wwPDB X-ray Structure Validation Summary Report (i)

Apr 22, 2025 – 01:50 pm BST

PDB ID	:	9FRW / pdb_00009frw
Title	:	Yeast 20S proteasome with human beta1i (1-51)
Authors	:	Maurits, E.; Huber, E.M.; Decker, P.M.; Wang, X.; Heinemeyer, W.; Florea, B.I.; Groll, M.; Overkleedt, H.S.
Deposited on	:	2024-06-19
Resolution	:	2.85 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

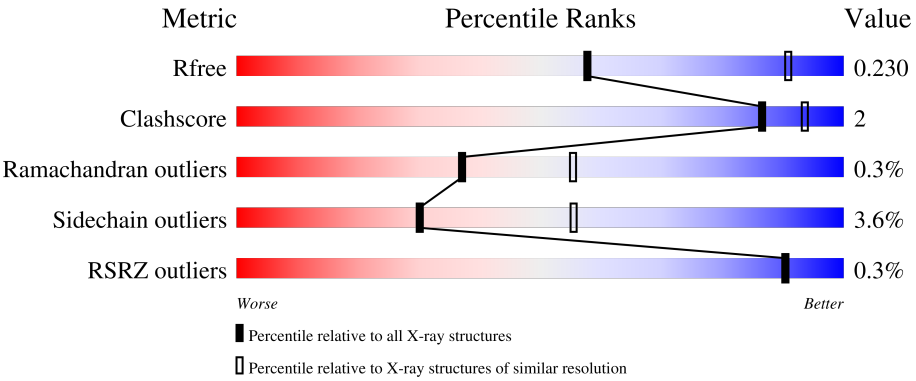
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	164625	1268 (2.88-2.84)
Clashscore	180529	1351 (2.88-2.84)
Ramachandran outliers	177936	1318 (2.88-2.84)
Sidechain outliers	177891	1319 (2.88-2.84)
RSRZ outliers	164620	1269 (2.88-2.84)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	97% ·
1	O	250	95% 5%
2	B	258	% 88% 7% 5%
2	P	258	% 88% 6% 5%
3	C	254	% 87% 6% · 6%

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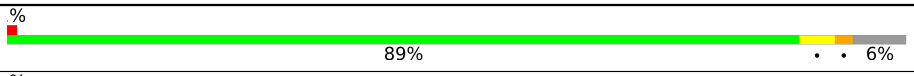
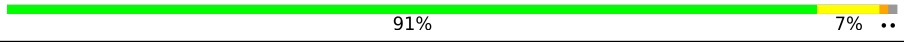
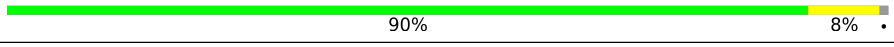
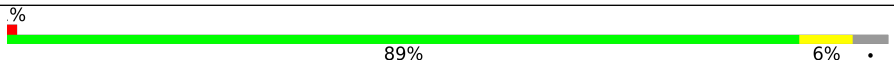
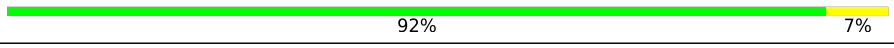
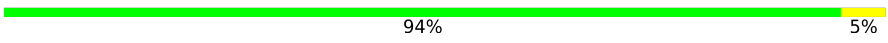
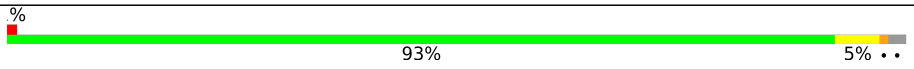
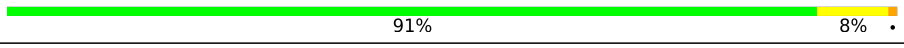
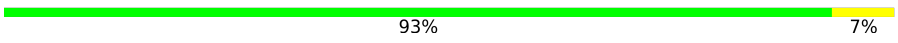
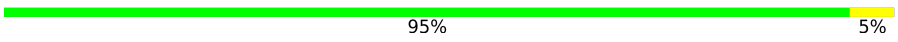
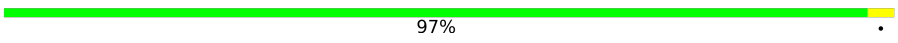
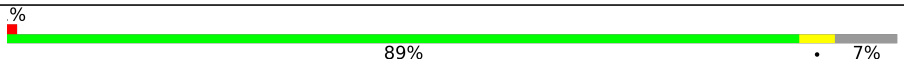
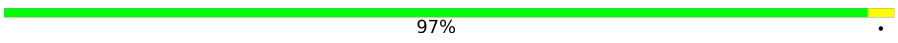
Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	

2 Entry composition (i)

There are 19 unique types of molecules in this entry. The entry contains 49457 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	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			
8	V	226	Total	C	N	O	S	0	1	0
			1727	1086	300	334	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	225	Total	C	N	O	S	0	0	0
			1761	1114	301	339	7			
13	a	228	Total	C	N	O	S	0	0	0
			1786	1131	305	343	7			

- Molecule 14 is a protein called Proteasome subunit beta type-9,Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1502	950	244	301	7			
14	b	196	Total	C	N	O	S	0	0	0
			1502	950	244	301	7			

- Molecule 15 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	G	1	Total	Cl	0	0
			1	1		

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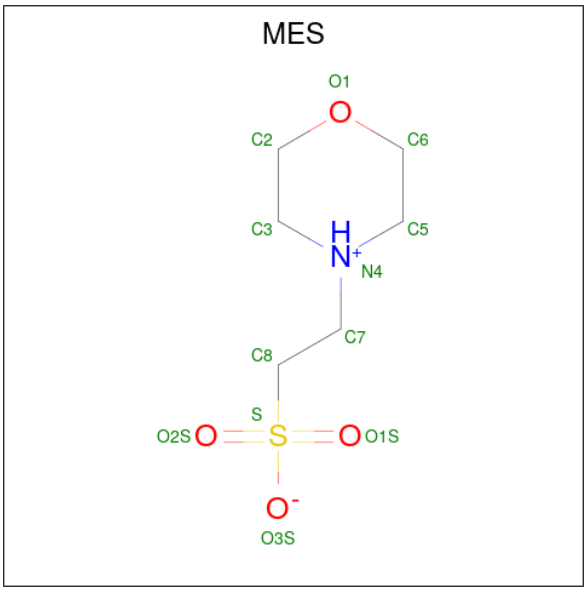
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	H	1	Total Cl 1 1	0	0
15	I	1	Total Cl 1 1	0	0
15	L	1	Total Cl 1 1	0	0
15	U	2	Total Cl 2 2	0	0
15	V	1	Total Cl 1 1	0	0

- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

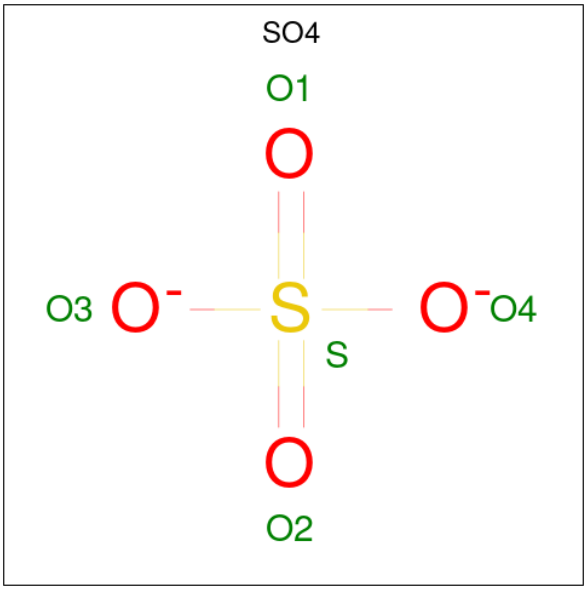
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Mg 1 1	0	0
16	I	1	Total Mg 1 1	0	0
16	K	1	Total Mg 1 1	0	0
16	N	1	Total Mg 1 1	0	0
16	U	1	Total Mg 1 1	0	0
16	V	1	Total Mg 1 1	0	0
16	W	1	Total Mg 1 1	0	0
16	Y	1	Total Mg 1 1	0	0
16	Z	1	Total Mg 1 1	0	0

- Molecule 17 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	M	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
17	a	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 18 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
18	N	1	Total	O	S		0	0
			5	4	1			
18	b	1	Total	O	S		0	0
			5	4	1			

- Molecule 19 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	A	4	Total O 4 4	0	0
19	B	8	Total O 8 8	0	0
19	C	6	Total O 6 6	0	0
19	D	6	Total O 6 6	0	0
19	E	6	Total O 6 6	0	0
19	F	1	Total O 1 1	0	0
19	G	6	Total O 6 6	0	0
19	H	5	Total O 5 5	0	0
19	I	3	Total O 3 3	0	0
19	J	8	Total O 8 8	0	0
19	K	13	Total O 13 13	0	0
19	L	7	Total O 7 7	0	0
19	M	9	Total O 9 9	0	0
19	N	2	Total O 2 2	0	0
19	O	3	Total O 3 3	0	0
19	P	4	Total O 4 4	0	0
19	Q	2	Total O 2 2	0	0
19	R	7	Total O 7 7	0	0
19	S	3	Total O 3 3	0	0
19	T	1	Total O 1 1	0	0
19	U	5	Total O 5 5	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	V	4	Total O 4 4	0	0
19	W	7	Total O 7 7	0	0
19	X	3	Total O 3 3	0	0
19	Y	9	Total O 9 9	0	0
19	Z	4	Total O 4 4	0	0
19	a	11	Total O 11 11	0	0
19	b	7	Total O 7 7	0	0

3 Residue-property plots (i)

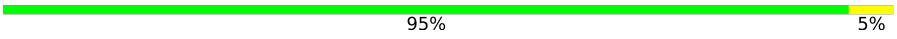
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

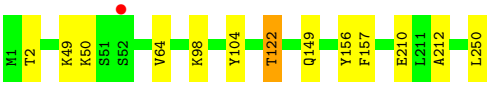
• Molecule 1: Proteasome subunit alpha type-2

Chain A:

• Molecule 1: Proteasome subunit alpha type-2

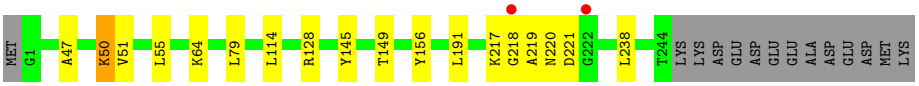
Chain O:





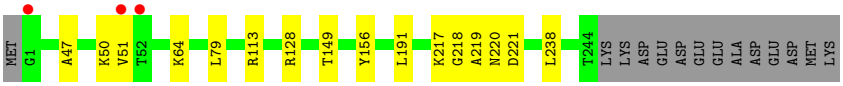
• Molecule 2: Proteasome subunit alpha type-3

Chain B:



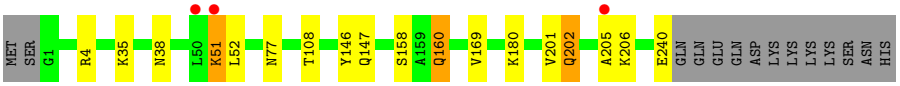
• Molecule 2: Proteasome subunit alpha type-3

Chain P:



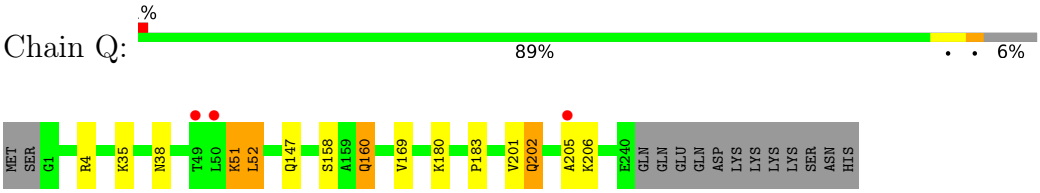
• Molecule 3: Proteasome subunit alpha type-4

Chain C:



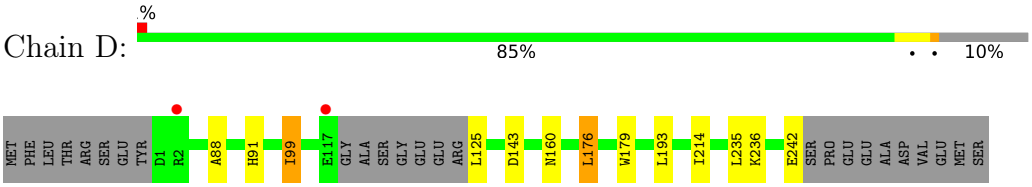
• Molecule 3: Proteasome subunit alpha type-4

Chain Q:



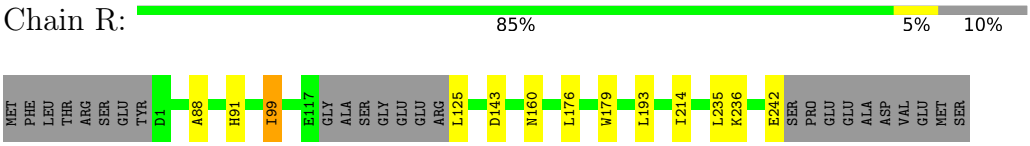
• Molecule 4: Proteasome subunit alpha type-5

Chain D:



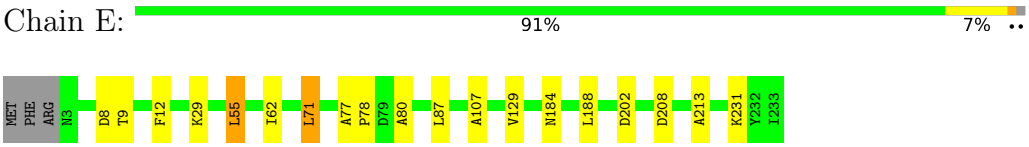
• Molecule 4: Proteasome subunit alpha type-5

Chain R:



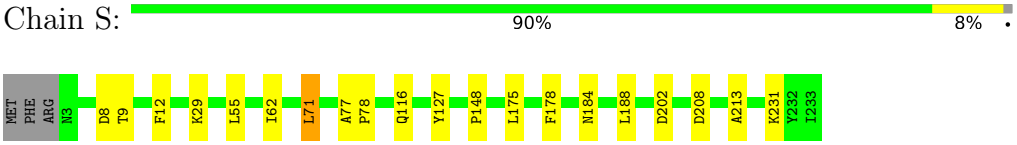
• Molecule 5: Proteasome subunit alpha type-6

Chain E:



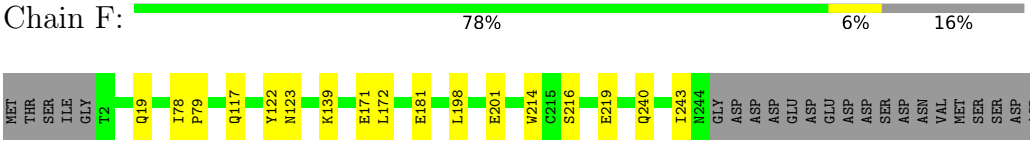
• Molecule 5: Proteasome subunit alpha type-6

Chain S:



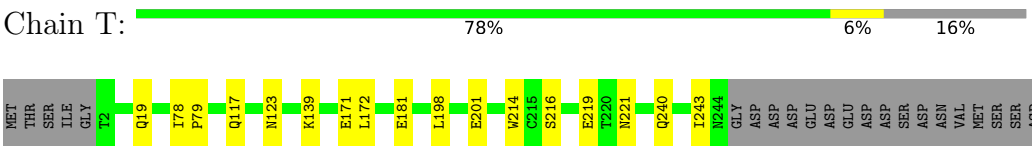
• Molecule 6: Probable proteasome subunit alpha type-7

Chain F:



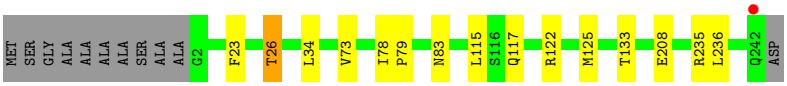
• Molecule 6: Probable proteasome subunit alpha type-7

Chain T:



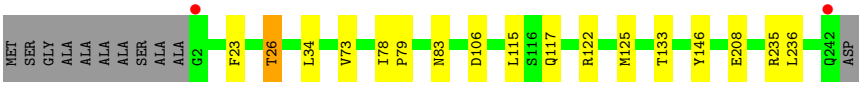
• Molecule 7: Proteasome subunit alpha type-1

Chain G:



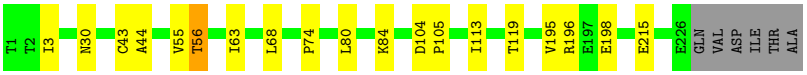
• Molecule 7: Proteasome subunit alpha type-1

Chain U:



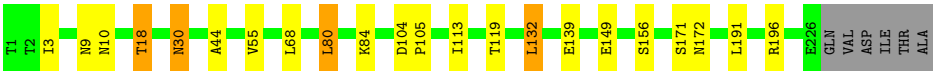
• Molecule 8: Proteasome subunit beta type-2

Chain H:



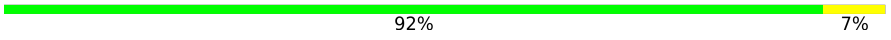
• Molecule 8: Proteasome subunit beta type-2

Chain V:



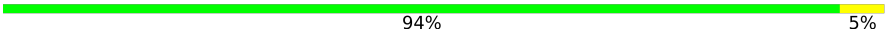
• Molecule 9: Proteasome subunit beta type-3

Chain I:



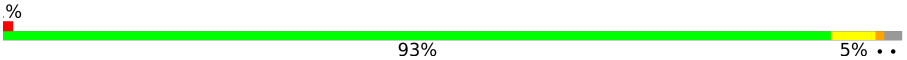
• Molecule 9: Proteasome subunit beta type-3

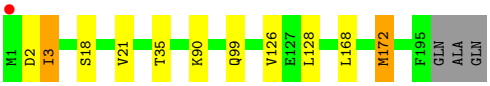
Chain W:



• Molecule 10: Proteasome subunit beta type-4

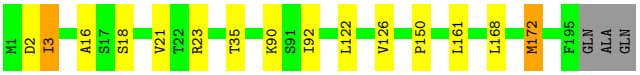
Chain J:





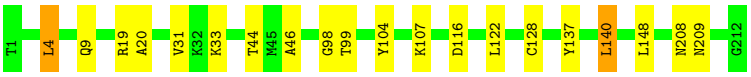
• Molecule 10: Proteasome subunit beta type-4

Chain X:



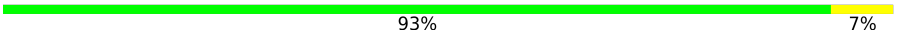
• Molecule 11: Proteasome subunit beta type-5

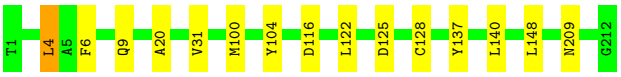
Chain K:



• Molecule 11: Proteasome subunit beta type-5

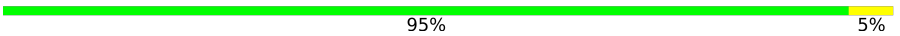
Chain Y:

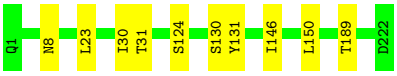




• Molecule 12: Proteasome subunit beta type-6

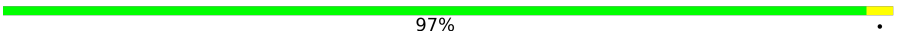
Chain L:

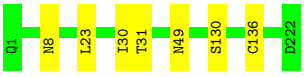




• Molecule 12: Proteasome subunit beta type-6

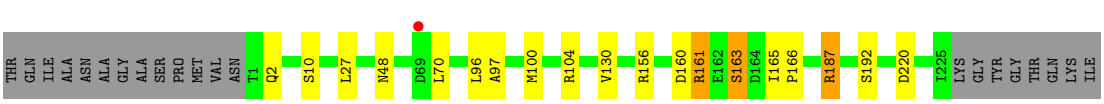
Chain Z:





• Molecule 13: Proteasome subunit beta type-7

Chain M:



• Molecule 13: Proteasome subunit beta type-7

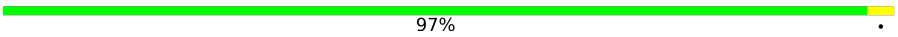
Chain a:

• Molecule 14: Proteasome subunit beta type-9,Proteasome subunit beta type-1

Chain N:

• Molecule 14: Proteasome subunit beta type-9,Proteasome subunit beta type-1

Chain b:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	135.43Å 301.91Å 145.53Å 90.00° 112.83° 90.00°	Depositor
Resolution (Å)	30.00 – 2.85 30.00 – 2.85	Depositor EDS
% Data completeness (in resolution range)	93.9 (30.00-2.85) 93.9 (30.00-2.85)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.28 (at 2.85Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.183 , 0.227 0.188 , 0.230	Depositor DCC
R_{free} test set	11725 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	56.4	Xtriage
Anisotropy	0.544	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 51.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	49457	wwPDB-VP
Average B, all atoms (Å^2)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SO4, MES, CL, MG

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	0.70	0/2642
1	O	0.67	0/1952	0.70	0/2642
2	B	0.66	0/1934	0.72	0/2618
2	P	0.67	0/1934	0.72	0/2618
3	C	0.67	0/1910	0.72	0/2586
3	Q	0.67	0/1910	0.72	0/2586
4	D	0.67	0/1837	0.71	0/2475
4	R	0.67	0/1837	0.71	0/2475
5	E	0.67	0/1800	0.72	0/2433
5	S	0.67	0/1800	0.72	0/2433
6	F	0.66	0/1932	0.71	0/2609
6	T	0.66	0/1932	0.71	0/2609
7	G	0.65	0/1945	0.70	0/2634
7	U	0.65	0/1945	0.70	0/2634
8	H	0.67	0/1750	0.72	0/2373
8	V	0.67	0/1758	0.72	0/2384
9	I	0.66	0/1611	0.71	0/2174
9	W	0.66	0/1611	0.71	0/2174
10	J	0.65	0/1589	0.71	0/2142
10	X	0.65	0/1589	0.71	0/2142
11	K	0.66	0/1681	0.72	0/2274
11	Y	0.66	0/1681	0.73	0/2274
12	L	0.65	0/1795	0.71	0/2420
12	Z	0.65	0/1795	0.71	0/2420
13	M	0.66	0/1791	0.74	0/2431
13	a	0.66	0/1817	0.74	0/2465
14	N	0.66	0/1531	0.71	0/2073
14	b	0.66	0/1531	0.72	0/2073
All	All	0.66	0/50150	0.72	0/67813

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 (i)

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	3	0
1	O	1915	0	1929	5	0
2	B	1904	0	1904	8	0
2	P	1904	0	1904	4	0
3	C	1881	0	1895	6	0
3	Q	1881	0	1895	5	0
4	D	1813	0	1797	4	0
4	R	1813	0	1797	3	0
5	E	1773	0	1775	8	0
5	S	1773	0	1775	7	0
6	F	1892	0	1883	5	0
6	T	1892	0	1883	4	0
7	G	1907	0	1901	5	0
7	U	1907	0	1901	7	0
8	H	1719	0	1719	8	0
8	V	1727	0	1724	23	0
9	I	1581	0	1574	8	0
9	W	1581	0	1574	6	0
10	J	1561	0	1569	5	0
10	X	1561	0	1569	8	0
11	K	1644	0	1595	12	0
11	Y	1644	0	1595	9	0
12	L	1757	0	1711	4	0
12	Z	1757	0	1711	1	0
13	M	1761	0	1765	9	0
13	a	1786	0	1790	0	0
14	N	1502	0	1460	13	0
14	b	1502	0	1460	0	0
15	G	1	0	0	0	0
15	H	1	0	0	0	0
15	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	L	1	0	0	0	0
15	U	2	0	0	0	0
15	V	1	0	0	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	U	1	0	0	0	0
16	V	1	0	0	0	0
16	W	1	0	0	0	0
16	Y	1	0	0	0	0
16	Z	1	0	0	0	0
17	M	12	0	13	0	0
17	a	12	0	13	0	0
18	N	5	0	0	0	0
18	b	5	0	0	0	0
19	A	4	0	0	0	0
19	B	8	0	0	0	0
19	C	6	0	0	0	0
19	D	6	0	0	0	0
19	E	6	0	0	0	0
19	F	1	0	0	0	0
19	G	6	0	0	0	0
19	H	5	0	0	0	0
19	I	3	0	0	0	0
19	J	8	0	0	0	0
19	K	13	0	0	0	0
19	L	7	0	0	0	0
19	M	9	0	0	0	0
19	N	2	0	0	0	0
19	O	3	0	0	0	0
19	P	4	0	0	0	0
19	Q	2	0	0	0	0
19	R	7	0	0	0	0
19	S	3	0	0	0	0
19	T	1	0	0	0	0
19	U	5	0	0	0	0
19	V	4	0	0	0	0
19	W	7	0	0	0	0
19	X	3	0	0	0	0
19	Y	9	0	0	0	0
19	Z	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	a	11	0	0	0	0
19	b	7	0	0	0	0
All	All	49457	0	49010	164	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 164 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)
13:M:161:ARG:HH11	13:M:161:ARG:HG3	1.37	0.89
8:V:18:THR:OG1	8:V:30:ASN:HA	1.76	0.86
10:X:92:ILE:HG21	10:X:122:LEU:HA	1.67	0.76
8:V:80:LEU:HD21	8:V:119:THR:HG21	1.69	0.75
13:M:161:ARG:HH11	13:M:161:ARG:CG	2.01	0.73

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%)	239 (96%)	8 (3%)	1 (0%)	30 49
1	O	248/250 (99%)	238 (96%)	8 (3%)	2 (1%)	16 32
2	B	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	7 16
2	P	242/258 (94%)	233 (96%)	5 (2%)	4 (2%)	7 16
3	C	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	16 32
3	Q	238/254 (94%)	228 (96%)	7 (3%)	3 (1%)	10 22
4	D	231/260 (89%)	226 (98%)	5 (2%)	0	100 100
4	R	231/260 (89%)	227 (98%)	4 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	229/234 (98%)	221 (96%)	8 (4%)	0	100	100
5	S	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
6	F	241/288 (84%)	236 (98%)	5 (2%)	0	100	100
6	T	241/288 (84%)	236 (98%)	5 (2%)	0	100	100
7	G	239/252 (95%)	232 (97%)	7 (3%)	0	100	100
7	U	239/252 (95%)	234 (98%)	5 (2%)	0	100	100
8	H	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
8	V	225/232 (97%)	219 (97%)	6 (3%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
10	X	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
11	K	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
11	Y	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
12	L	220/222 (99%)	214 (97%)	6 (3%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	223/246 (91%)	216 (97%)	6 (3%)	1 (0%)	30	49
13	a	226/246 (92%)	217 (96%)	9 (4%)	0	100	100
14	N	194/196 (99%)	191 (98%)	3 (2%)	0	100	100
14	b	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
All	All	6272/6614 (95%)	6094 (97%)	161 (3%)	17 (0%)	37	55

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
2	B	221	ASP
3	C	202	GLN
2	P	51	VAL
2	P	221	ASP

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	206 (99%)	3 (1%)	62	82
1	O	209/209 (100%)	206 (99%)	3 (1%)	62	82
2	B	203/216 (94%)	198 (98%)	5 (2%)	42	68
2	P	203/216 (94%)	198 (98%)	5 (2%)	42	68
3	C	212/226 (94%)	202 (95%)	10 (5%)	22	44
3	Q	212/226 (94%)	203 (96%)	9 (4%)	25	48
4	D	194/215 (90%)	185 (95%)	9 (5%)	23	44
4	R	194/215 (90%)	185 (95%)	9 (5%)	23	44
5	E	190/193 (98%)	180 (95%)	10 (5%)	19	38
5	S	190/193 (98%)	179 (94%)	11 (6%)	17	34
6	F	201/239 (84%)	192 (96%)	9 (4%)	23	45
6	T	201/239 (84%)	191 (95%)	10 (5%)	20	40
7	G	206/210 (98%)	197 (96%)	9 (4%)	24	46
7	U	206/210 (98%)	197 (96%)	9 (4%)	24	46
8	H	185/190 (97%)	177 (96%)	8 (4%)	25	47
8	V	186/190 (98%)	179 (96%)	7 (4%)	28	54
9	I	172/173 (99%)	169 (98%)	3 (2%)	56	78
9	W	172/173 (99%)	170 (99%)	2 (1%)	67	84
10	J	173/175 (99%)	167 (96%)	6 (4%)	31	57
10	X	173/175 (99%)	168 (97%)	5 (3%)	37	63
11	K	169/169 (100%)	162 (96%)	7 (4%)	26	50
11	Y	169/169 (100%)	162 (96%)	7 (4%)	26	50
12	L	185/185 (100%)	182 (98%)	3 (2%)	58	79
12	Z	185/185 (100%)	180 (97%)	5 (3%)	40	65
13	M	193/208 (93%)	184 (95%)	9 (5%)	22	44
13	a	195/208 (94%)	186 (95%)	9 (5%)	23	44
14	N	161/161 (100%)	156 (97%)	5 (3%)	35	61
14	b	161/161 (100%)	156 (97%)	5 (3%)	35	61
All	All	5309/5538 (96%)	5117 (96%)	192 (4%)	30	55

5 of 192 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	R	143	ASP
7	U	26	THR
4	R	235	LEU
5	S	202	ASP
7	U	235	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 104 such sidechains are listed below:

Mol	Chain	Res	Type
2	P	95	GLN
5	S	68	HIS
12	Z	49	ASN
2	P	123	GLN
3	Q	120	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 16 are monoatomic - leaving 4 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	$\#\|Z\|>2$
17	MES	M	301	-	12,12,12	0.73	0	14,16,16	0.39	0
18	SO4	b	201	-	4,4,4	0.39	0	6,6,6	0.05	0
18	SO4	N	201	-	4,4,4	0.39	0	6,6,6	0.05	0
17	MES	a	301	-	12,12,12	0.73	0	14,16,16	0.44	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
17	MES	M	301	-	-	0/6/14/14	0/1/1/1
17	MES	a	301	-	-	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.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	a	301	MES	C8-C7-N4-C5
17	a	301	MES	C7-C8-S-O3S
17	a	301	MES	C7-C8-S-O1S
17	a	301	MES	C7-C8-S-O2S

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^{th} 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	250/250 (100%)	-0.43	1 (0%) 89 88	50, 63, 91, 127	0
1	O	250/250 (100%)	-0.38	1 (0%) 89 88	52, 70, 104, 137	0
2	B	244/258 (94%)	-0.39	2 (0%) 82 81	49, 66, 101, 146	0
2	P	244/258 (94%)	-0.27	3 (1%) 76 74	50, 70, 107, 143	0
3	C	240/254 (94%)	-0.31	3 (1%) 74 72	53, 71, 121, 134	0
3	Q	240/254 (94%)	-0.16	3 (1%) 74 72	56, 78, 135, 165	0
4	D	235/260 (90%)	-0.27	2 (0%) 81 79	50, 73, 96, 133	0
4	R	235/260 (90%)	-0.41	0 100 100	53, 71, 97, 119	0
5	E	231/234 (98%)	-0.33	0 100 100	55, 74, 97, 124	0
5	S	231/234 (98%)	-0.32	0 100 100	54, 76, 101, 124	0
6	F	243/288 (84%)	-0.42	0 100 100	48, 70, 103, 137	0
6	T	243/288 (84%)	-0.29	0 100 100	52, 74, 113, 130	0
7	G	241/252 (95%)	-0.43	1 (0%) 89 88	46, 63, 91, 127	0
7	U	241/252 (95%)	-0.36	2 (0%) 82 81	53, 67, 94, 122	0
8	H	226/232 (97%)	-0.43	0 100 100	48, 61, 83, 119	0
8	V	226/232 (97%)	-0.41	0 100 100	38, 66, 87, 139	1 (0%)
9	I	204/205 (99%)	-0.56	0 100 100	42, 58, 81, 98	0
9	W	204/205 (99%)	-0.48	0 100 100	48, 61, 83, 102	0
10	J	195/198 (98%)	-0.49	1 (0%) 87 86	47, 60, 81, 114	0
10	X	195/198 (98%)	-0.46	0 100 100	50, 64, 83, 130	0
11	K	212/212 (100%)	-0.45	0 100 100	49, 62, 78, 92	0
11	Y	212/212 (100%)	-0.57	0 100 100	49, 60, 75, 99	0
12	L	222/222 (100%)	-0.42	0 100 100	49, 63, 91, 125	0
12	Z	222/222 (100%)	-0.46	0 100 100	47, 61, 85, 118	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	M	225/246 (91%)	-0.49	1 (0%) 89 88	49, 63, 85, 113	0
13	a	228/246 (92%)	-0.43	2 (0%) 81 79	47, 60, 87, 125	0
14	N	196/196 (100%)	-0.38	0 100 100	51, 63, 87, 111	0
14	b	196/196 (100%)	-0.39	0 100 100	49, 64, 90, 115	0
All	All	6331/6614 (95%)	-0.40	22 (0%) 90 90	38, 66, 100, 165	1 (0%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	1	GLY	4.5
3	Q	50	LEU	4.2
13	a	1	THR	3.9
7	U	2	GLY	3.8
3	C	50	LEU	3.7

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
17	MES	a	301	12/12	0.88	0.17	112,117,123,125	0
17	MES	M	301	12/12	0.89	0.15	116,122,126,128	0
18	SO4	b	201	5/5	0.93	0.12	98,99,106,107	0
18	SO4	N	201	5/5	0.94	0.19	89,90,95,97	0
16	MG	K	301	1/1	0.94	0.08	96,96,96,96	0
16	MG	Z	301	1/1	0.95	0.09	73,73,73,73	0
16	MG	W	301	1/1	0.96	0.17	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
16	MG	V	302	1/1	0.97	0.13	89,89,89,89	0
15	CL	V	301	1/1	0.97	0.14	79,79,79,79	0
16	MG	Y	301	1/1	0.97	0.06	61,61,61,61	0
15	CL	L	301	1/1	0.97	0.16	71,71,71,71	0
15	CL	H	301	1/1	0.98	0.14	67,67,67,67	0
16	MG	I	302	1/1	0.98	0.08	66,66,66,66	0
15	CL	U	302	1/1	0.98	0.07	58,58,58,58	0
16	MG	U	303	1/1	0.98	0.05	60,60,60,60	0
16	MG	N	202	1/1	0.99	0.08	63,63,63,63	0
15	CL	G	301	1/1	0.99	0.04	57,57,57,57	0
16	MG	G	302	1/1	0.99	0.03	67,67,67,67	0
15	CL	U	301	1/1	0.99	0.04	57,57,57,57	0
15	CL	I	301	1/1	0.99	0.10	61,61,61,61	0

6.5 Other polymers (i)

There are no such residues in this entry.