



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 01:06 PM BST

PDB ID : 4YA5
Title : Yeast 20S proteasome beta2-H114D mutant in complex with Ac-PAE-ep
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-02-17
Resolution : 2.50 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
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) : 2.13

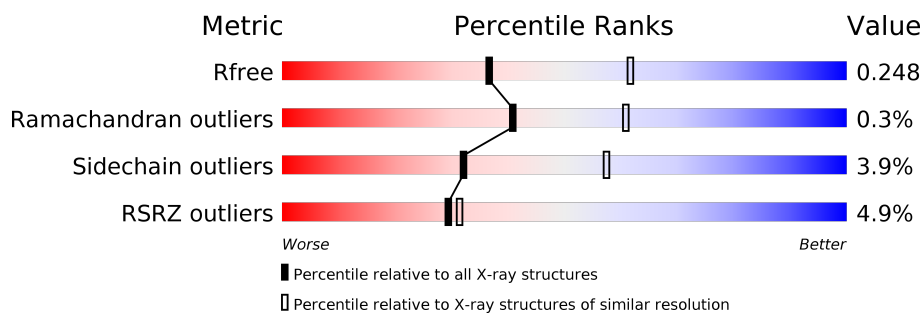
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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>5%</div> <div>98%</div> <div>.</div> </div>
1	O	250	<div> <div>5%</div> <div>98%</div> <div>.</div> </div>
2	B	258	<div> <div>8%</div> <div>90%</div> <div>5%</div> <div>5%</div> </div>
2	P	258	<div> <div>5%</div> <div>90%</div> <div>5%</div> <div>5%</div> </div>
3	C	254	<div> <div>9%</div> <div>89%</div> <div>6%</div> <div>6%</div> </div>
3	Q	254	<div> <div>15%</div> <div>89%</div> <div>6%</div> <div>6%</div> </div>
4	D	260	<div> <div>5%</div> <div>86%</div> <div>5%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
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	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 50389 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
			1717	1080	296	334	7			
8	V	226	Total	C	N	O	S	0	0	0
			1717	1080	296	334	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	114	ASP	HIS	engineered mutation	UNP P25043
V	114	ASP	HIS	engineered mutation	UNP P25043

- 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			
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-PAE-ep.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	c	5	Total	C	N	O	0	0	0
			28	18	3	7			
15	d	5	Total	C	N	O	0	0	0
			28	18	3	7			

- 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	2	Total	Mg	0	0
			2	2		
16	Z	1	Total	Mg	0	0
			1	1		
16	N	1	Total	Mg	0	0
			1	1		
16	L	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		

- Molecule 18 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	A	37	Total	O	0	0
			37	37		
18	B	27	Total	O	0	0
			27	27		
18	C	25	Total	O	0	0
			25	25		
18	D	27	Total	O	0	0
			27	27		
18	E	17	Total	O	0	0
			17	17		
18	F	32	Total	O	0	0
			32	32		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	G	52	Total 52	O 52	0	0
18	H	50	Total 50	O 50	0	0
18	I	39	Total 39	O 39	0	0
18	J	42	Total 42	O 42	0	0
18	K	41	Total 41	O 41	0	0
18	L	40	Total 40	O 40	0	0
18	M	50	Total 50	O 50	0	0
18	N	41	Total 41	O 41	0	0
18	O	26	Total 26	O 26	0	0
18	P	26	Total 26	O 26	0	0
18	Q	13	Total 13	O 13	0	0
18	R	18	Total 18	O 18	0	0
18	S	15	Total 15	O 15	0	0
18	T	28	Total 28	O 28	0	0
18	U	40	Total 40	O 40	0	0
18	V	38	Total 38	O 38	0	0
18	W	42	Total 42	O 42	0	0
18	X	37	Total 37	O 37	0	0
18	Y	36	Total 36	O 36	0	0
18	Z	40	Total 40	O 40	0	0
18	a	41	Total 41	O 41	0	0

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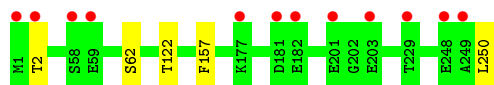
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	b	38	Total 38	O 38	0	0
18	c	3	Total 3	O 3	0	0
18	d	2	Total 2	O 2	0	0

3 Residue-property plots [i](#)

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

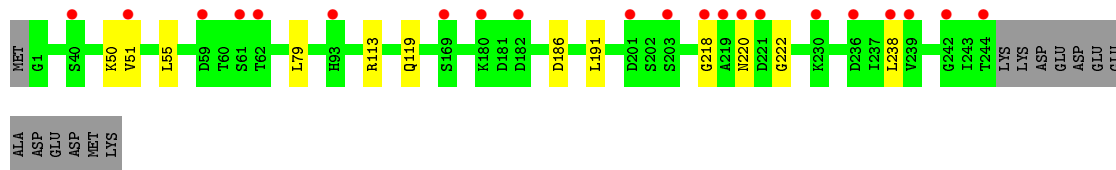
- Molecule 1: Proteasome subunit alpha type-2



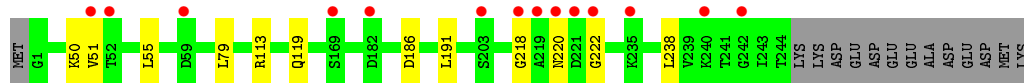
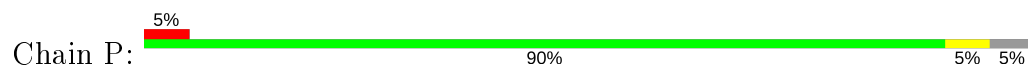
- Molecule 1: Proteasome subunit alpha type-2



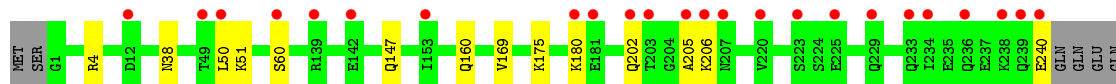
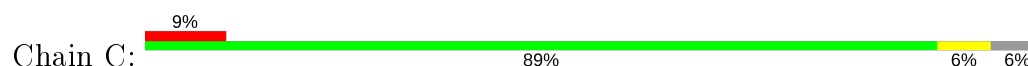
- Molecule 2: Proteasome subunit alpha type-3



- Molecule 2: Proteasome subunit alpha type-3

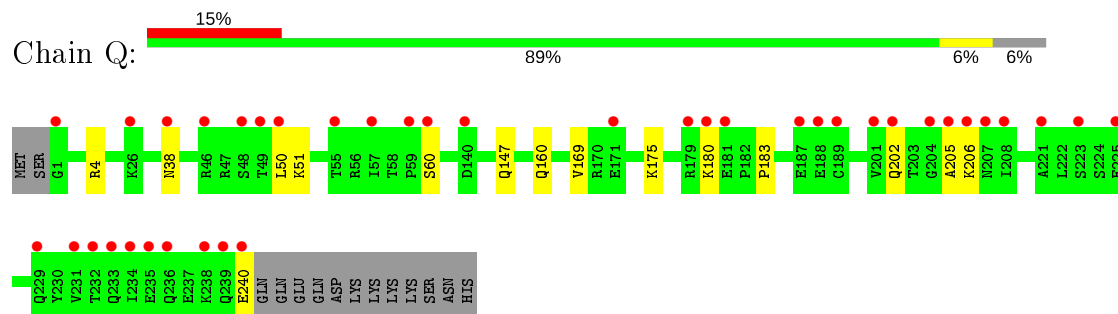


- Molecule 3: Proteasome subunit alpha type-4

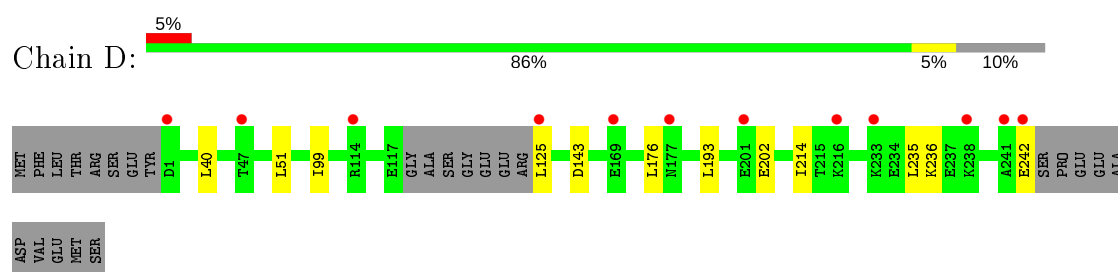


ASP
LYS
LYS
LYS
LYS
SER
ASN
HIS

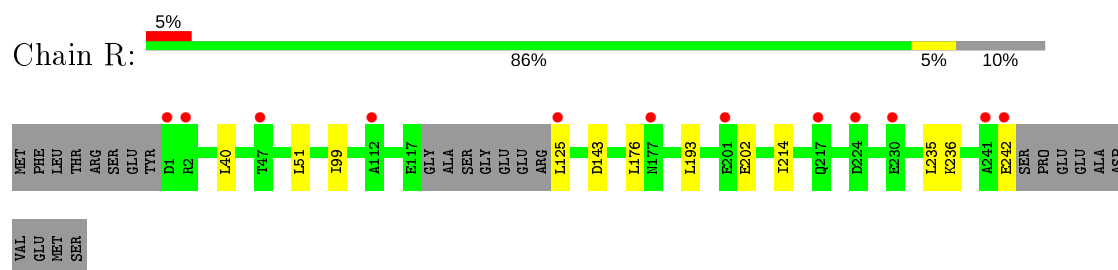
• Molecule 3: Proteasome subunit alpha type-4



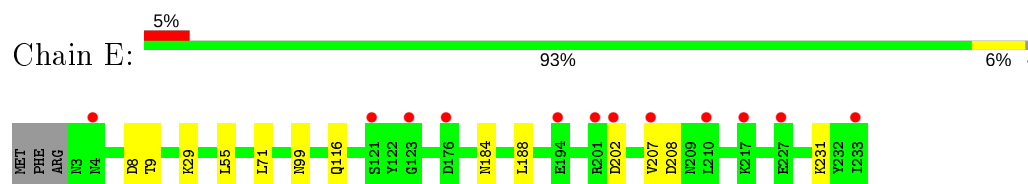
• Molecule 4: Proteasome subunit alpha type-5



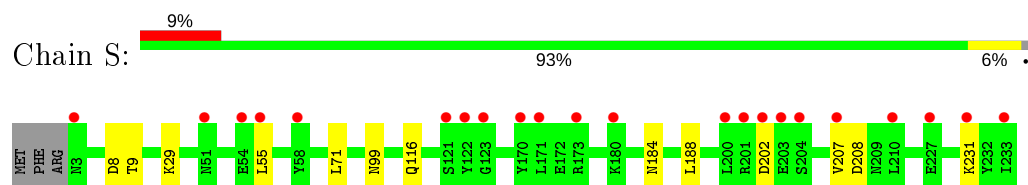
• Molecule 4: Proteasome subunit alpha type-5



• Molecule 5: Proteasome subunit alpha type-6

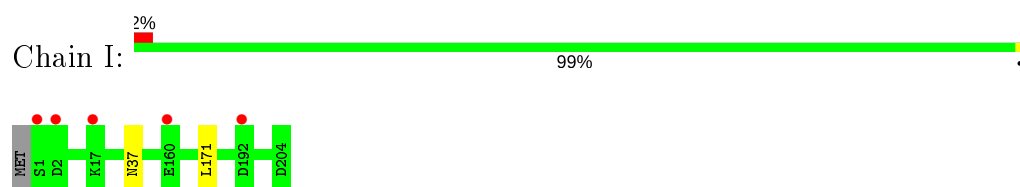


• Molecule 5: Proteasome subunit alpha type-6

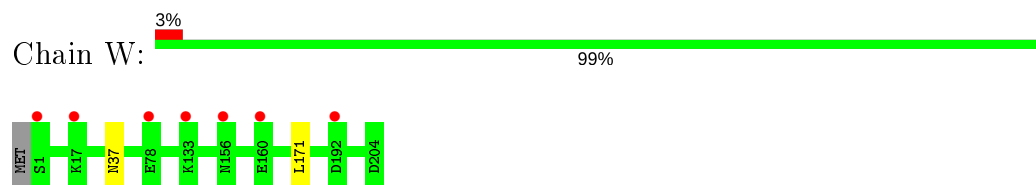


• Molecule 6: Probable proteasome subunit alpha type-7

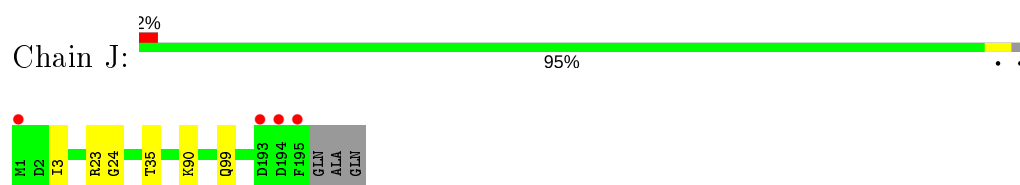




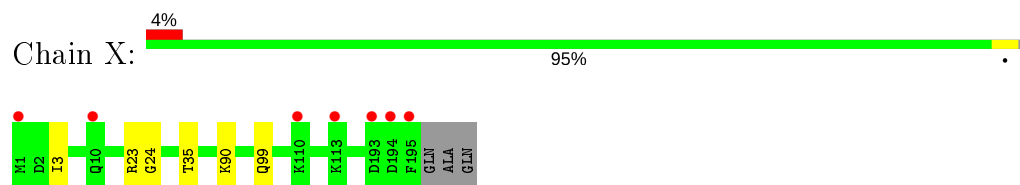
- Molecule 9: Proteasome subunit beta type-3



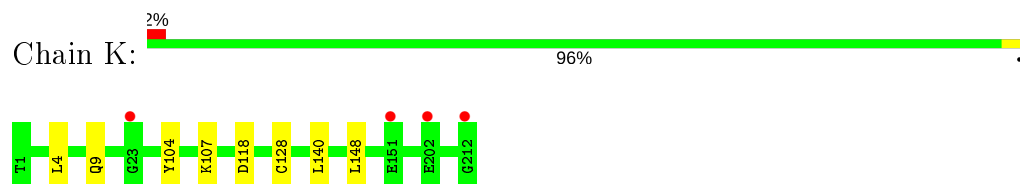
- Molecule 10: Proteasome subunit beta type-4



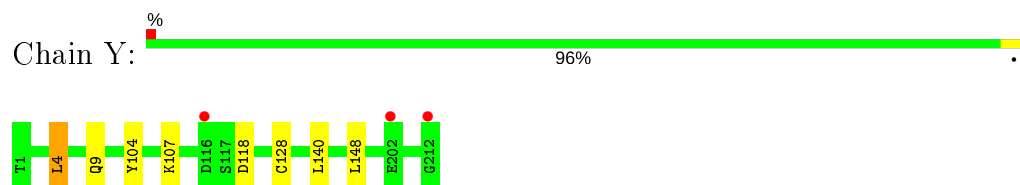
- Molecule 10: Proteasome subunit beta type-4



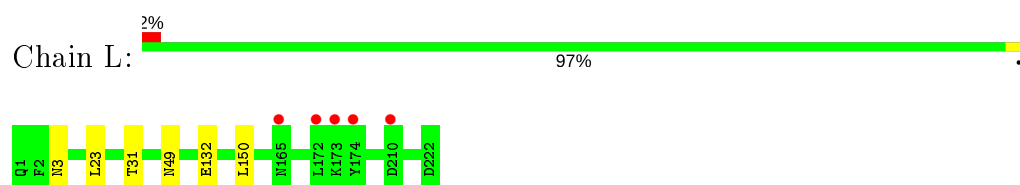
- Molecule 11: Proteasome subunit beta type-5



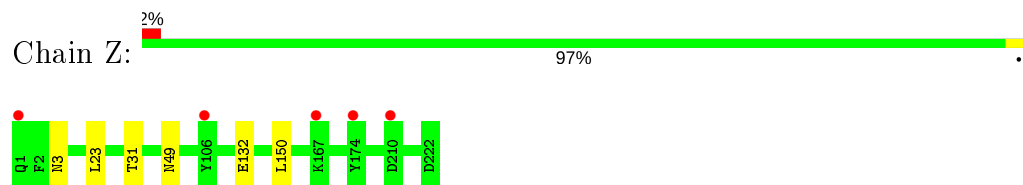
- Molecule 11: Proteasome subunit beta type-5



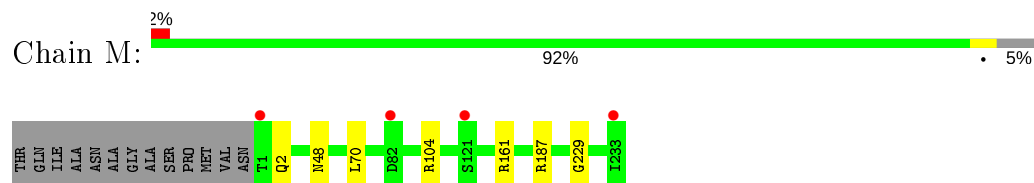
- Molecule 12: Proteasome subunit beta type-6



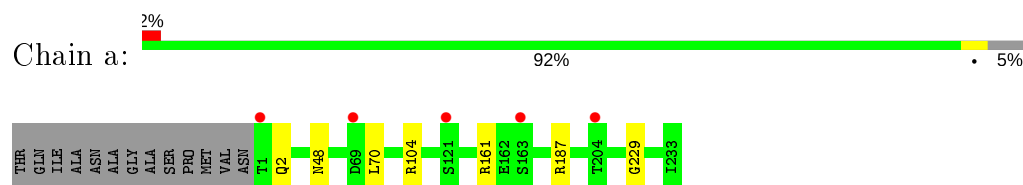
- Molecule 12: Proteasome subunit beta type-6



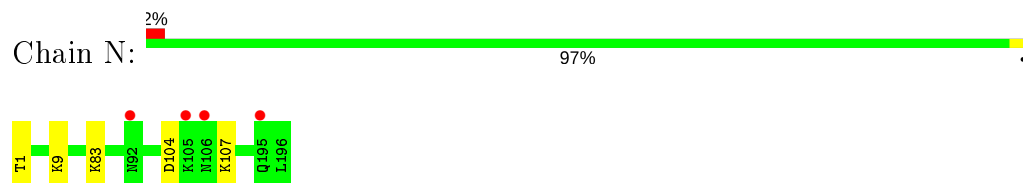
- Molecule 13: Proteasome subunit beta type-7



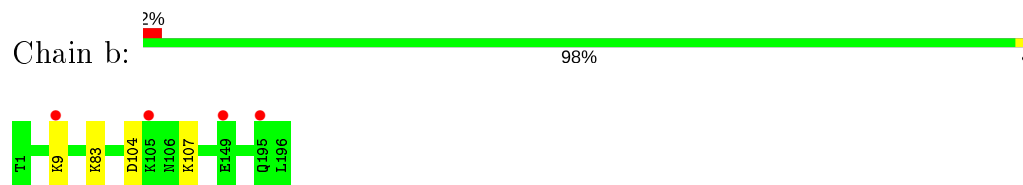
- Molecule 13: Proteasome subunit beta type-7



- Molecule 14: Proteasome subunit beta type-1



- Molecule 14: Proteasome subunit beta type-1



- Molecule 15: Ac-PAE-ep



- Molecule 15: Ac-PAE-ep



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.71Å 301.32Å 145.93Å 90.00° 113.18° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 15.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.9 (15.00-2.50) 95.9 (15.00-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.226 , 0.242 0.232 , 0.248	Depositor DCC
R_{free} test set	17789 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	44.2	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	50389	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, POL, GAU, ACE, CL

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	0.28	0/1952	0.47	0/2642
1	O	0.28	0/1952	0.47	0/2642
2	B	0.29	0/1934	0.50	0/2618
2	P	0.28	0/1934	0.50	0/2618
3	C	0.28	0/1910	0.51	0/2586
3	Q	0.28	0/1910	0.51	0/2586
4	D	0.28	0/1837	0.48	0/2475
4	R	0.28	0/1837	0.49	0/2475
5	E	0.28	0/1800	0.48	0/2433
5	S	0.28	0/1800	0.48	0/2433
6	F	0.28	0/1932	0.46	0/2609
6	T	0.28	0/1932	0.46	0/2609
7	G	0.28	0/1945	0.47	0/2634
7	U	0.28	0/1945	0.47	0/2634
8	H	0.26	0/1747	0.48	0/2369
8	V	0.26	0/1747	0.48	0/2369
9	I	0.29	0/1611	0.50	0/2174
9	W	0.29	0/1611	0.50	0/2174
10	J	0.27	0/1589	0.49	0/2142
10	X	0.27	0/1589	0.49	0/2142
11	K	0.27	0/1681	0.51	0/2274
11	Y	0.27	0/1681	0.51	1/2274 (0.0%)
12	L	0.28	0/1795	0.50	0/2420
12	Z	0.28	0/1795	0.50	0/2420
13	M	0.28	0/1855	0.51	0/2514
13	a	0.29	0/1855	0.51	0/2514
14	N	0.29	0/1541	0.50	1/2087 (0.0%)
14	b	0.27	0/1541	0.49	0/2087
15	c	2.57	1/13 (7.7%)	0.98	0/18
15	d	1.89	1/13 (7.7%)	0.94	0/18
All	All	0.28	2/50284 (0.0%)	0.49	2/67990 (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	-7.03	1.38	1.52
15	d	2	PRO	CA-C	-6.32	1.40	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	1	THR	N-CA-C	5.16	124.93	111.00
11	Y	4	LEU	CA-CB-CG	5.13	127.09	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	34	54
1	O	248/250 (99%)	238 (96%)	9 (4%)	1 (0%)	34	54
2	B	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	9	16
2	P	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	9	16
3	C	238/254 (94%)	233 (98%)	3 (1%)	2 (1%)	19	35
3	Q	238/254 (94%)	233 (98%)	2 (1%)	3 (1%)	12	21
4	D	231/260 (89%)	229 (99%)	2 (1%)	0	100	100
4	R	231/260 (89%)	229 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
5	S	229/234 (98%)	224 (98%)	5 (2%)	0	100	100
6	F	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
6	T	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
7	G	239/252 (95%)	238 (100%)	1 (0%)	0	100	100
7	U	239/252 (95%)	239 (100%)	0	0	100	100
8	H	224/232 (97%)	219 (98%)	5 (2%)	0	100	100
8	V	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
9	I	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
9	W	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
10	J	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	29	48
10	X	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	29	48
11	K	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
11	Y	210/212 (99%)	206 (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%)	223 (96%)	7 (3%)	1 (0%)	34	54
13	a	231/246 (94%)	224 (97%)	6 (3%)	1 (0%)	34	54
14	N	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
14	b	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
15	c	2/5 (40%)	2 (100%)	0	0	100	100
15	d	2/5 (40%)	2 (100%)	0	0	100	100
All	All	6288/6624 (95%)	6148 (98%)	121 (2%)	19 (0%)	41	61

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
2	B	222	GLY
3	C	202	GLN
2	P	51	VAL
2	P	222	GLY
3	Q	202	GLN
1	A	2	THR

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Mol	Chain	Res	Type
2	B	218	GLY
1	O	2	THR
2	P	218	GLY
2	B	220	ASN
3	C	205	ALA
2	P	220	ASN
3	Q	205	ALA
10	J	24	GLY
10	X	24	GLY
13	M	229	GLY
13	a	229	GLY
3	Q	183	PRO

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	80
1	O	209/209 (100%)	205 (98%)	4 (2%)	57	80
2	B	203/216 (94%)	195 (96%)	8 (4%)	32	57
2	P	203/216 (94%)	195 (96%)	8 (4%)	32	57
3	C	212/226 (94%)	200 (94%)	12 (6%)	20	39
3	Q	212/226 (94%)	200 (94%)	12 (6%)	20	39
4	D	194/215 (90%)	182 (94%)	12 (6%)	18	35
4	R	194/215 (90%)	182 (94%)	12 (6%)	18	35
5	E	190/193 (98%)	177 (93%)	13 (7%)	16	30
5	S	190/193 (98%)	177 (93%)	13 (7%)	16	30
6	F	201/239 (84%)	191 (95%)	10 (5%)	24	46
6	T	201/239 (84%)	191 (95%)	10 (5%)	24	46
7	G	206/210 (98%)	195 (95%)	11 (5%)	22	43
7	U	206/210 (98%)	195 (95%)	11 (5%)	22	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	H	185/190 (97%)	181 (98%)	4 (2%)	52	77
8	V	185/190 (97%)	181 (98%)	4 (2%)	52	77
9	I	172/173 (99%)	170 (99%)	2 (1%)	71	88
9	W	172/173 (99%)	170 (99%)	2 (1%)	71	88
10	J	173/175 (99%)	168 (97%)	5 (3%)	42	69
10	X	173/175 (99%)	168 (97%)	5 (3%)	42	69
11	K	169/169 (100%)	161 (95%)	8 (5%)	26	49
11	Y	169/169 (100%)	161 (95%)	8 (5%)	26	49
12	L	185/185 (100%)	179 (97%)	6 (3%)	39	65
12	Z	185/185 (100%)	179 (97%)	6 (3%)	39	65
13	M	199/208 (96%)	193 (97%)	6 (3%)	41	68
13	a	199/208 (96%)	193 (97%)	6 (3%)	41	68
14	N	162/162 (100%)	158 (98%)	4 (2%)	47	73
14	b	162/162 (100%)	158 (98%)	4 (2%)	47	73
15	c	1/1 (100%)	1 (100%)	0	100	100
15	d	1/1 (100%)	1 (100%)	0	100	100
All	All	5322/5542 (96%)	5112 (96%)	210 (4%)	32	57

All (210) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	SER
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	50	LYS
2	B	55	LEU
2	B	79	LEU
2	B	113	ARG
2	B	119	GLN
2	B	186	ASP
2	B	191	LEU
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	50	LEU

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Mol	Chain	Res	Type
3	C	51	LYS
3	C	60	SER
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	175	LYS
3	C	180	LYS
3	C	206	LYS
3	C	240	GLU
4	D	40	LEU
4	D	51	LEU
4	D	99	ILE
4	D	125	LEU
4	D	143	ASP
4	D	176	LEU
4	D	193	LEU
4	D	202	GLU
4	D	214	ILE
4	D	235	LEU
4	D	236	LYS
4	D	242	GLU
5	E	8	ASP
5	E	9	THR
5	E	29	LYS
5	E	55	LEU
5	E	71	LEU
5	E	99	ASN
5	E	116	GLN
5	E	184	ASN
5	E	188	LEU
5	E	202	ASP
5	E	207	VAL
5	E	208	ASP
5	E	231	LYS
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	172	LEU
6	F	181	GLU
6	F	201	GLU
6	F	202	ASP
6	F	207	ASP

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Mol	Chain	Res	Type
6	F	214	TRP
6	F	240	GLN
7	G	26	THR
7	G	75	ASN
7	G	83	ASN
7	G	115	LEU
7	G	117	GLN
7	G	122	ARG
7	G	125	MET
7	G	178	LYS
7	G	208	GLU
7	G	235	ARG
7	G	236	LEU
8	H	30	ASN
8	H	68	LEU
8	H	113	ILE
8	H	196	ARG
9	I	37	ASN
9	I	171	LEU
10	J	3	ILE
10	J	23	ARG
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
11	K	4	LEU
11	K	9	GLN
11	K	104	TYR
11	K	107	LYS
11	K	118	ASP
11	K	128	CYS
11	K	140	LEU
11	K	148	LEU
12	L	3	ASN
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	132	GLU
12	L	150	LEU
13	M	2	GLN
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG

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Mol	Chain	Res	Type
13	M	161	ARG
13	M	187	ARG
14	N	9	LYS
14	N	83	LYS
14	N	104	ASP
14	N	107	LYS
1	O	62	SER
1	O	122	THR
1	O	157	PHE
1	O	250	LEU
2	P	50	LYS
2	P	55	LEU
2	P	79	LEU
2	P	113	ARG
2	P	119	GLN
2	P	186	ASP
2	P	191	LEU
2	P	238	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	50	LEU
3	Q	51	LYS
3	Q	60	SER
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	175	LYS
3	Q	180	LYS
3	Q	206	LYS
3	Q	240	GLU
4	R	40	LEU
4	R	51	LEU
4	R	99	ILE
4	R	125	LEU
4	R	143	ASP
4	R	176	LEU
4	R	193	LEU
4	R	202	GLU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU

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Mol	Chain	Res	Type
5	S	8	ASP
5	S	9	THR
5	S	29	LYS
5	S	55	LEU
5	S	71	LEU
5	S	99	ASN
5	S	116	GLN
5	S	184	ASN
5	S	188	LEU
5	S	202	ASP
5	S	207	VAL
5	S	208	ASP
5	S	231	LYS
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	172	LEU
6	T	181	GLU
6	T	201	GLU
6	T	202	ASP
6	T	207	ASP
6	T	214	TRP
6	T	240	GLN
7	U	26	THR
7	U	75	ASN
7	U	83	ASN
7	U	115	LEU
7	U	117	GLN
7	U	122	ARG
7	U	125	MET
7	U	178	LYS
7	U	208	GLU
7	U	235	ARG
7	U	236	LEU
8	V	30	ASN
8	V	68	LEU
8	V	113	ILE
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU
10	X	3	ILE
10	X	23	ARG

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Mol	Chain	Res	Type
10	X	35	THR
10	X	90	LYS
10	X	99	GLN
11	Y	4	LEU
11	Y	9	GLN
11	Y	104	TYR
11	Y	107	LYS
11	Y	118	ASP
11	Y	128	CYS
11	Y	140	LEU
11	Y	148	LEU
12	Z	3	ASN
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	132	GLU
12	Z	150	LEU
13	a	2	GLN
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
14	b	9	LYS
14	b	83	LYS
14	b	104	ASP
14	b	107	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (116) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	20	GLN
2	B	58	GLN
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN
3	C	17	GLN
3	C	38	ASN
3	C	77	ASN

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Mol	Chain	Res	Type
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	91	HIS
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	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	191	GLN
6	F	240	GLN
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	167	GLN
8	H	66	HIS
8	H	165	ASN
9	I	37	ASN
10	J	55	GLN
10	J	146	HIS
11	K	85	ASN
11	K	176	ASN
11	K	190	ASN
11	K	208	ASN
12	L	3	ASN
12	L	49	ASN
12	L	70	ASN
12	L	79	HIS
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN

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Mol	Chain	Res	Type
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
1	O	94	HIS
2	P	20	GLN
2	P	58	GLN
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	176	GLN
3	Q	17	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
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	151	ASN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	191	GLN
6	T	240	GLN
7	U	30	ASN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	167	GLN
8	V	66	HIS

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Mol	Chain	Res	Type
8	V	165	ASN
9	W	37	ASN
10	X	55	GLN
10	X	86	GLN
10	X	146	HIS
11	Y	85	ASN
11	Y	176	ASN
11	Y	190	ASN
11	Y	208	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	158	ASN
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	194	ASN
13	a	213	GLN
14	b	38	HIS
14	b	141	ASN
14	b	161	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	GAU	d	4	15,14	5,8,8	1.24	1 (20%)	5,9,9	1.87	1 (20%)
15	GAU	c	4	15,14	5,8,8	1.33	1 (20%)	5,9,9	1.56	1 (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
15	GAU	d	4	15,14	-	2/5/7/7	-
15	GAU	c	4	15,14	-	2/5/7/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	d	4	GAU	C-CA	2.75	1.56	1.52
15	c	4	GAU	C-CA	2.72	1.56	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	d	4	GAU	CG-CB-CA	-3.66	105.04	112.74
15	c	4	GAU	CB-CA-N	-2.40	102.05	109.03

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	d	4	GAU	OXT-C-CA-CB
15	c	4	GAU	OXT-C-CA-CB
15	d	4	GAU	OXT-C-CA-N
15	c	4	GAU	OXT-C-CA-N

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 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	0.14	12 (4%)	30 32	31, 43, 77, 114	0
1	O	250/250 (100%)	0.25	12 (4%)	30 32	36, 52, 95, 125	0
2	B	244/258 (94%)	0.31	21 (8%)	10 10	30, 48, 89, 135	0
2	P	244/258 (94%)	0.41	14 (5%)	23 25	37, 54, 99, 145	0
3	C	240/254 (94%)	0.42	24 (10%)	7 6	31, 54, 115, 140	0
3	Q	240/254 (94%)	0.69	39 (16%)	1 1	36, 65, 144, 169	0
4	D	235/260 (90%)	0.25	12 (5%)	28 29	37, 56, 88, 132	0
4	R	235/260 (90%)	0.32	12 (5%)	28 29	40, 60, 99, 134	0
5	E	231/234 (98%)	0.37	12 (5%)	27 29	40, 58, 96, 144	0
5	S	231/234 (98%)	0.52	22 (9%)	8 8	41, 65, 107, 155	0
6	F	243/288 (84%)	0.19	14 (5%)	23 24	32, 50, 100, 130	0
6	T	243/288 (84%)	0.35	17 (6%)	16 16	36, 61, 120, 149	0
7	G	241/252 (95%)	0.10	11 (4%)	32 34	25, 45, 78, 130	0
7	U	241/252 (95%)	0.21	16 (6%)	18 19	34, 49, 81, 124	0
8	H	226/232 (97%)	0.12	7 (3%)	49 52	25, 41, 72, 133	0
8	V	226/232 (97%)	0.22	10 (4%)	34 37	32, 45, 74, 150	0
9	I	204/205 (99%)	-0.16	5 (2%)	57 61	26, 39, 66, 90	0
9	W	204/205 (99%)	-0.12	7 (3%)	45 48	30, 43, 71, 96	0
10	J	195/198 (98%)	-0.00	4 (2%)	63 66	30, 44, 69, 126	0
10	X	195/198 (98%)	0.07	7 (3%)	42 46	30, 45, 70, 132	0
11	K	212/212 (100%)	0.01	4 (1%)	66 69	28, 44, 67, 89	0
11	Y	212/212 (100%)	0.03	3 (1%)	75 77	33, 45, 69, 88	0
12	L	222/222 (100%)	0.03	5 (2%)	60 63	30, 46, 77, 110	0
12	Z	222/222 (100%)	0.07	5 (2%)	60 63	30, 44, 75, 109	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.08	4 (1%) 70 72	28, 43, 65, 83	0
13	a	233/246 (94%)	-0.05	5 (2%) 63 66	28, 42, 62, 79	0
14	N	196/196 (100%)	-0.08	4 (2%) 65 68	28, 39, 65, 94	0
14	b	196/196 (100%)	-0.02	4 (2%) 65 68	28, 40, 65, 99	0
15	c	2/5 (40%)	-0.31	0 100 100	52, 52, 52, 54	0
15	d	2/5 (40%)	-0.42	0 100 100	44, 44, 44, 51	0
All	All	6348/6624 (95%)	0.17	312 (4%) 29 31	25, 48, 93, 169	0

All (312) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	219	ALA	9.6
2	B	221	ASP	9.0
3	Q	49	THR	8.6
6	T	243	ILE	7.9
1	O	1	MET	7.6
2	P	220	ASN	7.6
10	J	1	MET	7.6
1	O	2	THR	7.0
1	A	2	THR	7.0
2	P	59	ASP	6.8
5	E	202	ASP	6.8
3	Q	206	LYS	6.7
7	U	242	GLN	6.7
10	X	1	MET	6.5
12	Z	174	TYR	6.3
6	F	205	GLU	6.0
10	X	193	ASP	5.9
2	P	221	ASP	5.9
3	Q	50	LEU	5.7
8	H	222	ASP	5.7
5	S	202	ASP	5.6
9	W	1	SER	5.5
3	Q	239	GLN	5.4
2	B	218	GLY	5.3
5	S	233	ILE	5.3
3	Q	48	SER	5.3
10	X	194	ASP	5.2
8	V	221	CYS	5.2
8	V	226	GLU	5.2

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Mol	Chain	Res	Type	RSRZ
3	C	240	GLU	5.2
2	P	218	GLY	5.1
8	V	223	ILE	5.1
2	B	59	ASP	5.0
14	b	195	GLN	5.0
8	V	222	ASP	5.0
12	L	172	LEU	5.0
1	O	250	LEU	5.0
3	C	50	LEU	5.0
5	E	233	ILE	5.0
1	A	248	GLU	4.9
10	J	193	ASP	4.9
8	H	221	CYS	4.8
6	F	2	THR	4.7
3	Q	229	GLN	4.6
11	Y	212	GLY	4.6
8	V	224	GLN	4.5
9	W	192	ASP	4.5
10	J	194	ASP	4.5
3	C	236	GLN	4.4
12	L	174	TYR	4.4
6	T	244	ASN	4.4
3	C	225	GLU	4.4
7	G	179	LYS	4.4
2	P	51	VAL	4.3
2	B	51	VAL	4.3
4	R	177	ASN	4.3
3	C	206	LYS	4.3
3	C	49	THR	4.2
7	U	206	GLY	4.1
3	Q	240	GLU	4.1
3	C	205	ALA	4.1
6	T	178	HIS	4.0
5	S	210	LEU	4.0
10	X	195	PHE	4.0
12	Z	1	GLN	3.9
3	Q	238	LYS	3.9
3	Q	180	LYS	3.9
3	C	223	SER	3.9
7	U	241	GLU	3.9
8	H	224	GLN	3.8
3	Q	233	GLN	3.8

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Mol	Chain	Res	Type	RSRZ
4	R	1	ASP	3.8
3	Q	225	GLU	3.8
9	I	160	GLU	3.7
3	Q	202	GLN	3.7
4	R	242	GLU	3.7
7	G	3	TYR	3.6
5	S	180	LYS	3.6
4	R	241	ALA	3.6
13	a	1	THR	3.6
6	F	244	ASN	3.6
3	C	60	SER	3.5
2	B	219	ALA	3.5
7	G	240	ALA	3.5
4	R	125	LEU	3.5
3	Q	181	GLU	3.5
3	C	238	LYS	3.5
5	S	3	ASN	3.4
5	E	201	ARG	3.4
3	C	12	ASP	3.4
5	S	122	TYR	3.4
1	A	1	MET	3.4
7	U	2	GLY	3.4
6	T	205	GLU	3.4
3	C	233	GLN	3.3
6	T	181	GLU	3.3
7	G	242	GLN	3.3
6	T	202	ASP	3.3
14	N	195	GLN	3.3
5	E	207	VAL	3.3
9	I	1	SER	3.3
6	F	215	CYS	3.2
8	H	198	GLU	3.2
2	B	242	GLY	3.2
8	V	145	ASP	3.2
6	F	174	LYS	3.2
2	B	182	ASP	3.2
5	S	227	GLU	3.2
3	Q	1	GLY	3.2
6	T	215	CYS	3.2
3	Q	60	SER	3.2
1	O	249	ALA	3.1
6	F	202	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
5	S	200	LEU	3.1
6	T	180	PRO	3.1
6	F	241	LYS	3.1
2	B	180	LYS	3.1
3	Q	236	GLN	3.1
3	Q	232	THR	3.1
3	Q	235	GLU	3.1
3	C	153	ILE	3.1
9	W	160	GLU	3.1
3	C	202	GLN	3.0
4	D	169	GLU	3.0
7	U	181	LYS	3.0
3	Q	205	ALA	3.0
2	B	220	ASN	3.0
11	K	212	GLY	3.0
2	P	52	THR	3.0
1	O	52	SER	3.0
5	S	58	TYR	3.0
5	S	204	SER	3.0
5	S	173	ARG	3.0
6	F	230	ASP	3.0
8	H	226	GLU	3.0
9	W	133	LYS	3.0
10	J	195	PHE	3.0
3	C	207	ASN	3.0
2	B	62	THR	2.9
4	D	125	LEU	2.9
2	P	242	GLY	2.9
3	Q	189	CYS	2.9
14	b	105	LYS	2.9
2	B	203	SER	2.9
13	M	1	THR	2.9
6	F	178	HIS	2.8
7	U	230	GLU	2.8
6	T	2	THR	2.8
3	C	181	GLU	2.8
2	P	203	SER	2.8
3	Q	26	LYS	2.8
3	Q	231	VAL	2.8
12	L	210	ASP	2.8
7	U	3	TYR	2.7
3	C	203	THR	2.7

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Mol	Chain	Res	Type	RSRZ
3	Q	55	THR	2.7
2	B	239	VAL	2.7
1	A	58	SER	2.7
6	F	243	ILE	2.7
3	C	142	GLU	2.7
5	E	217	LYS	2.7
2	B	238	LEU	2.7
14	N	105	LYS	2.7
1	A	182	GLU	2.7
4	D	242	GLU	2.7
5	E	210	LEU	2.7
2	B	230	LYS	2.7
7	U	179	LYS	2.7
7	U	222	ASP	2.7
1	O	229	THR	2.6
3	Q	204	GLY	2.6
7	G	241	GLU	2.6
3	Q	59	PRO	2.6
6	T	204	LYS	2.6
14	b	149	GLU	2.6
7	U	178	LYS	2.6
4	D	1	ASP	2.6
4	R	2	ARG	2.6
1	O	248	GLU	2.6
5	E	121	SER	2.6
1	A	181	ASP	2.6
10	X	113	LYS	2.6
12	Z	210	ASP	2.6
7	U	207	THR	2.5
9	I	17	LYS	2.5
3	C	139	ARG	2.5
6	F	218	SER	2.5
13	a	69	ASP	2.5
5	S	55	LEU	2.5
6	T	236	ILE	2.5
1	A	201	GLU	2.5
7	U	183	ASP	2.5
6	T	206	LYS	2.5
12	Z	167	LYS	2.5
9	W	78	GLU	2.5
11	K	23	GLY	2.5
2	B	236	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
3	Q	207	ASN	2.5
7	U	203	ASP	2.5
1	O	201	GLU	2.5
3	C	234	ILE	2.5
3	C	180	LYS	2.5
7	G	51	PRO	2.5
1	A	229	THR	2.5
2	P	222	GLY	2.5
5	S	123	GLY	2.5
7	U	188	GLU	2.4
12	L	165	ASN	2.4
4	R	47	THR	2.4
8	H	57	GLN	2.4
7	G	188	GLU	2.4
2	B	61	SER	2.4
4	D	233	LYS	2.4
5	E	123	GLY	2.4
14	N	92	ASN	2.4
13	M	121	SER	2.4
3	Q	201	VAL	2.4
5	S	207	VAL	2.4
5	E	4	ASN	2.4
3	Q	171	GLU	2.4
4	R	201	GLU	2.4
5	E	227	GLU	2.4
5	E	194	GLU	2.4
4	D	114	ARG	2.4
5	S	201	ARG	2.4
13	M	82	ASP	2.4
8	V	91	GLN	2.4
3	Q	223	SER	2.4
3	Q	38	ASN	2.3
2	B	201	ASP	2.3
2	P	182	ASP	2.3
4	R	224	ASP	2.3
4	R	217	GLN	2.3
11	K	151	GLU	2.3
3	Q	46	ARG	2.3
6	F	177	ASP	2.3
7	U	51	PRO	2.3
4	R	230	GLU	2.3
4	R	112	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
12	Z	106	TYR	2.3
5	E	176	ASP	2.3
4	D	216	LYS	2.3
4	D	241	ALA	2.3
14	b	9	LYS	2.3
6	F	180	PRO	2.3
7	U	201	MET	2.3
13	M	233	ILE	2.3
3	C	239	GLN	2.3
13	a	204	THR	2.3
3	C	220	VAL	2.3
12	L	173	LYS	2.3
14	N	106	ASN	2.3
1	O	230	ASP	2.3
3	Q	140	ASP	2.3
9	I	2	ASP	2.2
10	X	10	GLN	2.2
5	S	121	SER	2.2
1	A	177	LYS	2.2
2	B	40	SER	2.2
3	Q	179	ARG	2.2
5	S	51	ASN	2.2
1	O	178	ARG	2.2
2	P	235	LYS	2.2
3	Q	57	ILE	2.2
3	Q	234	ILE	2.2
8	V	198	GLU	2.2
3	C	229	GLN	2.1
7	G	237	VAL	2.1
4	D	177	ASN	2.1
3	Q	208	ILE	2.1
6	T	230	ASP	2.1
6	T	203	ASN	2.1
5	S	203	GLU	2.1
7	G	208	GLU	2.1
11	Y	202	GLU	2.1
5	S	231	LYS	2.1
13	a	163	SER	2.1
8	H	145	ASP	2.1
9	W	17	LYS	2.1
2	B	244	THR	2.1
4	D	47	THR	2.1

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Mol	Chain	Res	Type	RSRZ
5	S	171	LEU	2.1
6	F	217	LEU	2.1
6	T	55	LEU	2.1
6	T	198	LEU	2.1
6	T	235	ALA	2.1
2	B	169	SER	2.1
4	D	238	LYS	2.1
10	X	110	LYS	2.1
13	a	121	SER	2.1
5	S	170	TYR	2.1
8	V	149	GLU	2.1
2	B	93	HIS	2.1
11	K	202	GLU	2.1
3	Q	188	GLU	2.1
2	P	240	LYS	2.1
1	A	249	ALA	2.0
3	Q	221	ALA	2.0
2	P	169	SER	2.0
5	S	54	GLU	2.0
9	W	156	ASN	2.0
7	G	40	ASP	2.0
9	I	192	ASP	2.0
7	G	230	GLU	2.0
1	A	59	GLU	2.0
1	A	203	GLU	2.0
1	O	228	PRO	2.0
3	Q	187	GLU	2.0
4	D	201	GLU	2.0
1	O	177	LYS	2.0
8	V	218	VAL	2.0
11	Y	116	ASP	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	GAU	d	4	9/9	0.89	0.17	48,52,53,57	0
15	GAU	c	4	9/9	0.93	0.17	56,59,62,63	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
16	MG	I	301	1/1	0.91	0.20	63,63,63,63	0
16	MG	K	301	1/1	0.94	0.08	42,42,42,42	0
16	MG	G	301	1/1	0.95	0.08	43,43,43,43	0
16	MG	L	301	1/1	0.96	0.06	48,48,48,48	0
16	MG	Z	301	1/1	0.96	0.12	50,50,50,50	0
16	MG	N	201	1/1	0.96	0.12	47,47,47,47	0
16	MG	I	302	1/1	0.99	0.04	37,37,37,37	0
17	CL	G	302	1/1	0.99	0.10	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.