



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 25, 2020 – 06:46 PM BST

PDB ID : 4Y70
Title : Yeast 20S proteasome in complex with Ac-LAV-ep
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-02-13
Resolution : 2.40 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

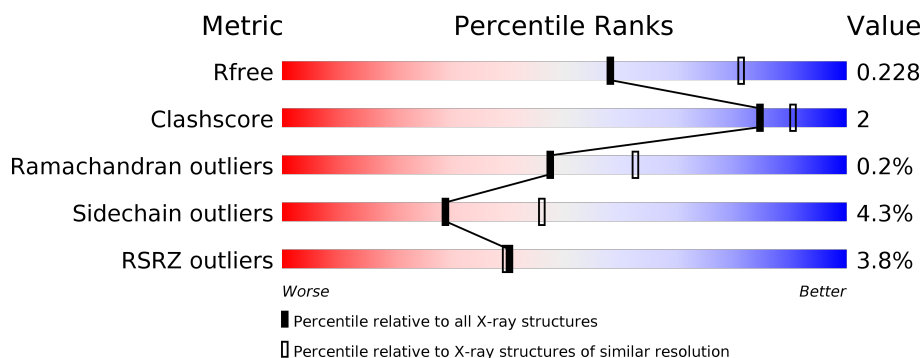
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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>3%</div> <div> <div></div> <div>93%</div> <div>7%</div> </div> </div>
1	O	250	<div> <div>4%</div> <div> <div></div> <div>91%</div> <div>8%</div> </div> </div>
2	B	258	<div> <div>9%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>5%</div> </div> </div>
2	P	258	<div> <div>7%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>5%</div> </div> </div>
3	C	254	<div> <div>7%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>6%</div> </div> </div>
3	Q	254	<div> <div>10%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>6%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
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	e	5	
15	f	5	
15	g	5	

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Mol	Chain	Length	Quality of chain
15	h	5	<div><div></div><div>80%</div><div>20%</div></div>

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 50716 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-LAV-ep.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	e	5	Total	C	N	O	0	0	0
			27	19	3	5			
15	f	5	Total	C	N	O	0	0	0
			27	19	3	5			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	g	5	Total	C	N	O	0	0	0
			27	19	3	5			
15	h	5	Total	C	N	O	0	0	0
			27	19	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	H	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		
17	U	1	Total	Cl	0	0
			1	1		

- Molecule 18 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
18	H	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	K	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
18	Y	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	58	Total	O	0	0
			58	58		
19	B	35	Total	O	0	0
			35	35		
19	C	41	Total	O	0	0
			41	41		
19	D	30	Total	O	0	0
			30	30		
19	E	17	Total	O	0	0
			17	17		
19	F	49	Total	O	0	0
			49	49		
19	G	57	Total	O	0	0
			57	57		
19	H	54	Total	O	0	0
			54	54		
19	I	61	Total	O	0	0
			61	61		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	J	64	Total O 64 64	0	0
19	K	51	Total O 51 51	0	0
19	L	67	Total O 67 67	0	0
19	M	55	Total O 55 55	0	0
19	N	39	Total O 39 39	0	0
19	O	36	Total O 36 36	0	0
19	P	28	Total O 28 28	0	0
19	Q	23	Total O 23 23	0	0
19	R	25	Total O 25 25	0	0
19	S	16	Total O 16 16	0	0
19	T	39	Total O 39 39	0	0
19	U	44	Total O 44 44	0	0
19	V	43	Total O 43 43	0	0
19	W	51	Total O 51 51	0	0
19	X	49	Total O 49 49	0	0
19	Y	33	Total O 33 33	0	0
19	Z	72	Total O 72 72	0	0
19	a	75	Total O 75 75	0	0
19	b	50	Total O 50 50	0	0
19	e	1	Total O 1 1	0	0
19	g	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	h	2	Total	O	0	0
			2	2		

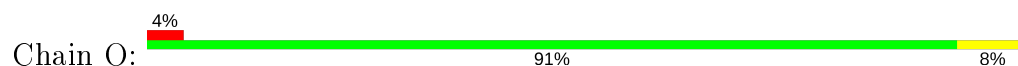
3 Residue-property plots [i](#)

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

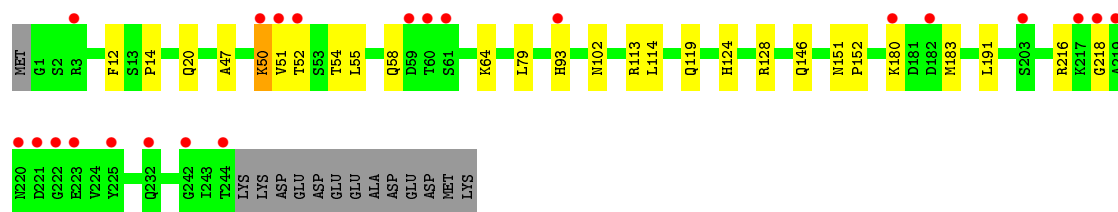
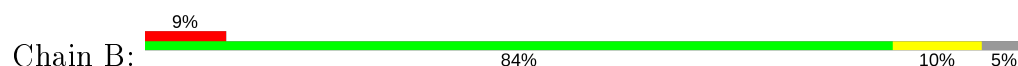
- Molecule 1: Proteasome subunit alpha type-2



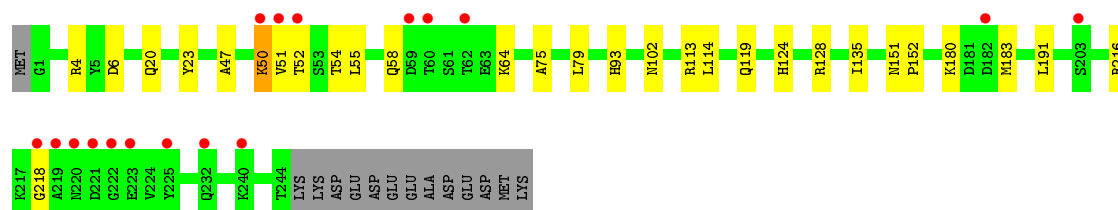
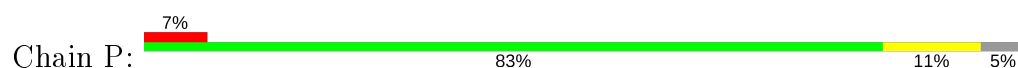
- Molecule 1: Proteasome subunit alpha type-2



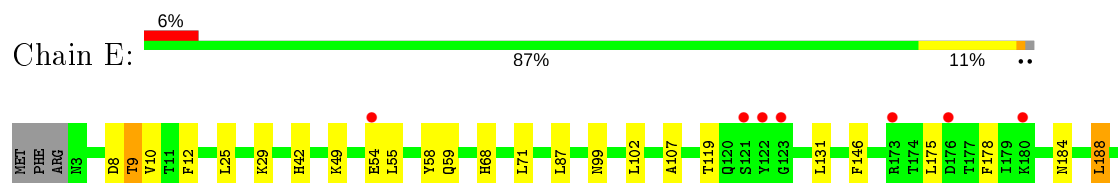
- Molecule 2: Proteasome subunit alpha type-3

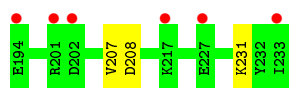


- Molecule 2: Proteasome subunit alpha type-3

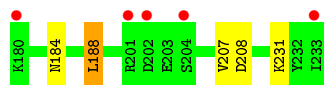
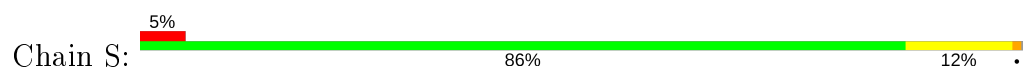


- Molecule 3: Proteasome subunit alpha type-4

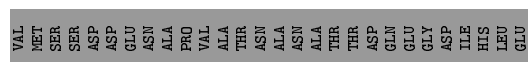
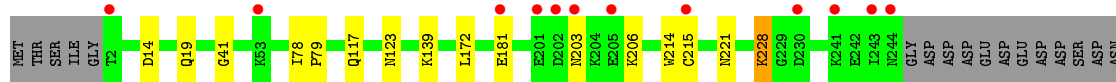
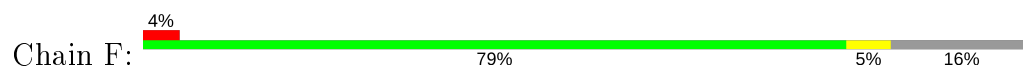




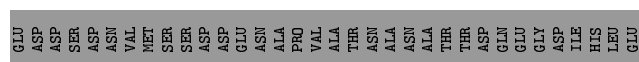
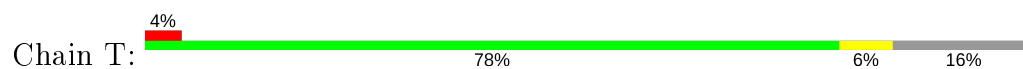
- Molecule 5: Proteasome subunit alpha type-6



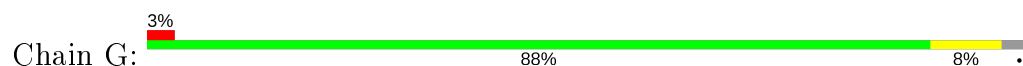
- Molecule 6: Probable proteasome subunit alpha type-7



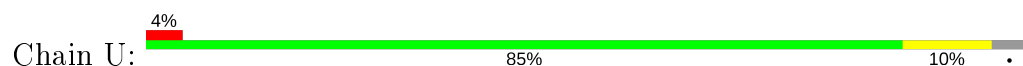
- Molecule 6: Probable proteasome subunit alpha type-7

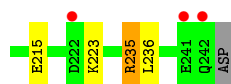


- Molecule 7: Proteasome subunit alpha type-1

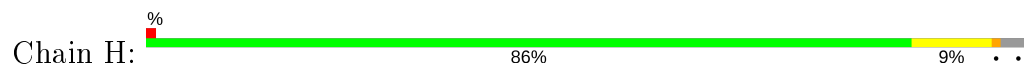


- Molecule 7: Proteasome subunit alpha type-1

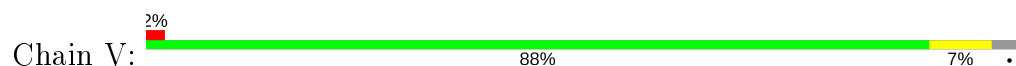




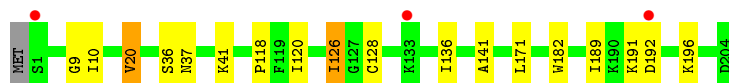
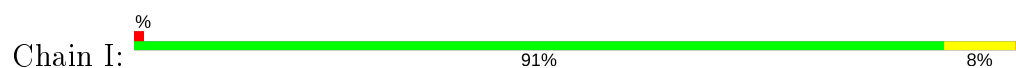
- Molecule 8: Proteasome subunit beta type-2



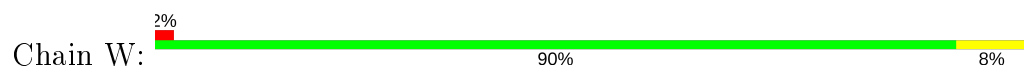
- Molecule 8: Proteasome subunit beta type-2



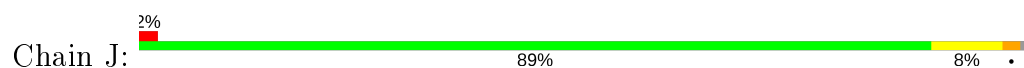
- Molecule 9: Proteasome subunit beta type-3



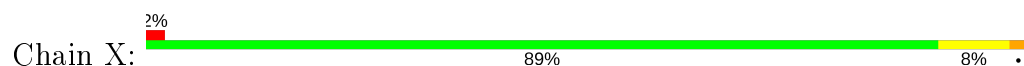
- Molecule 9: Proteasome subunit beta type-3



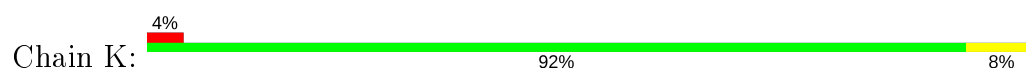
- Molecule 10: Proteasome subunit beta type-4



- Molecule 10: Proteasome subunit beta type-4



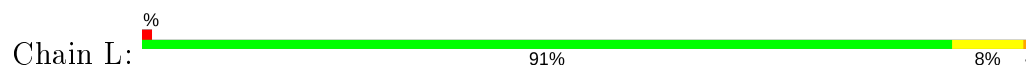
- Molecule 11: Proteasome subunit beta type-5



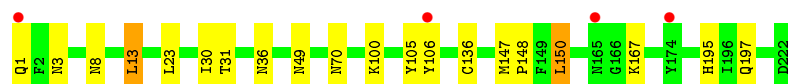
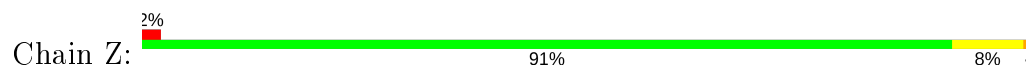
- Molecule 11: Proteasome subunit beta type-5



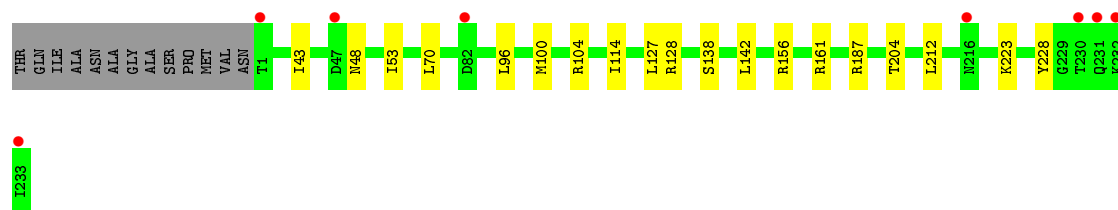
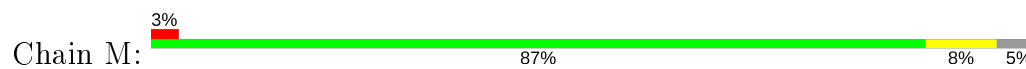
- Molecule 12: Proteasome subunit beta type-6



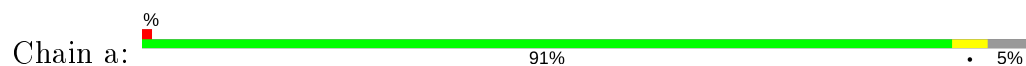
- Molecule 12: Proteasome subunit beta type-6



- Molecule 13: Proteasome subunit beta type-7

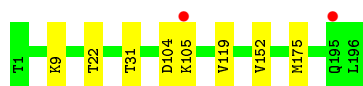


- Molecule 13: Proteasome subunit beta type-7

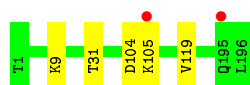


- Molecule 14: Proteasome subunit beta type-1

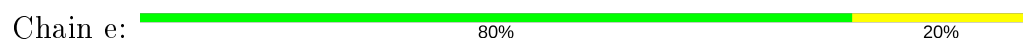




- Molecule 14: Proteasome subunit beta type-1



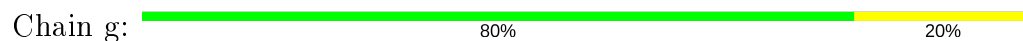
- Molecule 15: Ac-LAV-ep



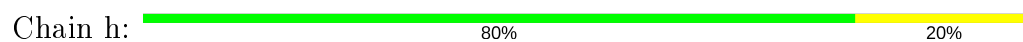
- Molecule 15: Ac-LAV-ep



- Molecule 15: Ac-LAV-ep



- Molecule 15: Ac-LAV-ep



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.94Å 299.89Å 144.86Å 90.00° 112.85° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 15.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.6 (15.00-2.40) 98.7 (15.00-2.40)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.97 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.208 , 0.226 0.210 , 0.228	Depositor DCC
R_{free} test set	20374 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	49.1	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 33.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	50716	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.49	0/2642
1	O	0.28	0/1952	0.49	0/2642
2	B	0.29	0/1934	0.52	0/2618
2	P	0.29	0/1934	0.52	0/2618
3	C	0.29	0/1910	0.52	0/2586
3	Q	0.29	0/1910	0.52	0/2586
4	D	0.29	0/1837	0.50	0/2475
4	R	0.28	0/1837	0.50	0/2475
5	E	0.29	0/1800	0.49	0/2433
5	S	0.29	0/1800	0.49	0/2433
6	F	0.29	0/1932	0.47	0/2609
6	T	0.29	0/1932	0.47	0/2609
7	G	0.29	0/1945	0.49	0/2634
7	U	0.29	0/1945	0.49	0/2634
8	H	0.34	1/1715 (0.1%)	0.55	1/2326 (0.0%)
8	V	0.33	0/1715	0.51	0/2326
9	I	0.30	0/1611	0.50	0/2174
9	W	0.29	0/1611	0.49	0/2174
10	J	0.27	0/1589	0.49	0/2142
10	X	0.28	0/1589	0.49	0/2142
11	K	0.32	0/1681	0.53	1/2274 (0.0%)
11	Y	0.32	0/1681	0.53	1/2274 (0.0%)
12	L	0.36	1/1795 (0.1%)	0.49	0/2420
12	Z	0.32	0/1795	0.49	0/2420
13	M	0.29	0/1855	0.52	0/2514
13	a	0.29	0/1855	0.52	0/2514
14	N	0.35	0/1541	0.49	0/2087
14	b	0.36	0/1541	0.49	0/2087
15	e	1.22	0/13	1.32	0/17
15	f	1.22	0/13	1.30	0/17
15	g	0.96	0/13	1.20	0/17
15	h	1.09	0/13	0.98	0/17

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.30	2/50246 (0.0%)	0.50	3/67936 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
8	H	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	114	HIS	CA-C	5.88	1.68	1.52
12	L	33	TYR	CE1-CZ	-5.53	1.31	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	4	LEU	CA-CB-CG	5.38	127.67	115.30
8	H	1	THR	N-CA-C	5.34	125.42	111.00
11	Y	4	LEU	CA-CB-CG	5.30	127.50	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	114	HIS	Mainchain

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	9	0
1	O	1915	0	1929	13	0
2	B	1904	0	1904	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	P	1904	0	1904	14	0
3	C	1881	0	1895	17	0
3	Q	1881	0	1895	17	0
4	D	1813	0	1797	10	0
4	R	1813	0	1797	12	0
5	E	1773	0	1775	9	0
5	S	1773	0	1775	12	0
6	F	1892	0	1883	5	0
6	T	1892	0	1883	7	0
7	G	1907	0	1901	8	0
7	U	1907	0	1901	14	0
8	H	1684	0	1685	10	0
8	V	1684	0	1685	7	0
9	I	1581	0	1574	11	0
9	W	1581	0	1574	10	0
10	J	1561	0	1569	11	0
10	X	1561	0	1569	11	0
11	K	1644	0	1592	12	0
11	Y	1644	0	1592	7	0
12	L	1757	0	1711	7	0
12	Z	1757	0	1711	8	0
13	M	1824	0	1832	6	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	1	0
14	b	1512	0	1481	0	0
15	e	27	0	33	0	0
15	f	27	0	34	0	0
15	g	27	0	33	0	0
15	h	27	0	33	0	0
16	G	1	0	0	0	0
16	H	1	0	0	0	0
16	I	2	0	0	0	0
16	K	1	0	0	0	0
16	L	1	0	0	0	0
16	N	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	H	12	0	13	0	0
18	K	12	0	13	0	0
18	Y	12	0	13	0	0
19	A	58	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	B	35	0	0	0	0
19	C	41	0	0	0	0
19	D	30	0	0	0	0
19	E	17	0	0	0	0
19	F	49	0	0	1	0
19	G	57	0	0	0	0
19	H	54	0	0	0	0
19	I	61	0	0	0	0
19	J	64	0	0	0	0
19	K	51	0	0	0	0
19	L	67	0	0	0	0
19	M	55	0	0	0	0
19	N	39	0	0	0	0
19	O	36	0	0	0	0
19	P	28	0	0	0	0
19	Q	23	0	0	0	0
19	R	25	0	0	0	0
19	S	16	0	0	0	0
19	T	39	0	0	0	0
19	U	44	0	0	0	0
19	V	43	0	0	0	0
19	W	51	0	0	0	0
19	X	49	0	0	0	0
19	Y	33	0	0	0	0
19	Z	72	0	0	0	0
19	a	75	0	0	0	0
19	b	50	0	0	0	0
19	e	1	0	0	0	0
19	g	1	0	0	0	0
19	h	2	0	0	0	0
All	All	50716	0	49228	214	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.

All (214) 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)
8:H:50:ALA:HB3	9:I:126:ILE:HD12	1.57	0.85
4:R:99:ILE:HD11	4:R:104:LEU:HB2	1.59	0.84
11:K:35:ILE:HD11	11:K:45:MET:SD	2.18	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:99:ILE:HD11	4:D:104:LEU:HB2	1.59	0.83
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.61	0.82
11:K:35:ILE:CD1	11:K:45:MET:SD	2.70	0.80
10:X:1:MET:O	10:X:2:ASP:HB2	1.83	0.78
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.66	0.78
10:J:1:MET:O	10:J:2:ASP:HB2	1.83	0.76
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.66	0.75
5:S:12:PHE:H	6:T:19:GLN:HE22	1.35	0.74
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.58	0.69
11:K:100:MET:CE	11:K:127:PHE:HB2	2.22	0.69
5:E:12:PHE:H	6:F:19:GLN:HE22	1.41	0.68
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.59	0.67
3:C:51:LYS:O	3:C:52:LEU:HB2	1.94	0.66
3:Q:51:LYS:O	3:Q:52:LEU:HB2	1.94	0.66
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.63	0.63
2:B:93:HIS:HB3	2:B:113:ARG:HH21	1.63	0.62
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.81	0.61
7:U:23:PHE:O	7:U:26:THR:HB	2.01	0.61
3:C:9:PHE:H	4:D:15:GLN:HE22	1.47	0.61
7:G:23:PHE:O	7:G:26:THR:HB	2.01	0.60
2:B:124:HIS:HB3	3:C:124:VAL:HG12	1.83	0.60
1:O:12:PHE:H	2:P:20:GLN:HE22	1.49	0.60
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.67	0.60
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.67	0.60
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.50	0.58
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.67	0.58
11:Y:53:GLN:O	11:Y:57:THR:HG23	2.03	0.58
11:K:5:ALA:HB3	11:K:100:MET:HE2	1.86	0.58
9:W:98:ARG:O	9:W:126:ILE:HD11	2.04	0.58
8:H:52:THR:O	8:H:56:THR:HB	2.03	0.58
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.68	0.58
8:V:52:THR:O	8:V:56:THR:HB	2.05	0.57
11:K:53:GLN:O	11:K:57:THR:HG23	2.04	0.57
14:N:152:VAL:HA	14:N:175:MET:HE1	1.86	0.56
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.87	0.56
8:H:50:ALA:CB	9:I:126:ILE:HD12	2.32	0.56
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.88	0.55
4:R:88:ALA:HA	4:R:99:ILE:HG21	1.88	0.55
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.88	0.55
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.89	0.55
5:E:9:THR:HG21	5:E:119:THR:HA	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.89	0.55
5:S:9:THR:HG21	5:S:119:THR:HA	1.89	0.54
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.56	0.54
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.89	0.53
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.91	0.53
1:A:12:PHE:H	2:B:20:GLN:HE22	1.55	0.53
10:J:1:MET:HA	10:J:34:LYS:HE3	1.91	0.53
2:P:216:ARG:HB3	2:P:218:GLY:H	1.74	0.53
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.91	0.53
10:J:174:MET:HA	10:X:174:MET:HA	1.91	0.53
1:O:7:PHE:HB3	3:Q:2:TYR:CE1	2.44	0.52
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.92	0.52
10:X:1:MET:HA	10:X:34:LYS:HE3	1.91	0.52
2:B:216:ARG:HB3	2:B:218:GLY:H	1.74	0.52
9:I:36:SER:HB2	10:J:126:VAL:HG11	1.92	0.52
10:J:1:MET:O	10:J:2:ASP:CB	2.58	0.52
12:L:195:HIS:HD2	12:L:197:GLN:H	1.56	0.52
8:H:50:ALA:HB3	9:I:126:ILE:CD1	2.35	0.52
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.92	0.52
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.92	0.52
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.92	0.52
1:O:119:GLN:O	1:O:122:THR:HB	2.10	0.51
10:X:1:MET:O	10:X:2:ASP:CB	2.58	0.51
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.92	0.51
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.92	0.51
2:B:146:GLN:HG2	3:C:57:ILE:HG21	1.91	0.51
3:C:202:GLN:HG3	3:C:203:THR:H	1.76	0.51
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.91	0.51
3:C:201:VAL:HG13	3:C:202:GLN:N	2.26	0.51
1:A:119:GLN:O	1:A:122:THR:HB	2.10	0.51
10:X:119:ILE:HG12	10:X:125:LYS:HG3	1.93	0.50
10:J:119:ILE:HG12	10:J:125:LYS:HG3	1.92	0.50
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.26	0.50
3:C:202:GLN:HG3	3:C:203:THR:N	2.27	0.50
13:M:127:LEU:HG	13:M:142:LEU:HD12	1.94	0.50
11:Y:35:ILE:HD11	11:Y:45:MET:SD	2.51	0.50
1:O:149:GLN:O	1:O:156:TYR:HA	2.11	0.50
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.94	0.50
6:F:19:GLN:NE2	19:F:301:HOH:O	2.45	0.50
3:Q:202:GLN:HG3	3:Q:203:THR:N	2.27	0.50
4:R:138:GLY:HA2	4:R:214:ILE:HG12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.60	0.49
1:A:149:GLN:O	1:A:156:TYR:HA	2.11	0.49
3:C:201:VAL:O	3:C:202:GLN:CB	2.60	0.49
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.93	0.49
3:Q:202:GLN:HG3	3:Q:203:THR:H	1.76	0.49
1:O:14:PRO:HA	2:P:23:TYR:CD1	2.48	0.49
4:D:138:GLY:HA2	4:D:214:ILE:HG12	1.94	0.49
2:P:47:ALA:HB1	2:P:64:LYS:HD2	1.95	0.49
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.13	0.49
12:L:8:ASN:HA	12:L:30:ILE:O	2.13	0.48
1:O:55:LEU:HB3	7:U:159:ALA:O	2.14	0.48
3:C:201:VAL:O	3:C:202:GLN:HB2	2.13	0.48
5:S:68:HIS:HE1	5:S:102:LEU:O	1.96	0.48
5:E:68:HIS:HE1	5:E:102:LEU:O	1.96	0.48
7:U:26:THR:HG21	7:U:131:ILE:HD12	1.96	0.48
7:G:195:GLU:HG3	7:G:235:ARG:HG3	1.94	0.48
3:Q:201:VAL:O	3:Q:202:GLN:HB2	2.13	0.48
7:U:195:GLU:HG3	7:U:235:ARG:HG3	1.95	0.47
1:O:83:ARG:HE	7:U:114:ASN:ND2	2.12	0.47
2:B:180:LYS:O	2:B:183:MET:HB2	2.15	0.47
9:W:101:PRO:HB3	9:W:126:ILE:HD12	1.97	0.47
9:W:20:VAL:HG23	9:W:189:ILE:HB	1.97	0.47
7:G:26:THR:HG21	7:G:131:ILE:HD12	1.97	0.47
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.45	0.47
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.45	0.46
6:F:228:LYS:HB2	6:F:228:LYS:HE3	1.60	0.46
1:A:55:LEU:HD12	7:G:170:THR:HG23	1.96	0.46
9:I:20:VAL:HG23	9:I:189:ILE:HB	1.96	0.46
7:U:187:GLU:HG2	7:U:192:LYS:HB2	1.96	0.46
9:I:120:ILE:HD12	9:I:136:ILE:HG12	1.98	0.46
3:Q:160:GLN:HE22	3:Q:170:ARG:HE	1.64	0.46
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	1.98	0.46
11:Y:37:ILE:HG23	11:Y:60:GLY:HA2	1.97	0.46
3:C:198:LEU:HA	3:C:201:VAL:HG12	1.98	0.46
4:D:155:THR:HG23	5:E:59:GLN:HE22	1.81	0.46
8:H:218:VAL:CG2	9:I:196:LYS:HB2	2.46	0.46
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.50	0.46
2:P:180:LYS:O	2:P:183:MET:HB2	2.15	0.46
5:S:131:LEU:HB2	5:S:146:PHE:HB3	1.98	0.46
2:B:12:PHE:H	3:C:17:GLN:HE22	1.62	0.46
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:42:HIS:HB2	5:E:188:LEU:HD12	1.98	0.46
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.51	0.46
7:G:187:GLU:HG2	7:G:192:LYS:HB2	1.97	0.45
8:H:50:ALA:HB2	9:I:128:CYS:HB2	1.99	0.45
4:R:155:THR:HG23	5:S:59:GLN:HE22	1.81	0.45
9:W:120:ILE:HD12	9:W:136:ILE:HG12	1.98	0.45
10:X:19:LYS:HD3	10:X:180:ILE:HG13	1.98	0.45
3:C:160:GLN:HE22	3:C:170:ARG:HE	1.63	0.45
10:J:21:VAL:HG11	11:K:122:LEU:HD11	1.98	0.45
11:K:37:ILE:HG23	11:K:60:GLY:HA2	1.97	0.45
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	1.98	0.45
1:A:222:LEU:HD13	1:A:232:GLY:HA2	1.99	0.45
5:E:131:LEU:HB2	5:E:146:PHE:HB3	1.97	0.45
13:M:228:TYR:HA	8:V:121:VAL:HG23	1.97	0.45
10:J:1:MET:HA	10:J:34:LYS:CE	2.47	0.45
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.52	0.45
5:S:109:HIS:HB3	6:T:82:ARG:NH2	2.32	0.44
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.32	0.44
10:J:19:LYS:HD3	10:J:180:ILE:HG13	1.97	0.44
1:O:222:LEU:HD13	1:O:232:GLY:HA2	1.99	0.44
5:S:42:HIS:HB2	5:S:188:LEU:HD12	1.98	0.44
4:R:9:PRO:HA	5:S:23:TYR:CD1	2.52	0.44
7:U:68:ARG:O	7:U:223:LYS:HA	2.18	0.44
2:P:50:LYS:HA	2:P:50:LYS:HE3	2.00	0.44
7:G:68:ARG:O	7:G:223:LYS:HA	2.18	0.44
12:L:147:MET:N	12:L:148:PRO:HD2	2.32	0.44
10:X:1:MET:HA	10:X:34:LYS:CE	2.47	0.44
3:C:11:PRO:HA	4:D:18:TYR:CD1	2.53	0.43
1:O:1:MET:CG	1:O:2:THR:H	2.32	0.43
13:M:96:LEU:O	13:M:100:MET:HG2	2.18	0.43
11:K:209:ASN:O	9:W:37:ASN:ND2	2.51	0.43
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.54	0.43
2:P:4:ARG:HG2	7:U:3:TYR:CZ	2.54	0.43
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.44	0.43
8:H:148:LYS:HE3	8:H:177:VAL:HG11	2.00	0.43
11:K:5:ALA:HB3	11:K:100:MET:CE	2.48	0.43
4:R:4:VAL:HG13	4:R:15:GLN:HG3	2.00	0.43
2:B:50:LYS:HE3	2:B:50:LYS:HA	2.00	0.43
3:C:169:VAL:HG23	3:C:196:SER:HB2	2.01	0.43
11:K:35:ILE:HD13	11:K:45:MET:SD	2.57	0.43
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:R:73:LEU:HD12	4:R:131:GLY:HA3	2.01	0.42
4:D:30:ILE:HD12	4:D:196:LEU:HG	2.01	0.42
3:Q:11:PRO:HA	4:R:18:TYR:CD1	2.55	0.42
11:K:6:PHE:HA	11:K:125:ASP:O	2.19	0.42
4:R:30:ILE:HD12	4:R:196:LEU:HG	2.01	0.42
6:T:228:LYS:HE3	6:T:228:LYS:HB2	1.59	0.42
4:D:4:VAL:HG13	4:D:15:GLN:HG3	2.00	0.42
1:O:54:PRO:HG2	7:U:174:GLU:HG2	2.02	0.42
13:M:156:ARG:HH11	8:V:165:ASN:HD22	1.66	0.42
8:V:148:LYS:HE3	8:V:177:VAL:HG11	2.00	0.42
3:C:35:LYS:HG2	3:C:158:SER:O	2.20	0.42
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.54	0.42
4:D:73:LEU:HD12	4:D:131:GLY:HA3	2.01	0.42
1:A:1:MET:CG	1:A:2:THR:H	2.32	0.42
11:Y:6:PHE:HA	11:Y:125:ASP:O	2.20	0.42
11:Y:45:MET:HG2	11:Y:52:CYS:HB3	2.00	0.42
5:E:49:LYS:HB3	5:E:58:TYR:HB3	2.02	0.42
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.55	0.42
2:B:14:PRO:HA	3:C:20:TYR:CD1	2.55	0.41
13:M:53:ILE:HG12	13:M:114:ILE:HG12	2.02	0.41
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	2.01	0.41
8:H:84:LYS:HG3	8:H:85:GLN:N	2.36	0.41
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.21	0.41
5:S:92:ASN:HD21	12:Z:70:ASN:ND2	2.18	0.41
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.41
6:F:41:GLY:HA3	6:F:215:CYS:O	2.21	0.41
2:P:75:ALA:HB3	2:P:135:ILE:HB	2.02	0.41
7:G:78:ILE:N	7:G:79:PRO:CD	2.83	0.41
12:L:100:LYS:HD3	12:L:105:TYR:CZ	2.56	0.41
1:A:110:LEU:O	1:A:114:VAL:HG23	2.20	0.41
8:H:113:ILE:HG12	8:H:119:THR:HG22	2.02	0.41
6:T:41:GLY:HA3	6:T:215:CYS:O	2.21	0.41
13:M:128:ARG:HH11	13:M:138:SER:HB2	1.85	0.41
6:T:155:GLY:HA3	7:U:59:THR:HG21	2.03	0.41
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.43	0.41
7:U:63:ILE:HD12	7:U:215:GLU:HG2	2.04	0.40
8:V:84:LYS:HG3	8:V:85:GLN:N	2.35	0.40
6:F:78:ILE:HB	6:F:79:PRO:HD3	2.03	0.40
1:O:110:LEU:O	1:O:114:VAL:HG23	2.21	0.40
6:T:78:ILE:HB	6:T:79:PRO:HD3	2.03	0.40
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:142:GLU:HA	3:Q:143:PRO:HD3	1.96	0.40
8:V:50:ALA:HB2	9:W:128:CYS:HB2	2.04	0.40
12:Z:100:LYS:HD3	12:Z:105:TYR:CZ	2.57	0.40
2:P:6:ASP:OD2	3:Q:4:ARG:HG3	2.21	0.40
1:A:83:ARG:HE	7:G:114:ASN:ND2	2.19	0.40
6:T:154:TRP:CZ3	7:U:60:VAL:HA	2.57	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%)	4 (2%)	2 (1%)	19	29
1	O	248/250 (99%)	242 (98%)	4 (2%)	2 (1%)	19	29
2	B	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	34	48
2	P	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	34	48
3	C	238/254 (94%)	228 (96%)	7 (3%)	3 (1%)	12	17
3	Q	238/254 (94%)	228 (96%)	7 (3%)	3 (1%)	12	17
4	D	231/260 (89%)	226 (98%)	5 (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%)	221 (96%)	8 (4%)	0	100	100
6	F	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
6	T	241/288 (84%)	234 (97%)	7 (3%)	0	100	100
7	G	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
7	U	239/252 (95%)	235 (98%)	4 (2%)	0	100	100
8	H	220/232 (95%)	214 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	V	220/232 (95%)	214 (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%)	187 (97%)	5 (3%)	1 (0%)	29	41
10	X	193/198 (98%)	187 (97%)	5 (3%)	1 (0%)	29	41
11	K	210/212 (99%)	207 (99%)	3 (1%)	0	100	100
11	Y	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
12	L	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
12	Z	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
13	M	231/246 (94%)	224 (97%)	7 (3%)	0	100	100
13	a	231/246 (94%)	224 (97%)	7 (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	e	2/5 (40%)	2 (100%)	0	0	100	100
15	f	2/5 (40%)	2 (100%)	0	0	100	100
15	g	2/5 (40%)	2 (100%)	0	0	100	100
15	h	2/5 (40%)	2 (100%)	0	0	100	100
All	All	6284/6634 (95%)	6113 (97%)	157 (2%)	14 (0%)	47	62

All (14) 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
1	A	3	ASP
1	O	3	ASP
1	A	2	THR
1	O	2	THR
3	C	183	PRO
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	75
1	O	209/209 (100%)	205 (98%)	4 (2%)	57	75
2	B	203/216 (94%)	193 (95%)	10 (5%)	25	40
2	P	203/216 (94%)	193 (95%)	10 (5%)	25	40
3	C	212/226 (94%)	204 (96%)	8 (4%)	33	51
3	Q	212/226 (94%)	204 (96%)	8 (4%)	33	51
4	D	194/215 (90%)	183 (94%)	11 (6%)	20	33
4	R	194/215 (90%)	183 (94%)	11 (6%)	20	33
5	E	190/193 (98%)	176 (93%)	14 (7%)	13	22
5	S	190/193 (98%)	176 (93%)	14 (7%)	13	22
6	F	201/239 (84%)	190 (94%)	11 (6%)	21	35
6	T	201/239 (84%)	190 (94%)	11 (6%)	21	35
7	G	206/210 (98%)	198 (96%)	8 (4%)	32	50
7	U	206/210 (98%)	198 (96%)	8 (4%)	32	50
8	H	181/190 (95%)	172 (95%)	9 (5%)	24	40
8	V	181/190 (95%)	174 (96%)	7 (4%)	32	50
9	I	172/173 (99%)	165 (96%)	7 (4%)	30	48
9	W	172/173 (99%)	166 (96%)	6 (4%)	36	55
10	J	173/175 (99%)	167 (96%)	6 (4%)	36	55
10	X	173/175 (99%)	167 (96%)	6 (4%)	36	55
11	K	169/169 (100%)	165 (98%)	4 (2%)	49	68
11	Y	169/169 (100%)	165 (98%)	4 (2%)	49	68
12	L	185/185 (100%)	176 (95%)	9 (5%)	25	40
12	Z	185/185 (100%)	176 (95%)	9 (5%)	25	40
13	M	199/208 (96%)	190 (96%)	9 (4%)	27	44
13	a	199/208 (96%)	190 (96%)	9 (4%)	27	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	162/162 (100%)	156 (96%)	6 (4%)	34	53
14	b	162/162 (100%)	157 (97%)	5 (3%)	40	60
15	e	1/1 (100%)	1 (100%)	0	100	100
15	f	1/1 (100%)	1 (100%)	0	100	100
15	g	1/1 (100%)	1 (100%)	0	100	100
15	h	1/1 (100%)	1 (100%)	0	100	100
All	All	5316/5544 (96%)	5088 (96%)	228 (4%)	29	46

All (228) 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
1	A	250	LEU
2	B	50	LYS
2	B	52	THR
2	B	54	THR
2	B	55	LEU
2	B	58	GLN
2	B	79	LEU
2	B	102	ASN
2	B	114	LEU
2	B	119	GLN
2	B	191	LEU
3	C	4	ARG
3	C	38	ASN
3	C	61	LYS
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	40	LEU
4	D	51	LEU
4	D	99	ILE
4	D	102	GLU
4	D	117	GLU
4	D	176	LEU

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Mol	Chain	Res	Type
4	D	193	LEU
4	D	214	ILE
4	D	236	LYS
4	D	242	GLU
5	E	8	ASP
5	E	9	THR
5	E	10	VAL
5	E	25	LEU
5	E	29	LYS
5	E	54	GLU
5	E	55	LEU
5	E	71	LEU
5	E	99	ASN
5	E	184	ASN
5	E	188	LEU
5	E	207	VAL
5	E	208	ASP
5	E	231	LYS
6	F	14	ASP
6	F	117	GLN
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
6	F	228	LYS
7	G	83	ASN
7	G	115	LEU
7	G	125	MET
7	G	154	TYR
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
7	G	236	LEU
8	H	22	GLN
8	H	30	ASN
8	H	31	CYS
8	H	34	LEU
8	H	43	CYS

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Mol	Chain	Res	Type
8	H	56	THR
8	H	68	LEU
8	H	127	LEU
8	H	196	ARG
9	I	20	VAL
9	I	37	ASN
9	I	126	ILE
9	I	171	LEU
9	I	182	TRP
9	I	191	LYS
9	I	192	ASP
10	J	23	ARG
10	J	35	THR
10	J	75	LEU
10	J	78	GLN
10	J	144	LEU
10	J	174	MET
11	K	4	LEU
11	K	9	GLN
11	K	106	ARG
11	K	118	ASP
12	L	1	GLN
12	L	3	ASN
12	L	13	LEU
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
13	M	204	THR
13	M	212	LEU
13	M	223	LYS
14	N	9	LYS
14	N	22	THR
14	N	31	THR

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Mol	Chain	Res	Type
14	N	104	ASP
14	N	105	LYS
14	N	119	VAL
1	O	17	LYS
1	O	61	LEU
1	O	157	PHE
1	O	250	LEU
2	P	50	LYS
2	P	52	THR
2	P	54	THR
2	P	55	LEU
2	P	58	GLN
2	P	79	LEU
2	P	102	ASN
2	P	114	LEU
2	P	119	GLN
2	P	191	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	61	LYS
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	40	LEU
4	R	51	LEU
4	R	99	ILE
4	R	102	GLU
4	R	117	GLU
4	R	176	LEU
4	R	193	LEU
4	R	214	ILE
4	R	236	LYS
4	R	242	GLU
5	S	8	ASP
5	S	9	THR
5	S	10	VAL
5	S	25	LEU
5	S	29	LYS
5	S	54	GLU

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Mol	Chain	Res	Type
5	S	55	LEU
5	S	71	LEU
5	S	99	ASN
5	S	184	ASN
5	S	188	LEU
5	S	207	VAL
5	S	208	ASP
5	S	231	LYS
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
6	T	228	LYS
7	U	83	ASN
7	U	115	LEU
7	U	125	MET
7	U	154	TYR
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
7	U	236	LEU
8	V	30	ASN
8	V	34	LEU
8	V	43	CYS
8	V	56	THR
8	V	68	LEU
8	V	127	LEU
8	V	196	ARG
9	W	20	VAL
9	W	37	ASN
9	W	171	LEU
9	W	182	TRP
9	W	191	LYS
9	W	192	ASP
10	X	23	ARG
10	X	35	THR

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Mol	Chain	Res	Type
10	X	75	LEU
10	X	78	GLN
10	X	144	LEU
10	X	174	MET
11	Y	4	LEU
11	Y	9	GLN
11	Y	106	ARG
11	Y	118	ASP
12	Z	1	GLN
12	Z	3	ASN
12	Z	13	LEU
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
13	a	204	THR
13	a	212	LEU
13	a	223	LYS
14	b	9	LYS
14	b	31	THR
14	b	104	ASP
14	b	105	LYS
14	b	119	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (136) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	20	GLN
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	155	ASN
2	B	176	GLN

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Mol	Chain	Res	Type
3	C	38	ASN
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	100	ASN
4	D	146	GLN
4	D	198	GLN
4	D	225	ASN
5	E	59	GLN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	147	GLN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	191	GLN
6	F	240	GLN
7	G	6	HIS
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	167	GLN
7	G	175	ASN
8	H	30	ASN
8	H	57	GLN
8	H	66	HIS
8	H	165	ASN
8	H	172	ASN
8	H	189	ASN
9	I	37	ASN
10	J	55	GLN
10	J	118	GLN
11	K	9	GLN
11	K	85	ASN

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Mol	Chain	Res	Type
11	K	176	ASN
12	L	1	GLN
12	L	3	ASN
12	L	49	ASN
12	L	70	ASN
12	L	80	ASN
12	L	158	ASN
12	L	165	ASN
12	L	195	HIS
13	M	2	GLN
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
14	N	38	HIS
14	N	161	GLN
1	O	94	HIS
2	P	20	GLN
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	176	GLN
3	Q	38	ASN
3	Q	77	ASN
3	Q	92	GLN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	100	ASN
4	R	146	GLN
4	R	198	GLN
4	R	225	ASN
5	S	59	GLN
5	S	68	HIS
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	147	GLN

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Mol	Chain	Res	Type
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
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	167	GLN
7	U	175	ASN
8	V	30	ASN
8	V	57	GLN
8	V	66	HIS
8	V	165	ASN
8	V	172	ASN
8	V	189	ASN
10	X	55	GLN
10	X	65	GLN
10	X	86	GLN
10	X	118	GLN
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
12	Z	1	GLN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	76	HIS
12	Z	80	ASN
12	Z	158	ASN
12	Z	165	ASN
12	Z	195	HIS
13	a	2	GLN
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	179	ASN
13	a	194	ASN

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Mol	Chain	Res	Type
13	a	213	GLN
14	b	38	HIS
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 ⓘ

4 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	VOL	h	4	11,15	6,6,6	1.15	0	4,7,7	1.50	1 (25%)
15	VOL	e	4	8,15	6,6,6	1.00	0	4,7,7	1.86	1 (25%)
15	VOL	g	4	8,15	6,6,6	1.09	1 (16%)	4,7,7	2.21	1 (25%)
15	VOL	f	4	11,15	6,6,6	1.18	1 (16%)	4,7,7	1.81	1 (25%)

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	VOL	h	4	11,15	-	2/6/6/6	-
15	VOL	e	4	8,15	-	3/6/6/6	-
15	VOL	g	4	8,15	-	4/6/6/6	-
15	VOL	f	4	11,15	-	2/6/6/6	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	f	4	VOL	CB-CA	2.15	1.56	1.53
15	g	4	VOL	OH-CH2	-2.03	1.33	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	g	4	VOL	OH-CH2-CA	-4.27	102.46	111.43
15	e	4	VOL	OH-CH2-CA	-3.36	104.37	111.43
15	f	4	VOL	OH-CH2-CA	-3.12	104.87	111.43
15	h	4	VOL	OH-CH2-CA	-2.83	105.48	111.43

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	h	4	VOL	N-CA-CH2-OH
15	e	4	VOL	N-CA-CB-CG2
15	f	4	VOL	N-CA-CH2-OH
15	g	4	VOL	N-CA-CB-CG2
15	f	4	VOL	CB-CA-CH2-OH
15	e	4	VOL	CH2-CA-CB-CG1
15	g	4	VOL	CH2-CA-CB-CG1
15	e	4	VOL	N-CA-CB-CG1
15	g	4	VOL	N-CA-CB-CG1
15	g	4	VOL	CB-CA-CH2-OH
15	h	4	VOL	CB-CA-CH2-OH

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 13 ligands modelled in this entry, 10 are monoatomic - leaving 3 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	Y	301	-	12,12,12	2.22	1 (8%)	14,16,16	1.74	4 (28%)
18	MES	K	302	-	12,12,12	2.31	1 (8%)	14,16,16	1.33	2 (14%)
18	MES	H	302	-	12,12,12	2.17	1 (8%)	14,16,16	1.43	3 (21%)

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	Y	301	-	-	0/6/14/14	0/1/1/1
18	MES	K	302	-	-	0/6/14/14	0/1/1/1
18	MES	H	302	-	-	4/6/14/14	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	K	302	MES	C8-S	-7.71	1.66	1.77
18	Y	301	MES	C8-S	-7.37	1.67	1.77
18	H	302	MES	C8-S	-7.22	1.67	1.77

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	Y	301	MES	C2-C3-N4	3.45	115.33	110.10
18	H	302	MES	O2S-S-C8	3.35	110.95	106.92
18	Y	301	MES	O3S-S-C8	2.85	110.38	105.77
18	K	302	MES	O3S-S-C8	2.57	109.92	105.77
18	Y	301	MES	O2S-S-C8	2.43	109.84	106.92
18	H	302	MES	O3S-S-C8	2.33	109.54	105.77
18	H	302	MES	O1S-S-C8	2.21	109.57	106.92
18	Y	301	MES	C5-N4-C3	2.15	113.66	108.83
18	K	302	MES	O2S-S-C8	2.08	109.42	106.92

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	H	302	MES	C7-C8-S-O1S
18	H	302	MES	C7-C8-S-O3S
18	H	302	MES	C7-C8-S-O2S
18	H	302	MES	N4-C7-C8-S

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, 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%)	-0.16	7 (2%)	53	51	35, 48, 82, 123	0
1	O	250/250 (100%)	-0.07	10 (4%)	38	37	39, 53, 96, 125	0
2	B	244/258 (94%)	0.12	22 (9%)	9	8	36, 53, 105, 163	0
2	P	244/258 (94%)	0.17	17 (6%)	16	15	39, 55, 108, 163	0
3	C	240/254 (94%)	0.11	19 (7%)	12	11	34, 54, 119, 153	0
3	Q	240/254 (94%)	0.43	25 (10%)	6	6	42, 70, 146, 194	0
4	D	235/260 (90%)	-0.18	5 (2%)	63	61	38, 56, 88, 130	0
4	R	235/260 (90%)	0.05	11 (4%)	31	30	44, 62, 100, 144	0
5	E	231/234 (98%)	0.05	13 (5%)	24	23	41, 61, 94, 136	0
5	S	231/234 (98%)	0.10	12 (5%)	27	26	43, 65, 102, 139	0
6	F	243/288 (84%)	-0.01	12 (4%)	29	28	40, 57, 105, 138	0
6	T	243/288 (84%)	-0.01	12 (4%)	29	28	39, 60, 107, 140	0
7	G	241/252 (95%)	-0.14	8 (3%)	46	45	34, 49, 92, 142	0
7	U	241/252 (95%)	-0.18	10 (4%)	37	36	37, 50, 82, 126	0
8	H	222/232 (95%)	-0.22	2 (0%)	84	82	35, 45, 71, 116	0
8	V	222/232 (95%)	-0.18	4 (1%)	68	66	36, 48, 73, 126	0
9	I	204/205 (99%)	-0.40	3 (1%)	73	72	32, 44, 69, 94	0
9	W	204/205 (99%)	-0.37	4 (1%)	65	63	33, 45, 72, 98	0
10	J	195/198 (98%)	-0.28	3 (1%)	73	72	33, 45, 70, 119	0
10	X	195/198 (98%)	-0.33	3 (1%)	73	72	35, 47, 70, 123	0
11	K	212/212 (100%)	-0.15	8 (3%)	40	39	34, 47, 74, 87	0
11	Y	212/212 (100%)	-0.06	9 (4%)	36	35	36, 49, 78, 103	0
12	L	222/222 (100%)	-0.35	3 (1%)	75	73	33, 46, 68, 92	0
12	Z	222/222 (100%)	-0.27	4 (1%)	68	66	36, 49, 74, 101	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.23	8 (3%) 45 44	31, 48, 72, 97	0
13	a	233/246 (94%)	-0.30	2 (0%) 84 82	33, 45, 67, 80	0
14	N	196/196 (100%)	-0.28	2 (1%) 82 80	36, 45, 69, 95	0
14	b	196/196 (100%)	-0.28	2 (1%) 82 80	36, 45, 70, 94	0
15	e	2/5 (40%)	-0.88	0 100 100	50, 50, 50, 53	0
15	f	2/5 (40%)	-0.25	0 100 100	62, 62, 62, 68	0
15	g	2/5 (40%)	-1.01	0 100 100	54, 54, 54, 62	0
15	h	2/5 (40%)	-0.48	0 100 100	63, 63, 63, 70	0
All	All	6344/6634 (95%)	-0.11	240 (3%) 40 39	31, 51, 93, 194	0

All (240) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	219	ALA	12.3
2	B	220	ASN	10.0
2	B	219	ALA	9.5
8	H	221	CYS	8.4
3	Q	49	THR	7.8
1	O	1	MET	7.3
8	V	222	ASP	7.2
3	Q	206	LYS	7.0
3	C	206	LYS	6.9
1	A	1	MET	6.9
2	P	218	GLY	6.8
8	V	221	CYS	6.7
3	Q	48	SER	6.7
5	S	202	ASP	6.5
5	E	202	ASP	6.2
2	P	51	VAL	6.1
11	Y	212	GLY	5.9
2	B	51	VAL	5.8
2	B	221	ASP	5.8
2	P	222	GLY	5.8
8	H	222	ASP	5.6
3	C	49	THR	5.4
2	P	220	ASN	5.4
2	P	221	ASP	5.3
1	O	249	ALA	5.2
3	Q	50	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
13	a	1	THR	4.9
10	J	1	MET	4.8
4	D	242	GLU	4.8
6	T	243	ILE	4.7
3	C	238	LYS	4.7
3	Q	239	GLN	4.6
10	X	1	MET	4.5
3	Q	51	LYS	4.5
3	C	225	GLU	4.5
4	R	241	ALA	4.5
7	U	222	ASP	4.4
10	X	194	ASP	4.4
2	B	218	GLY	4.4
3	Q	187	GLU	4.3
3	Q	240	GLU	4.3
9	W	1	SER	4.2
9	W	191	LYS	4.2
6	F	243	ILE	4.1
3	Q	238	LYS	4.1
3	C	202	GLN	4.1
3	Q	203	THR	4.1
3	Q	236	GLN	4.1
13	M	1	THR	4.0
3	C	48	SER	3.9
1	A	250	LEU	3.9
5	S	233	ILE	3.8
3	Q	225	GLU	3.8
2	B	182	ASP	3.8
1	O	2	THR	3.7
6	T	241	LYS	3.7
5	E	233	ILE	3.7
6	F	202	ASP	3.7
9	I	1	SER	3.7
6	F	244	ASN	3.7
4	R	242	GLU	3.7
13	M	233	ILE	3.7
13	M	232	LYS	3.7
10	J	194	ASP	3.6
3	C	240	GLU	3.6
3	Q	175	LYS	3.6
11	Y	147	ASP	3.6
5	E	122	TYR	3.6

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Mol	Chain	Res	Type	RSRZ
7	G	2	GLY	3.5
1	A	2	THR	3.5
3	Q	205	ALA	3.5
3	C	236	GLN	3.5
4	R	125	LEU	3.5
2	P	52	THR	3.4
6	T	53	LYS	3.4
3	C	205	ALA	3.4
13	M	216	ASN	3.4
5	S	180	LYS	3.4
7	G	3	TYR	3.4
2	P	59	ASP	3.4
3	C	239	GLN	3.3
2	B	52	THR	3.3
1	O	201	GLU	3.2
4	D	241	ALA	3.2
3	Q	55	THR	3.2
14	b	105	LYS	3.2
13	M	47	ASP	3.2
6	T	205	GLU	3.1
1	A	249	ALA	3.1
3	C	50	LEU	3.1
7	G	179	LYS	3.1
2	B	222	GLY	3.1
10	X	193	ASP	3.1
1	O	250	LEU	3.1
3	Q	223	SER	3.1
1	O	52	SER	3.1
6	T	181	GLU	3.1
6	T	2	THR	3.1
11	Y	182	GLU	3.0
7	G	242	GLN	3.0
4	R	1	ASP	3.0
5	E	123	GLY	3.0
2	B	60	THR	2.9
4	D	125	LEU	2.9
2	P	225	TYR	2.9
14	b	195	GLN	2.9
2	P	182	ASP	2.9
3	C	37	LYS	2.9
6	F	2	THR	2.9
12	Z	1	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
2	P	203	SER	2.9
7	U	3	TYR	2.9
11	K	182	GLU	2.8
6	F	181	GLU	2.8
9	W	192	ASP	2.8
1	A	248	GLU	2.8
6	F	205	GLU	2.8
2	B	242	GLY	2.8
10	J	193	ASP	2.8
11	Y	202	GLU	2.7
13	M	230	THR	2.7
3	Q	180	LYS	2.7
6	F	201	GLU	2.7
5	S	3	ASN	2.7
2	P	60	THR	2.7
3	Q	234	ILE	2.7
7	U	242	GLN	2.7
6	F	241	LYS	2.7
5	S	201	ARG	2.7
7	G	241	GLU	2.7
1	A	51	SER	2.7
5	E	54	GLU	2.6
1	O	53	SER	2.6
2	P	62	THR	2.6
6	F	215	CYS	2.6
3	Q	202	GLN	2.6
3	Q	141	ASP	2.6
11	K	147	ASP	2.6
9	W	133	LYS	2.6
2	B	203	SER	2.6
3	Q	232	THR	2.6
6	T	204	LYS	2.6
3	C	175	LYS	2.6
12	Z	174	TYR	2.6
11	Y	106	ARG	2.6
4	R	226	GLU	2.6
2	B	50	LYS	2.6
5	S	173	ARG	2.6
11	K	211	ILE	2.5
6	T	215	CYS	2.5
3	C	235	GLU	2.5
7	G	181	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	O	203	GLU	2.5
12	Z	165	ASN	2.5
5	E	201	ARG	2.5
4	R	177	ASN	2.5
5	E	176	ASP	2.5
11	K	183	ASP	2.5
3	Q	60	SER	2.5
7	U	181	LYS	2.5
6	T	230	ASP	2.5
3	Q	27	ARG	2.4
7	U	2	GLY	2.4
5	E	180	LYS	2.4
2	P	223	GLU	2.4
8	V	145	ASP	2.4
2	B	3	ARG	2.4
3	C	232	THR	2.4
4	D	47	THR	2.4
6	F	53	LYS	2.4
5	S	52	ALA	2.4
2	B	61	SER	2.4
2	B	59	ASP	2.4
6	T	166	GLN	2.4
4	R	230	GLU	2.4
9	I	133	LYS	2.3
14	N	195	GLN	2.3
4	R	54	ASP	2.3
5	S	163	ARG	2.3
5	S	54	GLU	2.3
5	E	121	SER	2.3
7	G	208	GLU	2.3
7	U	206	GLY	2.3
2	B	180	LYS	2.3
6	F	203	ASN	2.3
3	C	203	THR	2.3
11	Y	181	THR	2.3
2	P	240	LYS	2.3
5	E	227	GLU	2.3
1	O	50	LYS	2.3
2	B	232	GLN	2.3
5	S	30	GLN	2.3
12	L	1	GLN	2.3
13	M	82	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
2	P	50	LYS	2.2
4	D	238	LYS	2.2
2	B	244	THR	2.2
5	E	217	LYS	2.2
7	U	188	GLU	2.2
5	S	204	SER	2.2
2	P	232	GLN	2.2
4	R	217	GLN	2.2
9	I	192	ASP	2.2
12	Z	106	TYR	2.1
4	R	169	GLU	2.1
7	U	51	PRO	2.1
5	E	173	ARG	2.1
5	S	122	TYR	2.1
6	T	244	ASN	2.1
11	Y	104	TYR	2.1
11	K	212	GLY	2.1
11	Y	39	PRO	2.1
6	F	230	ASP	2.1
2	B	217	LYS	2.1
11	K	145	LYS	2.1
7	U	178	LYS	2.1
13	a	216	ASN	2.1
1	O	182	GLU	2.1
3	C	181	GLU	2.1
4	R	2	ARG	2.1
12	L	174	TYR	2.1
14	N	105	LYS	2.1
8	V	219	ASN	2.1
3	C	204	GLY	2.1
3	Q	181	GLU	2.1
1	A	54	PRO	2.1
7	G	240	ALA	2.1
11	K	39	PRO	2.1
2	B	93	HIS	2.0
7	U	241	GLU	2.0
12	L	172	LEU	2.0
3	C	180	LYS	2.0
6	T	180	PRO	2.0
2	B	223	GLU	2.0
5	E	194	GLU	2.0
13	M	231	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	225	TYR	2.0
11	K	151	GLU	2.0
11	Y	183	ASP	2.0
3	Q	167	LYS	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	VOL	h	4	7/7	0.84	0.22	56,69,78,80	0
15	VOL	g	4	7/7	0.88	0.19	54,61,70,74	0
15	VOL	e	4	7/7	0.89	0.17	47,56,61,62	0
15	VOL	f	4	7/7	0.92	0.21	57,68,71,73	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
18	MES	H	302	12/12	0.61	0.33	78,113,132,136	0
16	MG	H	301	1/1	0.78	0.15	65,65,65,65	0
18	MES	K	302	12/12	0.81	0.37	87,91,93,96	0
18	MES	Y	301	12/12	0.86	0.32	84,89,96,98	0
16	MG	I	301	1/1	0.92	0.18	56,56,56,56	0
16	MG	I	302	1/1	0.94	0.07	49,49,49,49	0
16	MG	K	301	1/1	0.95	0.09	51,51,51,51	0
16	MG	N	201	1/1	0.95	0.09	45,45,45,45	0
16	MG	G	301	1/1	0.96	0.04	41,41,41,41	0
16	MG	Z	301	1/1	0.98	0.11	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
17	CL	U	301	1/1	0.99	0.13	30,30,30,30	0
16	MG	L	301	1/1	0.99	0.08	44,44,44,44	0
17	CL	G	302	1/1	0.99	0.13	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.