



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 27, 2017 – 05:08 PM EDT

PDB ID : 5LF4
Title : Human 20S proteasome complex with Delanzomib at 2.0 Angstrom
Authors : Schrader, J.; Henneberg, F.; Mata, R.; Tittmann, K.; Schneider, T.R.; Stark, H.; Bourenkov, G.; Chari, A.
Deposited on : unknown
Resolution : 1.99 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

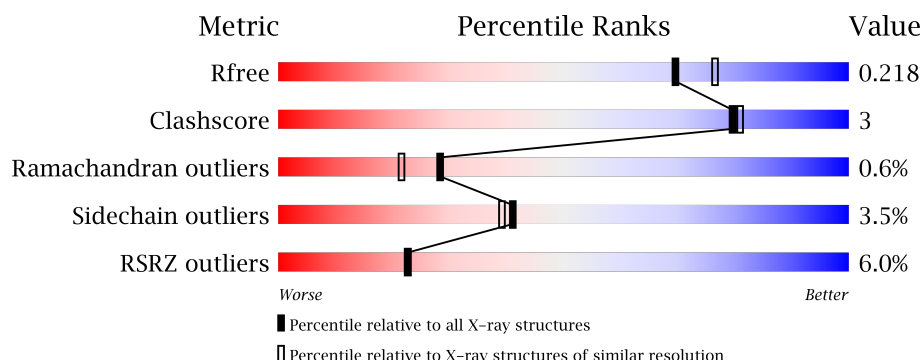
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	234	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>• •</div> </div> </div>
1	O	234	<div> <div>18%</div> <div> <div></div> <div>90%</div> <div>5%</div> <div>• •</div> </div> </div>
2	B	261	<div> <div>7%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>• 5%</div> </div> </div>
2	P	261	<div> <div>20%</div> <div> <div></div> <div>82%</div> <div>10%</div> <div>• 5%</div> </div> </div>
3	C	248	<div> <div>12%</div> <div> <div></div> <div>81%</div> <div>12%</div> <div>• •</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	Q	248	
4	D	241	
4	R	241	
5	E	263	
5	S	263	
6	F	255	
6	T	255	
7	G	246	
7	U	246	
8	H	234	
8	V	234	
9	I	205	
9	W	205	
10	J	201	
10	X	201	
11	K	204	
11	Y	204	
12	L	213	
12	Z	213	
13	M	219	
13	a	219	
14	N	205	
14	b	205	

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
15	CL	K	304	-	-	-	X
15	CL	M	301	-	-	-	X
15	CL	U	301	-	-	-	X
15	CL	a	302	-	-	-	X
18	1PE	H	305	-	-	-	X
18	1PE	I	303	-	-	-	X
18	1PE	L	301	-	-	-	X
18	1PE	L	302	-	-	-	X
18	1PE	N	304	-	-	-	X
18	1PE	W	303	-	-	-	X
18	1PE	Y	305	-	-	-	X
19	6V7	N	307	X	-	-	-
19	6V7	Y	306	X	-	-	-
7	6V1	U	47	X	-	-	-

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 52186 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	230	Total	C	N	O	S	0	3	0
			1788	1145	301	336	6			
1	O	230	Total	C	N	O	S	0	0	0
			1741	1111	293	331	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	248	Total	C	N	O	S	0	2	0
			1926	1220	332	363	11			
2	P	248	Total	C	N	O	S	0	2	0
			1909	1206	325	367	11			

- Molecule 3 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	237	Total	C	N	O	S	0	2	0
			1798	1121	320	352	5			
3	Q	239	Total	C	N	O	S	0	0	0
			1820	1136	320	359	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	233	Total	C	N	O	S	0	1	0
			1762	1105	290	356	11			
4	R	233	Total	C	N	O	S	0	1	0
			1753	1103	293	346	11			

- Molecule 5 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	234	Total	C	N	O	S	0	1	0
			1822	1144	325	342	11			
5	S	238	Total	C	N	O	S	0	3	0
			1875	1175	340	349	11			

- Molecule 6 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	239	Total	C	N	O	S	0	4	0
			1888	1198	325	353	12			
6	T	240	Total	C	N	O	S	0	1	0
			1856	1178	315	351	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	244	Total	C	N	O	S	0	2	0
			1912	1214	321	364	13			
7	U	238	Total	C	N	O	S	0	1	0
			1815	1147	304	350	14			

- Molecule 8 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	220	Total	C	N	O	S	0	2	0
			1664	1047	284	320	13			
8	V	220	Total	C	N	O	S	0	2	0
			1622	1023	269	318	12			

- 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	3	0
			1613	1028	270	295	20			
9	W	204	Total	C	N	O	S	0	2	0
			1599	1018	267	295	19			

- Molecule 10 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	196	Total	C	N	O	S	0	3	0
			1590	1021	271	288	10			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	196	Total	C	N	O	S	0	2	0
			1576	1012	267	287	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	200	Total	C	N	O	S	0	1	0
			1550	978	269	293	10			
11	Y	201	Total	C	N	O	S	0	3	0
			1580	996	280	294	10			

- Molecule 12 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	213	Total	C	N	O	S	0	2	0
			1636	1038	277	310	11			
12	Z	213	Total	C	N	O	S	0	1	0
			1642	1041	280	310	11			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	216	Total	C	N	O	S	0	1	0
			1692	1067	291	322	12			
13	a	216	Total	C	N	O	S	0	2	0
			1688	1064	291	321	12			

- Molecule 14 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	202	Total	C	N	O	S	0	1	0
			1519	953	258	295	13			
14	b	203	Total	C	N	O	S	0	1	0
			1524	956	259	296	13			

- Molecule 15 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	P	1	Total	Cl	0	0
			1	1		
15	K	3	Total	Cl	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	B	2	Total 2	Cl 2	0	0
15	W	1	Total 1	Cl 1	0	0
15	N	2	Total 2	Cl 2	0	0
15	S	3	Total 3	Cl 3	0	0
15	E	3	Total 3	Cl 3	0	0
15	b	1	Total 1	Cl 1	0	0
15	V	2	Total 2	Cl 2	0	0
15	A	4	Total 4	Cl 4	0	0
15	R	2	Total 2	Cl 2	0	0
15	M	3	Total 3	Cl 3	0	0
15	D	2	Total 2	Cl 2	0	0
15	I	1	Total 1	Cl 1	0	0
15	a	4	Total 4	Cl 4	0	0
15	U	1	Total 1	Cl 1	0	0
15	G	2	Total 2	Cl 2	0	0
15	Q	2	Total 2	Cl 2	0	0
15	H	2	Total 2	Cl 2	0	0
15	C	2	Total 2	Cl 2	0	0
15	O	4	Total 4	Cl 4	0	0
15	Y	4	Total 4	Cl 4	0	0
15	F	1	Total 1	Cl 1	0	0

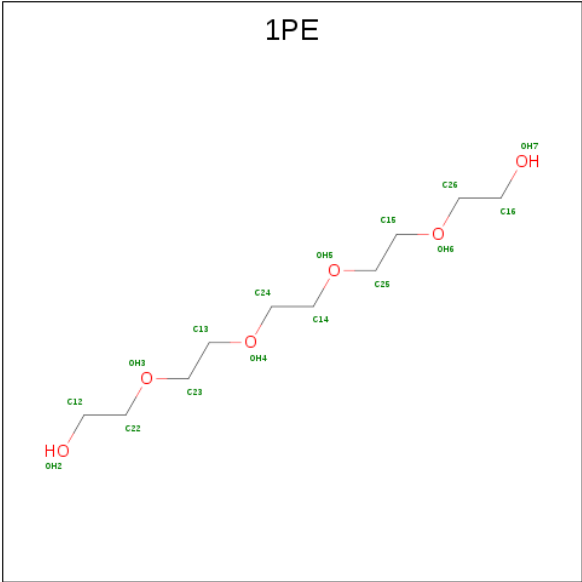
- Molecule 16 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total K 1 1	0	0
16	b	2	Total K 2 2	0	0
16	Z	1	Total K 1 1	0	0
16	N	2	Total K 2 2	0	0
16	U	1	Total K 1 1	0	0
16	L	1	Total K 1 1	0	0

- Molecule 17 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

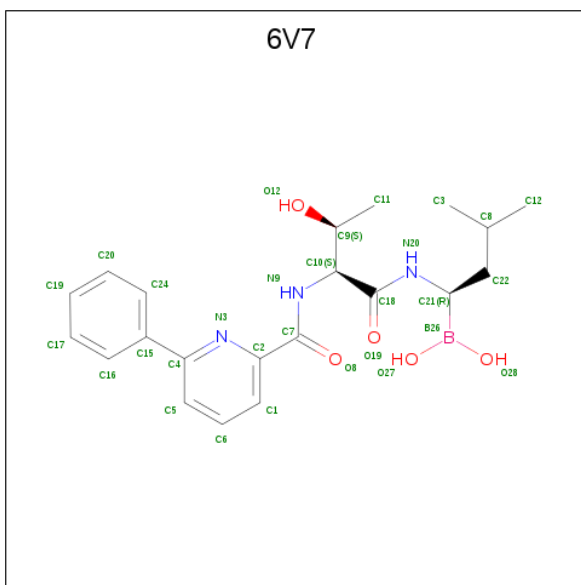
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	J	1	Total Mg 1 1	0	0
17	K	1	Total Mg 1 1	0	0
17	H	2	Total Mg 2 2	0	0
17	I	2	Total Mg 2 2	0	0
17	V	1	Total Mg 1 1	0	0
17	W	1	Total Mg 1 1	0	0
17	X	1	Total Mg 1 1	0	0
17	L	1	Total Mg 1 1	0	0

- Molecule 18 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	H	1	Total	C	O	0	0
			16	10	6		
18	I	1	Total	C	O	0	0
			16	10	6		
18	L	1	Total	C	O	0	0
			16	10	6		
18	L	1	Total	C	O	0	0
			16	10	6		
18	N	1	Total	C	O	0	0
			16	10	6		
18	N	1	Total	C	O	0	0
			16	10	6		
18	U	1	Total	C	O	0	0
			16	10	6		
18	W	1	Total	C	O	0	0
			16	10	6		
18	Y	1	Total	C	O	0	0
			16	10	6		

- Molecule 19 is [(1 {R})-3-methyl-1-[(2 {S},3 {S})-3-oxidanyl-2-[(6-phenylpyridin-2-yl)carbonylamino]butanoyl]amino]butyl]boronic acid (three-letter code: 6V7) (formula: C₂₁H₂₈BN₃O₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
19	K	1	Total	B	C	N	O	0	0
			30	1	21	3	5		
19	N	1	Total	B	C	N	O	0	0
			30	1	21	3	5		
19	Y	1	Total	B	C	N	O	0	0
			30	1	21	3	5		
19	b	1	Total	B	C	N	O	0	0
			30	1	21	3	5		

- Molecule 20 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	A	115	Total	O	0	0
			115	115		
20	B	129	Total	O	0	0
			129	129		
20	C	78	Total	O	0	0
			78	78		
20	D	98	Total	O	0	0
			98	98		
20	E	143	Total	O	0	0
			143	143		
20	F	186	Total	O	0	0
			186	186		
20	G	195	Total	O	0	0
			195	195		
20	H	164	Total	O	0	0
			164	164		

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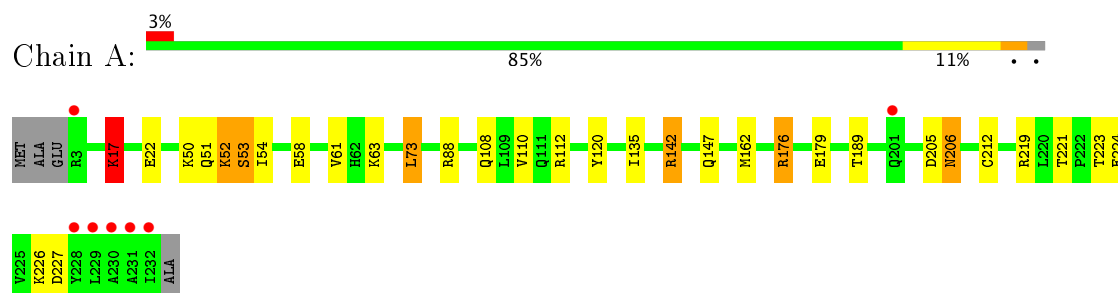
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	I	155	Total 155	O 155	0	0
20	J	141	Total 141	O 141	0	0
20	K	102	Total 102	O 102	0	0
20	L	124	Total 124	O 124	0	0
20	M	148	Total 148	O 148	0	0
20	N	168	Total 168	O 168	0	0
20	O	95	Total 95	O 95	0	0
20	P	124	Total 124	O 124	0	0
20	Q	75	Total 75	O 75	0	0
20	R	129	Total 129	O 129	0	0
20	S	128	Total 128	O 128	0	0
20	T	96	Total 96	O 96	0	0
20	U	113	Total 113	O 113	0	0
20	V	117	Total 117	O 117	0	0
20	W	123	Total 123	O 123	0	0
20	X	128	Total 128	O 128	0	0
20	Y	149	Total 149	O 149	0	0
20	Z	171	Total 171	O 171	0	0
20	a	172	Total 172	O 172	0	0
20	b	126	Total 126	O 126	0	0

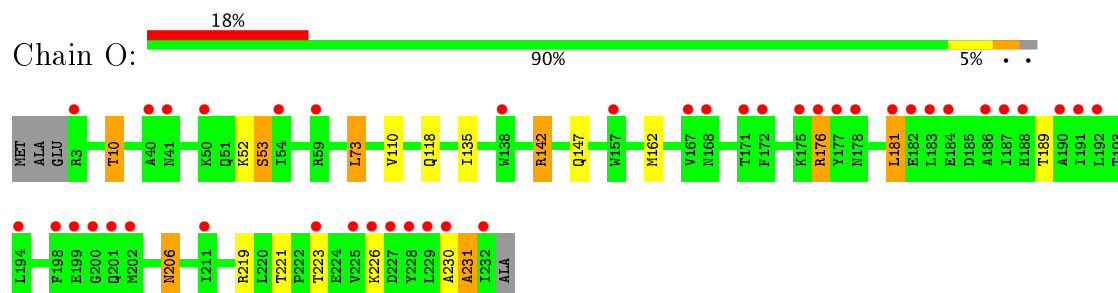
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

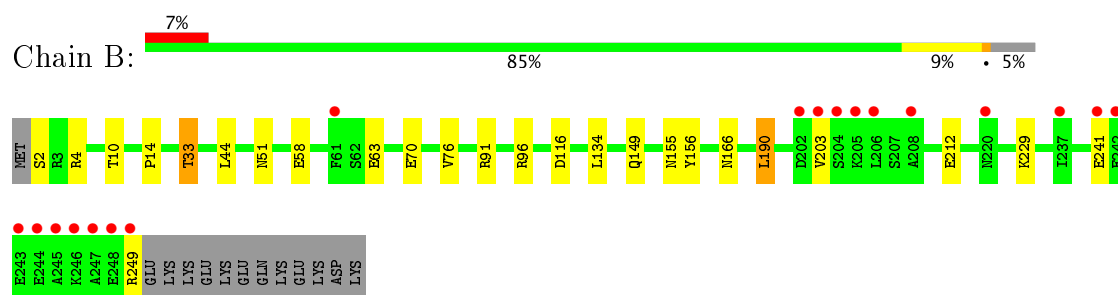
- Molecule 1: Proteasome subunit alpha type-2



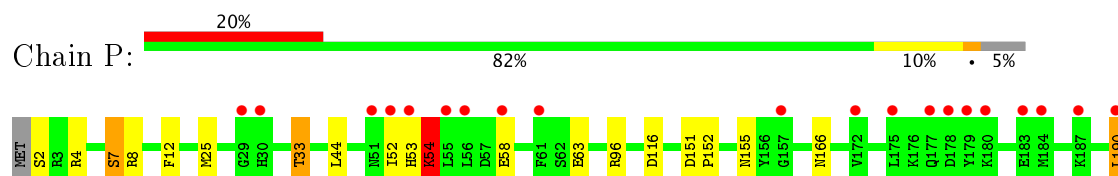
- Molecule 1: Proteasome subunit alpha type-2

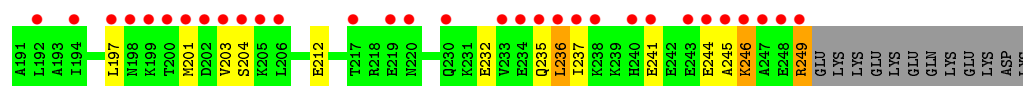


- Molecule 2: Proteasome subunit alpha type-4

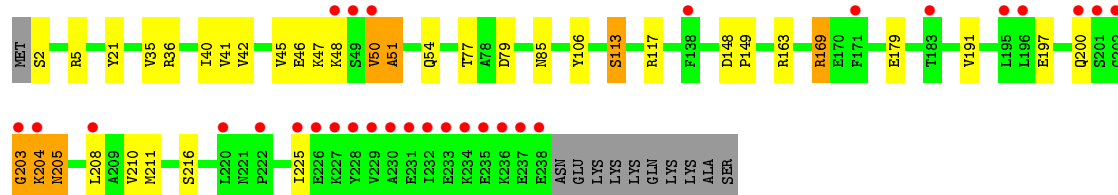
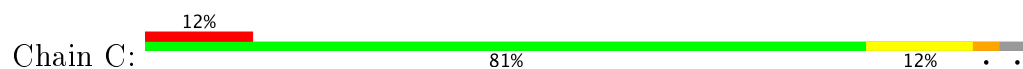


- Molecule 2: Proteasome subunit alpha type-4

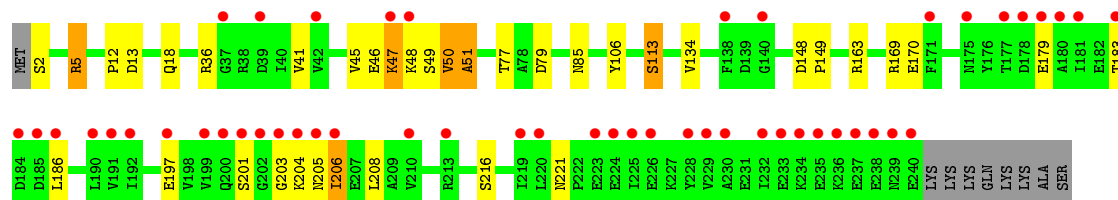
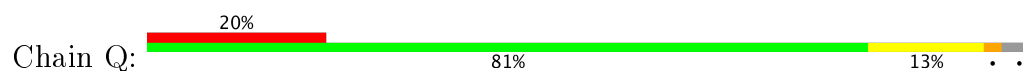




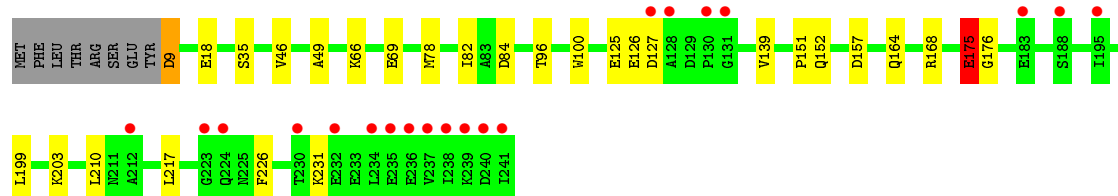
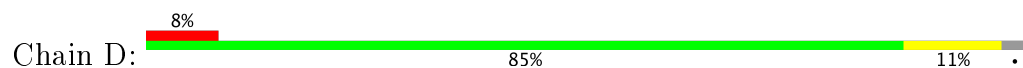
• Molecule 3: Proteasome subunit alpha type-7



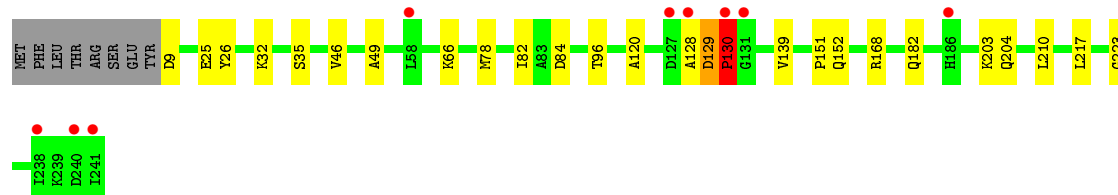
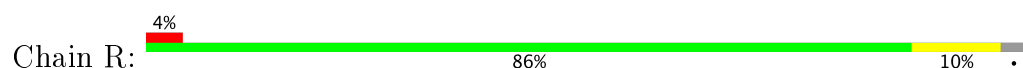
• Molecule 3: Proteasome subunit alpha type-7



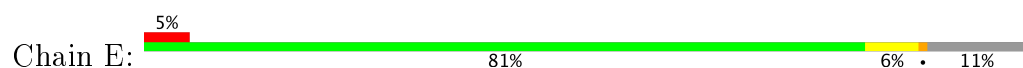
• Molecule 4: Proteasome subunit alpha type-5

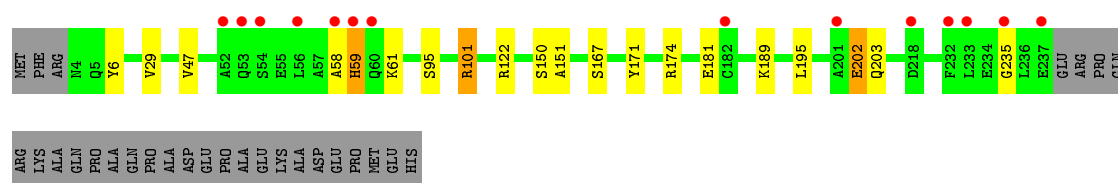


• Molecule 4: Proteasome subunit alpha type-5

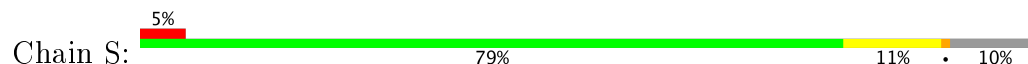


• Molecule 5: Proteasome subunit alpha type-1

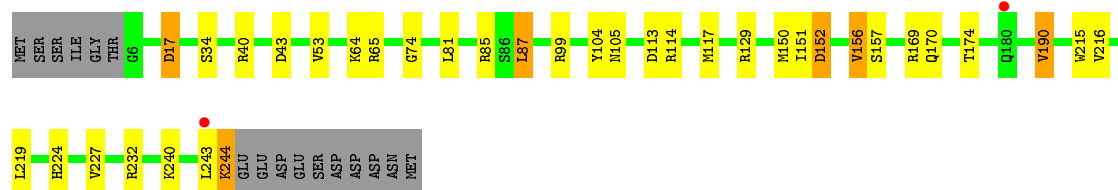




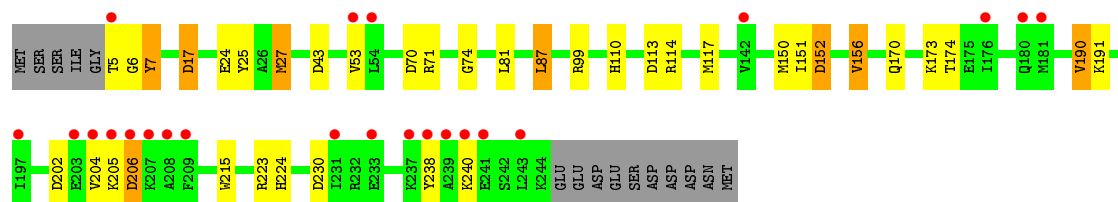
- Molecule 5: Proteasome subunit alpha type-1



- Molecule 6: Proteasome subunit alpha type-3



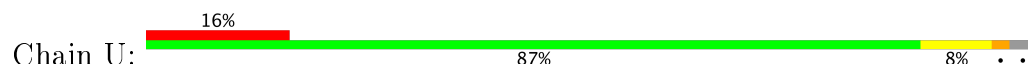
- Molecule 6: Proteasome subunit alpha type-3

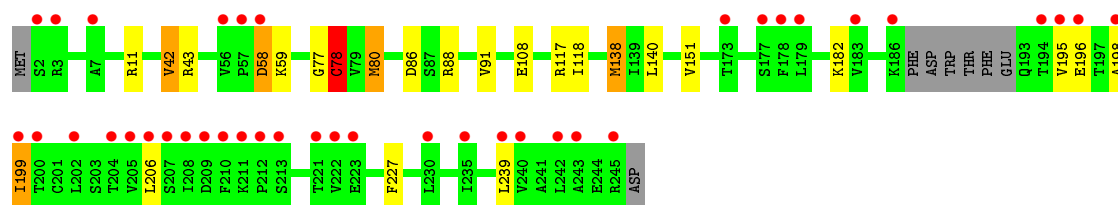


- Molecule 7: Proteasome subunit alpha type-6

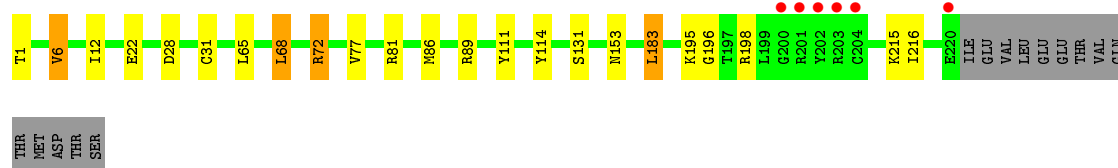
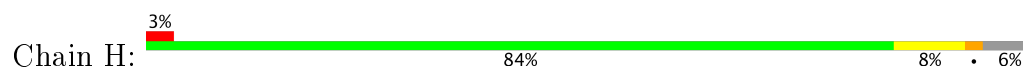


- Molecule 7: Proteasome subunit alpha type-6

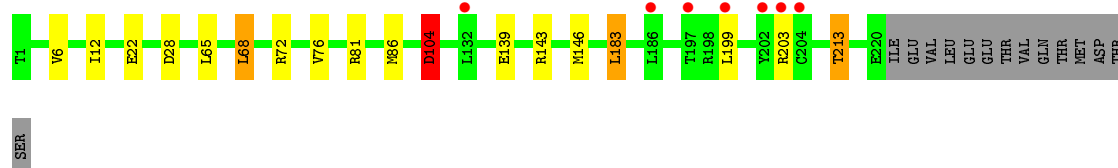
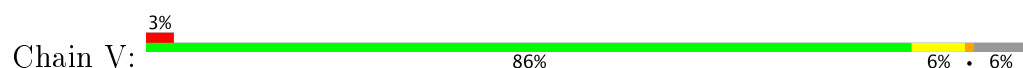




• Molecule 8: Proteasome subunit beta type-7



• Molecule 9: Proteasome subunit beta type-3



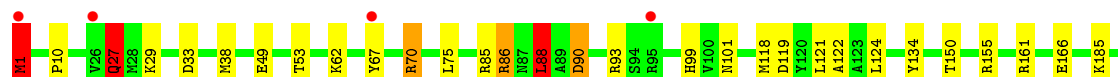
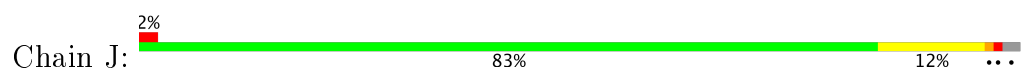
• Molecule 10: Proteasome subunit beta type-2



• Molecule 10: Proteasome subunit beta type-2

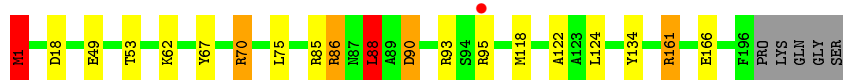


• Molecule 10: Proteasome subunit beta type-2




- Molecule 10: Proteasome subunit beta type-2

Chain X:  88% 7% ...




- Molecule 11: Proteasome subunit beta type-5

Chain K:  86% 11% ..




- Molecule 11: Proteasome subunit beta type-5

Chain Y:  83% 13% ..



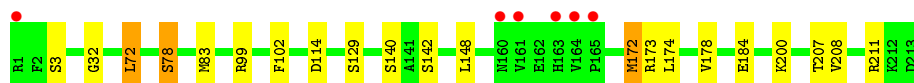
- Molecule 12: Proteasome subunit beta type-1

Chain L:  89% 9% .



- Molecule 12: Proteasome subunit beta type-1

Chain Z:  90% 8% .




- Molecule 13: Proteasome subunit beta type-4

Chain M:  89% 9% .

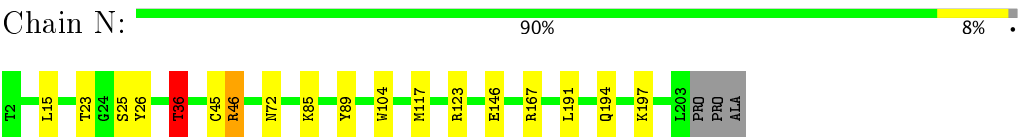


- Molecule 13: Proteasome subunit beta type-4

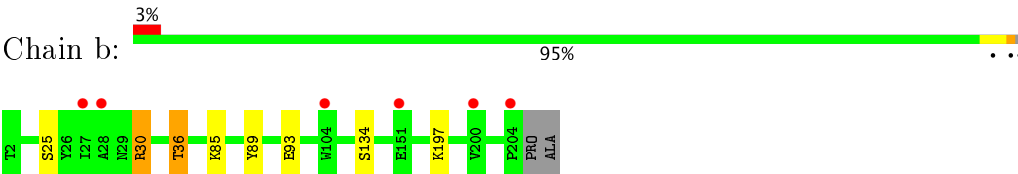
Chain a:  92% 6% .



● Molecule 14: Proteasome subunit beta type-6



● Molecule 14: Proteasome subunit beta type-6



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.45Å 202.76Å 314.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	170.38 – 1.99 48.90 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.0 (170.38-1.99) 99.0 (48.90-1.99)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.181 , 0.216 0.187 , 0.218	Depositor DCC
R_{free} test set	24259 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	35.9	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	52186	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.84% 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: MG, CL, 6V7, K, 6V1, 1PE, YCM

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	0.93	2/1833 (0.1%)	0.95	7/2489 (0.3%)
1	O	0.77	0/1778	0.89	6/2419 (0.2%)
2	B	0.94	1/1962 (0.1%)	0.98	7/2649 (0.3%)
2	P	0.84	2/1945 (0.1%)	0.95	6/2631 (0.2%)
3	C	0.84	1/1818 (0.1%)	0.98	6/2469 (0.2%)
3	Q	0.81	2/1834 (0.1%)	0.97	8/2490 (0.3%)
4	D	0.89	4/1789 (0.2%)	0.93	6/2424 (0.2%)
4	R	0.98	1/1780 (0.1%)	1.01	4/2408 (0.2%)
5	E	0.96	2/1842 (0.1%)	0.98	3/2493 (0.1%)
5	S	0.88	0/1901	0.95	3/2571 (0.1%)
6	F	1.13	2/1935 (0.1%)	1.13	17/2605 (0.7%)
6	T	0.93	2/1894 (0.1%)	1.05	17/2556 (0.7%)
7	G	1.09	3/1909 (0.2%)	0.97	8/2579 (0.3%)
7	U	0.84	3/1804 (0.2%)	0.93	8/2441 (0.3%)
8	H	1.10	4/1697 (0.2%)	1.21	12/2299 (0.5%)
8	V	0.87	2/1655 (0.1%)	1.02	10/2251 (0.4%)
9	I	1.07	2/1648 (0.1%)	1.23	12/2219 (0.5%)
9	W	0.87	2/1630 (0.1%)	1.09	8/2197 (0.4%)
10	J	0.97	0/1613	1.23	14/2180 (0.6%)
10	X	0.93	0/1599	1.15	11/2163 (0.5%)
11	K	0.97	1/1584 (0.1%)	1.04	9/2141 (0.4%)
11	Y	1.11	2/1620 (0.1%)	1.15	12/2185 (0.5%)
12	L	0.97	4/1672 (0.2%)	0.98	6/2257 (0.3%)
12	Z	1.14	6/1675 (0.4%)	1.06	5/2257 (0.2%)
13	M	1.04	0/1728	1.09	8/2339 (0.3%)
13	a	1.12	3/1724 (0.2%)	1.10	5/2336 (0.2%)
14	N	1.17	5/1548 (0.3%)	1.03	4/2095 (0.2%)
14	b	1.05	4/1554 (0.3%)	1.02	3/2104 (0.1%)
All	All	0.97	60/48971 (0.1%)	1.04	225/66247 (0.3%)

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
2	P	0	3
3	C	0	1
3	Q	0	3
4	D	0	4
4	R	0	2
5	E	0	1
6	T	0	1
7	U	1	0
9	I	0	1
9	W	0	1
10	J	0	2
10	X	0	1
13	a	0	1
All	All	1	21

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	108	GLU	CD-OE1	13.03	1.40	1.25
7	G	108	GLU	CD-OE2	8.40	1.34	1.25
12	Z	3	SER	CB-OG	8.15	1.52	1.42
6	F	104	TYR	CE2-CZ	8.09	1.49	1.38
6	F	104	TYR	CG-CD1	7.99	1.49	1.39

The worst 5 of 225 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	86	ARG	NE-CZ-NH2	-19.20	110.70	120.30
10	J	86	ARG	NE-CZ-NH1	18.23	129.41	120.30
9	I	69	ARG	NE-CZ-NH1	18.08	129.34	120.30
8	H	72	ARG	NE-CZ-NH2	-17.59	111.50	120.30
10	X	86	ARG	NE-CZ-NH2	-17.59	111.50	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	46	GLU	Peptide
4	D	127	ASP	Peptide
4	D	175[A]	GLU	Peptide
4	D	175[B]	GLU	Mainchain,Peptide
5	E	235	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	A	1788	0	1761	17	0
1	O	1741	0	1683	7	0
2	B	1926	0	1924	12	0
2	P	1909	0	1874	19	0
3	C	1798	0	1718	23	0
3	Q	1820	0	1749	11	0
4	D	1762	0	1709	9	0
4	R	1753	0	1726	11	0
5	E	1822	0	1779	7	0
5	S	1875	0	1818	20	0
6	F	1888	0	1882	14	0
6	T	1856	0	1816	11	0
7	G	1912	0	1882	10	0
7	U	1815	0	1748	10	0
8	H	1664	0	1681	10	0
8	V	1622	0	1595	4	0
9	I	1613	0	1646	12	0
9	W	1599	0	1621	8	0
10	J	1590	0	1581	19	0
10	X	1576	0	1561	13	0
11	K	1550	0	1503	8	0
11	Y	1580	0	1554	27	0
12	L	1636	0	1625	9	0
12	Z	1642	0	1635	3	0
13	M	1692	0	1670	7	0
13	a	1688	0	1658	0	0
14	N	1519	0	1492	7	0
14	b	1524	0	1492	0	0
15	A	4	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	B	2	0	0	1	0
15	C	2	0	0	0	0
15	D	2	0	0	0	0
15	E	3	0	0	0	0
15	F	1	0	0	0	0
15	G	2	0	0	0	0
15	H	2	0	0	1	0
15	I	1	0	0	0	0
15	K	3	0	0	0	0
15	M	3	0	0	1	0
15	N	2	0	0	1	0
15	O	4	0	0	0	0
15	P	1	0	0	0	0
15	Q	2	0	0	0	0
15	R	2	0	0	1	0
15	S	3	0	0	0	0
15	U	1	0	0	0	0
15	V	2	0	0	0	0
15	W	1	0	0	0	0
15	Y	4	0	0	0	0
15	a	4	0	0	0	0
15	b	1	0	0	0	0
16	G	1	0	0	0	0
16	L	1	0	0	0	0
16	N	2	0	0	0	0
16	U	1	0	0	0	0
16	Z	1	0	0	0	0
16	b	2	0	0	0	0
17	H	2	0	0	0	0
17	I	2	0	0	0	0
17	J	1	0	0	0	0
17	K	1	0	0	0	0
17	L	1	0	0	0	0
17	V	1	0	0	0	0
17	W	1	0	0	0	0
17	X	1	0	0	0	0
18	H	16	0	22	0	0
18	I	16	0	22	0	0
18	L	32	0	44	0	0
18	N	32	0	44	0	0
18	U	16	0	22	1	0
18	W	16	0	22	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Y	16	0	22	0	0
19	K	30	0	0	1	0
19	N	30	0	0	0	0
19	Y	30	0	0	1	0
19	b	30	0	0	0	0
20	A	115	0	0	4	0
20	B	129	0	0	2	0
20	C	78	0	0	2	0
20	D	98	0	0	1	0
20	E	143	0	0	1	0
20	F	186	0	0	4	0
20	G	195	0	0	4	0
20	H	164	0	0	4	0
20	I	155	0	0	1	0
20	J	141	0	0	2	0
20	K	102	0	0	0	0
20	L	124	0	0	2	0
20	M	148	0	0	0	0
20	N	168	0	0	1	0
20	O	95	0	0	1	0
20	P	124	0	0	1	0
20	Q	75	0	0	0	0
20	R	129	0	0	4	0
20	S	128	0	0	6	0
20	T	96	0	0	1	0
20	U	113	0	0	1	0
20	V	117	0	0	1	0
20	W	123	0	0	1	0
20	X	128	0	0	1	0
20	Y	149	0	0	0	0
20	Z	171	0	0	0	0
20	a	172	0	0	0	0
20	b	126	0	0	0	0
All	All	52186	0	47581	290	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 3.

The worst 5 of 290 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)
10:X:1:MET:HE1	10:X:134:TYR:H	1.36	0.91
11:Y:46:MET:HE2	11:Y:53:CYS:C	1.94	0.88
10:J:1[A]:MET:HE1	10:J:134:TYR:H	1.39	0.86
5:S:65[A]:HIS:CE1	20:S:402:HOH:O	2.32	0.81
5:E:47:VAL:HG12	5:E:195:LEU:HD22	1.63	0.80

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	231/234 (99%)	221 (96%)	6 (3%)	4 (2%)	11	4
1	O	228/234 (97%)	217 (95%)	7 (3%)	4 (2%)	10	4
2	B	248/261 (95%)	238 (96%)	9 (4%)	1 (0%)	38	33
2	P	248/261 (95%)	235 (95%)	10 (4%)	3 (1%)	15	8
3	C	236/248 (95%)	223 (94%)	7 (3%)	6 (2%)	6	2
3	Q	236/248 (95%)	221 (94%)	6 (2%)	9 (4%)	4	1
4	D	232/241 (96%)	222 (96%)	7 (3%)	3 (1%)	14	7
4	R	232/241 (96%)	222 (96%)	7 (3%)	3 (1%)	14	7
5	E	232/263 (88%)	226 (97%)	5 (2%)	1 (0%)	38	33
5	S	238/263 (90%)	228 (96%)	9 (4%)	1 (0%)	38	33
6	F	241/255 (94%)	238 (99%)	3 (1%)	0	100	100
6	T	239/255 (94%)	233 (98%)	4 (2%)	2 (1%)	22	15
7	G	241/246 (98%)	235 (98%)	6 (2%)	0	100	100
7	U	232/246 (94%)	227 (98%)	4 (2%)	1 (0%)	38	33
8	H	220/234 (94%)	217 (99%)	3 (1%)	0	100	100
8	V	220/234 (94%)	217 (99%)	2 (1%)	1 (0%)	32	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	205/205 (100%)	202 (98%)	3 (2%)	0	100	100
9	W	204/205 (100%)	199 (98%)	5 (2%)	0	100	100
10	J	195/201 (97%)	192 (98%)	3 (2%)	0	100	100
10	X	195/201 (97%)	193 (99%)	2 (1%)	0	100	100
11	K	199/204 (98%)	197 (99%)	2 (1%)	0	100	100
11	Y	202/204 (99%)	199 (98%)	2 (1%)	1 (0%)	32	26
12	L	213/213 (100%)	210 (99%)	3 (1%)	0	100	100
12	Z	212/213 (100%)	209 (99%)	3 (1%)	0	100	100
13	M	215/219 (98%)	209 (97%)	6 (3%)	0	100	100
13	a	216/219 (99%)	209 (97%)	7 (3%)	0	100	100
14	N	201/205 (98%)	199 (99%)	2 (1%)	0	100	100
14	b	202/205 (98%)	201 (100%)	1 (0%)	0	100	100
All	All	6213/6458 (96%)	6039 (97%)	134 (2%)	40 (1%)	28	21

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	LYS
1	A	53	SER
5	E	59	HIS
1	O	52	LYS
1	O	53	SER

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	185/191 (97%)	175 (95%)	10 (5%)	26	20
1	O	176/191 (92%)	165 (94%)	11 (6%)	21	15
2	B	200/221 (90%)	195 (98%)	5 (2%)	53	54
2	P	197/221 (89%)	187 (95%)	10 (5%)	28	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	179/210 (85%)	170 (95%)	9 (5%)	28	23
3	Q	184/210 (88%)	175 (95%)	9 (5%)	29	24
4	D	189/203 (93%)	183 (97%)	6 (3%)	44	42
4	R	187/203 (92%)	184 (98%)	3 (2%)	68	72
5	E	192/223 (86%)	184 (96%)	8 (4%)	34	30
5	S	197/223 (88%)	190 (96%)	7 (4%)	40	38
6	F	199/212 (94%)	191 (96%)	8 (4%)	36	32
6	T	192/212 (91%)	184 (96%)	8 (4%)	34	30
7	G	202/207 (98%)	195 (96%)	7 (4%)	41	39
7	U	186/207 (90%)	181 (97%)	5 (3%)	50	51
8	H	181/195 (93%)	175 (97%)	6 (3%)	43	41
8	V	172/195 (88%)	163 (95%)	9 (5%)	27	22
9	I	176/174 (101%)	174 (99%)	2 (1%)	78	82
9	W	173/174 (99%)	172 (99%)	1 (1%)	89	92
10	J	166/170 (98%)	159 (96%)	7 (4%)	34	30
10	X	165/170 (97%)	161 (98%)	4 (2%)	54	56
11	K	155/159 (98%)	148 (96%)	7 (4%)	32	27
11	Y	159/159 (100%)	156 (98%)	3 (2%)	62	66
12	L	175/178 (98%)	166 (95%)	9 (5%)	28	22
12	Z	175/178 (98%)	167 (95%)	8 (5%)	31	27
13	M	180/181 (99%)	175 (97%)	5 (3%)	49	49
13	a	178/181 (98%)	172 (97%)	6 (3%)	42	40
14	N	158/159 (99%)	154 (98%)	4 (2%)	53	54
14	b	158/159 (99%)	153 (97%)	5 (3%)	44	42
All	All	5036/5366 (94%)	4854 (96%)	182 (4%)	41	38

5 of 182 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	L	174	LEU
1	O	221	THR
12	Z	200	LYS
13	M	100	ARG
14	N	197	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	118	GLN
3	Q	18	GLN
13	a	89	HIS
1	O	206	ASN
2	P	40	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 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$
3	YCM	C	63	3	9,9,10	1.20	1 (11%)	4,10,12	1.84	2 (50%)
5	6V1	E	148	5	13,15,16	1.32	1 (7%)	12,20,22	3.08	6 (50%)
7	YCM	G	137	7	9,9,10	2.33	4 (44%)	4,10,12	3.13	2 (50%)
7	6V1	G	161	7	13,15,16	1.18	2 (15%)	12,20,22	2.39	7 (58%)
7	6V1	G	47	7	13,15,16	1.52	2 (15%)	12,20,22	1.08	1 (8%)
10	6V1	J	91	10	13,15,16	2.00	3 (23%)	12,20,22	4.08	8 (66%)
3	YCM	Q	63	3	9,9,10	1.77	2 (22%)	4,10,12	3.45	3 (75%)
5	6V1	S	148	5	13,15,16	1.53	4 (30%)	12,20,22	2.53	4 (33%)
7	YCM	U	137	7	9,9,10	1.43	2 (22%)	4,10,12	2.92	3 (75%)
7	6V1	U	161	7	13,15,16	1.28	2 (15%)	12,20,22	2.94	5 (41%)
7	6V1	U	47	7	13,15,16	1.48	3 (23%)	12,20,22	1.80	3 (25%)
10	6V1	X	91	10	13,15,16	1.64	3 (23%)	12,20,22	4.38	7 (58%)

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
3	YCM	C	63	3	-	0/6/8/10	0/0/0/0
5	6V1	E	148	5	-	1/6/25/27	0/1/1/1
7	YCM	G	137	7	-	0/6/8/10	0/0/0/0
7	6V1	G	161	7	-	0/6/25/27	0/1/1/1
7	6V1	G	47	7	-	0/6/25/27	0/1/1/1
10	6V1	J	91	10	-	0/6/25/27	0/1/1/1
3	YCM	Q	63	3	-	0/6/8/10	0/0/0/0
5	6V1	S	148	5	-	0/6/25/27	0/1/1/1
7	YCM	U	137	7	-	0/6/8/10	0/0/0/0
7	6V1	U	161	7	-	0/6/25/27	0/1/1/1
7	6V1	U	47	7	1/1/5/6	0/6/25/27	0/1/1/1
10	6V1	X	91	10	-	0/6/25/27	0/1/1/1

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	J	91	6V1	C1-SG	-5.89	1.76	1.83
3	Q	63	YCM	CD-SG	-3.87	1.73	1.81
10	X	91	6V1	C1-SG	-3.86	1.78	1.83
7	G	47	6V1	C2-N3	-3.69	1.33	1.38
7	G	137	YCM	CB-SG	-3.32	1.72	1.81

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	148	6V1	C2-N3-C4	-6.61	108.86	113.06
10	X	91	6V1	C2-N3-C4	-5.94	109.29	113.06
7	U	161	6V1	C2-N3-C4	-5.76	109.40	113.06
5	S	148	6V1	C2-N3-C4	-5.69	109.45	113.06
3	Q	63	YCM	CA-CB-SG	-4.91	100.72	113.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	148	6V1	C3-C6-N3-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 83 ligands modelled in this entry, 70 are monoatomic - leaving 13 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	1PE	H	305	-	15,15,15	0.47	0	14,14,14	0.57	0
18	1PE	I	303	-	15,15,15	0.55	0	14,14,14	1.10	2 (14%)
19	6V7	K	305	11	29,31,31	1.44	5 (17%)	34,42,42	1.72	9 (26%)
18	1PE	L	301	-	15,15,15	0.56	0	14,14,14	0.69	0
18	1PE	L	302	-	15,15,15	0.52	0	14,14,14	0.41	0
18	1PE	N	303	-	15,15,15	0.50	0	14,14,14	0.73	0
18	1PE	N	304	-	15,15,15	0.53	0	14,14,14	0.38	0
19	6V7	N	307	14	29,31,31	1.02	1 (3%)	34,42,42	1.51	7 (20%)
18	1PE	U	302	-	15,15,15	0.57	0	14,14,14	0.83	0
18	1PE	W	303	-	15,15,15	0.56	0	14,14,14	0.39	0
18	1PE	Y	305	-	15,15,15	0.53	0	14,14,14	0.52	0
19	6V7	Y	306	11	29,31,31	1.09	1 (3%)	34,42,42	1.33	5 (14%)
19	6V7	b	304	14	29,31,31	0.98	1 (3%)	34,42,42	1.47	4 (11%)

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	1PE	H	305	-	-	0/13/13/13	0/0/0/0
18	1PE	I	303	-	-	0/13/13/13	0/0/0/0
19	6V7	K	305	11	-	0/26/32/32	0/2/2/2
18	1PE	L	301	-	-	0/13/13/13	0/0/0/0
18	1PE	L	302	-	-	0/13/13/13	0/0/0/0
18	1PE	N	303	-	-	0/13/13/13	0/0/0/0
18	1PE	N	304	-	-	0/13/13/13	0/0/0/0
19	6V7	N	307	14	1/1/7/9	0/26/32/32	0/2/2/2
18	1PE	U	302	-	-	0/13/13/13	0/0/0/0
18	1PE	W	303	-	-	0/13/13/13	0/0/0/0
18	1PE	Y	305	-	-	0/13/13/13	0/0/0/0
19	6V7	Y	306	11	1/1/7/9	0/26/32/32	0/2/2/2
19	6V7	b	304	14	-	0/26/32/32	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	Y	306	6V7	O12-C9	-3.21	1.33	1.43
19	K	305	6V7	C11-C9	-2.54	1.43	1.51
19	b	304	6V7	C10-C18	-2.37	1.47	1.52
19	N	307	6V7	C2-N3	-2.04	1.31	1.34
19	K	305	6V7	C2-C7	-2.01	1.45	1.50

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	K	305	6V7	C6-C1-C2	-4.44	113.08	118.65
19	Y	306	6V7	O12-C9-C11	-3.44	98.94	109.70
19	K	305	6V7	O12-C9-C11	-3.28	99.45	109.70
19	K	305	6V7	C7-C2-N3	-3.17	112.30	117.47
19	K	305	6V7	C5-C4-N3	-2.54	118.53	121.97

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
19	N	307	6V7	C9
19	Y	306	6V7	C9

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	K	305	6V7	1	0
18	U	302	1PE	1	0
19	Y	306	6V7	1	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	A	230/234 (98%)	0.13	7 (3%) 51 51	27, 46, 86, 102	0
1	O	230/234 (98%)	0.81	41 (17%) 2 2	40, 68, 117, 148	0
2	B	248/261 (95%)	0.49	18 (7%) 16 16	32, 53, 98, 144	0
2	P	248/261 (95%)	1.02	51 (20%) 1 1	40, 64, 127, 174	0
3	C	236/248 (95%)	0.78	30 (12%) 4 4	36, 65, 112, 146	0
3	Q	238/248 (95%)	1.10	50 (21%) 1 1	33, 66, 138, 175	0
4	D	233/241 (96%)	0.38	20 (8%) 11 11	37, 62, 95, 139	0
4	R	233/241 (96%)	0.17	9 (3%) 40 40	30, 44, 75, 106	0
5	E	233/263 (88%)	0.27	14 (6%) 23 23	25, 41, 92, 116	0
5	S	237/263 (90%)	0.24	12 (5%) 29 29	32, 48, 86, 118	0
6	F	239/255 (93%)	-0.07	2 (0%) 86 85	22, 34, 59, 77	0
6	T	240/255 (94%)	0.47	23 (9%) 9 9	34, 57, 97, 137	0
7	G	241/246 (97%)	0.17	6 (2%) 58 57	23, 39, 73, 110	0
7	U	235/246 (95%)	0.85	39 (16%) 2 2	44, 67, 107, 136	0
8	H	220/234 (94%)	-0.02	6 (2%) 55 54	23, 35, 77, 133	0
8	V	220/234 (94%)	0.31	7 (3%) 48 48	34, 50, 91, 130	0
9	I	204/205 (99%)	0.11	2 (0%) 82 82	26, 36, 62, 81	0
9	W	204/205 (99%)	0.28	2 (0%) 82 82	34, 51, 80, 92	0
10	J	195/201 (97%)	0.05	4 (2%) 64 63	28, 43, 61, 84	0
10	X	195/201 (97%)	0.06	1 (0%) 90 90	32, 44, 60, 84	0
11	K	200/204 (98%)	0.25	4 (2%) 65 65	33, 47, 76, 97	0
11	Y	201/204 (98%)	0.13	3 (1%) 74 73	25, 35, 60, 81	0
12	L	213/213 (100%)	0.03	0 100 100	29, 49, 75, 95	0
12	Z	213/213 (100%)	0.12	6 (2%) 53 53	22, 36, 63, 86	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	216/219 (98%)	0.19	5 (2%) 61 60	23, 37, 65, 98	0
13	a	216/219 (98%)	0.07	3 (1%) 75 75	24, 38, 60, 86	0
14	N	202/205 (98%)	-0.07	0 100 100	22, 32, 55, 81	0
14	b	203/205 (99%)	0.27	6 (2%) 51 51	29, 41, 69, 97	0
All	All	6223/6458 (96%)	0.32	371 (5%) 23 23	22, 47, 93, 175	0

The worst 5 of 371 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	232	ILE	14.7
2	P	204	SER	13.5
4	D	241	ILE	10.8
2	P	203	VAL	10.8
3	Q	232	ILE	10.0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
7	6V1	G	161	15/16	0.94	0.14	-	32,53,59,62	0
10	6V1	J	91	15/16	0.94	0.18	-	32,51,60,60	0
3	YCM	C	63	10/11	0.92	0.11	-	58,62,76,78	0
5	6V1	E	148	15/16	0.93	0.14	-	31,59,70,71	0
7	6V1	G	47	15/16	0.94	0.15	-	39,60,67,69	0
10	6V1	X	91	15/16	0.92	0.20	-	34,57,64,68	0
7	YCM	U	137	10/11	0.91	0.14	-	54,64,77,80	0
3	YCM	Q	63	10/11	0.91	0.15	-	53,58,69,69	0
7	6V1	U	161	15/16	0.95	0.10	-	58,74,81,82	0
5	6V1	S	148	15/16	0.92	0.16	-	38,70,77,78	0
7	YCM	G	137	10/11	0.91	0.15	-	27,36,52,53	0
7	6V1	U	47	15/16	0.85	0.33	-	81,117,124,127	0

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
15	CL	K	304	1/1	0.91	0.20	9.02	80,80,80,80	0
18	1PE	H	305	16/16	0.84	0.26	9.01	60,83,112,113	0
18	1PE	N	304	16/16	0.82	0.31	5.57	72,74,112,114	0
18	1PE	L	302	16/16	0.80	0.35	5.18	75,84,119,120	0
18	1PE	I	303	16/16	0.89	0.16	3.41	60,62,82,83	0
15	CL	M	301	1/1	0.94	0.18	3.16	62,62,62,62	0
18	1PE	Y	305	16/16	0.82	0.16	3.15	59,75,81,84	0
15	CL	U	301	1/1	0.97	0.15	3.11	67,67,67,67	0
18	1PE	L	301	16/16	0.77	0.19	2.73	60,77,83,91	0
18	1PE	W	303	16/16	0.80	0.19	2.45	65,69,85,87	0
15	CL	a	302	1/1	0.89	0.17	2.29	69,69,69,69	0
15	CL	K	302	1/1	0.93	0.15	1.46	84,84,84,84	0
15	CL	E	303	1/1	0.96	0.13	1.42	74,74,74,74	0
15	CL	G	301	1/1	0.96	0.13	1.41	53,53,53,53	0
16	K	N	306	1/1	0.98	0.12	1.32	40,40,40,40	0
15	CL	S	301	1/1	0.95	0.14	1.25	81,81,81,81	0
15	CL	D	301	1/1	0.85	0.14	1.17	81,81,81,81	0
15	CL	Y	302	1/1	0.97	0.18	1.08	68,68,68,68	0
15	CL	Q	302	1/1	0.87	0.14	0.89	72,72,72,72	0
18	1PE	U	302	16/16	0.90	0.14	0.76	50,57,92,92	0
18	1PE	N	303	16/16	0.92	0.12	0.59	39,48,65,68	0
15	CL	A	304	1/1	0.92	0.10	0.34	63,63,63,63	0
19	6V7	N	307	30/30	0.97	0.11	0.32	25,26,37,38	0
15	CL	A	301	1/1	0.98	0.11	0.26	55,55,55,55	0
19	6V7	Y	306	30/30	0.96	0.12	0.25	24,28,34,37	0
19	6V7	K	305	30/30	0.94	0.11	0.10	34,37,46,49	0
19	6V7	b	304	30/30	0.95	0.14	0.08	32,36,44,45	0
15	CL	O	301	1/1	0.95	0.11	-0.13	61,61,61,61	0
15	CL	N	301	1/1	0.94	0.10	-0.40	68,68,68,68	0
15	CL	a	301	1/1	0.95	0.12	-0.46	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
16	K	b	303	1/1	0.96	0.10	-0.52	48,48,48,48	0
15	CL	Y	303	1/1	0.96	0.08	-0.76	68,68,68,68	0
16	K	Z	301	1/1	0.96	0.10	-0.87	41,41,41,41	0
15	CL	E	301	1/1	0.96	0.11	-0.95	68,68,68,68	0
15	CL	b	301	1/1	0.96	0.11	-0.99	69,69,69,69	0
15	CL	S	302	1/1	0.94	0.07	-1.15	72,72,72,72	0
15	CL	F	301	1/1	0.98	0.07	-1.34	61,61,61,61	0
15	CL	G	302	1/1	0.97	0.07	-1.41	68,68,68,68	0
15	CL	S	303	1/1	0.95	0.10	-1.56	59,59,59,59	0
15	CL	B	302	1/1	0.92	0.10	-1.57	64,64,64,64	0
17	MG	I	301	1/1	0.96	0.11	-1.60	33,33,33,33	0
17	MG	I	304	1/1	0.97	0.12	-1.75	29,29,29,29	0
16	K	U	303	1/1	0.96	0.08	-1.75	46,46,46,46	0
16	K	N	305	1/1	0.97	0.10	-2.06	41,41,41,41	0
15	CL	N	302	1/1	0.99	0.08	-2.15	59,59,59,59	0
17	MG	H	302	1/1	0.96	0.08	-2.16	32,32,32,32	0
17	MG	K	301	1/1	0.95	0.10	-2.51	37,37,37,37	0
16	K	G	303	1/1	0.98	0.06	-2.69	36,36,36,36	0
16	K	L	303	1/1	0.96	0.06	-3.34	53,53,53,53	0
17	MG	W	301	1/1	0.97	0.08	-3.36	37,37,37,37	0
17	MG	L	304	1/1	0.97	0.05	-3.66	39,39,39,39	0
16	K	b	302	1/1	0.96	0.09	-4.47	43,43,43,43	0
17	MG	V	301	1/1	0.58	0.23	-	85,85,85,85	0
15	CL	C	301	1/1	0.91	0.12	-	76,76,76,76	0
15	CL	O	303	1/1	0.82	0.10	-	99,99,99,99	0
15	CL	W	302	1/1	0.98	0.06	-	61,61,61,61	0
17	MG	X	301	1/1	0.98	0.08	-	58,58,58,58	0
15	CL	H	303	1/1	0.94	0.09	-	63,63,63,63	0
15	CL	K	303	1/1	0.91	0.12	-	74,74,74,74	0
15	CL	B	301	1/1	0.97	0.11	-	44,44,44,44	0
15	CL	M	302	1/1	0.97	0.10	-	42,42,42,42	0
15	CL	Y	301	1/1	0.97	0.14	-	69,69,69,69	0
15	CL	D	302	1/1	0.90	0.11	-	72,72,72,72	0
15	CL	O	304	1/1	0.87	0.12	-	77,77,77,77	0
15	CL	E	302	1/1	0.95	0.17	-	62,62,62,62	0
15	CL	M	303	1/1	0.92	0.11	-	65,65,65,65	0
15	CL	V	303	1/1	0.91	0.10	-	62,62,62,62	0
17	MG	H	301	1/1	0.94	0.16	-	71,71,71,71	0
15	CL	V	302	1/1	0.90	0.11	-	68,68,68,68	0
15	CL	I	302	1/1	0.94	0.08	-	51,51,51,51	0
15	CL	Q	301	1/1	0.97	0.14	-	84,84,84,84	0
15	CL	A	302	1/1	0.94	0.16	-	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
15	CL	H	304	1/1	0.97	0.06	-	50,50,50,50	0
15	CL	R	302	1/1	0.95	0.11	-	61,61,61,61	0
15	CL	C	302	1/1	0.95	0.13	-	76,76,76,76	0
15	CL	R	301	1/1	0.92	0.14	-	67,67,67,67	0
15	CL	P	301	1/1	0.96	0.14	-	56,56,56,56	0
17	MG	J	301	1/1	0.95	0.04	-	59,59,59,59	0
15	CL	Y	304	1/1	0.91	0.21	-	75,75,75,75	0
15	CL	a	304	1/1	0.93	0.14	-	67,67,67,67	0
15	CL	a	303	1/1	0.94	0.13	-	46,46,46,46	0
15	CL	O	302	1/1	0.96	0.09	-	72,72,72,72	0
15	CL	A	303	1/1	0.96	0.10	-	57,57,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.