



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 6, 2016 – 05:10 AM EDT

PDB ID : 5BXN
Title : Yeast 20S proteasome beta2-G170A mutant in complex with Bortezomib
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-06-09
Resolution : 2.80 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027674
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027674

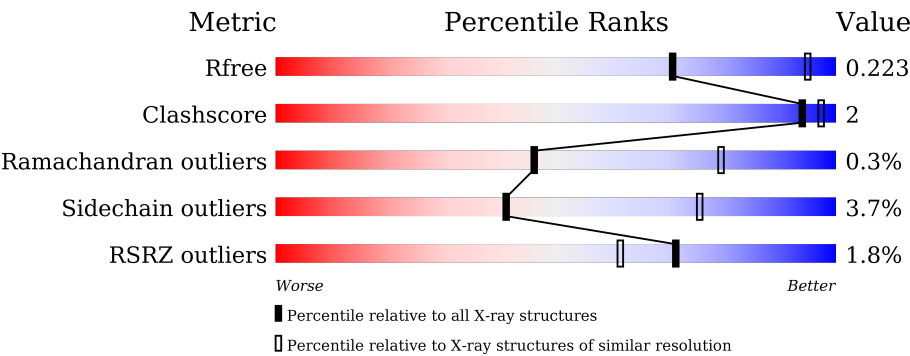
1 Overall quality at a glance ⓘ

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.





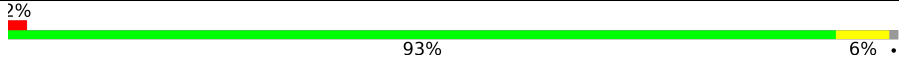
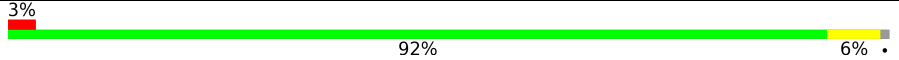
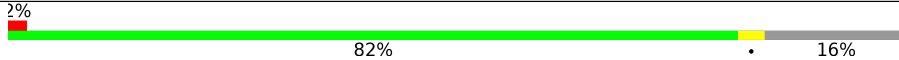
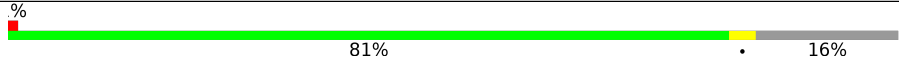
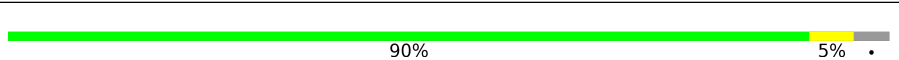
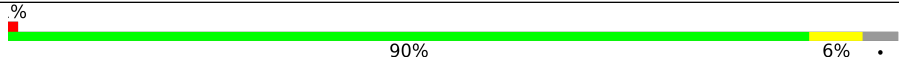
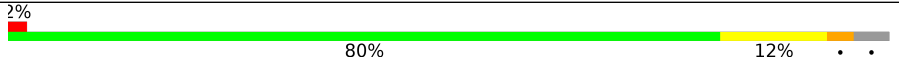
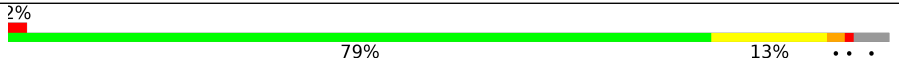
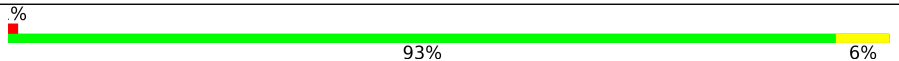
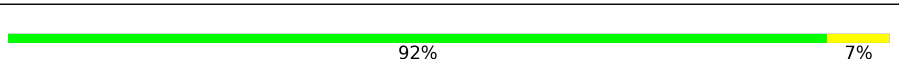
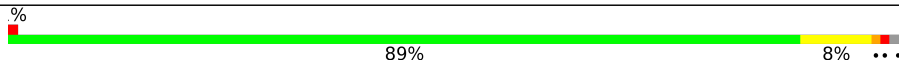
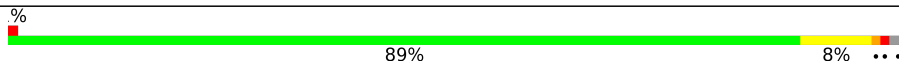
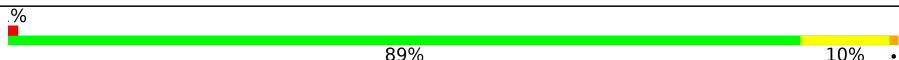
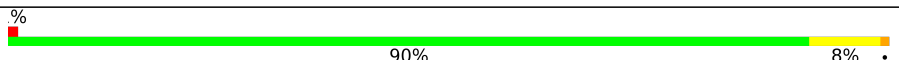
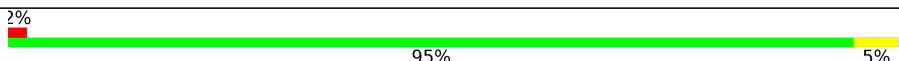
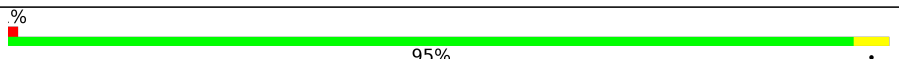
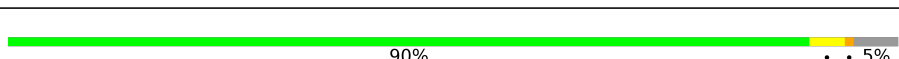
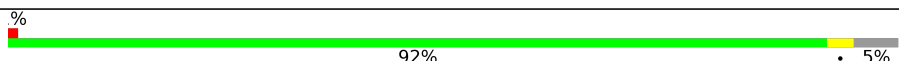
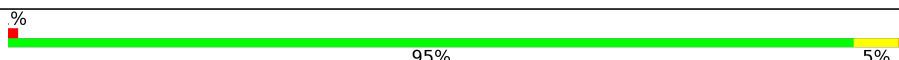
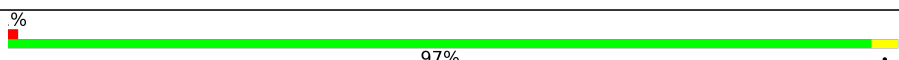
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	250	<div><div>2%</div><div>98%</div><div>•</div></div>
1	O	250	<div><div>2%</div><div>98%</div><div>•</div></div>
2	B	258	<div><div>2%</div><div>87%</div><div>7%</div><div>5%</div></div>
2	P	258	<div><div>3%</div><div>87%</div><div>7%</div><div>5%</div></div>
3	C	254	<div><div>4%</div><div>87%</div><div>6%</div><div>•</div><div>6%</div></div>
3	Q	254	<div><div>4%</div><div>87%</div><div>6%</div><div>•</div><div>6%</div></div>

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

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
15	MG	J	201	-	-	-	X
15	MG	Z	301	-	-	-	X
15	MG	Z	302	-	-	-	X
17	BO2	H	301	-	-	-	X
17	BO2	N	201	-	-	-	X
17	BO2	V	301	-	-	-	X
17	BO2	b	201	-	-	-	X

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 49853 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	222	Total	C	N	O	S	0	0	0
			1685	1062	293	323	7			
8	V	222	Total	C	N	O	S	0	0	0
			1685	1062	293	323	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	170	ALA	GLY	engineered mutation	UNP P25043
V	170	ALA	GLY	engineered mutation	UNP P25043

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

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

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

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

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

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

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

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

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

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

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

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

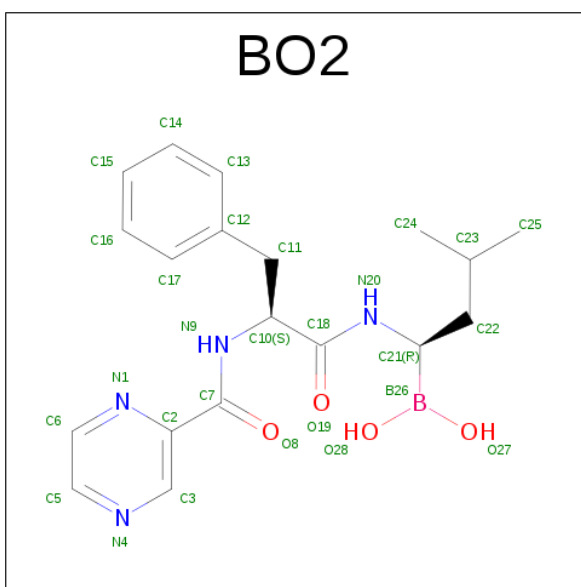
- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	G	1	Total Mg 1 1	0	0
15	J	1	Total Mg 1 1	0	0
15	K	1	Total Mg 1 1	0	0
15	I	1	Total Mg 1 1	0	0
15	V	1	Total Mg 1 1	0	0
15	Z	2	Total Mg 2 2	0	0
15	N	1	Total Mg 1 1	0	0
15	Y	1	Total Mg 1 1	0	0

- Molecule 16 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	b	1	Total Cl 1 1	0	0
16	N	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0

- Molecule 17 is N-[(1R)-1-(DIHYDROXYBORYL)-3-METHYLBUTYL]-N-(PYRAZIN-2-YLCARBONYL)-L-PHENYLALANINAMIDE (three-letter code: BO2) (formula: C₁₉H₂₅BN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	H	1	Total	B	C	N	O	0	0
			28	1	19	4	4		
17	K	1	Total	B	C	N	O	0	0
			28	1	19	4	4		
17	N	1	Total	B	C	N	O	0	0
			28	1	19	4	4		
17	V	1	Total	B	C	N	O	0	0
			28	1	19	4	4		
17	Y	1	Total	B	C	N	O	0	0
			28	1	19	4	4		
17	b	1	Total	B	C	N	O	0	0
			28	1	19	4	4		

- Molecule 18 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	A	15	Total	O	0	0
			15	15		
18	B	17	Total	O	0	0
			17	17		
18	C	14	Total	O	0	0
			14	14		
18	D	9	Total	O	0	0
			9	9		
18	E	6	Total	O	0	0
			6	6		
18	F	9	Total	O	0	0
			9	9		

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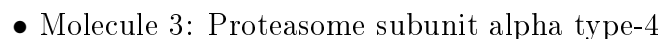
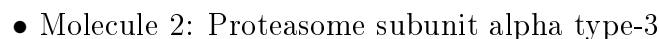
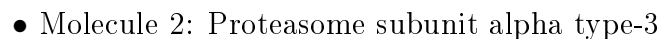
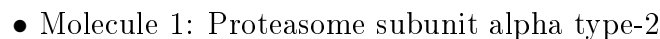
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
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18	H	22	Total 22	O 22	0	0
18	I	11	Total 11	O 11	0	0
18	J	18	Total 18	O 18	0	0
18	K	19	Total 19	O 19	0	0
18	L	20	Total 20	O 20	0	0
18	M	16	Total 16	O 16	0	0
18	N	9	Total 9	O 9	0	0
18	O	7	Total 7	O 7	0	0
18	P	17	Total 17	O 17	0	0
18	Q	6	Total 6	O 6	0	0
18	R	8	Total 8	O 8	0	0
18	S	7	Total 7	O 7	0	0
18	T	14	Total 14	O 14	0	0
18	U	14	Total 14	O 14	0	0
18	V	10	Total 10	O 10	0	0
18	W	10	Total 10	O 10	0	0
18	X	18	Total 18	O 18	0	0
18	Y	12	Total 12	O 12	0	0
18	Z	18	Total 18	O 18	0	0
18	a	21	Total 21	O 21	0	0

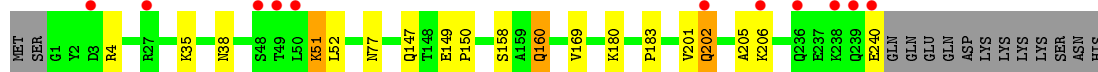
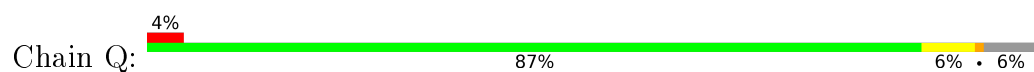
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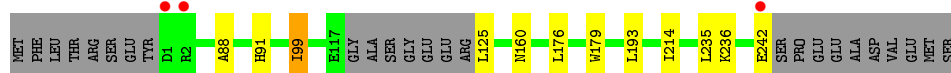
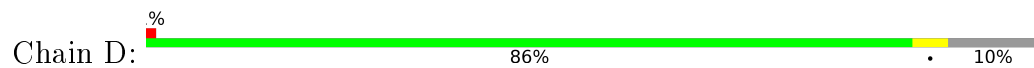
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
18	b	12	Total	O	0	0
			12	12		

- Molecule 1: Proteasome subunit alpha type-2

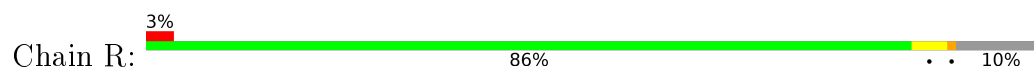




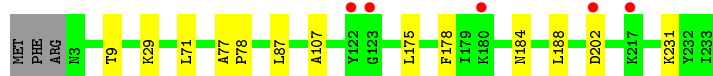
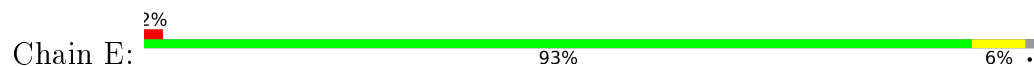
- Molecule 4: Proteasome subunit alpha type-5



- Molecule 4: Proteasome subunit alpha type-5



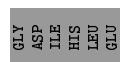
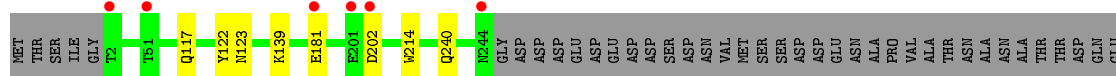
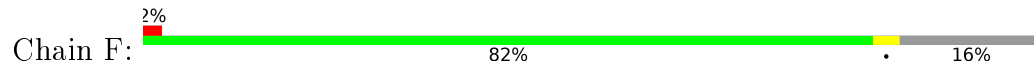
- Molecule 5: Proteasome subunit alpha type-6



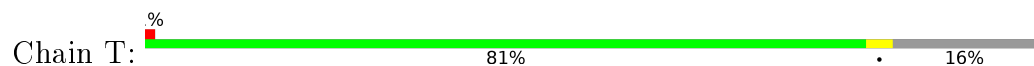
- Molecule 5: Proteasome subunit alpha type-6



- Molecule 6: Probable proteasome subunit alpha type-7

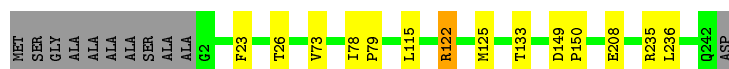


- Molecule 6: Probable proteasome subunit alpha type-7

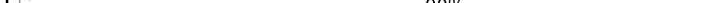


- Molecule 7: Proteasome subunit alpha type-1

Chain G:  90% 5% .

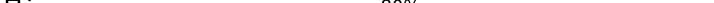


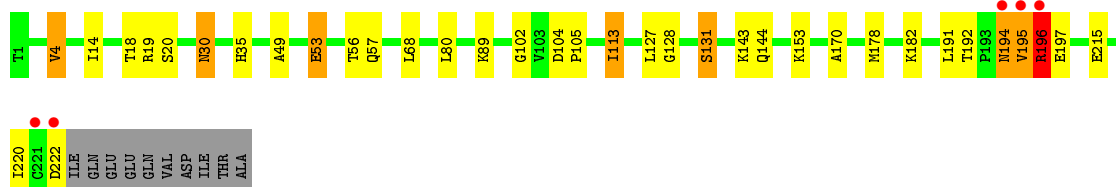
- Molecule 7: Proteasome subunit alpha type-1

Chain U:  90% 6% 4%

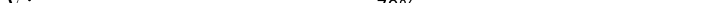


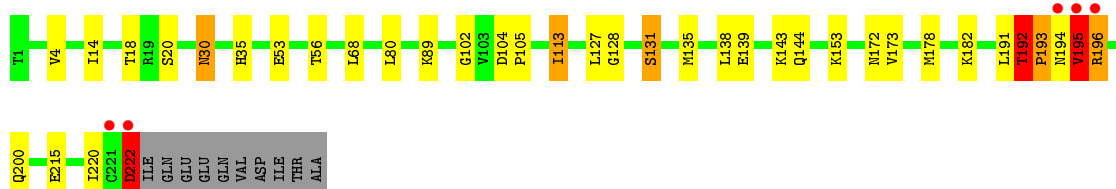
- Molecule 8: Proteasome subunit beta type-2

Chain H:  2% 80% 12%

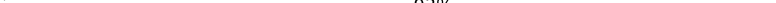


- Molecule 8: Proteasome subunit beta type-2

Chain V:  2% 79% 13% ...



- Molecule 9: Proteasome subunit beta type-3

Chain I:  93% 6% 1%




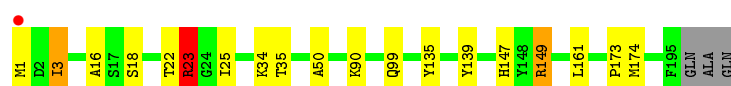
- Molecule 9: Proteasome subunit beta type-3

Chain W:  92% 7%




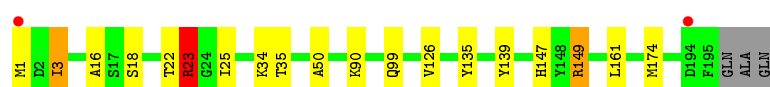
- Molecule 10: Proteasome subunit beta type-4

Chain J:  89% 8% ...



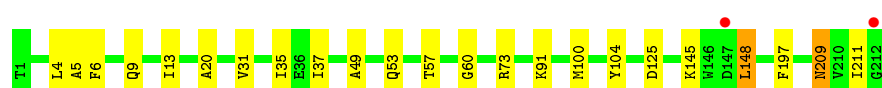
- Molecule 10: Proteasome subunit beta type-4

Chain X:  89% 8% ...



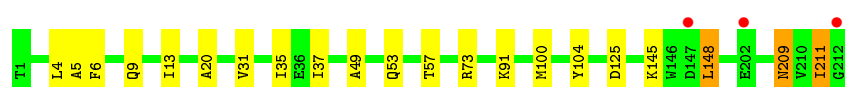
- Molecule 11: Proteasome subunit beta type-5

Chain K:  89% 10% .

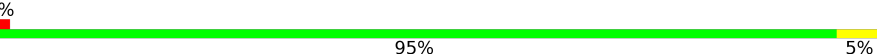


- Molecule 11: Proteasome subunit beta type-5

Chain Y:  90% 8% .



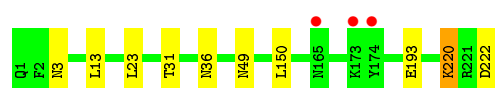
- Molecule 12: Proteasome subunit beta type-6

Chain L:  95% 5%




- Molecule 12: Proteasome subunit beta type-6

Chain Z:  95%




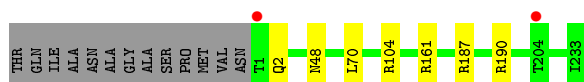
- Molecule 13: Proteasome subunit beta type-7

Chain M:  90% • • 5%

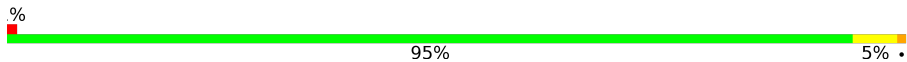


- Molecule 13: Proteasome subunit beta type-7

Chain a:  92% • 5%



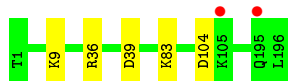
- Molecule 14: Proteasome subunit beta type-1

Chain N:  95% 5% •



- Molecule 14: Proteasome subunit beta type-1

Chain b:  97% •



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	134.22Å 300.86Å 144.10Å 90.00° 112.32° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.6 (15.00-2.80) 96.6 (15.00-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.198 , 0.218 0.203 , 0.223	Depositor DCC
R_{free} test set	12411 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	60.0	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 58.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	49853	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.30% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: BO2, MG, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.27	0/1952	0.46	0/2642
1	O	0.27	0/1952	0.46	0/2642
2	B	0.26	0/1934	0.50	0/2618
2	P	0.26	0/1934	0.50	0/2618
3	C	0.27	0/1910	0.50	0/2586
3	Q	0.27	0/1910	0.50	0/2586
4	D	0.26	0/1837	0.47	0/2475
4	R	0.26	0/1837	0.47	0/2475
5	E	0.26	0/1800	0.47	0/2433
5	S	0.26	0/1800	0.47	0/2433
6	F	0.27	0/1932	0.45	0/2609
6	T	0.26	0/1932	0.45	0/2609
7	G	0.27	0/1945	0.46	0/2634
7	U	0.26	0/1945	0.46	0/2634
8	H	0.46	2/1716 (0.1%)	0.73	3/2328 (0.1%)
8	V	0.47	3/1716 (0.2%)	0.72	3/2328 (0.1%)
9	I	0.27	0/1611	0.49	0/2174
9	W	0.27	0/1611	0.49	0/2174
10	J	0.27	0/1589	0.71	4/2142 (0.2%)
10	X	0.28	0/1589	0.75	4/2142 (0.2%)
11	K	0.26	0/1681	0.53	0/2274
11	Y	0.29	0/1681	0.53	0/2274
12	L	0.27	0/1795	0.51	0/2420
12	Z	0.32	0/1795	0.51	0/2420
13	M	0.27	0/1855	0.53	0/2514
13	a	0.27	0/1855	0.53	0/2514
14	N	0.25	0/1541	0.49	0/2087
14	b	0.25	0/1541	0.49	0/2087
All	All	0.29	5/50196 (0.0%)	0.53	14/67872 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying

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

Mol	Chain	#Chirality outliers	#Planarity outliers
8	V	0	1
10	X	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	4	VAL	CB-CG1	-6.63	1.39	1.52
8	H	4	VAL	CB-CG2	-6.55	1.39	1.52
8	V	4	VAL	CB-CG1	-6.31	1.39	1.52
8	V	4	VAL	CB-CG2	-5.77	1.40	1.52
8	V	193	PRO	N-CD	5.46	1.55	1.47

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	X	149	ARG	NE-CZ-NH2	-20.78	109.91	120.30
8	V	4	VAL	CG1-CB-CG2	-16.35	84.74	110.90
8	H	4	VAL	CG1-CB-CG2	-16.32	84.80	110.90
10	J	149	ARG	NE-CZ-NH1	-16.02	112.29	120.30
10	J	149	ARG	NE-CZ-NH2	14.32	127.46	120.30
10	X	149	ARG	CD-NE-CZ	12.23	140.72	123.60
10	X	149	ARG	NE-CZ-NH1	7.84	124.22	120.30
10	J	149	ARG	CD-NE-CZ	7.54	134.16	123.60
10	X	23	ARG	CG-CD-NE	6.06	124.53	111.80
8	H	192	THR	C-N-CD	6.02	141.05	128.40
10	J	23	ARG	CG-CD-NE	5.92	124.24	111.80
8	H	4	VAL	CB-CA-C	-5.79	100.41	111.40
8	V	192	THR	C-N-CD	5.55	140.05	128.40
8	V	222	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	V	193	PRO	Peptide
10	X	149	ARG	Sidechain

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	1	0
1	O	1915	0	1929	0	0
2	B	1904	0	1904	7	0
2	P	1904	0	1904	9	0
3	C	1881	0	1895	6	0
3	Q	1881	0	1895	6	0
4	D	1813	0	1797	4	0
4	R	1813	0	1797	5	0
5	E	1773	0	1775	3	0
5	S	1773	0	1775	5	0
6	F	1892	0	1883	1	0
6	T	1892	0	1883	1	0
7	G	1907	0	1901	5	0
7	U	1907	0	1901	4	0
8	H	1685	0	1689	22	0
8	V	1685	0	1689	22	0
9	I	1581	0	1574	6	0
9	W	1581	0	1574	8	0
10	J	1561	0	1569	11	0
10	X	1561	0	1569	12	0
11	K	1644	0	1594	12	0
11	Y	1644	0	1594	17	0
12	L	1757	0	1711	11	0
12	Z	1757	0	1711	3	0
13	M	1824	0	1832	4	0
13	a	1824	0	1832	0	0
14	N	1512	0	1480	3	0
14	b	1512	0	1480	0	0
15	G	1	0	0	0	0
15	I	1	0	0	0	0
15	J	1	0	0	0	0
15	K	1	0	0	0	0
15	N	1	0	0	0	0
15	V	1	0	0	0	0
15	Y	1	0	0	0	0
15	Z	2	0	0	0	0
16	G	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	N	1	0	0	0	0
16	U	1	0	0	0	0
16	b	1	0	0	0	0
17	H	28	0	25	2	0
17	K	28	0	25	1	0
17	N	28	0	25	0	0
17	V	28	0	25	0	0
17	Y	28	0	25	1	0
17	b	28	0	25	0	0
18	A	15	0	0	0	0
18	B	17	0	0	0	0
18	C	14	0	0	0	0
18	D	9	0	0	1	0
18	E	6	0	0	0	0
18	F	9	0	0	0	0
18	G	15	0	0	1	0
18	H	22	0	0	0	0
18	I	11	0	0	0	0
18	J	18	0	0	1	0
18	K	19	0	0	0	0
18	L	20	0	0	1	0
18	M	16	0	0	0	0
18	N	9	0	0	0	0
18	O	7	0	0	0	0
18	P	17	0	0	0	0
18	Q	6	0	0	0	0
18	R	8	0	0	0	0
18	S	7	0	0	0	0
18	T	14	0	0	0	0
18	U	14	0	0	0	0
18	V	10	0	0	0	0
18	W	10	0	0	0	0
18	X	18	0	0	1	0
18	Y	12	0	0	0	0
18	Z	18	0	0	0	0
18	a	21	0	0	0	0
18	b	12	0	0	0	0
All	All	49853	0	49216	165	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 (165) 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)
12:Z:193:GLU:OE1	12:Z:220:LYS:HE2	1.48	1.14
8:H:195:VAL:HG13	8:H:196:ARG:H	1.22	1.05
12:L:189:THR:HG22	8:V:196:ARG:NH1	1.94	0.81
12:L:189:THR:CG2	8:V:196:ARG:NH1	2.50	0.74
11:K:209:ASN:O	9:W:38:LYS:NZ	2.21	0.73
11:K:73:ARG:NH2	11:K:104:TYR:O	2.24	0.69
11:Y:73:ARG:NH2	11:Y:104:TYR:O	2.25	0.69
8:H:195:VAL:HG13	8:H:196:ARG:N	2.02	0.68
8:H:196:ARG:HG3	8:H:197:GLU:N	2.09	0.67
11:Y:35:ILE:HD11	11:Y:37:ILE:CG1	2.24	0.67
11:Y:35:ILE:C	11:Y:35:ILE:HD12	2.15	0.66
8:H:194:ASN:OD1	8:H:195:VAL:HB	1.96	0.66
10:J:139:TYR:OH	10:X:25:ILE:O	2.15	0.65
9:I:38:LYS:NZ	11:Y:209:ASN:O	2.30	0.64
8:V:172:ASN:ND2	8:V:192:THR:HG22	2.13	0.64
8:V:194:ASN:O	8:V:195:VAL:HG13	1.97	0.64
11:K:145:LYS:HB2	11:K:148:LEU:HD13	1.80	0.64
11:Y:35:ILE:HD11	11:Y:37:ILE:HG13	1.79	0.63
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	1.80	0.63
8:H:195:VAL:O	8:H:196:ARG:HB3	1.97	0.62
1:A:1:MET:HG3	6:F:122:TYR:CZ	2.34	0.62
9:I:125:LEU:HG	9:I:126:ILE:HG22	1.81	0.62
8:V:194:ASN:C	8:V:195:VAL:HG22	2.17	0.62
12:L:189:THR:CG2	8:V:196:ARG:HH11	2.12	0.62
9:W:125:LEU:HG	9:W:126:ILE:HG22	1.81	0.61
11:Y:35:ILE:CD1	11:Y:37:ILE:HG13	2.31	0.61
11:Y:35:ILE:HD12	11:Y:35:ILE:O	2.04	0.58
8:H:80:LEU:HD12	8:H:113:ILE:HD11	1.86	0.57
8:V:80:LEU:HD12	8:V:113:ILE:HD11	1.86	0.57
8:V:222:ASP:N	8:V:222:ASP:OD1	2.38	0.57
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.88	0.56
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.87	0.55
13:M:187:ARG:NH1	8:V:139:GLU:OE1	2.36	0.55
8:H:194:ASN:O	8:H:195:VAL:HG12	2.07	0.54
8:V:173:VAL:HB	8:V:191:LEU:HB2	1.89	0.54
8:H:35:HIS:CB	8:H:56:THR:HG21	2.37	0.54
7:U:23:PHE:O	7:U:26:THR:HB	2.08	0.53
8:H:195:VAL:CG1	8:H:196:ARG:H	2.03	0.53
11:K:49:ALA:HB3	17:K:301:BO2:H3	1.90	0.53
8:V:35:HIS:CB	8:V:56:THR:HG21	2.38	0.53
12:Z:31:THR:HG23	12:Z:36:ASN:HD21	1.73	0.53
11:Y:49:ALA:HB3	17:Y:301:BO2:H3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:201:VAL:O	3:C:202:GLN:CB	2.57	0.52
10:J:174:MET:HB2	18:J:310:HOH:O	2.08	0.52
12:L:31:THR:HG23	12:L:36:ASN:HD21	1.74	0.52
7:G:122:ARG:HD2	18:G:411:HOH:O	2.08	0.52
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.58	0.52
11:Y:35:ILE:HD11	11:Y:37:ILE:HG12	1.90	0.52
7:G:23:PHE:O	7:G:26:THR:HB	2.09	0.51
10:X:1:MET:HG2	10:X:34:LYS:HE3	1.93	0.49
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.94	0.49
10:J:25:ILE:O	10:X:139:TYR:OH	2.30	0.49
10:J:1:MET:HG2	10:J:34:LYS:HE3	1.93	0.49
12:L:4:PRO:O	13:M:104:ARG:NH1	2.44	0.48
3:C:160:GLN:HA	3:C:160:GLN:HE21	1.78	0.48
10:J:50:ALA:O	11:K:91:LYS:NZ	2.47	0.48
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.44	0.48
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.13	0.48
12:L:189:THR:HG22	8:V:196:ARG:HH11	1.69	0.48
3:Q:160:GLN:HA	3:Q:160:GLN:HE21	1.79	0.48
3:C:51:LYS:O	3:C:52:LEU:HB2	2.13	0.48
8:H:35:HIS:HB3	8:H:56:THR:HG21	1.95	0.48
10:X:174:MET:HB2	18:X:210:HOH:O	2.14	0.48
3:C:35:LYS:HG2	3:C:158:SER:O	2.13	0.47
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.96	0.47
2:B:221:ASP:O	2:B:223:GLU:N	2.48	0.47
12:L:135:GLN:HG3	18:L:303:HOH:O	2.14	0.47
11:Y:53:GLN:O	11:Y:57:THR:HG23	2.15	0.47
2:P:221:ASP:O	2:P:223:GLU:N	2.48	0.47
8:V:35:HIS:HB3	8:V:56:THR:HG21	1.96	0.47
8:V:128:GLY:O	8:V:131:SER:HB3	2.14	0.47
2:B:217:LYS:C	2:B:219:ALA:H	2.18	0.47
4:R:176:LEU:HA	5:S:55:LEU:HD21	1.97	0.47
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.15	0.46
8:H:128:GLY:O	8:H:131:SER:HB3	2.14	0.46
4:D:99:ILE:HG23	18:D:304:HOH:O	2.16	0.46
11:K:53:GLN:O	11:K:57:THR:HG23	2.15	0.45
2:P:50:LYS:HD3	2:P:50:LYS:HA	1.82	0.45
3:Q:201:VAL:O	3:Q:202:GLN:HB3	2.16	0.45
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	1.98	0.45
3:C:201:VAL:O	3:C:202:GLN:HB3	2.16	0.45
8:H:19:ARG:NE	8:H:170:ALA:HB3	2.31	0.45
2:P:217:LYS:C	2:P:219:ALA:H	2.18	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Y:5:ALA:HA	11:Y:13:ILE:O	2.16	0.45
2:P:145:TYR:OH	2:P:217:LYS:N	2.49	0.45
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.97	0.45
8:H:49:ALA:HA	17:H:301:BO2:C25	2.47	0.45
13:M:165:ILE:HB	13:M:166:PRO:HD3	1.99	0.45
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.47	0.45
8:V:135:MET:HE2	8:V:138:LEU:HD12	1.98	0.45
12:L:189:THR:HG21	8:V:196:ARG:HH11	1.82	0.45
2:B:145:TYR:OH	2:B:217:LYS:N	2.50	0.45
8:H:49:ALA:HA	17:H:301:BO2:H253	1.98	0.45
7:G:73:VAL:HG12	7:G:133:THR:HB	1.98	0.45
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.99	0.44
10:J:3:ILE:HG23	10:J:18:SER:HB3	2.00	0.44
13:M:96:LEU:O	13:M:100:MET:HG2	2.17	0.44
2:P:50:LYS:O	2:P:51:VAL:C	2.55	0.44
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.53	0.44
12:L:13:LEU:HD11	12:L:150:LEU:HD21	1.99	0.44
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.98	0.44
11:K:209:ASN:C	11:K:209:ASN:OD1	2.55	0.44
10:X:3:ILE:HG23	10:X:18:SER:HB3	1.99	0.44
11:K:5:ALA:HA	11:K:13:ILE:O	2.18	0.44
7:U:73:VAL:HG12	7:U:133:THR:HB	1.99	0.44
7:U:149:ASP:HB2	7:U:150:PRO:CD	2.48	0.44
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.99	0.44
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.99	0.44
2:B:50:LYS:O	2:B:51:VAL:C	2.56	0.43
11:Y:211:ILE:HG13	11:Y:211:ILE:H	1.72	0.43
12:Z:13:LEU:HD11	12:Z:150:LEU:HD21	2.00	0.43
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.49	0.43
8:H:102:GLY:HA2	8:H:178:MET:SD	2.59	0.43
11:Y:209:ASN:C	11:Y:209:ASN:OD1	2.57	0.43
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.53	0.43
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.48	0.43
2:P:47:ALA:HB1	2:P:64:LYS:HD2	2.01	0.43
14:N:176:VAL:HG12	14:N:178:LEU:HD13	2.01	0.43
8:H:196:ARG:HG3	8:H:197:GLU:H	1.83	0.43
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.49	0.43
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.99	0.43
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.42
9:I:10:ILE:HG21	9:I:141:ALA:HB3	2.01	0.42
11:K:6:PHE:HA	11:K:125:ASP:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:U:78:ILE:N	7:U:79:PRO:CD	2.82	0.42
8:H:194:ASN:OD1	8:H:195:VAL:N	2.52	0.42
8:H:215:GLU:HG2	9:I:197:ARG:HG2	2.00	0.42
11:Y:6:PHE:HA	11:Y:125:ASP:O	2.18	0.42
10:X:22:THR:O	10:X:23:ARG:NH2	2.53	0.42
10:X:50:ALA:O	11:Y:91:LYS:NZ	2.52	0.42
2:B:47:ALA:HB1	2:B:64:LYS:HD2	2.01	0.42
12:L:8:ASN:HA	12:L:30:ILE:O	2.20	0.42
4:R:176:LEU:HD11	5:S:54:GLU:HB2	2.01	0.42
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.55	0.42
8:H:18:THR:HB	8:H:30:ASN:HA	2.02	0.42
2:P:151:ASN:HB2	2:P:152:PRO:HD2	2.02	0.42
9:W:10:ILE:HG21	9:W:141:ALA:HB3	2.01	0.42
5:S:87:LEU:HD21	5:S:107:ALA:HB1	2.02	0.42
8:H:191:LEU:HA	8:H:191:LEU:HD23	1.87	0.41
2:P:145:TYR:OH	2:P:217:LYS:HB2	2.20	0.41
8:V:18:THR:HB	8:V:30:ASN:HA	2.02	0.41
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.03	0.41
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.50	0.41
8:V:194:ASN:O	8:V:195:VAL:HG22	2.20	0.41
5:E:87:LEU:HD21	5:E:107:ALA:HB1	2.02	0.41
4:D:88:ALA:HA	4:D:99:ILE:HG21	2.02	0.41
11:K:37:ILE:HG23	11:K:60:GLY:HA2	2.02	0.41
8:V:194:ASN:C	8:V:195:VAL:CG2	2.85	0.41
2:B:151:ASN:HB2	2:B:152:PRO:HD2	2.02	0.41
5:E:77:ALA:N	5:E:78:PRO:CD	2.84	0.41
10:J:22:THR:O	10:J:23:ARG:NH2	2.53	0.41
3:Q:149:GLU:HB2	3:Q:150:PRO:HD2	2.02	0.41
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.55	0.41
5:S:77:ALA:N	5:S:78:PRO:CD	2.84	0.41
10:J:135:TYR:HB3	10:X:25:ILE:HD11	2.03	0.41
14:N:175:MET:HB2	14:N:186:LEU:HB2	2.02	0.41
11:K:197:PHE:CE2	9:W:203:GLN:HG3	2.55	0.41
8:V:215:GLU:HG2	9:W:197:ARG:HG2	2.03	0.41
3:C:149:GLU:HB2	3:C:150:PRO:HD2	2.03	0.41
10:J:25:ILE:HD11	10:X:135:TYR:HB3	2.02	0.41
6:T:198:LEU:HD12	6:T:243:ILE:HG22	2.03	0.41
8:V:102:GLY:HA2	8:V:178:MET:SD	2.60	0.41
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.52	0.40
8:H:53:GLU:OE1	8:H:57:GLN:NE2	2.43	0.40
10:J:173:PRO:HB3	10:X:22:THR:HG21	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	238 (96%)	9 (4%)	1 (0%)	39	74
1	O	248/250 (99%)	238 (96%)	9 (4%)	1 (0%)	39	74
2	B	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	11	36
2	P	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	11	36
3	C	238/254 (94%)	233 (98%)	2 (1%)	3 (1%)	15	44
3	Q	238/254 (94%)	233 (98%)	2 (1%)	3 (1%)	15	44
4	D	231/260 (89%)	227 (98%)	4 (2%)	0	100	100
4	R	231/260 (89%)	228 (99%)	3 (1%)	0	100	100
5	E	229/234 (98%)	220 (96%)	9 (4%)	0	100	100
5	S	229/234 (98%)	220 (96%)	9 (4%)	0	100	100
6	F	241/288 (84%)	237 (98%)	4 (2%)	0	100	100
6	T	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
7	G	239/252 (95%)	238 (100%)	1 (0%)	0	100	100
7	U	239/252 (95%)	238 (100%)	1 (0%)	0	100	100
8	H	220/232 (95%)	212 (96%)	6 (3%)	2 (1%)	21	55
8	V	220/232 (95%)	211 (96%)	7 (3%)	2 (1%)	21	55
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%)	190 (98%)	3 (2%)	0	100	100
10	X	193/198 (98%)	190 (98%)	3 (2%)	0	100	100
11	K	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
11	Y	210/212 (99%)	206 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	231/246 (94%)	220 (95%)	11 (5%)	0	100	100
13	a	231/246 (94%)	220 (95%)	11 (5%)	0	100	100
14	N	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
14	b	194/196 (99%)	188 (97%)	6 (3%)	0	100	100
All	All	6276/6614 (95%)	6108 (97%)	148 (2%)	20 (0%)	46	79

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
2	B	222	GLY
3	C	202	GLN
2	P	51	VAL
2	P	222	GLY
3	Q	202	GLN
8	V	195	VAL
1	A	2	THR
2	B	218	GLY
1	O	2	THR
2	P	218	GLY
8	H	195	VAL
2	B	220	ASN
2	P	220	ASN
8	V	200	GLN
3	C	205	ALA
8	H	196	ARG
3	Q	205	ALA
3	C	183	PRO
3	Q	183	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	206 (99%)	3 (1%)	74	94
1	O	209/209 (100%)	206 (99%)	3 (1%)	74	94
2	B	203/216 (94%)	197 (97%)	6 (3%)	48	82
2	P	203/216 (94%)	198 (98%)	5 (2%)	55	86
3	C	212/226 (94%)	202 (95%)	10 (5%)	32	67
3	Q	212/226 (94%)	202 (95%)	10 (5%)	32	67
4	D	194/215 (90%)	186 (96%)	8 (4%)	37	72
4	R	194/215 (90%)	186 (96%)	8 (4%)	37	72
5	E	190/193 (98%)	183 (96%)	7 (4%)	41	76
5	S	190/193 (98%)	183 (96%)	7 (4%)	41	76
6	F	201/239 (84%)	194 (96%)	7 (4%)	43	77
6	T	201/239 (84%)	194 (96%)	7 (4%)	43	77
7	G	206/210 (98%)	200 (97%)	6 (3%)	50	83
7	U	206/210 (98%)	200 (97%)	6 (3%)	50	83
8	H	181/190 (95%)	163 (90%)	18 (10%)	10	28
8	V	181/190 (95%)	163 (90%)	18 (10%)	10	28
9	I	172/173 (99%)	168 (98%)	4 (2%)	58	88
9	W	172/173 (99%)	168 (98%)	4 (2%)	58	88
10	J	173/175 (99%)	166 (96%)	7 (4%)	38	73
10	X	173/175 (99%)	167 (96%)	6 (4%)	43	77
11	K	169/169 (100%)	162 (96%)	7 (4%)	37	72
11	Y	169/169 (100%)	163 (96%)	6 (4%)	42	76
12	L	185/185 (100%)	182 (98%)	3 (2%)	70	93
12	Z	185/185 (100%)	180 (97%)	5 (3%)	52	85
13	M	199/208 (96%)	192 (96%)	7 (4%)	43	77
13	a	199/208 (96%)	192 (96%)	7 (4%)	43	77
14	N	162/162 (100%)	157 (97%)	5 (3%)	47	81
14	b	162/162 (100%)	157 (97%)	5 (3%)	47	81
All	All	5312/5540 (96%)	5117 (96%)	195 (4%)	41	76

All (195) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	55	LEU
2	B	102	ASN
2	B	113	ARG
2	B	186	ASP
2	B	191	LEU
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	51	LYS
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	206	LYS
3	C	240	GLU
4	D	99	ILE
4	D	125	LEU
4	D	176	LEU
4	D	193	LEU
4	D	214	ILE
4	D	235	LEU
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	29	LYS
5	E	71	LEU
5	E	184	ASN
5	E	188	LEU
5	E	202	ASP
5	E	231	LYS
6	F	117	GLN
6	F	123	ASN
6	F	139	LYS
6	F	181	GLU
6	F	202	ASP
6	F	214	TRP
6	F	240	GLN
7	G	115	LEU
7	G	122	ARG

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Mol	Chain	Res	Type
7	G	125	MET
7	G	208	GLU
7	G	235	ARG
7	G	236	LEU
8	H	4	VAL
8	H	14	ILE
8	H	20	SER
8	H	30	ASN
8	H	53	GLU
8	H	68	LEU
8	H	89	LYS
8	H	113	ILE
8	H	127	LEU
8	H	131	SER
8	H	143	LYS
8	H	144	GLN
8	H	153	LYS
8	H	182	LYS
8	H	194	ASN
8	H	196	ARG
8	H	220	ILE
8	H	222	ASP
9	I	37	ASN
9	I	126	ILE
9	I	171	LEU
9	I	182	TRP
10	J	3	ILE
10	J	23	ARG
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
10	J	147	HIS
10	J	149	ARG
11	K	4	LEU
11	K	9	GLN
11	K	35	ILE
11	K	100	MET
11	K	148	LEU
11	K	209	ASN
11	K	211	ILE
12	L	3	ASN
12	L	23	LEU

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Mol	Chain	Res	Type
12	L	49	ASN
13	M	2	GLN
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	161	ARG
13	M	187	ARG
13	M	190	ARG
14	N	9	LYS
14	N	36	ARG
14	N	39	ASP
14	N	83	LYS
14	N	104	ASP
1	O	122	THR
1	O	157	PHE
1	O	250	LEU
2	P	55	LEU
2	P	113	ARG
2	P	186	ASP
2	P	191	LEU
2	P	238	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	51	LYS
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS
3	Q	206	LYS
3	Q	240	GLU
4	R	99	ILE
4	R	125	LEU
4	R	176	LEU
4	R	193	LEU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	71	LEU

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Mol	Chain	Res	Type
5	S	184	ASN
5	S	188	LEU
5	S	202	ASP
5	S	231	LYS
6	T	117	GLN
6	T	123	ASN
6	T	139	LYS
6	T	181	GLU
6	T	202	ASP
6	T	214	TRP
6	T	240	GLN
7	U	115	LEU
7	U	122	ARG
7	U	125	MET
7	U	208	GLU
7	U	235	ARG
7	U	236	LEU
8	V	14	ILE
8	V	20	SER
8	V	30	ASN
8	V	53	GLU
8	V	68	LEU
8	V	89	LYS
8	V	113	ILE
8	V	127	LEU
8	V	131	SER
8	V	143	LYS
8	V	144	GLN
8	V	153	LYS
8	V	182	LYS
8	V	192	THR
8	V	195	VAL
8	V	196	ARG
8	V	220	ILE
8	V	222	ASP
9	W	37	ASN
9	W	126	ILE
9	W	171	LEU
9	W	182	TRP
10	X	3	ILE
10	X	23	ARG
10	X	35	THR

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Mol	Chain	Res	Type
10	X	90	LYS
10	X	99	GLN
10	X	147	HIS
11	Y	4	LEU
11	Y	9	GLN
11	Y	100	MET
11	Y	148	LEU
11	Y	209	ASN
11	Y	211	ILE
12	Z	3	ASN
12	Z	23	LEU
12	Z	49	ASN
12	Z	220	LYS
12	Z	222	ASP
13	a	2	GLN
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	161	ARG
13	a	187	ARG
13	a	190	ARG
14	b	9	LYS
14	b	36	ARG
14	b	39	ASP
14	b	83	LYS
14	b	104	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (102) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	58	GLN
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
3	C	17	GLN
3	C	38	ASN
3	C	77	ASN
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	91	HIS

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Mol	Chain	Res	Type
4	D	146	GLN
4	D	225	ASN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	151	ASN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	191	GLN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
8	H	172	ASN
8	H	200	GLN
10	J	55	GLN
10	J	146	HIS
11	K	9	GLN
11	K	85	ASN
11	K	176	ASN
11	K	208	ASN
12	L	3	ASN
12	L	49	ASN
12	L	70	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	58	GLN
2	P	95	GLN

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Mol	Chain	Res	Type
2	P	119	GLN
2	P	123	GLN
3	Q	77	ASN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	91	HIS
4	R	146	GLN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	116	GLN
5	S	118	ASN
5	S	120	GLN
5	S	151	ASN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	191	GLN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
8	V	30	ASN
8	V	66	HIS
8	V	172	ASN
8	V	189	ASN
10	X	55	GLN
10	X	78	GLN
10	X	146	HIS
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
11	Y	208	ASN
12	Z	3	ASN
12	Z	49	ASN
12	Z	70	ASN
13	a	18	ASN

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Mol	Chain	Res	Type
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 ⓘ

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 13 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
17	BO2	H	301	8	28,29,29	1.78	2 (7%)	32,38,38	1.30	3 (9%)
17	BO2	K	301	11	28,29,29	1.49	5 (17%)	32,38,38	1.18	3 (9%)
17	BO2	N	201	14	28,29,29	1.49	4 (14%)	32,38,38	1.19	5 (15%)
17	BO2	V	301	8	28,29,29	1.50	2 (7%)	32,38,38	1.39	7 (21%)
17	BO2	Y	301	11	28,29,29	1.50	5 (17%)	32,38,38	1.22	3 (9%)
17	BO2	b	201	14	28,29,29	1.51	4 (14%)	32,38,38	1.17	5 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	BO2	H	301	8	-	0/22/28/28	0/2/2/2
17	BO2	K	301	11	-	0/22/28/28	0/2/2/2
17	BO2	N	201	14	-	0/22/28/28	0/2/2/2
17	BO2	V	301	8	-	2/22/28/28	0/2/2/2
17	BO2	Y	301	11	-	0/22/28/28	0/2/2/2
17	BO2	b	201	14	-	0/22/28/28	0/2/2/2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	H	301	BO2	C2-C7	-6.22	1.36	1.50
17	H	301	BO2	C11-C12	-5.77	1.37	1.51
17	V	301	BO2	C2-C7	-5.22	1.38	1.50
17	V	301	BO2	C11-C12	-4.74	1.39	1.51
17	Y	301	BO2	C2-C7	-4.69	1.39	1.50
17	K	301	BO2	C2-C7	-4.68	1.39	1.50
17	b	201	BO2	C2-C7	-4.49	1.40	1.50
17	N	201	BO2	C2-C7	-4.49	1.40	1.50
17	b	201	BO2	C11-C12	-4.02	1.41	1.51
17	Y	301	BO2	C11-C12	-3.98	1.41	1.51
17	K	301	BO2	C11-C12	-3.98	1.41	1.51
17	N	201	BO2	C11-C12	-3.95	1.41	1.51
17	Y	301	BO2	C5-N4	2.17	1.40	1.33
17	K	301	BO2	C5-N4	2.20	1.40	1.33
17	K	301	BO2	C6-N1	2.64	1.40	1.34
17	N	201	BO2	C3-N4	2.68	1.40	1.34
17	K	301	BO2	C3-N4	2.75	1.40	1.34
17	Y	301	BO2	C6-N1	2.76	1.40	1.34
17	b	201	BO2	C3-N4	2.82	1.40	1.34
17	Y	301	BO2	C3-N4	2.89	1.40	1.34
17	b	201	BO2	C6-N1	2.96	1.41	1.34
17	N	201	BO2	C6-N1	3.00	1.41	1.34

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	H	301	BO2	C22-C21-N20	-3.24	105.50	110.99
17	V	301	BO2	C6-C5-N4	-2.79	118.17	121.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	N	201	BO2	C21-C22-C23	-2.41	110.45	115.61
17	b	201	BO2	C21-C22-C23	-2.33	110.63	115.61
17	Y	301	BO2	C21-C22-C23	-2.32	110.64	115.61
17	N	201	BO2	C6-C5-N4	-2.29	118.84	121.95
17	V	301	BO2	C22-C21-N20	-2.27	107.13	110.99
17	H	301	BO2	C5-C6-N1	-2.24	119.43	122.23
17	V	301	BO2	C5-C6-N1	-2.24	119.43	122.23
17	K	301	BO2	C21-C22-C23	-2.23	110.83	115.61
17	b	201	BO2	C11-C10-N9	-2.23	106.08	110.81
17	N	201	BO2	C11-C10-N9	-2.12	106.32	110.81
17	b	201	BO2	C6-C5-N4	-2.08	119.13	121.95
17	V	301	BO2	C3-C2-N1	-2.08	119.12	121.69
17	V	301	BO2	C2-C3-N4	-2.08	119.52	122.05
17	Y	301	BO2	C5-C6-N1	-2.03	119.69	122.23
17	K	301	BO2	C5-C6-N1	-2.02	119.70	122.23
17	N	201	BO2	C7-C2-N1	2.18	120.25	117.67
17	b	201	BO2	C7-C2-N1	2.19	120.26	117.67
17	V	301	BO2	C5-N4-C3	2.45	121.31	116.82
17	N	201	BO2	C6-N1-C2	2.85	120.72	116.93
17	b	201	BO2	C6-N1-C2	2.85	120.73	116.93
17	H	301	BO2	C6-N1-C2	2.98	120.89	116.93
17	K	301	BO2	C6-N1-C2	3.21	121.20	116.93
17	Y	301	BO2	C6-N1-C2	3.34	121.37	116.93
17	V	301	BO2	C6-N1-C2	4.15	122.44	116.93

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	V	301	BO2	O8-C7-C2-C3
17	V	301	BO2	C3-C2-C7-N9

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	H	301	BO2	2	0
17	K	301	BO2	1	0
17	Y	301	BO2	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 ⓘ

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%)	-0.42	4 (1%) 74 66	46, 61, 102, 141	0
1	O	250/250 (100%)	-0.38	5 (2%) 68 58	46, 65, 110, 143	0
2	B	244/258 (94%)	-0.33	5 (2%) 68 58	46, 67, 113, 171	0
2	P	244/258 (94%)	-0.36	7 (2%) 55 43	49, 68, 110, 157	0
3	C	240/254 (94%)	-0.31	9 (3%) 44 32	42, 67, 127, 158	0
3	Q	240/254 (94%)	-0.04	11 (4%) 36 25	55, 85, 166, 186	0
4	D	235/260 (90%)	-0.44	3 (1%) 79 71	47, 69, 100, 145	0
4	R	235/260 (90%)	-0.24	7 (2%) 54 41	57, 81, 120, 162	0
5	E	231/234 (98%)	-0.22	5 (2%) 65 54	49, 76, 118, 164	0
5	S	231/234 (98%)	-0.10	8 (3%) 48 35	57, 86, 137, 175	0
6	F	243/288 (84%)	-0.47	6 (2%) 61 48	45, 68, 116, 147	0
6	T	243/288 (84%)	-0.36	3 (1%) 81 73	47, 78, 134, 166	0
7	G	241/252 (95%)	-0.48	0 100 100	46, 65, 103, 153	0
7	U	241/252 (95%)	-0.43	3 (1%) 81 73	49, 65, 101, 150	0
8	H	222/232 (95%)	-0.52	5 (2%) 64 52	37, 58, 92, 153	0
8	V	222/232 (95%)	-0.51	5 (2%) 64 52	37, 57, 93, 158	0
9	I	204/205 (99%)	-0.70	2 (0%) 84 77	39, 56, 86, 113	0
9	W	204/205 (99%)	-0.64	1 (0%) 91 88	37, 54, 85, 107	0
10	J	195/198 (98%)	-0.51	1 (0%) 91 88	39, 56, 88, 127	0
10	X	195/198 (98%)	-0.49	2 (1%) 84 77	42, 59, 86, 140	0
11	K	212/212 (100%)	-0.46	2 (0%) 85 79	39, 57, 91, 109	0
11	Y	212/212 (100%)	-0.38	3 (1%) 78 69	25, 59, 101, 122	0
12	L	222/222 (100%)	-0.49	4 (1%) 71 61	41, 59, 108, 139	0
12	Z	222/222 (100%)	-0.50	3 (1%) 78 69	40, 63, 112, 146	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.66	1 (0%)	93 90	40, 58, 81, 103	0
13	a	233/246 (94%)	-0.58	2 (0%)	85 79	41, 60, 84, 104	0
14	N	196/196 (100%)	-0.70	2 (1%)	84 77	40, 52, 83, 108	0
14	b	196/196 (100%)	-0.68	2 (1%)	84 77	40, 54, 83, 114	0
All	All	6336/6614 (95%)	-0.44	111 (1%)	71 61	25, 64, 115, 186	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	218	GLY	7.7
3	Q	50	LEU	6.7
2	B	220	ASN	5.7
8	V	222	ASP	5.6
2	B	219	ALA	5.6
11	Y	212	GLY	5.4
2	P	219	ALA	5.4
8	H	195	VAL	5.3
2	P	51	VAL	5.2
2	B	51	VAL	5.1
3	Q	49	THR	4.9
2	P	220	ASN	4.9
2	P	221	ASP	4.8
2	B	221	ASP	4.6
8	H	222	ASP	4.6
8	V	194	ASN	4.5
5	E	202	ASP	4.3
10	X	1	MET	4.2
5	S	202	ASP	4.1
3	C	206	LYS	4.0
8	H	194	ASN	4.0
1	A	1	MET	3.9
10	J	1	MET	3.8
3	Q	206	LYS	3.7
8	V	195	VAL	3.7
2	P	218	GLY	3.7
1	O	249	ALA	3.6
3	Q	238	LYS	3.6
1	O	2	THR	3.5
3	Q	239	GLN	3.5
9	W	1	SER	3.5
3	Q	240	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
7	U	242	GLN	3.3
3	C	238	LYS	3.3
3	Q	236	GLN	3.3
8	H	221	CYS	3.3
5	E	123	GLY	3.2
1	A	2	THR	3.2
12	L	162	PRO	3.1
6	F	51	THR	3.1
8	V	196	ARG	3.0
12	L	165	ASN	3.0
12	Z	173	LYS	3.0
8	V	221	CYS	3.0
12	L	163	GLY	2.9
5	S	165	GLN	2.9
3	C	49	THR	2.9
14	b	195	GLN	2.9
4	D	1	ASP	2.8
12	Z	174	TYR	2.8
4	R	241	ALA	2.8
5	S	227	GLU	2.7
1	A	229	THR	2.7
3	C	50	LEU	2.7
1	O	52	SER	2.7
5	S	180	LYS	2.7
11	Y	147	ASP	2.7
5	E	122	TYR	2.7
4	R	1	ASP	2.7
12	Z	165	ASN	2.6
12	L	174	TYR	2.6
6	F	2	THR	2.6
13	a	1	THR	2.6
3	Q	48	SER	2.6
1	A	249	ALA	2.6
4	R	230	GLU	2.6
6	T	244	ASN	2.5
3	C	1	GLY	2.5
6	F	202	ASP	2.5
1	O	1	MET	2.5
14	b	105	LYS	2.5
4	D	242	GLU	2.4
11	K	212	GLY	2.4
13	a	204	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	O	201	GLU	2.4
4	R	242	GLU	2.4
4	R	203	LYS	2.4
8	H	196	ARG	2.4
6	F	181	GLU	2.3
2	P	59	ASP	2.3
14	N	195	GLN	2.3
11	K	147	ASP	2.3
5	S	29	LYS	2.2
3	C	202	GLN	2.2
6	T	181	GLU	2.2
6	F	244	ASN	2.2
6	T	215	CYS	2.2
6	F	201	GLU	2.2
7	U	188	GLU	2.2
3	C	181	GLU	2.2
3	Q	202	GLN	2.2
4	R	239	GLU	2.2
3	C	216	ASP	2.2
3	Q	27	ARG	2.2
9	I	1	SER	2.1
9	I	192	ASP	2.1
13	M	47	ASP	2.1
5	S	201	ARG	2.1
5	S	51	ASN	2.1
5	E	180	LYS	2.1
14	N	105	LYS	2.1
7	U	241	GLU	2.1
10	X	194	ASP	2.1
5	S	54	GLU	2.1
11	Y	202	GLU	2.1
3	C	239	GLN	2.1
3	Q	3	ASP	2.0
4	R	2	ARG	2.0
2	P	230	LYS	2.0
4	D	2	ARG	2.0
5	E	217	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
15	MG	J	201	1/1	0.98	0.28	10.31	30,30,30,30	0
15	MG	Z	301	1/1	0.91	0.44	9.60	77,77,77,77	0
15	MG	Z	302	1/1	0.93	0.28	6.17	30,30,30,30	0
17	BO2	b	201	28/28	0.89	0.21	2.97	44,52,62,64	0
17	BO2	N	201	28/28	0.89	0.20	2.82	39,51,62,63	0
17	BO2	V	301	28/28	0.90	0.25	2.34	49,61,78,79	0
17	BO2	H	301	28/28	0.91	0.24	2.24	48,56,63,64	0
17	BO2	K	301	28/28	0.94	0.18	1.30	43,54,63,63	0
15	MG	I	301	1/1	0.95	0.18	1.17	66,66,66,66	0
17	BO2	Y	301	28/28	0.93	0.18	1.06	47,58,66,66	0
15	MG	N	202	1/1	0.93	0.13	0.70	58,58,58,58	0
16	CL	N	203	1/1	0.96	0.11	0.20	49,49,49,49	0
16	CL	b	202	1/1	0.96	0.10	-0.90	53,53,53,53	0
15	MG	K	302	1/1	0.95	0.08	-1.16	57,57,57,57	0
15	MG	Y	302	1/1	0.96	0.09	-1.31	48,48,48,48	0
15	MG	G	301	1/1	0.97	0.07	-1.55	54,54,54,54	0
15	MG	V	302	1/1	0.90	0.08	-1.80	72,72,72,72	0
16	CL	G	302	1/1	0.98	0.19	-	50,50,50,50	0
16	CL	U	301	1/1	0.99	0.20	-	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.