



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2024 – 12:13 PM EDT

PDB ID : 4X6Z
Title : Yeast 20S proteasome in complex with PR-VI modulator
Authors : Rostankowski, R.; Witkowska, J.; Borek, D.; Otwinowski, Z.; Jankowska, E.
Deposited on : 2014-12-09
Resolution : 2.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

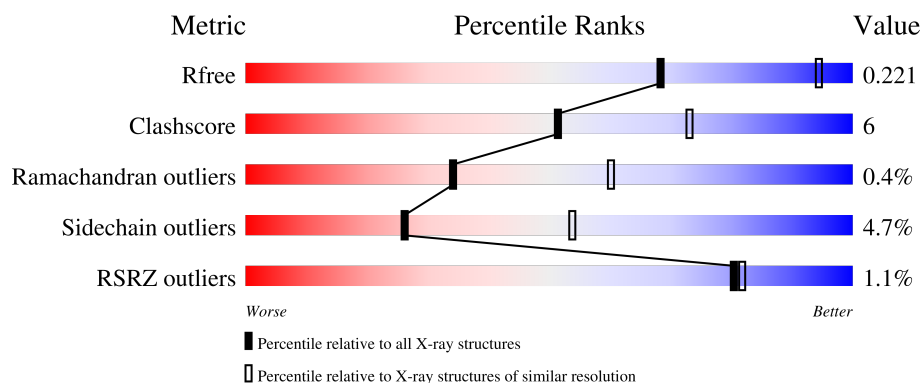
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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




























Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	1	241	
1	M	241	
2	2	266	
2	N	266	
3	A	252	

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Mol	Chain	Length	Quality of chain
3	O	252	
4	B	250	
4	P	250	
5	C	258	
5	Q	258	
6	D	254	
6	R	254	
7	E	260	
7	S	260	
8	F	234	
8	T	234	
9	G	288	
9	U	288	
10	H	215	
10	V	215	
11	I	261	
11	W	261	
12	J	205	
12	X	205	
13	K	198	
13	Y	198	
14	L	287	
14	Z	287	
15	a	13	
15	e	13	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
16	MPD	V	201	-	-	X	-
17	GOL	F	301	-	-	-	X
17	GOL	V	202	-	-	-	X
18	MG	S	303	-	-	-	X

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 50245 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 beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	222	Total	C	N	O	S	0	1	0
			1765	1120	306	335	4			
1	M	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 2 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	233	Total	C	N	O	S	0	1	0
			1833	1159	313	354	7			
2	N	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 3 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	242	Total	C	N	O	S	0	0	0
			1916	1218	321	369	8			
3	O	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	248	Total	C	N	O	S	0	0	0
			1898	1208	313	374	3			
4	P	249	Total	C	N	O	S	0	0	0
			1907	1214	314	376	3			

- Molecule 5 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
5	Q	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 6 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			
6	R	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			

- Molecule 7 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	7			
7	S	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	7			

- Molecule 8 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	232	Total	C	N	O	S	0	0	0
			1784	1120	311	349	4			
8	T	232	Total	C	N	O	S	0	0	0
			1784	1120	311	349	4			

- Molecule 9 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	G	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			
9	U	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			

- Molecule 10 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	196	Total	C	N	O	S	0	1	0
			1523	961	254	301	7			

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

- Molecule 11 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	221	Total	C	N	O	S	0	1	0
			1685	1065	292	321	7			
11	W	220	Total	C	N	O	S	0	2	0
			1683	1063	293	321	6			

- Molecule 12 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	J	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
12	X	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	196	Total	C	N	O	S	0	0	0
			1570	997	266	301	6			
13	Y	196	Total	C	N	O	S	0	0	0
			1570	997	266	301	6			

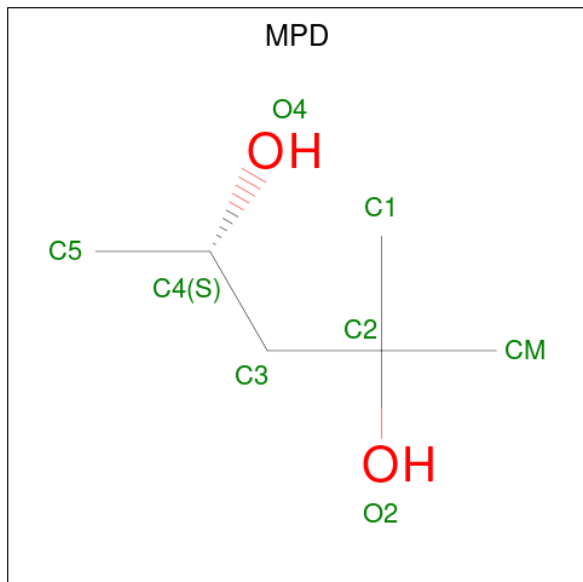
- Molecule 14 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			
14	Z	212	Total	C	N	O	S	0	1	0
			1650	1049	281	313	7			

- Molecule 15 is a protein called synthetic peptide (polymer).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	a	3	Total	C	N	O	0	0	0
			27	17	6	4			
15	e	3	Total	C	N	O	0	0	0
			27	17	6	4			

- Molecule 16 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	1	1	Total	C	O	0	0
			8	6	2		
16	2	1	Total	C	O	0	0
			8	6	2		
16	L	1	Total	C	O	0	0
			8	6	2		
16	M	1	Total	C	O	0	0
			8	6	2		
16	N	1	Total	C	O	0	0
			8	6	2		
16	T	1	Total	C	O	0	0
			8	6	2		
16	V	1	Total	C	O	0	0
			8	6	2		
16	X	1	Total	C	O	0	0
			8	6	2		
16	Z	1	Total	C	O	0	0
			8	6	2		

- Molecule 17 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
17	1	1	Total	C	O	0	0
			6	3	3		
17	1	1	Total	C	O	0	0
			6	3	3		
17	2	1	Total	C	O	0	0
			6	3	3		
17	2	1	Total	C	O	0	0
			6	3	3		
17	A	1	Total	C	O	0	0
			6	3	3		
17	A	1	Total	C	O	0	0
			6	3	3		
17	A	1	Total	C	O	0	0
			6	3	3		
17	A	1	Total	C	O	0	0
			6	3	3		
17	D	1	Total	C	O	0	0
			6	3	3		
17	E	1	Total	C	O	0	0
			6	3	3		
17	F	1	Total	C	O	0	0
			6	3	3		
17	F	1	Total	C	O	0	0
			6	3	3		
17	F	1	Total	C	O	0	0
			6	3	3		
17	F	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
17	G	1	Total	C	O	0	0
			6	3	3		
17	G	1	Total	C	O	0	0
			6	3	3		
17	H	1	Total	C	O	0	0
			6	3	3		
17	I	1	Total	C	O	0	0
			6	3	3		
17	I	1	Total	C	O	0	0
			6	3	3		
17	J	1	Total	C	O	0	0
			6	3	3		
17	K	1	Total	C	O	0	0
			6	3	3		
17	L	1	Total	C	O	0	0
			6	3	3		
17	L	1	Total	C	O	0	0
			6	3	3		
17	M	1	Total	C	O	0	0
			6	3	3		
17	M	1	Total	C	O	0	0
			6	3	3		
17	N	1	Total	C	O	0	0
			6	3	3		
17	N	1	Total	C	O	0	0
			6	3	3		
17	O	1	Total	C	O	0	0
			6	3	3		
17	O	1	Total	C	O	0	0
			6	3	3		
17	S	1	Total	C	O	0	0
			6	3	3		
17	T	1	Total	C	O	0	0
			6	3	3		
17	V	1	Total	C	O	0	0
			6	3	3		
17	V	1	Total	C	O	0	0
			6	3	3		
17	W	1	Total	C	O	0	0
			6	3	3		
17	X	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
17	Z	1	Total	C	O	0	0
			6	3	3		
17	Z	1	Total	C	O	0	0
			6	3	3		
17	Z	1	Total	C	O	0	0
			6	3	3		

- Molecule 18 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	1	1	Total	Mg	0	0
			1	1		
18	2	5	Total	Mg	0	0
			5	5		
18	B	1	Total	Mg	0	0
			1	1		
18	C	2	Total	Mg	0	0
			2	2		
18	D	1	Total	Mg	0	0
			1	1		
18	F	1	Total	Mg	0	0
			1	1		
18	H	4	Total	Mg	0	0
			4	4		
18	J	6	Total	Mg	0	0
			6	6		
18	K	2	Total	Mg	0	0
			2	2		
18	L	2	Total	Mg	0	0
			2	2		
18	M	4	Total	Mg	0	0
			4	4		
18	N	4	Total	Mg	0	0
			4	4		
18	O	1	Total	Mg	0	0
			1	1		
18	P	1	Total	Mg	0	0
			1	1		
18	Q	2	Total	Mg	0	0
			2	2		
18	R	3	Total	Mg	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	S	2	Total 2	Mg 2	0	0
18	T	2	Total 2	Mg 2	0	0
18	V	4	Total 4	Mg 4	0	0
18	W	1	Total 1	Mg 1	0	0
18	X	3	Total 3	Mg 3	0	0
18	Y	2	Total 2	Mg 2	0	0
18	Z	2	Total 2	Mg 2	0	0

- Molecule 19 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	1	14	Total 14	O 14	0	0
19	2	20	Total 20	O 20	0	0
19	A	13	Total 13	O 13	0	0
19	B	16	Total 16	O 16	0	0
19	C	5	Total 5	O 5	0	0
19	D	10	Total 10	O 10	0	0
19	E	11	Total 11	O 11	0	0
19	F	9	Total 9	O 9	0	0
19	G	14	Total 14	O 14	0	0
19	H	17	Total 17	O 17	0	0
19	I	15	Total 15	O 15	0	0
19	J	13	Total 13	O 13	0	0

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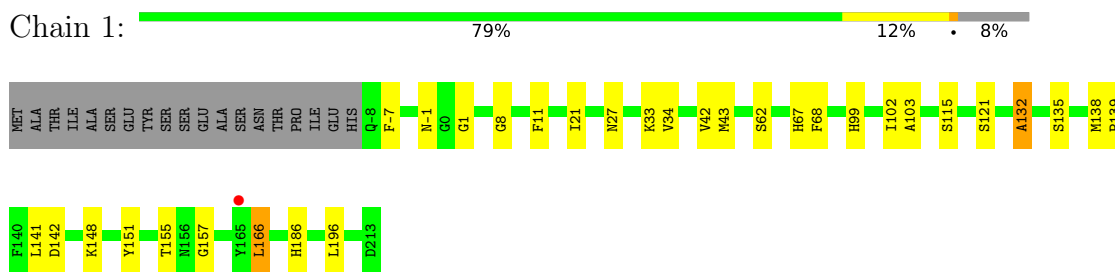
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	K	11	Total 11	O 11	0	0
19	L	14	Total 14	O 14	0	0
19	M	9	Total 9	O 9	0	0
19	N	15	Total 15	O 15	0	0
19	O	14	Total 14	O 14	0	0
19	P	13	Total 13	O 13	0	0
19	Q	13	Total 13	O 13	0	0
19	R	11	Total 11	O 11	0	0
19	S	10	Total 10	O 10	0	0
19	T	8	Total 8	O 8	0	0
19	U	17	Total 17	O 17	0	0
19	V	17	Total 17	O 17	0	0
19	W	12	Total 12	O 12	0	0
19	X	9	Total 9	O 9	0	0
19	Y	14	Total 14	O 14	0	0
19	Z	15	Total 15	O 15	0	0

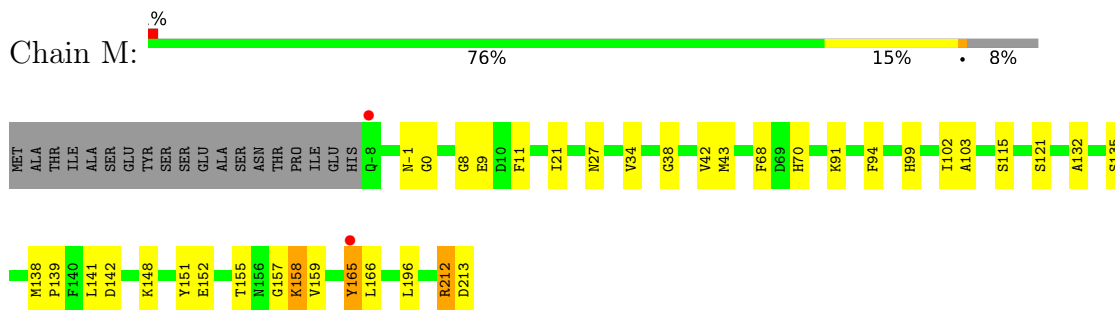
3 Residue-property plots [i](#)

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.

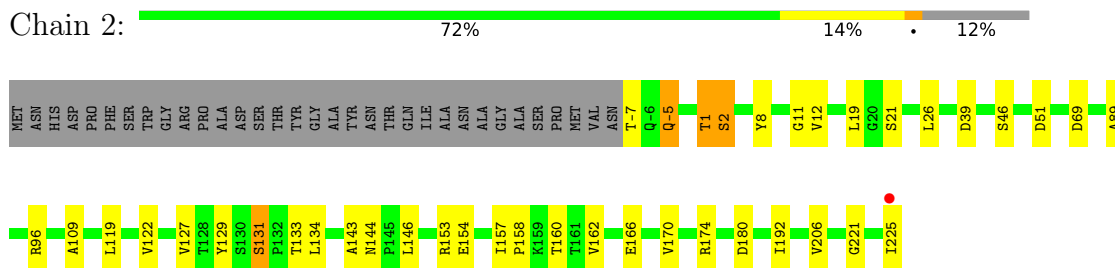
- Molecule 1: Proteasome subunit beta type-6



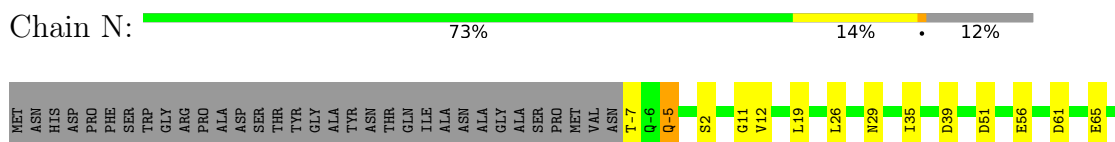
- Molecule 1: Proteasome subunit beta type-6



- Molecule 2: Proteasome subunit beta type-7

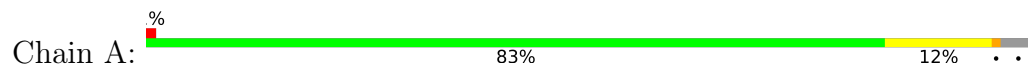


- Molecule 2: Proteasome subunit beta type-7

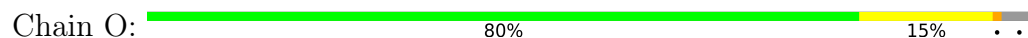




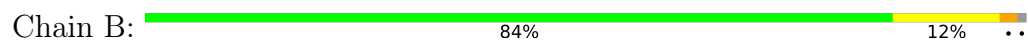
• Molecule 3: Proteasome subunit alpha type-1



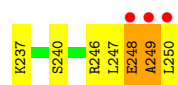
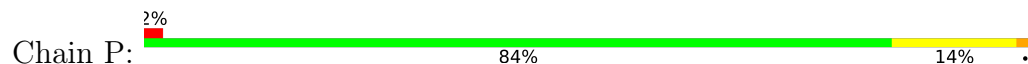
• Molecule 3: Proteasome subunit alpha type-1



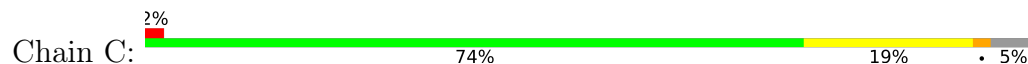
• Molecule 4: Proteasome subunit alpha type-2

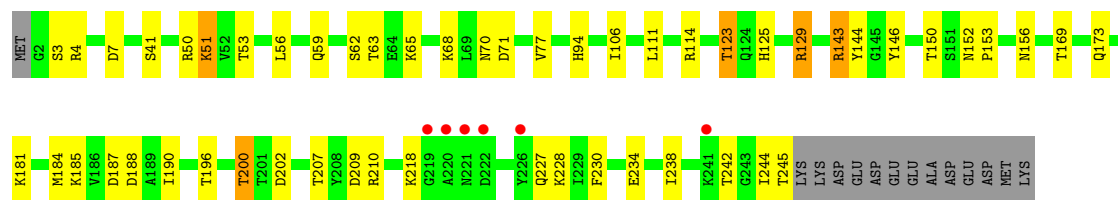


• Molecule 4: Proteasome subunit alpha type-2

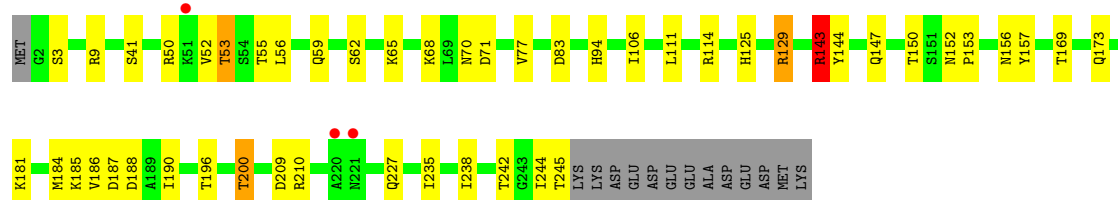
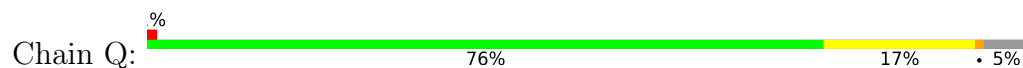


• Molecule 5: Proteasome subunit alpha type-3

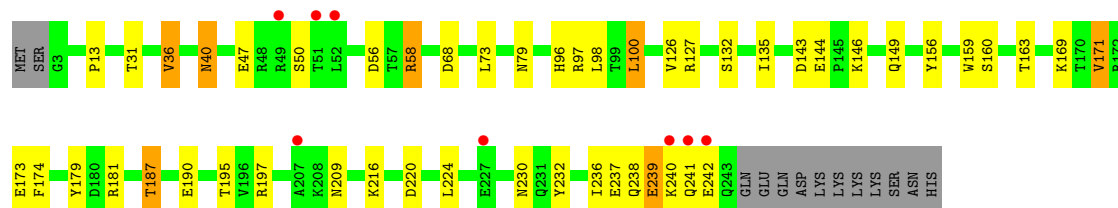
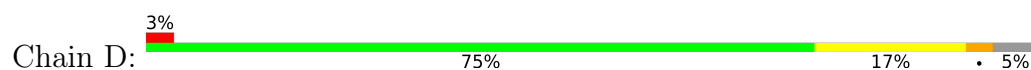




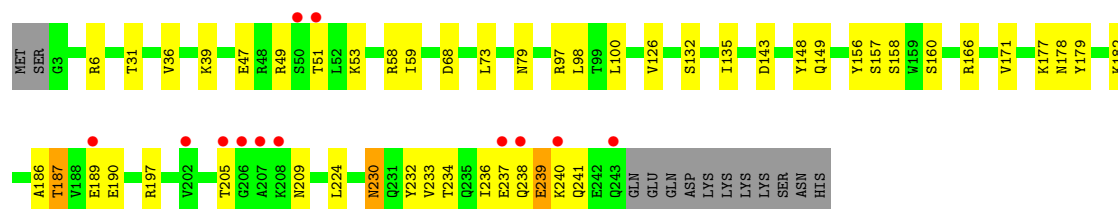
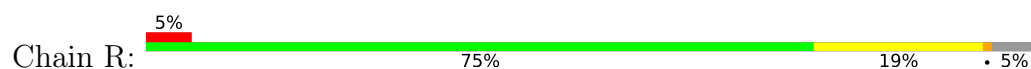
• Molecule 5: Proteasome subunit alpha type-3



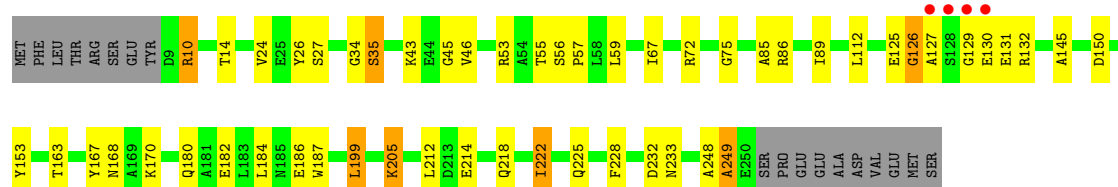
• Molecule 6: Proteasome subunit alpha type-4



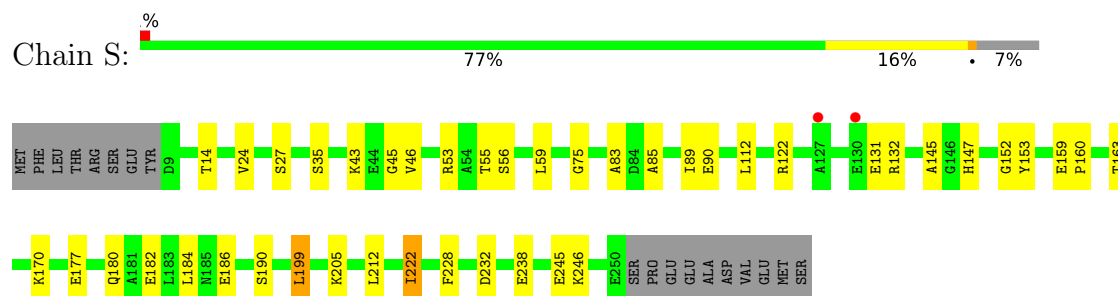
• Molecule 6: Proteasome subunit alpha type-4



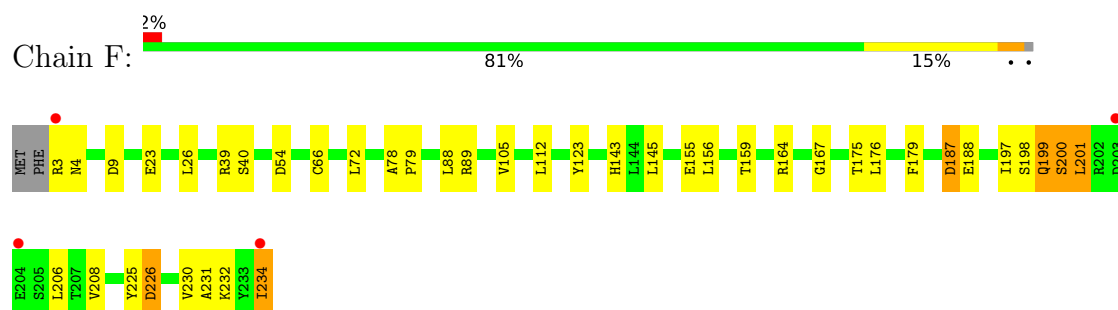
• Molecule 7: Proteasome subunit alpha type-5



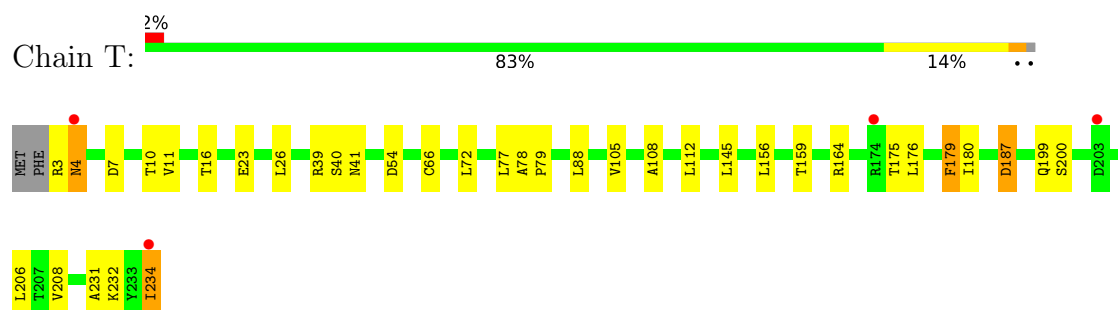
- Molecule 7: Proteasome subunit alpha type-5



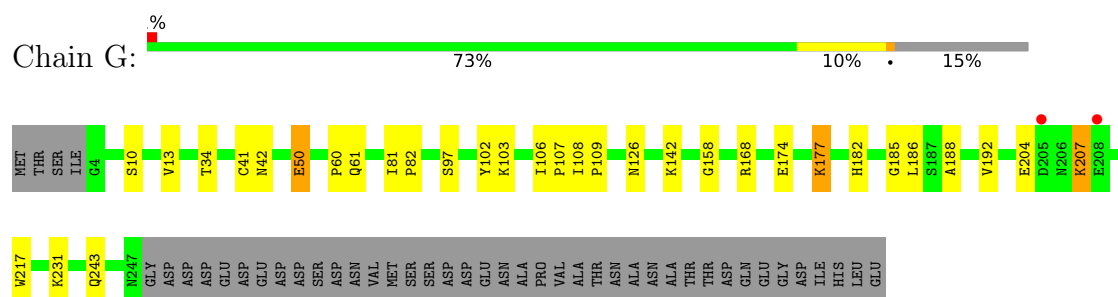
- Molecule 8: Proteasome subunit alpha type-6



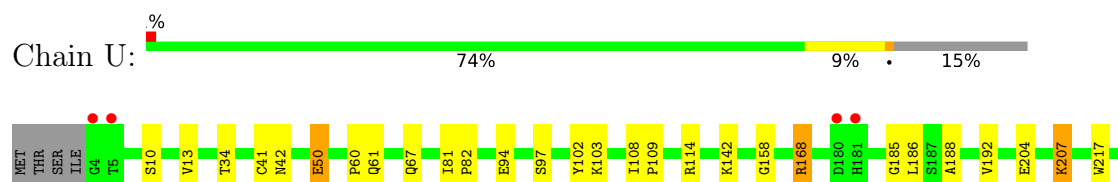
- Molecule 8: Proteasome subunit alpha type-6



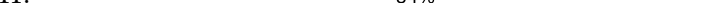
- Molecule 9: Probable proteasome subunit alpha type-7

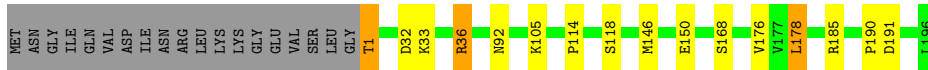


- Molecule 9: Probable proteasome subunit alpha type-7

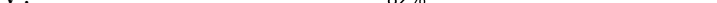


- Molecule 10: Proteasome subunit beta type-1

Chain H:  84% 6% • 9%



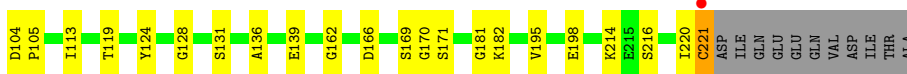
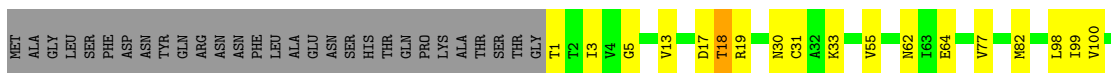
- Molecule 10: Proteasome subunit beta type-1

Chain V:  82% 8% 9%



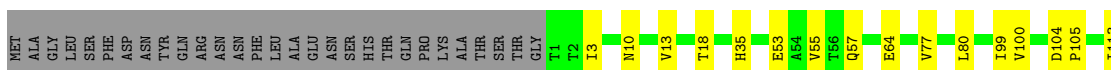
- Molecule 11: Proteasome subunit beta type-2

Chain I:  69% 15% • 15%



- Molecule 11: Proteasome subunit beta type-2

Chain W:  71% 13% 16%



- Molecule 12: Proteasome subunit beta type-3

Chain J: 89% 9%

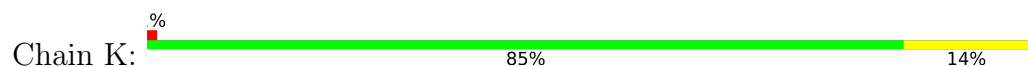


- Molecule 12: Proteasome subunit beta type-3

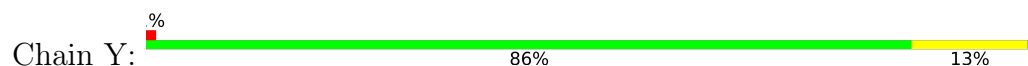
Chain X: 87% 11%



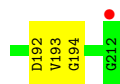
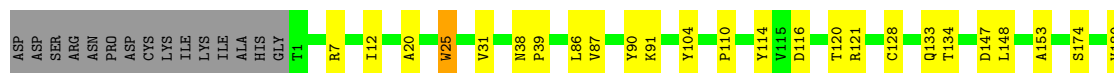
- Molecule 13: Proteasome subunit beta type-4



- Molecule 13: Proteasome subunit beta type-4



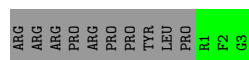
- Molecule 14: Proteasome subunit beta type-5



- Molecule 14: Proteasome subunit beta type-5



- Molecule 15: synthetic peptide (polymer)



- Molecule 15: synthetic peptide (polymer)

Chain e:

23%

77%

ARG	ARG	ARG	PRO	ARG	PRO	PRO	TYR	LEU	PRO	R11	F12	G13
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	133.35Å 300.79Å 144.58Å 90.00° 112.11° 90.00°	Depositor
Resolution (Å)	49.46 – 2.70 49.46 – 2.70	Depositor EDS
% Data completeness (in resolution range)	68.3 (49.46-2.70) 68.4 (49.46-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.19	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.177 , 0.222 0.181 , 0.221	Depositor DCC
R_{free} test set	9928 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	50245	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.31% 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: MPD, MG, GOL

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	1	0.72	0/1806	0.83	0/2434
1	M	0.74	0/1795	0.86	2/2420 (0.1%)
2	2	0.78	0/1864	0.92	0/2526
2	N	0.78	0/1855	0.91	2/2514 (0.1%)
3	A	0.79	1/1954 (0.1%)	0.87	0/2645
3	O	0.77	0/1945	0.87	0/2634
4	B	0.74	0/1935	0.85	1/2621 (0.0%)
4	P	0.68	0/1944	0.83	0/2632
5	C	0.75	0/1934	0.92	2/2618 (0.1%)
5	Q	0.74	0/1934	0.91	1/2618 (0.0%)
6	D	0.66	0/1919	0.83	1/2598 (0.0%)
6	R	0.64	0/1919	0.81	0/2598
7	E	0.70	0/1886	0.88	1/2541 (0.0%)
7	S	0.65	0/1886	0.86	0/2541
8	F	0.65	0/1811	0.80	0/2447
8	T	0.64	0/1811	0.83	1/2447 (0.0%)
9	G	0.70	0/1936	0.81	0/2614
9	U	0.70	0/1936	0.81	0/2614
10	H	0.80	0/1552	0.86	0/2101
10	V	0.81	0/1541	0.87	0/2087
11	I	0.74	0/1720	0.87	0/2333
11	W	0.74	0/1721	0.86	1/2334 (0.0%)
12	J	0.77	0/1611	0.90	4/2174 (0.2%)
12	X	0.78	1/1611 (0.1%)	0.89	4/2174 (0.2%)
13	K	0.76	0/1598	0.88	0/2154
13	Y	0.74	0/1598	0.87	0/2154
14	L	0.77	1/1681 (0.1%)	0.83	0/2274
14	Z	0.77	0/1690	0.86	0/2286
15	a	0.65	0/27	1.31	0/32
15	e	0.85	0/27	1.30	0/32
All	All	0.73	3/50447 (0.0%)	0.86	20/68197 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
11	I	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	X	196	ASP	CB-CG	5.80	1.64	1.51
14	L	25	TRP	CB-CG	-5.67	1.40	1.50
3	A	128	TYR	C-O	5.00	1.32	1.23

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	X	19	ARG	NE-CZ-NH2	-7.73	116.44	120.30
12	J	19	ARG	NE-CZ-NH1	7.57	124.08	120.30
12	X	19	ARG	NE-CZ-NH1	7.16	123.88	120.30
12	J	19	ARG	NE-CZ-NH2	-6.68	116.96	120.30
5	Q	143	ARG	NE-CZ-NH1	6.01	123.31	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	I	181	GLY	Peptide

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	1	1765	0	1724	18	0
1	M	1757	0	1711	23	0
2	2	1833	0	1837	29	0
2	N	1824	0	1832	19	0
3	A	1916	0	1905	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	O	1907	0	1901	18	0
4	B	1898	0	1906	23	0
4	P	1907	0	1917	24	0
5	C	1904	0	1901	41	0
5	Q	1904	0	1901	37	0
6	D	1890	0	1900	33	0
6	R	1890	0	1900	35	0
7	E	1861	0	1836	35	0
7	S	1861	0	1836	24	0
8	F	1784	0	1788	28	0
8	T	1784	0	1788	22	0
9	G	1896	0	1886	23	0
9	U	1896	0	1886	18	0
10	H	1523	0	1493	9	0
10	V	1512	0	1481	21	0
11	I	1685	0	1693	19	0
11	W	1683	0	1692	18	0
12	J	1581	0	1574	8	0
12	X	1581	0	1574	10	0
13	K	1570	0	1577	10	0
13	Y	1570	0	1577	10	0
14	L	1644	0	1595	15	0
14	Z	1650	0	1603	15	0
15	a	27	0	27	0	0
15	e	27	0	24	0	0
16	1	8	0	14	0	0
16	2	8	0	14	1	0
16	L	8	0	14	0	0
16	M	8	0	14	0	0
16	N	8	0	14	1	0
16	T	8	0	14	0	0
16	V	8	0	14	13	0
16	X	8	0	14	3	0
16	Z	8	0	14	2	0
17	1	12	0	16	0	0
17	2	12	0	16	0	0
17	A	24	0	32	0	0
17	D	6	0	8	2	0
17	E	6	0	8	0	0
17	F	24	0	32	0	0
17	G	12	0	16	0	0
17	H	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	I	12	0	16	0	0
17	J	6	0	8	0	0
17	K	6	0	8	0	0
17	L	12	0	16	0	0
17	M	12	0	16	0	0
17	N	12	0	16	0	0
17	O	12	0	16	0	0
17	S	6	0	8	0	0
17	T	6	0	8	0	0
17	V	12	0	16	0	0
17	W	6	0	8	0	0
17	X	6	0	8	0	0
17	Z	18	0	24	0	0
18	1	1	0	0	0	0
18	2	5	0	0	0	0
18	B	1	0	0	0	0
18	C	2	0	0	0	0
18	D	1	0	0	0	0
18	F	1	0	0	0	0
18	H	4	0	0	0	0
18	J	6	0	0	0	0
18	K	2	0	0	0	0
18	L	2	0	0	0	0
18	M	4	0	0	0	0
18	N	4	0	0	0	0
18	O	1	0	0	0	0
18	P	1	0	0	0	0
18	Q	2	0	0	0	0
18	R	3	0	0	0	0
18	S	2	0	0	0	0
18	T	2	0	0	0	0
18	V	4	0	0	0	0
18	W	1	0	0	0	0
18	X	3	0	0	0	0
18	Y	2	0	0	0	0
18	Z	2	0	0	0	0
19	1	14	0	0	1	0
19	2	20	0	0	1	0
19	A	13	0	0	0	0
19	B	16	0	0	1	0
19	C	5	0	0	0	0
19	D	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	E	11	0	0	1	0
19	F	9	0	0	0	0
19	G	14	0	0	1	0
19	H	17	0	0	0	0
19	I	15	0	0	0	0
19	J	13	0	0	0	0
19	K	11	0	0	0	0
19	L	14	0	0	0	0
19	M	9	0	0	1	0
19	N	15	0	0	0	0
19	O	14	0	0	0	0
19	P	13	0	0	1	0
19	Q	13	0	0	0	0
19	R	11	0	0	0	0
19	S	10	0	0	1	0
19	T	8	0	0	0	0
19	U	17	0	0	1	0
19	V	17	0	0	0	0
19	W	12	0	0	2	0
19	X	9	0	0	0	0
19	Y	14	0	0	0	0
19	Z	15	0	0	0	0
All	All	50245	0	49695	555	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 6.

The worst 5 of 555 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)
6:R:197:ARG:CG	6:R:236:ILE:HD11	1.80	1.11
6:D:232:TYR:O	6:D:236:ILE:HG12	1.54	1.06
6:D:238:GLN:OE1	6:D:238:GLN:N	1.97	0.97
6:R:197:ARG:HG2	6:R:236:ILE:HD11	1.45	0.93
6:R:197:ARG:HG3	6:R:236:ILE:CD1	2.01	0.91

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	1	221/241 (92%)	205 (93%)	15 (7%)	1 (0%)	29	54
1	M	220/241 (91%)	202 (92%)	17 (8%)	1 (0%)	29	54
2	2	232/266 (87%)	219 (94%)	12 (5%)	1 (0%)	34	60
2	N	231/266 (87%)	217 (94%)	14 (6%)	0	100	100
3	A	240/252 (95%)	235 (98%)	4 (2%)	1 (0%)	34	60
3	O	239/252 (95%)	235 (98%)	3 (1%)	1 (0%)	34	60
4	B	246/250 (98%)	231 (94%)	14 (6%)	1 (0%)	34	60
4	P	247/250 (99%)	233 (94%)	13 (5%)	1 (0%)	34	60
5	C	242/258 (94%)	228 (94%)	14 (6%)	0	100	100
5	Q	242/258 (94%)	230 (95%)	12 (5%)	0	100	100
6	D	239/254 (94%)	229 (96%)	9 (4%)	1 (0%)	34	60
6	R	239/254 (94%)	226 (95%)	12 (5%)	1 (0%)	34	60
7	E	240/260 (92%)	228 (95%)	9 (4%)	3 (1%)	12	30
7	S	240/260 (92%)	227 (95%)	11 (5%)	2 (1%)	19	43
8	F	230/234 (98%)	211 (92%)	16 (7%)	3 (1%)	12	30
8	T	230/234 (98%)	214 (93%)	15 (6%)	1 (0%)	34	60
9	G	242/288 (84%)	228 (94%)	13 (5%)	1 (0%)	34	60
9	U	242/288 (84%)	233 (96%)	9 (4%)	0	100	100
10	H	195/215 (91%)	187 (96%)	8 (4%)	0	100	100
10	V	194/215 (90%)	186 (96%)	8 (4%)	0	100	100
11	I	220/261 (84%)	211 (96%)	8 (4%)	1 (0%)	29	54
11	W	220/261 (84%)	214 (97%)	6 (3%)	0	100	100
12	J	202/205 (98%)	186 (92%)	14 (7%)	2 (1%)	15	37
12	X	202/205 (98%)	189 (94%)	11 (5%)	2 (1%)	15	37
13	K	194/198 (98%)	188 (97%)	5 (3%)	1 (0%)	29	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	Y	194/198 (98%)	186 (96%)	7 (4%)	1 (0%)	29	54
14	L	210/287 (73%)	204 (97%)	6 (3%)	0	100	100
14	Z	211/287 (74%)	202 (96%)	9 (4%)	0	100	100
15	a	1/13 (8%)	1 (100%)	0	0	100	100
15	e	1/13 (8%)	0	1 (100%)	0	100	100
All	All	6306/6964 (91%)	5985 (95%)	295 (5%)	26 (0%)	34	60

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	239	GLU
7	E	35	SER
7	E	249	ALA
4	P	249	ALA
6	R	239	GLU

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	1	186/201 (92%)	180 (97%)	6 (3%)	39	68
1	M	185/201 (92%)	178 (96%)	7 (4%)	33	62
2	2	200/224 (89%)	193 (96%)	7 (4%)	36	65
2	N	199/224 (89%)	191 (96%)	8 (4%)	31	60
3	A	207/210 (99%)	197 (95%)	10 (5%)	25	53
3	O	206/210 (98%)	196 (95%)	10 (5%)	25	52
4	B	207/209 (99%)	193 (93%)	14 (7%)	16	36
4	P	208/209 (100%)	196 (94%)	12 (6%)	20	43
5	C	203/216 (94%)	192 (95%)	11 (5%)	22	47
5	Q	203/216 (94%)	196 (97%)	7 (3%)	37	66
6	D	213/226 (94%)	203 (95%)	10 (5%)	26	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	R	213/226 (94%)	199 (93%)	14 (7%)	16	38
7	E	198/215 (92%)	185 (93%)	13 (7%)	16	38
7	S	198/215 (92%)	184 (93%)	14 (7%)	14	34
8	F	191/193 (99%)	181 (95%)	10 (5%)	23	49
8	T	191/193 (99%)	180 (94%)	11 (6%)	20	43
9	G	201/239 (84%)	194 (96%)	7 (4%)	36	65
9	U	201/239 (84%)	194 (96%)	7 (4%)	36	65
10	H	163/178 (92%)	154 (94%)	9 (6%)	21	46
10	V	162/178 (91%)	155 (96%)	7 (4%)	29	57
11	I	181/214 (85%)	169 (93%)	12 (7%)	16	38
11	W	181/214 (85%)	171 (94%)	10 (6%)	21	46
12	J	172/173 (99%)	168 (98%)	4 (2%)	50	78
12	X	172/173 (99%)	165 (96%)	7 (4%)	30	59
13	K	174/175 (99%)	166 (95%)	8 (5%)	27	54
13	Y	174/175 (99%)	166 (95%)	8 (5%)	27	54
14	L	169/235 (72%)	165 (98%)	4 (2%)	49	77
14	Z	170/235 (72%)	164 (96%)	6 (4%)	36	65
15	a	2/12 (17%)	2 (100%)	0	100	100
15	e	2/12 (17%)	2 (100%)	0	100	100
All	All	5332/5840 (91%)	5079 (95%)	253 (5%)	26	54

5 of 253 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	K	90	SER
10	V	190	PRO
3	O	134	MET
10	V	168	SER
12	X	185	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
3	O	209	HIS

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Mol	Chain	Res	Type
9	U	206	ASN
7	S	147	HIS
8	T	93	ASN
11	W	35	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 103 ligands modelled in this entry, 56 are monoatomic - leaving 47 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	$\# Z > 2$
16	MPD	Z	301	-	7,7,7	0.50	0	9,10,10	0.89	0
16	MPD	2	301	-	7,7,7	0.58	0	9,10,10	0.92	1 (11%)
17	GOL	O	302	-	5,5,5	0.29	0	5,5,5	0.59	0
17	GOL	T	302	-	5,5,5	0.64	0	5,5,5	0.87	0
17	GOL	J	202	-	5,5,5	0.60	0	5,5,5	0.41	0
17	GOL	M	303	-	5,5,5	0.54	0	5,5,5	0.34	0
17	GOL	Z	302	-	5,5,5	0.70	0	5,5,5	1.08	0
16	MPD	N	301	-	7,7,7	0.61	0	9,10,10	0.35	0
17	GOL	L	302	-	5,5,5	0.37	0	5,5,5	0.43	0
16	MPD	M	301	-	7,7,7	0.50	0	9,10,10	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
17	GOL	G	302	-	5,5,5	0.33	0	5,5,5	0.49	0
17	GOL	F	302	-	5,5,5	0.30	0	5,5,5	0.41	0
17	GOL	S	301	-	5,5,5	0.56	0	5,5,5	0.32	0
17	GOL	W	301	-	5,5,5	0.55	0	5,5,5	0.87	0
17	GOL	K	201	-	5,5,5	0.46	0	5,5,5	0.87	0
17	GOL	G	301	-	5,5,5	0.34	0	5,5,5	0.68	0
17	GOL	2	303	-	5,5,5	0.28	0	5,5,5	0.93	0
17	GOL	M	302	-	5,5,5	0.53	0	5,5,5	1.01	0
17	GOL	Z	303	-	5,5,5	0.33	0	5,5,5	0.87	0
17	GOL	Z	304	-	5,5,5	0.45	0	5,5,5	0.58	0
16	MPD	V	201	-	7,7,7	0.82	0	9,10,10	1.69	1 (11%)
17	GOL	E	301	-	5,5,5	0.39	0	5,5,5	1.13	0
17	GOL	F	303	-	5,5,5	0.30	0	5,5,5	0.52	0
17	GOL	V	203	-	5,5,5	1.21	0	5,5,5	1.50	1 (20%)
17	GOL	F	301	-	5,5,5	0.59	0	5,5,5	0.43	0
16	MPD	1	301	-	7,7,7	0.81	0	9,10,10	0.93	1 (11%)
17	GOL	A	302	-	5,5,5	0.24	0	5,5,5	0.44	0
17	GOL	I	302	-	5,5,5	0.46	0	5,5,5	0.64	0
17	GOL	V	202	-	5,5,5	0.49	0	5,5,5	0.32	0
17	GOL	O	301	-	5,5,5	0.71	0	5,5,5	0.67	0
17	GOL	N	302	-	5,5,5	0.56	0	5,5,5	0.61	0
17	GOL	2	302	-	5,5,5	0.55	0	5,5,5	0.29	0
17	GOL	X	202	-	5,5,5	0.40	0	5,5,5	0.72	0
17	GOL	D	301	-	5,5,5	0.89	0	5,5,5	1.19	0
17	GOL	H	201	-	5,5,5	0.15	0	5,5,5	0.59	0
16	MPD	X	201	-	7,7,7	0.60	0	9,10,10	0.65	0
16	MPD	L	301	-	7,7,7	0.71	0	9,10,10	0.66	0
17	GOL	A	301	-	5,5,5	0.60	0	5,5,5	0.54	0
17	GOL	A	303	-	5,5,5	0.74	0	5,5,5	1.22	0
17	GOL	F	304	-	5,5,5	0.39	0	5,5,5	0.62	0
16	MPD	T	301	-	7,7,7	1.08	1 (14%)	9,10,10	0.95	1 (11%)
17	GOL	1	302	-	5,5,5	0.45	0	5,5,5	0.27	0
17	GOL	1	303	-	5,5,5	0.55	0	5,5,5	0.42	0
17	GOL	I	301	-	5,5,5	0.81	0	5,5,5	0.72	0
17	GOL	L	303	-	5,5,5	0.40	0	5,5,5	0.36	0
17	GOL	N	303	-	5,5,5	0.23	0	5,5,5	0.68	0
17	GOL	A	304	-	5,5,5	0.42	0	5,5,5	0.77	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	MPD	Z	301	-	-	3/5/5/5	-
16	MPD	2	301	-	-	2/5/5/5	-
17	GOL	O	302	-	-	2/4/4/4	-
17	GOL	T	302	-	-	4/4/4/4	-
17	GOL	J	202	-	-	2/4/4/4	-
17	GOL	M	303	-	-	2/4/4/4	-
17	GOL	Z	302	-	-	1/4/4/4	-
16	MPD	N	301	-	-	2/5/5/5	-
17	GOL	L	302	-	-	2/4/4/4	-
16	MPD	M	301	-	-	3/5/5/5	-
17	GOL	G	302	-	-	4/4/4/4	-
17	GOL	F	302	-	-	0/4/4/4	-
17	GOL	S	301	-	-	2/4/4/4	-
17	GOL	W	301	-	-	3/4/4/4	-
17	GOL	K	201	-	-	4/4/4/4	-
17	GOL	G	301	-	-	1/4/4/4	-
17	GOL	2	303	-	-	0/4/4/4	-
17	GOL	M	302	-	-	2/4/4/4	-
17	GOL	Z	303	-	-	2/4/4/4	-
17	GOL	Z	304	-	-	2/4/4/4	-
16	MPD	V	201	-	-	2/5/5/5	-
17	GOL	E	301	-	-	2/4/4/4	-
17	GOL	F	303	-	-	2/4/4/4	-
17	GOL	V	203	-	-	4/4/4/4	-
17	GOL	F	301	-	-	4/4/4/4	-
16	MPD	1	301	-	-	1/5/5/5	-
17	GOL	A	302	-	-	0/4/4/4	-
17	GOL	I	302	-	-	2/4/4/4	-
17	GOL	V	202	-	-	2/4/4/4	-
17	GOL	O	301	-	-	0/4/4/4	-
17	GOL	N	302	-	-	2/4/4/4	-
17	GOL	2	302	-	-	4/4/4/4	-
17	GOL	X	202	-	-	2/4/4/4	-
17	GOL	D	301	-	-	2/4/4/4	-
17	GOL	H	201	-	-	1/4/4/4	-
16	MPD	X	201	-	-	0/5/5/5	-
16	MPD	L	301	-	-	2/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	GOL	A	301	-	-	2/4/4/4	-
17	GOL	A	303	-	-	4/4/4/4	-
17	GOL	F	304	-	-	0/4/4/4	-
16	MPD	T	301	-	-	2/5/5/5	-
17	GOL	1	302	-	-	0/4/4/4	-
17	GOL	1	303	-	-	4/4/4/4	-
17	GOL	I	301	-	-	3/4/4/4	-
17	GOL	L	303	-	-	2/4/4/4	-
17	GOL	N	303	-	-	2/4/4/4	-
17	GOL	A	304	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	T	301	MPD	C3-C2	2.30	1.59	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	V	201	MPD	O2-C2-C1	-4.06	95.05	108.08
16	1	301	MPD	CM-C2-C1	-2.17	106.04	110.57
17	V	203	GOL	O1-C1-C2	2.13	120.42	110.20
16	2	301	MPD	O2-C2-CM	-2.12	101.26	108.08
16	T	301	MPD	CM-C2-C1	-2.07	106.26	110.57

There are no chirality outliers.

5 of 94 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	M	301	MPD	C2-C3-C4-O4
16	Z	301	MPD	C2-C3-C4-O4
17	1	303	GOL	C1-C2-C3-O3
17	2	302	GOL	C1-C2-C3-O3
17	A	303	GOL	O1-C1-C2-C3

There are no ring outliers.

6 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	Z	301	MPD	2	0
16	2	301	MPD	1	0
16	N	301	MPD	1	0
16	V	201	MPD	13	0
17	D	301	GOL	2	0
16	X	201	MPD	3	0

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	1	222/241 (92%)	-0.53	1 (0%) 91 92	22, 40, 65, 98	0
1	M	222/241 (92%)	-0.57	2 (0%) 84 85	22, 39, 64, 98	0
2	2	233/266 (87%)	-0.74	1 (0%) 92 93	19, 33, 52, 86	0
2	N	233/266 (87%)	-0.68	1 (0%) 92 93	19, 34, 55, 90	0
3	A	242/252 (96%)	-0.62	2 (0%) 86 87	19, 36, 65, 126	0
3	O	241/252 (95%)	-0.58	0 100 100	22, 39, 70, 91	0
4	B	248/250 (99%)	-0.55	1 (0%) 92 93	20, 37, 67, 104	0
4	P	249/250 (99%)	-0.40	4 (1%) 72 74	23, 44, 77, 110	0
5	C	244/258 (94%)	-0.35	6 (2%) 57 59	23, 44, 86, 129	0
5	Q	244/258 (94%)	-0.35	3 (1%) 79 80	26, 46, 88, 141	0
6	D	241/254 (94%)	-0.28	8 (3%) 46 46	24, 47, 103, 133	0
6	R	241/254 (94%)	-0.13	12 (4%) 28 27	30, 53, 108, 125	0
7	E	242/260 (93%)	-0.35	4 (1%) 70 72	26, 47, 86, 160	0
7	S	242/260 (93%)	-0.43	2 (0%) 86 87	27, 51, 81, 119	0
8	F	232/234 (99%)	-0.35	4 (1%) 70 72	29, 49, 76, 101	0
8	T	232/234 (99%)	-0.25	4 (1%) 70 72	29, 52, 79, 105	0
9	G	244/288 (84%)	-0.50	2 (0%) 86 87	23, 41, 78, 117	0
9	U	244/288 (84%)	-0.45	4 (1%) 72 74	22, 44, 83, 104	0
10	H	196/215 (91%)	-0.76	0 100 100	17, 27, 51, 84	0
10	V	196/215 (91%)	-0.71	0 100 100	18, 29, 56, 77	0
11	I	221/261 (84%)	-0.56	1 (0%) 91 92	20, 34, 59, 94	0
11	W	220/261 (84%)	-0.66	0 100 100	23, 37, 60, 77	0
12	J	204/205 (99%)	-0.56	1 (0%) 91 92	23, 35, 72, 91	0
12	X	204/205 (99%)	-0.56	0 100 100	22, 36, 71, 100	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	K	196/198 (98%)	-0.66	1 (0%) 91 92	20, 36, 57, 93	0
13	Y	196/198 (98%)	-0.60	2 (1%) 82 83	25, 39, 59, 99	0
14	L	212/287 (73%)	-0.62	1 (0%) 91 92	21, 37, 56, 66	0
14	Z	212/287 (73%)	-0.62	0 100 100	22, 38, 58, 76	0
15	a	3/13 (23%)	0.57	0 100 100	63, 63, 78, 96	0
15	e	3/13 (23%)	-0.02	0 100 100	54, 54, 60, 83	1 (33%)
All	All	6359/6964 (91%)	-0.51	67 (1%) 80 82	17, 40, 76, 160	1 (0%)

The worst 5 of 67 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	Q	220	ALA	5.9
3	A	252	ASP	5.5
11	I	221	CYS	5.4
4	P	250	LEU	4.8
5	Q	221	ASN	4.8

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
17	GOL	V	202	6/6	0.58	0.60	89,93,98,98	0
17	GOL	F	301	6/6	0.62	0.53	64,75,77,79	0
16	MPD	T	301	8/8	0.68	0.30	52,70,76,77	0
18	MG	S	303	1/1	0.74	0.40	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
17	GOL	D	301	6/6	0.77	0.37	64,69,72,75	0
17	GOL	T	302	6/6	0.77	0.29	53,67,67,68	0
17	GOL	S	301	6/6	0.79	0.25	63,65,69,69	0
17	GOL	A	301	6/6	0.79	0.26	51,58,60,63	0
17	GOL	V	203	6/6	0.82	0.23	43,55,58,59	0
18	MG	T	303	1/1	0.82	0.23	51,51,51,51	0
17	GOL	A	302	6/6	0.86	0.30	67,70,71,73	0
16	MPD	V	201	8/8	0.86	0.29	38,42,55,56	0
16	MPD	Z	301	8/8	0.86	0.28	56,65,76,84	0
17	GOL	F	303	6/6	0.86	0.25	56,64,73,74	0
16	MPD	M	301	8/8	0.86	0.33	66,83,98,111	0
16	MPD	N	301	8/8	0.87	0.17	60,65,69,69	0
16	MPD	X	201	8/8	0.88	0.25	67,81,88,90	0
17	GOL	I	301	6/6	0.88	0.19	64,68,72,72	0
16	MPD	L	301	8/8	0.89	0.26	55,70,75,76	0
17	GOL	I	302	6/6	0.89	0.19	53,58,59,60	0
18	MG	2	307	1/1	0.89	0.14	53,53,53,53	0
18	MG	K	202	1/1	0.89	0.19	35,35,35,35	0
17	GOL	F	302	6/6	0.89	0.17	52,59,66,66	0
16	MPD	1	301	8/8	0.89	0.29	58,64,66,70	0
17	GOL	X	202	6/6	0.90	0.32	47,48,50,51	0
17	GOL	A	303	6/6	0.90	0.21	44,49,55,57	0
18	MG	F	305	1/1	0.90	0.27	50,50,50,50	0
17	GOL	L	303	6/6	0.90	0.26	49,55,59,60	0
17	GOL	2	303	6/6	0.90	0.23	51,54,56,62	0
17	GOL	W	301	6/6	0.90	0.21	51,57,58,64	0
18	MG	W	302	1/1	0.90	0.14	37,37,37,37	0
17	GOL	O	301	6/6	0.91	0.15	53,54,60,60	0
17	GOL	E	301	6/6	0.91	0.31	50,53,54,56	0
18	MG	P	301	1/1	0.91	0.34	49,49,49,49	0
17	GOL	G	301	6/6	0.91	0.22	52,55,57,57	0
17	GOL	Z	304	6/6	0.91	0.23	49,54,57,60	0
18	MG	V	207	1/1	0.91	0.14	39,39,39,39	0
17	GOL	G	302	6/6	0.91	0.29	61,63,64,64	0
17	GOL	M	302	6/6	0.92	0.22	33,37,41,41	0
17	GOL	J	202	6/6	0.92	0.18	56,61,71,75	0
17	GOL	L	302	6/6	0.92	0.21	70,73,75,82	0
16	MPD	2	301	8/8	0.92	0.19	61,65,74,74	0
18	MG	M	305	1/1	0.92	0.35	55,55,55,55	0
17	GOL	H	201	6/6	0.93	0.22	62,68,72,75	0
18	MG	B	301	1/1	0.93	0.12	42,42,42,42	0
17	GOL	F	304	6/6	0.93	0.23	50,56,60,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
17	GOL	2	302	6/6	0.93	0.15	39,43,49,51	0
18	MG	M	304	1/1	0.93	0.19	40,40,40,40	0
17	GOL	M	303	6/6	0.93	0.25	62,72,77,77	0
18	MG	N	306	1/1	0.93	0.16	39,39,39,39	0
17	GOL	1	303	6/6	0.93	0.27	58,61,61,62	0
17	GOL	Z	302	6/6	0.93	0.14	47,56,58,59	0
17	GOL	K	201	6/6	0.93	0.34	57,62,63,63	0
18	MG	1	304	1/1	0.93	0.06	35,35,35,35	0
18	MG	2	305	1/1	0.93	0.15	39,39,39,39	0
18	MG	N	307	1/1	0.94	0.09	27,27,27,27	0
18	MG	O	303	1/1	0.94	0.15	34,34,34,34	0
18	MG	J	201	1/1	0.94	0.11	36,36,36,36	0
18	MG	R	301	1/1	0.94	0.07	28,28,28,28	0
17	GOL	1	302	6/6	0.94	0.19	54,58,62,64	0
17	GOL	N	303	6/6	0.94	0.18	44,51,52,52	0
18	MG	V	206	1/1	0.94	0.18	28,28,28,28	0
17	GOL	A	304	6/6	0.94	0.22	48,50,51,51	0
18	MG	2	304	1/1	0.94	0.15	22,22,22,22	0
18	MG	X	205	1/1	0.94	0.14	35,35,35,35	0
18	MG	Y	201	1/1	0.94	0.18	40,40,40,40	0
18	MG	J	206	1/1	0.95	0.11	42,42,42,42	0
18	MG	T	304	1/1	0.95	0.12	47,47,47,47	0
18	MG	J	207	1/1	0.95	0.16	34,34,34,34	0
18	MG	D	302	1/1	0.95	0.10	27,27,27,27	0
17	GOL	O	302	6/6	0.95	0.21	63,67,69,70	0
18	MG	2	306	1/1	0.95	0.09	43,43,43,43	0
18	MG	M	306	1/1	0.95	0.19	37,37,37,37	0
17	GOL	Z	303	6/6	0.96	0.21	36,40,41,42	0
17	GOL	N	302	6/6	0.96	0.10	50,57,60,62	0
18	MG	X	204	1/1	0.96	0.11	35,35,35,35	0
18	MG	H	205	1/1	0.96	0.11	29,29,29,29	0
18	MG	R	303	1/1	0.96	0.12	39,39,39,39	0
18	MG	Y	202	1/1	0.96	0.21	31,31,31,31	0
18	MG	V	204	1/1	0.97	0.06	21,21,21,21	0
18	MG	V	205	1/1	0.97	0.15	33,33,33,33	0
18	MG	J	203	1/1	0.97	0.10	30,30,30,30	0
18	MG	Q	301	1/1	0.97	0.12	25,25,25,25	0
18	MG	J	204	1/1	0.97	0.13	35,35,35,35	0
18	MG	X	203	1/1	0.97	0.14	26,26,26,26	0
18	MG	H	203	1/1	0.97	0.25	38,38,38,38	0
18	MG	2	308	1/1	0.97	0.07	32,32,32,32	0
18	MG	H	202	1/1	0.97	0.07	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
18	MG	L	304	1/1	0.97	0.17	30,30,30,30	0
18	MG	N	304	1/1	0.98	0.07	34,34,34,34	0
18	MG	S	302	1/1	0.98	0.05	31,31,31,31	0
18	MG	N	305	1/1	0.98	0.19	28,28,28,28	0
18	MG	L	305	1/1	0.98	0.09	32,32,32,32	0
18	MG	K	203	1/1	0.98	0.11	25,25,25,25	0
18	MG	Z	305	1/1	0.98	0.06	31,31,31,31	0
18	MG	Z	306	1/1	0.98	0.12	35,35,35,35	0
18	MG	C	301	1/1	0.99	0.20	20,20,20,20	0
18	MG	Q	302	1/1	0.99	0.05	30,30,30,30	0
18	MG	J	205	1/1	0.99	0.04	23,23,23,23	0
18	MG	R	302	1/1	0.99	0.06	26,26,26,26	0
18	MG	C	302	1/1	0.99	0.07	28,28,28,28	0
18	MG	M	307	1/1	0.99	0.06	25,25,25,25	0
18	MG	H	204	1/1	0.99	0.24	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.