



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 03:01 PM UTC

PDB ID : 4J70 / pdb_00004j70
Title : Yeast 20S proteasome in complex with the belactosin derivative 3e
Authors : Kawamura, S.; Unno, Y.; List, A.; Tanaka, M.; Sasaki, T.; Arisawa, M.; Asai, A.; Groll, M.; Shuto, S.
Deposited on : 2013-02-12
Resolution : 2.80 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

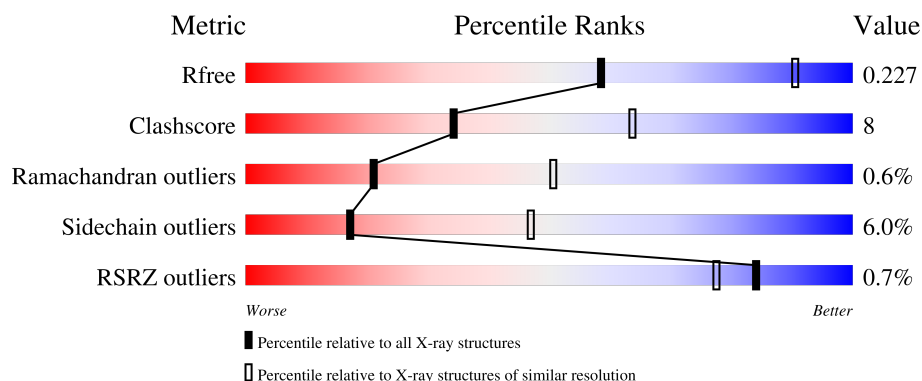
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

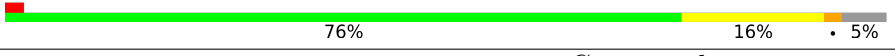
The reported resolution of this entry is 2.80 Å.

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.



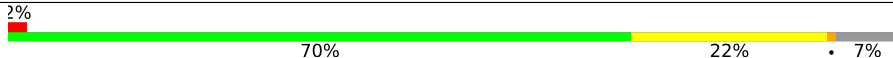
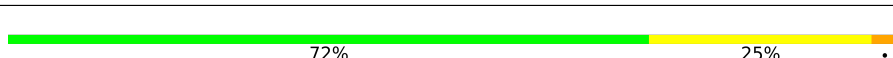
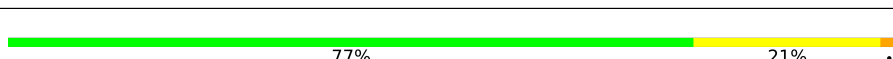
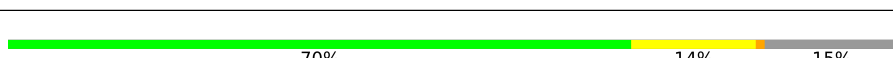
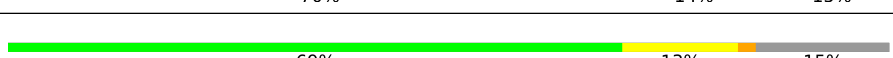
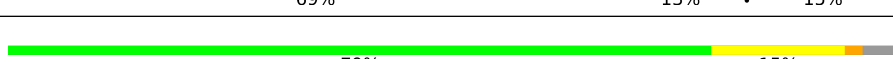
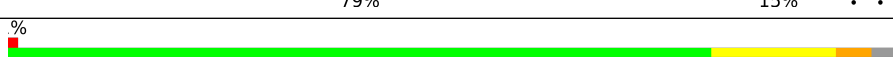
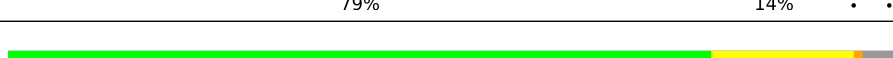
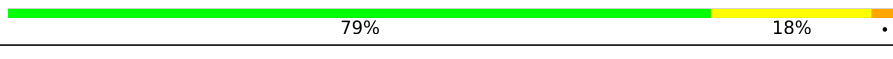
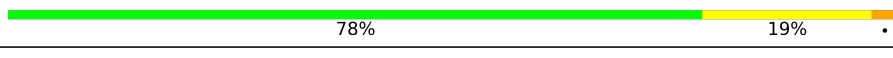
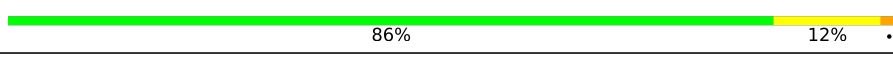
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	
1	O	250	
2	B	258	
2	P	258	
3	C	254	

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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	233	
13	a	233	
14	N	196	
14	b	196	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 50956 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 component Y7.

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 component Y13.

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 component PRE6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			
3	Q	241	Total	C	N	O	S	0	0	0
			1890	1181	331	374	4			

- Molecule 4 is a protein called Proteasome component PUP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	7			
4	R	242	Total	C	N	O	S	0	0	0
			1861	1162	314	378	7			

- Molecule 5 is a protein called Proteasome component PRE5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			
5	S	233	Total	C	N	O	S	0	0	0
			1795	1129	312	350	4			

- Molecule 6 is a protein called Proteasome component C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			
6	T	244	Total	C	N	O	S	0	0	0
			1896	1205	330	357	4			

- Molecule 7 is a protein called Proteasome component C7-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			
7	U	243	Total	C	N	O	S	0	0	0
			1921	1221	322	370	8			

- Molecule 8 is a protein called Proteasome component PUP1.

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 component PUP3.

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 component C11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	198	Total	C	N	O	S	0	0	0
			1585	1005	269	305	6			

- Molecule 11 is a protein called Proteasome component PRE2.

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 component C5.

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			

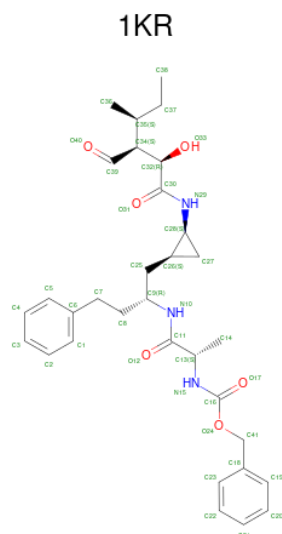
- Molecule 13 is a protein called Proteasome component PRE4.

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 component PRE3.

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 benzyl [(2S)-1-({(2R)-1-[(1S,2S)-2-{{(2R,3S,4S)-3-formyl-2-hydroxy-4-methylhexanoyl}amino}cyclopropyl]-4-phenylbutan-2-yl}amino)-1-oxopropan-2-yl]carbamate (CCD ID: 1KR) (formula: C₃₂H₄₃N₃O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
15	K	1	Total 41	C 32	N 3	O 6	0	0
15	Y	1	Total 41	C 32	N 3	O 6	0	0

- Molecule 16 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	A	55	Total O 55 55	0	0
16	B	37	Total O 37 37	0	0
16	C	45	Total O 45 45	0	0
16	D	39	Total O 39 39	0	0
16	E	22	Total O 22 22	0	0
16	F	46	Total O 46 46	0	0
16	G	63	Total O 63 63	0	0
16	H	52	Total O 52 52	0	0
16	I	67	Total O 67 67	0	0
16	J	55	Total O 55 55	0	0

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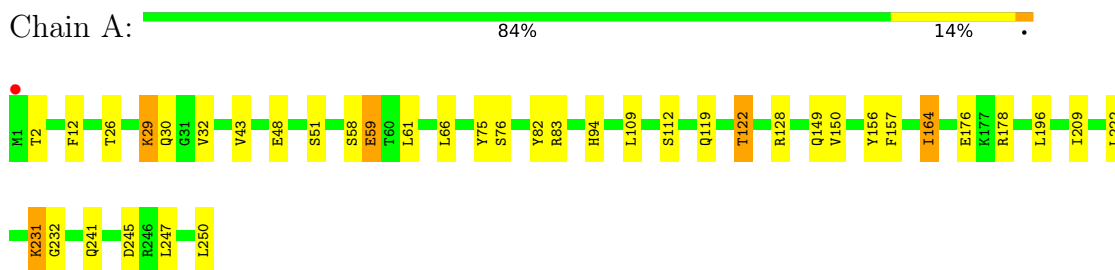
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	K	40	Total 40	O 40	0	0
16	L	57	Total 57	O 57	0	0
16	M	75	Total 75	O 75	0	0
16	N	54	Total 54	O 54	0	0
16	O	31	Total 31	O 31	0	0
16	P	31	Total 31	O 31	0	0
16	Q	26	Total 26	O 26	0	0
16	R	30	Total 30	O 30	0	0
16	S	23	Total 23	O 23	0	0
16	T	43	Total 43	O 43	0	0
16	U	59	Total 59	O 59	0	0
16	V	51	Total 51	O 51	0	0
16	W	62	Total 62	O 62	0	0
16	X	46	Total 46	O 46	0	0
16	Y	49	Total 49	O 49	0	0
16	Z	51	Total 51	O 51	0	0
16	a	72	Total 72	O 72	0	0
16	b	55	Total 55	O 55	0	0

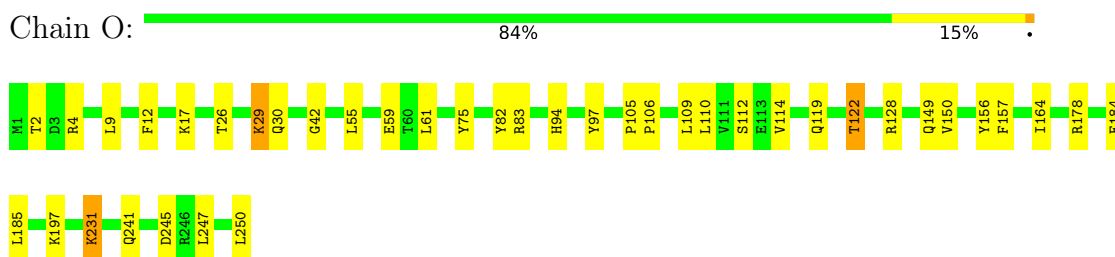
3 Residue-property plots [i](#)

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

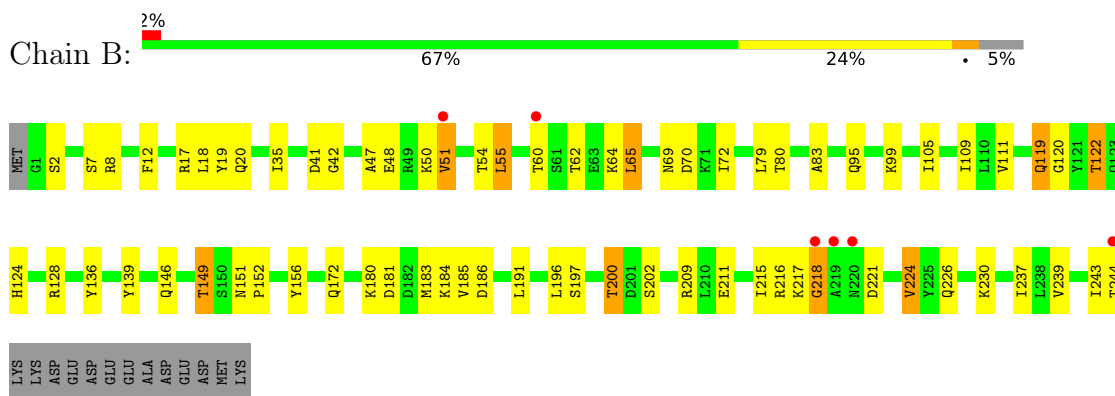
• Molecule 1: Proteasome component Y7



• Molecule 1: Proteasome component Y7

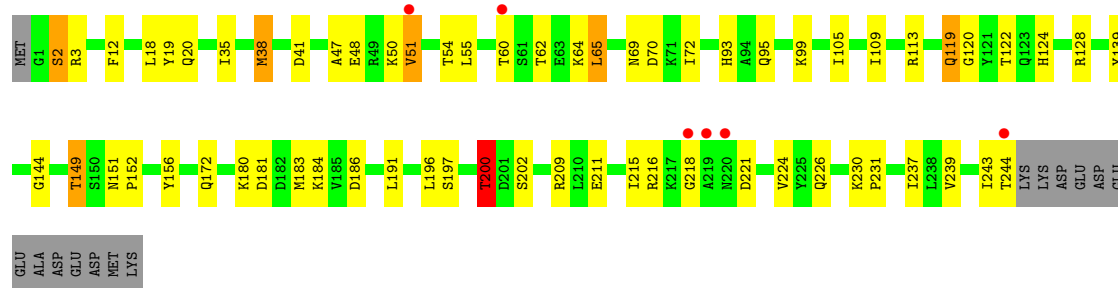


• Molecule 2: Proteasome component Y13

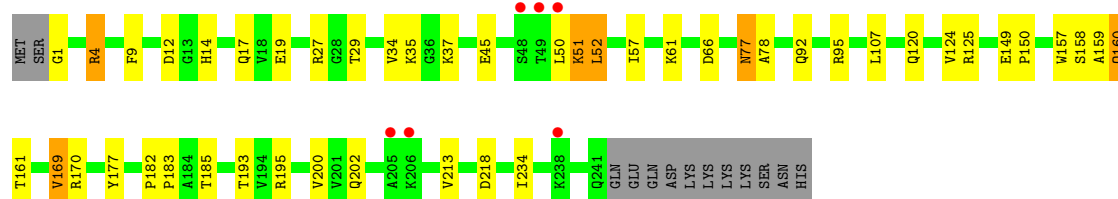
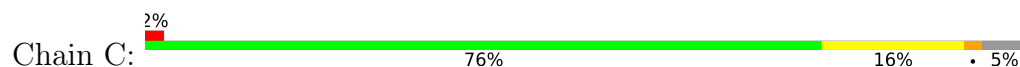


• Molecule 2: Proteasome component Y13

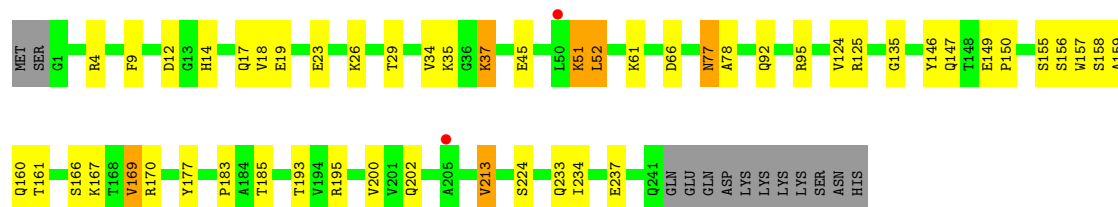
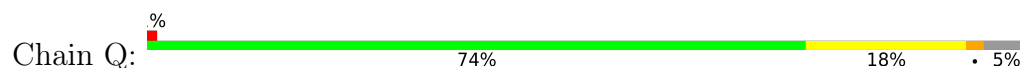




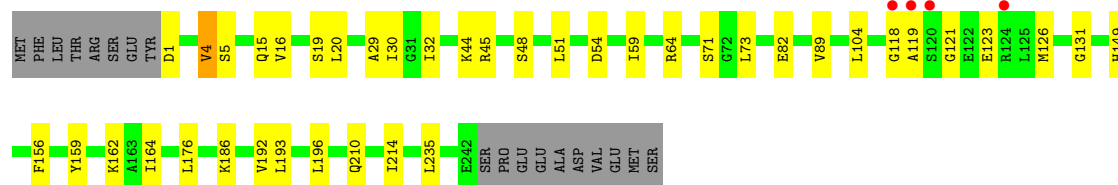
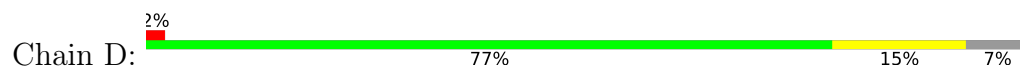
• Molecule 3: Proteasome component PRE6



• Molecule 3: Proteasome component PRE6

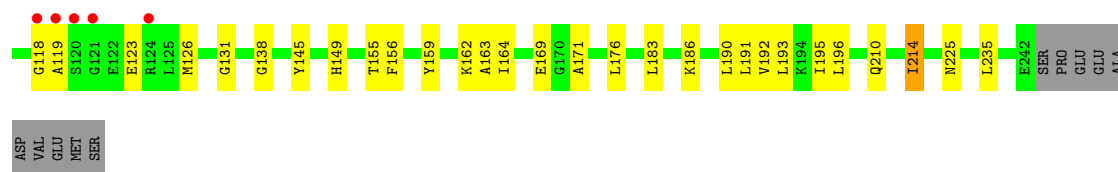


• Molecule 4: Proteasome component PUP2



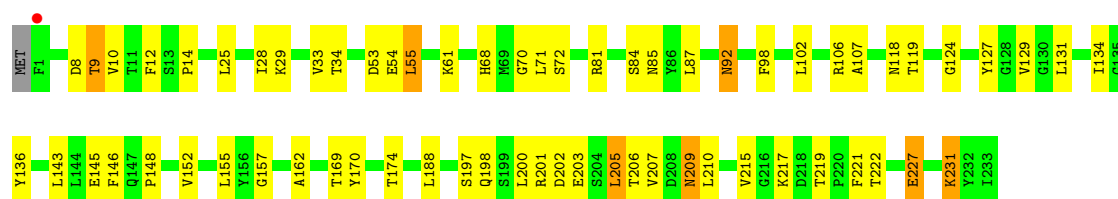
• Molecule 4: Proteasome component PUP2





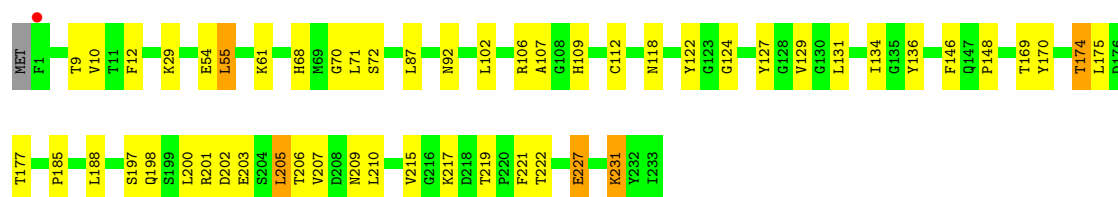
• Molecule 5: Proteasome component PRE5

Chain E: 72% 25% .



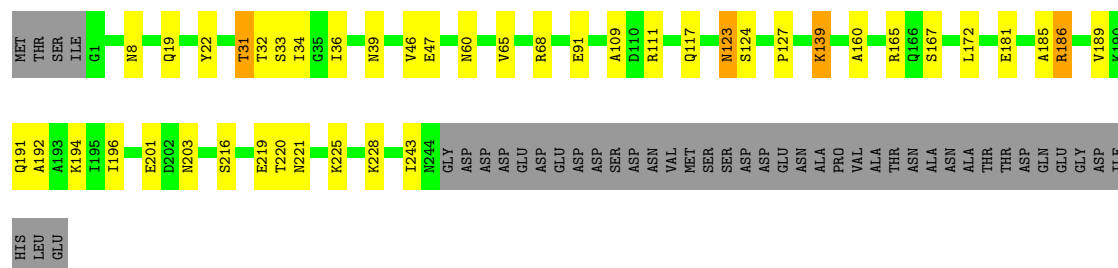
• Molecule 5: Proteasome component PRE5

Chain S: 77% 21% .



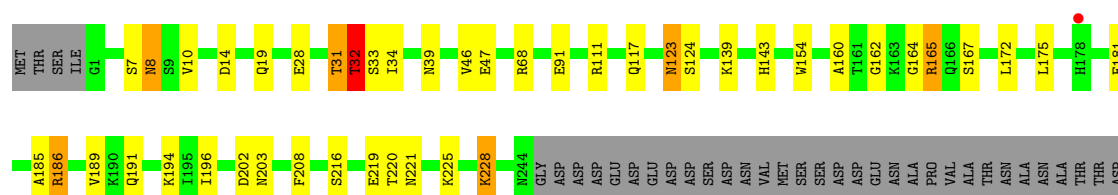
• Molecule 6: Proteasome component C1

Chain F: 70% 14% 15% .



• Molecule 6: Proteasome component C1

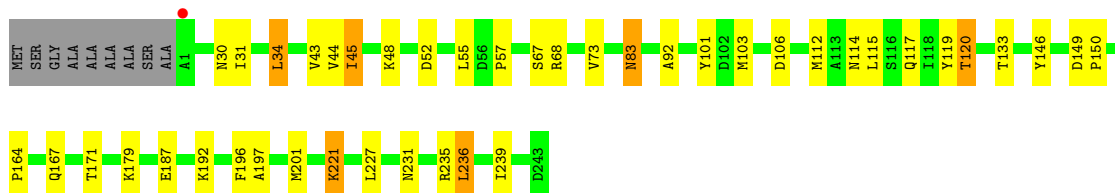
Chain T: 69% 13% 15% .



GLN
GLU
GLY
GLY
ASP
ILE
HIS
LEU
GLU

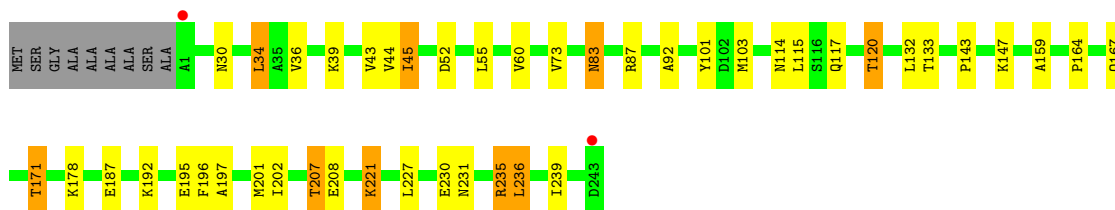
• Molecule 7: Proteasome component C7-alpha

Chain G: 79% 15% . .



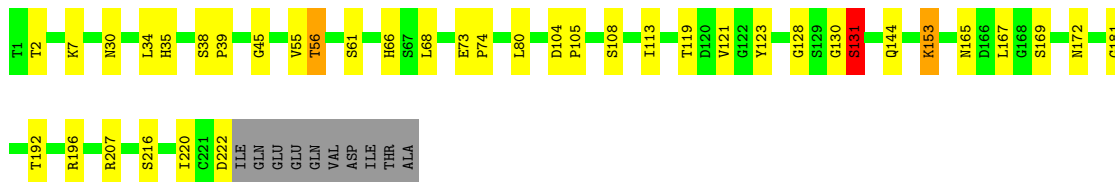
• Molecule 7: Proteasome component C7-alpha

Chain U: 79% 14% . .



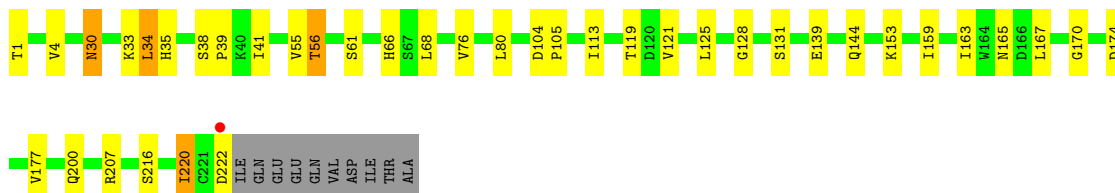
• Molecule 8: Proteasome component PUP1

Chain H: 79% 16% . .



• Molecule 8: Proteasome component PUP1

Chain V: 79% 15% . .

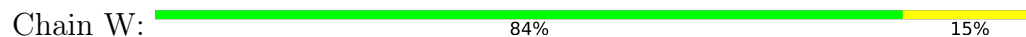


• Molecule 9: Proteasome component PUP3

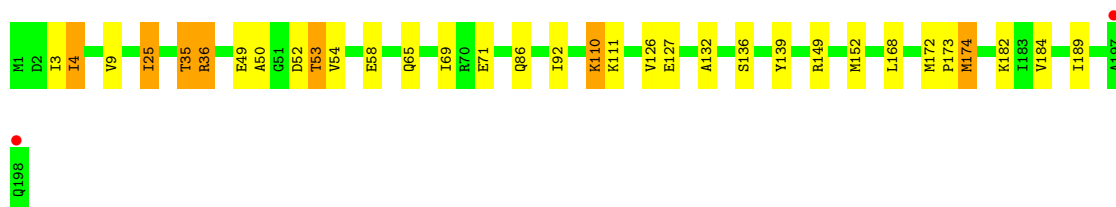
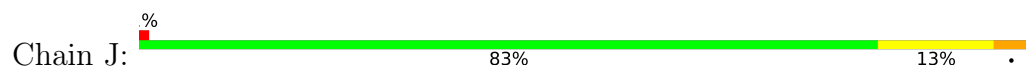
Chain I: 84% 15%



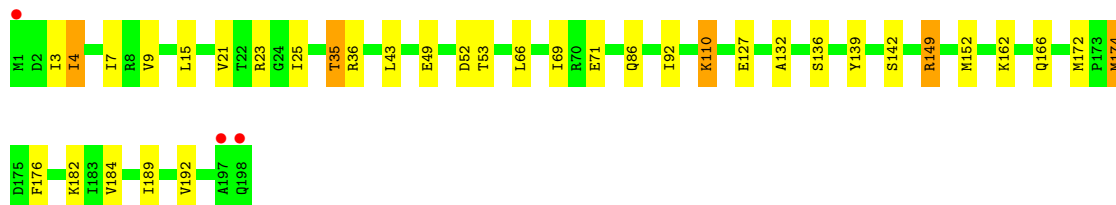
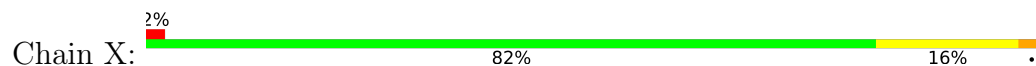
- Molecule 9: Proteasome component PUP3



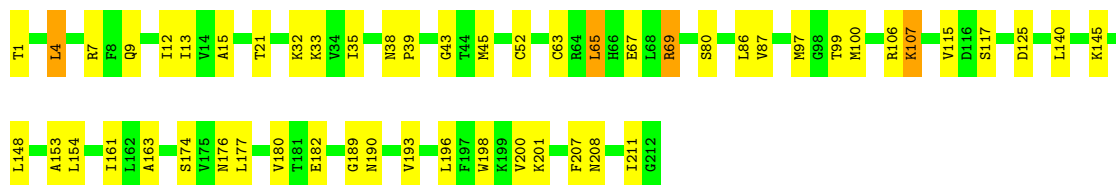
- Molecule 10: Proteasome component C11



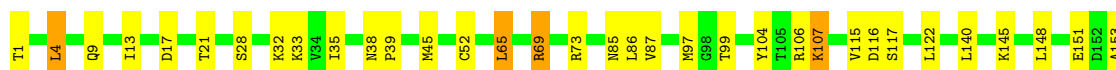
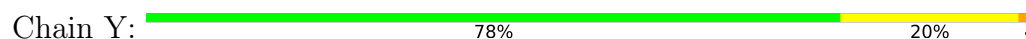
- Molecule 10: Proteasome component C11



- Molecule 11: Proteasome component PRE2



- Molecule 11: Proteasome component PRE2





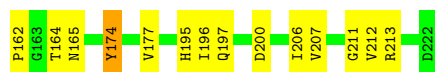
• Molecule 12: Proteasome component C5

Chain L: 79% 18% .



• Molecule 12: Proteasome component C5

Chain Z: 78% 19% .



• Molecule 13: Proteasome component PRE4

Chain M: 84% 15% .



• Molecule 13: Proteasome component PRE4

Chain a: 86% 12% .

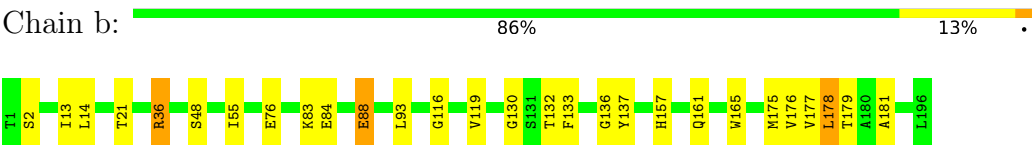


• Molecule 14: Proteasome component PRE3

Chain N: 85% 14% .



● Molecule 14: Proteasome component PRE3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	137.08Å 301.71Å 146.23Å 90.00° 113.69° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.9 (15.00-2.80) 98.2 (15.00-2.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 2.81Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.172 , 0.224 0.175 , 0.227	Depositor DCC
R_{free} test set	13052 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	50.2	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.7	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	50956	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 1KR

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	0.90	0/1952	1.05	2/2642 (0.1%)
1	O	0.85	0/1952	1.01	1/2642 (0.0%)
2	B	0.89	0/1934	1.06	2/2618 (0.1%)
2	P	0.88	0/1934	1.07	3/2618 (0.1%)
3	C	0.85	0/1919	1.05	2/2598 (0.1%)
3	Q	0.80	0/1919	1.05	2/2598 (0.1%)
4	D	0.86	0/1886	1.06	0/2541
4	R	0.87	0/1886	1.09	4/2541 (0.2%)
5	E	0.84	0/1823	1.04	2/2463 (0.1%)
5	S	0.83	0/1823	1.04	0/2463
6	F	0.88	0/1936	1.10	2/2614 (0.1%)
6	T	0.86	0/1936	1.11	3/2614 (0.1%)
7	G	0.92	0/1959	1.07	2/2652 (0.1%)
7	U	0.89	0/1959	1.07	0/2652
8	H	0.93	1/1715 (0.1%)	1.13	2/2326 (0.1%)
8	V	0.94	0/1715	1.09	0/2326
9	I	0.97	0/1611	1.07	1/2174 (0.0%)
9	W	0.93	0/1611	1.05	2/2174 (0.1%)
10	J	0.94	0/1613	1.10	2/2173 (0.1%)
10	X	0.96	1/1613 (0.1%)	1.11	2/2173 (0.1%)
11	K	0.94	1/1681 (0.1%)	1.10	2/2274 (0.1%)
11	Y	0.92	1/1681 (0.1%)	1.06	2/2274 (0.1%)
12	L	0.96	0/1795	1.08	5/2420 (0.2%)
12	Z	0.93	1/1795 (0.1%)	1.10	6/2420 (0.2%)
13	M	0.94	0/1855	1.09	1/2514 (0.0%)
13	a	0.92	0/1855	1.14	4/2514 (0.2%)
14	N	1.00	0/1541	1.14	3/2087 (0.1%)
14	b	0.93	0/1541	1.13	2/2087 (0.1%)
All	All	0.90	5/50440 (0.0%)	1.08	59/68192 (0.1%)

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
12	L	0	1
12	Z	0	1
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	Y	1	THR	C-N	8.05	1.45	1.33
11	K	1	THR	C-N	7.85	1.44	1.33
8	H	169	SER	C-O	6.06	1.31	1.23
12	Z	213	ARG	CA-C	5.88	1.59	1.52
10	X	149	ARG	CA-C	5.30	1.57	1.52

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	8	ASN	N-CA-C	7.37	119.00	110.97
13	a	35	ARG	N-CA-C	7.37	119.00	110.97
14	b	116	GLY	N-CA-C	6.74	121.89	114.40
10	X	192	VAL	CB-CA-C	-6.72	104.68	111.80
2	P	224	VAL	N-CA-C	6.70	118.22	108.58

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	H	181	GLY	Peptide
12	L	174	TYR	Peptide
12	Z	174	TYR	Peptide

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	29	0
1	O	1915	0	1929	32	0
2	B	1904	0	1904	52	0
2	P	1904	0	1904	53	0
3	C	1890	0	1903	42	0
3	Q	1890	0	1903	42	0
4	D	1861	0	1839	25	0
4	R	1861	0	1839	33	0
5	E	1795	0	1800	39	0
5	S	1795	0	1800	32	0
6	F	1896	0	1889	24	0
6	T	1896	0	1889	30	0
7	G	1921	0	1913	35	0
7	U	1921	0	1913	39	0
8	H	1684	0	1688	18	0
8	V	1684	0	1688	25	0
9	I	1581	0	1574	20	0
9	W	1581	0	1574	19	0
10	J	1585	0	1590	28	0
10	X	1585	0	1590	28	0
11	K	1644	0	1594	34	0
11	Y	1644	0	1594	28	0
12	L	1757	0	1711	31	0
12	Z	1757	0	1711	29	0
13	M	1824	0	1832	31	0
13	a	1824	0	1832	25	0
14	N	1512	0	1481	21	0
14	b	1512	0	1481	20	0
15	K	41	0	41	4	0
15	Y	41	0	42	2	0
16	A	55	0	0	0	0
16	B	37	0	0	2	0
16	C	45	0	0	4	0
16	D	39	0	0	2	0
16	E	22	0	0	3	0
16	F	46	0	0	4	0
16	G	63	0	0	2	0
16	H	52	0	0	1	0
16	I	67	0	0	3	0
16	J	55	0	0	3	0
16	K	40	0	0	0	0
16	L	57	0	0	3	0
16	M	75	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	N	54	0	0	1	0
16	O	31	0	0	2	0
16	P	31	0	0	1	0
16	Q	26	0	0	3	0
16	R	30	0	0	6	0
16	S	23	0	0	4	0
16	T	43	0	0	1	0
16	U	59	0	0	7	0
16	V	51	0	0	2	0
16	W	62	0	0	2	0
16	X	46	0	0	1	0
16	Y	49	0	0	3	0
16	Z	51	0	0	4	0
16	a	72	0	0	1	0
16	b	55	0	0	2	0
All	All	50956	0	49377	754	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 8.

The worst 5 of 754 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:174:MET:HE3	10:X:174:MET:CE	1.45	1.44
10:J:174:MET:CE	10:X:174:MET:HE3	1.45	1.44
7:U:92:ALA:HA	7:U:103:MET:HE2	1.34	1.10
1:O:128:ARG:HH21	7:U:120:THR:HG22	1.14	1.07
7:G:92:ALA:HA	7:G:103:MET:HE2	1.38	1.03

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%)	240 (97%)	7 (3%)	1 (0%)	30	60
1	O	248/250 (99%)	238 (96%)	9 (4%)	1 (0%)	30	60
2	B	242/258 (94%)	226 (93%)	13 (5%)	3 (1%)	10	34
2	P	242/258 (94%)	225 (93%)	14 (6%)	3 (1%)	10	34
3	C	239/254 (94%)	232 (97%)	4 (2%)	3 (1%)	9	31
3	Q	239/254 (94%)	231 (97%)	5 (2%)	3 (1%)	9	31
4	D	240/260 (92%)	225 (94%)	13 (5%)	2 (1%)	16	44
4	R	240/260 (92%)	229 (95%)	9 (4%)	2 (1%)	16	44
5	E	231/234 (99%)	217 (94%)	11 (5%)	3 (1%)	9	31
5	S	231/234 (99%)	216 (94%)	11 (5%)	4 (2%)	7	25
6	F	242/288 (84%)	230 (95%)	12 (5%)	0	100	100
6	T	242/288 (84%)	228 (94%)	14 (6%)	0	100	100
7	G	241/252 (96%)	233 (97%)	8 (3%)	0	100	100
7	U	241/252 (96%)	232 (96%)	9 (4%)	0	100	100
8	H	220/232 (95%)	211 (96%)	8 (4%)	1 (0%)	24	55
8	V	220/232 (95%)	212 (96%)	8 (4%)	0	100	100
9	I	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
9	W	202/205 (98%)	194 (96%)	8 (4%)	0	100	100
10	J	196/198 (99%)	190 (97%)	5 (3%)	1 (0%)	24	55
10	X	196/198 (99%)	191 (97%)	4 (2%)	1 (0%)	24	55
11	K	210/212 (99%)	204 (97%)	5 (2%)	1 (0%)	24	55
11	Y	210/212 (99%)	205 (98%)	4 (2%)	1 (0%)	24	55
12	L	220/222 (99%)	203 (92%)	15 (7%)	2 (1%)	14	41
12	Z	220/222 (99%)	204 (93%)	14 (6%)	2 (1%)	14	41
13	M	231/233 (99%)	219 (95%)	11 (5%)	1 (0%)	30	60
13	a	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
14	N	194/196 (99%)	187 (96%)	7 (4%)	0	100	100
14	b	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
All	All	6312/6588 (96%)	6027 (96%)	250 (4%)	35 (1%)	21	51

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	52	LEU
2	P	51	VAL
3	Q	52	LEU
2	B	218	GLY

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%)	198 (95%)	11 (5%)	20	52
1	O	209/209 (100%)	198 (95%)	11 (5%)	20	52
2	B	203/216 (94%)	187 (92%)	16 (8%)	11	35
2	P	203/216 (94%)	189 (93%)	14 (7%)	14	41
3	C	213/226 (94%)	202 (95%)	11 (5%)	21	53
3	Q	213/226 (94%)	202 (95%)	11 (5%)	21	53
4	D	198/215 (92%)	185 (93%)	13 (7%)	15	43
4	R	198/215 (92%)	184 (93%)	14 (7%)	13	39
5	E	192/193 (100%)	170 (88%)	22 (12%)	5	18
5	S	192/193 (100%)	172 (90%)	20 (10%)	7	22
6	F	201/239 (84%)	184 (92%)	17 (8%)	10	31
6	T	201/239 (84%)	185 (92%)	16 (8%)	11	34
7	G	207/210 (99%)	197 (95%)	10 (5%)	23	56
7	U	207/210 (99%)	193 (93%)	14 (7%)	14	42
8	H	181/190 (95%)	166 (92%)	15 (8%)	10	32
8	V	181/190 (95%)	169 (93%)	12 (7%)	15	43
9	I	172/173 (99%)	167 (97%)	5 (3%)	37	73
9	W	172/173 (99%)	166 (96%)	6 (4%)	32	67
10	J	175/175 (100%)	166 (95%)	9 (5%)	21	54
10	X	175/175 (100%)	165 (94%)	10 (6%)	18	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K	169/169 (100%)	158 (94%)	11 (6%)	15	43
11	Y	169/169 (100%)	158 (94%)	11 (6%)	15	43
12	L	185/185 (100%)	177 (96%)	8 (4%)	26	60
12	Z	185/185 (100%)	178 (96%)	7 (4%)	29	64
13	M	199/199 (100%)	193 (97%)	6 (3%)	36	72
13	a	199/199 (100%)	192 (96%)	7 (4%)	32	67
14	N	162/162 (100%)	157 (97%)	5 (3%)	35	70
14	b	162/162 (100%)	155 (96%)	7 (4%)	26	60
All	All	5332/5522 (97%)	5013 (94%)	319 (6%)	17	47

5 of 319 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	T	39	ASN
10	X	174	MET
6	T	172	LEU
8	V	34	LEU
12	Z	49	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 205 such sidechains are listed below:

Mol	Chain	Res	Type
2	P	95	GLN
5	S	184	ASN
13	a	213	GLN
2	P	155	ASN
4	R	146	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands 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	1KR	K	301	11	43,43,43	1.76	6 (13%)	51,57,57	1.94	12 (23%)
15	1KR	Y	301	11	43,43,43	1.79	8 (18%)	51,57,57	1.91	10 (19%)

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	1KR	K	301	11	-	17/46/51/51	0/3/3/3
15	1KR	Y	301	11	-	14/46/51/51	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	Y	301	1KR	C5-C6	6.11	1.51	1.38
15	K	301	1KR	C5-C6	5.67	1.50	1.38
15	Y	301	1KR	O40-C39	3.78	1.34	1.20
15	K	301	1KR	C27-C28	3.72	1.54	1.49
15	Y	301	1KR	C27-C28	3.61	1.54	1.49

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	Y	301	1KR	C28-N29-C30	-6.96	111.15	123.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	K	301	1KR	C28-N29-C30	-6.06	112.71	123.25
15	K	301	1KR	C14-C13-C11	4.91	119.46	110.14
15	Y	301	1KR	C26-C25-C9	-4.72	107.84	115.62
15	Y	301	1KR	C13-N15-C16	3.99	128.14	120.59

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

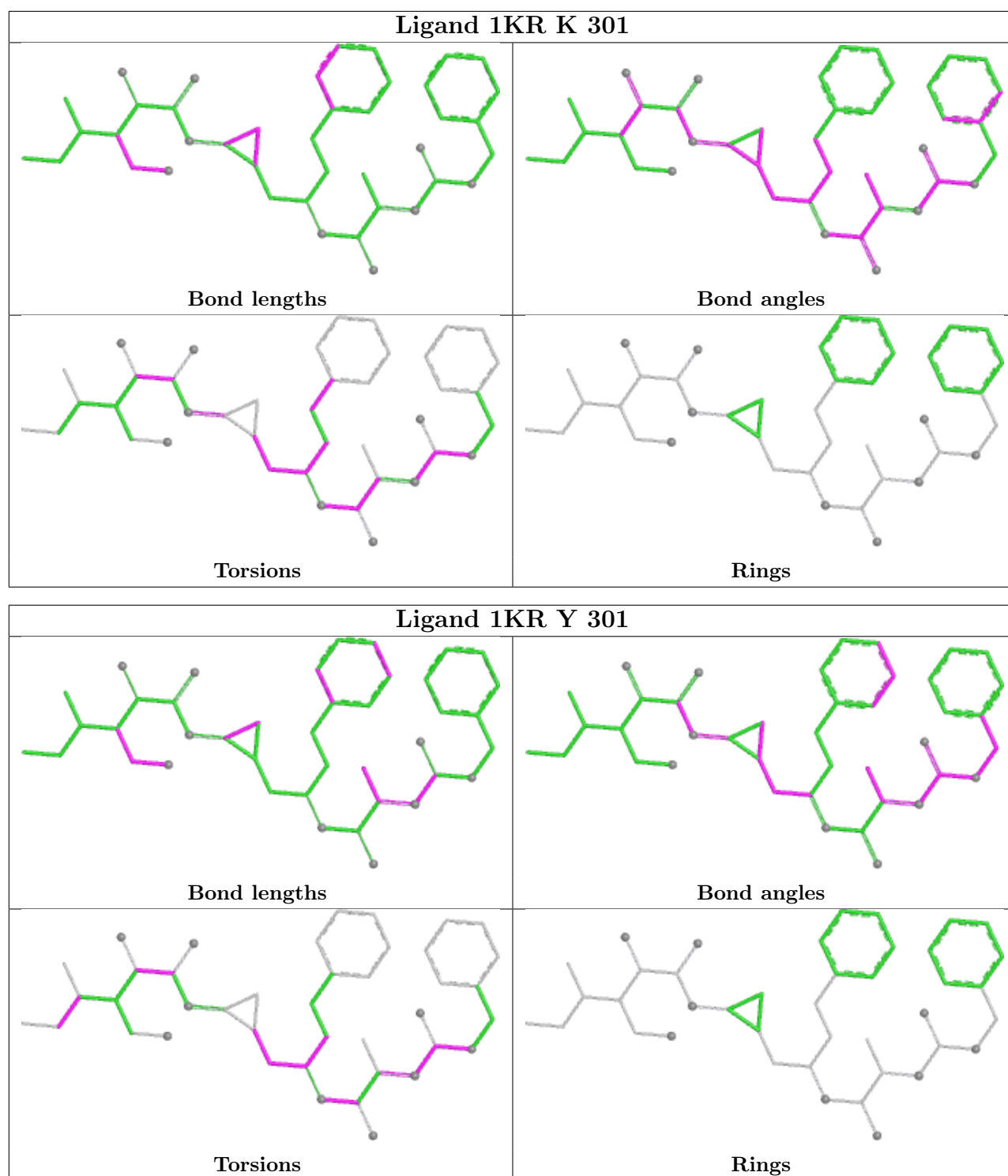
Mol	Chain	Res	Type	Atoms
15	K	301	1KR	O17-C16-O24-C41
15	K	301	1KR	N15-C16-O24-C41
15	K	301	1KR	O24-C16-N15-C13
15	K	301	1KR	O12-C11-C13-C14
15	K	301	1KR	N10-C11-C13-C14

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	K	301	1KR	4	0
15	Y	301	1KR	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.97	1 (0%) 88 84	28, 43, 74, 146	0
1	O	250/250 (100%)	-0.84	0 100 100	30, 51, 87, 142	0
2	B	244/258 (94%)	-0.72	6 (2%) 58 48	27, 48, 104, 154	0
2	P	244/258 (94%)	-0.63	6 (2%) 58 48	33, 52, 105, 156	0
3	C	241/254 (94%)	-0.69	6 (2%) 58 48	28, 52, 111, 147	0
3	Q	241/254 (94%)	-0.49	2 (0%) 82 75	33, 58, 125, 153	0
4	D	242/260 (93%)	-0.74	4 (1%) 69 60	32, 51, 89, 185	0
4	R	242/260 (93%)	-0.69	5 (2%) 63 54	34, 54, 94, 195	0
5	E	233/234 (99%)	-0.65	1 (0%) 88 84	36, 55, 87, 152	0
5	S	233/234 (99%)	-0.58	1 (0%) 88 84	35, 58, 97, 146	0
6	F	244/288 (84%)	-0.86	0 100 100	30, 47, 92, 128	0
6	T	244/288 (84%)	-0.62	1 (0%) 88 84	32, 52, 98, 134	0
7	G	243/252 (96%)	-0.90	1 (0%) 88 84	24, 43, 80, 157	0
7	U	243/252 (96%)	-0.84	2 (0%) 82 75	29, 46, 83, 149	0
8	H	222/232 (95%)	-1.07	0 100 100	26, 40, 65, 99	0
8	V	222/232 (95%)	-1.01	1 (0%) 87 82	29, 42, 70, 112	0
9	I	204/205 (99%)	-1.11	1 (0%) 87 82	26, 40, 64, 99	0
9	W	204/205 (99%)	-1.05	0 100 100	27, 41, 66, 115	0
10	J	198/198 (100%)	-0.96	2 (1%) 79 72	28, 42, 68, 184	0
10	X	198/198 (100%)	-0.94	3 (1%) 72 63	30, 43, 71, 162	0
11	K	212/212 (100%)	-1.04	0 100 100	27, 42, 61, 76	0
11	Y	212/212 (100%)	-1.06	0 100 100	29, 43, 64, 80	0
12	L	222/222 (100%)	-0.97	0 100 100	27, 44, 73, 117	0
12	Z	222/222 (100%)	-1.01	0 100 100	28, 43, 70, 108	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/233 (100%)	-1.08	0 100 100	29, 44, 61, 83	0
13	a	233/233 (100%)	-1.04	0 100 100	26, 43, 60, 77	0
14	N	196/196 (100%)	-1.05	0 100 100	27, 39, 63, 90	0
14	b	196/196 (100%)	-1.06	0 100 100	24, 40, 66, 90	0
All	All	6368/6588 (96%)	-0.87	43 (0%) 84 77	24, 46, 87, 195	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	119	ALA	5.8
2	B	218	GLY	5.2
3	Q	50	LEU	4.4
10	J	197	ALA	4.2
4	R	121	GLY	4.1

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

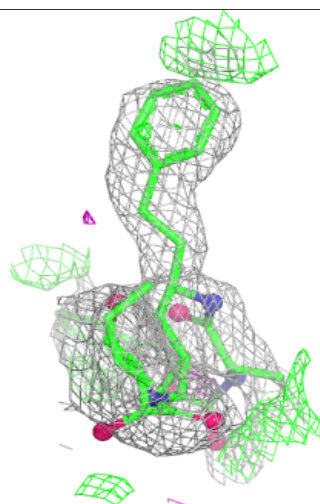
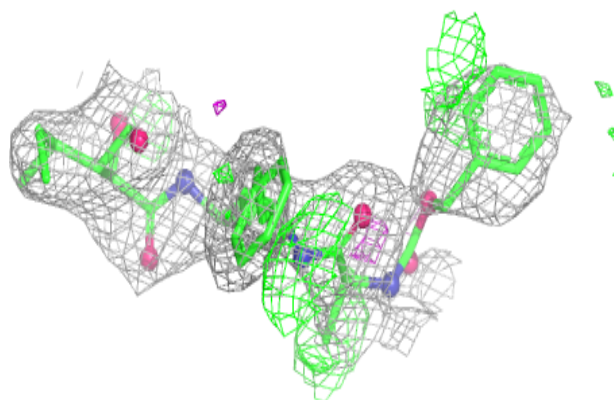
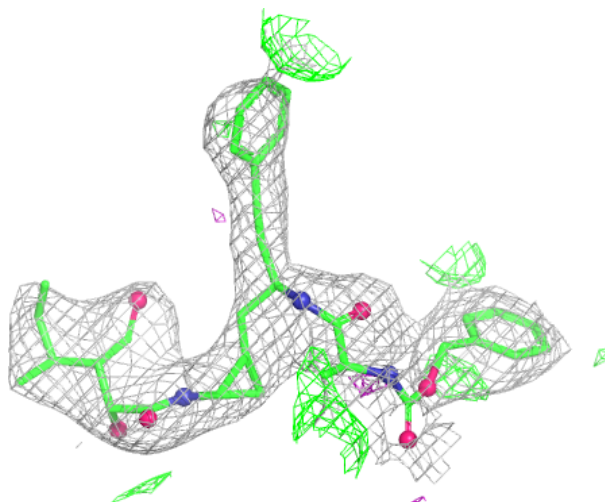
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	1KR	K	301	41/41	0.90	0.14	40,81,141,150	0
15	1KR	Y	301	41/41	0.91	0.13	37,81,137,168	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

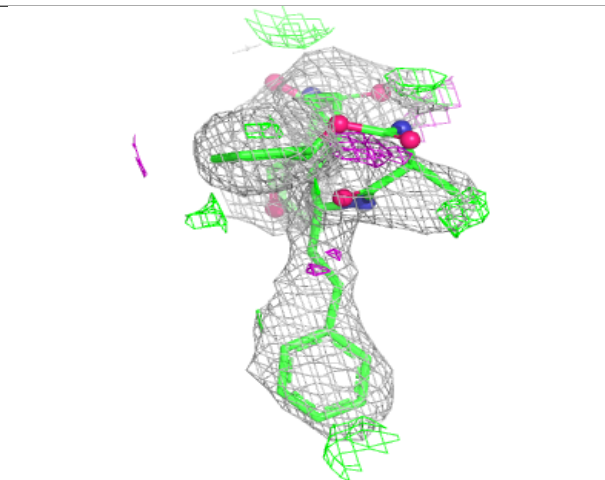
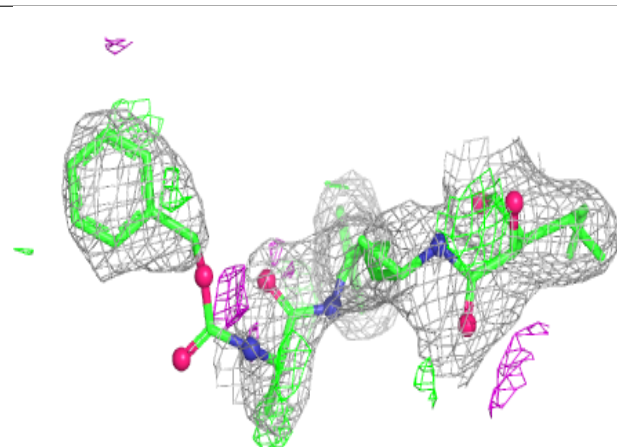
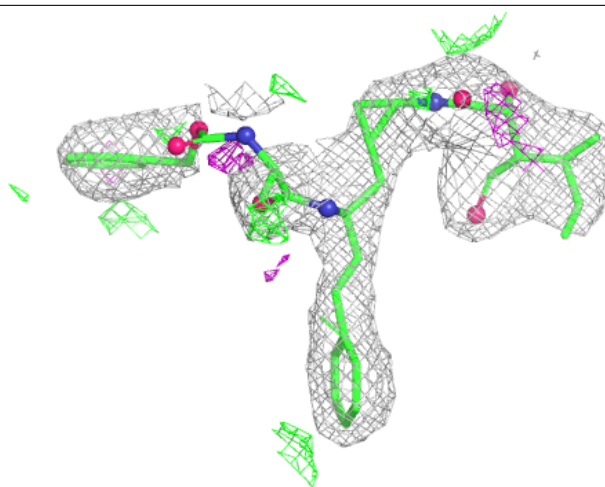
Electron density around 1KR K 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 1KR Y 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.