



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 27, 2017 – 05:26 PM EDT

PDB ID : 5LF6
Title : Human 20S proteasome complex with Z-LLY-ketoaldehyde at 2.1 Angstrom
Authors : Schrader, J.; Henneberg, F.; Mata, R.; Tittmann, K.; Schneider, T.R.; Stark, H.; Bourenkov, G.; Chari, A.
Deposited on : unknown
Resolution : 2.07 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

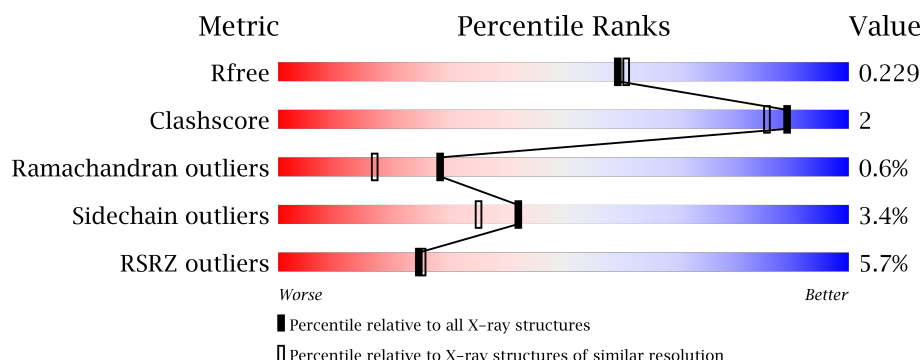
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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	2028 (2.08-2.04)
Clashscore	112137	2143 (2.08-2.04)
Ramachandran outliers	110173	2126 (2.08-2.04)
Sidechain outliers	110143	2126 (2.08-2.04)
RSRZ outliers	101464	2035 (2.08-2.04)

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>6%</div> <div>87%</div> <div>10%</div> <div>..</div> </div>
1	O	234	<div> <div>17%</div> <div>89%</div> <div>7%</div> <div>..</div> </div>
2	B	261	<div> <div>6%</div> <div>88%</div> <div>7%</div> <div>5%</div> </div>
2	P	261	<div> <div>15%</div> <div>84%</div> <div>10%</div> <div>5%</div> </div>
3	C	248	<div> <div>13%</div> <div>86%</div> <div>7%</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	c	3	
11	d	3	
12	K	204	
12	Y	204	
13	L	213	
13	Z	213	
14	M	219	
14	a	219	
15	N	205	
15	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
16	CL	K	302	-	-	-	X
16	CL	K	304	-	-	-	X
16	CL	N	301	-	-	-	X
16	CL	S	301	-	-	-	X
16	CL	Y	302	-	-	-	X
19	1PE	I	303	-	-	-	X
19	1PE	I	304	-	-	-	X
19	1PE	L	301	-	-	-	X
19	1PE	M	304	-	-	-	X
19	1PE	N	305	-	-	-	X
19	1PE	W	303	-	-	-	X
19	1PE	Z	301	-	-	-	X
19	1PE	a	304	-	-	-	X
20	PHQ	c	101	-	-	-	X
20	PHQ	d	101	-	-	-	X
7	6V1	U	47	X	-	-	-

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 51953 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			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	148	6V1	CYS	modified residue	UNP P25786
S	148	6V1	CYS	modified residue	UNP P25786

- 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			
10	X	196	Total	C	N	O	S	0	2	0
			1576	1012	267	287	10			

- Molecule 11 is a protein called LLY-ketoaldehyde peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	c	3	Total	C	N	O	0	0	0
			30	22	3	5			
11	d	3	Total	C	N	O	0	0	0
			30	22	3	5			

- Molecule 12 is a protein called Proteasome subunit beta type-5.

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

- Molecule 13 is a protein called Proteasome subunit beta type-1.

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

- Molecule 14 is a protein called Proteasome subunit beta type-4.

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

- Molecule 15 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	N	202	Total	C	N	O	S	0	1	0
			1516	950	258	295	13			
15	b	203	Total	C	N	O	S	0	1	0
			1524	956	259	296	13			

- Molecule 16 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	P	1	Total	Cl	0	0
			1	1		
16	K	3	Total	Cl	0	0
			3	3		
16	B	2	Total	Cl	0	0
			2	2		
16	W	1	Total	Cl	0	0
			1	1		
16	N	4	Total	Cl	0	0
			4	4		
16	S	3	Total	Cl	0	0
			3	3		
16	E	3	Total	Cl	0	0
			3	3		
16	b	3	Total	Cl	0	0
			3	3		
16	V	2	Total	Cl	0	0
			2	2		
16	A	4	Total	Cl	0	0
			4	4		
16	R	2	Total	Cl	0	0
			2	2		
16	M	3	Total	Cl	0	0
			3	3		
16	D	2	Total	Cl	0	0
			2	2		
16	I	1	Total	Cl	0	0
			1	1		
16	a	3	Total	Cl	0	0
			3	3		
16	U	1	Total	Cl	0	0
			1	1		
16	G	2	Total	Cl	0	0
			2	2		
16	Q	2	Total	Cl	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	H	2	Total 2	Cl 2	0	0
16	C	2	Total 2	Cl 2	0	0
16	O	4	Total 4	Cl 4	0	0
16	Y	4	Total 4	Cl 4	0	0
16	F	1	Total 1	Cl 1	0	0

- Molecule 17 is POTASSIUM ION (three-letter code: K) (formula: K).

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

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

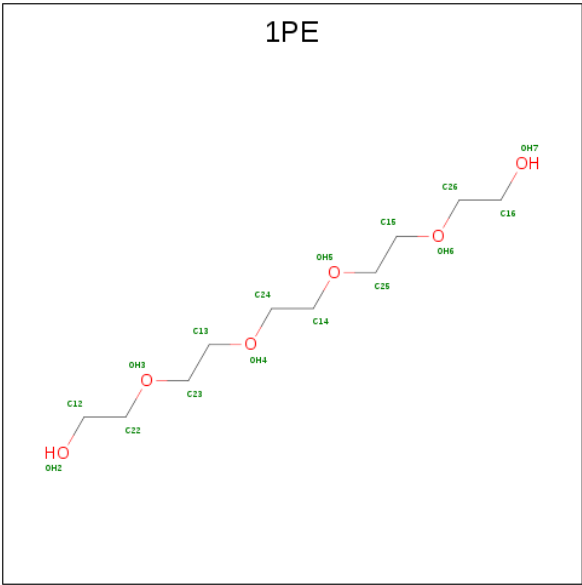
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	J	1	Total 1	Mg 1	0	0
18	K	1	Total 1	Mg 1	0	0
18	H	2	Total 2	Mg 2	0	0
18	I	2	Total 2	Mg 2	0	0
18	V	1	Total 1	Mg 1	0	0
18	W	1	Total 1	Mg 1	0	0

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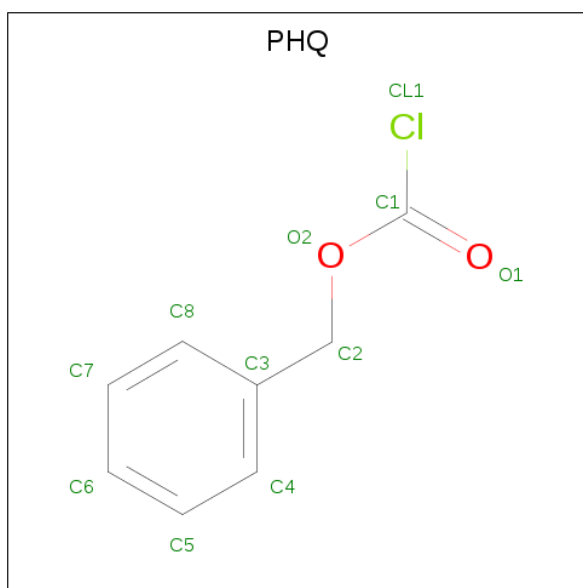
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	X	1	Total	Mg	0	0
			1	1		
18	L	1	Total	Mg	0	0
			1	1		

- Molecule 19 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	I	1	Total	C	O	0	0
			16	10	6		
19	I	1	Total	C	O	0	0
			16	10	6		
19	L	1	Total	C	O	0	0
			16	10	6		
19	M	1	Total	C	O	0	0
			16	10	6		
19	N	1	Total	C	O	0	0
			16	10	6		
19	W	1	Total	C	O	0	0
			16	10	6		
19	Z	1	Total	C	O	0	0
			16	10	6		
19	a	1	Total	C	O	0	0
			16	10	6		
19	b	1	Total	C	O	0	0
			16	10	6		

- Molecule 20 is benzyl chlorocarbonate (three-letter code: PHQ) (formula: $C_8H_7ClO_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
20	c	1	Total	C	O	0	0
			10	8	2		
20	d	1	Total	C	O	0	0
			10	8	2		

- Molecule 21 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
21	A	108	Total	O	0	0
			108	108		
21	B	119	Total	O	0	0
			119	119		
21	C	75	Total	O	0	0
			75	75		
21	D	86	Total	O	0	0
			86	86		
21	E	137	Total	O	0	0
			137	137		
21	F	179	Total	O	0	0
			179	179		
21	G	190	Total	O	0	0
			190	190		
21	H	150	Total	O	0	0
			150	150		
21	I	157	Total	O	0	0
			157	157		

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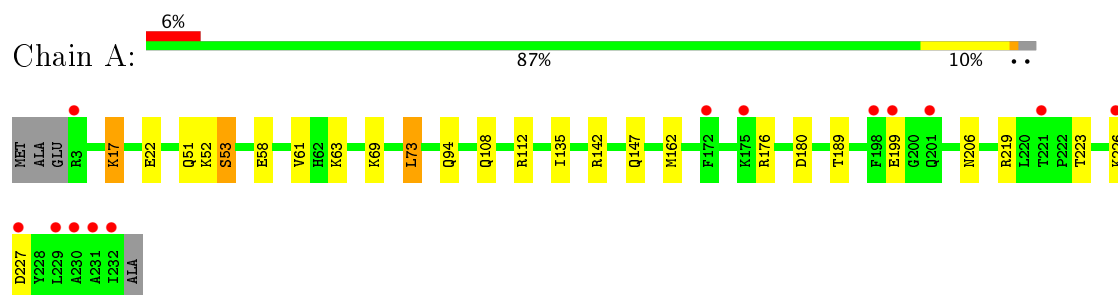
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
21	J	133	Total 133	O 133	0	0
21	c	3	Total 3	O 3	0	0
21	K	92	Total 92	O 92	0	0
21	L	121	Total 121	O 121	0	0
21	M	145	Total 145	O 145	0	0
21	N	156	Total 156	O 156	0	0
21	O	89	Total 89	O 89	0	0
21	P	109	Total 109	O 109	0	0
21	Q	71	Total 71	O 71	0	0
21	R	119	Total 119	O 119	0	0
21	S	124	Total 124	O 124	0	0
21	T	91	Total 91	O 91	0	0
21	U	103	Total 103	O 103	0	0
21	V	109	Total 109	O 109	0	0
21	W	108	Total 108	O 108	0	0
21	X	124	Total 124	O 124	0	0
21	d	2	Total 2	O 2	0	0
21	Y	141	Total 141	O 141	0	0
21	Z	167	Total 167	O 167	0	0
21	a	172	Total 172	O 172	0	0
21	b	121	Total 121	O 121	0	0

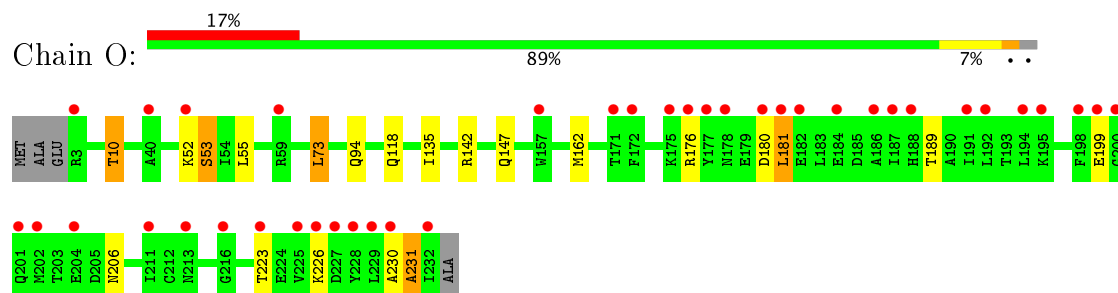
3 Residue-property plots [i](#)

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.

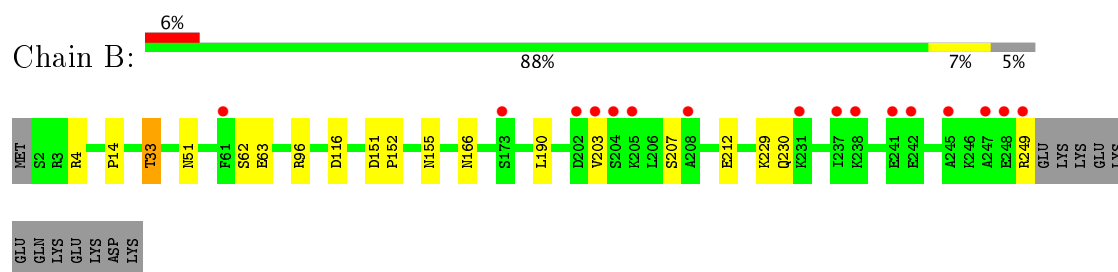
- Molecule 1: Proteasome subunit alpha type-2



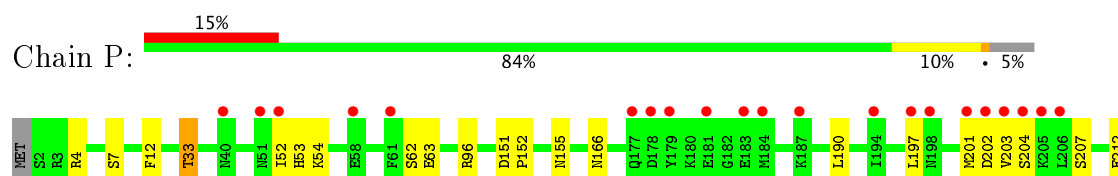
- Molecule 1: Proteasome subunit alpha type-2

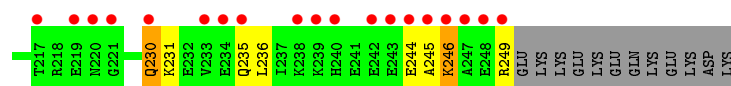


- Molecule 2: Proteasome subunit alpha type-4

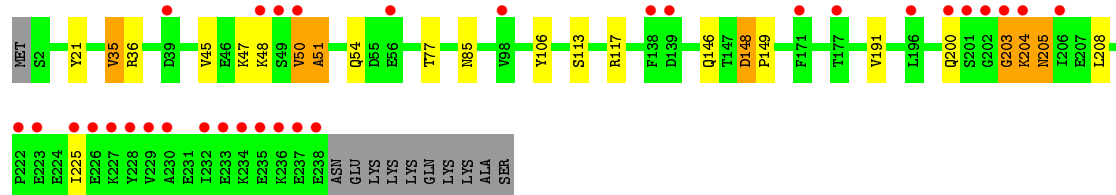
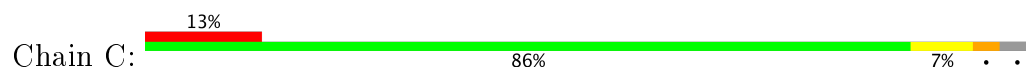


- Molecule 2: Proteasome subunit alpha type-4

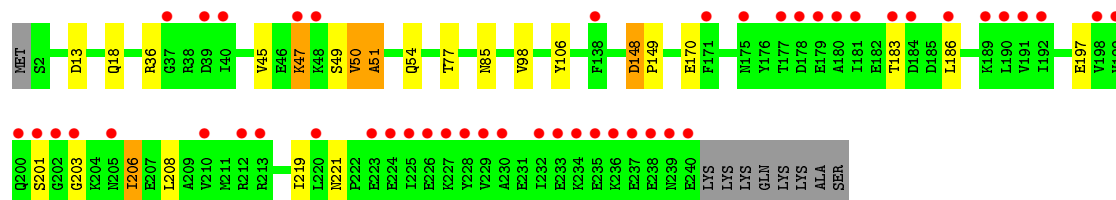
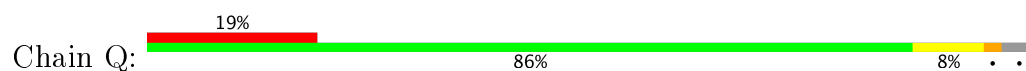




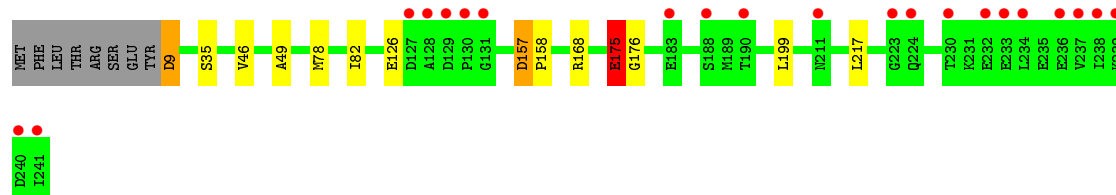
• Molecule 3: Proteasome subunit alpha type-7



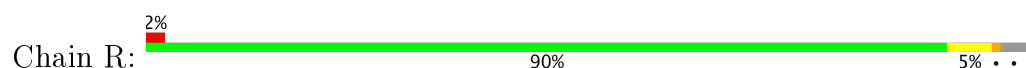
• Molecule 3: Proteasome subunit alpha type-7



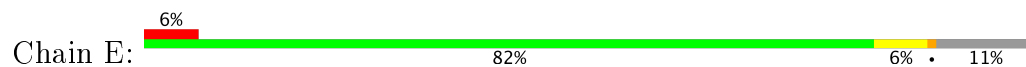
• Molecule 4: Proteasome subunit alpha type-5



• Molecule 4: Proteasome subunit alpha type-5



• Molecule 5: Proteasome subunit alpha type-1



ALA
GLN
PRO
ALA
GLN
PRO
ALA
ASP
GLU
PRO
ALA
GLY
LYS
ALA
ASP
GLU
PRO
MET
GLU
HIS

• Molecule 5: Proteasome subunit alpha type-1

Chain S: 5% 83% 7% 10%

MET F2 R3 N4 R18 E23 V45 L46 V47 A48 L49 K50 Q53 L56 A57 A58 H59 H65 R101 R122 N152 Y153 F164 A158 R174 H175 M176 F179 L195 K217 E234 G235 L236 E237 E238 R239 PRO GLN ARG LYS ALA GLN PRO ALA GLN

PRO
ALA
ASP
GLU
PRO
ALA
GLY
LYS
ALA
ASP
GLU
PRO
MET
GLU
HIS

• Molecule 6: Proteasome subunit alpha type-3

Chain F: 0% 82% 11% 6%

MET SER SER ILE GLY THR G6 D17 K28 S33 S34 V53 K64 R65 L81 R85 S86 L87 R99 N105 D113 R114 M117 C133 I151 D152 V156 R169 V190 V204 W215 E218 L219 T220 N221 V227 R232 K240

L243 K244 GLU GLU ASP ASP ASP ASP MET

• Molecule 6: Proteasome subunit alpha type-3

Chain T: 6% 82% 11% 6%

MET SER SER ILE GLY T5 G6 Y7 D17 M27 S33 S34 V53 L57 M63 K64 R65 L81 R85 S86 L87 D113 R114 M117 C133 D152 V156 R169 Q170 A171 A172 K173 V190 K191 I199 D202 E203 V204 K205 D206 K207 A208 F209

K215 R223 D230 Y238 K239 K240 S242 L243 K244 GLU ASP ASP SER ASP ASP ASP MET

• Molecule 7: Proteasome subunit alpha type-6

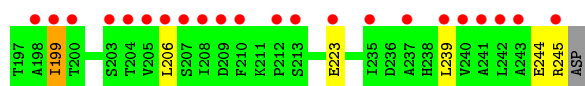
Chain G: 4% 93% 5% 2%

MET S2 R3 G8 V49 P57 I72 C78 R88 E108 L114 R117 D120 L140 V183 K186 F187 D188 V189 T190 L206 D209 V219 R245 ASP

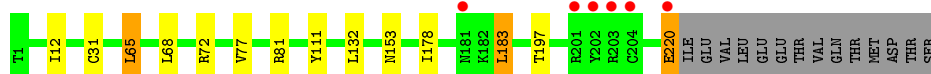
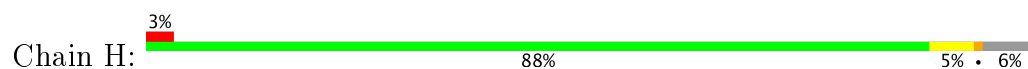
• Molecule 7: Proteasome subunit alpha type-6

Chain U: 14% 87% 7% 2%

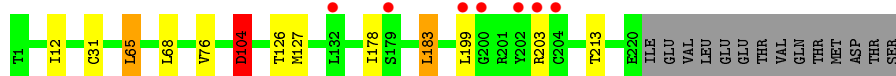
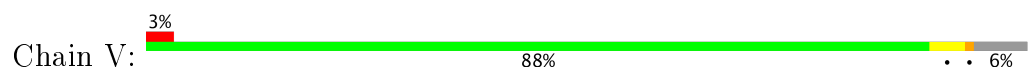
MET S2 R3 R11 R43 D46 V56 P57 D58 K59 D62 I72 C78 V79 R80 D86 S87 R88 V91 E108 L114 R117 I118 L140 V151 T173 T176 S177 F178 L179 V183 K186 PHE ASP TRP THR PHE GLU Q193 T194 V195 E196



- Molecule 8: Proteasome subunit beta type-7



- Molecule 8: Proteasome subunit beta type-7



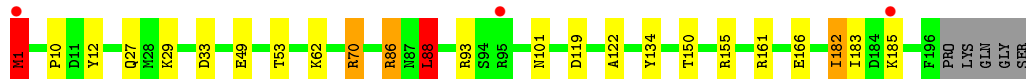
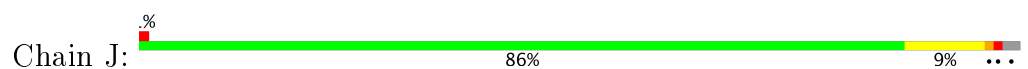
- Molecule 9: Proteasome subunit beta type-3



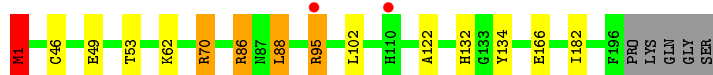
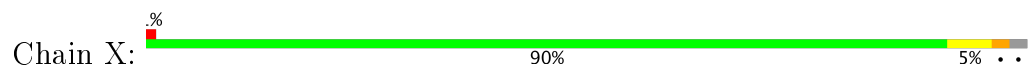
- Molecule 9: Proteasome subunit beta type-3



- Molecule 10: Proteasome subunit beta type-2



- Molecule 10: Proteasome subunit beta type-2



- Molecule 11: LLY-ketoaldehyde peptide




There are no outlier residues recorded for this chain.

- Molecule 11: LLY-ketoaldehyde peptide

Chain d:  100%


There are no outlier residues recorded for this chain.

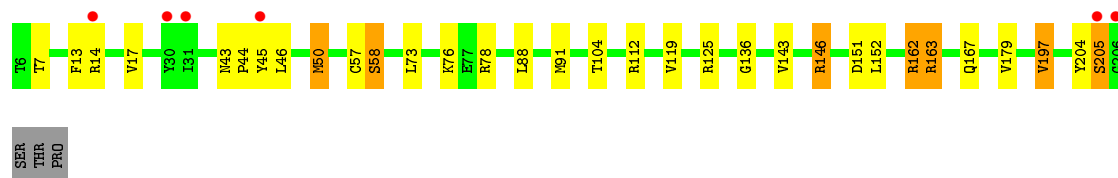
- Molecule 12: Proteasome subunit beta type-5

Chain K:  86% 10% ..



- Molecule 12: Proteasome subunit beta type-5

Chain Y:  83% 12% ..



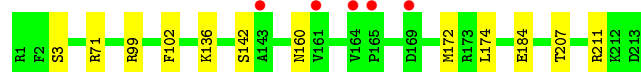
- Molecule 13: Proteasome subunit beta type-1

Chain L:  93% 7%



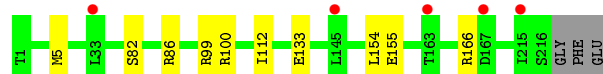
- Molecule 13: Proteasome subunit beta type-1

Chain Z:  94% 6% 2%



- Molecule 14: Proteasome subunit beta type-4

Chain M:  94% 5% 2%

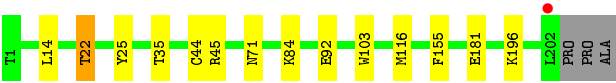


- Molecule 14: Proteasome subunit beta type-4

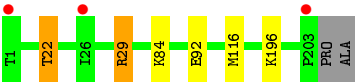
Chain a:  94% 5% 1%



● Molecule 15: Proteasome subunit beta type-6



● Molecule 15: 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	113.87Å 203.48Å 315.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	171.02 – 2.07 49.08 – 2.07	Depositor EDS
% Data completeness (in resolution range)	96.4 (171.02-2.07) 96.4 (49.08-2.07)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 2.07Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.186 , 0.227 0.193 , 0.229	Depositor DCC
R_{free} test set	21152 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	43.8	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.4	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	51953	wwPDB-VP
Average B, all atoms (Å ²)	54.0	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, K, 6V1, 1PE, YCM, 6VF, PHQ

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	0.71	0/1833	0.81	2/2489 (0.1%)
1	O	0.61	0/1778	0.79	2/2419 (0.1%)
2	B	0.78	0/1962	0.86	4/2649 (0.2%)
2	P	0.65	0/1945	0.84	2/2631 (0.1%)
3	C	0.73	1/1818 (0.1%)	0.91	2/2469 (0.1%)
3	Q	0.70	1/1834 (0.1%)	0.89	2/2490 (0.1%)
4	D	0.69	0/1789	0.85	5/2424 (0.2%)
4	R	0.81	1/1780 (0.1%)	0.93	5/2408 (0.2%)
5	E	0.74	0/1842	0.85	2/2493 (0.1%)
5	S	0.75	0/1901	0.86	2/2571 (0.1%)
6	F	0.87	1/1935 (0.1%)	0.95	8/2605 (0.3%)
6	T	0.78	0/1894	0.96	11/2556 (0.4%)
7	G	0.84	3/1909 (0.2%)	0.86	5/2579 (0.2%)
7	U	0.69	1/1804 (0.1%)	0.85	6/2441 (0.2%)
8	H	0.84	0/1697	0.93	4/2299 (0.2%)
8	V	0.69	0/1655	0.87	3/2251 (0.1%)
9	I	0.82	0/1648	1.05	9/2219 (0.4%)
9	W	0.65	0/1630	0.96	7/2197 (0.3%)
10	J	0.84	0/1613	0.99	7/2180 (0.3%)
10	X	0.73	0/1599	0.96	4/2163 (0.2%)
11	c	0.69	0/15	1.15	0/19
11	d	0.85	0/15	1.08	0/19
12	K	0.77	0/1584	0.96	10/2141 (0.5%)
12	Y	0.88	0/1620	1.08	11/2185 (0.5%)
13	L	0.71	0/1672	0.86	3/2257 (0.1%)
13	Z	0.87	2/1675 (0.1%)	0.91	4/2257 (0.2%)
14	M	0.81	0/1728	0.93	3/2339 (0.1%)
14	a	0.87	1/1724 (0.1%)	0.95	3/2336 (0.1%)
15	N	0.90	0/1545	0.89	3/2091 (0.1%)
15	b	0.88	1/1554 (0.1%)	0.90	4/2104 (0.2%)
All	All	0.77	12/48998 (0.0%)	0.91	133/66281 (0.2%)

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	4
3	Q	0	2
4	D	0	2
4	R	0	2
6	T	0	1
7	U	1	0
9	I	0	1
9	W	0	1
10	J	0	2
10	X	0	1
14	a	0	1
All	All	1	17

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	108	GLU	CD-OE1	9.58	1.36	1.25
15	b	92	GLU	CD-OE2	7.86	1.34	1.25
3	Q	13	ASP	CB-CG	6.72	1.65	1.51
14	a	75	GLU	CD-OE1	5.71	1.31	1.25
7	G	108	GLU	CD-OE2	5.66	1.31	1.25

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	I	69	ARG	NE-CZ-NH1	14.57	127.58	120.30
9	W	69	ARG	NE-CZ-NH1	13.28	126.94	120.30
9	I	69	ARG	NE-CZ-NH2	-11.86	114.37	120.30
10	J	86	ARG	NE-CZ-NH2	-11.17	114.72	120.30
9	W	69	ARG	NE-CZ-NH2	-11.02	114.79	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	175[A]	GLU	Peptide
4	D	175[B]	GLU	Peptide
9	I	78	GLY	Peptide
10	J	1[A]	MET	Peptide
10	J	1[B]	MET	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	9	0
1	O	1741	0	1683	6	0
2	B	1926	0	1924	6	0
2	P	1909	0	1874	8	0
3	C	1798	0	1718	15	0
3	Q	1820	0	1749	7	0
4	D	1762	0	1709	3	0
4	R	1753	0	1726	6	0
5	E	1822	0	1779	9	0
5	S	1875	0	1818	21	0
6	F	1888	0	1882	13	0
6	T	1856	0	1816	8	0
7	G	1912	0	1882	5	0
7	U	1815	0	1748	10	0
8	H	1664	0	1681	7	0
8	V	1622	0	1595	5	0
9	I	1613	0	1646	6	0
9	W	1599	0	1621	6	0
10	J	1590	0	1581	17	0
10	X	1576	0	1561	12	0
11	c	30	0	21	0	0
11	d	30	0	21	0	0
12	K	1550	0	1503	7	0
12	Y	1580	0	1554	19	0
13	L	1636	0	1625	5	0
13	Z	1642	0	1635	3	0
14	M	1692	0	1670	4	0
14	a	1688	0	1658	0	0
15	N	1516	0	1487	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	b	1524	0	1496	0	0
16	A	4	0	0	1	0
16	B	2	0	0	1	0
16	C	2	0	0	0	0
16	D	2	0	0	0	0
16	E	3	0	0	0	0
16	F	1	0	0	0	0
16	G	2	0	0	1	0
16	H	2	0	0	0	0
16	I	1	0	0	0	0
16	K	3	0	0	0	0
16	M	3	0	0	0	0
16	N	4	0	0	0	0
16	O	4	0	0	0	0
16	P	1	0	0	0	0
16	Q	2	0	0	0	0
16	R	2	0	0	0	0
16	S	3	0	0	0	0
16	U	1	0	0	0	0
16	V	2	0	0	0	0
16	W	1	0	0	0	0
16	Y	4	0	0	0	0
16	a	3	0	0	0	0
16	b	3	0	0	0	0
17	G	1	0	0	0	0
17	L	1	0	0	0	0
17	N	1	0	0	0	0
17	U	1	0	0	0	0
17	Z	1	0	0	0	0
17	b	1	0	0	0	0
18	H	2	0	0	0	0
18	I	2	0	0	0	0
18	J	1	0	0	0	0
18	K	1	0	0	0	0
18	L	1	0	0	0	0
18	V	1	0	0	0	0
18	W	1	0	0	0	0
18	X	1	0	0	0	0
19	I	32	0	44	0	0
19	L	16	0	22	0	0
19	M	16	0	22	0	0
19	N	16	0	22	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	W	16	0	22	0	0
19	Z	16	0	22	0	0
19	a	16	0	22	0	0
19	b	16	0	22	0	0
20	c	10	0	7	0	0
20	d	10	0	7	0	0
21	A	108	0	0	1	0
21	B	119	0	0	0	0
21	C	75	0	0	0	0
21	D	86	0	0	0	0
21	E	137	0	0	2	0
21	F	179	0	0	6	0
21	G	190	0	0	0	0
21	H	150	0	0	2	0
21	I	157	0	0	1	0
21	J	133	0	0	3	0
21	K	92	0	0	0	0
21	L	121	0	0	0	0
21	M	145	0	0	0	0
21	N	156	0	0	1	0
21	O	89	0	0	1	0
21	P	109	0	0	0	0
21	Q	71	0	0	1	0
21	R	119	0	0	0	0
21	S	124	0	0	5	0
21	T	91	0	0	1	0
21	U	103	0	0	0	0
21	V	109	0	0	0	0
21	W	108	0	0	1	0
21	X	124	0	0	1	0
21	Y	141	0	0	0	0
21	Z	167	0	0	1	0
21	a	172	0	0	0	0
21	b	121	0	0	0	0
21	c	3	0	0	0	0
21	d	2	0	0	0	0
All	All	51953	0	47636	201	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 201 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)
5:S:152[B]:ASN:ND2	21:S:401:HOH:O	2.07	0.87
5:S:65[A]:HIS:CE1	21:S:402:HOH:O	2.29	0.84
10:J:185:LYS:NZ	21:J:401:HOH:O	2.10	0.84
12:Y:50:MET:HE1	12:Y:58:SER:HA	1.63	0.80
10:J:1[A]:MET:HE1	10:J:134:TYR:H	1.50	0.75

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	231/234 (99%)	218 (94%)	9 (4%)	4 (2%)	11	3
1	O	228/234 (97%)	214 (94%)	9 (4%)	5 (2%)	8	1
2	B	248/261 (95%)	234 (94%)	13 (5%)	1 (0%)	38	27
2	P	248/261 (95%)	234 (94%)	12 (5%)	2 (1%)	22	11
3	C	236/248 (95%)	217 (92%)	14 (6%)	5 (2%)	8	2
3	Q	236/248 (95%)	217 (92%)	12 (5%)	7 (3%)	5	1
4	D	232/241 (96%)	223 (96%)	6 (3%)	3 (1%)	14	5
4	R	232/241 (96%)	221 (95%)	8 (3%)	3 (1%)	14	5
5	E	232/263 (88%)	226 (97%)	4 (2%)	2 (1%)	20	9
5	S	238/263 (90%)	231 (97%)	6 (2%)	1 (0%)	38	27
6	F	241/255 (94%)	238 (99%)	3 (1%)	0	100	100
6	T	239/255 (94%)	230 (96%)	6 (2%)	3 (1%)	14	5
7	G	241/246 (98%)	235 (98%)	6 (2%)	0	100	100
7	U	232/246 (94%)	227 (98%)	3 (1%)	2 (1%)	20	9
8	H	220/234 (94%)	217 (99%)	3 (1%)	0	100	100
8	V	220/234 (94%)	216 (98%)	3 (1%)	1 (0%)	32	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	205/205 (100%)	200 (98%)	5 (2%)	0	100	100
9	W	204/205 (100%)	198 (97%)	6 (3%)	0	100	100
10	J	195/201 (97%)	191 (98%)	4 (2%)	0	100	100
10	X	195/201 (97%)	192 (98%)	3 (2%)	0	100	100
12	K	199/204 (98%)	196 (98%)	3 (2%)	0	100	100
12	Y	202/204 (99%)	198 (98%)	3 (2%)	1 (0%)	32	21
13	L	213/213 (100%)	211 (99%)	2 (1%)	0	100	100
13	Z	212/213 (100%)	210 (99%)	2 (1%)	0	100	100
14	M	215/219 (98%)	208 (97%)	7 (3%)	0	100	100
14	a	216/219 (99%)	207 (96%)	9 (4%)	0	100	100
15	N	201/205 (98%)	200 (100%)	1 (0%)	0	100	100
15	b	202/205 (98%)	201 (100%)	1 (0%)	0	100	100
All	All	6213/6458 (96%)	6010 (97%)	163 (3%)	40 (1%)	28	17

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	LYS
1	A	53	SER
4	D	176	GLY
5	E	59	HIS
1	O	52	LYS

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%)	174 (94%)	11 (6%)	23	13
1	O	176/191 (92%)	166 (94%)	10 (6%)	24	14
2	B	200/221 (90%)	193 (96%)	7 (4%)	41	33
2	P	197/221 (89%)	184 (93%)	13 (7%)	19	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	179/210 (85%)	171 (96%)	8 (4%)	32	23
3	Q	184/210 (88%)	175 (95%)	9 (5%)	29	20
4	D	189/203 (93%)	184 (97%)	5 (3%)	51	46
4	R	187/203 (92%)	184 (98%)	3 (2%)	68	64
5	E	192/223 (86%)	185 (96%)	7 (4%)	40	32
5	S	197/223 (88%)	195 (99%)	2 (1%)	80	79
6	F	199/212 (94%)	189 (95%)	10 (5%)	28	19
6	T	192/212 (91%)	182 (95%)	10 (5%)	27	17
7	G	202/207 (98%)	197 (98%)	5 (2%)	53	47
7	U	186/207 (90%)	181 (97%)	5 (3%)	50	44
8	H	181/195 (93%)	175 (97%)	6 (3%)	43	36
8	V	172/195 (88%)	165 (96%)	7 (4%)	35	27
9	I	176/174 (101%)	174 (99%)	2 (1%)	78	76
9	W	173/174 (99%)	172 (99%)	1 (1%)	89	89
10	J	166/170 (98%)	160 (96%)	6 (4%)	40	32
10	X	165/170 (97%)	161 (98%)	4 (2%)	54	49
11	c	2/2 (100%)	2 (100%)	0	100	100
11	d	2/2 (100%)	2 (100%)	0	100	100
12	K	155/159 (98%)	146 (94%)	9 (6%)	23	13
12	Y	159/159 (100%)	152 (96%)	7 (4%)	33	24
13	L	175/178 (98%)	169 (97%)	6 (3%)	42	35
13	Z	175/178 (98%)	172 (98%)	3 (2%)	66	62
14	M	180/181 (99%)	176 (98%)	4 (2%)	57	52
14	a	178/181 (98%)	172 (97%)	6 (3%)	42	35
15	N	157/159 (99%)	154 (98%)	3 (2%)	62	58
15	b	158/159 (99%)	154 (98%)	4 (2%)	53	47
All	All	5039/5370 (94%)	4866 (97%)	173 (3%)	42	35

5 of 173 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	L	102	PHE
1	O	206	ASN

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Mol	Chain	Res	Type
12	Y	197	VAL
13	L	174	LEU
15	N	84	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
14	M	162	GLN
2	P	109	GLN
13	Z	157	ASN
1	O	118	GLN
1	O	206	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	1.12	1 (11%)	4,10,12	1.41	1 (25%)
5	6V1	E	148	5	13,15,16	1.25	2 (15%)	12,20,22	2.44	5 (41%)
7	YCM	G	137	7	9,9,10	2.08	5 (55%)	4,10,12	2.99	1 (25%)
7	6V1	G	161	7	13,15,16	1.42	2 (15%)	12,20,22	2.32	5 (41%)
7	6V1	G	47	7	13,15,16	1.67	2 (15%)	12,20,22	1.24	2 (16%)
10	6V1	J	91	10	13,15,16	1.51	1 (7%)	12,20,22	4.06	7 (58%)
3	YCM	Q	63	3	9,9,10	1.53	2 (22%)	4,10,12	4.24	3 (75%)
5	6V1	S	148	5	13,15,16	1.39	3 (23%)	12,20,22	2.32	5 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	YCM	U	137	7	9,9,10	1.12	1 (11%)	4,10,12	2.23	1 (25%)
7	6V1	U	161	7	13,15,16	1.30	2 (15%)	12,20,22	3.17	5 (41%)
7	6V1	U	47	7	13,15,16	1.31	2 (15%)	12,20,22	1.84	3 (25%)
10	6V1	X	91	10	13,15,16	1.81	3 (23%)	12,20,22	4.29	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	-	0/6/25/27	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 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	X	91	6V1	C1-SG	-4.48	1.77	1.83
10	J	91	6V1	C1-SG	-4.21	1.78	1.83
7	G	47	6V1	C4-N3	-3.89	1.31	1.38
7	G	47	6V1	C2-N3	-3.66	1.33	1.38
7	G	161	6V1	C4-N3	-3.33	1.32	1.38

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	U	161	6V1	C2-N3-C4	-7.56	108.26	113.06
3	Q	63	YCM	CE-CD-SG	-6.26	98.41	113.17
10	X	91	6V1	C2-N3-C4	-5.82	109.36	113.06
5	E	148	6V1	C2-N3-C4	-5.38	109.64	113.06
10	J	91	6V1	C2-N3-C4	-5.09	109.83	113.06

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 82 ligands modelled in this entry, 71 are monoatomic - leaving 11 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	$\# Z > 2$
19	1PE	I	303	-	15,15,15	0.58	0	14,14,14	1.09	2 (14%)
19	1PE	I	304	-	15,15,15	0.52	0	14,14,14	0.51	0
19	1PE	L	301	-	15,15,15	0.59	0	14,14,14	0.71	0
19	1PE	M	304	-	15,15,15	0.54	0	14,14,14	0.37	0
19	1PE	N	305	-	15,15,15	0.57	0	14,14,14	0.57	0
19	1PE	W	303	-	15,15,15	0.53	0	14,14,14	0.42	0
19	1PE	Z	301	-	15,15,15	0.55	0	14,14,14	0.39	0
19	1PE	a	304	-	15,15,15	0.53	0	14,14,14	0.41	0
19	1PE	b	304	-	15,15,15	0.68	0	14,14,14	0.77	0
20	PHQ	c	101	11	9,10,11	1.93	3 (33%)	10,11,13	2.42	1 (10%)
20	PHQ	d	101	11	9,10,11	2.19	4 (44%)	10,11,13	2.48	1 (10%)

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
19	1PE	I	303	-	-	0/13/13/13	0/0/0/0
19	1PE	I	304	-	-	0/13/13/13	0/0/0/0
19	1PE	L	301	-	-	0/13/13/13	0/0/0/0
19	1PE	M	304	-	-	0/13/13/13	0/0/0/0
19	1PE	N	305	-	-	0/13/13/13	0/0/0/0
19	1PE	W	303	-	-	0/13/13/13	0/0/0/0
19	1PE	Z	301	-	-	0/13/13/13	0/0/0/0
19	1PE	a	304	-	-	0/13/13/13	0/0/0/0
19	1PE	b	304	-	-	0/13/13/13	0/0/0/0
20	PHQ	c	101	11	-	0/4/4/5	0/1/1/1
20	PHQ	d	101	11	-	0/4/4/5	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	d	101	PHQ	C8-C3	2.16	1.43	1.38
20	c	101	PHQ	C4-C3	2.19	1.43	1.38
20	d	101	PHQ	C4-C3	2.30	1.43	1.38
20	c	101	PHQ	O2-C1	3.01	1.41	1.32
20	d	101	PHQ	C2-C3	3.13	1.57	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	I	303	1PE	OH5-C25-C15	2.28	120.85	110.41
19	I	303	1PE	C25-OH5-C14	2.73	125.12	113.30
20	c	101	PHQ	O2-C2-C3	7.32	127.59	109.41
20	d	101	PHQ	O2-C2-C3	7.47	127.96	109.41

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 ⓘ

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%)	0.07	13 (5%) 24 25	34, 52, 90, 106	0
1	O	230/234 (98%)	0.71	39 (16%) 2 1	43, 70, 110, 140	0
2	B	248/261 (95%)	0.29	16 (6%) 20 20	36, 56, 99, 133	0
2	P	248/261 (95%)	0.83	40 (16%) 2 2	45, 66, 117, 153	0
3	C	236/248 (95%)	0.69	32 (13%) 3 3	41, 67, 112, 136	0
3	Q	238/248 (95%)	1.02	48 (20%) 1 1	36, 68, 128, 154	0
4	D	233/241 (96%)	0.27	21 (9%) 10 10	41, 67, 99, 141	0
4	R	233/241 (96%)	-0.02	5 (2%) 64 66	32, 47, 75, 115	0
5	E	233/263 (88%)	0.17	15 (6%) 20 20	32, 47, 98, 121	0
5	S	237/263 (90%)	0.13	14 (5%) 23 24	36, 50, 89, 110	0
6	F	239/255 (93%)	-0.11	2 (0%) 86 87	30, 39, 64, 80	0
6	T	240/255 (94%)	0.27	16 (6%) 19 19	36, 55, 92, 134	0
7	G	241/246 (97%)	0.22	9 (3%) 42 44	30, 43, 80, 113	0
7	U	235/246 (95%)	0.72	35 (14%) 3 2	46, 64, 98, 116	0
8	H	220/234 (94%)	-0.09	6 (2%) 55 58	30, 39, 70, 117	0
8	V	220/234 (94%)	0.15	7 (3%) 48 51	38, 54, 85, 123	0
9	I	204/205 (99%)	0.02	1 (0%) 90 92	31, 40, 61, 73	0
9	W	204/205 (99%)	0.08	3 (1%) 74 75	40, 55, 81, 93	0
10	J	195/201 (97%)	-0.14	3 (1%) 74 75	33, 43, 61, 85	0
10	X	195/201 (97%)	-0.03	2 (1%) 82 84	34, 47, 62, 86	0
11	c	2/3 (66%)	0.46	0 100 100	40, 40, 40, 43	0
11	d	2/3 (66%)	0.29	0 100 100	32, 32, 32, 36	0
12	K	200/204 (98%)	0.15	3 (1%) 74 75	38, 51, 78, 95	0
12	Y	201/204 (98%)	0.07	6 (2%) 51 54	30, 40, 61, 78	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	L	213/213 (100%)	-0.08	0	100 100	36, 54, 77, 91	0
13	Z	213/213 (100%)	0.11	5 (2%)	61 63	30, 40, 64, 78	0
14	M	216/219 (98%)	0.15	5 (2%)	61 63	30, 43, 68, 103	0
14	a	216/219 (98%)	-0.00	3 (1%)	75 77	30, 42, 64, 97	0
15	N	202/205 (98%)	-0.09	1 (0%)	90 92	29, 37, 59, 94	0
15	b	203/205 (99%)	0.13	3 (1%)	74 75	33, 42, 71, 99	0
All	All	6227/6464 (96%)	0.21	353 (5%)	24 25	29, 50, 93, 154	0

The worst 5 of 353 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	204	SER	19.2
1	O	232	ILE	11.3
3	Q	232	ILE	10.0
2	P	203	VAL	9.8
3	Q	238	GLU	9.5

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

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	U	47	15/16	0.85	0.33	-	79,115,121,123	0
7	YCM	G	137	10/11	0.89	0.14	-	37,44,55,55	0
3	YCM	C	63	10/11	0.90	0.12	-	63,66,76,78	0
7	6V1	G	161	15/16	0.94	0.12	-	40,59,63,63	0
7	6V1	U	161	15/16	0.91	0.11	-	60,86,92,92	0
7	YCM	U	137	10/11	0.86	0.18	-	55,65,80,83	0
5	6V1	E	148	15/16	0.91	0.14	-	39,64,73,74	0
7	6V1	G	47	15/16	0.94	0.13	-	42,67,70,75	0
10	6V1	X	91	15/16	0.93	0.18	-	41,58,63,71	0
3	YCM	Q	63	10/11	0.91	0.14	-	57,61,67,67	0
10	6V1	J	91	15/16	0.94	0.17	-	37,57,65,66	0
5	6V1	S	148	15/16	0.92	0.15	-	40,71,78,81	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
19	1PE	I	304	16/16	0.79	0.29	21.24	69,85,101,102	0
19	1PE	Z	301	16/16	0.78	0.17	7.07	59,72,80,84	0
20	PHQ	d	101	10/11	0.69	0.28	5.17	46,72,78,79	0
20	PHQ	c	101	10/11	0.65	0.24	4.77	49,78,81,83	0
16	CL	K	302	1/1	0.87	0.26	4.73	92,92,92,92	0
16	CL	S	301	1/1	0.93	0.23	4.03	76,76,76,76	0
19	1PE	I	303	16/16	0.83	0.16	3.89	59,68,77,84	0
16	CL	K	304	1/1	0.88	0.15	3.69	79,79,79,79	0
19	1PE	N	305	16/16	0.84	0.16	3.59	44,57,68,68	0
19	1PE	M	304	16/16	0.79	0.32	3.33	69,80,114,115	0
19	1PE	a	304	16/16	0.86	0.26	2.97	62,70,101,101	0
19	1PE	L	301	16/16	0.70	0.17	2.81	65,79,84,90	0
16	CL	Y	302	1/1	0.87	0.30	2.63	90,90,90,90	0
19	1PE	W	303	16/16	0.81	0.18	2.58	68,73,84,87	0
16	CL	N	301	1/1	0.93	0.20	2.51	55,55,55,55	0
16	CL	E	303	1/1	0.95	0.13	1.19	75,75,75,75	0
19	1PE	b	304	16/16	0.84	0.16	1.09	50,58,92,98	0
16	CL	S	303	1/1	0.98	0.14	0.61	60,60,60,60	0
16	CL	M	301	1/1	0.95	0.13	0.41	67,67,67,67	0
16	CL	E	301	1/1	0.95	0.13	-0.10	69,69,69,69	0
16	CL	D	301	1/1	0.82	0.11	-0.20	83,83,83,83	0
16	CL	b	303	1/1	0.96	0.15	-0.20	64,64,64,64	0
16	CL	a	301	1/1	0.93	0.10	-0.69	69,69,69,69	0
16	CL	G	301	1/1	0.96	0.10	-0.78	52,52,52,52	0
16	CL	B	302	1/1	0.93	0.12	-0.88	69,69,69,69	0
16	CL	S	302	1/1	0.94	0.09	-0.99	76,76,76,76	0
16	CL	b	302	1/1	0.98	0.12	-1.14	68,68,68,68	0
17	K	Z	302	1/1	0.97	0.11	-1.37	44,44,44,44	0
16	CL	N	304	1/1	0.96	0.10	-1.51	50,50,50,50	0
16	CL	O	301	1/1	0.96	0.07	-1.62	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
16	CL	Y	303	1/1	0.93	0.07	-1.69	66,66,66,66	0
16	CL	N	303	1/1	0.93	0.10	-1.83	70,70,70,70	0
16	CL	A	301	1/1	0.97	0.06	-2.21	64,64,64,64	0
16	CL	F	301	1/1	0.97	0.05	-2.45	60,60,60,60	0
16	CL	U	301	1/1	0.96	0.06	-2.77	67,67,67,67	0
18	MG	I	305	1/1	0.97	0.09	-2.86	29,29,29,29	0
18	MG	I	301	1/1	0.93	0.07	-2.87	34,34,34,34	0
18	MG	W	301	1/1	0.94	0.06	-2.91	43,43,43,43	0
18	MG	K	301	1/1	0.97	0.08	-3.03	40,40,40,40	0
16	CL	A	304	1/1	0.93	0.06	-3.07	63,63,63,63	0
17	K	L	302	1/1	0.96	0.05	-3.29	58,58,58,58	0
17	K	U	302	1/1	0.95	0.06	-3.38	46,46,46,46	0
18	MG	H	302	1/1	0.99	0.05	-3.47	34,34,34,34	0
17	K	G	303	1/1	0.97	0.05	-4.17	38,38,38,38	0
18	MG	L	303	1/1	0.99	0.04	-4.30	43,43,43,43	0
17	K	N	306	1/1	0.97	0.07	-4.50	44,44,44,44	0
17	K	b	305	1/1	0.96	0.09	-4.84	49,49,49,49	0
16	CL	A	303	1/1	0.97	0.15	-	58,58,58,58	0
16	CL	O	303	1/1	0.77	0.25	-	103,103,103,103	0
16	CL	V	302	1/1	0.91	0.13	-	73,73,73,73	0
16	CL	W	302	1/1	0.94	0.07	-	61,61,61,61	0
16	CL	Y	301	1/1	0.93	0.09	-	71,71,71,71	0
18	MG	H	301	1/1	0.94	0.09	-	48,48,48,48	0
16	CL	D	302	1/1	0.88	0.11	-	77,77,77,77	0
16	CL	O	302	1/1	0.93	0.08	-	71,71,71,71	0
16	CL	Q	302	1/1	0.96	0.10	-	77,77,77,77	0
16	CL	M	302	1/1	0.98	0.12	-	44,44,44,44	0
16	CL	Y	304	1/1	0.92	0.17	-	73,73,73,73	0
16	CL	C	301	1/1	0.84	0.10	-	74,74,74,74	0
16	CL	N	302	1/1	0.96	0.16	-	66,66,66,66	0
16	CL	K	303	1/1	0.91	0.20	-	73,73,73,73	0
16	CL	a	303	1/1	0.84	0.08	-	69,69,69,69	0
16	CL	B	301	1/1	0.97	0.12	-	46,46,46,46	0
16	CL	A	302	1/1	0.92	0.11	-	76,76,76,76	0
18	MG	X	301	1/1	0.97	0.09	-	54,54,54,54	0
16	CL	R	301	1/1	0.94	0.18	-	63,63,63,63	0
16	CL	b	301	1/1	0.94	0.16	-	66,66,66,66	0
16	CL	G	302	1/1	0.96	0.06	-	76,76,76,76	0
16	CL	E	302	1/1	0.96	0.14	-	61,61,61,61	0
16	CL	O	304	1/1	0.87	0.14	-	80,80,80,80	0
16	CL	C	302	1/1	0.89	0.09	-	79,79,79,79	0
16	CL	a	302	1/1	0.96	0.11	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
16	CL	M	303	1/1	0.92	0.09	-	61,61,61,61	0
16	CL	R	302	1/1	0.93	0.12	-	62,62,62,62	0
16	CL	V	303	1/1	0.92	0.10	-	66,66,66,66	0
16	CL	H	303	1/1	0.89	0.08	-	63,63,63,63	0
16	CL	H	304	1/1	0.96	0.08	-	57,57,57,57	0
18	MG	J	301	1/1	0.95	0.06	-	55,55,55,55	0
16	CL	I	302	1/1	0.92	0.12	-	57,57,57,57	0
16	CL	Q	301	1/1	0.66	0.20	-	98,98,98,98	0
16	CL	P	301	1/1	0.93	0.13	-	65,65,65,65	0
18	MG	V	301	1/1	0.93	0.21	-	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.