



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2016 – 04:34 PM EDT

PDB ID : 5LE5
Title : Native human 20S proteasome at 1.8 Angstrom
Authors : Schrader, J.; Henneberg, F.; Mata, R.; Tittmann, K.; Schneider, T.R.; Stark, H.; Bourenkov, G.; Chari, A.
Deposited on : 2016-06-29
Resolution : 1.80 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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-20027939

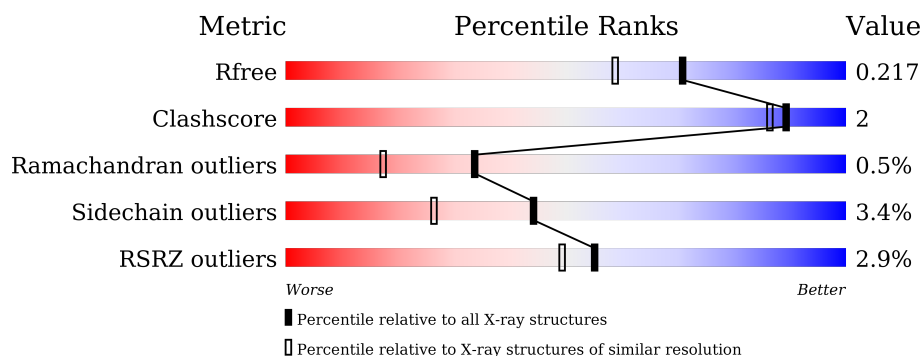
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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>2%</div> <div>89%</div> <div>8%</div> <div>..</div> </div>
1	O	234	<div> <div>7%</div> <div>87%</div> <div>9%</div> <div>...</div> </div>
2	B	261	<div> <div>3%</div> <div>88%</div> <div>6%</div> <div>5%</div> </div>
2	P	261	<div> <div>7%</div> <div>84%</div> <div>8%</div> <div>.. 5%</div> </div>
3	C	248	<div> <div>8%</div> <div>80%</div> <div>14%</div> <div>..</div> </div>
3	Q	248	<div> <div>6%</div> <div>81%</div> <div>12%</div> <div>6%</div> </div>

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
15	CL	B	302	-	-	-	X
15	CL	E	303	-	-	-	X
15	CL	K	305	-	-	-	X
15	CL	M	301	-	-	-	X
15	CL	M	302	-	-	-	X
15	CL	Q	302	-	-	-	X
15	CL	S	301	-	-	-	X
15	CL	a	301	-	-	-	X
16	1PE	I	303	-	-	-	X
16	1PE	I	304	-	-	-	X
16	1PE	L	301	-	-	-	X
16	1PE	W	303	-	-	-	X
16	1PE	Z	301	-	-	-	X
16	1PE	a	304	-	-	-	X
16	1PE	b	505	-	-	-	X
7	6V1	U	47	X	-	-	-

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 52161 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	2	0
			1799	1151	307	335	6			
1	O	230	Total	C	N	O	S	0	0	0
			1779	1136	301	336	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	1	0
			1942	1226	332	373	11			
2	P	247	Total	C	N	O	S	0	2	0
			1919	1211	326	371	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	0	0
			1836	1152	328	351	5			
3	Q	234	Total	C	N	O	S	0	0	0
			1821	1143	319	354	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	2	0
			1783	1118	294	360	11			
4	R	233	Total	C	N	O	S	0	1	0
			1773	1115	295	352	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	0	0
			1833	1150	328	344	11			
5	S	238	Total	C	N	O	S	0	3	0
			1880	1179	339	351	11			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	239	Total	C	N	O	S	0	4	0
			1890	1200	323	355	12			
6	T	240	Total	C	N	O	S	0	1	0
			1867	1186	320	349	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
			1928	1223	322	370	13			
7	U	235	Total	C	N	O	S	0	0	0
			1820	1151	306	350	13			

- 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
			1672	1053	286	320	13			
8	V	220	Total	C	N	O	S	0	2	0
			1655	1042	278	322	13			

- 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	6	0
			1633	1039	274	301	19			
9	W	204	Total	C	N	O	S	0	2	0
			1604	1021	269	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	2	0
			1585	1017	268	290	10			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	196	Total	C	N	O	S	0	2	0
			1590	1019	270	291	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	201	Total	C	N	O	S	0	0	0
			1543	974	267	293	9			
11	Y	199	Total	C	N	O	S	0	3	0
			1564	988	275	291	10			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	213	Total	C	N	O	S	0	2	0
			1656	1048	283	314	11			
12	Z	213	Total	C	N	O	S	0	1	0
			1644	1043	281	309	11			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	216	Total	C	N	O	S	0	0	0
			1687	1064	291	320	12			
13	a	216	Total	C	N	O	S	0	1	0
			1688	1065	291	320	12			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	202	Total	C	N	O	S	0	1	0
			1515	951	258	293	13			
14	b	203	Total	C	N	O	S	0	1	0
			1526	958	259	296	13			

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

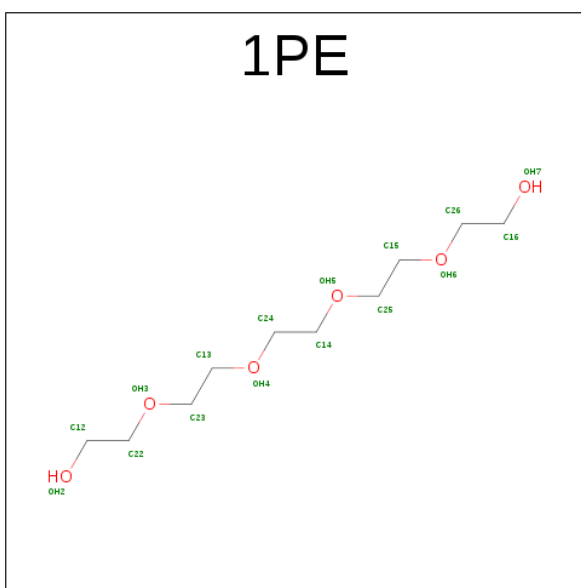
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	P	1	Total	Cl	0	0
			1	1		
15	K	4	Total	Cl	0	0
			4	4		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	B	2	Total 2	Cl 2	0	0
15	W	1	Total 1	Cl 1	0	0
15	N	3	Total 3	Cl 3	0	0
15	S	3	Total 3	Cl 3	0	0
15	E	3	Total 3	Cl 3	0	0
15	b	3	Total 3	Cl 3	0	0
15	V	2	Total 2	Cl 2	0	0
15	A	4	Total 4	Cl 4	0	0
15	R	2	Total 2	Cl 2	0	0
15	M	4	Total 4	Cl 4	0	0
15	D	2	Total 2	Cl 2	0	0
15	I	1	Total 1	Cl 1	0	0
15	a	3	Total 3	Cl 3	0	0
15	U	1	Total 1	Cl 1	0	0
15	G	2	Total 2	Cl 2	0	0
15	Q	2	Total 2	Cl 2	0	0
15	H	2	Total 2	Cl 2	0	0
15	C	2	Total 2	Cl 2	0	0
15	O	4	Total 4	Cl 4	0	0
15	Y	5	Total 5	Cl 5	0	0
15	F	1	Total 1	Cl 1	0	0

- Molecule 16 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	G	1	Total	K	0	0
			1	1		
17	b	1	Total	K	0	0
			1	1		

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

- Molecule 19 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	A	112	Total 112	O 112	0	0
19	B	123	Total 123	O 123	0	0
19	C	75	Total 75	O 75	0	0
19	D	83	Total 83	O 83	0	0
19	E	134	Total 134	O 134	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	F	189	Total 189	O 189	0	0
19	G	190	Total 190	O 190	0	0
19	H	151	Total 151	O 151	0	0
19	I	149	Total 149	O 149	0	0
19	J	127	Total 127	O 127	0	0
19	K	108	Total 108	O 108	0	0
19	L	115	Total 115	O 115	0	0
19	M	155	Total 155	O 155	0	0
19	N	164	Total 164	O 164	0	0
19	O	85	Total 85	O 85	0	0
19	P	111	Total 111	O 111	0	0
19	Q	66	Total 66	O 66	0	0
19	R	126	Total 126	O 126	0	0
19	S	115	Total 115	O 115	0	0
19	T	85	Total 85	O 85	0	0
19	U	100	Total 100	O 100	0	0
19	V	108	Total 108	O 108	0	0
19	W	117	Total 117	O 117	0	0
19	X	120	Total 120	O 120	0	0
19	Y	145	Total 145	O 145	0	0
19	Z	168	Total 168	O 168	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	a	164	Total 164	O 164	0	0
19	b	127	Total 127	O 127	0	0

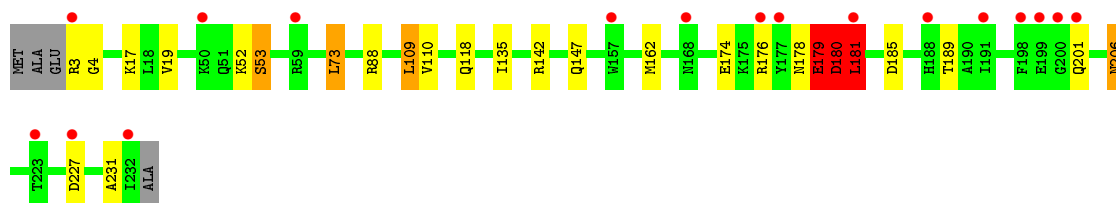
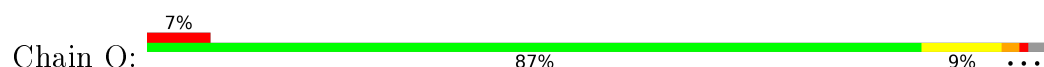
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

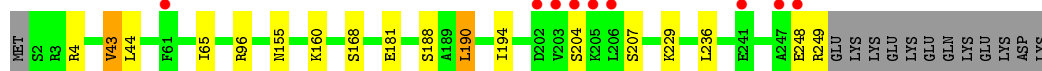
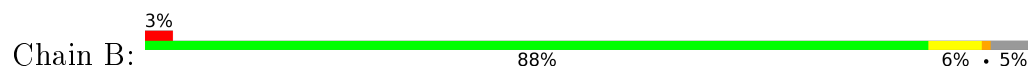
- Molecule 1: Proteasome subunit alpha type-2



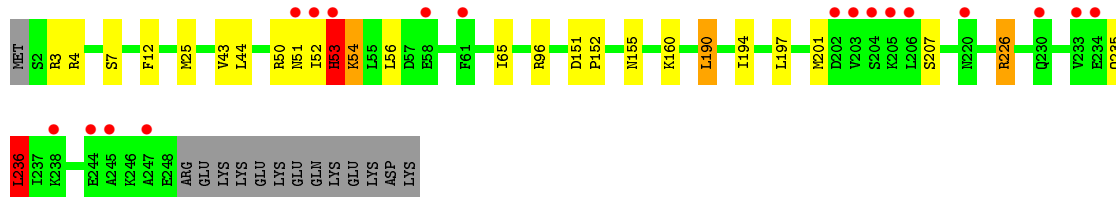
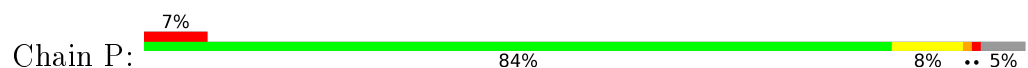
- Molecule 1: Proteasome subunit alpha type-2



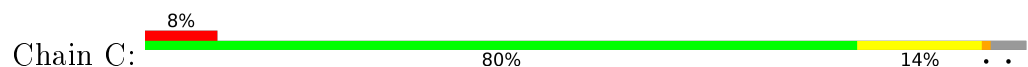
- Molecule 2: Proteasome subunit alpha type-4

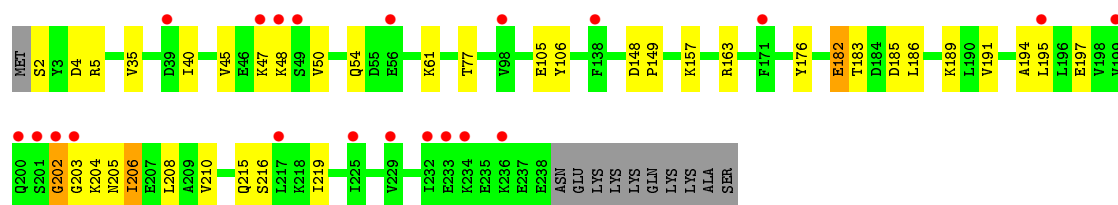


- Molecule 2: Proteasome subunit alpha type-4

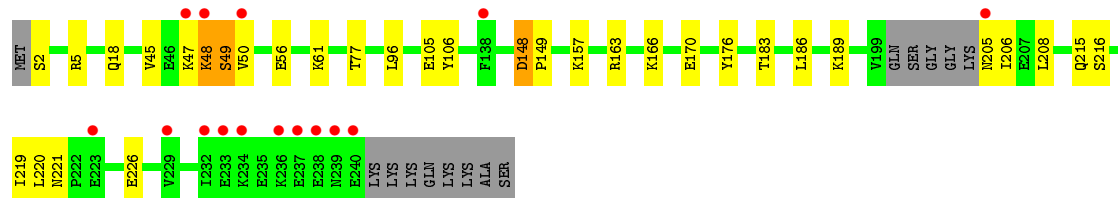
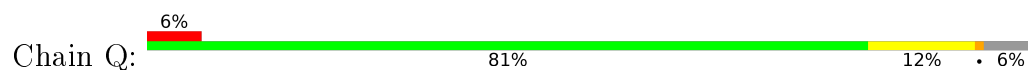


- Molecule 3: Proteasome subunit alpha type-7

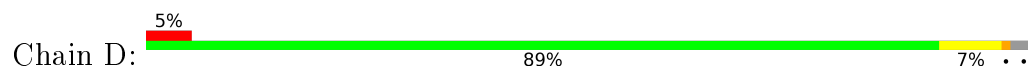




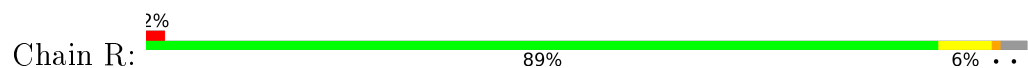
• Molecule 3: Proteasome subunit alpha type-7



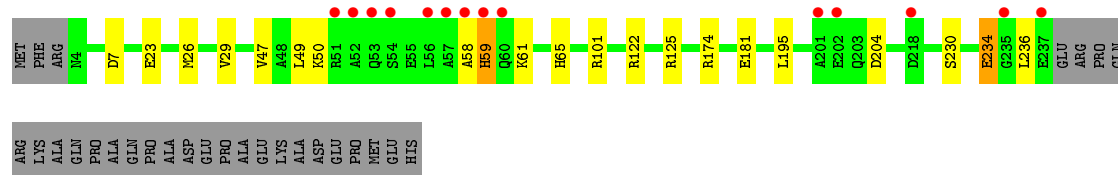
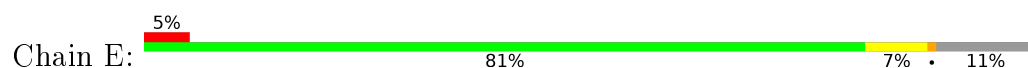
• Molecule 4: Proteasome subunit alpha type-5



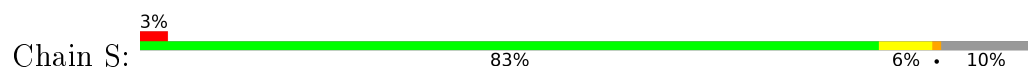
• Molecule 4: Proteasome subunit alpha type-5



• Molecule 5: Proteasome subunit alpha type-1




• Molecule 5: Proteasome subunit alpha type-1



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


• Molecule 6: Proteasome subunit alpha type-3

Chain F:  84% 8% 6%

MET SER SER ILE GLY THR G6 D17 V30 E31 V53 R85 S86 L87 E94 N105 M117 A127 C133 D152 V156 R169 V190 D206 R207 A208 W215 L219 T220 N221 V227 D230 E231 R232 K240 L243 K244 GLU GLU ASP

GLU SER SER ASP ASP ASP ASN MET

• Molecule 6: Proteasome subunit alpha type-3

Chain T:  5% 83% 9% 6%

MET SER SER ILE GLY THR T5 D17 M27 V30 E31 I37 D43 V53 L54 M63 G74 L81 R85 S86 L87 L108 R109 H110 M117 C133 Y140 Q170 T174 Q180 V190 V204 K205 D206 K207 A208 F209 W215 E218


H224 E225 I226 E234 K244 GLU GLU ASP ASP ASP ASP ASP MET

• Molecule 7: Proteasome subunit alpha type-6

Chain G:  1% 91% 6% 2%

MET S2 R11 V42 R43 V49 I72 C78 R88 E108 L114 R117 L140 E146 V151 V183 F187 D188 H189 E192 Q193 L206 V219 R245 ASP


• Molecule 7: Proteasome subunit alpha type-6

Chain U:  6% 87% 7% 2%

MET S2 R3 S6 R11 V42 R43 V51 F57 D58 K59 I72 G77 C78 R88 L114 R117 L140 V151 S177 K184 LYS PHE ASP THR PHE GLU GLN T194 V195 E196 T197 A198 I199 L206 S207 I208 P212 E223 F227


V240 A241 L242 A243 E244 R245 ASP

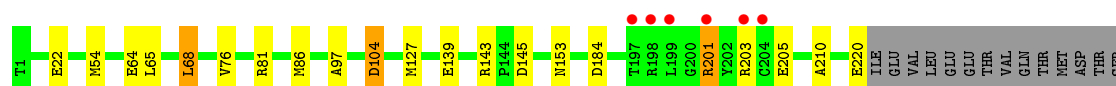
• Molecule 8: Proteasome subunit beta type-7

Chain H:  2% 87% 7% 6%

T1 E22 C31 C43 L65 R72 R81 M86 R89 L98 R143 E150 M153 K195 G196 T197 R198 L199 G200 R201 Y202 R203 C204 I216 E220 ILE GLU VAL LEU GLU GLU THR VAL GLN THR MET ASP THR SER

• Molecule 8: Proteasome subunit beta type-7

Chain V:  3% 85% 8% 6%



- Molecule 9: Proteasome subunit beta type-3

Chain I: 95%



- Molecule 9: Proteasome subunit beta type-3

Chain W: 96%



- Molecule 10: Proteasome subunit beta type-2

Chain J: 85%



- Molecule 10: Proteasome subunit beta type-2

Chain X: 88%



- Molecule 11: Proteasome subunit beta type-5

Chain K: 91%



- Molecule 11: Proteasome subunit beta type-5

Chain Y: 89%



- Molecule 12: Proteasome subunit beta type-1

Chain L: 92%



- Molecule 12: Proteasome subunit beta type-1

Chain Z: 94% 5% .



- Molecule 13: Proteasome subunit beta type-4

Chain M: 92% 7% .



- Molecule 13: Proteasome subunit beta type-4

Chain a: 94% . .



- Molecule 14: Proteasome subunit beta type-6

Chain N: 93% 5% .



- Molecule 14: Proteasome subunit beta type-6

Chain b: 97% . .



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.44Å 202.77Å 316.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	170.66 – 1.80 106.77 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (170.66-1.80) 99.9 (106.77-1.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.182 , 0.212 0.190 , 0.217	Depositor DCC
R_{free} test set	33208 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.1	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	52161	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.79% 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

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	0.73	1/1844 (0.1%)	0.82	1/2500 (0.0%)
1	O	0.64	0/1818	0.86	5/2467 (0.2%)
2	B	0.81	2/1975 (0.1%)	0.94	4/2665 (0.2%)
2	P	0.75	0/1955	0.90	6/2642 (0.2%)
3	C	1.16	3/1851 (0.2%)	0.91	3/2502 (0.1%)
3	Q	0.79	1/1835 (0.1%)	0.89	2/2485 (0.1%)
4	D	0.76	1/1810 (0.1%)	0.91	4/2448 (0.2%)
4	R	0.81	0/1800	0.94	4/2431 (0.2%)
5	E	0.75	1/1851 (0.1%)	0.91	3/2502 (0.1%)
5	S	0.71	0/1908	0.91	6/2577 (0.2%)
6	F	0.91	1/1937 (0.1%)	1.01	9/2607 (0.3%)
6	T	0.77	0/1905	0.96	8/2567 (0.3%)
7	G	0.91	1/1925 (0.1%)	0.92	8/2598 (0.3%)
7	U	0.69	0/1806	0.84	4/2438 (0.2%)
8	H	0.85	1/1705 (0.1%)	0.98	6/2307 (0.3%)
8	V	0.68	0/1688	0.90	4/2288 (0.2%)
9	I	0.82	0/1668	0.97	5/2247 (0.2%)
9	W	0.68	0/1636	1.00	9/2205 (0.4%)
10	J	0.95	3/1605 (0.2%)	0.99	2/2170 (0.1%)
10	X	0.84	2/1613 (0.1%)	0.98	8/2180 (0.4%)
11	K	0.79	0/1574	1.00	7/2128 (0.3%)
11	Y	0.85	0/1604	1.04	10/2165 (0.5%)
12	L	0.73	1/1692 (0.1%)	0.87	3/2281 (0.1%)
12	Z	0.84	2/1677 (0.1%)	1.06	4/2260 (0.2%)
13	M	0.82	1/1720 (0.1%)	0.97	4/2328 (0.2%)
13	a	0.86	0/1724	0.98	7/2334 (0.3%)
14	N	0.94	4/1544 (0.3%)	0.94	4/2090 (0.2%)
14	b	0.86	4/1556 (0.3%)	0.91	2/2107 (0.1%)
All	All	0.82	29/49226 (0.1%)	0.94	142/66519 (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	1
3	C	0	1
3	Q	0	2
4	D	0	3
7	U	1	0
9	I	0	1
10	X	0	1
12	Z	0	1
All	All	1	10

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	182	GLU	CG-CD	27.93	1.93	1.51
3	C	182	GLU	CD-OE2	-24.47	0.98	1.25
7	G	108	GLU	CD-OE1	14.97	1.42	1.25
3	Q	189	LYS	C-O	11.20	1.44	1.23
14	b	150	GLU	CD-OE1	9.45	1.36	1.25

The worst 5 of 142 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	Z	99	ARG	NE-CZ-NH2	-17.26	111.67	120.30
12	Z	99	ARG	NE-CZ-NH1	16.34	128.47	120.30
9	W	69	ARG	NE-CZ-NH1	14.69	127.64	120.30
9	W	69	ARG	NE-CZ-NH2	-12.94	113.83	120.30
13	M	151	ARG	NE-CZ-NH1	11.86	126.23	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	202	GLY	Peptide
4	D	175[A]	GLU	Peptide
4	D	175[B]	GLU	Mainchain,Peptide

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Mol	Chain	Res	Type	Group
9	I	78[B]	GLY	Peptide
2	P	54	LYS	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	1799	0	1793	8	0
1	O	1779	0	1747	13	0
2	B	1942	0	1938	6	0
2	P	1919	0	1895	16	0
3	C	1836	0	1821	20	0
3	Q	1821	0	1788	12	0
4	D	1783	0	1751	6	0
4	R	1773	0	1760	9	0
5	E	1833	0	1797	8	0
5	S	1880	0	1850	10	0
6	F	1890	0	1886	11	0
6	T	1867	0	1847	8	0
7	G	1928	0	1905	10	0
7	U	1820	0	1792	10	0
8	H	1672	0	1703	5	0
8	V	1655	0	1661	9	0
9	I	1633	0	1660	4	0
9	W	1604	0	1626	3	0
10	J	1585	0	1568	19	0
10	X	1590	0	1580	7	0
11	K	1543	0	1495	4	0
11	Y	1564	0	1539	9	0
12	L	1656	0	1655	7	0
12	Z	1644	0	1644	3	0
13	M	1687	0	1666	4	0
13	a	1688	0	1666	0	0
14	N	1515	0	1492	2	0
14	b	1526	0	1503	0	0
15	A	4	0	0	0	0
15	B	2	0	0	1	0
15	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	D	2	0	0	0	0
15	E	3	0	0	0	0
15	F	1	0	0	0	0
15	G	2	0	0	0	0
15	H	2	0	0	1	0
15	I	1	0	0	0	0
15	K	4	0	0	0	0
15	M	4	0	0	1	0
15	N	3	0	0	0	0
15	O	4	0	0	0	0
15	P	1	0	0	0	0
15	Q	2	0	0	0	0
15	R	2	0	0	1	0
15	S	3	0	0	0	0
15	U	1	0	0	0	0
15	V	2	0	0	0	0
15	W	1	0	0	0	0
15	Y	5	0	0	1	0
15	a	3	0	0	0	0
15	b	3	0	0	0	0
16	G	16	0	22	1	0
16	I	32	0	44	0	0
16	L	16	0	22	0	0
16	W	16	0	22	0	0
16	Z	16	0	22	0	0
16	a	16	0	22	0	0
16	b	32	0	44	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	A	112	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	B	123	0	0	0	0
19	C	75	0	0	0	0
19	D	83	0	0	0	0
19	E	134	0	0	1	0
19	F	189	0	0	5	0
19	G	190	0	0	4	0
19	H	151	0	0	2	0
19	I	149	0	0	1	0
19	J	127	0	0	1	0
19	K	108	0	0	0	0
19	L	115	0	0	1	0
19	M	155	0	0	0	0
19	N	164	0	0	0	0
19	O	85	0	0	1	0
19	P	111	0	0	1	0
19	Q	66	0	0	0	0
19	R	126	0	0	2	0
19	S	115	0	0	3	0
19	T	85	0	0	1	0
19	U	100	0	0	0	0
19	V	108	0	0	2	0
19	W	117	0	0	3	0
19	X	120	0	0	1	0
19	Y	145	0	0	0	0
19	Z	168	0	0	0	0
19	a	164	0	0	0	0
19	b	127	0	0	0	0
All	All	52161	0	48226	213	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 213 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)
3:C:182:GLU:CG	3:C:182:GLU:CD	1.93	1.34
10:J:1:MET:HG3	10:J:134:TYR:CD2	1.92	1.04
10:J:183:ILE:O	10:J:184:ASP:OD1	1.83	0.97
9:I:16[A]:LYS:O	19:I:401:HOH:O	1.85	0.95
10:J:1:MET:HG3	10:J:134:TYR:HD2	1.36	0.91

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	230/234 (98%)	220 (96%)	6 (3%)	4 (2%)	11	2
1	O	228/234 (97%)	214 (94%)	7 (3%)	7 (3%)	5	0
2	B	247/261 (95%)	238 (96%)	9 (4%)	0	100	100
2	P	247/261 (95%)	234 (95%)	11 (4%)	2 (1%)	24	8
3	C	234/248 (94%)	224 (96%)	6 (3%)	4 (2%)	11	2
3	Q	229/248 (92%)	218 (95%)	6 (3%)	5 (2%)	8	1
4	D	233/241 (97%)	223 (96%)	6 (3%)	4 (2%)	11	2
4	R	232/241 (96%)	223 (96%)	6 (3%)	3 (1%)	15	4
5	E	231/263 (88%)	226 (98%)	4 (2%)	1 (0%)	39	23
5	S	238/263 (90%)	234 (98%)	4 (2%)	0	100	100
6	F	241/255 (94%)	238 (99%)	3 (1%)	0	100	100
6	T	239/255 (94%)	233 (98%)	4 (2%)	2 (1%)	24	8
7	G	241/246 (98%)	237 (98%)	4 (2%)	0	100	100
7	U	228/246 (93%)	224 (98%)	4 (2%)	0	100	100
8	H	220/234 (94%)	217 (99%)	3 (1%)	0	100	100
8	V	220/234 (94%)	215 (98%)	4 (2%)	1 (0%)	34	17
9	I	208/205 (102%)	204 (98%)	4 (2%)	0	100	100
9	W	204/205 (100%)	198 (97%)	6 (3%)	0	100	100
10	J	195/201 (97%)	192 (98%)	3 (2%)	0	100	100
10	X	195/201 (97%)	192 (98%)	3 (2%)	0	100	100
11	K	199/204 (98%)	195 (98%)	4 (2%)	0	100	100
11	Y	200/204 (98%)	197 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L	213/213 (100%)	211 (99%)	2 (1%)	0	100	100
12	Z	212/213 (100%)	210 (99%)	2 (1%)	0	100	100
13	M	214/219 (98%)	208 (97%)	6 (3%)	0	100	100
13	a	215/219 (98%)	209 (97%)	6 (3%)	0	100	100
14	N	201/205 (98%)	198 (98%)	3 (2%)	0	100	100
14	b	202/205 (98%)	199 (98%)	3 (2%)	0	100	100
All	All	6196/6458 (96%)	6031 (97%)	132 (2%)	33 (0%)	34	17

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	LYS
1	A	53	SER
4	D	127	ASP
4	D	176	GLY
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	188/191 (98%)	177 (94%)	11 (6%)	24	9
1	O	184/191 (96%)	172 (94%)	12 (6%)	21	7
2	B	205/221 (93%)	198 (97%)	7 (3%)	44	26
2	P	201/221 (91%)	190 (94%)	11 (6%)	27	10
3	C	189/210 (90%)	181 (96%)	8 (4%)	36	18
3	Q	189/210 (90%)	176 (93%)	13 (7%)	19	6
4	D	194/203 (96%)	187 (96%)	7 (4%)	42	24
4	R	192/203 (95%)	189 (98%)	3 (2%)	70	59
5	E	195/223 (87%)	188 (96%)	7 (4%)	42	24
5	S	201/223 (90%)	194 (96%)	7 (4%)	43	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	200/212 (94%)	192 (96%)	8 (4%)	38	20
6	T	194/212 (92%)	184 (95%)	10 (5%)	29	12
7	G	206/207 (100%)	201 (98%)	5 (2%)	57	41
7	U	192/207 (93%)	187 (97%)	5 (3%)	54	37
8	H	183/195 (94%)	179 (98%)	4 (2%)	60	45
8	V	180/195 (92%)	172 (96%)	8 (4%)	35	17
9	I	178/174 (102%)	178 (100%)	0	100	100
9	W	174/174 (100%)	174 (100%)	0	100	100
10	J	166/170 (98%)	160 (96%)	6 (4%)	42	24
10	X	168/170 (99%)	164 (98%)	4 (2%)	57	41
11	K	153/159 (96%)	144 (94%)	9 (6%)	24	9
11	Y	157/159 (99%)	152 (97%)	5 (3%)	46	29
12	L	179/178 (101%)	170 (95%)	9 (5%)	30	13
12	Z	176/178 (99%)	171 (97%)	5 (3%)	51	35
13	M	179/181 (99%)	175 (98%)	4 (2%)	60	45
13	a	179/181 (99%)	174 (97%)	5 (3%)	51	35
14	N	157/159 (99%)	155 (99%)	2 (1%)	76	68
14	b	159/159 (100%)	158 (99%)	1 (1%)	90	88
All	All	5118/5366 (95%)	4942 (97%)	176 (3%)	44	26

5 of 176 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	L	174	LEU
1	O	206	ASN
11	Y	141[A]	ARG
13	M	100	ARG
1	O	118	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	118	GLN
3	Q	239	ASN
12	Z	157	ASN

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Mol	Chain	Res	Type
1	O	206	ASN
2	P	109	GLN

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	7,9,10	1.23	1 (14%)	5,10,12	1.66	2 (40%)
5	6V1	E	148	5	11,15,16	1.50	4 (36%)	11,20,22	2.43	3 (27%)
7	YCM	G	137	7	7,9,10	3.10	4 (57%)	5,10,12	6.74	4 (80%)
7	6V1	G	161	7	11,15,16	1.67	3 (27%)	11,20,22	2.59	6 (54%)
7	6V1	G	47	7	11,15,16	2.14	4 (36%)	11,20,22	4.27	4 (36%)
10	6V1	J	91	10	11,15,16	2.16	1 (9%)	11,20,22	6.12	8 (72%)
3	YCM	Q	63	3	7,9,10	2.08	2 (28%)	5,10,12	3.76	3 (60%)
5	6V1	S	148	5	11,15,16	1.60	2 (18%)	11,20,22	2.62	4 (36%)
7	YCM	U	137	7	7,9,10	1.85	2 (28%)	5,10,12	2.25	3 (60%)
7	6V1	U	161	7	11,15,16	1.55	3 (27%)	11,20,22	2.41	5 (45%)
7	6V1	U	47	7	11,15,16	1.20	1 (9%)	11,20,22	2.98	4 (36%)
10	6V1	X	91	10	11,15,16	2.40	2 (18%)	11,20,22	6.04	7 (63%)

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	-	1/6/25/27	0/1/1/1
7	YCM	U	137	7	-	0/6/8/10	0/0/0/0
7	6V1	U	161	7	-	0/6/25/27	0/1/1/1
7	6V1	U	47	7	1/1/5/6	0/6/25/27	0/1/1/1
10	6V1	X	91	10	-	0/6/25/27	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	X	91	6V1	C1-SG	-6.87	1.74	1.83
10	J	91	6V1	C1-SG	-6.55	1.75	1.83
7	G	137	YCM	CB-SG	-5.97	1.69	1.81
3	Q	63	YCM	CD-SG	-4.41	1.72	1.81
7	U	137	YCM	CB-SG	-4.06	1.73	1.81

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	47	6V1	C5-C1-C2	-12.69	94.32	103.98
10	J	91	6V1	C6-N3-C4	-7.48	115.29	123.24
10	X	91	6V1	C6-N3-C4	-6.95	115.85	123.24
3	Q	63	YCM	CA-CB-SG	-4.75	101.60	112.84
10	X	91	6V1	O8-C4-C5	-4.59	121.23	127.38

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	U	47	6V1	C1

All (1) torsion outliers are listed below:

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

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, 73 are monoatomic - leaving 9 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
16	1PE	G	303	-	15,15,15	0.58	0	14,14,14	0.71	0
16	1PE	I	303	-	15,15,15	0.56	0	14,14,14	0.87	1 (7%)
16	1PE	I	304	-	15,15,15	0.55	0	14,14,14	0.65	0
16	1PE	L	301	-	15,15,15	0.62	0	14,14,14	0.74	1 (7%)
16	1PE	W	303	-	15,15,15	0.57	0	14,14,14	0.51	0
16	1PE	Z	301	-	15,15,15	0.64	0	14,14,14	0.63	0
16	1PE	a	304	-	15,15,15	0.55	0	14,14,14	0.58	0
16	1PE	b	504	-	15,15,15	0.63	0	14,14,14	0.78	0
16	1PE	b	505	-	15,15,15	0.68	0	14,14,14	0.39	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	1PE	G	303	-	-	0/13/13/13	0/0/0/0
16	1PE	I	303	-	-	0/13/13/13	0/0/0/0
16	1PE	I	304	-	-	0/13/13/13	0/0/0/0
16	1PE	L	301	-	-	0/13/13/13	0/0/0/0
16	1PE	W	303	-	-	0/13/13/13	0/0/0/0
16	1PE	Z	301	-	-	0/13/13/13	0/0/0/0
16	1PE	a	304	-	-	0/13/13/13	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
16	1PE	b	504	-	-	0/13/13/13	0/0/0/0
16	1PE	b	505	-	-	0/13/13/13	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	L	301	1PE	C26-OH6-C15	2.14	122.45	113.31
16	I	303	1PE	C25-OH5-C14	2.15	122.49	113.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	G	303	1PE	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	230/234 (98%)	-0.11	4 (1%) 73 69	27, 42, 75, 87	0
1	O	230/234 (98%)	0.34	17 (7%) 17 14	36, 56, 93, 119	0
2	B	248/261 (95%)	0.11	9 (3%) 46 40	31, 48, 85, 130	0
2	P	247/261 (94%)	0.24	18 (7%) 18 14	35, 53, 91, 133	0
3	C	236/248 (95%)	0.47	21 (8%) 12 9	32, 57, 97, 128	0
3	Q	233/248 (93%)	0.29	15 (6%) 23 18	31, 54, 95, 127	0
4	D	233/241 (96%)	0.23	13 (5%) 28 22	35, 55, 85, 106	0
4	R	233/241 (96%)	-0.11	5 (2%) 67 62	29, 40, 62, 82	0
5	E	233/263 (88%)	0.09	14 (6%) 25 20	25, 39, 82, 98	0
5	S	237/263 (90%)	-0.05	8 (3%) 49 43	31, 43, 72, 94	0
6	F	239/255 (93%)	-0.15	0 100 100	22, 32, 52, 72	0
6	T	240/255 (94%)	0.17	12 (5%) 32 27	32, 49, 79, 105	0
7	G	241/246 (97%)	-0.10	3 (1%) 81 78	23, 35, 65, 89	0
7	U	232/246 (94%)	0.23	14 (6%) 25 20	38, 56, 86, 122	0
8	H	220/234 (94%)	-0.00	4 (1%) 71 67	25, 32, 62, 87	0
8	V	220/234 (94%)	-0.07	6 (2%) 58 53	34, 44, 78, 100	0
9	I	204/205 (99%)	-0.25	0 100 100	25, 32, 51, 64	0
9	W	204/205 (99%)	-0.22	2 (0%) 84 82	32, 44, 66, 72	0
10	J	195/201 (97%)	-0.17	1 (0%) 91 90	28, 38, 55, 70	0
10	X	195/201 (97%)	-0.22	0 100 100	30, 38, 54, 69	0
11	K	201/204 (98%)	-0.28	0 100 100	32, 41, 65, 90	0
11	Y	199/204 (97%)	-0.27	0 100 100	26, 33, 51, 62	0
12	L	213/213 (100%)	-0.11	0 100 100	29, 45, 65, 83	0
12	Z	213/213 (100%)	-0.16	1 (0%) 91 90	24, 34, 55, 73	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	216/219 (98%)	-0.10	2 (0%) 85 83	24, 35, 59, 94	0
13	a	216/219 (98%)	-0.14	2 (0%) 85 83	24, 36, 57, 82	0
14	N	202/205 (98%)	-0.08	3 (1%) 76 72	23, 32, 52, 91	0
14	b	203/205 (99%)	-0.13	4 (1%) 68 64	30, 38, 63, 90	0
All	All	6213/6458 (96%)	-0.01	178 (2%) 55 49	22, 42, 78, 133	0

The worst 5 of 178 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	232	ILE	13.9
2	B	203	VAL	10.2
4	D	241	ILE	9.2
2	P	204	SER	9.0
2	P	203	VAL	8.8

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	6V1	S	148	15/16	0.89	0.19	-	35,56,62,64	0
7	YCM	G	137	10/11	0.89	0.12	-	27,34,48,49	0
7	6V1	U	47	15/16	0.83	0.29	-	64,96,103,104	0
7	6V1	G	161	15/16	0.94	0.12	-	28,44,50,52	0
3	YCM	C	63	10/11	0.87	0.11	-	48,50,59,60	0
10	6V1	J	91	15/16	0.90	0.19	-	31,44,50,50	0
5	6V1	E	148	15/16	0.89	0.15	-	29,45,55,55	0
7	6V1	G	47	15/16	0.89	0.17	-	33,52,55,55	0
7	YCM	U	137	10/11	0.83	0.15	-	46,54,72,72	0
3	YCM	Q	63	10/11	0.90	0.09	-	45,48,59,60	0
7	6V1	U	161	15/16	0.94	0.11	-	48,62,69,70	0
10	6V1	X	91	15/16	0.92	0.16	-	32,47,53,53	0

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
15	CL	K	305	1/1	0.91	0.29	10.66	60,60,60,60	0
15	CL	M	301	1/1	0.93	0.18	9.93	52,52,52,52	0
16	1PE	I	304	16/16	0.80	0.25	9.44	48,61,71,75	0
15	CL	S	301	1/1	0.97	0.28	9.01	59,59,59,59	0
16	1PE	L	301	16/16	0.83	0.17	7.39	49,62,66,69	0
16	1PE	b	505	16/16	0.79	0.23	6.86	64,67,78,78	0
15	CL	E	303	1/1	0.95	0.15	5.96	54,54,54,54	0
15	CL	a	301	1/1	0.96	0.13	5.96	53,53,53,53	0
16	1PE	I	303	16/16	0.85	0.14	5.71	48,52,60,68	0
16	1PE	a	304	16/16	0.78	0.22	5.04	57,62,69,71	0
15	CL	M	302	1/1	0.86	0.17	4.65	62,62,62,62	0
16	1PE	Z	301	16/16	0.86	0.15	4.58	51,61,64,64	0
16	1PE	W	303	16/16	0.84	0.14	4.18	55,58,64,66	0
15	CL	Q	302	1/1	0.96	0.21	3.35	54,54,54,54	0
15	CL	B	302	1/1	0.94	0.17	2.49	54,54,54,54	0
15	CL	D	301	1/1	0.96	0.19	1.75	61,61,61,61	0
15	CL	A	304	1/1	0.98	0.12	1.47	52,52,52,52	0
15	CL	K	303	1/1	0.97	0.12	1.38	62,62,62,62	0
16	1PE	b	504	16/16	0.85	0.13	1.07	41,50,67,68	0
15	CL	b	502	1/1	0.79	0.10	0.83	59,59,59,59	0
16	1PE	G	303	16/16	0.91	0.12	0.19	34,42,51,56	0
15	CL	C	301	1/1	0.92	0.11	-0.16	56,56,56,56	0
15	CL	U	301	1/1	0.98	0.10	-0.23	51,51,51,51	0
18	MG	L	303	1/1	0.97	0.09	-0.87	33,33,33,33	0
15	CL	G	301	1/1	0.98	0.10	-0.89	41,41,41,41	0
17	K	b	506	1/1	0.95	0.07	-0.98	38,38,38,38	0
15	CL	E	301	1/1	0.99	0.08	-1.06	54,54,54,54	0
18	MG	I	301	1/1	0.96	0.07	-1.11	29,29,29,29	0
15	CL	Y	303	1/1	0.95	0.06	-1.24	56,56,56,56	0
15	CL	A	301	1/1	0.95	0.07	-1.37	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
15	CL	b	503	1/1	0.98	0.07	-1.43	44,44,44,44	0
17	K	N	504	1/1	0.97	0.06	-1.46	37,37,37,37	0
15	CL	F	301	1/1	0.94	0.07	-1.60	46,46,46,46	0
15	CL	O	301	1/1	0.95	0.05	-1.67	49,49,49,49	0
15	CL	G	302	1/1	0.93	0.05	-1.80	56,56,56,56	0
15	CL	N	503	1/1	0.99	0.07	-2.07	40,40,40,40	0
18	MG	K	301	1/1	0.93	0.07	-2.16	33,33,33,33	0
18	MG	I	305	1/1	0.99	0.07	-2.38	26,26,26,26	0
15	CL	N	501	1/1	0.97	0.07	-2.68	42,42,42,42	0
18	MG	W	301	1/1	0.96	0.07	-2.99	34,34,34,34	0
17	K	Z	302	1/1	0.99	0.06	-3.08	34,34,34,34	0
15	CL	S	303	1/1	0.97	0.06	-3.22	48,48,48,48	0
17	K	U	302	1/1	0.96	0.06	-3.46	38,38,38,38	0
17	K	L	302	1/1	0.98	0.05	-3.61	42,42,42,42	0
18	MG	H	302	1/1	0.99	0.05	-4.50	29,29,29,29	0
17	K	G	304	1/1	0.99	0.07	-4.59	28,28,28,28	0
15	CL	K	304	1/1	0.91	0.15	-	52,52,52,52	0
15	CL	N	502	1/1	0.99	0.05	-	43,43,43,43	0
15	CL	P	301	1/1	0.94	0.06	-	45,45,45,45	0
18	MG	J	301	1/1	0.91	0.06	-	41,41,41,41	0
15	CL	a	303	1/1	0.96	0.08	-	52,52,52,52	0
18	MG	X	301	1/1	0.89	0.06	-	44,44,44,44	0
15	CL	b	501	1/1	0.97	0.07	-	44,44,44,44	0
18	MG	V	301	1/1	0.74	0.18	-	48,48,48,48	0
15	CL	S	302	1/1	0.93	0.13	-	54,54,54,54	0
15	CL	O	304	1/1	0.92	0.14	-	55,55,55,55	0
15	CL	Q	301	1/1	0.97	0.16	-	62,62,62,62	0
18	MG	H	301	1/1	0.71	0.10	-	45,45,45,45	0
15	CL	I	302	1/1	0.96	0.06	-	40,40,40,40	0
15	CL	M	303	1/1	0.99	0.05	-	38,38,38,38	0
15	CL	B	301	1/1	0.96	0.09	-	37,37,37,37	0
15	CL	E	302	1/1	0.96	0.07	-	49,49,49,49	0
15	CL	V	302	1/1	0.92	0.10	-	50,50,50,50	0
15	CL	M	304	1/1	0.96	0.04	-	49,49,49,49	0
15	CL	A	302	1/1	0.91	0.07	-	61,61,61,61	0
15	CL	K	302	1/1	0.97	0.07	-	41,41,41,41	0
15	CL	a	302	1/1	0.97	0.06	-	42,42,42,42	0
15	CL	Y	304	1/1	0.93	0.07	-	51,51,51,51	0
15	CL	A	303	1/1	0.99	0.07	-	42,42,42,42	0
15	CL	Y	302	1/1	0.99	0.07	-	47,47,47,47	0
15	CL	V	303	1/1	0.91	0.09	-	59,59,59,59	0
15	CL	W	302	1/1	0.97	0.05	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
15	CL	H	303	1/1	0.88	0.11	-	51,51,51,51	0
15	CL	Y	301	1/1	0.98	0.09	-	33,33,33,33	0
15	CL	D	302	1/1	0.92	0.10	-	53,53,53,53	0
15	CL	O	303	1/1	0.80	0.37	-	74,74,74,74	0
15	CL	R	301	1/1	0.97	0.09	-	50,50,50,50	0
15	CL	C	302	1/1	0.86	0.14	-	63,63,63,63	0
15	CL	O	302	1/1	0.96	0.07	-	59,59,59,59	0
15	CL	H	304	1/1	0.99	0.06	-	47,47,47,47	0
15	CL	R	302	1/1	0.97	0.15	-	48,48,48,48	0
15	CL	Y	305	1/1	0.91	0.09	-	54,54,54,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.