



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 6, 2023 – 07:56 am GMT

PDB ID : 4Y7Y
Title : Yeast 20S proteasome in complex with Ac-LAA-ep
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-02-16
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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

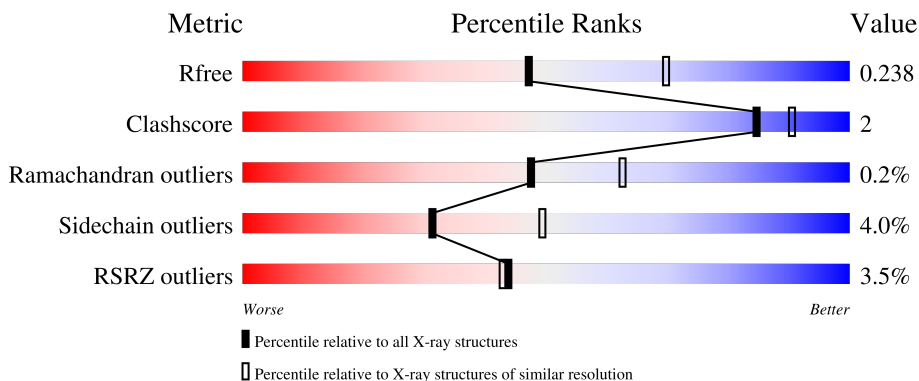
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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 style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 96%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 2%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 0%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 0%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">96% .</p>
1	O	250	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 95%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 0%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 0%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">95% 5%</p>
2	B	258	<div style="display: flex; align-items: center;"> <div style="width: 7%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 87%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 8%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 5%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 0%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">87% 8% 5%</p>
2	P	258	<div style="display: flex; align-items: center;"> <div style="width: 9%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 87%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 8%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 5%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 0%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">87% 8% 5%</p>
3	C	254	<div style="display: flex; align-items: center;"> <div style="width: 7%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 87%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 6%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 6%; height: 10px; background-color: orange; margin-right: 2px;"></div> <div style="width: 0%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">87% 6% • 6%</p>



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Mol	Chain	Length	Quality of chain
3	Q	254	9% 87% 6% • 6%
4	D	260	2% 85% 5% • 10%
4	R	260	3% 83% 7% • 10%
5	E	234	4% 90% 8% •
5	S	234	6% 90% 8% •
6	F	288	3% 80% 5% 16%
6	T	288	4% 80% 5% 16%
7	G	252	4% 90% 5% •
7	U	252	2% 90% 6% •
8	H	232	2% 88% 7% •
8	V	232	% 87% 9% •
9	I	205	% 92% 7% •
9	W	205	2% 93% 6% •
10	J	198	3% 86% 10% • • •
10	X	198	3% 86% 10% • • •
11	K	212	2% 85% 12% •
11	Y	212	2% 86% 10% •
12	L	222	2% 94% 6%
12	Z	222	% 93% 6% •
13	M	246	2% 89% 5% 5%
13	a	246	2% 92% • 5%
14	N	196	% 97% •
14	b	196	% 98% •
15	c	5	100%
15	d	5	100%

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Mol	Chain	Length	Quality of chain
15	e	5	 100%
15	f	5	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
18	MES	V	301	-	-	-	X

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 50481 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
			Total	C	N	O	S			
1	A	250	Total 1915	C 1219	N 315	O 377	S 4	0	0	0
1	O	250	Total 1915	C 1219	N 315	O 377	S 4	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	240	Total 1881	C 1176	N 329	O 372	S 4	0	0	0
3	Q	240	Total 1881	C 1176	N 329	O 372	S 4	0	0	0

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
8	H	222	Total 1684	C 1061	N 293	O 323	S 7	0	0	0
8	V	222	Total 1691	C 1066	N 295	O 323	S 7	0	1	0

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
9	I	204	Total 1581	C 1010	N 258	O 305	S 8	0	0	0
9	W	204	Total 1581	C 1010	N 258	O 305	S 8	0	0	0

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	222	1757	1115	303	335	4	0	0	0
12	Z	222	1764	1120	305	335	4	0	1	0

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

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

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

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

- Molecule 15 is a protein called Ac-LAA-ep.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
15	c	5	25	17	3	5	0	0	0
15	d	5	25	17	3	5	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	e	5	Total	C	N	O	0	0	0
			25	17	3	5			
15	f	5	Total	C	N	O	0	0	0
			25	17	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	I	2	Total	Mg	0	0
			2	2		
16	K	1	Total	Mg	0	0
			1	1		
16	L	1	Total	Mg	0	0
			1	1		
16	N	1	Total	Mg	0	0
			1	1		
16	Z	1	Total	Mg	0	0
			1	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	G	1	Total	Cl	0	0
			1	1		
17	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
			Total	C	N	O	S		
18	H	1	12	6	1	4	1	0	0
18	K	1	12	6	1	4	1	0	0
18	V	1	12	6	1	4	1	0	0
18	Y	1	12	6	1	4	1	0	0

- Molecule 19 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	A	51	Total	O	0	0
			51	51		
19	B	35	Total	O	0	0
			35	35		
19	C	36	Total	O	0	0
			36	36		
19	D	21	Total	O	0	0
			21	21		
19	E	18	Total	O	0	0
			18	18		
19	F	30	Total	O	0	0
			30	30		
19	G	45	Total	O	0	0
			45	45		
19	H	51	Total	O	0	0
			51	51		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	I	49	Total O 49 49	0	0
19	J	44	Total O 44 44	0	0
19	K	40	Total O 40 40	0	0
19	L	49	Total O 49 49	0	0
19	M	40	Total O 40 40	0	0
19	N	35	Total O 35 35	0	0
19	O	32	Total O 32 32	0	0
19	P	29	Total O 29 29	0	0
19	Q	18	Total O 18 18	0	0
19	R	25	Total O 25 25	0	0
19	S	14	Total O 14 14	0	0
19	T	31	Total O 31 31	0	0
19	U	52	Total O 52 52	0	0
19	V	29	Total O 29 29	0	0
19	W	32	Total O 32 32	0	0
19	X	27	Total O 27 27	0	0
19	Y	43	Total O 43 43	0	0
19	Z	43	Total O 43 43	0	0
19	a	54	Total O 54 54	0	0
19	b	38	Total O 38 38	0	0
19	e	1	Total O 1 1	0	0

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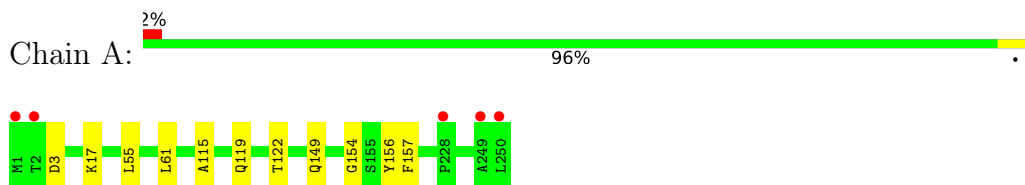
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
19	f	2	Total	O	0	0
			2	2		

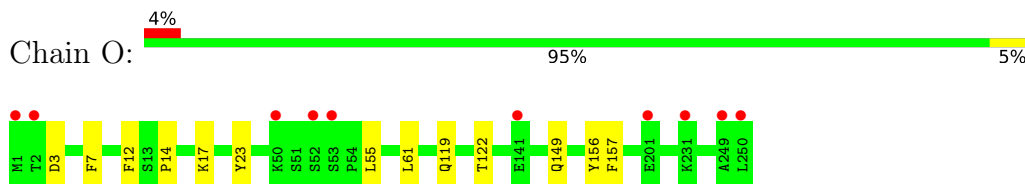
3 Residue-property plots [i](#)

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.

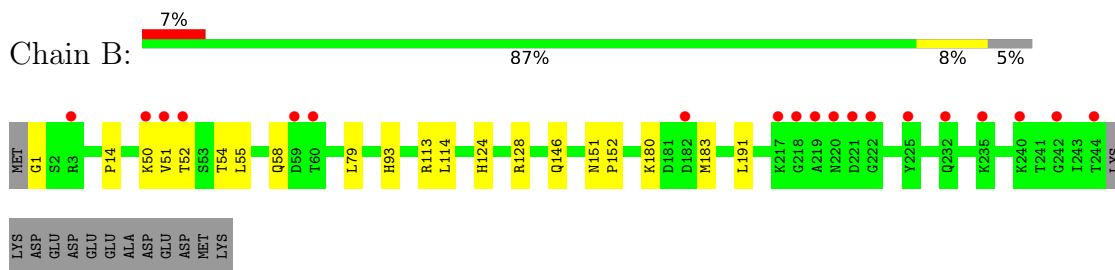
- Molecule 1: Proteasome subunit alpha type-2



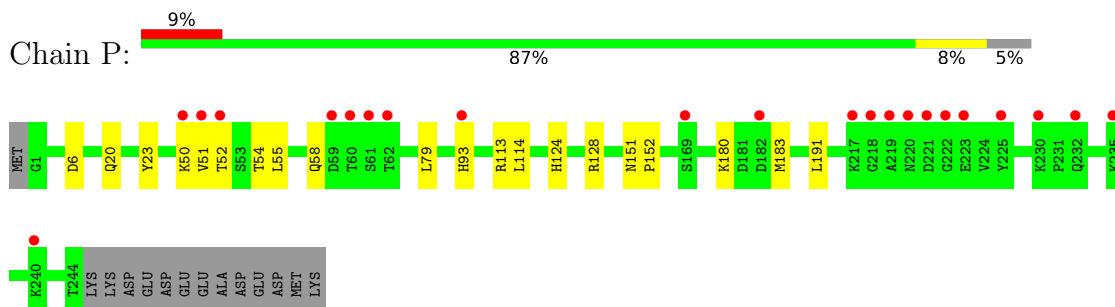
- Molecule 1: Proteasome subunit alpha type-2



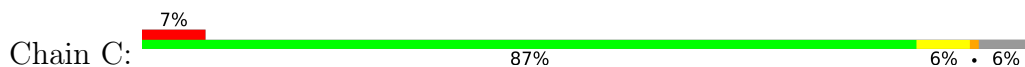
- Molecule 2: Proteasome subunit alpha type-3

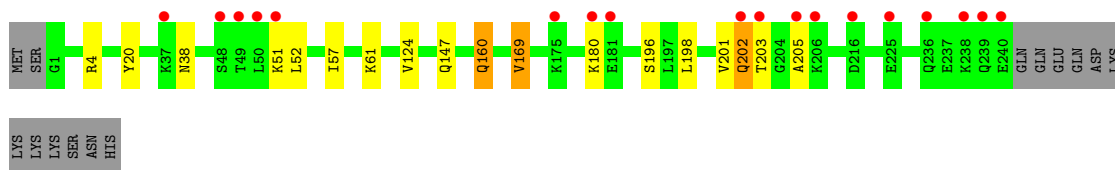


- Molecule 2: Proteasome subunit alpha type-3

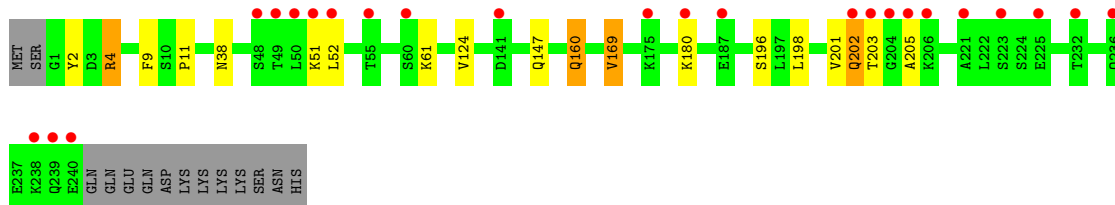
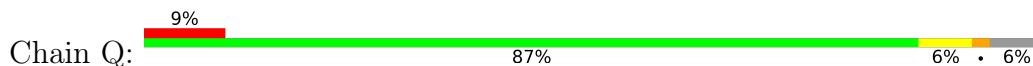


- Molecule 3: Proteasome subunit alpha type-4

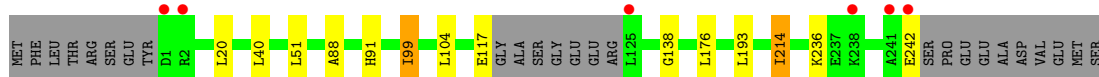
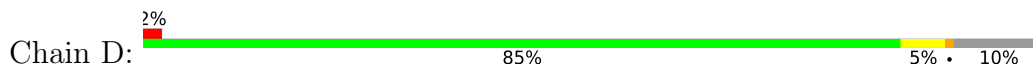




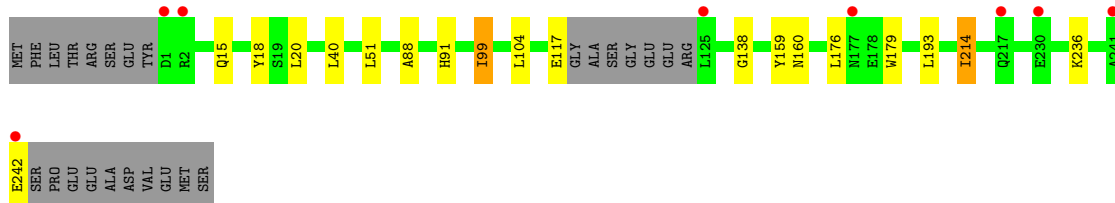
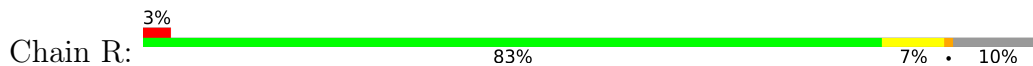
• Molecule 3: Proteasome subunit alpha type-4



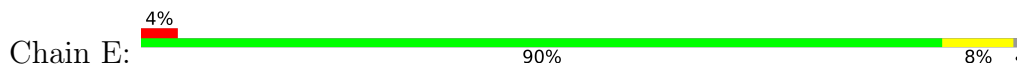
• Molecule 4: Proteasome subunit alpha type-5



• Molecule 4: Proteasome subunit alpha type-5



• Molecule 5: Proteasome subunit alpha type-6

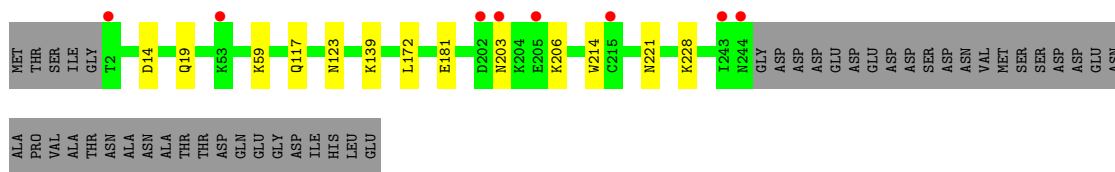
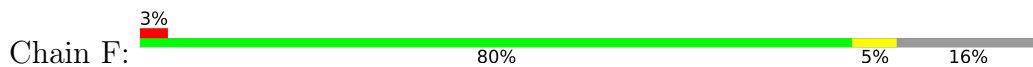


• Molecule 5: Proteasome subunit alpha type-6

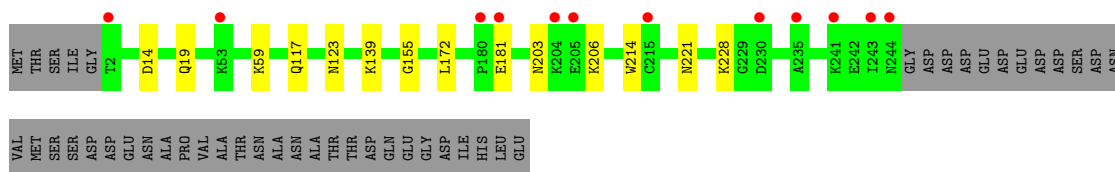
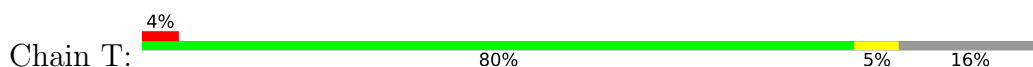




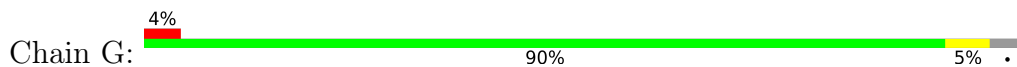
● Molecule 6: Probable proteasome subunit alpha type-7



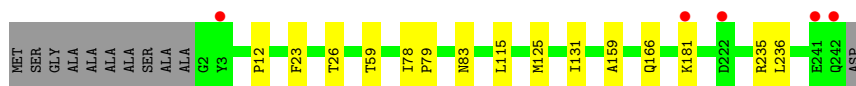
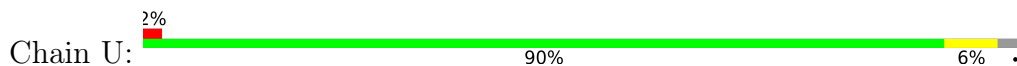
● Molecule 6: Probable proteasome subunit alpha type-7



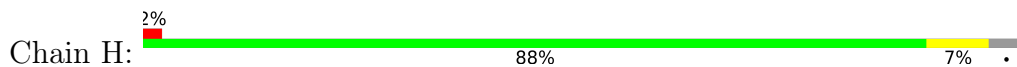
● Molecule 7: Proteasome subunit alpha type-1



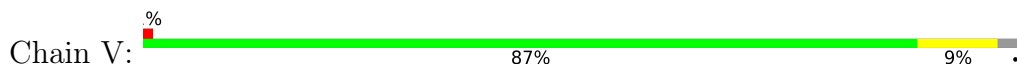
● Molecule 7: Proteasome subunit alpha type-1



● Molecule 8: Proteasome subunit beta type-2

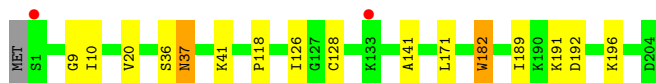
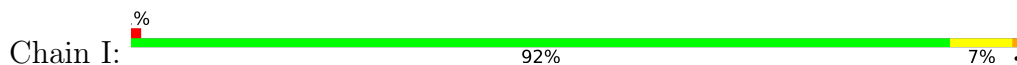


● Molecule 8: Proteasome subunit beta type-2

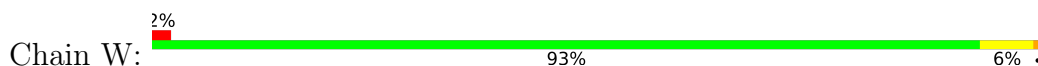




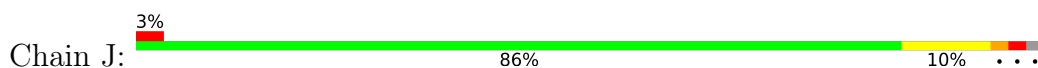
- Molecule 9: Proteasome subunit beta type-3



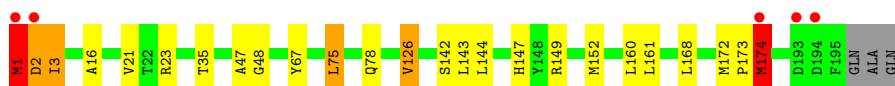
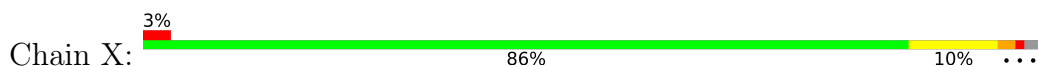
- Molecule 9: Proteasome subunit beta type-3



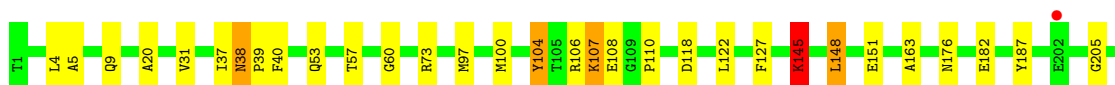
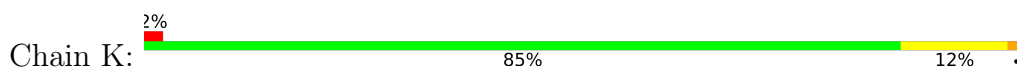
- Molecule 10: Proteasome subunit beta type-4



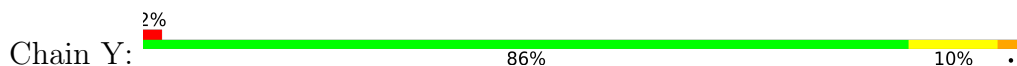
- Molecule 10: Proteasome subunit beta type-4

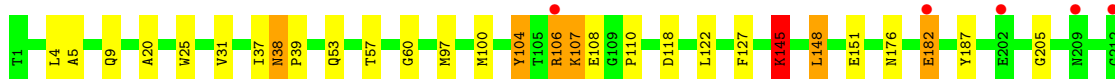


- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5

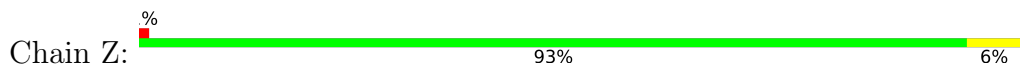




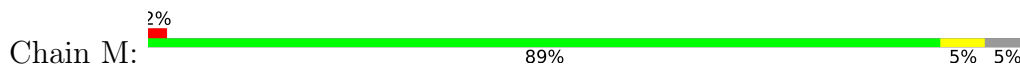
- Molecule 12: Proteasome subunit beta type-6



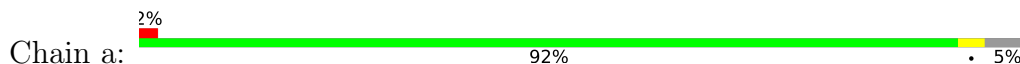
- Molecule 12: Proteasome subunit beta type-6



- Molecule 13: Proteasome subunit beta type-7



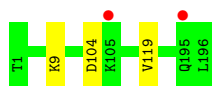
- Molecule 13: Proteasome subunit beta type-7



- Molecule 14: Proteasome subunit beta type-1



- Molecule 14: Proteasome subunit beta type-1



- Molecule 15: Ac-LAA-ep

Chain c:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: Ac-LAA-ep

Chain d:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: Ac-LAA-ep

Chain e:  100%

There are no outlier residues recorded for this chain.

- Molecule 15: Ac-LAA-ep

Chain f:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	136.68Å 299.82Å 144.75Å 90.00° 113.07° 90.00°	Depositor
Resolution (Å)	15.00 – 2.40 15.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.5 (15.00-2.40) 98.5 (15.00-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.212 , 0.235 0.215 , 0.238	Depositor DCC
R_{free} test set	20390 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtrriage
Anisotropy	0.101	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	50481	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.11% 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: ACE, CL, MG, MES, 2A1, POL

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	0.27	0/1952	0.48	0/2642
2	B	0.28	0/1934	0.51	0/2618
2	P	0.28	0/1934	0.50	0/2618
3	C	0.28	0/1910	0.52	0/2586
3	Q	0.28	0/1910	0.51	0/2586
4	D	0.27	0/1837	0.49	0/2475
4	R	0.27	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	0.48	0/2634
7	U	0.28	0/1945	0.48	0/2634
8	H	0.26	0/1715	0.50	0/2326
8	V	0.28	0/1726	0.49	0/2341
9	I	0.28	0/1611	0.49	0/2174
9	W	0.28	0/1611	0.49	0/2174
10	J	0.38	1/1589 (0.1%)	0.68	6/2142 (0.3%)
10	X	0.36	1/1589 (0.1%)	0.74	5/2142 (0.2%)
11	K	0.35	0/1681	0.63	2/2274 (0.1%)
11	Y	0.31	0/1681	0.76	4/2274 (0.2%)
12	L	0.28	0/1795	0.49	0/2420
12	Z	0.37	2/1806 (0.1%)	0.55	2/2435 (0.1%)
13	M	0.28	0/1855	0.52	0/2514
13	a	0.28	0/1855	0.52	0/2514
14	N	0.26	0/1541	0.48	0/2087
14	b	0.29	0/1541	0.48	0/2087
15	c	0.36	0/13	1.25	0/17
15	d	0.27	0/13	1.24	0/17
15	e	0.37	0/13	1.24	0/17
15	f	0.28	0/13	1.24	0/17

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.29	4/50268 (0.0%)	0.53	19/67966 (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
10	X	0	1
11	Y	0	1
12	Z	0	2
All	All	0	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	Z	108[A]	HIS	CA-C	6.56	1.70	1.52
12	Z	108[B]	HIS	CA-C	6.56	1.70	1.52
10	X	2	ASP	N-CA	-6.46	1.33	1.46
10	J	2	ASP	N-CA	-5.96	1.34	1.46

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Y	106	ARG	NE-CZ-NH2	-15.31	112.65	120.30
10	X	174	MET	CA-CB-CG	14.29	137.59	113.30
11	Y	145	LYS	CD-CE-NZ	13.20	142.06	111.70
10	J	174	MET	CA-CB-CG	12.16	133.98	113.30
11	K	145	LYS	CD-CE-NZ	11.19	137.43	111.70
10	X	1	MET	CG-SD-CE	-10.95	82.68	100.20
11	Y	106	ARG	NE-CZ-NH1	9.44	125.02	120.30
10	X	174	MET	CG-SD-CE	-8.77	86.18	100.20
11	Y	106	ARG	CD-NE-CZ	6.70	132.98	123.60
10	J	2	ASP	N-CA-CB	-6.64	98.65	110.60
11	K	97	MET	CB-CG-SD	-6.21	93.78	112.40
10	J	1	MET	CG-SD-CE	-6.02	90.57	100.20
10	J	1	MET	C-N-CA	-5.88	107.00	121.70
10	J	174	MET	CG-SD-CE	-5.57	91.29	100.20
10	X	1	MET	C-N-CA	-5.52	107.91	121.70
12	Z	108[A]	HIS	CA-C-N	-5.44	105.23	117.20
12	Z	108[B]	HIS	CA-C-N	-5.44	105.23	117.20
10	J	1	MET	CA-CB-CG	-5.09	104.65	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	X	174	MET	N-CA-CB	5.06	119.70	110.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	X	1	MET	Peptide
11	Y	106	ARG	Sidechain
12	Z	108[A]	HIS	Mainchain
12	Z	108[B]	HIS	Mainchain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	5	0
1	O	1915	0	1929	8	0
2	B	1904	0	1904	10	0
2	P	1904	0	1904	9	0
3	C	1881	0	1895	11	0
3	Q	1881	0	1895	12	0
4	D	1813	0	1797	4	0
4	R	1813	0	1797	8	0
5	E	1773	0	1775	6	0
5	S	1773	0	1775	6	0
6	F	1892	0	1883	2	0
6	T	1892	0	1883	4	0
7	G	1907	0	1901	4	0
7	U	1907	0	1901	6	0
8	H	1684	0	1685	8	0
8	V	1691	0	1692	9	0
9	I	1581	0	1574	10	0
9	W	1581	0	1574	8	0
10	J	1561	0	1569	38	0
10	X	1561	0	1569	35	0
11	K	1644	0	1592	24	0
11	Y	1644	0	1592	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L	1757	0	1711	4	0
12	Z	1764	0	1718	5	0
13	M	1824	0	1832	4	0
13	a	1824	0	1832	0	0
14	N	1512	0	1481	1	0
14	b	1512	0	1481	0	0
15	c	25	0	25	0	0
15	d	25	0	25	0	0
15	e	25	0	25	0	0
15	f	25	0	25	0	0
16	G	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	V	12	0	13	1	0
18	Y	12	0	13	0	0
19	A	51	0	0	0	0
19	B	35	0	0	0	0
19	C	36	0	0	0	0
19	D	21	0	0	0	0
19	E	18	0	0	0	0
19	F	30	0	0	0	0
19	G	45	0	0	0	0
19	H	51	0	0	0	0
19	I	49	0	0	0	0
19	J	44	0	0	1	0
19	K	40	0	0	1	0
19	L	49	0	0	0	0
19	M	40	0	0	0	0
19	N	35	0	0	0	0
19	O	32	0	0	0	0
19	P	29	0	0	0	0
19	Q	18	0	0	0	0
19	R	25	0	0	0	0
19	S	14	0	0	0	0
19	T	31	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	U	52	0	0	0	0
19	V	29	0	0	0	0
19	W	32	0	0	0	0
19	X	27	0	0	0	0
19	Y	43	0	0	0	0
19	Z	43	0	0	0	0
19	a	54	0	0	0	0
19	b	38	0	0	0	0
19	e	1	0	0	0	0
19	f	2	0	0	0	0
All	All	50481	0	49222	217	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 (217) 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)
10:J:1:MET:SD	10:J:47:ALA:HB1	1.50	1.50
10:J:1:MET:CE	10:J:47:ALA:HB1	1.54	1.38
10:J:1:MET:CE	10:J:47:ALA:CB	2.07	1.31
10:X:1:MET:O	10:X:2:ASP:CG	1.75	1.25
10:J:1:MET:SD	10:J:47:ALA:CB	2.33	1.17
10:J:1:MET:HE3	10:J:47:ALA:HA	1.15	1.14
10:J:174:MET:HE2	10:J:174:MET:N	1.63	1.12
10:X:174:MET:HE2	10:X:174:MET:N	1.65	1.11
10:J:1:MET:HE3	10:J:47:ALA:CA	1.79	1.10
10:X:1:MET:C	10:X:2:ASP:CG	2.08	1.10
11:K:182:GLU:OE2	19:K:401:HOH:O	1.69	1.08
10:J:1:MET:HE1	10:J:47:ALA:CB	1.83	1.01
10:X:1:MET:CA	10:X:2:ASP:OD2	2.10	1.00
10:X:174:MET:N	10:X:174:MET:CE	2.28	0.97
10:J:1:MET:CE	10:J:47:ALA:CA	2.39	0.96
10:X:1:MET:C	10:X:2:ASP:OD2	2.05	0.94
10:J:174:MET:N	10:J:174:MET:CE	2.31	0.93
10:X:1:MET:N	10:X:2:ASP:OD2	2.03	0.91
10:J:1:MET:N	10:J:2:ASP:OD2	1.93	0.89
11:K:73:ARG:NH2	11:K:104:TYR:O	2.06	0.88
10:J:1:MET:SD	10:J:48:GLY:N	2.47	0.87
11:K:40:PHE:CD1	11:K:73:ARG:NH1	2.44	0.86
10:X:1:MET:O	10:X:2:ASP:OD1	1.93	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:1:MET:CE	10:J:47:ALA:HA	2.02	0.82
10:J:1:MET:HE1	10:J:47:ALA:HB2	1.63	0.81
10:X:174:MET:CE	10:X:174:MET:H	1.91	0.80
10:J:1:MET:SD	10:J:47:ALA:C	2.60	0.80
10:J:1:MET:HE1	10:J:47:ALA:HB1	1.47	0.78
8:H:50:ALA:HB3	9:I:126:ILE:HD12	1.70	0.73
11:Y:145:LYS:HG3	11:Y:148:LEU:HD13	1.70	0.72
12:Z:13:LEU:HD13	12:Z:150:LEU:HD21	1.73	0.70
12:L:13:LEU:HD13	12:L:150:LEU:HD21	1.73	0.70
4:D:99:ILE:HD11	4:D:104:LEU:HB2	1.75	0.69
10:J:1:MET:SD	10:J:47:ALA:CA	2.80	0.68
11:K:100:MET:HE3	11:K:127:PHE:HB2	1.74	0.68
4:R:99:ILE:HD11	4:R:104:LEU:HB2	1.74	0.68
8:V:114[B]:HIS:CD2	8:V:116:HIS:H	2.13	0.67
8:V:50:ALA:HB3	9:W:126:ILE:HD12	1.77	0.66
11:Y:100:MET:HE3	11:Y:127:PHE:HB2	1.80	0.64
10:J:1:MET:HB3	19:J:229:HOH:O	1.98	0.64
10:J:174:MET:HE2	10:J:174:MET:CA	2.23	0.64
10:J:149:ARG:NH1	11:Y:205:GLY:O	2.31	0.63
10:J:149:ARG:HH12	11:Y:205:GLY:C	2.01	0.63
11:K:205:GLY:C	10:X:149:ARG:HH12	2.01	0.62
10:J:173:PRO:C	10:J:174:MET:HE2	2.19	0.62
10:X:174:MET:CE	10:X:174:MET:CA	2.77	0.62
11:Y:5:ALA:HB3	11:Y:100:MET:HE2	1.82	0.61
11:K:205:GLY:O	10:X:149:ARG:NH1	2.33	0.60
10:J:174:MET:CE	10:J:174:MET:CA	2.67	0.60
10:X:1:MET:O	10:X:2:ASP:OD2	2.10	0.60
10:X:174:MET:N	10:X:174:MET:HE3	2.14	0.60
10:X:174:MET:H	10:X:174:MET:HE3	1.65	0.59
11:K:145:LYS:HG3	11:K:148:LEU:HD13	1.85	0.58
11:K:106:ARG:HD3	11:K:182:GLU:OE2	2.04	0.58
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.85	0.57
11:K:38:ASN:CB	11:K:39:PRO:CD	2.81	0.57
8:V:114[B]:HIS:HD2	8:V:116:HIS:H	1.51	0.57
11:Y:38:ASN:CB	11:Y:39:PRO:CD	2.81	0.57
10:J:174:MET:CE	10:J:174:MET:H	2.15	0.57
11:Y:107:LYS:HG3	11:Y:108:GLU:HG3	1.88	0.56
7:G:23:PHE:O	7:G:26:THR:HB	2.05	0.56
7:U:23:PHE:O	7:U:26:THR:HB	2.05	0.56
11:Y:104:TYR:CZ	11:Y:110:PRO:HD3	2.41	0.56
3:Q:160:GLN:HA	3:Q:160:GLN:HE21	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.06	0.56
2:B:124:HIS:HB3	3:C:124:VAL:HG12	1.88	0.56
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.71	0.56
11:K:107:LYS:HG3	11:K:108:GLU:HG3	1.87	0.56
11:K:5:ALA:HB3	11:K:100:MET:HE2	1.88	0.56
11:K:104:TYR:CZ	11:K:110:PRO:HD3	2.41	0.56
3:C:51:LYS:O	3:C:52:LEU:HB2	2.06	0.55
10:J:21:VAL:HG11	11:K:122:LEU:HD11	1.89	0.55
11:K:100:MET:CE	11:K:127:PHE:HB2	2.37	0.54
8:V:47:GLY:HA2	18:V:301:MES:H81	1.89	0.54
11:Y:100:MET:CE	11:Y:127:PHE:HB2	2.37	0.54
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.90	0.53
5:S:12:PHE:H	6:T:19:GLN:HE22	1.56	0.53
6:T:19:GLN:NE2	19:T:301:HOH:O	2.41	0.53
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.91	0.53
10:J:149:ARG:NH1	11:Y:205:GLY:C	2.62	0.53
14:N:152:VAL:HA	14:N:175:MET:HE1	1.91	0.53
10:X:174:MET:CA	10:X:174:MET:HE3	2.39	0.52
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.75	0.52
10:J:173:PRO:O	10:X:174:MET:HB2	2.10	0.52
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.92	0.52
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.92	0.52
11:Y:145:LYS:HG3	11:Y:148:LEU:CD1	2.39	0.52
5:E:12:PHE:H	6:F:19:GLN:HE22	1.57	0.51
11:K:38:ASN:HB2	11:K:39:PRO:CD	2.40	0.51
11:K:205:GLY:C	10:X:149:ARG:NH1	2.64	0.51
10:X:173:PRO:C	10:X:174:MET:HE2	2.28	0.51
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.75	0.50
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.94	0.50
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.94	0.50
1:A:55:LEU:HD12	7:G:170:THR:HG23	1.93	0.50
10:J:1:MET:CG	10:J:48:GLY:N	2.75	0.50
9:I:37:ASN:HB3	9:I:182:TRP:CE3	2.47	0.49
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.94	0.49
9:W:37:ASN:HB3	9:W:182:TRP:CE3	2.47	0.49
3:C:201:VAL:O	3:C:202:GLN:CB	2.61	0.49
2:B:146:GLN:HG2	3:C:57:ILE:HG21	1.93	0.49
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.94	0.49
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.94	0.49
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.61	0.49
8:H:52:THR:O	8:H:56:THR:HB	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:1:MET:SD	10:X:48:GLY:N	2.87	0.48
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.94	0.48
3:C:201:VAL:HG13	3:C:202:GLN:N	2.29	0.48
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.96	0.48
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.96	0.48
11:K:37:ILE:HG23	11:K:60:GLY:HA2	1.96	0.48
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.14	0.48
11:Y:37:ILE:HG23	11:Y:60:GLY:HA2	1.96	0.47
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.29	0.47
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	1.96	0.47
1:O:55:LEU:HB3	7:U:159:ALA:O	2.14	0.47
6:T:155:GLY:HA3	7:U:59:THR:HG21	1.97	0.47
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.96	0.47
8:H:218:VAL:CG2	9:I:196:LYS:HB2	2.45	0.47
3:Q:201:VAL:O	3:Q:202:GLN:HB2	2.14	0.47
10:X:1:MET:CG	10:X:48:GLY:N	2.77	0.47
12:L:8:ASN:HA	12:L:30:ILE:O	2.14	0.47
8:V:52:THR:O	8:V:56:THR:HB	2.14	0.47
3:C:201:VAL:O	3:C:202:GLN:HB2	2.14	0.47
1:O:7:PHE:HB3	3:Q:2:TYR:CE1	2.49	0.47
10:J:174:MET:HA	10:X:174:MET:HA	1.96	0.47
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.49	0.46
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	1.98	0.46
5:E:9:THR:HG21	5:E:119:THR:HA	1.97	0.46
5:S:9:THR:HG21	5:S:119:THR:HA	1.98	0.46
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.52	0.45
9:W:20:VAL:HG23	9:W:189:ILE:HB	1.98	0.45
11:K:176:ASN:ND2	11:K:187:TYR:OH	2.49	0.45
4:R:88:ALA:HA	4:R:99:ILE:HG21	1.98	0.45
9:W:36:SER:CB	10:X:126:VAL:HG11	2.47	0.45
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.51	0.45
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.31	0.45
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.98	0.45
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.46	0.45
2:P:93:HIS:HB3	2:P:113:ARG:HH21	1.81	0.45
11:Y:176:ASN:ND2	11:Y:187:TYR:OH	2.49	0.45
1:A:149:GLN:O	1:A:156:TYR:HA	2.17	0.45
1:O:14:PRO:HA	2:P:23:TYR:CD1	2.52	0.45
2:B:93:HIS:HB3	2:B:113:ARG:HH21	1.81	0.45
12:L:147:MET:N	12:L:148:PRO:HD2	2.32	0.45
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.52	0.45
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.99	0.44
1:O:119:GLN:O	1:O:122:THR:HB	2.17	0.44
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.99	0.44
10:J:174:MET:N	10:J:174:MET:HE3	2.24	0.44
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.53	0.44
9:I:20:VAL:HG23	9:I:189:ILE:HB	1.98	0.44
1:O:149:GLN:O	1:O:156:TYR:HA	2.17	0.44
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.47	0.44
1:A:119:GLN:O	1:A:122:THR:HB	2.17	0.44
2:B:14:PRO:HA	3:C:20:TYR:CD1	2.53	0.44
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.53	0.44
8:H:50:ALA:CB	9:I:126:ILE:HD12	2.45	0.44
6:T:228:LYS:HB2	6:T:228:LYS:HE3	1.79	0.44
9:W:36:SER:HB2	10:X:126:VAL:HG11	2.00	0.43
1:O:12:PHE:H	2:P:20:GLN:HE22	1.67	0.43
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.99	0.43
7:U:26:THR:HG21	7:U:131:ILE:HD12	2.01	0.43
11:Y:53:GLN:O	11:Y:57:THR:HG23	2.18	0.43
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.49	0.43
10:X:168:LEU:O	10:X:172:MET:HB2	2.18	0.43
3:C:198:LEU:HA	3:C:201:VAL:HG12	2.01	0.43
11:K:38:ASN:HB2	11:K:39:PRO:HD2	2.01	0.43
13:M:127:LEU:HG	13:M:142:LEU:HD12	2.01	0.43
3:Q:198:LEU:HA	3:Q:201:VAL:HG12	2.01	0.43
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.48	0.42
10:X:1:MET:HA	10:X:2:ASP:OD2	2.13	0.42
10:X:1:MET:SD	10:X:47:ALA:C	2.97	0.42
10:J:147:HIS:HB2	10:J:160:LEU:HD11	2.02	0.42
11:K:53:GLN:O	11:K:57:THR:HG23	2.19	0.42
2:B:1:GLY:HA3	5:E:122:TYR:CD1	2.54	0.42
2:P:6:ASP:OD2	3:Q:4:ARG:HG3	2.20	0.42
7:G:26:THR:HG21	7:G:131:ILE:HD12	2.01	0.42
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.42
1:A:115:ALA:HB1	1:A:154:GLY:O	2.20	0.42
8:H:50:ALA:HB2	9:I:128:CYS:HB2	2.02	0.42
10:J:149:ARG:HB2	10:J:152:MET:HG3	2.02	0.42
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.42
11:K:106:ARG:HD2	11:K:106:ARG:HA	1.79	0.42
12:L:195:HIS:HD2	12:L:197:GLN:H	1.68	0.42
10:J:1:MET:HG3	10:J:48:GLY:CA	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:2:ASP:O	10:X:3:ILE:C	2.58	0.41
10:X:149:ARG:HB2	10:X:152:MET:HG3	2.02	0.41
12:Z:195:HIS:HD2	12:Z:197:GLN:H	1.68	0.41
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.68	0.41
2:B:14:PRO:HA	3:C:20:TYR:CE1	2.53	0.41
9:I:36:SER:CB	10:J:126:VAL:HG11	2.50	0.41
5:S:131:LEU:HB2	5:S:146:PHE:HB3	2.02	0.41
10:J:143:LEU:HD21	10:J:163:LEU:HB3	2.03	0.41
10:J:168:LEU:O	10:J:172:MET:HB2	2.20	0.41
13:M:43:ILE:HA	13:M:44:PRO:HD3	1.97	0.41
8:V:1:THR:CG2	8:V:3:ILE:HG23	2.51	0.41
10:X:147:HIS:HB2	10:X:160:LEU:HD11	2.02	0.41
8:H:1:THR:CG2	8:H:3:ILE:HG23	2.50	0.41
11:K:163:ALA:HB1	10:X:142:SER:HB2	2.02	0.41
4:R:138:GLY:HA2	4:R:214:ILE:HG12	2.02	0.41
6:F:228:LYS:HE3	6:F:228:LYS:HB2	1.78	0.41
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.56	0.41
13:M:96:LEU:O	13:M:100:MET:HG2	2.21	0.41
4:D:138:GLY:HA2	4:D:214:ILE:HG12	2.02	0.41
8:H:84:LYS:HG3	8:H:85:GLN:N	2.36	0.41
5:E:131:LEU:HB2	5:E:146:PHE:HB3	2.02	0.41
11:K:5:ALA:HB3	11:K:100:MET:CE	2.50	0.40
13:M:228:TYR:HA	8:V:121:VAL:HG23	2.02	0.40
8:V:84:LYS:HG3	8:V:85:GLN:N	2.36	0.40
11:Y:25:TRP:CH2	12:Z:144:SER:HA	2.56	0.40
2:B:180:LYS:O	2:B:183:MET:HB2	2.21	0.40
2:P:180:LYS:O	2:P:183:MET:HB2	2.21	0.40
3:Q:11:PRO:HA	4:R:18:TYR:CD1	2.57	0.40
10:X:173:PRO:HB2	10:X:174:MET:HE2	2.04	0.40
11:Y:182:GLU:H	11:Y:182:GLU:HG3	1.62	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%)	5 (2%)	1 (0%)	34	48
1	O	248/250 (99%)	242 (98%)	5 (2%)	1 (0%)	34	48
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%)	230 (97%)	6 (2%)	2 (1%)	19	29
3	Q	238/254 (94%)	230 (97%)	6 (2%)	2 (1%)	19	29
4	D	231/260 (89%)	227 (98%)	4 (2%)	0	100	100
4	R	231/260 (89%)	227 (98%)	4 (2%)	0	100	100
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%)	233 (97%)	8 (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%)	216 (98%)	4 (2%)	0	100	100
8	V	221/232 (95%)	217 (98%)	4 (2%)	0	100	100
9	I	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
9	W	202/205 (98%)	195 (96%)	7 (4%)	0	100	100
10	J	193/198 (98%)	187 (97%)	4 (2%)	2 (1%)	15	23
10	X	193/198 (98%)	187 (97%)	5 (3%)	1 (0%)	29	41
11	K	210/212 (99%)	205 (98%)	5 (2%)	0	100	100
11	Y	210/212 (99%)	205 (98%)	5 (2%)	0	100	100
12	L	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
12	Z	221/222 (100%)	217 (98%)	4 (2%)	0	100	100
13	M	231/246 (94%)	225 (97%)	6 (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	c	2/5 (40%)	2 (100%)	0	0	100	100
15	d	2/5 (40%)	2 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	e	2/5 (40%)	2 (100%)	0	0	100	100
15	f	2/5 (40%)	2 (100%)	0	0	100	100
All	All	6286/6634 (95%)	6124 (97%)	151 (2%)	11 (0%)	47	62

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
10	J	2	ASP
10	J	3	ILE
2	P	51	VAL
3	Q	202	GLN
10	X	3	ILE
3	C	205	ALA
3	Q	205	ALA
1	A	3	ASP
1	O	3	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	206 (99%)	3 (1%)	67	82
1	O	209/209 (100%)	206 (99%)	3 (1%)	67	82
2	B	203/216 (94%)	195 (96%)	8 (4%)	32	50
2	P	203/216 (94%)	195 (96%)	8 (4%)	32	50
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%)	184 (95%)	10 (5%)	23	38
4	R	194/215 (90%)	184 (95%)	10 (5%)	23	38
5	E	190/193 (98%)	179 (94%)	11 (6%)	20	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	S	190/193 (98%)	179 (94%)	11 (6%)	20	32
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%)	199 (97%)	7 (3%)	37	56
7	U	206/210 (98%)	199 (97%)	7 (3%)	37	56
8	H	181/190 (95%)	173 (96%)	8 (4%)	28	45
8	V	182/190 (96%)	173 (95%)	9 (5%)	25	40
9	I	172/173 (99%)	167 (97%)	5 (3%)	42	62
9	W	172/173 (99%)	167 (97%)	5 (3%)	42	62
10	J	173/175 (99%)	164 (95%)	9 (5%)	23	38
10	X	173/175 (99%)	164 (95%)	9 (5%)	23	38
11	K	169/169 (100%)	160 (95%)	9 (5%)	22	37
11	Y	169/169 (100%)	158 (94%)	11 (6%)	17	27
12	L	185/185 (100%)	178 (96%)	7 (4%)	33	51
12	Z	186/185 (100%)	179 (96%)	7 (4%)	33	51
13	M	199/208 (96%)	192 (96%)	7 (4%)	36	55
13	a	199/208 (96%)	192 (96%)	7 (4%)	36	55
14	N	162/162 (100%)	159 (98%)	3 (2%)	57	75
14	b	162/162 (100%)	159 (98%)	3 (2%)	57	75
15	c	1/1 (100%)	1 (100%)	0	100	100
15	d	1/1 (100%)	1 (100%)	0	100	100
15	e	1/1 (100%)	1 (100%)	0	100	100
15	f	1/1 (100%)	1 (100%)	0	100	100
All	All	5318/5544 (96%)	5103 (96%)	215 (4%)	31	49

All (215) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	61	LEU
1	A	157	PHE
2	B	50	LYS
2	B	52	THR
2	B	54	THR

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Mol	Chain	Res	Type
2	B	55	LEU
2	B	58	GLN
2	B	79	LEU
2	B	114	LEU
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	117	GLU
4	D	176	LEU
4	D	193	LEU
4	D	214	ILE
4	D	236	LYS
4	D	242	GLU
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	184	ASN
5	E	188	LEU
5	E	207	VAL
5	E	231	LYS
6	F	14	ASP
6	F	59	LYS
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	172	LEU
6	F	181	GLU
6	F	203	ASN

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Mol	Chain	Res	Type
6	F	206	LYS
6	F	214	TRP
6	F	221	ASN
7	G	83	ASN
7	G	115	LEU
7	G	125	MET
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
7	G	236	LEU
8	H	30	ASN
8	H	31	CYS
8	H	34	LEU
8	H	43	CYS
8	H	56	THR
8	H	68	LEU
8	H	127	LEU
8	H	196	ARG
9	I	37	ASN
9	I	171	LEU
9	I	182	TRP
9	I	191	LYS
9	I	192	ASP
10	J	1	MET
10	J	23	ARG
10	J	35	THR
10	J	75	LEU
10	J	78	GLN
10	J	126	VAL
10	J	143	LEU
10	J	144	LEU
10	J	174	MET
11	K	4	LEU
11	K	9	GLN
11	K	38	ASN
11	K	104	TYR
11	K	107	LYS
11	K	118	ASP
11	K	145	LYS
11	K	148	LEU
11	K	151	GLU
12	L	1	GLN

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Mol	Chain	Res	Type
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	223	LYS
14	N	9	LYS
14	N	104	ASP
14	N	119	VAL
1	O	17	LYS
1	O	61	LEU
1	O	157	PHE
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	114	LEU
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	117	GLU
4	R	176	LEU
4	R	193	LEU

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Mol	Chain	Res	Type
4	R	214	ILE
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	10	VAL
5	S	25	LEU
5	S	29	LYS
5	S	54	GLU
5	S	55	LEU
5	S	71	LEU
5	S	184	ASN
5	S	188	LEU
5	S	207	VAL
5	S	231	LYS
6	T	14	ASP
6	T	59	LYS
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	172	LEU
6	T	181	GLU
6	T	203	ASN
6	T	206	LYS
6	T	214	TRP
6	T	221	ASN
7	U	83	ASN
7	U	115	LEU
7	U	125	MET
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
7	U	236	LEU
8	V	30	ASN
8	V	31	CYS
8	V	34	LEU
8	V	43	CYS
8	V	56	THR
8	V	57	GLN
8	V	68	LEU
8	V	127	LEU
8	V	196	ARG
9	W	37	ASN

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Mol	Chain	Res	Type
9	W	171	LEU
9	W	182	TRP
9	W	191	LYS
9	W	192	ASP
10	X	1	MET
10	X	23	ARG
10	X	35	THR
10	X	75	LEU
10	X	78	GLN
10	X	126	VAL
10	X	143	LEU
10	X	144	LEU
10	X	174	MET
11	Y	4	LEU
11	Y	9	GLN
11	Y	38	ASN
11	Y	97	MET
11	Y	104	TYR
11	Y	107	LYS
11	Y	118	ASP
11	Y	145	LYS
11	Y	148	LEU
11	Y	151	GLU
11	Y	182	GLU
12	Z	1	GLN
12	Z	23	LEU
12	Z	49	ASN
12	Z	106	TYR
12	Z	136	CYS
12	Z	150	LEU
12	Z	167	LYS
13	a	43	ILE
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
13	a	223	LYS
14	b	9	LYS
14	b	104	ASP
14	b	119	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (101)

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
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	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	191	GLN
6	F	240	GLN
7	G	6	HIS
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	167	GLN
8	H	57	GLN
8	H	66	HIS
10	J	55	GLN
10	J	146	HIS
10	J	147	HIS
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
12	L	3	ASN

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Mol	Chain	Res	Type
12	L	49	ASN
12	L	70	ASN
12	L	158	ASN
13	M	18	ASN
13	M	48	ASN
13	M	102	GLN
13	M	179	ASN
13	M	194	ASN
13	M	213	GLN
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	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	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	116	GLN
5	S	120	GLN
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	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	167	GLN
8	V	116	HIS

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Mol	Chain	Res	Type
10	X	55	GLN
10	X	86	GLN
10	X	146	HIS
10	X	147	HIS
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	179	ASN
13	a	194	ASN
13	a	213	GLN
14	b	161	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 9 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	MES	V	301	-	12,12,12	2.31	1 (8%)	14,16,16	1.18	2 (14%)
18	MES	H	301	-	12,12,12	2.24	1 (8%)	14,16,16	1.30	3 (21%)
18	MES	K	302	-	12,12,12	2.39	1 (8%)	14,16,16	1.33	2 (14%)
18	MES	Y	301	-	12,12,12	2.36	1 (8%)	14,16,16	1.29	2 (14%)

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	V	301	-	-	5/6/14/14	0/1/1/1
18	MES	H	301	-	-	0/6/14/14	0/1/1/1
18	MES	K	302	-	-	0/6/14/14	0/1/1/1
18	MES	Y	301	-	-	0/6/14/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	K	302	MES	C8-S	-8.01	1.66	1.77
18	Y	301	MES	C8-S	-7.92	1.66	1.77
18	V	301	MES	C8-S	-7.72	1.66	1.77
18	H	301	MES	C8-S	-7.47	1.66	1.77

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	Y	301	MES	O2S-S-C8	2.92	110.44	106.92
18	K	302	MES	O3S-S-C8	2.91	110.48	105.77
18	H	301	MES	O2S-S-C8	2.63	110.09	106.92
18	K	302	MES	O2S-S-C8	2.50	109.93	106.92
18	V	301	MES	O2S-S-C8	2.49	109.91	106.92
18	Y	301	MES	O3S-S-C8	2.49	109.79	105.77
18	H	301	MES	O3S-S-C8	2.25	109.41	105.77
18	H	301	MES	O1S-S-C8	2.21	109.58	106.92
18	V	301	MES	O3S-S-C8	2.10	109.16	105.77

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	V	301	MES	C7-C8-S-O1S
18	V	301	MES	C7-C8-S-O3S
18	V	301	MES	C7-C8-S-O2S
18	V	301	MES	C8-C7-N4-C5
18	V	301	MES	C8-C7-N4-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	V	301	MES	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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%)	-0.15	5 (2%) 65 63	35, 49, 85, 124	0
1	O	250/250 (100%)	-0.06	10 (4%) 38 37	40, 57, 102, 132	0
2	B	244/258 (94%)	0.11	19 (7%) 13 11	35, 54, 106, 159	0
2	P	244/258 (94%)	0.16	22 (9%) 9 8	41, 58, 109, 161	0
3	C	240/254 (94%)	0.10	18 (7%) 14 13	36, 57, 120, 161	0
3	Q	240/254 (94%)	0.35	24 (10%) 7 6	43, 72, 153, 196	0
4	D	235/260 (90%)	-0.18	6 (2%) 56 54	40, 58, 91, 137	0
4	R	235/260 (90%)	-0.05	8 (3%) 45 44	45, 64, 100, 150	0
5	E	231/234 (98%)	0.06	10 (4%) 35 33	43, 63, 100, 146	0
5	S	231/234 (98%)	0.19	15 (6%) 18 17	46, 71, 111, 147	0
6	F	243/288 (84%)	-0.14	8 (3%) 46 45	38, 58, 107, 139	0
6	T	243/288 (84%)	0.02	12 (4%) 29 28	37, 64, 116, 154	0
7	G	241/252 (95%)	-0.16	10 (4%) 37 36	35, 51, 93, 148	0
7	U	241/252 (95%)	-0.18	5 (2%) 63 61	38, 53, 86, 132	0
8	H	222/232 (95%)	-0.18	4 (1%) 68 66	36, 48, 76, 115	0
8	V	222/232 (95%)	-0.13	3 (1%) 75 73	37, 52, 83, 126	0
9	I	204/205 (99%)	-0.34	2 (0%) 82 80	33, 46, 77, 97	0
9	W	204/205 (99%)	-0.32	4 (1%) 65 63	35, 49, 80, 103	0
10	J	195/198 (98%)	-0.18	5 (2%) 56 54	34, 49, 76, 122	0
10	X	195/198 (98%)	-0.18	5 (2%) 56 54	34, 53, 75, 131	0
11	K	212/212 (100%)	-0.12	4 (1%) 66 64	36, 51, 84, 99	0
11	Y	212/212 (100%)	-0.06	5 (2%) 59 57	37, 51, 85, 110	0
12	L	222/222 (100%)	-0.35	4 (1%) 68 66	33, 48, 76, 101	0
12	Z	222/222 (100%)	-0.29	3 (1%) 75 73	35, 50, 79, 104	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.30	5 (2%) 63 61	31, 50, 74, 94	0
13	a	233/246 (94%)	-0.30	4 (1%) 70 68	34, 49, 71, 90	0
14	N	196/196 (100%)	-0.35	1 (0%) 91 89	35, 46, 74, 99	0
14	b	196/196 (100%)	-0.31	2 (1%) 82 80	36, 47, 74, 99	0
15	c	2/5 (40%)	-0.62	0 100 100	54, 54, 54, 57	0
15	d	2/5 (40%)	-0.48	0 100 100	59, 59, 59, 65	0
15	e	2/5 (40%)	-0.75	0 100 100	54, 54, 54, 60	0
15	f	2/5 (40%)	-0.52	0 100 100	60, 60, 60, 67	0
All	All	6344/6634 (95%)	-0.11	223 (3%) 44 43	31, 54, 98, 196	0

All (223) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	J	1	MET	12.6
10	X	1	MET	10.2
3	Q	49	THR	9.5
2	B	220	ASN	9.3
2	P	219	ALA	9.2
3	C	206	LYS	8.2
1	A	1	MET	7.9
8	V	222	ASP	7.6
3	Q	206	LYS	7.5
2	B	219	ALA	7.5
8	H	221	CYS	7.0
3	Q	50	LEU	6.7
2	B	221	ASP	6.5
2	B	51	VAL	6.4
2	P	222	GLY	6.3
8	V	221	CYS	6.2
2	P	51	VAL	6.1
2	P	220	ASN	6.1
1	O	1	MET	6.0
2	B	218	GLY	5.9
5	S	202	ASP	5.7
3	Q	48	SER	5.7
9	I	1	SER	5.6
10	X	194	ASP	5.5
2	P	221	ASP	5.4
3	C	225	GLU	5.3

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Mol	Chain	Res	Type	RSRZ
5	E	202	ASP	5.2
3	C	205	ALA	5.1
3	Q	236	GLN	5.0
4	R	241	ALA	4.9
3	Q	51	LYS	4.8
3	C	49	THR	4.7
13	a	1	THR	4.7
3	Q	205	ALA	4.6
3	C	202	GLN	4.6
6	T	243	ILE	4.6
1	O	249	ALA	4.6
8	H	222	ASP	4.5
3	C	50	LEU	4.5
10	J	2	ASP	4.5
4	D	242	GLU	4.5
2	P	52	THR	4.5
9	W	1	SER	4.5
3	Q	240	GLU	4.4
10	X	2	ASP	4.4
2	P	218	GLY	4.3
3	Q	239	GLN	4.3
3	C	238	LYS	4.3
1	A	249	ALA	4.2
7	U	222	ASP	4.1
1	A	250	LEU	4.0
6	T	241	LYS	4.0
3	Q	238	LYS	4.0
1	O	250	LEU	4.0
5	E	233	ILE	3.9
1	A	2	THR	3.9
5	E	123	GLY	3.9
4	R	125	LEU	3.9
1	O	52	SER	3.8
11	Y	212	GLY	3.7
2	B	60	THR	3.7
2	B	52	THR	3.7
13	M	1	THR	3.7
4	D	241	ALA	3.7
2	B	242	GLY	3.7
1	O	201	GLU	3.6
3	Q	204	GLY	3.6
10	J	194	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
6	T	53	LYS	3.6
12	Z	1	GLN	3.6
7	G	242	GLN	3.5
5	S	233	ILE	3.5
3	C	236	GLN	3.4
10	X	193	ASP	3.4
4	R	242	GLU	3.4
5	S	180	LYS	3.4
1	O	2	THR	3.4
6	T	2	THR	3.3
7	G	2	GLY	3.3
2	B	240	LYS	3.3
8	V	145	ASP	3.3
6	F	243	ILE	3.3
2	B	225	TYR	3.2
3	Q	187	GLU	3.2
6	T	181	GLU	3.2
3	Q	223	SER	3.2
6	F	53	LYS	3.2
2	B	222	GLY	3.2
7	G	3	TYR	3.1
7	U	242	GLN	3.1
3	Q	203	THR	3.1
5	S	171	LEU	3.1
4	R	1	ASP	3.1
6	T	244	ASN	3.1
6	F	215	CYS	3.0
3	C	239	GLN	3.0
9	W	191	LYS	3.0
5	E	54	GLU	3.0
2	P	59	ASP	2.9
2	B	232	GLN	2.9
5	S	3	ASN	2.9
5	S	122	TYR	2.9
2	P	182	ASP	2.9
3	C	48	SER	2.9
11	Y	202	GLU	2.9
12	Z	210	ASP	2.8
13	a	233	ILE	2.8
5	S	52	ALA	2.8
2	B	217	LYS	2.8
6	T	204	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
13	M	216	ASN	2.8
11	K	211	ILE	2.8
13	M	233	ILE	2.8
6	F	2	THR	2.8
5	S	204	SER	2.8
5	E	201	ARG	2.8
6	F	205	GLU	2.8
5	E	122	TYR	2.7
8	H	217	ILE	2.7
3	C	216	ASP	2.7
13	M	232	LYS	2.7
14	b	195	GLN	2.7
4	R	217	GLN	2.7
3	Q	232	THR	2.7
3	C	51	LYS	2.7
7	G	181	LYS	2.7
11	K	209	ASN	2.7
2	P	169	SER	2.6
9	W	192	ASP	2.6
10	J	174	MET	2.6
3	C	175	LYS	2.6
11	Y	209	ASN	2.6
11	K	212	GLY	2.6
7	U	181	LYS	2.6
3	Q	55	THR	2.6
4	D	125	LEU	2.6
2	P	225	TYR	2.6
3	Q	60	SER	2.5
6	T	205	GLU	2.5
6	T	230	ASP	2.5
8	H	198	GLU	2.5
4	D	2	ARG	2.5
6	F	202	ASP	2.5
5	S	30	GLN	2.5
1	O	231	LYS	2.5
2	P	230	LYS	2.5
3	C	180	LYS	2.5
3	Q	221	ALA	2.5
3	Q	225	GLU	2.5
10	X	174	MET	2.4
3	C	37	LYS	2.4
4	R	2	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
2	P	50	LYS	2.4
4	D	1	ASP	2.4
5	S	194	GLU	2.4
5	E	180	LYS	2.4
7	G	240	ALA	2.4
3	C	240	GLU	2.4
5	S	54	GLU	2.4
2	B	59	ASP	2.4
3	Q	141	ASP	2.4
2	P	62	THR	2.4
4	R	230	GLU	2.4
7	U	241	GLU	2.4
3	C	181	GLU	2.3
7	G	188	GLU	2.3
2	P	60	THR	2.3
13	a	232	LYS	2.3
14	b	105	LYS	2.3
3	Q	202	GLN	2.3
6	T	180	PRO	2.3
4	R	177	ASN	2.3
6	T	215	CYS	2.3
13	a	216	ASN	2.3
3	Q	175	LYS	2.3
10	J	193	ASP	2.3
6	F	244	ASN	2.3
5	S	173	ARG	2.3
7	G	241	GLU	2.3
9	W	131	GLU	2.3
11	Y	182	GLU	2.3
2	P	217	LYS	2.2
9	I	133	LYS	2.2
1	O	141	GLU	2.2
3	Q	180	LYS	2.2
11	Y	106	ARG	2.2
6	F	203	ASN	2.2
2	B	182	ASP	2.2
5	E	176	ASP	2.2
5	E	203	GLU	2.2
1	O	53	SER	2.2
12	L	106	TYR	2.2
4	D	238	LYS	2.2
7	G	51	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
12	L	174	TYR	2.2
5	E	194	GLU	2.2
2	B	244	THR	2.2
3	C	203	THR	2.2
2	B	235	LYS	2.1
7	G	179	LYS	2.1
2	P	235	LYS	2.1
12	Z	165	ASN	2.1
6	T	235	ALA	2.1
12	L	1	GLN	2.1
7	U	3	TYR	2.1
1	O	50	LYS	2.1
2	P	61	SER	2.1
2	P	240	LYS	2.1
3	Q	52	LEU	2.1
2	P	223	GLU	2.1
1	A	228	PRO	2.1
2	P	93	HIS	2.1
12	L	172	LEU	2.1
5	S	203	GLU	2.1
11	K	202	GLU	2.1
2	B	50	LYS	2.1
5	S	225	ASP	2.0
2	B	3	ARG	2.0
13	M	47	ASP	2.0
5	S	163	ARG	2.0
7	G	222	ASP	2.0
14	N	105	LYS	2.0
2	P	232	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
18	MES	H	301	12/12	0.77	0.34	76,104,129,131	0
18	MES	V	301	12/12	0.80	0.43	82,119,139,142	0
16	MG	I	302	1/1	0.84	0.09	52,52,52,52	0
16	MG	K	301	1/1	0.88	0.14	51,51,51,51	0
18	MES	K	302	12/12	0.92	0.26	70,80,84,84	0
16	MG	Z	301	1/1	0.92	0.15	65,65,65,65	0
18	MES	Y	301	12/12	0.92	0.24	64,79,81,82	0
16	MG	N	201	1/1	0.96	0.10	43,43,43,43	0
16	MG	G	301	1/1	0.96	0.08	43,43,43,43	0
16	MG	I	301	1/1	0.96	0.10	48,48,48,48	0
16	MG	L	301	1/1	0.99	0.04	45,45,45,45	0
17	CL	U	301	1/1	0.99	0.17	30,30,30,30	0
17	CL	G	302	1/1	1.00	0.14	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.