



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:48 PM GMT

PDB ID : 4Y7X  
Title : Yeast 20S proteasome in complex with Ac-PAA-ep  
Authors : Huber, E.M.; Groll, M.  
Deposited on : 2015-02-16  
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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-20026982

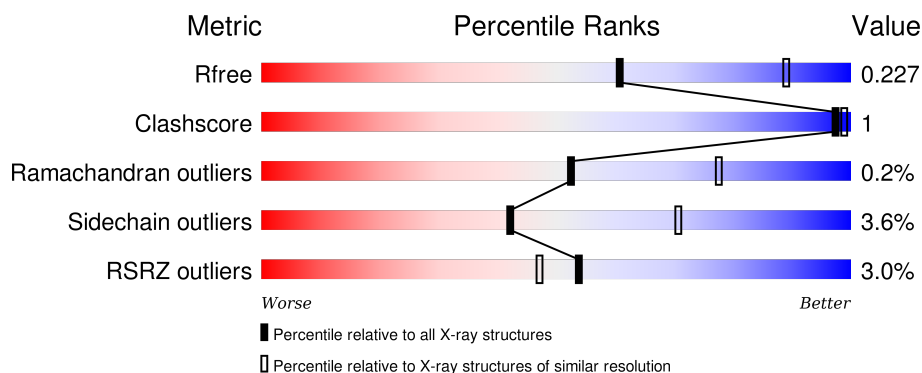
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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  $\geq 3$ , 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	250	<div> <div>2%</div> <div>98%</div> <div>.</div> </div>
1	O	250	<div> <div>4%</div> <div>98%</div> <div>.</div> </div>
2	B	258	<div> <div>6%</div> <div>90%</div> <div>• • 5%</div> </div>
2	P	258	<div> <div>5%</div> <div>90%</div> <div>• • 5%</div> </div>
3	C	254	<div> <div>6%</div> <div>89%</div> <div>5% • 6%</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	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	
15	c	5	
15	d	5	

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	I	301	-	-	-	X
18	MES	K	302	-	-	-	X
18	MES	d	101	-	-	-	X

## 2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 49992 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	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			
3	Q	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			
4	R	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			
5	S	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			
6	T	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			
7	U	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			

- Molecule 8 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	7			
8	V	222	Total	C	N	O	S	0	0	0
			1684	1061	293	323	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	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	7			
11	Y	212	Total	C	N	O	S	0	0	0
			1644	1045	280	312	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 Ac-PPA-ep.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	c	5	Total	C	N	O	0	0	0
			24	16	3	5			
15	d	5	Total	C	N	O	0	0	0
			24	16	3	5			

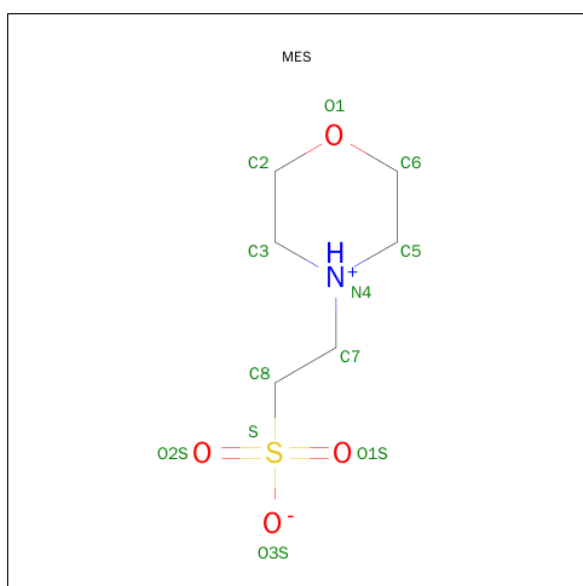
- Molecule 16 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	G	1	Total	Mg	0	0
			1	1		
16	K	1	Total	Mg	0	0
			1	1		
16	I	1	Total	Mg	0	0
			1	1		
16	V	1	Total	Mg	0	0
			1	1		
16	Z	1	Total	Mg	0	0
			1	1		
16	N	1	Total	Mg	0	0
			1	1		
16	Y	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	U	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	K	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	d	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 19 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	A	30	Total	O	0	0
			30	30		
19	B	19	Total	O	0	0
			19	19		
19	C	20	Total	O	0	0
			20	20		
19	D	11	Total	O	0	0
			11	11		
19	E	10	Total	O	0	0
			10	10		
19	F	18	Total	O	0	0
			18	18		
19	G	29	Total	O	0	0
			29	29		
19	H	29	Total	O	0	0
			29	29		
19	I	23	Total	O	0	0
			23	23		
19	J	25	Total	O	0	0
			25	25		
19	K	23	Total	O	0	0
			23	23		
19	L	27	Total	O	0	0
			27	27		
19	M	26	Total	O	0	0
			26	26		
19	N	22	Total	O	0	0
			22	22		
19	O	19	Total	O	0	0
			19	19		
19	P	18	Total	O	0	0
			18	18		
19	Q	15	Total	O	0	0
			15	15		
19	R	8	Total	O	0	0
			8	8		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	S	5	Total 5	O 5	0	0
19	T	14	Total 14	O 14	0	0
19	U	35	Total 35	O 35	0	0
19	V	24	Total 24	O 24	0	0
19	W	18	Total 18	O 18	0	0
19	X	23	Total 23	O 23	0	0
19	Y	22	Total 22	O 22	0	0
19	Z	29	Total 29	O 29	0	0
19	a	35	Total 35	O 35	0	0
19	b	34	Total 34	O 34	0	0
19	c	1	Total 1	O 1	0	0
19	d	3	Total 3	O 3	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.

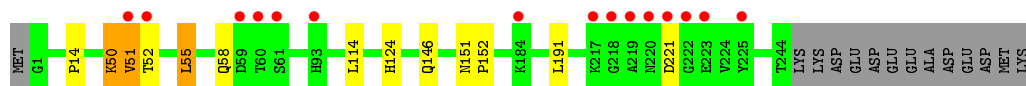
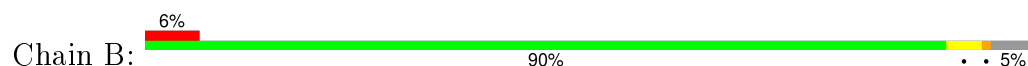
- Molecule 1: Proteasome subunit alpha type-2



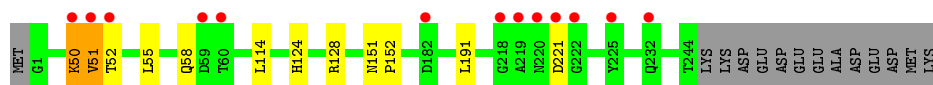
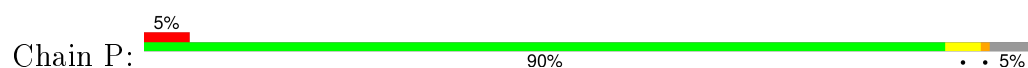
- Molecule 1: Proteasome subunit alpha type-2



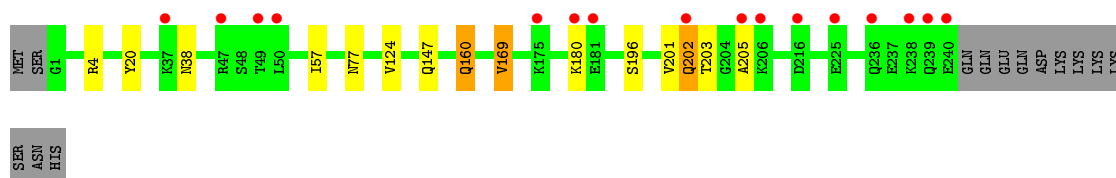
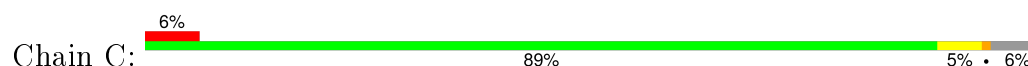
- Molecule 2: Proteasome subunit alpha type-3



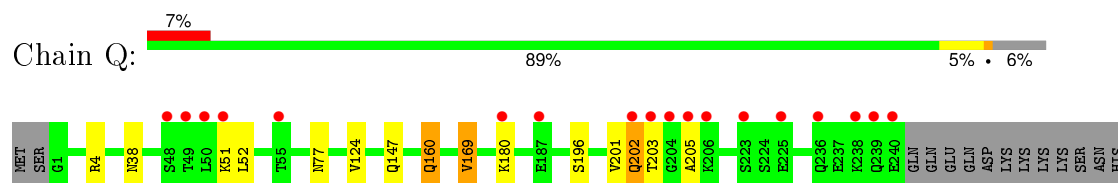
- Molecule 2: Proteasome subunit alpha type-3



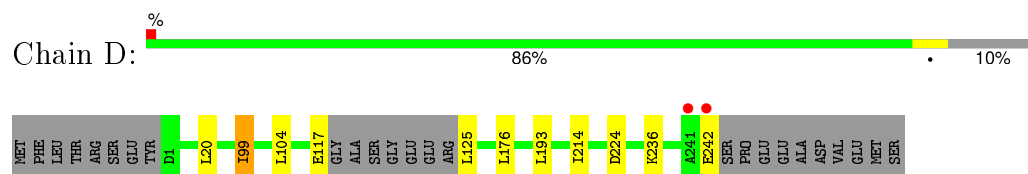
- Molecule 3: Proteasome subunit alpha type-4



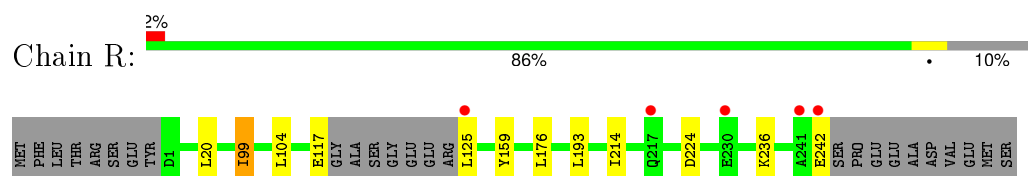
- Molecule 3: Proteasome subunit alpha type-4



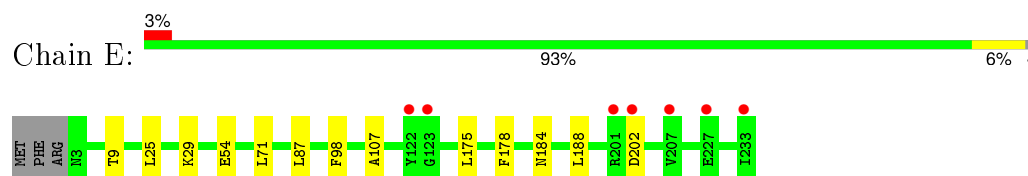
- Molecule 4: Proteasome subunit alpha type-5



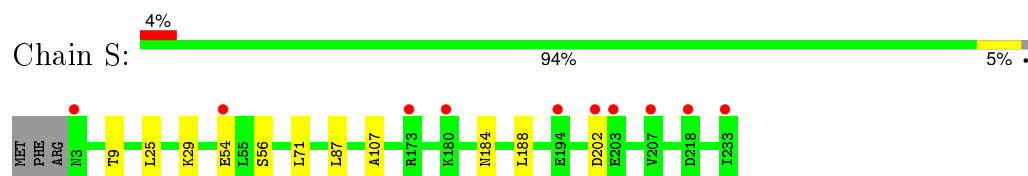
- Molecule 4: Proteasome subunit alpha type-5



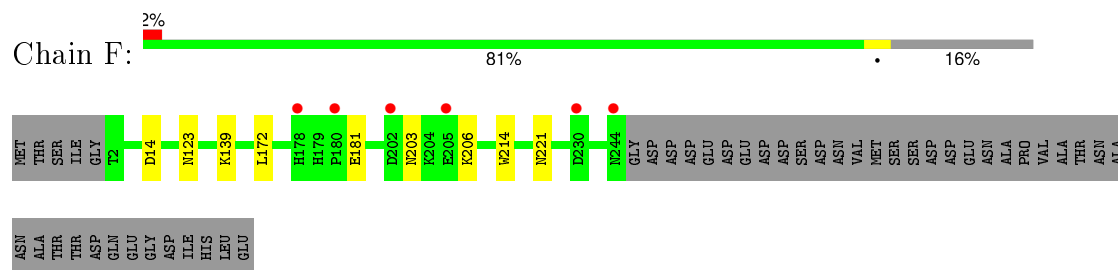
- Molecule 5: Proteasome subunit alpha type-6



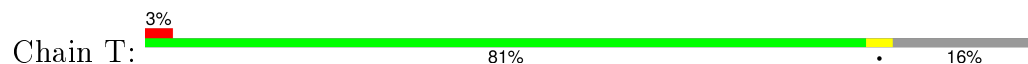
- Molecule 5: Proteasome subunit alpha type-6

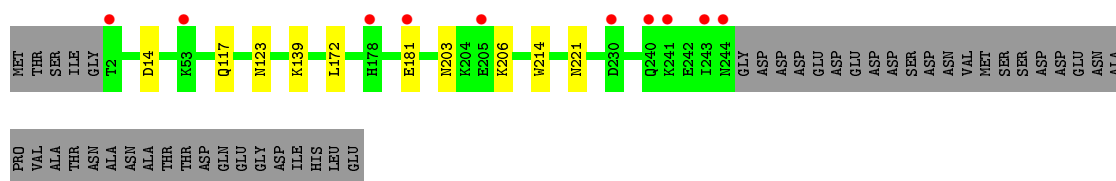


- Molecule 6: Probable proteasome subunit alpha type-7

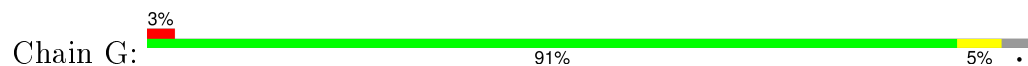


- Molecule 6: Probable proteasome subunit alpha type-7

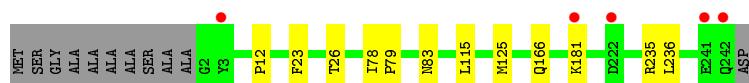
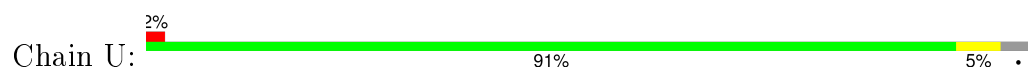




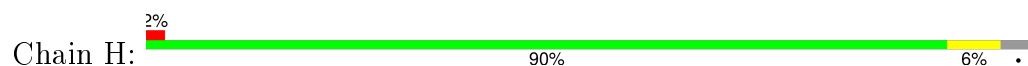
- Molecule 7: Proteasome subunit alpha type-1



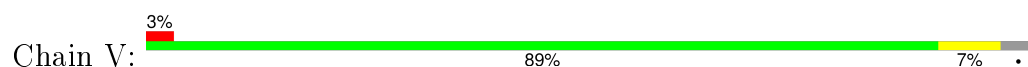
- Molecule 7: Proteasome subunit alpha type-1



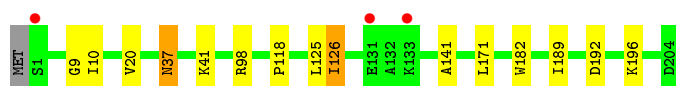
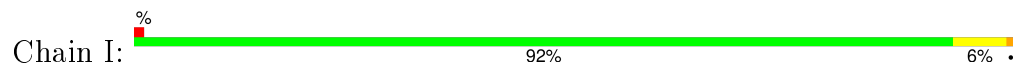
- Molecule 8: Proteasome subunit beta type-2



- Molecule 8: Proteasome subunit beta type-2



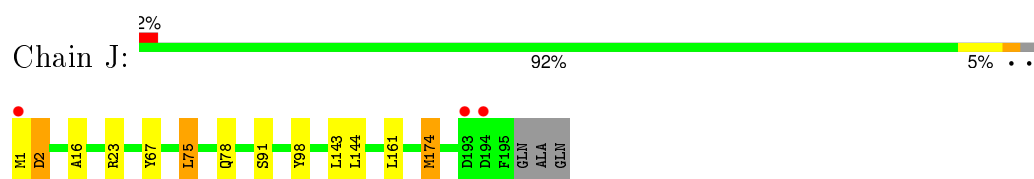
- Molecule 9: Proteasome subunit beta type-3



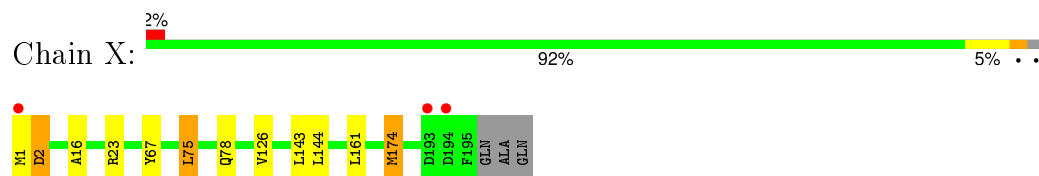
- Molecule 9: Proteasome subunit beta type-3



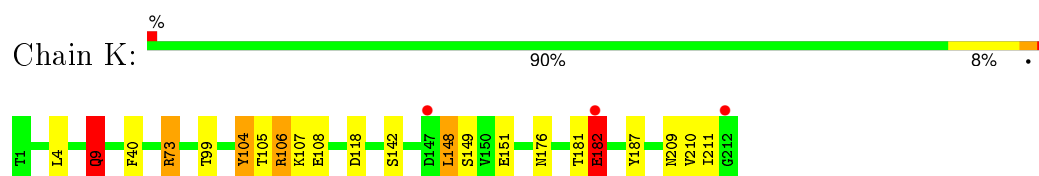
- Molecule 10: Proteasome subunit beta type-4



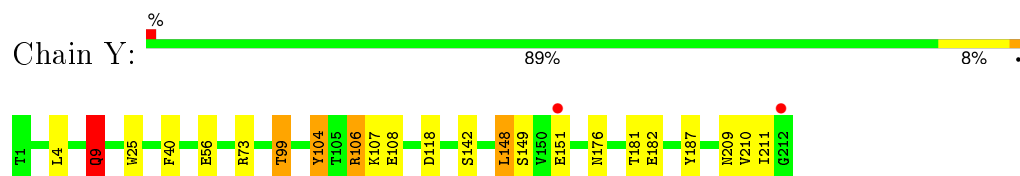
- Molecule 10: Proteasome subunit beta type-4



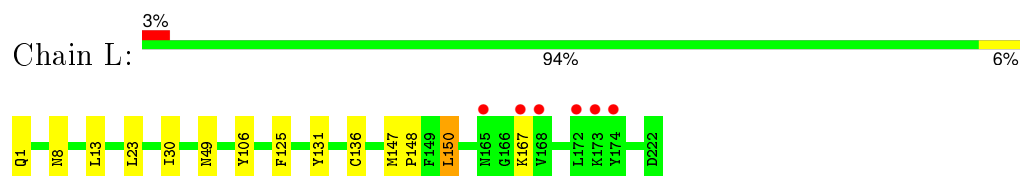
- Molecule 11: Proteasome subunit beta type-5



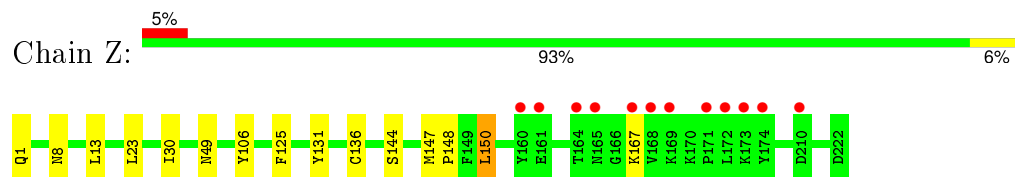
- Molecule 11: Proteasome subunit beta type-5



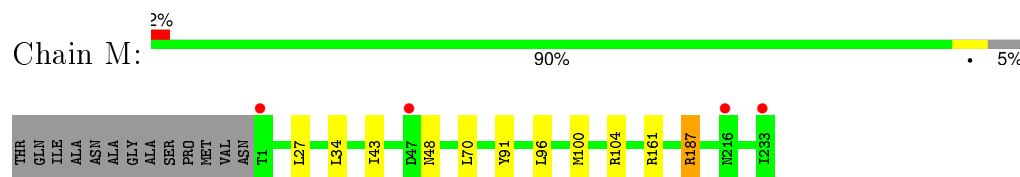
- Molecule 12: Proteasome subunit beta type-6



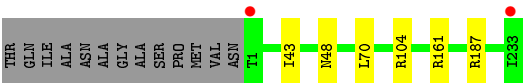
- Molecule 12: Proteasome subunit beta type-6



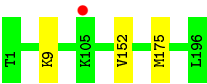
- Molecule 13: Proteasome subunit beta type-7



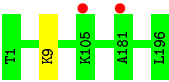
- Molecule 13: Proteasome subunit beta type-7



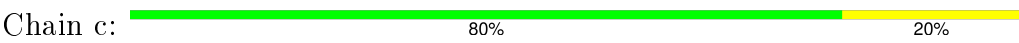
• Molecule 14: Proteasome subunit beta type-1



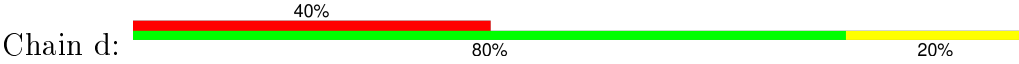
• Molecule 14: Proteasome subunit beta type-1



• Molecule 15: Ac-PPA-ep



• Molecule 15: Ac-PPA-ep



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	137.07Å 300.98Å 146.03Å 90.00° 113.29° 90.00°	Depositor
Resolution (Å)	15.00 – 2.60 15.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.2 (15.00-2.60) 98.2 (15.00-2.60)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.71 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.202 , 0.225 0.205 , 0.227	Depositor DCC
$R_{free}$ test set	16214 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.1	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 33.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 324291 reflections (0.000%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	49992	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, ACE, CL, POL, MES, 2A1

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	0.27	0/1952	0.47	0/2642
1	O	0.27	0/1952	0.47	0/2642
2	B	0.27	0/1934	0.49	0/2618
2	P	0.27	0/1934	0.49	0/2618
3	C	0.28	0/1910	0.50	0/2586
3	Q	0.28	0/1910	0.50	0/2586
4	D	0.27	0/1837	0.47	0/2475
4	R	0.27	0/1837	0.47	0/2475
5	E	0.27	0/1800	0.47	0/2433
5	S	0.27	0/1800	0.47	0/2433
6	F	0.28	0/1932	0.45	0/2609
6	T	0.27	0/1932	0.45	0/2609
7	G	0.28	0/1945	0.47	0/2634
7	U	0.28	0/1945	0.47	0/2634
8	H	0.30	0/1715	0.48	0/2326
8	V	0.31	0/1715	0.49	0/2326
9	I	0.27	0/1611	0.48	0/2174
9	W	0.28	0/1611	0.48	0/2174
10	J	0.27	0/1589	0.49	0/2142
10	X	0.27	0/1589	0.49	0/2142
11	K	0.29	0/1681	0.59	2/2274 (0.1%)
11	Y	0.34	0/1681	0.58	1/2274 (0.0%)
12	L	0.28	0/1795	0.47	0/2420
12	Z	0.28	0/1795	0.47	0/2420
13	M	0.28	0/1855	0.51	0/2514
13	a	0.28	0/1855	0.51	0/2514
14	N	0.27	0/1541	0.46	0/2087
14	b	0.27	0/1541	0.46	0/2087
15	c	1.90	1/13 (7.7%)	1.35	0/18
15	d	1.88	1/13 (7.7%)	1.37	0/18
All	All	0.28	2/50220 (0.0%)	0.49	3/67904 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	c	2	PRO	CA-C	-6.64	1.39	1.52
15	d	2	PRO	CA-C	-6.58	1.39	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Y	210	VAL	CG1-CB-CG2	-9.28	96.06	110.90
11	K	210	VAL	CG1-CB-CG2	-8.11	97.92	110.90
11	K	182	GLU	CA-CB-CG	7.24	129.32	113.40

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	2	0
1	O	1915	0	1929	2	0
2	B	1904	0	1904	8	0
2	P	1904	0	1904	5	0
3	C	1881	0	1895	9	0
3	Q	1881	0	1895	7	0
4	D	1813	0	1797	1	0
4	R	1813	0	1797	2	0
5	E	1773	0	1775	3	0
5	S	1773	0	1775	2	0
6	F	1892	0	1883	0	0
6	T	1892	0	1883	0	0
7	G	1907	0	1901	3	0
7	U	1907	0	1901	3	0
8	H	1684	0	1688	7	0
8	V	1684	0	1688	7	0
9	I	1581	0	1574	11	0
9	W	1581	0	1574	10	0
10	J	1561	0	1569	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	X	1561	0	1569	6	0
11	K	1644	0	1592	10	0
11	Y	1644	0	1592	14	0
12	L	1757	0	1711	4	0
12	Z	1757	0	1711	5	0
13	M	1824	0	1832	4	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	1	0
14	b	1512	0	1481	0	0
15	c	24	0	26	0	0
15	d	24	0	26	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	Y	1	0	0	0	0
16	Z	1	0	0	0	0
17	G	1	0	0	0	0
17	U	1	0	0	0	0
18	K	12	0	13	0	0
18	d	12	0	13	0	0
19	A	30	0	0	0	0
19	B	19	0	0	0	0
19	C	20	0	0	0	0
19	D	11	0	0	0	0
19	E	10	0	0	0	0
19	F	18	0	0	0	0
19	G	29	0	0	0	0
19	H	29	0	0	0	0
19	I	23	0	0	0	0
19	J	25	0	0	0	0
19	K	23	0	0	1	0
19	L	27	0	0	0	0
19	M	26	0	0	0	0
19	N	22	0	0	0	0
19	O	19	0	0	0	0
19	P	18	0	0	0	0
19	Q	15	0	0	0	0
19	R	8	0	0	0	0
19	S	5	0	0	0	0
19	T	14	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	U	35	0	0	0	0
19	V	24	0	0	0	0
19	W	18	0	0	0	0
19	X	23	0	0	0	0
19	Y	22	0	0	0	0
19	Z	29	0	0	0	0
19	a	35	0	0	0	0
19	b	34	0	0	0	0
19	c	1	0	0	0	0
19	d	3	0	0	0	0
All	All	49992	0	49140	113	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 1.

All (113) 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:106:ARG:NH1	11:Y:182:GLU:OE2	1.68	1.26
11:Y:40:PHE:CD1	11:Y:73:ARG:NH1	2.26	1.03
11:Y:40:PHE:CG	11:Y:73:ARG:NH1	2.47	0.82
11:Y:73:ARG:NH2	11:Y:104:TYR:O	2.20	0.74
10:J:1:MET:O	10:J:2:ASP:HB2	1.88	0.73
10:X:1:MET:O	10:X:2:ASP:HB2	1.88	0.72
8:H:3:ILE:HG22	8:H:16:ALA:HB2	1.83	0.60
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.87	0.57
9:I:98:ARG:CD	9:I:126:ILE:HD12	2.34	0.57
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.87	0.57
9:W:125:LEU:HG	9:W:126:ILE:HG22	1.87	0.57
9:W:98:ARG:CD	9:W:126:ILE:HD12	2.35	0.56
8:V:84:LYS:HA	8:V:113:ILE:HD11	1.87	0.56
14:N:152:VAL:HA	14:N:175:MET:HE1	1.88	0.55
9:I:125:LEU:HG	9:I:126:ILE:HG22	1.87	0.55
11:Y:106:ARG:CZ	11:Y:182:GLU:OE2	2.52	0.55
11:K:40:PHE:CD1	11:K:73:ARG:NH1	2.75	0.54
9:I:98:ARG:HD2	9:I:126:ILE:HD12	1.90	0.54
11:Y:176:ASN:ND2	11:Y:187:TYR:OH	2.40	0.53
9:W:98:ARG:HD2	9:W:126:ILE:HD12	1.90	0.53
11:K:176:ASN:ND2	11:K:187:TYR:OH	2.41	0.53
11:K:209:ASN:O	9:W:37:ASN:ND2	2.43	0.51
8:V:3:ILE:HG21	8:V:44:ALA:HB3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:23:PHE:O	7:U:26:THR:HB	2.12	0.50
7:G:23:PHE:O	7:G:26:THR:HB	2.12	0.50
3:C:160:GLN:HA	3:C:160:GLN:HE21	1.77	0.50
8:V:22:GLN:HG3	8:V:27:ALA:HB2	1.93	0.50
11:Y:104:TYR:HB3	11:Y:182:GLU:HA	1.94	0.50
4:R:99:ILE:HD11	4:R:104:LEU:HB2	1.94	0.50
3:C:201:VAL:O	3:C:202:GLN:CB	2.61	0.49
8:H:218:VAL:CG2	9:I:196:LYS:HB2	2.42	0.49
3:Q:160:GLN:HA	3:Q:160:GLN:HE21	1.76	0.49
11:Y:56:GLU:OE2	11:Y:99:THR:OG1	2.22	0.48
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.60	0.48
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.49	0.48
4:D:99:ILE:HD11	4:D:104:LEU:HB2	1.95	0.48
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.49	0.48
3:C:201:VAL:HG13	3:C:202:GLN:N	2.29	0.47
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.29	0.47
10:J:91:SER:HG	10:J:98:TYR:H	1.63	0.47
11:K:73:ARG:NH1	19:K:408:HOH:O	2.48	0.47
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.97	0.47
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.97	0.47
11:K:104:TYR:HB3	11:K:182:GLU:HA	1.97	0.46
11:K:73:ARG:HH21	11:K:105:THR:HA	1.80	0.46
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.98	0.46
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.98	0.46
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.97	0.46
11:Y:107:LYS:HG3	11:Y:108:GLU:HG3	1.98	0.46
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.98	0.45
8:H:22:GLN:HG3	8:H:27:ALA:HB2	1.97	0.45
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.97	0.45
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.99	0.45
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.97	0.45
11:K:107:LYS:HG3	11:K:108:GLU:HG3	1.98	0.45
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.98	0.45
3:Q:201:VAL:O	3:Q:202:GLN:HB2	2.17	0.45
8:H:99:ILE:HG13	8:H:127:LEU:HD22	1.99	0.45
10:J:174:MET:HA	10:X:174:MET:HA	1.99	0.45
8:V:3:ILE:HG22	8:V:4:VAL:N	2.32	0.44
13:M:96:LEU:O	13:M:100:MET:HG2	2.17	0.44
8:H:3:ILE:HG21	8:H:44:ALA:HB1	2.00	0.44
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.98	0.44
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:1:MET:O	10:X:2:ASP:CB	2.60	0.44
1:A:55:LEU:HD12	7:G:170:THR:HG23	2.00	0.44
10:X:16:ALA:HB2	10:X:161:LEU:HD21	2.00	0.44
10:J:16:ALA:HB2	10:J:161:LEU:HD21	2.00	0.44
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.33	0.43
11:Y:9:GLN:NE2	11:Y:148:LEU:O	2.51	0.43
3:C:201:VAL:O	3:C:202:GLN:HB2	2.17	0.43
11:K:104:TYR:CD1	11:K:182:GLU:HB2	2.53	0.43
11:K:9:GLN:NE2	11:K:148:LEU:O	2.52	0.43
13:M:187:ARG:NH1	8:V:139:GLU:OE1	2.48	0.43
9:I:126:ILE:HG13	9:I:126:ILE:O	2.18	0.43
10:J:1:MET:O	10:J:2:ASP:CB	2.60	0.43
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.49	0.43
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.53	0.43
11:Y:25:TRP:CH2	12:Z:144:SER:HA	2.54	0.42
12:L:147:MET:N	12:L:148:PRO:HD2	2.34	0.42
8:H:218:VAL:HG21	9:I:196:LYS:HB2	2.01	0.42
2:B:14:PRO:HA	3:C:20:TYR:CD1	2.55	0.42
11:Y:40:PHE:CE1	11:Y:73:ARG:NH1	2.81	0.42
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.49	0.42
11:K:106:ARG:HA	11:K:106:ARG:HD2	1.78	0.42
2:P:151:ASN:HB2	2:P:152:PRO:HD2	2.02	0.42
2:B:151:ASN:HB2	2:B:152:PRO:HD2	2.02	0.42
2:B:146:GLN:HG2	3:C:57:ILE:HG21	2.01	0.42
9:I:37:ASN:ND2	11:Y:209:ASN:O	2.53	0.42
7:G:78:ILE:N	7:G:79:PRO:CD	2.83	0.41
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	2.02	0.41
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.55	0.41
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.41
5:E:98:PHE:O	13:M:91:TYR:HA	2.20	0.41
13:M:27:LEU:HD21	13:M:34:LEU:HD22	2.02	0.41
2:B:124:HIS:HB3	3:C:124:VAL:HG12	2.02	0.41
2:P:50:LYS:O	2:P:51:VAL:C	2.58	0.41
12:L:8:ASN:HA	12:L:30:ILE:O	2.20	0.41
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.56	0.41
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.86	0.41
9:W:20:VAL:HG23	9:W:189:ILE:HB	2.02	0.41
1:A:176:GLU:HG2	2:B:55:LEU:HD13	2.03	0.41
12:L:125:PHE:CD2	12:L:131:TYR:HB3	2.56	0.41
11:Y:106:ARG:HD3	11:Y:182:GLU:OE2	2.21	0.40
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:W:126:ILE:O	9:W:126:ILE:HG13	2.20	0.40
9:I:20:VAL:HG23	9:I:189:ILE:HB	2.02	0.40
2:B:14:PRO:HA	3:C:20:TYR:CE1	2.55	0.40
2:B:50:LYS:O	2:B:51:VAL:C	2.59	0.40
8:V:98:LEU:HB2	8:V:113:ILE:HG22	2.04	0.40
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.57	0.40
9:W:36:SER:HB2	10:X:126:VAL:HG11	2.02	0.40
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.21	0.40

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%)	242 (98%)	6 (2%)	0	100	100
1	O	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
2	B	242/258 (94%)	233 (96%)	7 (3%)	2 (1%)	24	46
2	P	242/258 (94%)	233 (96%)	7 (3%)	2 (1%)	24	46
3	C	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	24	46
3	Q	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	24	46
4	D	231/260 (89%)	227 (98%)	4 (2%)	0	100	100
4	R	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
5	E	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
5	S	229/234 (98%)	223 (97%)	6 (3%)	0	100	100
6	F	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
6	T	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
7	G	239/252 (95%)	235 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	U	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
8	H	220/232 (95%)	214 (97%)	6 (3%)	0	100	100
8	V	220/232 (95%)	214 (97%)	6 (3%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	34	60
10	X	193/198 (98%)	190 (98%)	2 (1%)	1 (0%)	34	60
11	K	210/212 (99%)	205 (98%)	4 (2%)	1 (0%)	34	60
11	Y	210/212 (99%)	205 (98%)	4 (2%)	1 (0%)	34	60
12	L	220/222 (99%)	217 (99%)	3 (1%)	0	100	100
12	Z	220/222 (99%)	217 (99%)	3 (1%)	0	100	100
13	M	231/246 (94%)	225 (97%)	6 (3%)	0	100	100
13	a	231/246 (94%)	225 (97%)	6 (3%)	0	100	100
14	N	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
14	b	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
15	c	1/5 (20%)	1 (100%)	0	0	100	100
15	d	1/5 (20%)	1 (100%)	0	0	100	100
All	All	6278/6624 (95%)	6117 (97%)	149 (2%)	12 (0%)	52	77

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
10	J	2	ASP
2	P	51	VAL
3	Q	202	GLN
10	X	2	ASP
3	C	205	ALA
3	Q	205	ALA
11	Y	9	GLN
2	B	221	ASP
11	K	9	GLN
2	P	221	ASP



### 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%)	206 (99%)	3 (1%)	74	90
1	O	209/209 (100%)	206 (99%)	3 (1%)	74	90
2	B	203/216 (94%)	197 (97%)	6 (3%)	48	76
2	P	203/216 (94%)	197 (97%)	6 (3%)	48	76
3	C	212/226 (94%)	204 (96%)	8 (4%)	40	68
3	Q	212/226 (94%)	204 (96%)	8 (4%)	40	68
4	D	194/215 (90%)	184 (95%)	10 (5%)	29	54
4	R	194/215 (90%)	184 (95%)	10 (5%)	29	54
5	E	190/193 (98%)	182 (96%)	8 (4%)	36	65
5	S	190/193 (98%)	182 (96%)	8 (4%)	36	65
6	F	201/239 (84%)	192 (96%)	9 (4%)	34	62
6	T	201/239 (84%)	191 (95%)	10 (5%)	30	56
7	G	206/210 (98%)	199 (97%)	7 (3%)	44	72
7	U	206/210 (98%)	199 (97%)	7 (3%)	44	72
8	H	181/190 (95%)	176 (97%)	5 (3%)	51	78
8	V	181/190 (95%)	176 (97%)	5 (3%)	51	78
9	I	172/173 (99%)	167 (97%)	5 (3%)	50	77
9	W	172/173 (99%)	167 (97%)	5 (3%)	50	77
10	J	173/175 (99%)	167 (96%)	6 (4%)	43	71
10	X	173/175 (99%)	167 (96%)	6 (4%)	43	71
11	K	169/169 (100%)	155 (92%)	14 (8%)	14	27
11	Y	169/169 (100%)	157 (93%)	12 (7%)	18	36
12	L	185/185 (100%)	178 (96%)	7 (4%)	40	68
12	Z	185/185 (100%)	178 (96%)	7 (4%)	40	68
13	M	199/208 (96%)	193 (97%)	6 (3%)	48	76
13	a	199/208 (96%)	193 (97%)	6 (3%)	48	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	162/162 (100%)	161 (99%)	1 (1%)	90	97
14	b	162/162 (100%)	161 (99%)	1 (1%)	90	97
15	c	1/1 (100%)	1 (100%)	0	100	100
15	d	1/1 (100%)	1 (100%)	0	100	100
All	All	5314/5542 (96%)	5125 (96%)	189 (4%)	42	71

All (189) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	61	LEU
1	A	157	PHE
2	B	50	LYS
2	B	52	THR
2	B	55	LEU
2	B	58	GLN
2	B	114	LEU
2	B	191	LEU
3	C	4	ARG
3	C	38	ASN
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	203	THR
4	D	20	LEU
4	D	99	ILE
4	D	117	GLU
4	D	125	LEU
4	D	176	LEU
4	D	193	LEU
4	D	214	ILE
4	D	224	ASP
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	25	LEU
5	E	29	LYS
5	E	54	GLU
5	E	71	LEU

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Mol	Chain	Res	Type
5	E	184	ASN
5	E	188	LEU
5	E	202	ASP
6	F	14	ASP
6	F	123	ASN
6	F	139	LYS
6	F	172	LEU
6	F	181	GLU
6	F	203	ASN
6	F	206	LYS
6	F	214	TRP
6	F	221	ASN
7	G	83	ASN
7	G	115	LEU
7	G	125	MET
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
7	G	236	LEU
8	H	30	ASN
8	H	56	THR
8	H	68	LEU
8	H	127	LEU
8	H	196	ARG
9	I	37	ASN
9	I	126	ILE
9	I	171	LEU
9	I	182	TRP
9	I	192	ASP
10	J	23	ARG
10	J	75	LEU
10	J	78	GLN
10	J	143	LEU
10	J	144	LEU
10	J	174	MET
11	K	4	LEU
11	K	9	GLN
11	K	73	ARG
11	K	99	THR
11	K	104	TYR
11	K	106	ARG
11	K	118	ASP

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Mol	Chain	Res	Type
11	K	142	SER
11	K	148	LEU
11	K	149	SER
11	K	151	GLU
11	K	181	THR
11	K	182	GLU
11	K	211	ILE
12	L	1	GLN
12	L	23	LEU
12	L	49	ASN
12	L	106	TYR
12	L	136	CYS
12	L	150	LEU
12	L	167	LYS
13	M	43	ILE
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	161	ARG
13	M	187	ARG
14	N	9	LYS
1	O	17	LYS
1	O	61	LEU
1	O	157	PHE
2	P	50	LYS
2	P	52	THR
2	P	55	LEU
2	P	58	GLN
2	P	114	LEU
2	P	191	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	203	THR
4	R	20	LEU
4	R	99	ILE
4	R	117	GLU
4	R	125	LEU

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Mol	Chain	Res	Type
4	R	176	LEU
4	R	193	LEU
4	R	214	ILE
4	R	224	ASP
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	25	LEU
5	S	29	LYS
5	S	54	GLU
5	S	71	LEU
5	S	184	ASN
5	S	188	LEU
5	S	202	ASP
6	T	14	ASP
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	172	LEU
6	T	181	GLU
6	T	203	ASN
6	T	206	LYS
6	T	214	TRP
6	T	221	ASN
7	U	83	ASN
7	U	115	LEU
7	U	125	MET
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
7	U	236	LEU
8	V	30	ASN
8	V	56	THR
8	V	68	LEU
8	V	127	LEU
8	V	196	ARG
9	W	37	ASN
9	W	126	ILE
9	W	171	LEU
9	W	182	TRP
9	W	192	ASP
10	X	23	ARG

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Mol	Chain	Res	Type
10	X	75	LEU
10	X	78	GLN
10	X	143	LEU
10	X	144	LEU
10	X	174	MET
11	Y	4	LEU
11	Y	9	GLN
11	Y	99	THR
11	Y	104	TYR
11	Y	106	ARG
11	Y	118	ASP
11	Y	142	SER
11	Y	148	LEU
11	Y	149	SER
11	Y	151	GLU
11	Y	181	THR
11	Y	211	ILE
12	Z	1	GLN
12	Z	23	LEU
12	Z	49	ASN
12	Z	106	TYR
12	Z	136	CYS
12	Z	150	LEU
12	Z	167	LYS
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
14	b	9	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (83) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	20	GLN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN
3	C	38	ASN

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Mol	Chain	Res	Type
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
4	D	91	HIS
4	D	100	ASN
4	D	146	GLN
4	D	225	ASN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	120	GLN
5	E	184	ASN
6	F	86	ASN
6	F	117	GLN
6	F	191	GLN
6	F	240	GLN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
8	H	57	GLN
10	J	55	GLN
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
12	L	3	ASN
12	L	70	ASN
12	L	158	ASN
12	L	159	GLN
13	M	48	ASN
13	M	102	GLN
13	M	194	ASN
13	M	213	GLN
1	O	94	HIS
2	P	119	GLN
2	P	123	GLN
2	P	176	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN

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Mol	Chain	Res	Type
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	146	GLN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	116	GLN
5	S	120	GLN
5	S	184	ASN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	191	GLN
6	T	240	GLN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
8	V	22	GLN
8	V	57	GLN
10	X	55	GLN
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
12	Z	3	ASN
12	Z	70	ASN
12	Z	79	HIS
12	Z	158	ASN
13	a	48	ASN
13	a	102	GLN
13	a	194	ASN
13	a	213	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.



## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 9 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
18	MES	K	302	-	12,12,12	2.10	1 (8%)	15,16,16	1.60	3 (20%)
18	MES	d	101	-	12,12,12	2.08	1 (8%)	15,16,16	1.72	3 (20%)

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	K	302	-	-	0/6/14/14	0/1/1/1
18	MES	d	101	-	-	0/6/14/14	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	K	302	MES	C8-S	-6.96	1.67	1.77
18	d	101	MES	C8-S	-6.90	1.67	1.77

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	d	101	MES	O3S-S-C8	2.24	109.65	104.99
18	K	302	MES	O3S-S-C8	2.38	109.94	104.99
18	K	302	MES	O1S-S-C8	3.22	109.15	106.87
18	d	101	MES	O1S-S-C8	3.50	109.34	106.87
18	K	302	MES	O2S-S-C8	3.73	109.51	106.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	d	101	MES	O2S-S-C8	4.29	109.90	106.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [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, 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%)	-0.32	6 (2%) 62 56	34, 46, 78, 121	0
1	O	250/250 (100%)	-0.25	11 (4%) 38 30	37, 53, 95, 126	0
2	B	244/258 (94%)	-0.10	15 (6%) 25 18	33, 51, 100, 158	0
2	P	244/258 (94%)	-0.06	13 (5%) 30 23	37, 56, 104, 161	0
3	C	240/254 (94%)	-0.07	16 (6%) 21 15	34, 54, 120, 157	0
3	Q	240/254 (94%)	0.13	18 (7%) 17 12	41, 67, 148, 186	0
4	D	235/260 (90%)	-0.36	2 (0%) 85 83	38, 56, 88, 133	0
4	R	235/260 (90%)	-0.24	5 (2%) 67 61	41, 60, 98, 148	0
5	E	231/234 (98%)	-0.18	7 (3%) 54 47	40, 58, 93, 138	0
5	S	231/234 (98%)	-0.10	10 (4%) 39 31	40, 64, 101, 140	0
6	F	243/288 (84%)	-0.34	6 (2%) 61 54	33, 51, 103, 132	0
6	T	243/288 (84%)	-0.18	10 (4%) 41 33	31, 59, 111, 148	0
7	G	241/252 (95%)	-0.33	7 (2%) 55 48	31, 48, 87, 142	0
7	U	241/252 (95%)	-0.37	5 (2%) 67 61	35, 48, 79, 123	0
8	H	222/232 (95%)	-0.15	5 (2%) 64 57	35, 46, 87, 125	0
8	V	222/232 (95%)	-0.11	6 (2%) 58 51	35, 49, 87, 133	0
9	I	204/205 (99%)	-0.53	3 (1%) 76 71	30, 45, 75, 93	0
9	W	204/205 (99%)	-0.51	4 (1%) 68 63	32, 46, 77, 97	0
10	J	195/198 (98%)	-0.43	3 (1%) 76 71	30, 47, 73, 114	0
10	X	195/198 (98%)	-0.44	3 (1%) 76 71	33, 48, 74, 124	0
11	K	212/212 (100%)	-0.26	3 (1%) 78 74	33, 50, 85, 104	0
11	Y	212/212 (100%)	-0.28	2 (0%) 85 83	34, 49, 86, 105	0
12	L	222/222 (100%)	-0.32	6 (2%) 58 51	31, 49, 86, 121	0
12	Z	222/222 (100%)	-0.22	12 (5%) 29 22	32, 48, 91, 129	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
13	M	233/246 (94%)	-0.51	4 (1%) 73 68	28, 46, 71, 93	0
13	a	233/246 (94%)	-0.52	2 (0%) 85 83	30, 45, 68, 89	0
14	N	196/196 (100%)	-0.56	1 (0%) 91 90	31, 41, 69, 94	0
14	b	196/196 (100%)	-0.54	2 (1%) 84 81	32, 42, 68, 90	0
15	c	2/5 (40%)	1.59	0 100 100	79, 79, 79, 87	0
15	d	2/5 (40%)	2.97	2 (100%) 0 0	81, 81, 81, 91	0
All	All	6340/6624 (95%)	-0.28	189 (2%) 54 47	28, 51, 95, 186	0

All (189) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	219	ALA	10.1
2	P	222	GLY	8.8
3	C	206	LYS	7.6
1	O	1	MET	7.4
2	B	220	ASN	7.4
3	Q	49	THR	7.3
1	A	1	MET	7.1
3	Q	50	LEU	6.6
2	B	219	ALA	6.6
2	B	221	ASP	6.6
8	H	221	CYS	6.5
8	V	221	CYS	6.3
2	B	51	VAL	6.3
10	X	1	MET	5.9
8	V	222	ASP	5.9
12	L	172	LEU	5.6
2	B	218	GLY	5.4
2	P	221	ASP	5.4
2	P	51	VAL	5.1
3	Q	206	LYS	5.1
5	S	202	ASP	5.0
12	Z	172	LEU	4.9
10	X	194	ASP	4.9
2	P	218	GLY	4.8
3	C	49	THR	4.7
5	E	202	ASP	4.7
3	C	236	GLN	4.7
3	Q	239	GLN	4.7
8	H	222	ASP	4.7

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Mol	Chain	Res	Type	RSRZ
12	Z	174	TYR	4.7
2	P	220	ASN	4.6
10	J	1	MET	4.6
3	Q	236	GLN	4.5
9	W	1	SER	4.5
3	Q	51	LYS	4.5
3	C	238	LYS	4.4
3	Q	48	SER	4.3
2	P	59	ASP	4.1
4	D	242	GLU	4.0
3	C	205	ALA	3.9
6	T	244	ASN	3.9
9	I	1	SER	3.8
6	F	202	ASP	3.8
6	T	178	HIS	3.8
12	L	174	TYR	3.7
3	C	202	GLN	3.7
3	Q	238	LYS	3.7
10	J	194	ASP	3.7
12	Z	167	LYS	3.7
15	d	2	PRO	3.7
3	Q	225	GLU	3.6
10	X	193	ASP	3.6
9	I	133	LYS	3.5
5	E	123	GLY	3.5
2	P	52	THR	3.5
3	C	239	GLN	3.5
3	Q	203	THR	3.5
4	R	242	GLU	3.4
6	F	244	ASN	3.4
7	U	222	ASP	3.4
12	Z	160	TYR	3.3
8	H	215	GLU	3.3
1	O	201	GLU	3.3
12	Z	161	GLU	3.2
8	H	198	GLU	3.2
4	D	241	ALA	3.2
3	Q	240	GLU	3.2
7	G	2	GLY	3.2
12	Z	165	ASN	3.2
2	B	222	GLY	3.1
1	O	249	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
7	G	242	GLN	3.1
6	F	205	GLU	3.1
6	T	243	ILE	3.1
5	S	54	GLU	3.1
3	C	50	LEU	3.1
7	G	181	LYS	3.1
3	Q	202	GLN	3.0
1	A	249	ALA	3.0
6	T	241	LYS	2.9
9	W	133	LYS	2.9
7	U	242	GLN	2.8
13	a	1	THR	2.8
5	E	233	ILE	2.8
3	Q	205	ALA	2.8
3	Q	204	GLY	2.8
9	W	191	LYS	2.8
14	N	105	LYS	2.8
3	C	240	GLU	2.7
8	V	215	GLU	2.7
11	K	182	GLU	2.7
12	L	173	LYS	2.7
12	Z	210	ASP	2.7
5	E	201	ARG	2.7
1	O	52	SER	2.7
11	K	147	ASP	2.7
5	S	180	LYS	2.7
1	O	231	LYS	2.7
3	Q	223	SER	2.7
6	F	178	HIS	2.6
1	O	2	THR	2.6
10	J	193	ASP	2.6
1	A	248	GLU	2.6
1	A	2	THR	2.6
1	A	250	LEU	2.6
12	L	167	LYS	2.5
1	O	250	LEU	2.5
3	C	37	LYS	2.5
3	C	181	GLU	2.5
2	B	217	LYS	2.5
1	O	229	THR	2.5
5	S	173	ARG	2.5
2	B	225	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
6	T	205	GLU	2.5
6	T	2	THR	2.5
7	G	3	TYR	2.5
4	R	125	LEU	2.4
2	B	60	THR	2.4
2	B	61	SER	2.4
3	Q	187	GLU	2.4
14	b	105	LYS	2.4
2	P	225	TYR	2.4
13	M	47	ASP	2.4
5	E	122	TYR	2.4
3	Q	180	LYS	2.4
2	B	52	THR	2.4
2	P	60	THR	2.4
9	W	192	ASP	2.4
13	M	1	THR	2.4
12	Z	171	PRO	2.3
4	R	241	ALA	2.3
7	G	179	LYS	2.3
12	L	165	ASN	2.3
1	A	201	GLU	2.3
5	S	194	GLU	2.3
7	G	240	ALA	2.3
8	V	145	ASP	2.3
11	K	212	GLY	2.3
3	C	225	GLU	2.3
8	V	207	ARG	2.3
12	Z	169	LYS	2.3
15	d	3	ALA	2.3
3	C	175	LYS	2.2
7	U	3	TYR	2.2
4	R	217	GLN	2.2
6	T	181	GLU	2.2
12	Z	168	VAL	2.2
1	O	53	SER	2.2
3	C	180	LYS	2.2
8	H	219	ASN	2.2
2	P	182	ASP	2.2
9	I	131	GLU	2.2
6	T	53	LYS	2.2
6	T	230	ASP	2.2
12	Z	164	THR	2.2

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Mol	Chain	Res	Type	RSRZ
13	M	233	ILE	2.2
5	S	3	ASN	2.2
8	V	212	VAL	2.2
7	U	241	GLU	2.2
5	S	233	ILE	2.2
13	M	216	ASN	2.1
4	R	230	GLU	2.1
6	F	180	PRO	2.1
5	S	218	ASP	2.1
3	C	47	ARG	2.1
2	B	184	LYS	2.1
1	O	248	GLU	2.1
11	Y	151	GLU	2.1
13	a	233	ILE	2.1
6	F	230	ASP	2.1
2	B	59	ASP	2.1
5	S	207	VAL	2.1
12	Z	173	LYS	2.1
2	B	93	HIS	2.1
3	C	216	ASP	2.1
7	U	181	LYS	2.1
1	O	178	ARG	2.1
2	B	223	GLU	2.1
5	E	227	GLU	2.1
11	Y	212	GLY	2.1
5	E	207	VAL	2.0
5	S	203	GLU	2.0
7	G	241	GLU	2.0
14	b	181	ALA	2.0
3	Q	55	THR	2.0
12	L	168	VAL	2.0
2	P	232	GLN	2.0
6	T	240	GLN	2.0
2	P	50	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.



### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. 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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
18	MES	K	302	12/12	0.87	0.39	6.03	81,85,88,92	0
18	MES	d	101	12/12	0.84	0.36	3.64	74,83,85,90	0
16	MG	I	301	1/1	0.91	0.22	3.01	49,49,49,49	0
16	MG	Z	301	1/1	0.94	0.14	-0.25	52,52,52,52	0
16	MG	N	201	1/1	0.96	0.10	-0.36	42,42,42,42	0
16	MG	G	301	1/1	0.96	0.06	-1.38	44,44,44,44	0
16	MG	V	301	1/1	0.94	0.10	-1.63	55,55,55,55	0
16	MG	Y	301	1/1	0.96	0.07	-2.93	52,52,52,52	0
16	MG	K	301	1/1	0.96	0.06	-4.12	52,52,52,52	0
17	CL	U	301	1/1	0.98	0.20	-	30,30,30,30	0
17	CL	G	302	1/1	0.99	0.11	-	30,30,30,30	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.