0/3/3/3
17	04C	Y	301	11	-	11/44/52/52	0/3/3/3
17	04C	V	301	8	-	10/44/52/52	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	K	303	MES	C8-S	-7.46	1.67	1.77
18	Y	303	MES	C8-S	-7.34	1.67	1.77
17	Y	301	04C	C10-C9	5.50	1.62	1.53
17	V	301	04C	C10-C9	5.17	1.62	1.53
17	H	301	04C	C10-C9	5.12	1.62	1.53
17	K	301	04C	C10-C9	5.06	1.62	1.53
17	K	301	04C	C40-C41	-4.73	1.40	1.51
17	N	201	04C	C10-C9	4.52	1.61	1.53
17	b	201	04C	C10-C9	4.51	1.61	1.53
17	N	201	04C	C40-C41	-4.49	1.40	1.51
17	b	201	04C	C40-C41	-4.42	1.40	1.51
17	Y	301	04C	C40-C41	-4.41	1.40	1.51
17	H	301	04C	C40-C41	-4.28	1.41	1.51
17	Y	301	04C	C7-C6	-4.25	1.41	1.51
17	V	301	04C	C40-C41	-4.24	1.41	1.51
17	K	301	04C	C7-C6	-4.18	1.41	1.51
17	H	301	04C	C7-C6	-3.77	1.42	1.51
17	b	201	04C	C7-C6	-3.68	1.42	1.51
17	N	201	04C	C7-C6	-3.68	1.42	1.51
17	V	301	04C	C7-C6	-3.49	1.43	1.51
17	H	301	04C	C11-C10	2.14	1.58	1.53
17	V	301	04C	C11-C10	2.03	1.58	1.53

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	N	201	04C	C11-C10-C12	-4.38	104.18	109.76
17	Y	301	04C	O13-C12-C10	-4.20	102.87	111.51
17	b	201	04C	C11-C10-C12	-3.97	104.71	109.76
17	N	201	04C	C29-C30-N31	-3.70	104.82	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	K	301	04C	O13-C12-C10	-3.63	104.05	111.51
17	b	201	04C	C29-C30-N31	-3.49	105.29	113.41
17	H	301	04C	O34-C33-C32	-3.39	104.46	111.77
17	V	301	04C	O34-C33-C32	-3.24	104.80	111.77
17	K	301	04C	C41-C40-C24	-3.07	105.20	113.36
17	Y	301	04C	C41-C40-C24	-3.04	105.27	113.36
17	H	301	04C	C11-C10-C12	-2.89	106.08	109.76
17	K	301	04C	O34-C33-C32	-2.83	105.67	111.77
17	Y	301	04C	C46-O45-C44	-2.82	111.46	117.50
17	K	301	04C	C46-O45-C44	-2.80	111.50	117.50
17	K	301	04C	C30-N31-C36	-2.77	106.83	111.14
18	K	303	MES	O1S-S-C8	2.76	110.89	106.73
17	Y	301	04C	O34-C33-C32	-2.75	105.86	111.77
17	b	201	04C	C35-C36-N31	-2.73	105.97	110.12
17	N	201	04C	C35-C36-N31	-2.70	106.01	110.12
17	b	201	04C	C7-C6-C5	2.67	125.87	120.90
17	Y	301	04C	C30-N31-C36	-2.67	106.99	111.14
17	V	301	04C	C46-O45-C44	-2.63	111.86	117.50
17	N	201	04C	C7-C6-C5	2.62	125.77	120.90
17	Y	301	04C	C7-C8-N22	-2.61	106.37	110.08
17	N	201	04C	O34-C33-C32	-2.61	106.16	111.77
17	b	201	04C	O34-C33-C32	-2.59	106.19	111.77
17	V	301	04C	C11-C10-C12	-2.58	106.47	109.76
17	H	301	04C	C46-O45-C44	-2.55	112.03	117.50
18	Y	303	MES	O1S-S-C8	2.42	110.39	106.73
17	K	301	04C	C7-C8-N22	-2.42	106.65	110.08
17	b	201	04C	C7-C6-C1	-2.36	116.52	120.90
17	N	201	04C	C7-C6-C1	-2.33	116.57	120.90
17	V	301	04C	C7-C6-C5	2.25	125.09	120.90
17	N	201	04C	C41-C40-C24	-2.24	107.40	113.36
17	b	201	04C	C41-C40-C24	-2.22	107.46	113.36
17	V	301	04C	C30-N31-C36	-2.19	107.74	111.14
17	H	301	04C	C7-C6-C5	2.18	124.97	120.90
17	K	301	04C	C7-C6-C1	-2.17	116.86	120.90
17	H	301	04C	C30-N31-C36	-2.16	107.78	111.14
17	Y	301	04C	C7-C6-C5	2.15	124.91	120.90
17	V	301	04C	C7-C6-C1	-2.15	116.90	120.90
17	K	301	04C	C7-C6-C5	2.14	124.88	120.90
17	H	301	04C	C7-C6-C1	-2.13	116.93	120.90
17	Y	301	04C	C7-C6-C1	-2.11	116.98	120.90
17	Y	301	04C	C29-C30-N31	-2.03	108.70	113.41
17	V	301	04C	C32-N31-C36	2.01	113.17	108.84

There are no chirality outliers.

All (76) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	H	301	04C	C11-C10-C9-C8
17	K	301	04C	C11-C10-C9-C8
17	K	301	04C	C12-C10-C9-C8
17	N	201	04C	C11-C10-C9-C8
17	N	201	04C	C9-C10-C12-O13
17	N	201	04C	C11-C10-C12-O13
17	V	301	04C	C11-C10-C9-C8
17	Y	301	04C	C11-C10-C9-C8
17	Y	301	04C	C12-C10-C9-C8
17	b	201	04C	C11-C10-C9-C8
17	b	201	04C	C9-C10-C12-O13
17	b	201	04C	C11-C10-C12-O13
17	H	301	04C	C47-C44-O45-C46
17	H	301	04C	C43-C44-O45-C46
17	K	301	04C	C43-C44-O45-C46
17	V	301	04C	C47-C44-O45-C46
17	V	301	04C	C43-C44-O45-C46
17	Y	301	04C	C43-C44-O45-C46
17	Y	301	04C	C47-C44-O45-C46
17	K	301	04C	C47-C44-O45-C46
17	N	201	04C	C47-C44-O45-C46
17	b	201	04C	C47-C44-O45-C46
17	N	201	04C	C43-C44-O45-C46
17	b	201	04C	C43-C44-O45-C46
17	H	301	04C	N25-C24-C40-C41
17	N	201	04C	N25-C24-C40-C41
17	V	301	04C	N25-C24-C40-C41
17	b	201	04C	N25-C24-C40-C41
17	N	201	04C	C5-C6-C7-C8
17	b	201	04C	C5-C6-C7-C8
17	N	201	04C	C1-C6-C7-C8
17	b	201	04C	C1-C6-C7-C8
17	V	301	04C	C5-C6-C7-C8
17	H	301	04C	C5-C6-C7-C8
17	N	201	04C	N28-C29-C30-N31
17	b	201	04C	N28-C29-C30-N31
17	N	201	04C	C23-C24-C40-C41
17	H	301	04C	C1-C6-C7-C8
17	V	301	04C	C1-C6-C7-C8
17	K	301	04C	C11-C10-C9-O21

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Mol	Chain	Res	Type	Atoms
17	Y	301	04C	C11-C10-C9-O21
17	b	201	04C	C23-C24-C40-C41
17	K	301	04C	C5-C6-C7-C8
17	Y	301	04C	C5-C6-C7-C8
17	Y	301	04C	C1-C6-C7-C8
17	K	301	04C	C1-C6-C7-C8
17	N	201	04C	O37-C29-C30-N31
17	b	201	04C	O37-C29-C30-N31
17	H	301	04C	C11-C10-C9-O21
17	V	301	04C	C11-C10-C9-O21
17	N	201	04C	C6-C7-C8-N22
17	b	201	04C	C6-C7-C8-N22
17	H	301	04C	C23-C24-C40-C41
17	V	301	04C	C23-C24-C40-C41
17	N	201	04C	C29-C30-N31-C32
17	b	201	04C	C29-C30-N31-C32
17	K	301	04C	C12-C10-C9-O21
17	Y	301	04C	C12-C10-C9-O21
17	b	201	04C	C11-C10-C9-O21
17	N	201	04C	C29-C30-N31-C36
17	b	201	04C	C29-C30-N31-C36
17	H	301	04C	C6-C7-C8-N22
17	K	301	04C	C6-C7-C8-N22
17	V	301	04C	C6-C7-C8-N22
17	Y	301	04C	C6-C7-C8-N22
17	Y	301	04C	O49-C23-C24-N25
17	N	201	04C	C11-C10-C9-O21
17	K	301	04C	O49-C23-C24-N25
17	Y	301	04C	N22-C23-C24-N25
17	K	301	04C	N22-C23-C24-N25
17	H	301	04C	C12-C10-C9-C8
17	N	201	04C	C12-C10-C9-C8
17	V	301	04C	C12-C10-C9-C8
17	b	201	04C	C12-C10-C9-C8
17	N	201	04C	C6-C7-C8-C9
17	b	201	04C	C6-C7-C8-C9

There are no ring outliers.

6 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	K	301	04C	5	0

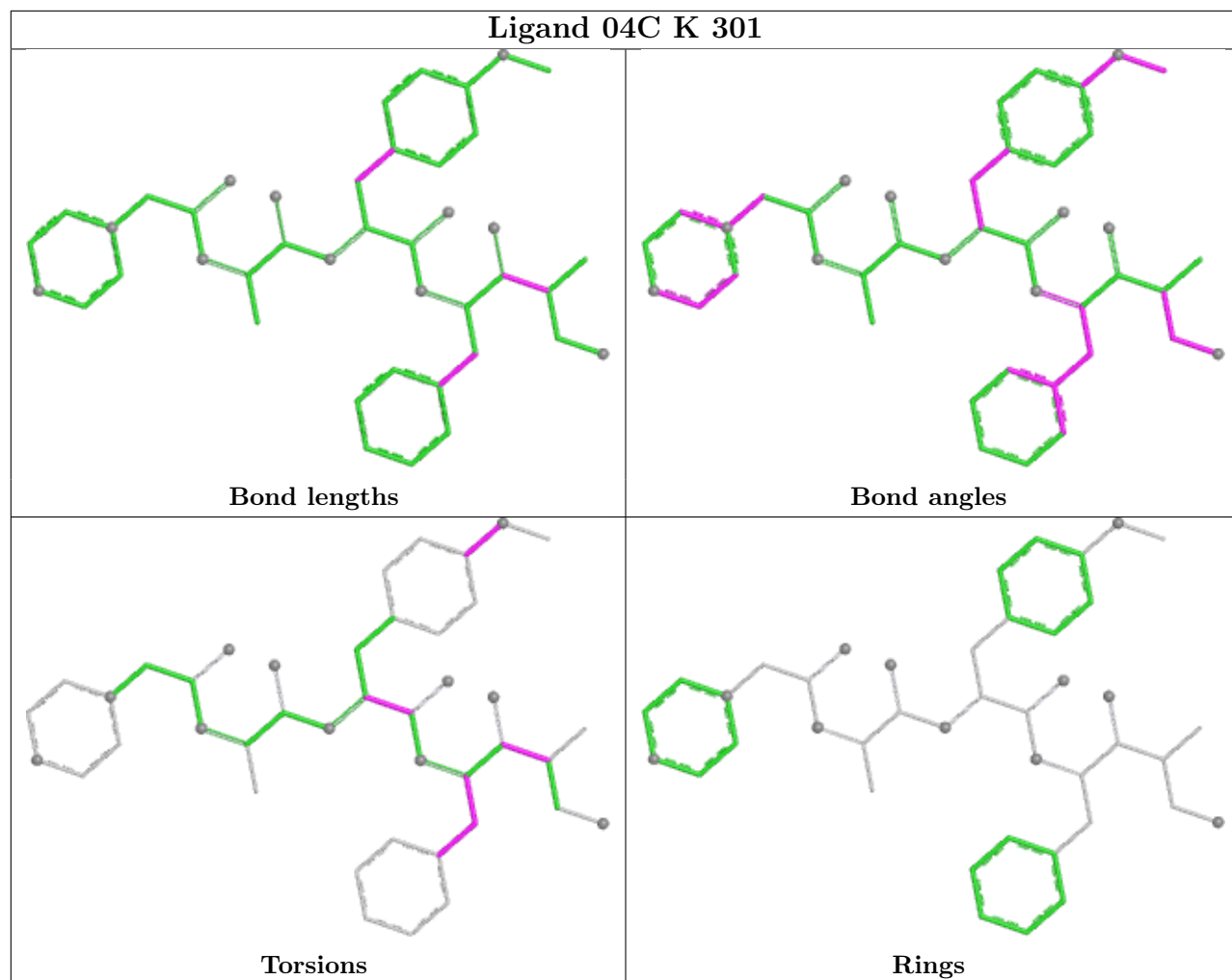
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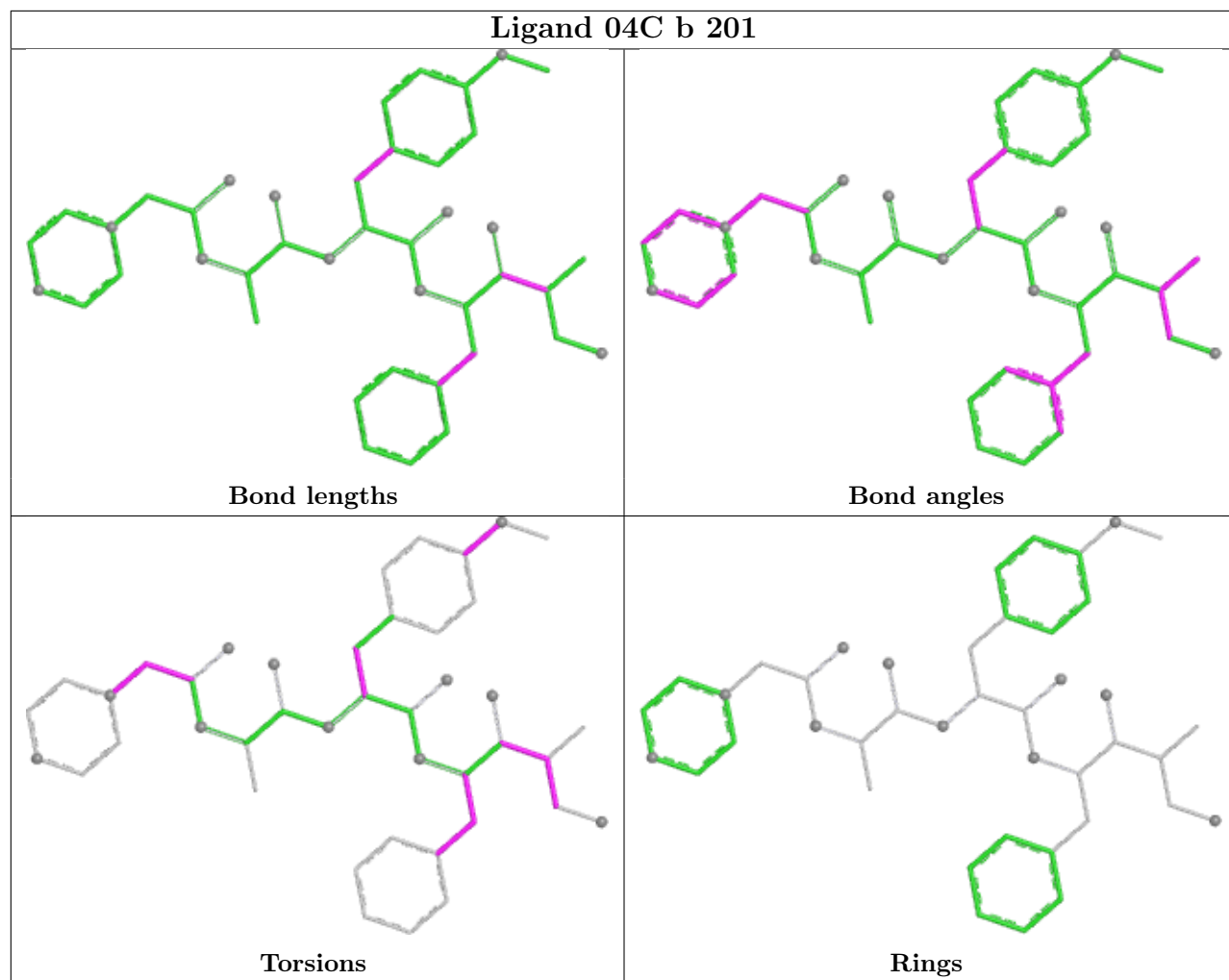
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	b	201	04C	4	0
17	H	301	04C	3	0
17	N	201	04C	3	0
17	Y	301	04C	6	0
17	V	301	04C	4	0

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.

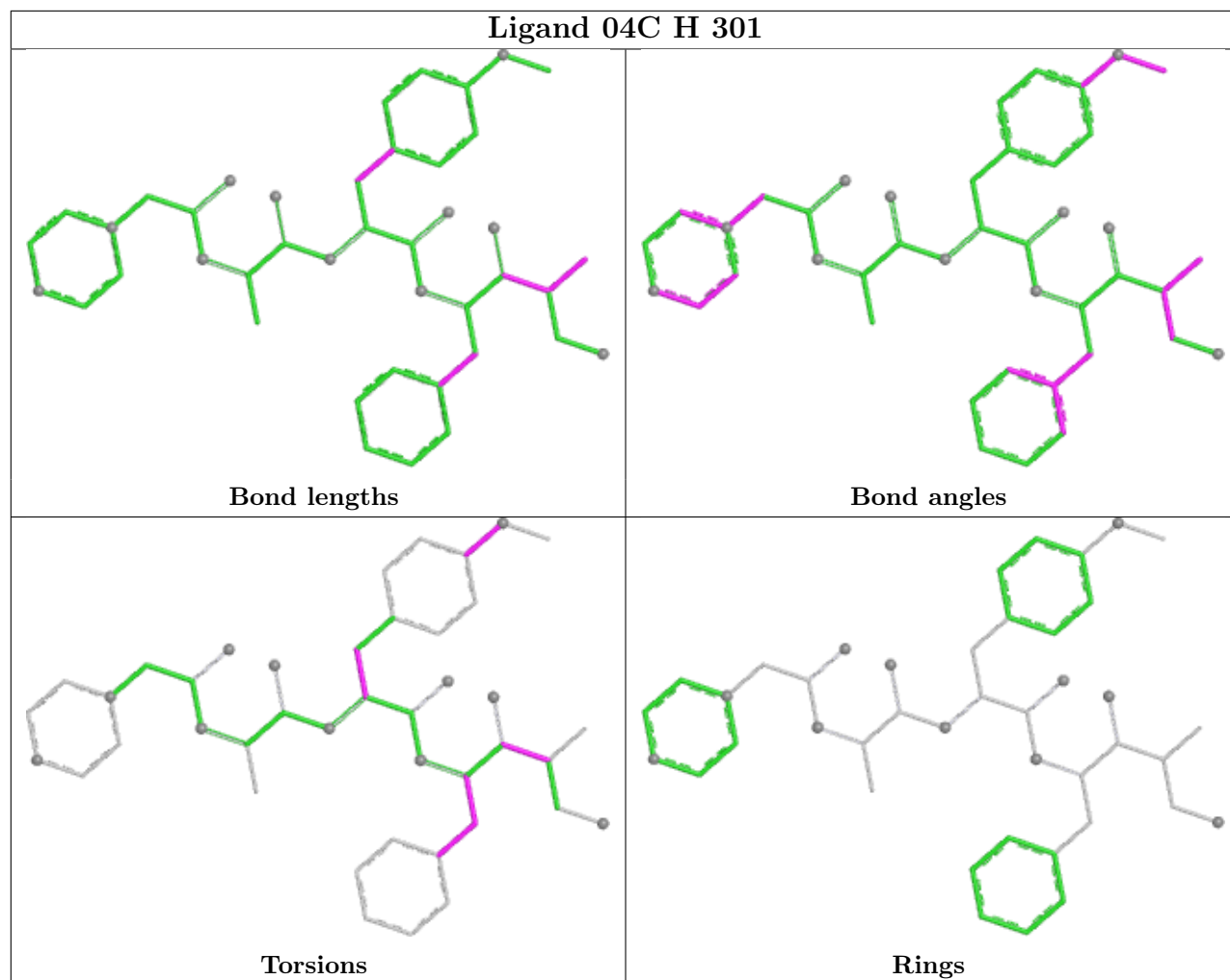
Ligand 04C K 301



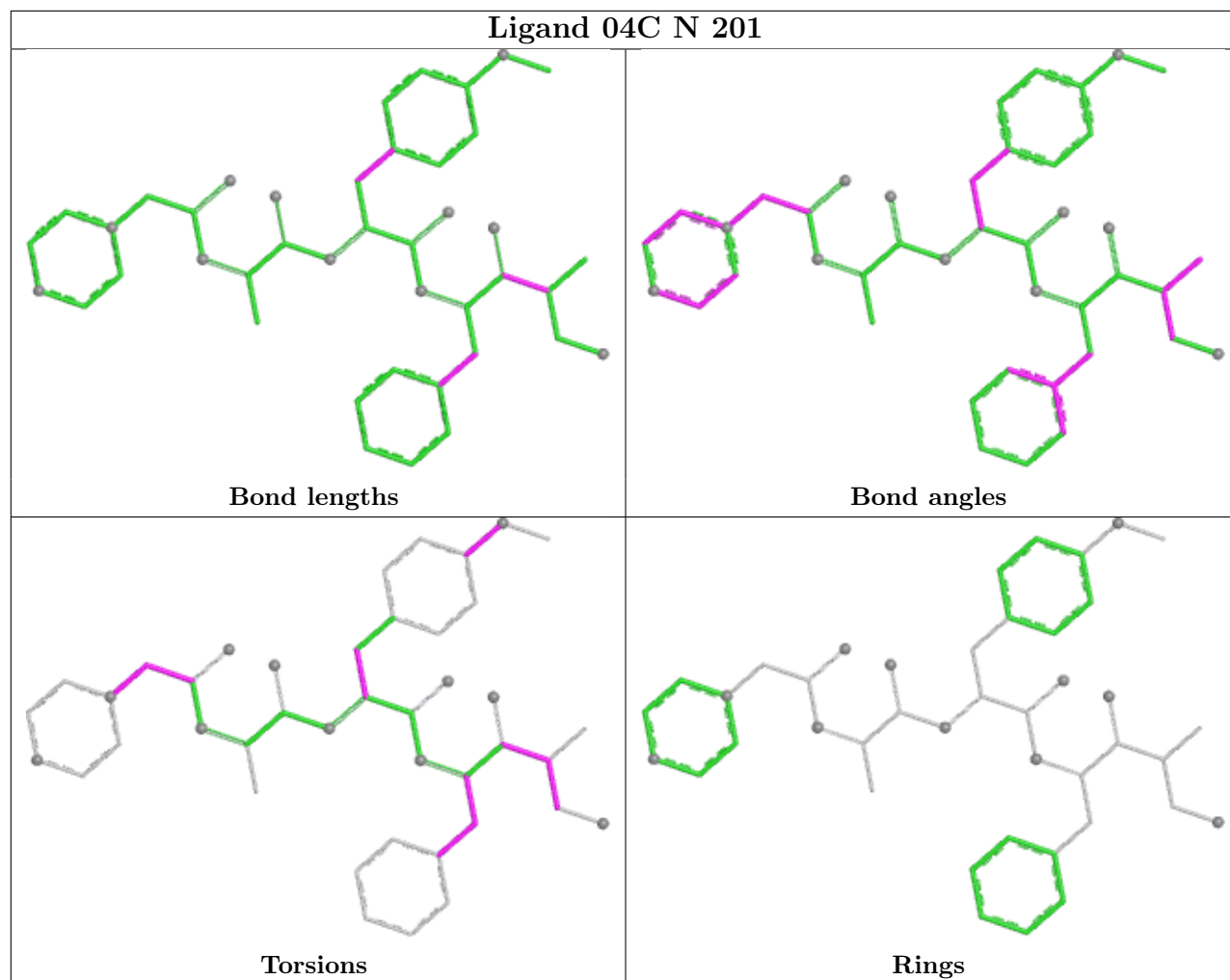
Ligand 04C b 201



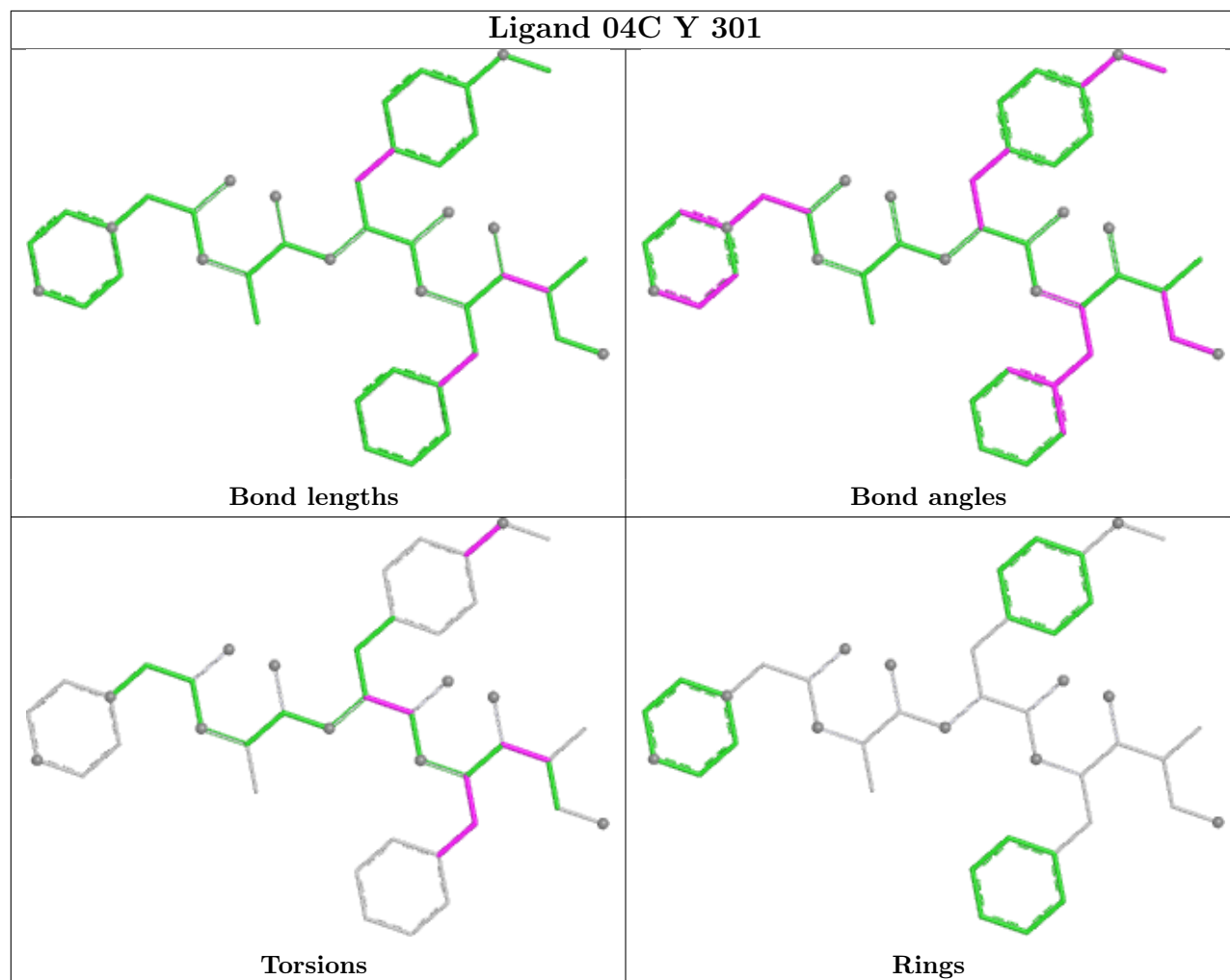
Ligand 04C H 301

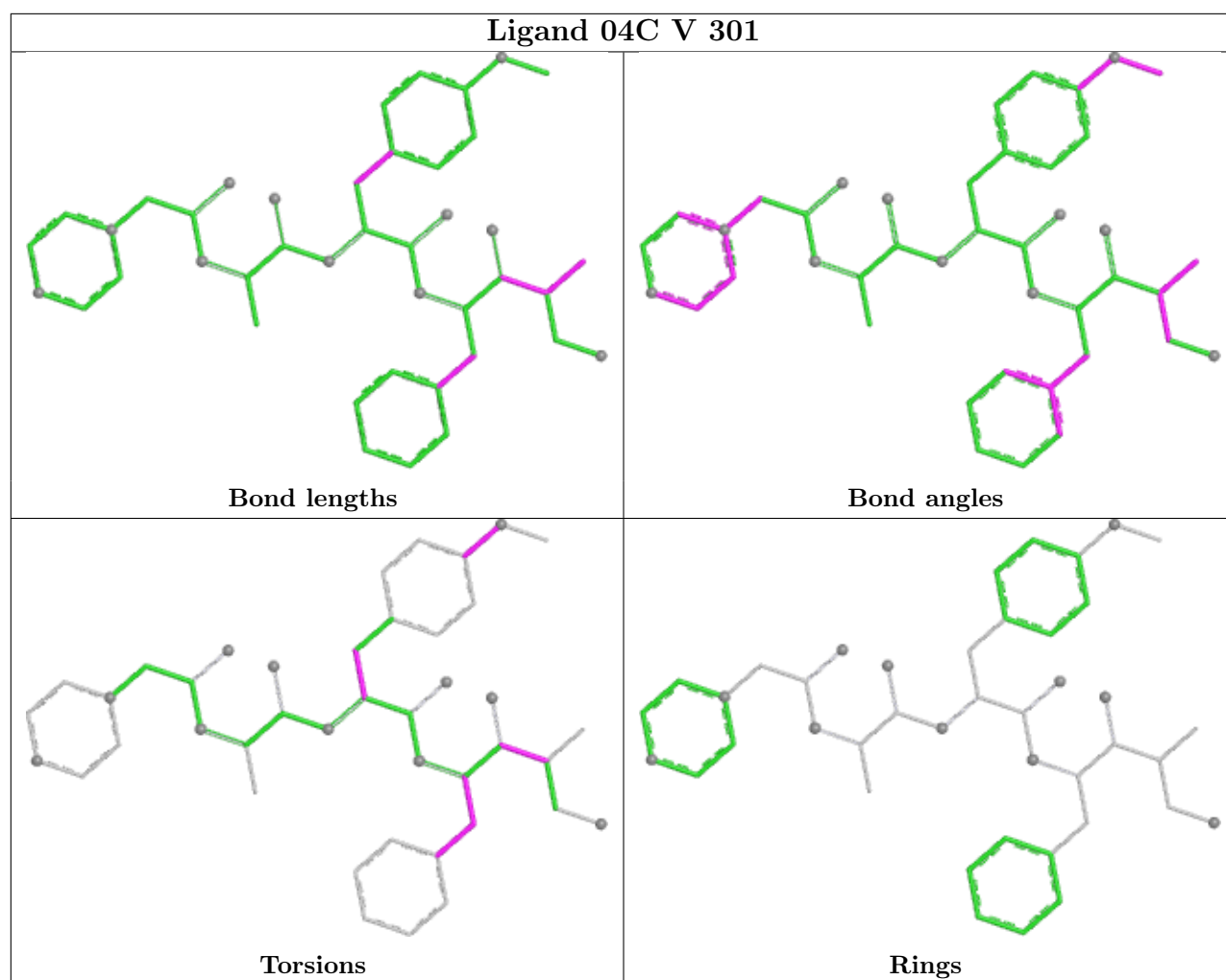


Ligand 04C N 201



Ligand 04C Y 301





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%)	-0.19	2 (0%) 82 75	41, 57, 99, 139	0
1	O	250/250 (100%)	-0.09	5 (2%) 65 56	43, 63, 106, 142	0
2	B	244/258 (94%)	-0.14	4 (1%) 70 61	39, 59, 106, 169	0
2	P	244/258 (94%)	-0.17	5 (2%) 65 56	42, 61, 108, 167	0
3	C	240/254 (94%)	-0.14	3 (1%) 75 66	38, 62, 125, 161	0
3	Q	240/254 (94%)	0.03	6 (2%) 58 48	45, 76, 153, 202	0
4	D	235/260 (90%)	-0.25	2 (0%) 81 74	41, 64, 95, 140	0
4	R	235/260 (90%)	-0.17	0 100 100	49, 69, 108, 153	0
5	E	231/234 (98%)	-0.08	0 100 100	46, 69, 106, 150	0
5	S	231/234 (98%)	-0.06	0 100 100	47, 70, 108, 139	0
6	F	243/288 (84%)	0.18	9 (3%) 45 36	44, 66, 116, 149	0
6	T	243/288 (84%)	0.01	3 (1%) 76 68	42, 67, 118, 154	0
7	G	241/252 (95%)	0.19	6 (2%) 58 48	43, 63, 104, 152	0
7	U	241/252 (95%)	0.01	1 (0%) 88 84	42, 60, 96, 144	0
8	H	222/232 (95%)	0.25	12 (5%) 31 24	42, 60, 96, 140	0
8	V	222/232 (95%)	0.29	12 (5%) 31 24	43, 64, 95, 143	0
9	I	204/205 (99%)	-0.49	3 (1%) 72 63	35, 50, 81, 104	0
9	W	204/205 (99%)	-0.43	3 (1%) 72 63	37, 52, 83, 99	0
10	J	195/198 (98%)	-0.60	1 (0%) 87 82	34, 48, 73, 118	0
10	X	195/198 (98%)	-0.58	1 (0%) 87 82	37, 50, 78, 127	0
11	K	212/212 (100%)	-0.49	0 100 100	25, 52, 77, 95	0
11	Y	212/212 (100%)	-0.50	1 (0%) 87 82	20, 52, 80, 106	0
12	L	222/222 (100%)	-0.36	1 (0%) 87 82	37, 54, 82, 108	0
12	Z	222/222 (100%)	-0.38	0 100 100	35, 54, 83, 109	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	225/246 (91%)	-0.19	2 (0%) 81 74	35, 56, 82, 100	0
13	a	225/246 (91%)	-0.26	1 (0%) 88 84	36, 54, 81, 111	0
14	N	196/196 (100%)	-0.09	0 100 100	32, 56, 86, 108	0
14	b	196/196 (100%)	-0.06	1 (0%) 87 82	31, 55, 83, 103	0
All	All	6320/6614 (95%)	-0.16	84 (1%) 75 66	20, 59, 102, 202	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	X	1	MET	5.0
3	Q	50	LEU	5.0
2	B	219	ALA	4.9
2	B	51	VAL	4.5
2	P	219	ALA	3.9
1	O	1	MET	3.6
11	Y	212	GLY	3.6
10	J	1	MET	3.6
12	L	163	GLY	3.5
6	T	178	HIS	3.5
13	M	69	ASP	3.4
8	H	212	VAL	3.3
1	O	53	SER	3.3
6	F	202	ASP	3.1
6	F	215	CYS	3.1
13	M	1	THR	3.1
9	W	130	ASP	3.0
8	V	32	ALA	3.0
3	Q	51	LYS	3.0
14	b	103	ASP	3.0
3	Q	49	THR	3.0
9	I	130	ASP	3.0
13	a	1	THR	2.9
1	O	249	ALA	2.9
9	I	131	GLU	2.8
7	G	31	ILE	2.8
6	F	178	HIS	2.8
1	A	1	MET	2.8
8	V	196	ARG	2.8
6	F	180	PRO	2.8
2	P	51	VAL	2.7
8	H	222	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
8	V	1	THR	2.7
8	H	208	GLY	2.7
6	F	206	LYS	2.7
1	O	226	GLY	2.7
3	Q	205	ALA	2.6
7	U	222	ASP	2.6
3	C	204	GLY	2.6
2	P	1	GLY	2.5
1	O	206	GLY	2.5
8	H	10	ASN	2.5
3	Q	240	GLU	2.5
7	G	204	ALA	2.5
8	H	32	ALA	2.5
9	W	124	ASP	2.5
7	G	171	THR	2.5
6	F	244	ASN	2.5
8	H	220	ILE	2.4
8	V	207	ARG	2.4
3	C	205	ALA	2.4
8	H	204	LYS	2.4
8	H	209	THR	2.4
2	B	220	ASN	2.4
8	V	28	ASP	2.4
4	D	240	ALA	2.4
2	P	52	THR	2.4
3	Q	206	LYS	2.4
4	D	2	ARG	2.4
8	V	191	LEU	2.3
9	W	131	GLU	2.3
7	G	222	ASP	2.3
8	H	213	LEU	2.3
9	I	124	ASP	2.3
8	H	217	ILE	2.3
6	F	241	LYS	2.2
7	G	40	ASP	2.2
8	V	220	ILE	2.2
8	V	20	SER	2.2
1	A	249	ALA	2.2
8	V	214	LYS	2.2
6	F	176	VAL	2.2
2	B	52	THR	2.1
2	P	225	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
8	V	31	CYS	2.1
8	V	2	THR	2.1
8	V	221	CYS	2.1
8	H	207	ARG	2.1
8	H	20	SER	2.1
6	T	179	HIS	2.1
6	T	59	LYS	2.0
3	C	203	THR	2.0
6	F	177	ASP	2.0
7	G	207	THR	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	04C	V	301	42/42	0.42	0.22	40,51,90,100	0
17	04C	H	301	42/42	0.45	0.22	40,57,79,83	0
18	MES	Y	303	12/12	0.84	0.20	57,83,86,86	0
18	MES	K	303	12/12	0.88	0.19	61,86,89,98	0
15	MG	Z	301	1/1	0.89	0.11	71,71,71,71	0
17	04C	N	201	42/42	0.90	0.10	30,38,47,52	0
17	04C	b	201	42/42	0.90	0.10	29,38,53,59	0
17	04C	Y	301	42/42	0.93	0.09	19,36,59,61	0
17	04C	K	301	42/42	0.94	0.08	23,39,56,58	0
16	CL	G	302	1/1	0.96	0.07	43,43,43,43	0
15	MG	V	302	1/1	0.97	0.07	66,66,66,66	0
16	CL	U	301	1/1	0.98	0.08	42,42,42,42	0
15	MG	N	202	1/1	0.98	0.07	48,48,48,48	0

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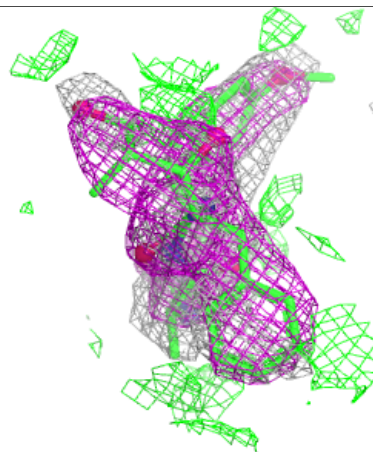
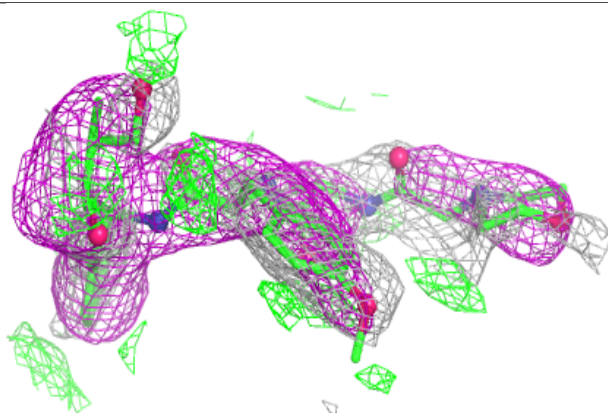
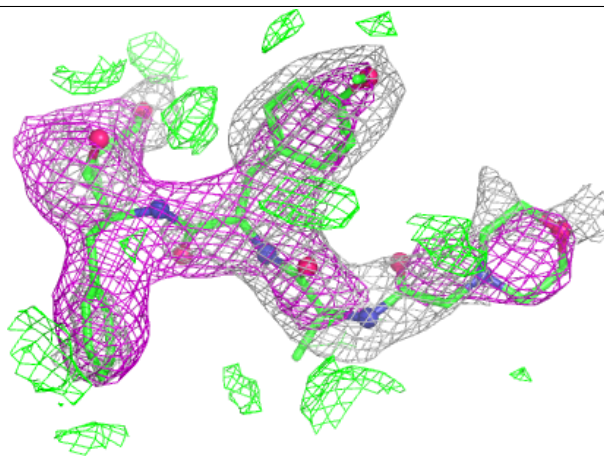
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
15	MG	Y	302	1/1	0.98	0.06	54,54,54,54	0
15	MG	K	302	1/1	0.99	0.07	58,58,58,58	0
15	MG	G	301	1/1	0.99	0.07	54,54,54,54	0
15	MG	I	301	1/1	0.99	0.03	48,48,48,48	0

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.

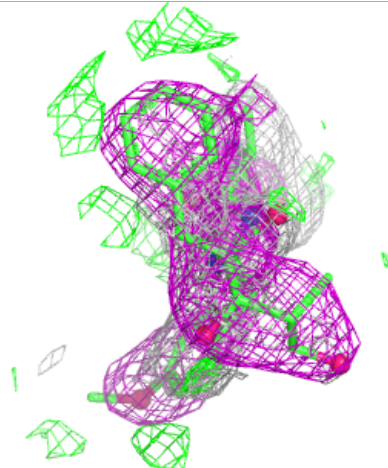
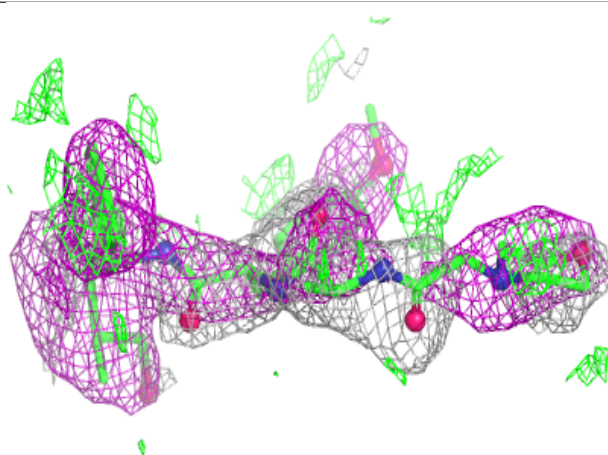
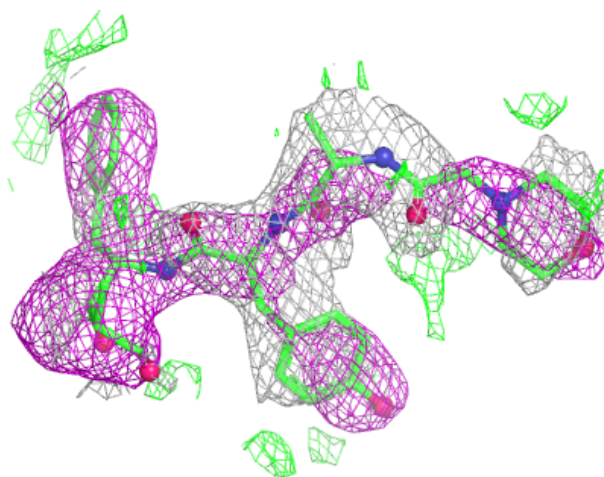
Electron density around 04C V 301:

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



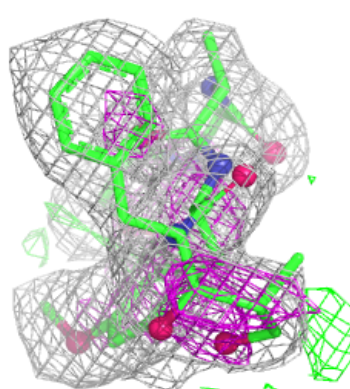
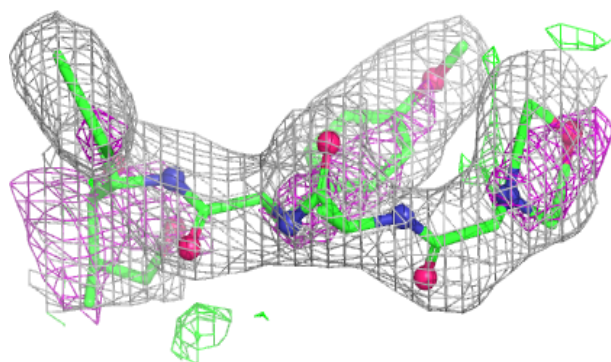
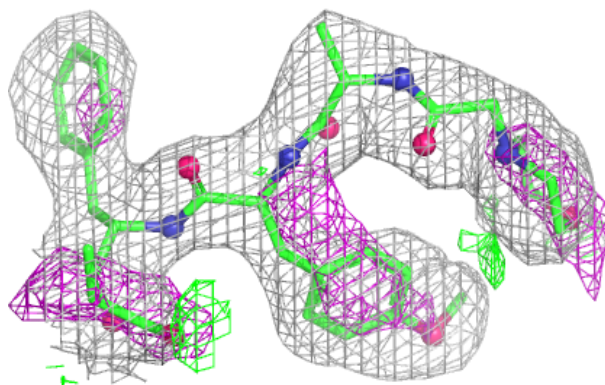
Electron density around 04C H 301:

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

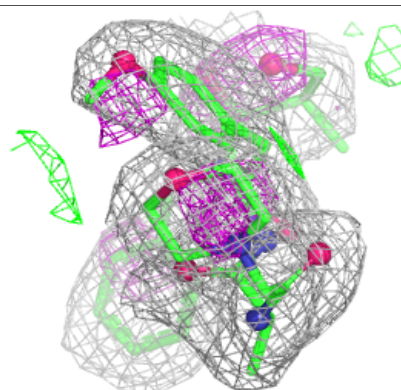
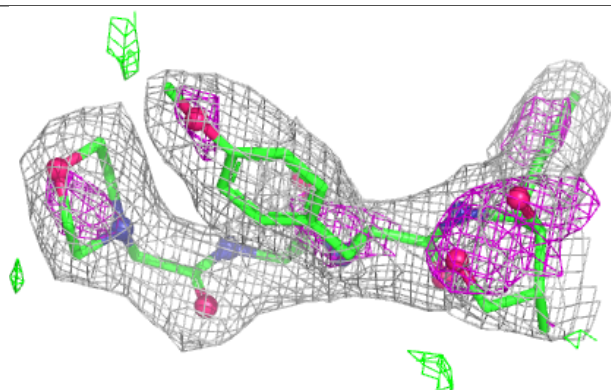
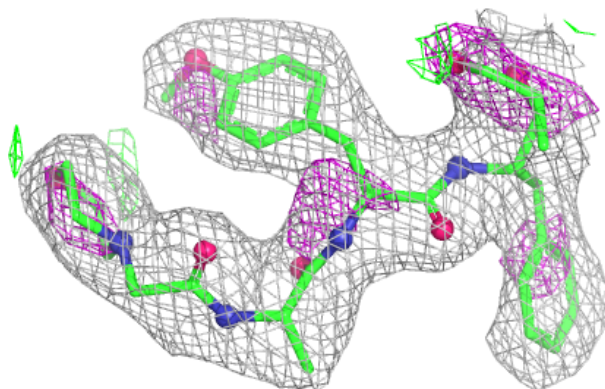


Electron density around 04C N 201:

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

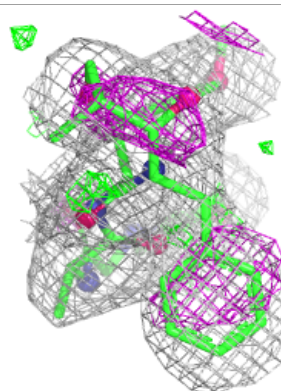
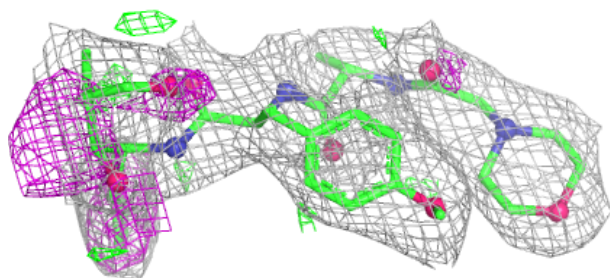
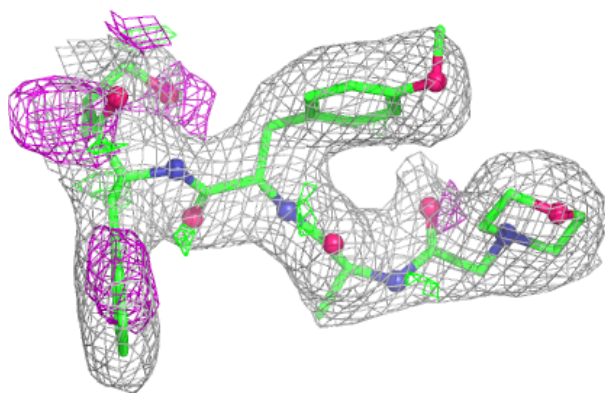
**Electron density around 04C b 201:**

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

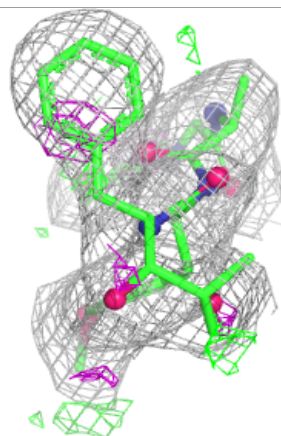
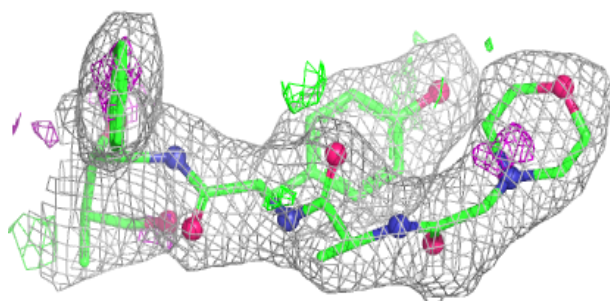
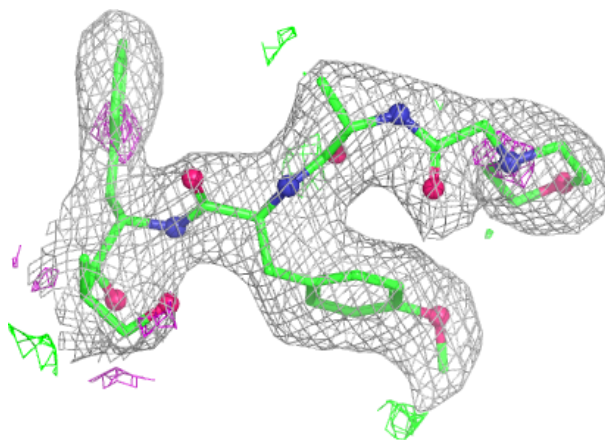


Electron density around 04C Y 301:

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

**Electron density around 04C K 301:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.