



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 7, 2023 – 06:16 am GMT

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 : 2016-06-30
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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

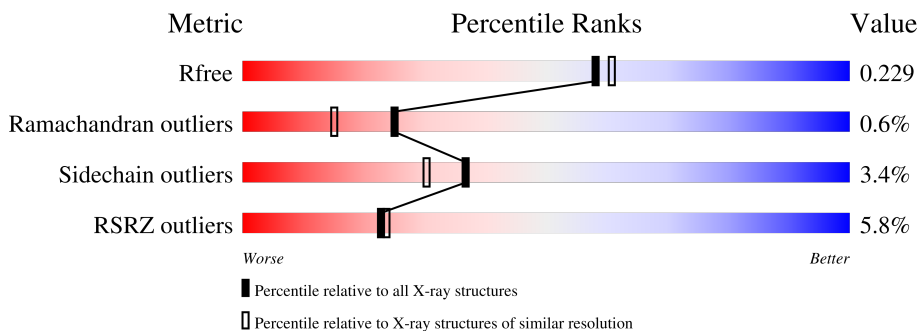
1 Overall quality at a glance i

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}	130704	2684 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	234	6% (poor fit), 91% (0-1 outliers), 6% (2-3 outliers), 0% (4+ outliers), 0% (not modelled)
1	O	234	18% (poor fit), 92% (0-1 outliers), 6% (2-3 outliers), 0% (4+ outliers), 0% (not modelled)
2	B	261	6% (poor fit), 91% (0-1 outliers), 5% (2-3 outliers), 0% (4+ outliers), 0% (not modelled)
2	P	261	15% (poor fit), 87% (0-1 outliers), 8% (2-3 outliers), 5% (4+ outliers), 0% (not modelled)
3	C	248	13% (poor fit), 89% (0-1 outliers), 6% (2-3 outliers), 0% (4+ outliers), 0% (not modelled)
3	Q	248	19% (poor fit), 89% (0-1 outliers), 7% (2-3 outliers), 0% (4+ outliers), 0% (not modelled)

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Mol	Chain	Length	Quality of chain
4	D	241	9% 93% ..
4	R	241	2% 92%
5	E	263	6% 85% • 11%
5	S	263	5% 88% • 10%
6	F	255	% 87% 6% 6%
6	T	255	7% 86% 8% 6%
7	G	246	4% 95%
7	U	246	15% 90% 7% .
8	H	234	3% 90% • 6%
8	V	234	3% 91% • 6%
9	I	205	96% .
9	W	205	% 97% .
10	J	201	% 93%
10	X	201	% 94%
11	c	3	100%
11	d	3	100%
12	K	204	2% 90% 7% .
12	Y	204	3% 91% 7% .
13	L	213	97% .
13	Z	213	2% 96% .
14	M	219	2% 96%
14	a	219	% 94% 5% .
15	N	205	96%
15	b	205	% 96%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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
			Total	C	N	O			
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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
			Total	C	N	O	S			
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	A	4	Total	Cl	0	0
			4	4		
16	B	2	Total	Cl	0	0
			2	2		
16	C	2	Total	Cl	0	0
			2	2		
16	D	2	Total	Cl	0	0
			2	2		
16	E	3	Total	Cl	0	0
			3	3		
16	F	1	Total	Cl	0	0
			1	1		
16	G	2	Total	Cl	0	0
			2	2		
16	H	2	Total	Cl	0	0
			2	2		
16	I	1	Total	Cl	0	0
			1	1		
16	K	3	Total	Cl	0	0
			3	3		
16	M	3	Total	Cl	0	0
			3	3		
16	N	4	Total	Cl	0	0
			4	4		
16	O	4	Total	Cl	0	0
			4	4		
16	P	1	Total	Cl	0	0
			1	1		
16	Q	2	Total	Cl	0	0
			2	2		
16	R	2	Total	Cl	0	0
			2	2		
16	S	3	Total	Cl	0	0
			3	3		
16	U	1	Total	Cl	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	V	2	Total 2	Cl 2	0	0
16	W	1	Total 1	Cl 1	0	0
16	Y	4	Total 4	Cl 4	0	0
16	a	3	Total 3	Cl 3	0	0
16	b	3	Total 3	Cl 3	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	L	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	Z	1	Total 1	K 1	0	0
17	b	1	Total 1	K 1	0	0

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

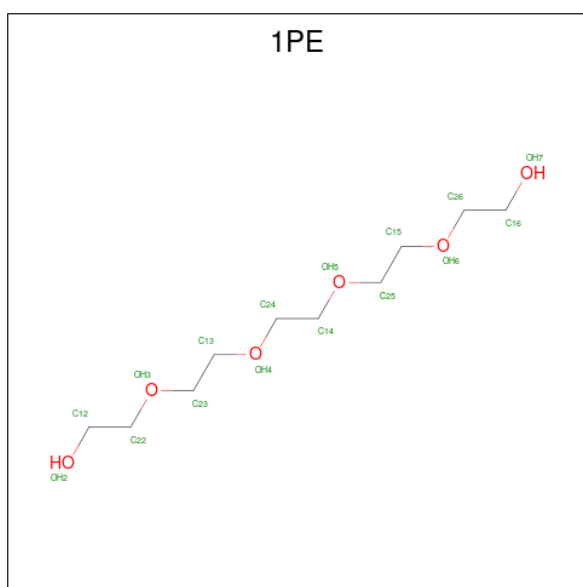
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	H	2	Total 2	Mg 2	0	0
18	I	2	Total 2	Mg 2	0	0
18	J	1	Total 1	Mg 1	0	0
18	K	1	Total 1	Mg 1	0	0
18	L	1	Total 1	Mg 1	0	0
18	V	1	Total 1	Mg 1	0	0

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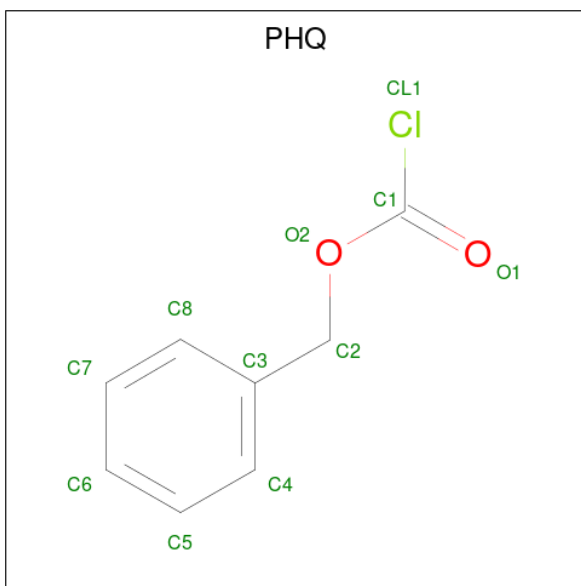
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
18	W	1	Total Mg 1 1	0	0
18	X	1	Total Mg 1 1	0	0

- Molecule 19 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



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

- Molecule 20 is benzyl chlorocarbonate (three-letter code: PHQ) (formula: C₈H₇ClO₂).



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

- Molecule 21 is water.

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

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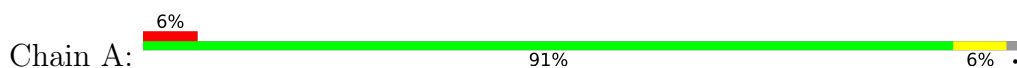
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
21	J	133	Total O 133 133	0	0
21	c	3	Total O 3 3	0	0
21	K	92	Total O 92 92	0	0
21	L	121	Total O 121 121	0	0
21	M	145	Total O 145 145	0	0
21	N	156	Total O 156 156	0	0
21	O	89	Total O 89 89	0	0
21	P	109	Total O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

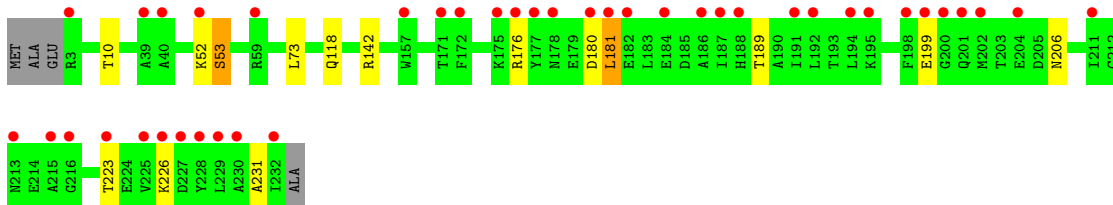
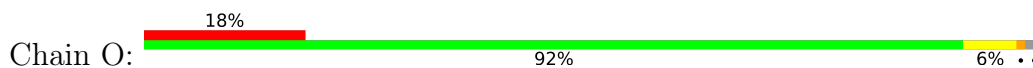
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

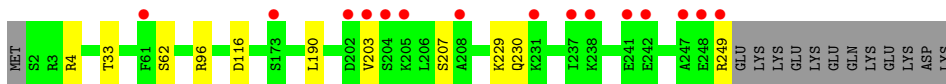
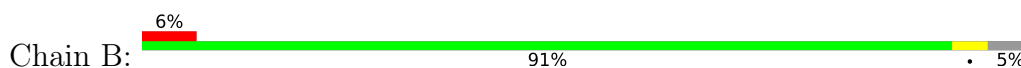
- Molecule 1: Proteasome subunit alpha type-2



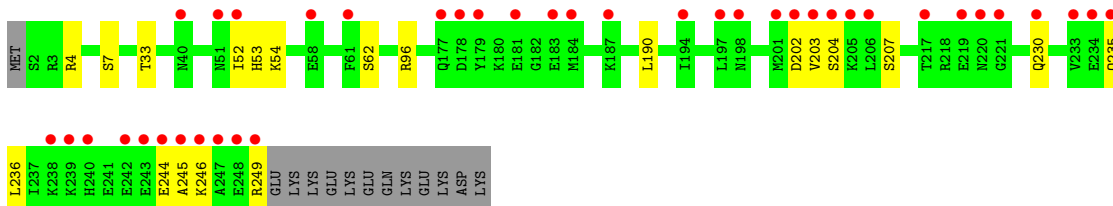
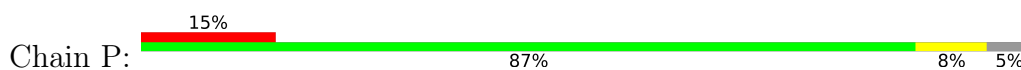
- Molecule 1: Proteasome subunit alpha type-2



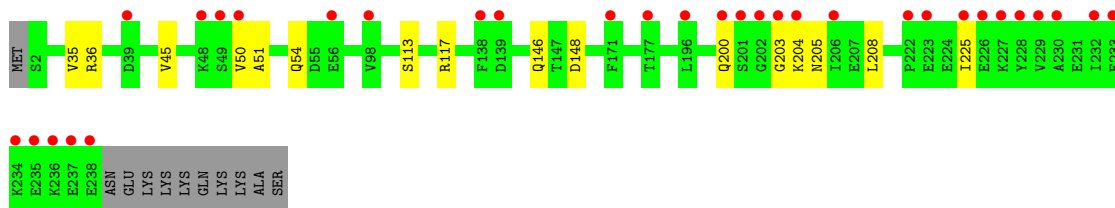
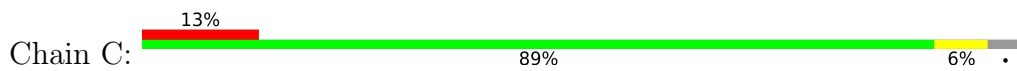
- Molecule 2: Proteasome subunit alpha type-4



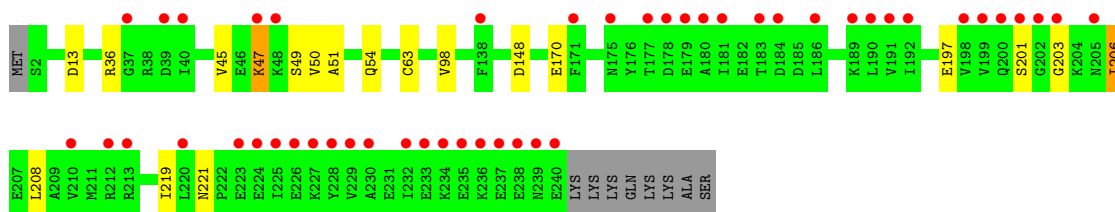
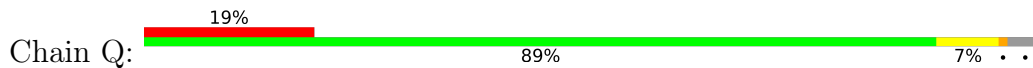
- Molecule 2: Proteasome subunit alpha type-4



- Molecule 3: Proteasome subunit alpha type-7



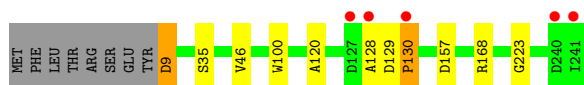
• Molecule 3: Proteasome subunit alpha type-7



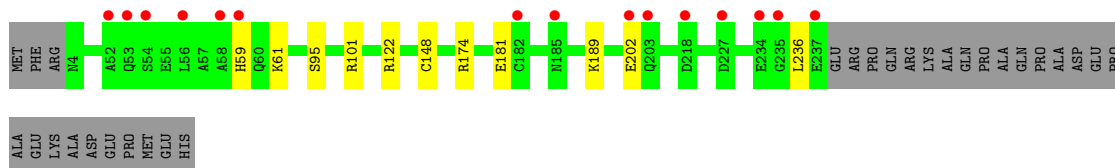
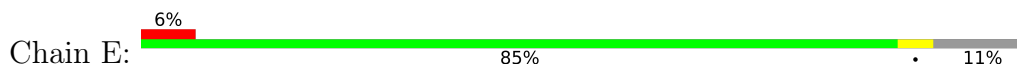
• Molecule 4: Proteasome subunit alpha type-5



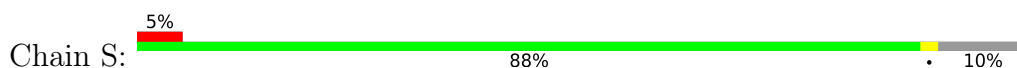
• Molecule 4: Proteasome subunit alpha type-5

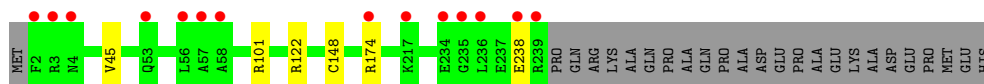


• Molecule 5: Proteasome subunit alpha type-1

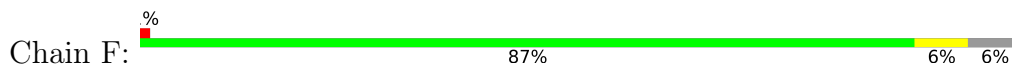


• Molecule 5: Proteasome subunit alpha type-1

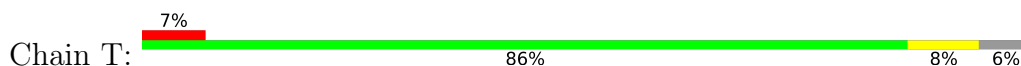




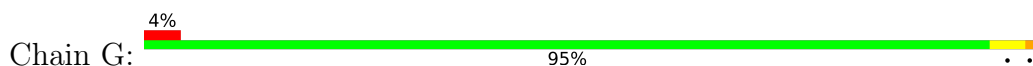
- Molecule 6: Proteasome subunit alpha type-3



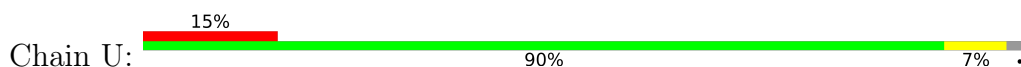
- Molecule 6: Proteasome subunit alpha type-3



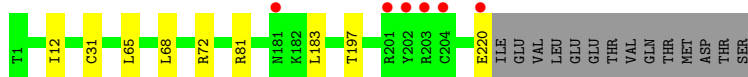
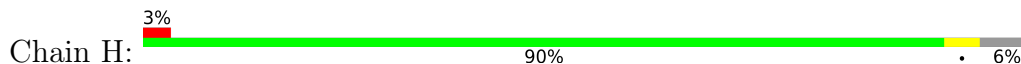
- Molecule 7: Proteasome subunit alpha type-6



- Molecule 7: Proteasome subunit alpha type-6

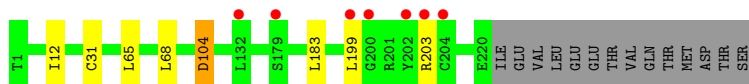


- Molecule 8: Proteasome subunit beta type-7



- Molecule 8: Proteasome subunit beta type-7





- Molecule 9: Proteasome subunit beta type-3

Chain I: 96%



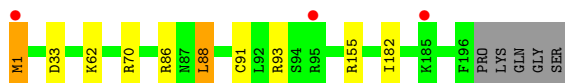
- Molecule 9: Proteasome subunit beta type-3

Chain W: 97%



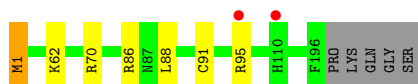
- Molecule 10: Proteasome subunit beta type-2

Chain J: 93%



- Molecule 10: Proteasome subunit beta type-2

Chain X: 94%



- Molecule 11: LLY-ketoaldehyde peptide

Chain c: 100%

There are no outlier residues recorded for this chain.

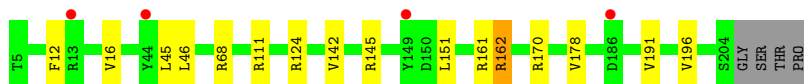
- Molecule 11: LLY-ketoaldehyde peptide

Chain d: 100%

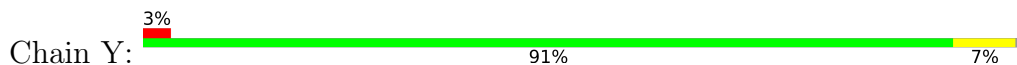
There are no outlier residues recorded for this chain.

- Molecule 12: Proteasome subunit beta type-5

Chain K: 90%



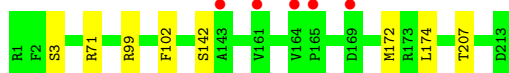
- Molecule 12: Proteasome subunit beta type-5



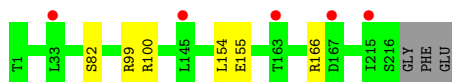
- Molecule 13: Proteasome subunit beta type-1



- Molecule 13: Proteasome subunit beta type-1



- Molecule 14: Proteasome subunit beta type-4



- Molecule 14: Proteasome subunit beta type-4



- 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)	Xtrriage
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 (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	43.8	Xtrriage
Anisotropy	0.245	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
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

Xtrriage'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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PHQ, K, CL, 6V1, MG, 1PE, 6VF, 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	0.71	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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	9 2
1	O	228/234 (97%)	214 (94%)	9 (4%)	5 (2%)	6 1
2	B	248/261 (95%)	234 (94%)	13 (5%)	1 (0%)	34 25
2	P	248/261 (95%)	234 (94%)	12 (5%)	2 (1%)	19 9
3	C	236/248 (95%)	217 (92%)	14 (6%)	5 (2%)	7 1
3	Q	236/248 (95%)	217 (92%)	12 (5%)	7 (3%)	4 0
4	D	232/241 (96%)	223 (96%)	6 (3%)	3 (1%)	12 4
4	R	232/241 (96%)	221 (95%)	8 (3%)	3 (1%)	12 4
5	E	232/263 (88%)	226 (97%)	4 (2%)	2 (1%)	17 8
5	S	238/263 (90%)	231 (97%)	6 (2%)	1 (0%)	34 25
6	F	241/255 (94%)	238 (99%)	3 (1%)	0	100 100
6	T	239/255 (94%)	230 (96%)	6 (2%)	3 (1%)	12 4
7	G	241/246 (98%)	235 (98%)	6 (2%)	0	100 100
7	U	232/246 (94%)	227 (98%)	3 (1%)	2 (1%)	17 8
8	H	220/234 (94%)	217 (99%)	3 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	V	220/234 (94%)	216 (98%)	3 (1%)	1 (0%)	29	19
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
11	c	1/3 (33%)	1 (100%)	0	0	100	100
11	d	1/3 (33%)	1 (100%)	0	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%)	29	19
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	6215/6464 (96%)	6012 (97%)	163 (3%)	40 (1%)	25	15

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 [i](#)

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%)	19	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	176/191 (92%)	166 (94%)	10 (6%)	20	12
2	B	200/221 (90%)	193 (96%)	7 (4%)	36	29
2	P	197/221 (89%)	184 (93%)	13 (7%)	16	9
3	C	179/210 (85%)	171 (96%)	8 (4%)	27	20
3	Q	184/210 (88%)	175 (95%)	9 (5%)	25	17
4	D	189/203 (93%)	184 (97%)	5 (3%)	46	40
4	R	187/203 (92%)	184 (98%)	3 (2%)	62	59
5	E	192/223 (86%)	185 (96%)	7 (4%)	35	28
5	S	197/223 (88%)	195 (99%)	2 (1%)	76	75
6	F	199/212 (94%)	189 (95%)	10 (5%)	24	16
6	T	192/212 (91%)	182 (95%)	10 (5%)	23	14
7	G	202/207 (98%)	197 (98%)	5 (2%)	47	41
7	U	186/207 (90%)	181 (97%)	5 (3%)	44	39
8	H	181/195 (93%)	175 (97%)	6 (3%)	38	31
8	V	172/195 (88%)	165 (96%)	7 (4%)	30	23
9	I	176/174 (101%)	174 (99%)	2 (1%)	73	72
9	W	173/174 (99%)	172 (99%)	1 (1%)	86	86
10	J	166/170 (98%)	160 (96%)	6 (4%)	35	28
10	X	165/170 (97%)	161 (98%)	4 (2%)	49	43
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%)	20	11
12	Y	159/159 (100%)	152 (96%)	7 (4%)	28	21
13	L	175/178 (98%)	169 (97%)	6 (3%)	37	30
13	Z	175/178 (98%)	172 (98%)	3 (2%)	60	57
14	M	180/181 (99%)	176 (98%)	4 (2%)	52	46
14	a	178/181 (98%)	172 (97%)	6 (3%)	37	30
15	N	157/159 (99%)	154 (98%)	3 (2%)	57	53
15	b	158/159 (99%)	154 (98%)	4 (2%)	47	41
All	All	5039/5370 (94%)	4866 (97%)	173 (3%)	37	30

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

Mol	Chain	Res	Type
3	Q	148	ASP
8	V	68	LEU
3	Q	208	LEU
6	T	86	SER
10	X	62	LYS

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

Mol	Chain	Res	Type
6	T	63	ASN
12	Y	167	GLN
6	T	68	ASN
8	V	193	ASN
14	a	89	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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
10	6V1	J	91	10	12,15,16	1.69	2 (16%)	9,20,22	4.60	6 (66%)
7	6V1	U	161	7	12,15,16	1.58	3 (25%)	9,20,22	3.78	5 (55%)
5	6V1	E	148	5	12,15,16	2.12	3 (25%)	9,20,22	2.76	4 (44%)
5	6V1	S	148	5	12,15,16	1.93	3 (25%)	9,20,22	2.61	4 (44%)
3	YCM	Q	63	3	7,9,10	1.25	1 (14%)	4,10,12	3.61	3 (75%)
7	YCM	G	137	7	7,9,10	1.71	2 (28%)	4,10,12	2.38	1 (25%)
3	YCM	C	63	3	7,9,10	0.99	0	4,10,12	0.84	0
7	YCM	U	137	7	7,9,10	0.94	0	4,10,12	1.65	1 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	6V1	X	91	10	12,15,16	2.00	3 (25%)	9,20,22	4.84	6 (66%)
7	6V1	G	47	7	12,15,16	2.18	3 (25%)	9,20,22	1.35	2 (22%)
7	6V1	G	161	7	12,15,16	1.64	3 (25%)	9,20,22	2.63	4 (44%)
7	6V1	U	47	7	12,15,16	1.78	3 (25%)	9,20,22	2.16	3 (33%)

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
10	6V1	J	91	10	-	2/6/25/27	0/1/1/1
7	6V1	U	161	7	-	3/6/25/27	0/1/1/1
5	6V1	E	148	5	-	2/6/25/27	0/1/1/1
5	6V1	S	148	5	-	0/6/25/27	0/1/1/1
3	YCM	Q	63	3	-	3/6/8/10	-
3	YCM	C	63	3	-	0/6/8/10	-
7	YCM	G	137	7	-	3/6/8/10	-
7	YCM	U	137	7	-	1/6/8/10	-
10	6V1	X	91	10	-	2/6/25/27	0/1/1/1
7	6V1	G	47	7	-	0/6/25/27	0/1/1/1
7	6V1	G	161	7	-	3/6/25/27	0/1/1/1
7	6V1	U	47	7	1/1/5/6	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)
5	E	148	6V1	CB-SG	-5.78	1.75	1.82
10	X	91	6V1	C1-SG	-4.95	1.77	1.83
5	S	148	6V1	CB-SG	-4.76	1.76	1.82
7	G	47	6V1	CB-SG	-4.69	1.77	1.82
10	J	91	6V1	C1-SG	-4.65	1.78	1.83

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	X	91	6V1	C5-C4-N3	8.45	113.11	108.13
10	J	91	6V1	C5-C4-N3	8.14	112.93	108.13
7	U	161	6V1	C2-N3-C4	-8.05	108.26	113.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	91	6V1	C6-N3-C2	6.34	131.40	123.36
10	X	91	6V1	O7-C2-N3	6.33	131.88	124.14

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	G	137	YCM	CE-CD-SG-CB
7	G	137	YCM	SG-CD-CE-NZ2
10	J	91	6V1	C3-C6-N3-C2
10	J	91	6V1	C3-C6-N3-C4
3	Q	63	YCM	CE-CD-SG-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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	0.57	0	14,14,14	1.10	2 (14%)
19	1PE	M	304	-	15,15,15	0.53	0	14,14,14	0.38	0
19	1PE	N	305	-	15,15,15	0.57	0	14,14,14	0.58	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
20	PHQ	c	101	11	9,10,11	1.75	3 (33%)	10,11,13	2.48	1 (10%)
20	PHQ	d	101	11	9,10,11	1.93	4 (44%)	10,11,13	2.53	1 (10%)
19	1PE	I	304	-	15,15,15	0.51	0	14,14,14	0.52	0
19	1PE	b	304	-	15,15,15	0.67	0	14,14,14	0.78	0
19	1PE	a	304	-	15,15,15	0.52	0	14,14,14	0.41	0
19	1PE	W	303	-	15,15,15	0.52	0	14,14,14	0.43	0
19	1PE	L	301	-	15,15,15	0.59	0	14,14,14	0.72	0
19	1PE	Z	301	-	15,15,15	0.54	0	14,14,14	0.40	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	1PE	I	303	-	-	8/13/13/13	-
19	1PE	M	304	-	-	7/13/13/13	-
19	1PE	N	305	-	-	6/13/13/13	-
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
19	1PE	I	304	-	-	8/13/13/13	-
19	1PE	b	304	-	-	8/13/13/13	-
19	1PE	a	304	-	-	5/13/13/13	-
19	1PE	W	303	-	-	6/13/13/13	-
19	1PE	L	301	-	-	6/13/13/13	-
19	1PE	Z	301	-	-	6/13/13/13	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	c	101	PHQ	C2-C3	3.18	1.58	1.50
20	d	101	PHQ	C2-C3	3.07	1.57	1.50
20	d	101	PHQ	O2-C1	3.02	1.45	1.33
20	d	101	PHQ	C4-C3	2.22	1.43	1.38
20	c	101	PHQ	O2-C1	2.18	1.41	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	d	101	PHQ	O2-C2-C3	7.73	127.96	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	c	101	PHQ	O2-C2-C3	7.57	127.59	109.40
19	I	303	1PE	C25-OH5-C14	2.73	125.12	113.29
19	I	303	1PE	OH5-C25-C15	2.32	120.85	110.39

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	I	303	1PE	C15-C25-OH5-C14
19	I	304	1PE	C24-C14-OH5-C25
19	I	304	1PE	OH7-C16-C26-OH6
19	M	304	1PE	OH4-C13-C23-OH3
19	I	304	1PE	OH4-C13-C23-OH3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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%) 23 24	34, 52, 90, 106	0
1	O	230/234 (98%)	0.71	41 (17%) 1 1	43, 70, 110, 140	0
2	B	248/261 (95%)	0.29	15 (6%) 21 22	36, 56, 99, 133	0
2	P	248/261 (95%)	0.84	40 (16%) 1 1	45, 66, 117, 153	0
3	C	236/248 (95%)	0.69	32 (13%) 3 2	41, 67, 112, 136	0
3	Q	238/248 (95%)	1.02	48 (20%) 1 0	36, 68, 128, 154	0
4	D	233/241 (96%)	0.28	21 (9%) 9 9	41, 67, 99, 141	0
4	R	233/241 (96%)	-0.02	5 (2%) 63 65	32, 47, 75, 115	0
5	E	233/263 (88%)	0.17	15 (6%) 19 19	32, 47, 98, 121	0
5	S	237/263 (90%)	0.13	14 (5%) 22 23	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	17 (7%) 16 16	36, 55, 92, 134	0
7	G	241/246 (97%)	0.22	10 (4%) 37 39	30, 43, 80, 113	0
7	U	235/246 (95%)	0.72	37 (15%) 2 1	46, 64, 98, 116	0
8	H	220/234 (94%)	-0.09	6 (2%) 54 57	30, 39, 70, 117	0
8	V	220/234 (94%)	0.15	7 (3%) 47 50	38, 54, 85, 123	0
9	I	204/205 (99%)	0.02	1 (0%) 91 91	31, 40, 61, 73	0
9	W	204/205 (99%)	0.08	3 (1%) 73 75	40, 55, 81, 92	0
10	J	195/201 (97%)	-0.14	3 (1%) 73 75	33, 43, 61, 85	0
10	X	195/201 (97%)	-0.03	2 (1%) 82 83	34, 47, 62, 86	0
11	c	2/3 (66%)	0.47	0 100 100	40, 40, 40, 43	0
11	d	2/3 (66%)	0.31	0 100 100	32, 32, 32, 36	0
12	K	200/204 (98%)	0.15	4 (2%) 65 67	38, 51, 78, 95	0
12	Y	201/204 (98%)	0.07	6 (2%) 50 53	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%) 60 63	30, 40, 64, 78	0
14	M	216/219 (98%)	0.15	5 (2%) 60 63	30, 43, 68, 103	0
14	a	216/219 (98%)	0.00	3 (1%) 75 76	30, 42, 64, 97	0
15	N	202/205 (98%)	-0.08	1 (0%) 91 91	29, 37, 59, 94	0
15	b	203/205 (99%)	0.13	3 (1%) 73 75	33, 42, 71, 99	0
All	All	6227/6464 (96%)	0.22	359 (5%) 23 24	29, 50, 93, 154	0

The worst 5 of 359 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	204	SER	19.2
1	O	232	ILE	11.2
3	Q	232	ILE	10.0
2	P	203	VAL	9.8
3	Q	238	GLU	9.6

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	6V1	U	47	15/16	0.85	0.33	79,115,121,123	0
7	YCM	U	137	10/11	0.85	0.18	55,65,80,83	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
3	YCM	Q	63	10/11	0.91	0.14	57,61,67,67	0
7	6V1	U	161	15/16	0.91	0.11	60,86,92,92	0
5	6V1	E	148	15/16	0.92	0.14	39,64,73,74	0
5	6V1	S	148	15/16	0.92	0.15	40,71,78,81	0
10	6V1	X	91	15/16	0.93	0.18	41,58,63,71	0
7	6V1	G	161	15/16	0.94	0.12	40,59,63,63	0
10	6V1	J	91	15/16	0.94	0.17	37,57,65,66	0
7	6V1	G	47	15/16	0.94	0.13	42,67,70,75	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
20	PHQ	c	101	10/11	0.65	0.24	49,78,81,83	0
16	CL	Q	301	1/1	0.66	0.20	98,98,98,98	0
20	PHQ	d	101	10/11	0.69	0.28	46,72,78,79	0
19	1PE	L	301	16/16	0.70	0.17	65,79,84,90	0
16	CL	O	303	1/1	0.77	0.25	103,103,103,103	0
19	1PE	Z	301	16/16	0.78	0.17	59,72,80,84	0
19	1PE	M	304	16/16	0.79	0.32	69,80,114,115	0
19	1PE	I	304	16/16	0.79	0.29	69,85,101,102	0
19	1PE	W	303	16/16	0.81	0.18	68,73,84,87	0
16	CL	D	301	1/1	0.82	0.11	83,83,83,83	0
19	1PE	I	303	16/16	0.83	0.16	59,68,77,84	0
16	CL	a	303	1/1	0.84	0.08	69,69,69,69	0
19	1PE	b	304	16/16	0.84	0.16	50,58,92,98	0
19	1PE	N	305	16/16	0.84	0.16	44,57,68,68	0
16	CL	C	301	1/1	0.84	0.10	74,74,74,74	0
19	1PE	a	304	16/16	0.86	0.26	62,70,101,101	0
16	CL	O	304	1/1	0.87	0.14	80,80,80,80	0
16	CL	K	302	1/1	0.87	0.27	92,92,92,92	0
16	CL	Y	302	1/1	0.87	0.30	90,90,90,90	0
16	CL	D	302	1/1	0.88	0.11	77,77,77,77	0
16	CL	K	304	1/1	0.88	0.15	79,79,79,79	0
16	CL	C	302	1/1	0.89	0.10	79,79,79,79	0
16	CL	H	303	1/1	0.89	0.08	63,63,63,63	0
16	CL	V	302	1/1	0.91	0.14	73,73,73,73	0
16	CL	K	303	1/1	0.91	0.20	73,73,73,73	0
16	CL	A	302	1/1	0.92	0.11	76,76,76,76	0
16	CL	I	302	1/1	0.92	0.12	57,57,57,57	0
16	CL	M	303	1/1	0.92	0.09	61,61,61,61	0
16	CL	V	303	1/1	0.92	0.10	66,66,66,66	0
16	CL	B	302	1/1	0.92	0.12	69,69,69,69	0
16	CL	Y	304	1/1	0.92	0.16	73,73,73,73	0
16	CL	R	302	1/1	0.93	0.12	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
16	CL	S	301	1/1	0.93	0.24	76,76,76,76	0
16	CL	O	302	1/1	0.93	0.08	71,71,71,71	0
16	CL	A	304	1/1	0.93	0.06	63,63,63,63	0
16	CL	Y	301	1/1	0.93	0.09	71,71,71,71	0
16	CL	N	301	1/1	0.93	0.19	55,55,55,55	0
16	CL	P	301	1/1	0.93	0.13	65,65,65,65	0
16	CL	a	301	1/1	0.93	0.10	69,69,69,69	0
16	CL	N	303	1/1	0.93	0.10	70,70,70,70	0
18	MG	I	301	1/1	0.93	0.08	34,34,34,34	0
18	MG	V	301	1/1	0.93	0.21	58,58,58,58	0
16	CL	Y	303	1/1	0.94	0.07	66,66,66,66	0
16	CL	W	302	1/1	0.94	0.07	61,61,61,61	0
18	MG	W	301	1/1	0.94	0.06	43,43,43,43	0
16	CL	R	301	1/1	0.94	0.18	63,63,63,63	0
16	CL	S	302	1/1	0.94	0.09	76,76,76,76	0
16	CL	b	301	1/1	0.94	0.16	66,66,66,66	0
18	MG	H	301	1/1	0.94	0.09	48,48,48,48	0
16	CL	M	301	1/1	0.95	0.13	67,67,67,67	0
18	MG	J	301	1/1	0.95	0.06	55,55,55,55	0
16	CL	E	303	1/1	0.95	0.13	75,75,75,75	0
17	K	U	302	1/1	0.95	0.06	46,46,46,46	0
16	CL	E	301	1/1	0.95	0.13	69,69,69,69	0
16	CL	O	301	1/1	0.96	0.07	63,63,63,63	0
16	CL	G	301	1/1	0.96	0.09	52,52,52,52	0
16	CL	G	302	1/1	0.96	0.06	76,76,76,76	0
16	CL	a	302	1/1	0.96	0.11	48,48,48,48	0
16	CL	U	301	1/1	0.96	0.06	67,67,67,67	0
16	CL	E	302	1/1	0.96	0.14	61,61,61,61	0
16	CL	b	303	1/1	0.96	0.15	64,64,64,64	0
17	K	L	302	1/1	0.96	0.05	58,58,58,58	0
16	CL	N	302	1/1	0.96	0.16	66,66,66,66	0
17	K	b	305	1/1	0.96	0.09	49,49,49,49	0
16	CL	H	304	1/1	0.96	0.08	57,57,57,57	0
16	CL	Q	302	1/1	0.96	0.11	77,77,77,77	0
16	CL	N	304	1/1	0.96	0.10	50,50,50,50	0
16	CL	B	301	1/1	0.97	0.12	46,46,46,46	0
16	CL	A	303	1/1	0.97	0.15	58,58,58,58	0
17	K	G	303	1/1	0.97	0.05	38,38,38,38	0
18	MG	I	305	1/1	0.97	0.09	29,29,29,29	0
16	CL	A	301	1/1	0.97	0.06	64,64,64,64	0
18	MG	K	301	1/1	0.97	0.08	40,40,40,40	0
17	K	N	306	1/1	0.97	0.07	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
16	CL	F	301	1/1	0.97	0.05	60,60,60,60	0
18	MG	X	301	1/1	0.97	0.09	54,54,54,54	0
17	K	Z	302	1/1	0.97	0.11	44,44,44,44	0
16	CL	b	302	1/1	0.98	0.12	68,68,68,68	0
16	CL	M	302	1/1	0.98	0.12	44,44,44,44	0
16	CL	S	303	1/1	0.98	0.14	60,60,60,60	0
18	MG	H	302	1/1	0.99	0.05	34,34,34,34	0
18	MG	L	303	1/1	0.99	0.04	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.