



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 3, 2024 – 08:13 pm BST

PDB ID : 9FT0  
Title : Yeast 20S proteasome in complex with epoxyketone inhibitor 42  
Authors : Maurits, E.; Huber, E.M.; Dekker, P.M.; Wang, X.; Heinemeyer, W.; Florea, B.I.; Groll, M.; Overkleeft, H.S.  
Deposited on : 2024-06-23  
Resolution : 2.75 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](mailto: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>.

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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	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

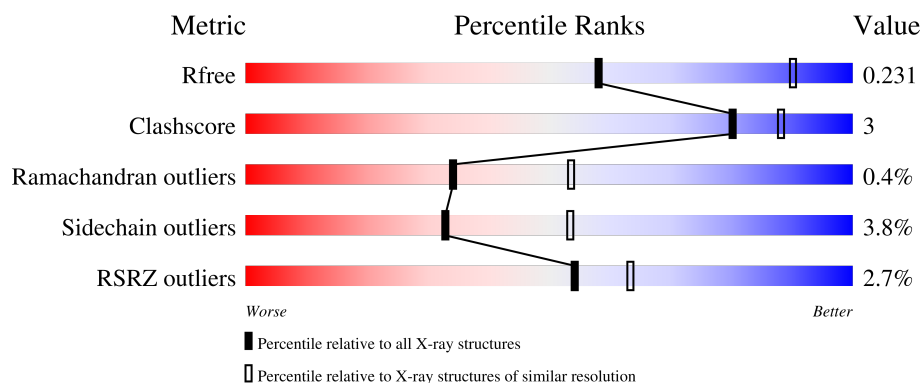
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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  $\geq 3$ , 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	250	<div> <div>2%</div> <div>94%</div> <div>6%</div> </div>
1	O	250	<div> <div>2%</div> <div>92%</div> <div>7%</div> </div>
2	B	258	<div> <div>5%</div> <div>84%</div> <div>10%</div> <div>5%</div> </div>
2	P	258	<div> <div>5%</div> <div>84%</div> <div>10%</div> <div>5%</div> </div>
3	C	254	<div> <div>4%</div> <div>85%</div> <div>9%</div> <div>5%</div> </div>



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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	231	
8	V	231	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	211	
11	Y	211	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	
15	e	4	
15	f	4	

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Mol	Chain	Length	Quality of chain
15	g	4	
15	h	4	

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	MG	Z	301	-	-	-	X

## 2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 49929 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	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			
3	Q	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			

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

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

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			
5	S	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			
6	T	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			
7	U	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			

- Molecule 8 is a protein called proteasome endopeptidase complex.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	221	Total	C	N	O	S	0	0	0
			1677	1057	292	321	7			
8	V	221	Total	C	N	O	S	0	0	0
			1677	1057	292	321	7			

- 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	0	0
			1581	1010	258	305	8			
9	W	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

- Molecule 11 is a protein called proteasome endopeptidase complex.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	211	Total	C	N	O	S	0	0	0
			1637	1041	279	310	7			
11	Y	211	Total	C	N	O	S	0	0	0
			1637	1041	279	310	7			

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			
13	a	233	Total	C	N	O	S	0	0	0
			1824	1154	312	351	7			

- Molecule 14 is a protein called Proteasome subunit beta type-1.

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

- Molecule 15 is a protein called 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C]PYRAZOLE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	e	4	Total	C	N	O	0	0	0
			51	36	5	10			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	f	4	Total	C	N	O	0	0	0
			51	36	5	10			
15	g	4	Total	C	N	O	0	0	0
			51	36	5	10			
15	h	4	Total	C	N	O	0	0	0
			51	36	5	10			

- Molecule 16 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

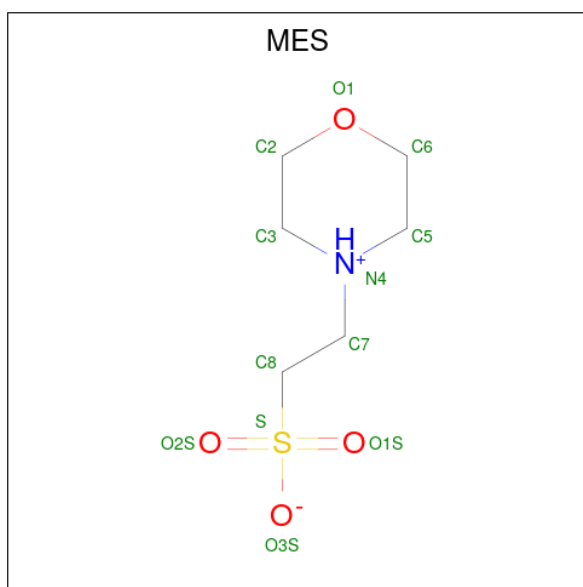
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	G	1	Total	Mg	0	0
			1	1		
16	I	1	Total	Mg	0	0
			1	1		
16	K	1	Total	Mg	0	0
			1	1		
16	N	1	Total	Mg	0	0
			1	1		
16	V	1	Total	Mg	0	0
			1	1		
16	W	1	Total	Mg	0	0
			1	1		
16	X	1	Total	Mg	0	0
			1	1		
16	Y	1	Total	Mg	0	0
			1	1		
16	Z	1	Total	Mg	0	0
			1	1		

- Molecule 17 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	G	1	Total	Cl	0	0
			1	1		
17	N	2	Total	Cl	0	0
			2	2		
17	U	1	Total	Cl	0	0
			1	1		
17	b	1	Total	Cl	0	0
			1	1		

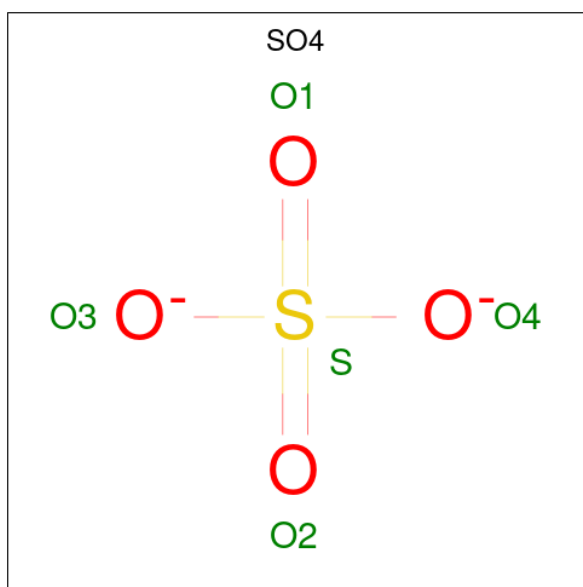
- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	H	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	K	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	X	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 19 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	f	1	Total	O S	0	0
			5	4 1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
19	g	1	Total	O	S	0	0
			5	4	1		
19	h	1	Total	O	S	0	0
			5	4	1		

- Molecule 20 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	A	2	Total	O	0	0
			2	2		
20	B	6	Total	O	0	0
			6	6		
20	C	3	Total	O	0	0
			3	3		
20	D	2	Total	O	0	0
			2	2		
20	E	4	Total	O	0	0
			4	4		
20	F	5	Total	O	0	0
			5	5		
20	G	4	Total	O	0	0
			4	4		
20	H	4	Total	O	0	0
			4	4		
20	I	3	Total	O	0	0
			3	3		
20	J	7	Total	O	0	0
			7	7		
20	K	6	Total	O	0	0
			6	6		
20	L	5	Total	O	0	0
			5	5		
20	M	5	Total	O	0	0
			5	5		
20	N	8	Total	O	0	0
			8	8		
20	O	2	Total	O	0	0
			2	2		
20	P	6	Total	O	0	0
			6	6		
20	Q	3	Total	O	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
20	R	2	Total	O	0	0
			2	2		
20	S	4	Total	O	0	0
			4	4		
20	T	7	Total	O	0	0
			7	7		
20	U	8	Total	O	0	0
			8	8		
20	V	3	Total	O	0	0
			3	3		
20	W	5	Total	O	0	0
			5	5		
20	X	11	Total	O	0	0
			11	11		
20	Y	7	Total	O	0	0
			7	7		
20	Z	10	Total	O	0	0
			10	10		
20	a	10	Total	O	0	0
			10	10		
20	b	7	Total	O	0	0
			7	7		
20	g	1	Total	O	0	0
			1	1		

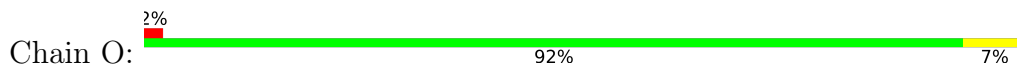
### 3 Residue-property plots [i](#)

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.

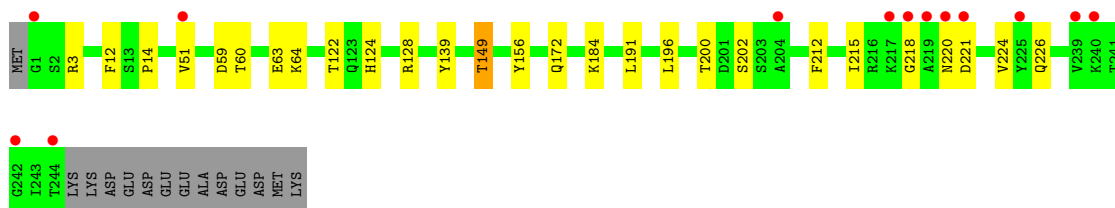
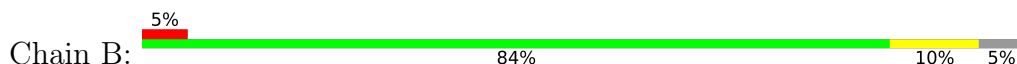
- Molecule 1: Proteasome subunit alpha type-2



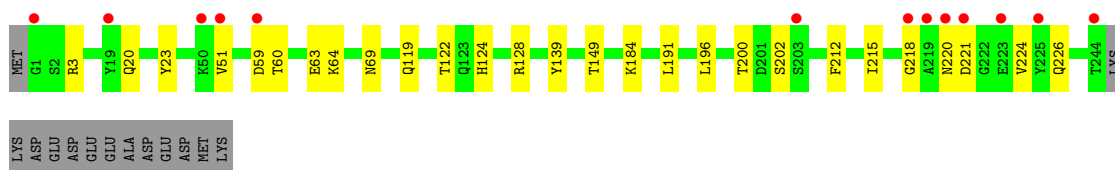
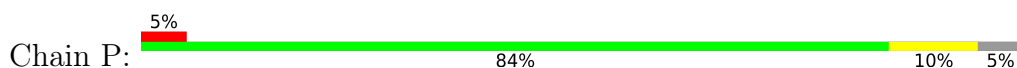
- Molecule 1: Proteasome subunit alpha type-2



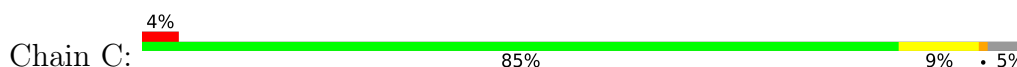
- Molecule 2: Proteasome subunit alpha type-3

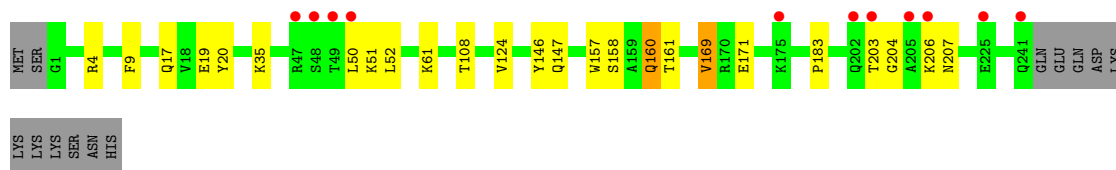


- Molecule 2: Proteasome subunit alpha type-3

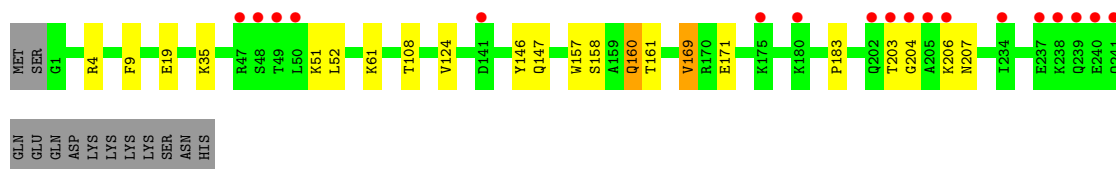
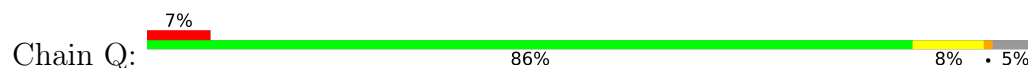


- Molecule 3: Proteasome subunit alpha type-4

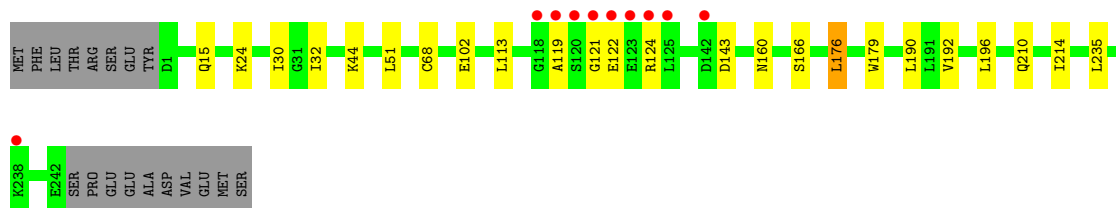
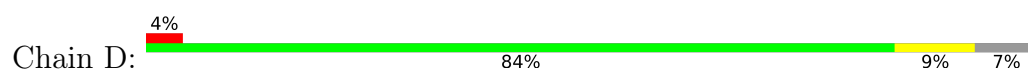




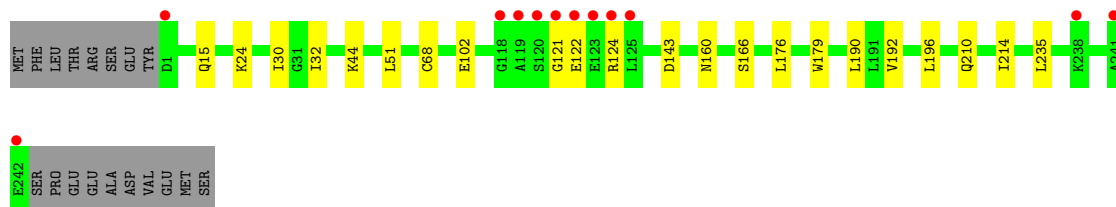
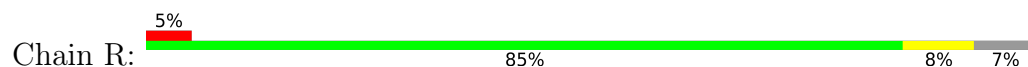
• Molecule 3: Proteasome subunit alpha type-4



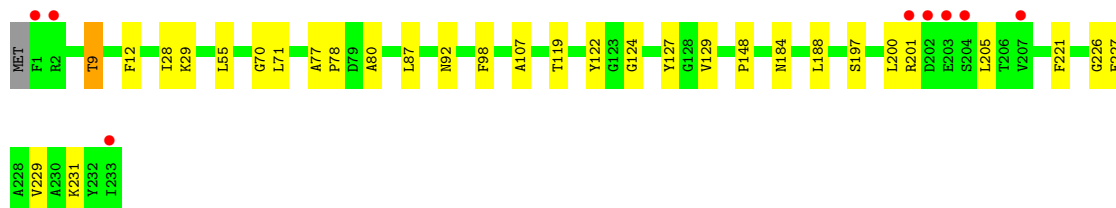
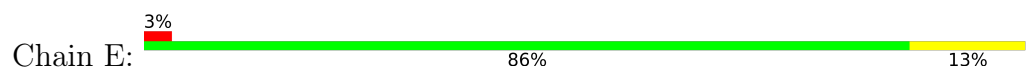
• Molecule 4: Proteasome subunit alpha type-5



• Molecule 4: Proteasome subunit alpha type-5



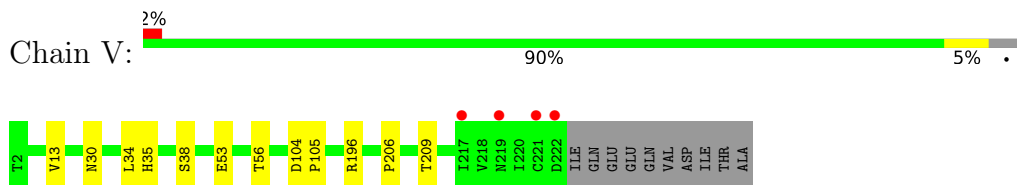
• Molecule 5: Proteasome subunit alpha type-6



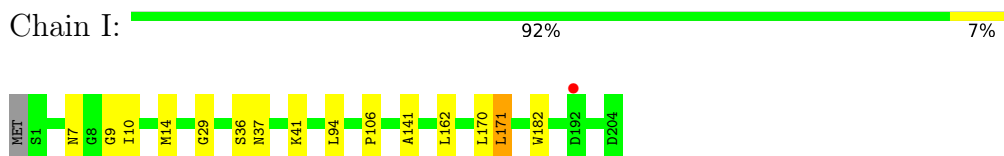
• Molecule 5: Proteasome subunit alpha type-6



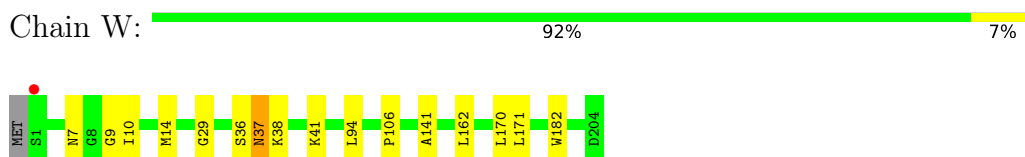
- Molecule 8: proteasome endopeptidase complex



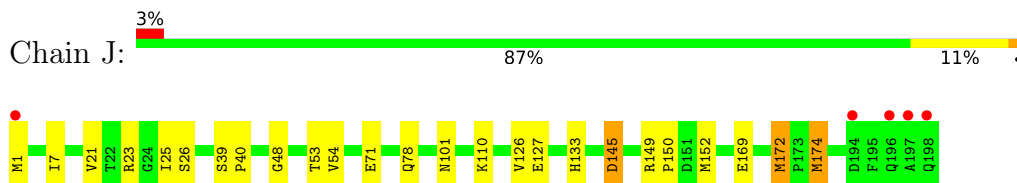
- Molecule 9: Proteasome subunit beta type-3



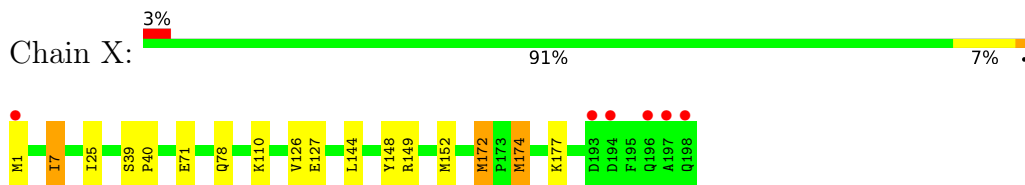
- Molecule 9: Proteasome subunit beta type-3



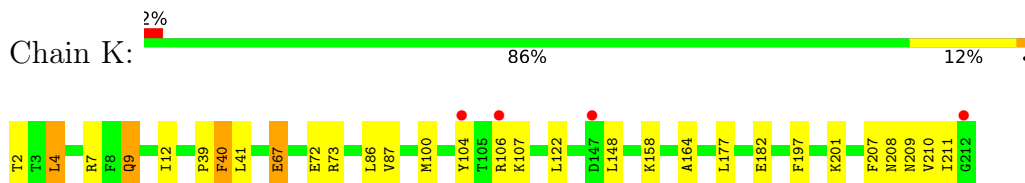
- Molecule 10: Proteasome subunit beta type-4



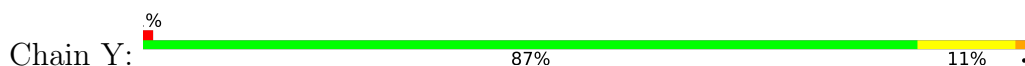
- Molecule 10: Proteasome subunit beta type-4

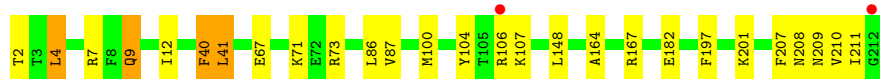


- Molecule 11: proteasome endopeptidase complex



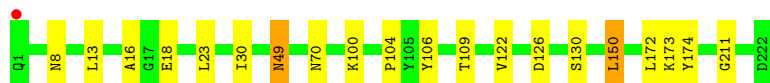
- Molecule 11: proteasome endopeptidase complex





- Molecule 12: Proteasome subunit beta type-6

Chain L: 91% 8% .



- Molecule 12: Proteasome subunit beta type-6

Chain Z: 91% 8% .



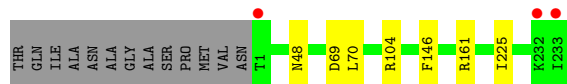
- Molecule 13: Proteasome subunit beta type-7

Chain M: 87% 8% 5%



- Molecule 13: Proteasome subunit beta type-7

Chain a: 92% 5%



- Molecule 14: Proteasome subunit beta type-1

Chain N: 94% 6%




- Molecule 14: Proteasome subunit beta type-1

Chain b: 98%



- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-C]PYRAZOLE



Chain e:  25% 75%

00EI	S2	Y3	A1IFL4
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- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-.C.]PYRAZOLE

Chain f:  50% 50%


00EI	S2	Y3	A1IFL4
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- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-.C.]PYRAZOLE

Chain g:  50% 50%

00EI	S2	Y3	A1IFL4
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- Molecule 15: 3-PYRIDIN-4-YL-2,4-DIHYDRO-INDENO[1,2-.C.]PYRAZOLE

Chain h:  75% 25%

00EI	S2	Y3	A1IFL4
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.52Å 299.48Å 145.00Å 90.00° 112.90° 90.00°	Depositor
Resolution (Å)	30.00 – 2.75 29.89 – 2.75	Depositor EDS
% Data completeness (in resolution range)	96.3 (30.00-2.75) 96.4 (29.89-2.75)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.76Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.190 , 0.232 0.195 , 0.231	Depositor DCC
$R_{free}$ test set	13235 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	56.2	Xtriage
Anisotropy	0.750	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 26.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	49929	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: A1IFL, MES, SO4, 00E, CL, MG, HSE, 0A1

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	0.66	0/1952	0.71	0/2642
1	O	0.67	0/1952	0.71	0/2642
2	B	0.66	0/1934	0.72	0/2618
2	P	0.66	0/1934	0.72	0/2618
3	C	0.67	0/1919	0.72	0/2598
3	Q	0.67	0/1919	0.72	0/2598
4	D	0.67	0/1886	0.72	0/2541
4	R	0.67	0/1886	0.72	0/2541
5	E	0.67	0/1823	0.72	0/2463
5	S	0.67	0/1823	0.72	0/2463
6	F	0.66	0/1936	0.71	0/2614
6	T	0.66	0/1936	0.71	0/2614
7	G	0.65	0/1959	0.71	0/2652
7	U	0.65	0/1959	0.71	0/2652
8	H	0.67	0/1708	0.72	0/2316
8	V	0.67	0/1708	0.73	0/2316
9	I	0.66	0/1611	0.71	0/2174
9	W	0.66	0/1611	0.71	0/2174
10	J	0.67	0/1613	0.75	0/2173
10	X	0.66	0/1613	0.74	0/2173
11	K	0.66	0/1674	0.77	0/2264
11	Y	0.66	0/1674	0.78	0/2264
12	L	0.66	0/1795	0.72	0/2420
12	Z	0.66	0/1795	0.73	0/2420
13	M	0.66	0/1855	0.72	0/2514
13	a	0.66	0/1855	0.73	0/2514
14	N	0.66	0/1541	0.71	0/2087
14	b	0.66	0/1541	0.71	0/2087
All	All	0.66	0/50412	0.72	0/68152

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 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	1915	0	1929	8	0
1	O	1915	0	1929	11	0
2	B	1904	0	1904	12	0
2	P	1904	0	1904	10	0
3	C	1890	0	1903	11	0
3	Q	1890	0	1903	8	0
4	D	1861	0	1839	11	0
4	R	1861	0	1839	8	0
5	E	1795	0	1800	19	0
5	S	1795	0	1800	15	0
6	F	1896	0	1889	4	0
6	T	1896	0	1889	8	0
7	G	1921	0	1913	10	0
7	U	1921	0	1913	12	0
8	H	1677	0	1678	5	0
8	V	1677	0	1678	3	0
9	I	1581	0	1574	8	0
9	W	1581	0	1574	10	0
10	J	1585	0	1590	14	0
10	X	1585	0	1590	13	0
11	K	1637	0	1585	18	0
11	Y	1637	0	1585	19	0
12	L	1757	0	1711	11	0
12	Z	1757	0	1711	14	0
13	M	1824	0	1832	7	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	5	0
14	b	1512	0	1481	0	0
15	e	51	0	23	0	0
15	f	51	0	23	0	0
15	g	51	0	23	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	h	51	0	23	0	0
16	G	1	0	0	0	0
16	I	1	0	0	0	0
16	K	1	0	0	0	0
16	N	1	0	0	0	0
16	V	1	0	0	0	0
16	W	1	0	0	0	0
16	X	1	0	0	0	0
16	Y	1	0	0	0	0
16	Z	1	0	0	0	0
17	G	1	0	0	0	0
17	N	2	0	0	1	0
17	U	1	0	0	0	0
17	b	1	0	0	0	0
18	H	12	0	13	2	0
18	K	12	0	13	0	0
18	X	12	0	13	0	0
19	f	5	0	0	0	0
19	g	5	0	0	0	0
19	h	5	0	0	0	0
20	A	2	0	0	0	0
20	B	6	0	0	0	0
20	C	3	0	0	0	0
20	D	2	0	0	0	0
20	E	4	0	0	0	0
20	F	5	0	0	0	0
20	G	4	0	0	0	0
20	H	4	0	0	0	0
20	I	3	0	0	0	0
20	J	7	0	0	1	0
20	K	6	0	0	0	0
20	L	5	0	0	0	0
20	M	5	0	0	0	0
20	N	8	0	0	0	0
20	O	2	0	0	0	0
20	P	6	0	0	0	0
20	Q	3	0	0	0	0
20	R	2	0	0	0	0
20	S	4	0	0	0	0
20	T	7	0	0	0	0
20	U	8	0	0	0	0
20	V	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	W	5	0	0	0	0
20	X	11	0	0	0	0
20	Y	7	0	0	0	0
20	Z	10	0	0	0	0
20	a	10	0	0	0	0
20	b	7	0	0	0	0
20	g	1	0	0	0	0
All	All	49929	0	49387	230	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 230 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)
11:Y:104:TYR:CZ	11:Y:182:GLU:HG3	2.07	0.90
11:K:104:TYR:CZ	11:K:182:GLU:HG3	2.08	0.88
6:T:91:GLU:HG2	6:T:111:ARG:HB3	1.67	0.76
6:F:91:GLU:HG2	6:F:111:ARG:HB3	1.68	0.75
11:K:104:TYR:CE1	11:K:182:GLU:HG3	2.22	0.74

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	248/250 (99%)	240 (97%)	6 (2%)	2 (1%)	19 34
1	O	248/250 (99%)	241 (97%)	5 (2%)	2 (1%)	19 34
2	B	242/258 (94%)	232 (96%)	7 (3%)	3 (1%)	13 23
2	P	242/258 (94%)	232 (96%)	7 (3%)	3 (1%)	13 23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	239/254 (94%)	227 (95%)	9 (4%)	3 (1%)	12	21
3	Q	239/254 (94%)	228 (95%)	8 (3%)	3 (1%)	12	21
4	D	240/260 (92%)	230 (96%)	8 (3%)	2 (1%)	19	34
4	R	240/260 (92%)	230 (96%)	8 (3%)	2 (1%)	19	34
5	E	231/234 (99%)	218 (94%)	11 (5%)	2 (1%)	17	31
5	S	231/234 (99%)	218 (94%)	11 (5%)	2 (1%)	17	31
6	F	242/288 (84%)	234 (97%)	8 (3%)	0	100	100
6	T	242/288 (84%)	234 (97%)	8 (3%)	0	100	100
7	G	241/252 (96%)	234 (97%)	6 (2%)	1 (0%)	34	53
7	U	241/252 (96%)	234 (97%)	6 (2%)	1 (0%)	34	53
8	H	219/231 (95%)	214 (98%)	5 (2%)	0	100	100
8	V	219/231 (95%)	214 (98%)	5 (2%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
9	W	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	J	196/198 (99%)	191 (97%)	5 (3%)	0	100	100
10	X	196/198 (99%)	191 (97%)	5 (3%)	0	100	100
11	K	209/211 (99%)	204 (98%)	5 (2%)	0	100	100
11	Y	209/211 (99%)	205 (98%)	4 (2%)	0	100	100
12	L	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	231/246 (94%)	220 (95%)	11 (5%)	0	100	100
13	a	231/246 (94%)	221 (96%)	10 (4%)	0	100	100
14	N	194/196 (99%)	186 (96%)	8 (4%)	0	100	100
14	b	194/196 (99%)	185 (95%)	9 (5%)	0	100	100
All	All	6308/6610 (95%)	6081 (96%)	201 (3%)	26 (0%)	34	53

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	166	LYS
3	C	203	THR
5	E	201	ARG
1	O	166	LYS
3	Q	203	THR

### 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	209/209 (100%)	205 (98%)	4 (2%)	57	73
1	O	209/209 (100%)	206 (99%)	3 (1%)	67	79
2	B	203/216 (94%)	195 (96%)	8 (4%)	32	52
2	P	203/216 (94%)	193 (95%)	10 (5%)	25	43
3	C	213/226 (94%)	204 (96%)	9 (4%)	30	49
3	Q	213/226 (94%)	204 (96%)	9 (4%)	30	49
4	D	198/215 (92%)	190 (96%)	8 (4%)	31	51
4	R	198/215 (92%)	190 (96%)	8 (4%)	31	51
5	E	192/193 (100%)	186 (97%)	6 (3%)	40	60
5	S	192/193 (100%)	186 (97%)	6 (3%)	40	60
6	F	201/239 (84%)	191 (95%)	10 (5%)	24	42
6	T	201/239 (84%)	191 (95%)	10 (5%)	24	42
7	G	207/210 (99%)	199 (96%)	8 (4%)	32	52
7	U	207/210 (99%)	199 (96%)	8 (4%)	32	52
8	H	180/189 (95%)	174 (97%)	6 (3%)	38	58
8	V	180/189 (95%)	174 (97%)	6 (3%)	38	58
9	I	172/173 (99%)	169 (98%)	3 (2%)	60	76
9	W	172/173 (99%)	169 (98%)	3 (2%)	60	76
10	J	175/175 (100%)	163 (93%)	12 (7%)	15	27
10	X	175/175 (100%)	168 (96%)	7 (4%)	31	51
11	K	168/168 (100%)	158 (94%)	10 (6%)	19	33
11	Y	168/168 (100%)	157 (94%)	11 (6%)	17	30
12	L	185/185 (100%)	176 (95%)	9 (5%)	25	43
12	Z	185/185 (100%)	176 (95%)	9 (5%)	25	43
13	M	199/208 (96%)	192 (96%)	7 (4%)	36	56
13	a	199/208 (96%)	192 (96%)	7 (4%)	36	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
14	N	162/162 (100%)	159 (98%)	3 (2%)	57 73
14	b	162/162 (100%)	159 (98%)	3 (2%)	57 73
All	All	5328/5536 (96%)	5125 (96%)	203 (4%)	33 53

5 of 203 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	P	220	ASN
6	T	181	GLU
13	a	225	ILE
3	Q	61	LYS
4	R	190	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
12	Z	3	ASN
12	Z	165	ASN
12	L	1	GLN
11	K	209	ASN
13	a	48	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
15	0A1	h	3	15	12,13,14	1.96	1 (8%)	13,16,18	1.18	2 (15%)
15	00E	h	1	15	9,9,10	0.59	0	10,10,12	0.97	0
15	HSE	g	2	15	5,6,7	0.68	0	2,6,8	1.27	0
15	00E	g	1	15	9,9,10	0.53	0	10,10,12	1.50	2 (20%)
15	0A1	e	3	15	12,13,14	1.82	1 (8%)	13,16,18	1.56	2 (15%)
15	0A1	g	3	15	12,13,14	1.60	1 (8%)	13,16,18	1.07	2 (15%)
15	HSE	f	2	15	5,6,7	1.34	1 (20%)	2,6,8	1.55	1 (50%)
15	00E	f	1	15	9,9,10	0.68	0	10,10,12	1.13	0
15	HSE	e	2	15	5,6,7	1.12	1 (20%)	2,6,8	1.13	0
15	0A1	f	3	15	12,13,14	2.22	2 (16%)	13,16,18	1.18	1 (7%)
15	00E	e	1	15	9,9,10	0.60	0	10,10,12	1.59	1 (10%)
15	HSE	h	2	15	5,6,7	1.07	0	2,6,8	0.63	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
15	0A1	h	3	15	-	2/7/8/10	0/1/1/1
15	00E	h	1	15	-	0/2/11/12	0/1/1/1
15	HSE	g	2	15	-	1/4/5/7	-
15	00E	g	1	15	-	2/2/11/12	0/1/1/1
15	0A1	e	3	15	-	4/7/8/10	0/1/1/1
15	0A1	g	3	15	-	2/7/8/10	0/1/1/1
15	HSE	f	2	15	-	1/4/5/7	-
15	00E	f	1	15	-	0/2/11/12	0/1/1/1
15	HSE	e	2	15	-	3/4/5/7	-
15	0A1	f	3	15	-	3/7/8/10	0/1/1/1
15	00E	e	1	15	-	0/2/11/12	0/1/1/1
15	HSE	h	2	15	-	1/4/5/7	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	f	3	0A1	CB-CG	-6.75	1.35	1.51
15	e	3	0A1	CB-CG	-6.08	1.36	1.51
15	h	3	0A1	CB-CG	-6.02	1.36	1.51
15	g	3	0A1	CB-CG	-5.34	1.38	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	f	2	HSE	C3-CA	-2.80	1.49	1.53

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	e	3	0A1	CM-OH-CZ	-3.82	109.22	117.51
15	e	1	00E	CA-NB-CD2	-3.34	106.75	110.48
15	g	1	00E	CE2-CD2-NB	3.06	114.74	110.10
15	e	3	0A1	CG-CB-CA	-3.00	108.03	114.10
15	g	1	00E	CA-NB-CD2	-2.50	107.69	110.48

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	g	1	00E	C-CA-NB-CD1
15	e	2	HSE	O-C-CA-C3
15	e	2	HSE	CA-C3-C4-O3
15	f	2	HSE	C4-C3-CA-C
15	g	2	HSE	CA-C3-C4-O3

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 20 ligands modelled in this entry, 14 are monoatomic - leaving 6 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	SO4	g	101	-	4,4,4	0.56	0	6,6,6	0.09	0
18	MES	K	302	-	12,12,12	0.75	0	14,16,16	0.50	0
18	MES	H	301	-	12,12,12	0.72	0	14,16,16	0.37	0
18	MES	X	202	-	12,12,12	0.77	0	14,16,16	0.38	0
19	SO4	h	101	-	4,4,4	0.38	0	6,6,6	0.05	0
19	SO4	f	101	-	4,4,4	0.67	0	6,6,6	0.09	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
18	MES	H	301	-	-	2/6/14/14	0/1/1/1
18	MES	X	202	-	-	2/6/14/14	0/1/1/1
18	MES	K	302	-	-	4/6/14/14	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	K	302	MES	C7-C8-S-O1S
18	X	202	MES	C8-C7-N4-C3
18	K	302	MES	C7-C8-S-O3S
18	K	302	MES	C8-C7-N4-C3
18	K	302	MES	C7-C8-S-O2S

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	H	301	MES	2	0

## 5.7 Other polymers ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	250/250 (100%)	-0.18	6 (2%) 59 68	49, 65, 94, 137	0
1	O	250/250 (100%)	-0.14	6 (2%) 59 68	56, 73, 106, 145	0
2	B	244/258 (94%)	0.09	13 (5%) 26 31	53, 72, 114, 147	0
2	P	244/258 (94%)	0.04	13 (5%) 26 31	56, 73, 120, 153	0
3	C	241/254 (94%)	0.01	11 (4%) 32 39	53, 75, 131, 143	0
3	Q	241/254 (94%)	0.21	18 (7%) 14 17	57, 84, 146, 165	0
4	D	242/260 (93%)	0.10	10 (4%) 37 44	55, 76, 114, 153	0
4	R	242/260 (93%)	0.11	12 (4%) 28 35	58, 81, 121, 162	0
5	E	233/234 (99%)	-0.04	8 (3%) 45 53	57, 77, 112, 140	0
5	S	233/234 (99%)	0.08	12 (5%) 27 33	57, 80, 114, 160	0
6	F	244/288 (84%)	-0.15	8 (3%) 46 54	52, 70, 106, 138	0
6	T	244/288 (84%)	0.01	12 (4%) 29 36	55, 73, 112, 138	0
7	G	243/252 (96%)	-0.24	5 (2%) 63 72	50, 65, 96, 148	0
7	U	243/252 (96%)	-0.22	3 (1%) 79 85	53, 66, 93, 148	0
8	H	221/231 (95%)	-0.22	2 (0%) 84 89	51, 62, 86, 141	0
8	V	221/231 (95%)	-0.16	4 (1%) 68 76	53, 66, 92, 136	0
9	I	204/205 (99%)	-0.43	1 (0%) 91 94	48, 61, 84, 112	0
9	W	204/205 (99%)	-0.36	1 (0%) 91 94	46, 64, 85, 102	0
10	J	198/198 (100%)	-0.16	5 (2%) 57 66	48, 64, 90, 148	0
10	X	198/198 (100%)	-0.20	6 (3%) 50 59	51, 66, 90, 149	0
11	K	211/211 (100%)	-0.12	4 (1%) 66 75	48, 63, 90, 111	0
11	Y	211/211 (100%)	-0.24	2 (0%) 84 89	52, 63, 91, 109	0
12	L	222/222 (100%)	-0.35	1 (0%) 91 94	48, 65, 88, 103	0
12	Z	222/222 (100%)	-0.25	3 (1%) 75 82	50, 65, 92, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
13	M	233/246 (94%)	-0.37	2 (0%) 84 89	48, 63, 84, 110	0
13	a	233/246 (94%)	-0.29	3 (1%) 77 84	46, 62, 82, 111	0
14	N	196/196 (100%)	-0.34	1 (0%) 91 94	47, 59, 88, 113	0
14	b	196/196 (100%)	-0.35	1 (0%) 91 94	46, 59, 86, 108	0
15	e	0/4	-	-	-	-
15	f	0/4	-	-	-	-
15	g	0/4	-	-	-	-
15	h	0/4	-	-	-	-
All	All	6364/6626 (96%)	-0.14	173 (2%) 54 63	46, 68, 108, 165	0

The worst 5 of 173 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	R	120	SER	11.8
4	D	118	GLY	11.2
4	R	121	GLY	10.9
4	D	119	ALA	9.6
4	D	121	GLY	9.6

## 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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
15	HSE	g	2	7/8	0.87	0.21	66,70,73,76	7
15	00E	g	1	9/10	0.90	0.29	77,82,84,84	9
15	00E	e	1	9/10	0.90	0.28	72,73,76,76	9
15	0A1	e	3	13/14	0.91	0.21	61,63,67,67	13
15	HSE	e	2	7/8	0.93	0.18	56,63,67,67	7
15	0A1	g	3	13/14	0.94	0.23	63,66,67,68	13
15	HSE	f	2	7/8	0.95	0.13	51,57,60,65	0
15	00E	h	1	9/10	0.96	0.20	64,71,72,72	0
15	00E	f	1	9/10	0.96	0.20	62,74,76,76	0
15	0A1	f	3	13/14	0.97	0.14	50,52,63,64	0
15	HSE	h	2	7/8	0.98	0.13	57,60,64,68	0
15	0A1	h	3	13/14	0.98	0.14	46,54,57,58	0

### 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

### 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
16	MG	Z	301	1/1	0.44	0.43	98,98,98,98	0
16	MG	G	301	1/1	0.81	0.26	75,75,75,75	0
18	MES	H	301	12/12	0.88	0.26	60,64,68,68	12
16	MG	W	301	1/1	0.91	0.22	78,78,78,78	0
16	MG	V	301	1/1	0.92	0.17	112,112,112,112	0
16	MG	N	201	1/1	0.94	0.21	74,74,74,74	0
17	CL	N	203	1/1	0.95	0.17	95,95,95,95	0
16	MG	K	301	1/1	0.95	0.23	89,89,89,89	0
19	SO4	f	101	5/5	0.95	0.25	100,107,110,110	0
17	CL	U	301	1/1	0.96	0.07	66,66,66,66	0
17	CL	b	201	1/1	0.96	0.07	70,70,70,70	0
19	SO4	h	101	5/5	0.96	0.24	70,72,73,76	5
18	MES	X	202	12/12	0.97	0.13	69,78,84,86	0
16	MG	I	301	1/1	0.97	0.13	75,75,75,75	0
19	SO4	g	101	5/5	0.97	0.25	78,83,88,88	5
18	MES	K	302	12/12	0.97	0.17	75,82,86,88	0
17	CL	N	202	1/1	0.98	0.08	70,70,70,70	0
17	CL	G	302	1/1	0.98	0.06	59,59,59,59	0
16	MG	X	201	1/1	0.99	0.32	52,52,52,52	0
16	MG	Y	301	1/1	0.99	0.05	84,84,84,84	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.