



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 06:17 AM UTC

PDB ID : 5CGG / pdb_00005cgg
Title : Yeast 20S proteasome beta5-G48C mutant in complex with alpha-chloroacetamide 1
Authors : Dubiella, C.; Groll, M.
Deposited on : 2015-07-09
Resolution : 2.90 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
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

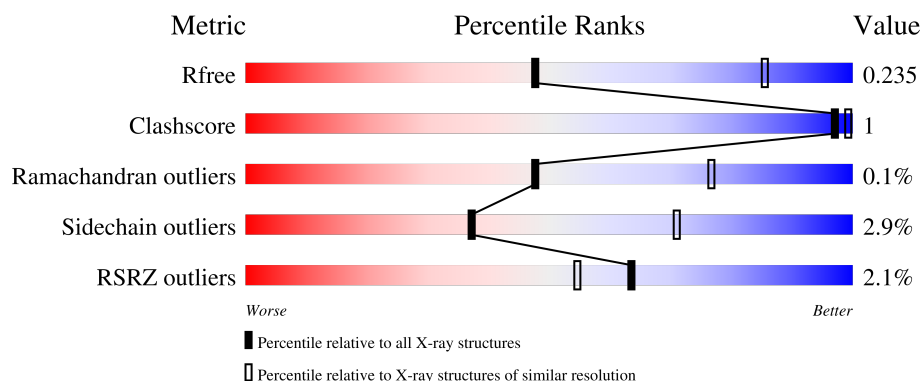
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

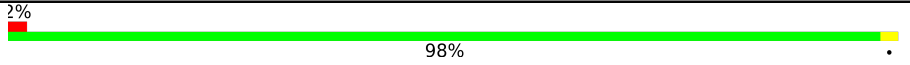
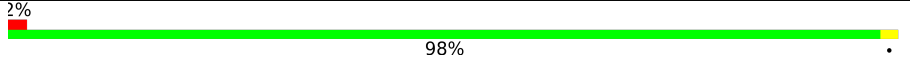
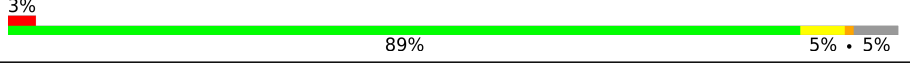
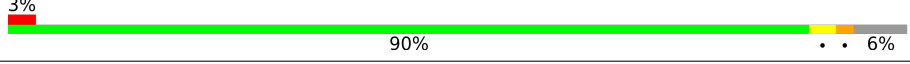
The reported resolution of this entry is 2.90 Å.

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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	
1	O	250	
2	B	258	
2	P	258	
3	C	254	

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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	
15	g	6	
15	h	6	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 49712 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
			1914	1219	315	376	4			
1	O	250	Total	C	N	O	S	0	0	0
			1914	1219	315	376	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
			1772	1114	307	347	4			
5	S	231	Total	C	N	O	S	0	0	0
			1772	1114	307	347	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
			1906	1214	320	364	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
			1580	1010	258	304	8			
9	W	204	Total	C	N	O	S	0	0	0
			1580	1010	258	304	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
			1645	1046	280	311	8			
11	Y	212	Total	C	N	O	S	0	0	0
			1645	1046	280	311	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	48	CYS	GLY	engineered mutation	UNP P30656
Y	48	CYS	GLY	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
			1756	1115	303	334	4			
12	Z	222	Total	C	N	O	S	0	0	0
			1756	1115	303	334	4			

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1823	1154	312	350	7			
13	a	233	Total	C	N	O	S	0	0	0
			1823	1154	312	350	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
			1511	955	250	299	7			
14	b	196	Total	C	N	O	S	0	0	0
			1511	955	250	299	7			

- Molecule 15 is a protein called carfilzomib alpha-chloroacetamide 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	g	6	Total	C	N	O	0	0	0
			46	34	6	6			
15	h	6	Total	C	N	O	0	0	0
			46	34	6	6			

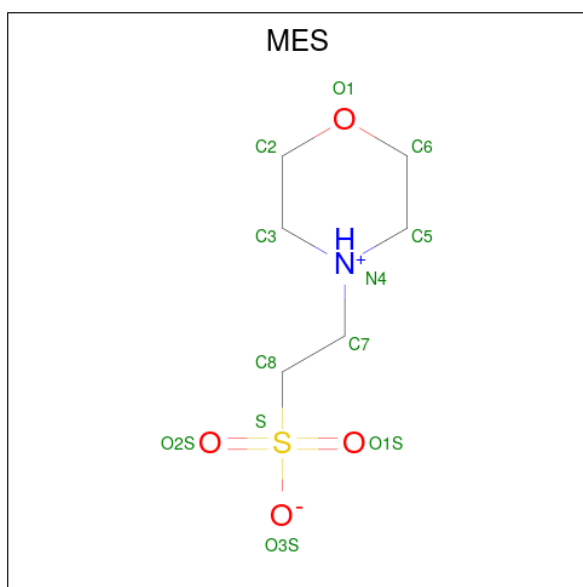
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	G	1	Total	Mg	0	0
			1	1		
16	I	2	Total	Mg	0	0
			2	2		
16	J	1	Total	Mg	0	0
			1	1		
16	K	1	Total	Mg	0	0
			1	1		
16	N	1	Total	Mg	0	0
			1	1		
16	V	1	Total	Mg	0	0
			1	1		
16	Z	1	Total	Mg	0	0
			1	1		

- Molecule 17 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- 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	10	Total	O	0	0
			10	10		
19	B	17	Total	O	0	0
			17	17		
19	C	9	Total	O	0	0
			9	9		
19	D	5	Total	O	0	0
			5	5		
19	E	7	Total	O	0	0
			7	7		
19	F	16	Total	O	0	0
			16	16		
19	G	13	Total	O	0	0
			13	13		
19	H	14	Total	O	0	0
			14	14		
19	I	9	Total	O	0	0
			9	9		
19	J	19	Total	O	0	0
			19	19		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	K	9	Total O 9 9	0	0
19	L	10	Total O 10 10	0	0
19	M	12	Total O 12 12	0	0
19	N	13	Total O 13 13	0	0
19	O	8	Total O 8 8	0	0
19	P	4	Total O 4 4	0	0
19	Q	10	Total O 10 10	0	0
19	R	4	Total O 4 4	0	0
19	S	6	Total O 6 6	0	0
19	T	12	Total O 12 12	0	0
19	U	15	Total O 15 15	0	0
19	V	13	Total O 13 13	0	0
19	W	8	Total O 8 8	0	0
19	X	8	Total O 8 8	0	0
19	Y	8	Total O 8 8	0	0
19	Z	10	Total O 10 10	0	0
19	a	12	Total O 12 12	0	0
19	b	17	Total O 17 17	0	0
19	h	1	Total O 1 1	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.

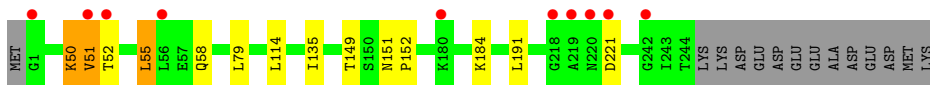
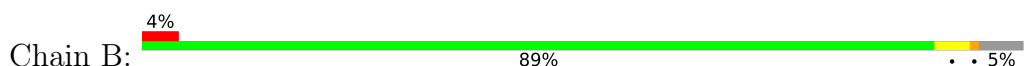
- Molecule 1: Proteasome subunit alpha type-2



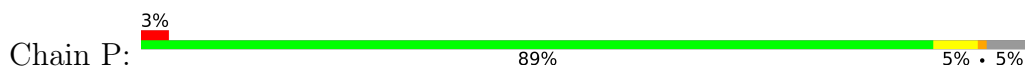
- Molecule 1: Proteasome subunit alpha type-2



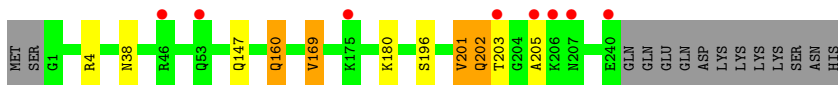
- Molecule 2: Proteasome subunit alpha type-3



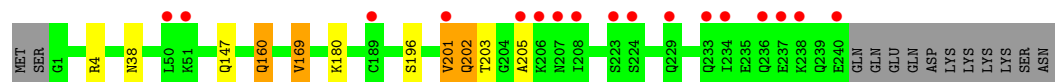
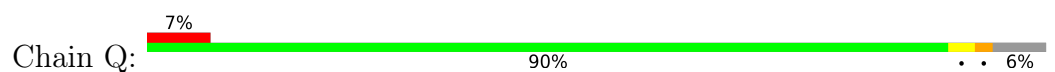
- Molecule 2: Proteasome subunit alpha type-3



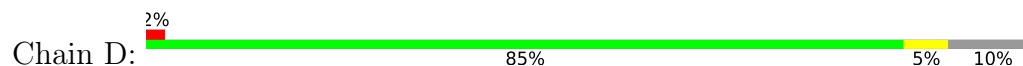
- Molecule 3: Proteasome subunit alpha type-4



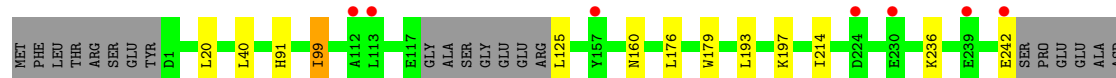
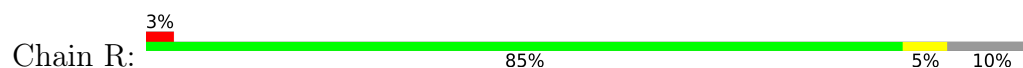
- Molecule 3: Proteasome subunit alpha type-4



- Molecule 4: Proteasome subunit alpha type-5



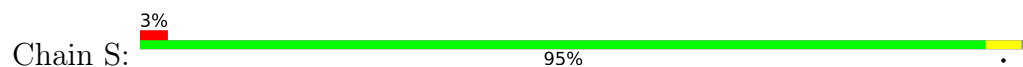
- Molecule 4: Proteasome subunit alpha type-5



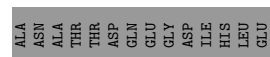
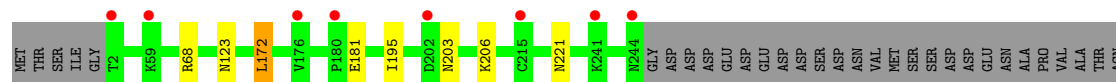
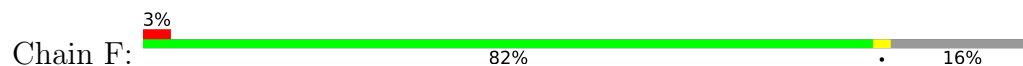
- Molecule 5: Proteasome subunit alpha type-6



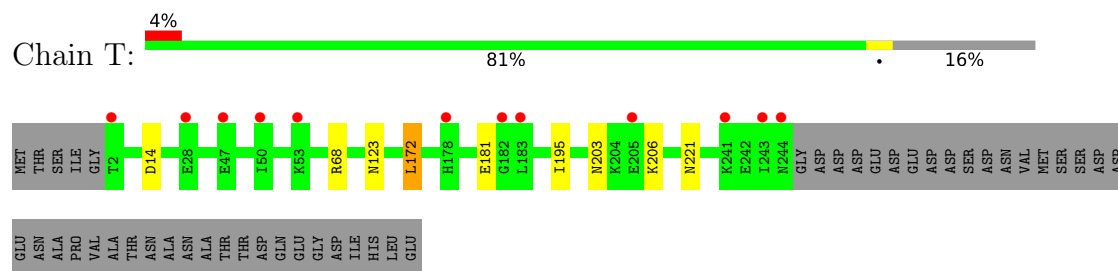
- Molecule 5: Proteasome subunit alpha type-6



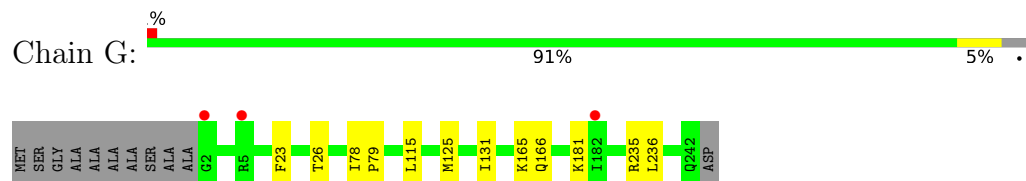
- Molecule 6: Probable proteasome subunit alpha type-7



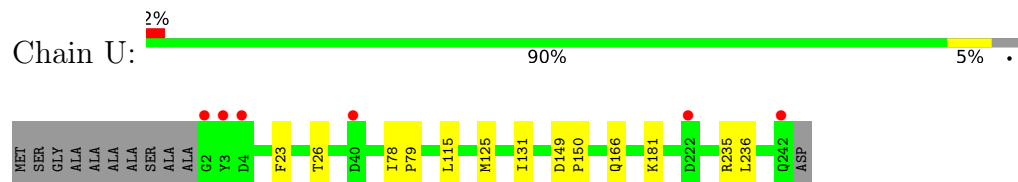
- Molecule 6: Probable proteasome subunit alpha type-7



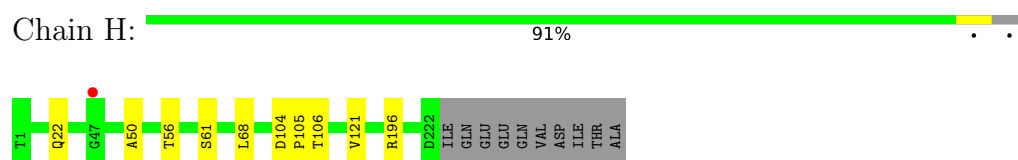
- Molecule 7: Proteasome subunit alpha type-1



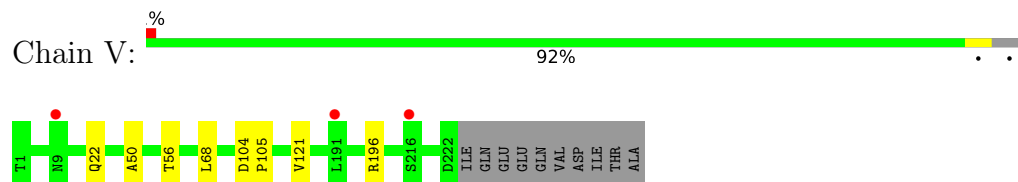
- Molecule 7: Proteasome subunit alpha type-1



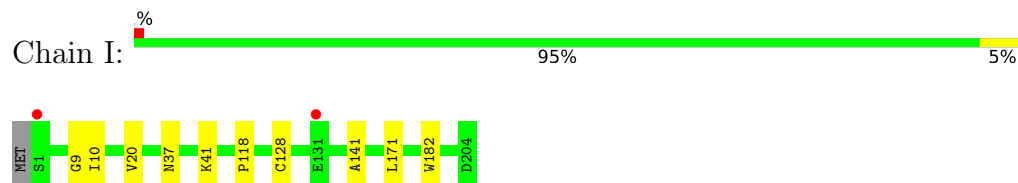
- Molecule 8: Proteasome subunit beta type-2



- Molecule 8: Proteasome subunit beta type-2

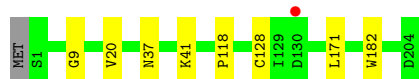


- Molecule 9: Proteasome subunit beta type-3



- 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



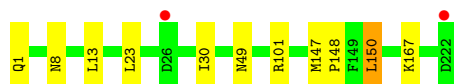
- Molecule 11: Proteasome subunit beta type-5



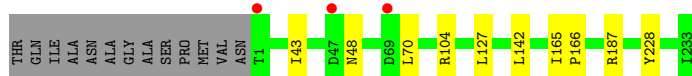
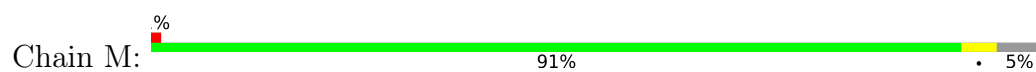
- Molecule 12: Proteasome subunit beta type-6



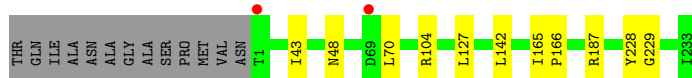
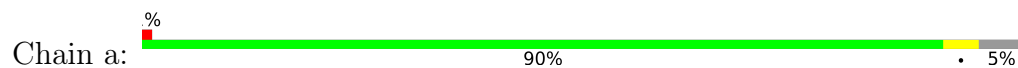
- Molecule 12: Proteasome subunit beta type-6



- Molecule 13: Proteasome subunit beta type-7



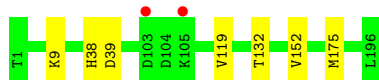
- Molecule 13: Proteasome subunit beta type-7



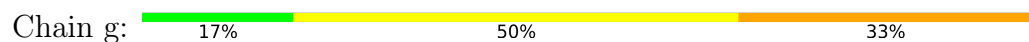
- Molecule 14: Proteasome subunit beta type-1



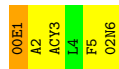
- Molecule 14: Proteasome subunit beta type-1



- Molecule 15: carfilzomib alpha-chloroacetamide 1



- Molecule 15: carfilzomib alpha-chloroacetamide 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	134.44Å 300.47Å 144.74Å 90.00° 113.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.90 15.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	95.7 (15.00-2.90) 95.0 (15.00-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.204 , 0.231 0.210 , 0.235	Depositor DCC
R_{free} test set	11055 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	49712	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.40% 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: MES, CL, MG, 00E, ACY, DPP, 02N

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	0/1951	0.69	0/2642
1	O	0.40	0/1951	0.69	0/2642
2	B	0.39	0/1934	0.67	0/2618
2	P	0.39	0/1934	0.67	0/2618
3	C	0.40	0/1910	0.70	1/2586 (0.0%)
3	Q	0.39	0/1910	0.70	1/2586 (0.0%)
4	D	0.39	0/1837	0.65	0/2475
4	R	0.38	0/1837	0.65	0/2475
5	E	0.39	0/1799	0.67	0/2433
5	S	0.39	0/1799	0.67	0/2433
6	F	0.39	0/1932	0.69	0/2609
6	T	0.39	0/1932	0.69	0/2609
7	G	0.38	0/1945	0.67	0/2634
7	U	0.39	0/1944	0.67	0/2632
8	H	0.38	0/1715	0.65	0/2326
8	V	0.39	0/1715	0.65	0/2326
9	I	0.37	0/1610	0.65	0/2174
9	W	0.37	0/1610	0.66	0/2174
10	J	0.37	0/1589	0.66	0/2142
10	X	0.37	0/1589	0.66	0/2142
11	K	0.37	0/1682	0.65	0/2277
11	Y	0.38	0/1682	0.65	0/2277
12	L	0.38	0/1794	0.66	0/2420
12	Z	0.38	0/1794	0.66	0/2420
13	M	0.39	0/1854	0.67	0/2514
13	a	0.39	0/1854	0.67	0/2514
14	N	0.37	0/1540	0.67	0/2087
14	b	0.36	0/1540	0.67	0/2087
15	g	1.66	1/19 (5.3%)	1.65	1/24 (4.2%)
15	h	1.54	1/19 (5.3%)	1.15	0/24
All	All	0.39	2/50221 (0.0%)	0.67	3/67920 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	g	5	PHE	CB-CG	-6.03	1.36	1.50
15	h	5	PHE	CB-CG	-5.66	1.37	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	g	5	PHE	CA-CB-CG	-6.60	107.20	113.80
3	C	201	VAL	N-CA-C	5.36	115.80	110.23
3	Q	201	VAL	N-CA-C	5.30	115.74	110.23

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	1914	0	1929	2	0
1	O	1914	0	1929	0	0
2	B	1904	0	1904	5	0
2	P	1904	0	1904	4	0
3	C	1881	0	1895	4	0
3	Q	1881	0	1895	4	0
4	D	1813	0	1797	3	0
4	R	1813	0	1797	2	0
5	E	1772	0	1775	2	0
5	S	1772	0	1775	2	0
6	F	1892	0	1883	1	0
6	T	1892	0	1883	1	0
7	G	1907	0	1901	4	0
7	U	1906	0	1901	4	0
8	H	1684	0	1688	5	0
8	V	1684	0	1688	3	0
9	I	1580	0	1574	4	0
9	W	1580	0	1574	3	0
10	J	1561	0	1569	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	X	1561	0	1569	4	0
11	K	1645	0	1596	9	0
11	Y	1645	0	1596	10	0
12	L	1756	0	1711	3	0
12	Z	1756	0	1711	4	0
13	M	1823	0	1832	3	0
13	a	1823	0	1832	3	0
14	N	1511	0	1481	2	0
14	b	1511	0	1481	3	0
15	g	46	0	44	4	0
15	h	46	0	44	6	0
16	G	1	0	0	0	0
16	I	2	0	0	0	0
16	J	1	0	0	0	0
16	K	1	0	0	0	0
16	N	1	0	0	0	0
16	V	1	0	0	0	0
16	Z	1	0	0	0	0
17	G	2	0	0	0	0
17	N	1	0	0	0	0
17	U	1	0	0	0	0
18	K	12	0	13	0	0
18	Y	12	0	13	0	0
19	A	10	0	0	0	0
19	B	17	0	0	0	0
19	C	9	0	0	0	0
19	D	5	0	0	1	0
19	E	7	0	0	0	0
19	F	16	0	0	0	0
19	G	13	0	0	1	0
19	H	14	0	0	0	0
19	I	9	0	0	0	0
19	J	19	0	0	0	0
19	K	9	0	0	0	0
19	L	10	0	0	0	0
19	M	12	0	0	0	0
19	N	13	0	0	0	0
19	O	8	0	0	0	0
19	P	4	0	0	0	0
19	Q	10	0	0	0	0
19	R	4	0	0	0	0
19	S	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	T	12	0	0	0	0
19	U	15	0	0	0	0
19	V	13	0	0	0	0
19	W	8	0	0	0	0
19	X	8	0	0	0	0
19	Y	8	0	0	0	0
19	Z	10	0	0	0	0
19	a	12	0	0	1	0
19	b	17	0	0	0	0
19	h	1	0	0	0	0
All	All	49712	0	49184	92	0

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

All (92) 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)
15:g:1:00E:O	15:g:2:DPP:HB3	1.88	0.73
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.73	0.71
15:h:1:00E:O	15:h:2:DPP:HB3	1.90	0.70
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.73	0.69
11:Y:45:MET:SD	15:h:6:02N:H27B	2.33	0.68
11:K:31:VAL:HG11	15:g:6:02N:C23	2.30	0.62
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.83	0.60
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.84	0.59
11:Y:45:MET:SD	15:h:6:02N:C27	2.91	0.59
14:N:152:VAL:HA	14:N:175:MET:HE1	1.87	0.56
14:b:152:VAL:HA	14:b:175:MET:HE1	1.87	0.56
11:K:35:ILE:HB	11:K:45:MET:CE	2.35	0.55
11:Y:31:VAL:HG11	15:h:6:02N:C23	2.37	0.55
11:Y:35:ILE:HB	11:Y:45:MET:CE	2.36	0.55
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.44	0.53
3:C:201:VAL:O	3:C:202:GLN:CB	2.57	0.53
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.44	0.53
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.58	0.52
7:G:23:PHE:O	7:G:26:THR:HB	2.11	0.50
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.94	0.49
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.94	0.49
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.94	0.49
7:U:23:PHE:O	7:U:26:THR:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:174:MET:HA	10:X:174:MET:HA	1.93	0.49
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.94	0.49
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.96	0.48
11:K:45:MET:SD	15:g:6:02N:H27B	2.54	0.48
12:Z:101:ARG:NH2	15:h:3:ACY:H3	2.30	0.47
2:P:50:LYS:O	2:P:51:VAL:C	2.57	0.47
11:K:35:ILE:HB	11:K:45:MET:HE3	1.96	0.47
8:H:106:THR:HG23	19:a:303:HOH:O	2.15	0.47
2:B:50:LYS:O	2:B:51:VAL:C	2.58	0.46
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.97	0.46
11:Y:35:ILE:HB	11:Y:45:MET:HE3	1.97	0.46
6:F:172:LEU:CD1	6:F:195:ILE:HD13	2.46	0.46
8:H:50:ALA:HB2	9:I:128:CYS:HB2	1.98	0.46
6:T:172:LEU:CD1	6:T:195:ILE:HD13	2.46	0.45
7:U:26:THR:HG21	7:U:131:ILE:HD12	1.99	0.45
11:K:116:ASP:OD1	11:K:116:ASP:C	2.60	0.45
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.98	0.44
11:K:31:VAL:HG11	15:g:6:02N:C22	2.48	0.44
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.98	0.44
4:D:113:LEU:HB2	19:D:301:HOH:O	2.18	0.44
13:M:165:ILE:HB	13:M:166:PRO:HD3	2.00	0.44
13:a:165:ILE:HB	13:a:166:PRO:HD3	2.00	0.44
7:U:78:ILE:N	7:U:79:PRO:CD	2.81	0.44
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.48	0.43
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.43
9:I:20:VAL:HG13	9:I:118:PRO:HB3	2.00	0.43
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.48	0.43
8:V:50:ALA:HB2	9:W:128:CYS:HB2	2.01	0.43
10:X:3:ILE:HD12	10:X:176:PHE:CG	2.54	0.43
3:C:201:VAL:HG13	3:C:202:GLN:N	2.34	0.43
1:A:176:GLU:HG2	2:B:55:LEU:HD13	2.00	0.43
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.84	0.42
9:W:9:GLY:HA3	9:W:41:LYS:HE2	2.01	0.42
9:W:20:VAL:HG13	9:W:118:PRO:HB3	2.01	0.42
7:G:26:THR:HG21	7:G:131:ILE:HD12	2.00	0.42
11:K:5:ALA:HB3	11:K:100:MET:CE	2.50	0.42
11:Y:45:MET:HB3	15:h:6:02N:H25	2.01	0.42
9:I:9:GLY:HA3	9:I:41:LYS:HE2	2.02	0.42
13:M:127:LEU:HG	13:M:142:LEU:HD12	2.02	0.42
11:Y:5:ALA:HB3	11:Y:100:MET:CE	2.50	0.42
14:b:38:HIS:O	14:b:39:ASP:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:3:ILE:HD12	10:J:176:PHE:CG	2.54	0.42
13:M:228:TYR:HA	8:V:121:VAL:HG23	2.01	0.42
14:N:133:PHE:HA	14:b:132:THR:O	2.20	0.42
11:Y:116:ASP:OD1	11:Y:116:ASP:C	2.62	0.42
11:Y:4:LEU:C	11:Y:4:LEU:HD22	2.45	0.41
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.84	0.41
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.55	0.41
8:H:121:VAL:HG23	13:a:228:TYR:HA	2.03	0.41
12:L:8:ASN:HA	12:L:30:ILE:O	2.20	0.41
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.34	0.41
11:K:4:LEU:HD22	11:K:4:LEU:C	2.45	0.41
13:a:127:LEU:HG	13:a:142:LEU:HD12	2.02	0.41
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.35	0.41
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.20	0.41
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.50	0.41
9:I:10:ILE:HG21	9:I:141:ALA:HB3	2.03	0.41
1:A:99:ARG:HE	8:H:61:SER:HG	1.69	0.41
2:B:135:ILE:HG12	2:B:149:THR:HG22	2.03	0.41
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.55	0.41
7:G:165:LYS:HD2	19:G:409:HOH:O	2.21	0.41
2:P:135:ILE:HG12	2:P:149:THR:HG22	2.03	0.41
5:S:77:ALA:N	5:S:78:PRO:CD	2.84	0.41
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.51	0.40
2:P:151:ASN:HB2	2:P:152:PRO:HD2	2.03	0.40
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.52	0.40
2:B:151:ASN:HB2	2:B:152:PRO:HD2	2.03	0.40
5:E:77:ALA:N	5:E:78:PRO:CD	2.84	0.40
12:L:147:MET:N	12:L:148:PRO:HD2	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	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%)	6 (2%)	2 (1%)	16	44
2	P	242/258 (94%)	234 (97%)	6 (2%)	2 (1%)	16	44
3	C	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	16	44
3	Q	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	16	44
4	D	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
4	R	231/260 (89%)	225 (97%)	6 (3%)	0	100	100
5	E	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
5	S	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
6	F	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
6	T	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
7	G	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
7	U	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
8	H	220/232 (95%)	213 (97%)	7 (3%)	0	100	100
8	V	220/232 (95%)	214 (97%)	6 (3%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
10	X	193/198 (98%)	189 (98%)	4 (2%)	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%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	231/246 (94%)	221 (96%)	10 (4%)	0	100	100
13	a	231/246 (94%)	221 (96%)	9 (4%)	1 (0%)	30	59
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	6276/6614 (95%)	6099 (97%)	168 (3%)	9 (0%)	48	77

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
2	P	51	VAL
3	Q	202	GLN
3	C	205	ALA
3	Q	205	ALA
2	B	221	ASP
2	P	221	ASP
13	a	229	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	205 (98%)	4 (2%)	50	79
1	O	209/209 (100%)	205 (98%)	4 (2%)	50	79
2	B	203/216 (94%)	195 (96%)	8 (4%)	28	63
2	P	203/216 (94%)	195 (96%)	8 (4%)	28	63
3	C	212/226 (94%)	205 (97%)	7 (3%)	33	67
3	Q	212/226 (94%)	205 (97%)	7 (3%)	33	67
4	D	194/215 (90%)	184 (95%)	10 (5%)	21	52
4	R	194/215 (90%)	184 (95%)	10 (5%)	21	52
5	E	190/193 (98%)	185 (97%)	5 (3%)	40	73
5	S	190/193 (98%)	185 (97%)	5 (3%)	40	73
6	F	201/239 (84%)	194 (96%)	7 (4%)	32	66
6	T	201/239 (84%)	193 (96%)	8 (4%)	28	62
7	G	206/210 (98%)	200 (97%)	6 (3%)	37	71
7	U	206/210 (98%)	200 (97%)	6 (3%)	37	71
8	H	181/190 (95%)	177 (98%)	4 (2%)	45	77
8	V	181/190 (95%)	177 (98%)	4 (2%)	45	77
9	I	172/173 (99%)	169 (98%)	3 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	W	172/173 (99%)	169 (98%)	3 (2%)	53	82
10	J	173/175 (99%)	169 (98%)	4 (2%)	44	76
10	X	173/175 (99%)	169 (98%)	4 (2%)	44	76
11	K	170/170 (100%)	166 (98%)	4 (2%)	43	75
11	Y	170/170 (100%)	166 (98%)	4 (2%)	43	75
12	L	185/185 (100%)	179 (97%)	6 (3%)	34	68
12	Z	185/185 (100%)	180 (97%)	5 (3%)	39	73
13	M	199/208 (96%)	194 (98%)	5 (2%)	42	74
13	a	199/208 (96%)	194 (98%)	5 (2%)	42	74
14	N	162/162 (100%)	159 (98%)	3 (2%)	50	79
14	b	162/162 (100%)	160 (99%)	2 (1%)	63	86
15	g	2/2 (100%)	1 (50%)	1 (50%)	0	0
15	h	2/2 (100%)	2 (100%)	0	100	100
All	All	5318/5546 (96%)	5166 (97%)	152 (3%)	37	71

All (152) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
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	55	LEU
2	B	58	GLN
2	B	79	LEU
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

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Mol	Chain	Res	Type
4	D	20	LEU
4	D	40	LEU
4	D	99	ILE
4	D	125	LEU
4	D	176	LEU
4	D	193	LEU
4	D	197	LYS
4	D	214	ILE
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	29	LYS
5	E	54	GLU
5	E	71	LEU
5	E	188	LEU
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	115	LEU
7	G	125	MET
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
7	G	236	LEU
8	H	22	GLN
8	H	56	THR
8	H	68	LEU
8	H	196	ARG
9	I	37	ASN
9	I	171	LEU
9	I	182	TRP
10	J	23	ARG
10	J	75	LEU
10	J	144	LEU
10	J	174	MET
11	K	4	LEU
11	K	35	ILE
11	K	73	ARG

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Mol	Chain	Res	Type
11	K	106	ARG
12	L	1	GLN
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
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
14	N	9	LYS
14	N	22	THR
14	N	119	VAL
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	55	LEU
2	P	58	GLN
2	P	79	LEU
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
4	R	40	LEU
4	R	99	ILE
4	R	125	LEU
4	R	176	LEU
4	R	193	LEU
4	R	197	LYS
4	R	214	ILE

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Mol	Chain	Res	Type
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	54	GLU
5	S	71	LEU
5	S	188	LEU
6	T	14	ASP
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	115	LEU
7	U	125	MET
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
7	U	236	LEU
8	V	22	GLN
8	V	56	THR
8	V	68	LEU
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU
9	W	182	TRP
10	X	23	ARG
10	X	75	LEU
10	X	144	LEU
10	X	174	MET
11	Y	4	LEU
11	Y	35	ILE
11	Y	73	ARG
11	Y	106	ARG
12	Z	1	GLN
12	Z	23	LEU
12	Z	49	ASN
12	Z	150	LEU
12	Z	167	LYS
13	a	43	ILE

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Mol	Chain	Res	Type
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	187	ARG
14	b	9	LYS
14	b	119	VAL
15	g	4	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (117) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	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	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
3	C	233	GLN
4	D	91	HIS
4	D	100	ASN
4	D	106	GLN
4	D	180	HIS
4	D	217	GLN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	151	ASN
5	E	165	GLN
5	E	184	ASN
6	F	86	ASN
6	F	123	ASN
6	F	179	HIS
6	F	240	GLN

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Mol	Chain	Res	Type
7	G	30	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	175	ASN
8	H	30	ASN
8	H	66	HIS
8	H	86	HIS
8	H	165	ASN
8	H	172	ASN
8	H	189	ASN
9	I	37	ASN
9	I	44	HIS
9	I	63	ASN
10	J	37	GLN
10	J	55	GLN
10	J	63	ASN
10	J	78	GLN
10	J	146	HIS
11	K	9	GLN
11	K	85	ASN
11	K	143	ASN
11	K	176	ASN
11	K	208	ASN
12	L	3	ASN
12	L	70	ASN
12	L	79	HIS
12	L	158	ASN
13	M	194	ASN
13	M	213	GLN
14	N	38	HIS
1	O	30	GLN
1	O	218	ASN
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	147	GLN
3	Q	160	GLN

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Mol	Chain	Res	Type
3	Q	233	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	180	HIS
4	R	217	GLN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	151	ASN
5	S	165	GLN
5	S	184	ASN
6	T	86	ASN
6	T	123	ASN
6	T	240	GLN
7	U	30	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	175	ASN
8	V	66	HIS
8	V	86	HIS
9	W	37	ASN
9	W	63	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	85	ASN
11	Y	143	ASN
11	Y	176	ASN
11	Y	208	ASN
12	Z	70	ASN
12	Z	79	HIS
13	a	149	HIS
13	a	194	ASN

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Mol	Chain	Res	Type
13	a	213	GLN
14	b	141	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
15	DPP	g	2	15	4,5,6	1.19	1 (25%)	1,5,7	0.08	0
15	DPP	h	2	15	4,5,6	0.97	0	1,5,7	0.24	0
15	00E	h	1	15	9,9,10	0.49	0	10,10,12	2.11	5 (50%)
15	00E	g	1	15	9,9,10	0.73	0	10,10,12	2.69	3 (30%)

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
15	DPP	g	2	15	-	2/2/4/6	-
15	DPP	h	2	15	-	2/2/4/6	-
15	00E	h	1	15	-	2/2/11/12	0/1/1/1
15	00E	g	1	15	-	2/2/11/12	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	g	2	DPP	CB-CA	-2.12	1.49	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	g	1	00E	C-CA-NB	-6.77	99.86	112.80
15	h	1	00E	C-CA-NB	-3.18	106.73	112.80
15	h	1	00E	CA-NB-CD1	-3.08	107.28	110.49
15	g	1	00E	CA-NB-CD2	-3.08	107.28	110.49
15	h	1	00E	CA-NB-CD2	-2.67	107.71	110.49
15	h	1	00E	OZ-CE2-CD2	-2.50	106.39	111.77
15	g	1	00E	CD2-NB-CD1	2.49	114.21	108.84
15	h	1	00E	CD2-NB-CD1	2.28	113.75	108.84

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	g	1	00E	C-CA-NB-CD1
15	g	1	00E	C-CA-NB-CD2
15	h	1	00E	C-CA-NB-CD1
15	h	1	00E	C-CA-NB-CD2
15	g	2	DPP	N-CA-CB-NG
15	g	2	DPP	C-CA-CB-NG
15	h	2	DPP	C-CA-CB-NG
15	h	2	DPP	N-CA-CB-NG

There are no ring outliers.

4 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	g	2	DPP	1	0
15	h	2	DPP	1	0
15	h	1	00E	1	0
15	g	1	00E	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 12 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
18	MES	Y	301	-	12,12,12	2.26	1 (8%)	15,16,16	1.07	1 (6%)
18	MES	K	302	-	12,12,12	2.26	1 (8%)	15,16,16	0.98	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	MES	Y	301	-	-	0/6/14/14	0/1/1/1
18	MES	K	302	-	-	0/6/14/14	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	K	302	MES	C8-S	-7.52	1.67	1.77
18	Y	301	MES	C8-S	-7.50	1.67	1.77

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	Y	301	MES	O3S-S-C8	2.62	111.12	106.00
18	K	302	MES	O3S-S-C8	2.20	110.31	106.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
15	h	1
15	g	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	h	3:ACY	C	4:LEU	N	4.86
1	g	3:ACY	C	4:LEU	N	4.48

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%)	0.03	4 (1%) 70 62	36, 51, 91, 148	0
1	O	250/250 (100%)	0.05	6 (2%) 59 50	41, 60, 100, 144	0
2	B	244/258 (94%)	0.22	10 (4%) 41 33	40, 60, 105, 158	0
2	P	244/258 (94%)	0.16	9 (3%) 45 37	41, 62, 106, 159	0
3	C	240/254 (94%)	0.18	8 (3%) 49 40	36, 60, 122, 159	0
3	Q	240/254 (94%)	0.47	17 (7%) 22 17	47, 75, 152, 181	0
4	D	235/260 (90%)	0.07	5 (2%) 63 54	41, 62, 92, 142	0
4	R	235/260 (90%)	0.21	7 (2%) 52 43	47, 67, 106, 148	0
5	E	231/234 (98%)	0.16	2 (0%) 81 75	43, 65, 98, 138	0
5	S	231/234 (98%)	0.35	8 (3%) 47 38	43, 71, 119, 147	0
6	F	243/288 (84%)	0.08	8 (3%) 49 40	39, 59, 108, 133	0
6	T	243/288 (84%)	0.33	12 (4%) 35 27	40, 70, 125, 161	0
7	G	241/252 (95%)	0.04	3 (1%) 76 69	35, 53, 91, 142	0
7	U	241/252 (95%)	0.02	6 (2%) 58 48	36, 56, 91, 135	0
8	H	222/232 (95%)	0.18	1 (0%) 87 83	39, 52, 87, 116	0
8	V	222/232 (95%)	0.27	3 (1%) 73 65	41, 56, 88, 123	0
9	I	204/205 (99%)	-0.18	2 (0%) 79 73	34, 50, 78, 103	0
9	W	204/205 (99%)	-0.10	1 (0%) 87 83	33, 50, 79, 105	0
10	J	195/198 (98%)	-0.15	1 (0%) 87 83	34, 51, 79, 119	0
10	X	195/198 (98%)	-0.05	3 (1%) 72 64	35, 54, 81, 132	0
11	K	212/212 (100%)	-0.05	2 (0%) 81 75	36, 53, 83, 101	0
11	Y	212/212 (100%)	0.06	3 (1%) 73 65	41, 55, 90, 113	0
12	L	222/222 (100%)	-0.05	1 (0%) 87 83	32, 53, 85, 112	0
12	Z	222/222 (100%)	-0.03	2 (0%) 81 75	35, 52, 87, 110	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.09	3 (1%) 75 67	31, 51, 76, 92	0
13	a	233/246 (94%)	-0.08	2 (0%) 81 75	32, 51, 76, 89	0
14	N	196/196 (100%)	0.00	2 (1%) 79 73	34, 47, 75, 97	0
14	b	196/196 (100%)	-0.01	2 (1%) 79 73	36, 49, 78, 101	0
15	g	2/6 (33%)	0.40	0 100 100	47, 47, 47, 47	0
15	h	2/6 (33%)	0.43	0 100 100	51, 51, 51, 51	0
All	All	6340/6626 (95%)	0.08	133 (2%) 63 54	31, 56, 102, 181	0

All (133) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	X	1	MET	6.1
1	A	1	MET	5.3
3	Q	50	LEU	4.8
1	O	1	MET	4.5
10	J	1	MET	4.5
2	B	219	ALA	4.4
3	Q	51	LYS	4.4
2	P	218	GLY	4.3
13	a	69	ASP	3.9
3	C	203	THR	3.8
13	a	1	THR	3.8
7	U	2	GLY	3.7
2	P	52	THR	3.6
7	U	242	GLN	3.5
11	Y	212	GLY	3.5
6	F	202	ASP	3.5
9	W	130	ASP	3.4
3	Q	205	ALA	3.3
3	Q	189	CYS	3.3
4	D	240	ALA	3.2
6	T	178	HIS	3.2
6	T	243	ILE	3.2
3	Q	206	LYS	3.0
14	N	103	ASP	3.0
5	S	58	TYR	3.0
6	T	205	GLU	3.0
2	B	51	VAL	3.0
11	Y	118	ASP	3.0
5	S	52	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
3	Q	201	VAL	3.0
4	D	239	GLU	2.9
2	P	220	ASN	2.9
3	Q	238	LYS	2.8
2	P	93	HIS	2.8
3	Q	233	GLN	2.8
11	Y	147	ASP	2.8
4	D	117	GLU	2.8
3	Q	234	ILE	2.8
7	U	222	ASP	2.8
5	S	207	VAL	2.7
3	C	205	ALA	2.7
2	B	220	ASN	2.7
14	b	103	ASP	2.7
9	I	131	GLU	2.7
2	P	219	ALA	2.7
4	R	112	ALA	2.7
13	M	1	THR	2.7
5	S	173	ARG	2.7
6	T	241	LYS	2.7
6	T	2	THR	2.7
2	B	221	ASP	2.7
5	E	122	TYR	2.6
13	M	69	ASP	2.6
6	F	59	LYS	2.6
1	O	184	GLU	2.6
1	A	249	ALA	2.6
3	C	175	LYS	2.6
3	Q	240	GLU	2.6
13	M	47	ASP	2.6
3	C	206	LYS	2.5
4	R	157	TYR	2.5
5	E	233	ILE	2.5
2	P	60	THR	2.5
10	X	11	ASP	2.5
6	T	50	ILE	2.5
6	F	215	CYS	2.5
11	K	73	ARG	2.5
4	D	224	ASP	2.5
5	S	233	ILE	2.5
8	H	47	GLY	2.5
1	O	2	THR	2.5

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Mol	Chain	Res	Type	RSRZ
4	R	113	LEU	2.5
6	F	180	PRO	2.5
6	F	176	VAL	2.4
2	P	209	ARG	2.4
3	Q	236	GLN	2.4
7	U	40	ASP	2.4
11	K	212	GLY	2.4
4	R	230	GLU	2.4
3	Q	224	SER	2.4
3	Q	208	ILE	2.3
12	L	163	GLY	2.3
5	S	122	TYR	2.3
6	T	182	GLY	2.3
1	O	53	SER	2.3
3	C	46	ARG	2.3
12	Z	222	ASP	2.3
2	B	180	LYS	2.3
4	D	238	LYS	2.2
9	I	1	SER	2.2
1	O	249	ALA	2.2
1	A	4	ARG	2.2
7	G	5	ARG	2.2
2	B	52	THR	2.2
4	R	239	GLU	2.2
2	B	56	LEU	2.2
6	T	47	GLU	2.2
6	T	244	ASN	2.1
8	V	9	ASN	2.1
7	U	4	ASP	2.1
6	T	53	LYS	2.1
2	B	1	GLY	2.1
6	T	183	LEU	2.1
10	X	194	ASP	2.1
2	B	242	GLY	2.1
7	G	2	GLY	2.1
3	C	240	GLU	2.1
2	P	51	VAL	2.1
2	P	217	LYS	2.1
3	C	207	ASN	2.1
6	F	244	ASN	2.1
14	b	105	LYS	2.1
1	A	55	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
12	Z	26	ASP	2.1
3	C	53	GLN	2.1
3	Q	229	GLN	2.1
3	Q	207	ASN	2.1
2	B	218	GLY	2.1
14	N	47	GLY	2.1
1	O	4	ARG	2.1
6	F	2	THR	2.1
3	Q	237	GLU	2.1
5	S	209	ASN	2.0
8	V	191	LEU	2.0
4	R	242	GLU	2.0
6	T	28	GLU	2.0
6	F	241	LYS	2.0
3	Q	223	SER	2.0
8	V	216	SER	2.0
5	S	205	LEU	2.0
7	G	182	ILE	2.0
4	R	224	ASP	2.0
7	U	3	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	DPP	h	2	6/7	0.60	0.14	52,54,55,57	0
15	00E	h	1	9/10	0.62	0.19	56,59,60,64	0
15	00E	g	1	9/10	0.67	0.20	53,54,57,59	0
15	DPP	g	2	6/7	0.84	0.09	48,50,52,56	0

6.3 Carbohydrates [i](#)

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(Å ²)	Q<0.9
16	MG	V	301	1/1	0.73	0.13	67,67,67,67	0
17	CL	G	303	1/1	0.94	0.13	30,30,30,30	0
18	MES	K	302	12/12	0.95	0.12	40,43,52,58	0
18	MES	Y	301	12/12	0.95	0.12	40,42,55,55	0
16	MG	I	301	1/1	0.96	0.16	61,61,61,61	0
16	MG	J	201	1/1	0.96	0.13	30,30,30,30	0
17	CL	N	202	1/1	0.97	0.08	30,30,30,30	0
16	MG	I	302	1/1	0.97	0.09	42,42,42,42	0
16	MG	N	201	1/1	0.97	0.06	42,42,42,42	0
17	CL	U	301	1/1	0.98	0.10	44,44,44,44	0
16	MG	K	301	1/1	0.98	0.07	43,43,43,43	0
16	MG	Z	301	1/1	0.98	0.03	52,52,52,52	0
17	CL	G	302	1/1	0.99	0.04	42,42,42,42	0
16	MG	G	301	1/1	0.99	0.04	42,42,42,42	0

6.5 Other polymers

There are no such residues in this entry.