



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 15, 2026 – 01:39 AM UTC

PDB ID : 9QCF / pdb_00009qcf
Title : Yeast 20S proteasome mutant: beta1_G128V
Authors : Huber, E.M.; Heinemeyer, W.; Groll, M.
Deposited on : 2025-03-04
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
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

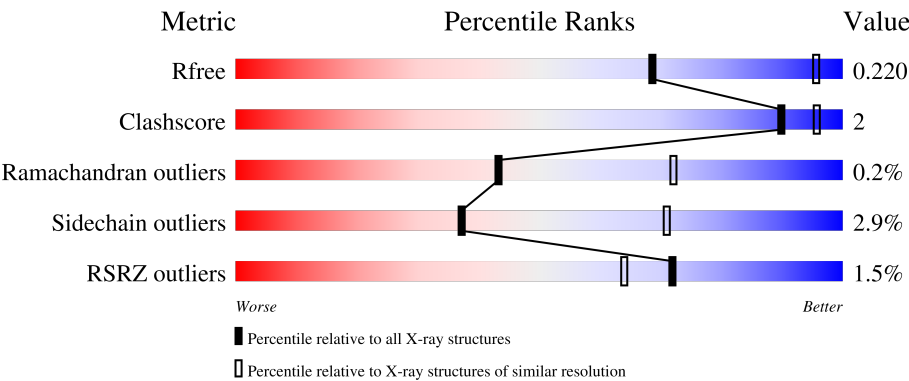
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	98%
1	O	250	98%
2	B	258	90% 5%
2	P	258	90% 5%
3	C	254	91% 6%

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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	246	
13	a	246	
14	N	215	
14	b	215	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 49433 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	191	Total	C	N	O	S	0	0	0
			1474	931	246	291	6			
14	b	191	Total	C	N	O	S	0	0	0
			1474	931	246	291	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	128	VAL	GLY	conflict	UNP P38624
b	128	VAL	GLY	conflict	UNP P38624

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 16 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 17 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	2	Total O 2 2	0	0
17	B	8	Total O 8 8	0	0
17	C	9	Total O 9 9	0	0
17	D	3	Total O 3 3	0	0
17	E	4	Total O 4 4	0	0
17	F	6	Total O 6 6	0	0
17	G	6	Total O 6 6	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	H	9	Total O 9 9	0	0
17	I	4	Total O 4 4	0	0
17	J	8	Total O 8 8	0	0
17	K	12	Total O 12 12	0	0
17	L	11	Total O 11 11	0	0
17	M	10	Total O 10 10	0	0
17	N	8	Total O 8 8	0	0
17	O	3	Total O 3 3	0	0
17	P	8	Total O 8 8	0	0
17	Q	6	Total O 6 6	0	0
17	R	6	Total O 6 6	0	0
17	S	5	Total O 5 5	0	0
17	T	4	Total O 4 4	0	0
17	U	7	Total O 7 7	0	0
17	V	11	Total O 11 11	0	0
17	W	5	Total O 5 5	0	0
17	X	9	Total O 9 9	0	0
17	Y	12	Total O 12 12	0	0
17	Z	12	Total O 12 12	0	0
17	a	9	Total O 9 9	0	0
17	b	4	Total O 4 4	0	0

3 Residue-property plots [i](#)

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

- Molecule 1: Proteasome subunit alpha type-2



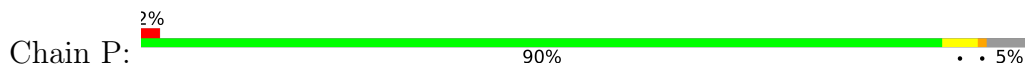
- Molecule 1: Proteasome subunit alpha type-2



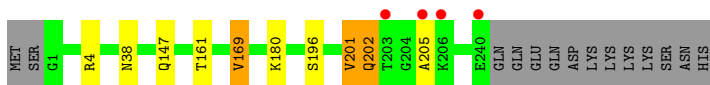
- Molecule 2: Proteasome subunit alpha type-3



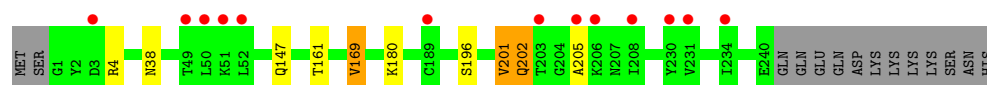
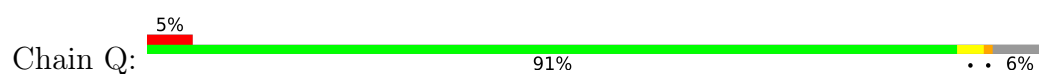
- Molecule 2: Proteasome subunit alpha type-3



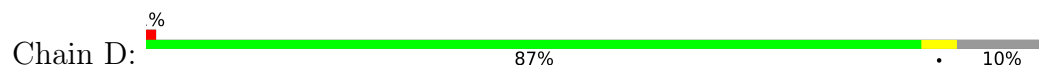
- Molecule 3: Proteasome subunit alpha type-4



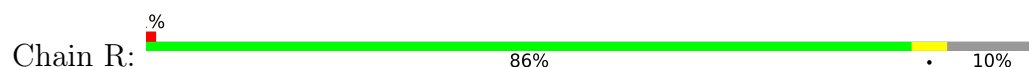
- Molecule 3: Proteasome subunit alpha type-4



- Molecule 4: Proteasome subunit alpha type-5



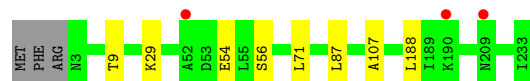
- Molecule 4: Proteasome subunit alpha type-5



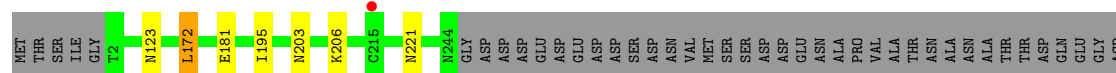
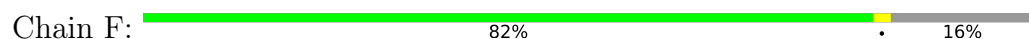
- Molecule 5: Proteasome subunit alpha type-6



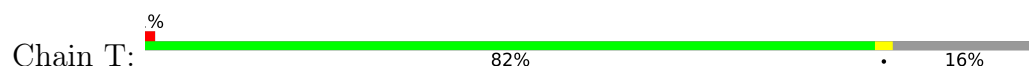
- Molecule 5: Proteasome subunit alpha type-6

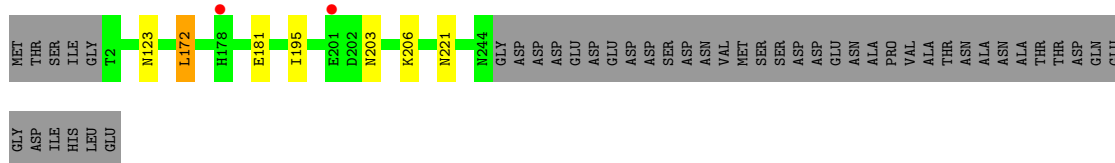


- Molecule 6: Probable proteasome subunit alpha type-7



- Molecule 6: Probable proteasome subunit alpha type-7





- Molecule 7: Proteasome subunit alpha type-1

Chain G: 90% 5%



- Molecule 7: Proteasome subunit alpha type-1

Chain U: 90% 5%



- Molecule 8: Proteasome subunit beta type-2

Chain H: 92% 5%



- Molecule 8: Proteasome subunit beta type-2

Chain V: 92% 5%



- Molecule 9: Proteasome subunit beta type-3

Chain I: 93% 7%

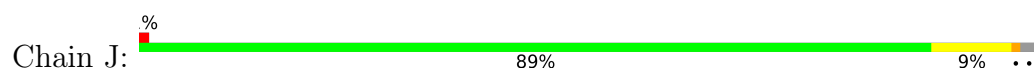


- Molecule 9: Proteasome subunit beta type-3

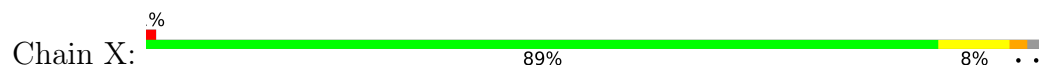
Chain W: 92% 8%



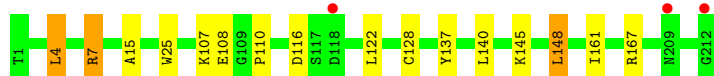
- Molecule 10: Proteasome subunit beta type-4



- Molecule 10: Proteasome subunit beta type-4



- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5



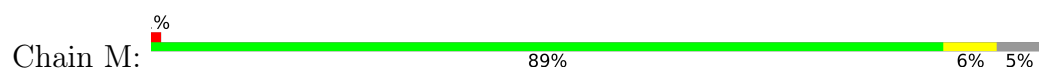
- Molecule 12: Proteasome subunit beta type-6



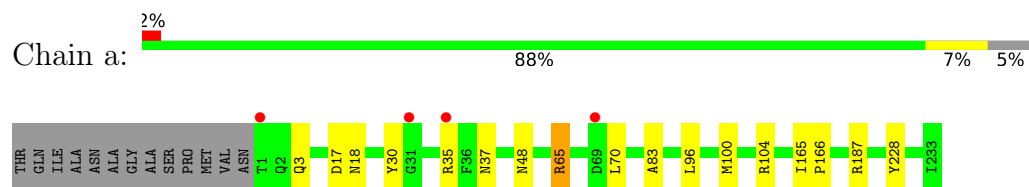
- Molecule 12: Proteasome subunit beta type-6



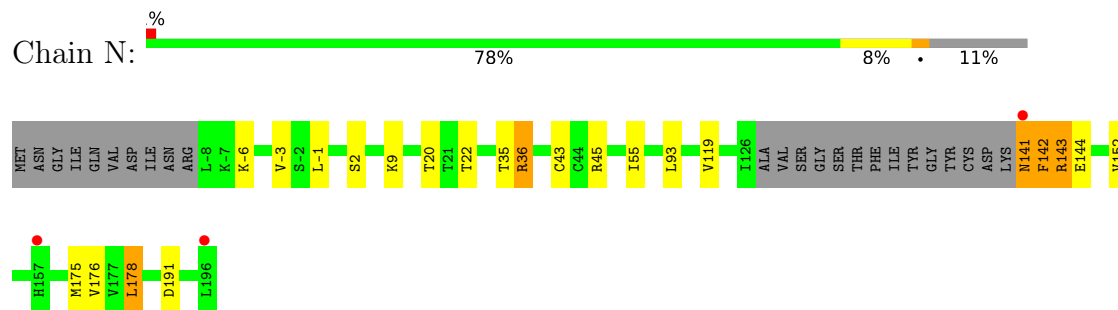
- Molecule 13: Proteasome subunit beta type-7



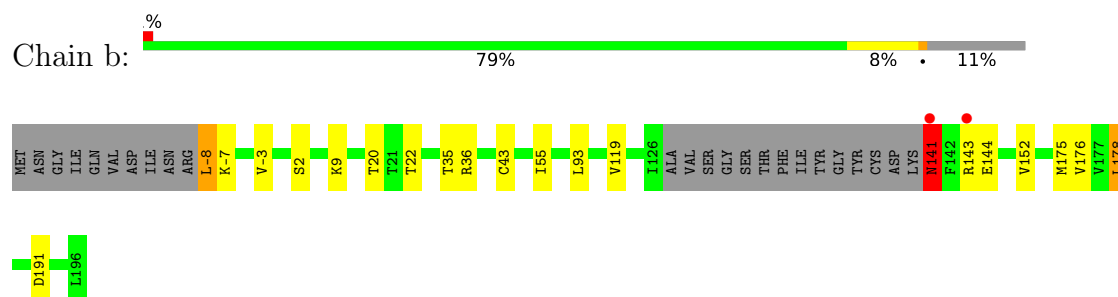
- Molecule 13: Proteasome subunit beta type-7



- Molecule 14: Proteasome subunit beta type-1



- Molecule 14: Proteasome subunit beta type-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	134.91Å 301.57Å 144.43Å 90.00° 112.99° 90.00°	Depositor
Resolution (Å)	15.00 – 2.90 15.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (15.00-2.90) 96.8 (15.00-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.188 , 0.214 0.194 , 0.220	Depositor DCC
R_{free} test set	11327 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	61.6	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 57.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	49433	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.26% 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: CL, MG

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	0.39	0/1952	0.68	0/2642
1	O	0.39	0/1952	0.68	0/2642
2	B	0.39	0/1934	0.66	0/2618
2	P	0.39	0/1934	0.66	0/2618
3	C	0.39	0/1910	0.70	1/2586 (0.0%)
3	Q	0.39	0/1910	0.70	1/2586 (0.0%)
4	D	0.38	0/1837	0.65	0/2475
4	R	0.38	0/1837	0.65	0/2475
5	E	0.38	0/1800	0.66	0/2433
5	S	0.38	0/1800	0.66	0/2433
6	F	0.40	0/1932	0.71	0/2609
6	T	0.39	0/1932	0.71	0/2609
7	G	0.38	0/1945	0.66	0/2634
7	U	0.39	0/1945	0.66	0/2634
8	H	0.35	0/1715	0.68	0/2326
8	V	0.35	0/1715	0.68	0/2326
9	I	0.36	0/1611	0.72	0/2174
9	W	0.36	0/1611	0.72	0/2174
10	J	0.48	0/1589	0.77	0/2142
10	X	0.47	0/1589	0.73	0/2142
11	K	0.35	0/1681	0.69	0/2274
11	Y	0.35	0/1681	0.69	0/2274
12	L	0.35	0/1795	0.69	0/2420
12	Z	0.35	0/1795	0.69	0/2420
13	M	0.37	0/1855	0.73	1/2514 (0.0%)
13	a	0.37	0/1855	0.73	0/2514
14	N	0.37	0/1499	0.70	0/2027
14	b	0.36	0/1499	0.73	1/2027 (0.0%)
All	All	0.38	0/50110	0.69	4/67748 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	201	VAL	N-CA-C	5.46	115.90	110.23
3	Q	201	VAL	N-CA-C	5.39	115.84	110.23
14	b	141	ASN	CB-CA-C	5.32	120.22	110.10
13	M	10	SER	N-CA-C	5.05	117.42	110.35

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1915	0	1929	1	0
1	O	1915	0	1929	1	0
2	B	1904	0	1904	4	0
2	P	1904	0	1904	4	0
3	C	1881	0	1895	4	0
3	Q	1881	0	1895	4	0
4	D	1813	0	1797	1	0
4	R	1813	0	1797	2	0
5	E	1773	0	1775	1	0
5	S	1773	0	1775	2	0
6	F	1892	0	1883	1	0
6	T	1892	0	1883	1	0
7	G	1907	0	1901	4	0
7	U	1907	0	1901	5	0
8	H	1684	0	1688	3	0
8	V	1684	0	1688	3	0
9	I	1581	0	1574	7	0
9	W	1581	0	1574	9	0
10	J	1561	0	1569	20	0
10	X	1561	0	1569	15	0
11	K	1644	0	1595	20	0
11	Y	1644	0	1595	21	0
12	L	1757	0	1711	7	0
12	Z	1757	0	1711	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	1824	0	1832	17	0
13	a	1824	0	1832	10	0
14	N	1474	0	1463	14	0
14	b	1474	0	1463	9	0
15	G	2	0	0	0	0
15	I	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	1	0	0	0	0
16	G	1	0	0	0	0
16	N	1	0	0	0	0
16	U	1	0	0	0	0
16	b	1	0	0	0	0
17	A	2	0	0	0	0
17	B	8	0	0	0	0
17	C	9	0	0	0	0
17	D	3	0	0	0	0
17	E	4	0	0	0	0
17	F	6	0	0	0	0
17	G	6	0	0	0	0
17	H	9	0	0	0	0
17	I	4	0	0	0	0
17	J	8	0	0	0	0
17	K	12	0	0	0	0
17	L	11	0	0	0	0
17	M	10	0	0	0	0
17	N	8	0	0	1	0
17	O	3	0	0	0	0
17	P	8	0	0	0	0
17	Q	6	0	0	0	0
17	R	6	0	0	0	0
17	S	5	0	0	0	0
17	T	4	0	0	0	0
17	U	7	0	0	0	0
17	V	11	0	0	0	0
17	W	5	0	0	0	0
17	X	9	0	0	0	0
17	Y	12	0	0	0	0
17	Z	12	0	0	0	0
17	a	9	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	b	4	0	0	1	0
All	All	49433	0	49032	177	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 (177) 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)
13:a:65:ARG:HG2	13:a:65:ARG:HH21	1.19	1.07
13:M:30:TYR:CD1	13:M:35:ARG:NE	2.31	0.97
13:M:30:TYR:CE1	13:M:35:ARG:NH2	2.42	0.88
14:N:141:ASN:O	14:N:141:ASN:ND2	2.08	0.86
14:b:141:ASN:ND2	14:b:141:ASN:O	2.09	0.84
13:M:30:TYR:CE1	13:M:35:ARG:CZ	2.63	0.81
11:Y:4:LEU:CD1	11:Y:161:ILE:HD11	2.12	0.79
13:M:30:TYR:HB2	13:M:35:ARG:HG3	1.64	0.79
11:K:7:ARG:HD2	11:K:110:PRO:O	1.84	0.77
13:M:30:TYR:HD1	13:M:35:ARG:NE	1.83	0.75
11:Y:4:LEU:HD13	11:Y:15:ALA:O	1.85	0.75
10:J:143:LEU:CD2	10:J:163:LEU:HD23	2.17	0.75
10:X:144:LEU:HD11	10:X:164:CYS:SG	2.27	0.74
10:J:144:LEU:CD1	10:J:164:CYS:SG	2.78	0.71
10:X:143:LEU:CD2	10:X:163:LEU:HD23	2.20	0.71
11:Y:4:LEU:HD12	11:Y:161:ILE:HD11	1.72	0.70
13:M:30:TYR:CD1	13:M:35:ARG:CZ	2.76	0.69
11:K:4:LEU:CD1	11:K:161:ILE:HD11	2.23	0.68
13:a:30:TYR:HB2	13:a:35:ARG:HG3	1.74	0.68
11:Y:4:LEU:C	11:Y:4:LEU:HD22	2.18	0.68
11:K:4:LEU:HD22	11:K:4:LEU:C	2.19	0.68
13:M:30:TYR:HE1	13:M:35:ARG:NH2	1.92	0.68
10:J:22:THR:O	10:J:23:ARG:NH1	2.27	0.66
10:J:143:LEU:HD21	10:J:163:LEU:HD23	1.80	0.63
13:a:65:ARG:HG2	13:a:65:ARG:NH2	2.00	0.63
10:J:144:LEU:HD11	10:J:164:CYS:SG	2.39	0.62
13:a:65:ARG:HH21	13:a:65:ARG:CG	2.02	0.62
10:J:144:LEU:HD13	10:J:164:CYS:SG	2.41	0.61
11:Y:4:LEU:HD12	11:Y:161:ILE:CD1	2.30	0.60
10:X:25:ILE:HD11	11:Y:134:THR:HG21	1.83	0.60
11:Y:4:LEU:HD13	11:Y:4:LEU:H	1.68	0.58
10:X:67:TYR:CE1	10:X:75:LEU:HD13	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:152:VAL:HA	14:N:175:MET:HE1	1.87	0.57
13:M:30:TYR:HE1	13:M:35:ARG:HH21	1.53	0.57
10:J:23:ARG:HG3	10:J:28:LEU:CD1	2.34	0.57
14:b:152:VAL:HA	14:b:175:MET:HE1	1.86	0.57
10:J:67:TYR:CE1	10:J:75:LEU:HD13	2.39	0.57
13:M:30:TYR:HB2	13:M:35:ARG:CG	2.34	0.57
11:Y:4:LEU:HD11	11:Y:15:ALA:HB3	1.87	0.56
8:V:91:GLN:OE1	14:b:-7:LYS:NZ	2.39	0.55
11:K:4:LEU:H	11:K:4:LEU:HD13	1.71	0.55
11:K:7:ARG:CD	11:K:110:PRO:O	2.53	0.55
10:J:168:LEU:O	10:J:172:MET:HB2	2.05	0.55
11:Y:4:LEU:CD1	11:Y:161:ILE:CD1	2.83	0.54
11:K:4:LEU:HD13	11:K:15:ALA:O	2.07	0.54
14:N:141:ASN:HD22	14:N:141:ASN:C	2.09	0.54
11:Y:4:LEU:HD22	11:Y:4:LEU:O	2.08	0.54
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	1.88	0.54
11:K:4:LEU:HB3	11:K:128:CYS:SG	2.48	0.54
14:N:142:PHE:CD2	14:N:142:PHE:C	2.85	0.54
3:C:201:VAL:O	3:C:202:GLN:CB	2.57	0.53
11:K:145:LYS:HB2	11:K:148:LEU:HD13	1.89	0.53
10:J:23:ARG:HG3	10:J:28:LEU:HD12	1.90	0.53
10:X:144:LEU:CD1	10:X:164:CYS:SG	2.95	0.53
11:Y:4:LEU:HD13	11:Y:4:LEU:N	2.24	0.53
14:N:36:ARG:HD2	17:N:305:HOH:O	2.09	0.52
13:M:30:TYR:CE1	13:M:35:ARG:NE	2.76	0.52
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.57	0.52
1:A:176:GLU:HG2	2:B:55:LEU:HD13	1.91	0.52
11:K:4:LEU:HD13	11:K:4:LEU:N	2.25	0.52
10:J:143:LEU:HD21	10:J:163:LEU:CD2	2.40	0.51
10:X:143:LEU:HD21	10:X:163:LEU:HD23	1.93	0.51
10:J:144:LEU:O	10:J:148:TYR:HB3	2.12	0.50
3:C:169:VAL:HG23	3:C:196:SER:HB2	1.94	0.50
14:b:-8:LEU:N	17:b:301:HOH:O	2.45	0.50
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.95	0.49
13:M:30:TYR:CD1	13:M:35:ARG:CD	2.94	0.49
3:Q:169:VAL:HG23	3:Q:196:SER:HB2	1.94	0.49
14:b:35:THR:OG1	14:b:43:CYS:SG	2.71	0.49
10:J:138:PHE:O	11:Y:134:THR:HB	2.13	0.49
11:K:4:LEU:C	11:K:4:LEU:CD2	2.85	0.49
14:N:35:THR:OG1	14:N:43:CYS:SG	2.71	0.49
14:N:-3:VAL:CG1	14:N:20:THR:CG2	2.91	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:96:LEU:O	13:M:100:MET:HG2	2.13	0.48
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.94	0.48
13:M:165:ILE:HB	13:M:166:PRO:HD3	1.96	0.48
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.94	0.48
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.95	0.48
13:a:96:LEU:O	13:a:100:MET:HG2	2.13	0.48
11:K:4:LEU:HD22	11:K:4:LEU:O	2.13	0.48
9:I:20:VAL:HG13	9:I:118:PRO:HB3	1.96	0.48
11:K:4:LEU:CD1	11:K:161:ILE:CD1	2.92	0.47
13:a:165:ILE:HB	13:a:166:PRO:HD3	1.96	0.47
9:W:20:VAL:HG13	9:W:118:PRO:HB3	1.96	0.47
10:X:143:LEU:HD23	10:X:163:LEU:HD23	1.94	0.47
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.50	0.47
10:J:174:MET:HE2	10:X:174:MET:HA	1.97	0.47
11:K:4:LEU:HD12	11:K:161:ILE:HD11	1.97	0.47
11:K:167:ARG:NH1	9:W:34:GLY:O	2.43	0.47
11:Y:4:LEU:C	11:Y:4:LEU:CD2	2.86	0.47
14:N:143:ARG:HG3	14:N:143:ARG:NH1	2.30	0.47
7:G:23:PHE:O	7:G:26:THR:HB	2.16	0.46
14:b:141:ASN:ND2	14:b:141:ASN:C	2.72	0.46
12:Z:147:MET:N	12:Z:148:PRO:HD2	2.31	0.46
7:U:23:PHE:O	7:U:26:THR:HB	2.15	0.46
10:J:172:MET:HB3	10:J:172:MET:HE3	1.81	0.46
6:T:172:LEU:CD1	6:T:195:ILE:HD13	2.46	0.46
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.98	0.45
10:J:144:LEU:O	10:J:148:TYR:CB	2.64	0.45
11:K:25:TRP:HH2	12:L:147:MET:HB3	1.82	0.45
6:F:172:LEU:CD1	6:F:195:ILE:HD13	2.46	0.45
9:I:34:GLY:O	11:Y:167:ARG:NH1	2.45	0.45
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.98	0.45
9:I:163:PHE:CE1	9:I:197:ARG:HD2	2.52	0.45
13:M:3:GLN:HG3	13:M:3:GLN:O	2.16	0.44
2:P:86:LEU:HB3	2:P:114:LEU:HD21	1.99	0.44
9:I:20:VAL:HG23	9:I:189:ILE:HB	1.99	0.44
2:P:95:GLN:HB3	9:W:68:TYR:CD2	2.52	0.44
14:b:-3:VAL:CG1	14:b:20:THR:CG2	2.94	0.44
2:B:86:LEU:HB3	2:B:114:LEU:HD21	1.99	0.44
9:W:163:PHE:CE1	9:W:197:ARG:HD2	2.52	0.44
12:L:147:MET:N	12:L:148:PRO:HD2	2.32	0.44
12:L:13:LEU:CD1	12:L:150:LEU:HD21	2.48	0.44
14:N:141:ASN:ND2	14:N:141:ASN:C	2.73	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:X:2:ASP:OD2	10:X:174:MET:CE	2.66	0.44
11:K:128:CYS:HB2	11:K:137:TYR:CZ	2.53	0.44
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.53	0.43
10:X:2:ASP:OD2	10:X:174:MET:HE1	2.18	0.43
11:Y:4:LEU:HD11	11:Y:161:ILE:HG12	1.99	0.43
11:Y:107:LYS:HG3	11:Y:108:GLU:HG3	2.00	0.43
12:L:4:PRO:O	13:M:104:ARG:NH1	2.47	0.43
13:a:3:GLN:O	13:a:3:GLN:HG3	2.18	0.43
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.53	0.43
5:S:87:LEU:HD21	5:S:107:ALA:HB1	2.01	0.43
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.49	0.43
9:W:20:VAL:HG23	9:W:189:ILE:HB	1.99	0.43
12:Z:13:LEU:CD1	12:Z:150:LEU:HD21	2.48	0.43
14:b:55:ILE:HD11	14:b:93:LEU:HD13	2.01	0.43
7:G:78:ILE:N	7:G:79:PRO:CD	2.82	0.43
12:Z:17:GLY:HA3	12:Z:20:PHE:CE1	2.53	0.43
14:N:55:ILE:HD11	14:N:93:LEU:HD13	2.00	0.43
9:W:148:MET:HE2	9:W:172:ASN:HB2	2.00	0.43
2:P:50:LYS:O	2:P:51:VAL:C	2.62	0.43
9:I:148:MET:HE2	9:I:172:ASN:HB2	2.01	0.43
7:U:78:ILE:N	7:U:79:PRO:CD	2.82	0.43
11:Y:128:CYS:HB2	11:Y:137:TYR:CZ	2.54	0.43
8:H:102:GLY:HA2	8:H:178:MET:SD	2.59	0.42
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.48	0.42
9:I:65:MET:O	9:I:68:TYR:HB3	2.19	0.42
3:Q:161:THR:HG21	3:Q:169:VAL:HG13	2.01	0.42
10:X:144:LEU:O	10:X:148:TYR:HB3	2.19	0.42
10:J:23:ARG:HG3	10:J:28:LEU:HD11	2.00	0.42
12:L:17:GLY:HA3	12:L:20:PHE:CE1	2.54	0.42
7:U:73:VAL:HG12	7:U:133:THR:HB	2.02	0.42
3:C:161:THR:HG21	3:C:169:VAL:HG13	2.01	0.42
2:B:50:LYS:O	2:B:51:VAL:C	2.62	0.42
7:G:73:VAL:HG12	7:G:133:THR:HB	2.01	0.42
8:H:139:GLU:OE1	13:a:187:ARG:NH1	2.51	0.42
11:K:107:LYS:HG3	11:K:108:GLU:HG3	2.01	0.42
10:J:21:VAL:HG11	11:K:122:LEU:HD11	2.02	0.42
11:K:128:CYS:HB2	11:K:137:TYR:CE2	2.55	0.42
14:N:143:ARG:CG	14:N:143:ARG:HH11	2.33	0.42
11:K:4:LEU:HD12	11:K:161:ILE:CD1	2.50	0.41
14:b:176:VAL:HG12	14:b:178:LEU:HD13	2.02	0.41
5:E:87:LEU:HD21	5:E:107:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:Y:128:CYS:HB2	11:Y:137:TYR:CE2	2.56	0.41
10:J:3:ILE:HD11	10:J:172:MET:HE2	2.03	0.41
10:X:143:LEU:HD21	10:X:163:LEU:CD2	2.51	0.41
11:Y:25:TRP:HH2	12:Z:147:MET:HB3	1.85	0.41
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.56	0.41
13:a:17:ASP:OD1	13:a:18:ASN:N	2.53	0.41
9:W:65:MET:O	9:W:68:TYR:HB3	2.20	0.41
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	2.01	0.41
3:C:201:VAL:HG13	3:C:202:GLN:N	2.35	0.41
14:N:35:THR:HG21	13:a:228:TYR:HE2	1.86	0.41
14:N:-1:LEU:HD11	14:N:45:ARG:NH1	2.35	0.41
14:N:176:VAL:HG12	14:N:178:LEU:HD13	2.02	0.41
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.51	0.41
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.56	0.41
12:L:8:ASN:HA	12:L:30:ILE:O	2.21	0.40
12:L:125:PHE:CD2	12:L:131:TYR:HB3	2.56	0.40
13:M:187:ARG:NH1	8:V:139:GLU:OE1	2.52	0.40
9:W:28:LEU:HD23	9:W:35:VAL:HB	2.03	0.40
3:Q:201:VAL:HG13	3:Q:202:GLN:N	2.36	0.40
10:X:3:ILE:HD12	10:X:176:PHE:CG	2.56	0.40
13:M:30:TYR:HD1	13:M:35:ARG:HE	1.58	0.40
7:U:26:THR:HG21	7:U:131:ILE:HD12	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
1	O	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
2	B	242/258 (94%)	236 (98%)	4 (2%)	2 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	P	242/258 (94%)	236 (98%)	4 (2%)	2 (1%)	16	44
3	C	238/254 (94%)	229 (96%)	7 (3%)	2 (1%)	16	44
3	Q	238/254 (94%)	229 (96%)	7 (3%)	2 (1%)	16	44
4	D	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
4	R	231/260 (89%)	226 (98%)	5 (2%)	0	100	100
5	E	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
5	S	229/234 (98%)	222 (97%)	7 (3%)	0	100	100
6	F	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
6	T	241/288 (84%)	235 (98%)	6 (2%)	0	100	100
7	G	239/252 (95%)	234 (98%)	5 (2%)	0	100	100
7	U	239/252 (95%)	234 (98%)	5 (2%)	0	100	100
8	H	220/232 (95%)	213 (97%)	7 (3%)	0	100	100
8	V	220/232 (95%)	213 (97%)	7 (3%)	0	100	100
9	I	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
9	W	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
10	J	193/198 (98%)	190 (98%)	3 (2%)	0	100	100
10	X	193/198 (98%)	190 (98%)	3 (2%)	0	100	100
11	K	210/212 (99%)	204 (97%)	6 (3%)	0	100	100
11	Y	210/212 (99%)	205 (98%)	5 (2%)	0	100	100
12	L	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	231/246 (94%)	219 (95%)	11 (5%)	1 (0%)	30	59
13	a	231/246 (94%)	218 (94%)	12 (5%)	1 (0%)	30	59
14	N	187/215 (87%)	178 (95%)	9 (5%)	0	100	100
14	b	187/215 (87%)	178 (95%)	9 (5%)	0	100	100
All	All	6262/6652 (94%)	6076 (97%)	176 (3%)	10 (0%)	43	72

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
3	C	202	GLN
2	P	51	VAL

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Mol	Chain	Res	Type
3	Q	202	GLN
3	C	205	ALA
3	Q	205	ALA
2	B	221	ASP
13	M	83	ALA
2	P	221	ASP
13	a	83	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	205 (98%)	4 (2%)	50	79
1	O	209/209 (100%)	205 (98%)	4 (2%)	50	79
2	B	203/216 (94%)	196 (97%)	7 (3%)	32	66
2	P	203/216 (94%)	196 (97%)	7 (3%)	32	66
3	C	212/226 (94%)	207 (98%)	5 (2%)	43	75
3	Q	212/226 (94%)	207 (98%)	5 (2%)	43	75
4	D	194/215 (90%)	186 (96%)	8 (4%)	27	61
4	R	194/215 (90%)	186 (96%)	8 (4%)	27	61
5	E	190/193 (98%)	185 (97%)	5 (3%)	40	73
5	S	190/193 (98%)	185 (97%)	5 (3%)	40	73
6	F	201/239 (84%)	195 (97%)	6 (3%)	36	70
6	T	201/239 (84%)	195 (97%)	6 (3%)	36	70
7	G	206/210 (98%)	201 (98%)	5 (2%)	43	75
7	U	206/210 (98%)	201 (98%)	5 (2%)	43	75
8	H	181/190 (95%)	177 (98%)	4 (2%)	45	77
8	V	181/190 (95%)	177 (98%)	4 (2%)	45	77
9	I	172/173 (99%)	170 (99%)	2 (1%)	63	86
9	W	172/173 (99%)	170 (99%)	2 (1%)	63	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	173/175 (99%)	170 (98%)	3 (2%)	53	82
10	X	173/175 (99%)	167 (96%)	6 (4%)	32	66
11	K	169/169 (100%)	164 (97%)	5 (3%)	36	70
11	Y	169/169 (100%)	165 (98%)	4 (2%)	43	75
12	L	185/185 (100%)	179 (97%)	6 (3%)	34	68
12	Z	185/185 (100%)	179 (97%)	6 (3%)	34	68
13	M	199/208 (96%)	194 (98%)	5 (2%)	42	74
13	a	199/208 (96%)	194 (98%)	5 (2%)	42	74
14	N	159/179 (89%)	147 (92%)	12 (8%)	12	37
14	b	159/179 (89%)	148 (93%)	11 (7%)	14	41
All	All	5306/5574 (95%)	5151 (97%)	155 (3%)	37	71

All (155) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	61	LEU
1	A	122	THR
1	A	157	PHE
2	B	50	LYS
2	B	55	LEU
2	B	58	GLN
2	B	79	LEU
2	B	114	LEU
2	B	184	LYS
2	B	191	LEU
3	C	4	ARG
3	C	38	ASN
3	C	147	GLN
3	C	169	VAL
3	C	180	LYS
4	D	20	LEU
4	D	99	ILE
4	D	176	LEU
4	D	193	LEU
4	D	197	LYS
4	D	214	ILE
4	D	236	LYS

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Mol	Chain	Res	Type
4	D	242	GLU
5	E	9	THR
5	E	29	LYS
5	E	54	GLU
5	E	71	LEU
5	E	188	LEU
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	203	ASN
6	F	206	LYS
6	F	221	ASN
7	G	115	LEU
7	G	125	MET
7	G	166	GLN
7	G	181	LYS
7	G	235	ARG
8	H	68	LEU
8	H	127	LEU
8	H	153	LYS
8	H	196	ARG
9	I	37	ASN
9	I	171	LEU
10	J	75	LEU
10	J	136	SER
10	J	143	LEU
11	K	4	LEU
11	K	7	ARG
11	K	116	ASP
11	K	140	LEU
11	K	148	LEU
12	L	1	GLN
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	150	LEU
12	L	167	LYS
13	M	37	ASN
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	146	PHE

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Mol	Chain	Res	Type
14	N	-6	LYS
14	N	2	SER
14	N	9	LYS
14	N	22	THR
14	N	36	ARG
14	N	119	VAL
14	N	141	ASN
14	N	142	PHE
14	N	143	ARG
14	N	144	GLU
14	N	178	LEU
14	N	191	ASP
1	O	17	LYS
1	O	61	LEU
1	O	122	THR
1	O	157	PHE
2	P	50	LYS
2	P	55	LEU
2	P	58	GLN
2	P	79	LEU
2	P	114	LEU
2	P	184	LYS
2	P	191	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	147	GLN
3	Q	169	VAL
3	Q	180	LYS
4	R	20	LEU
4	R	99	ILE
4	R	176	LEU
4	R	193	LEU
4	R	197	LYS
4	R	214	ILE
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	54	GLU
5	S	71	LEU
5	S	188	LEU
6	T	123	ASN

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Mol	Chain	Res	Type
6	T	172	LEU
6	T	181	GLU
6	T	203	ASN
6	T	206	LYS
6	T	221	ASN
7	U	115	LEU
7	U	125	MET
7	U	166	GLN
7	U	181	LYS
7	U	235	ARG
8	V	68	LEU
8	V	127	LEU
8	V	153	LYS
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU
10	X	23	ARG
10	X	75	LEU
10	X	136	SER
10	X	143	LEU
10	X	172	MET
10	X	174	MET
11	Y	4	LEU
11	Y	116	ASP
11	Y	140	LEU
11	Y	148	LEU
12	Z	1	GLN
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	150	LEU
12	Z	167	LYS
13	a	37	ASN
13	a	48	ASN
13	a	65	ARG
13	a	70	LEU
13	a	104	ARG
14	b	-8	LEU
14	b	2	SER
14	b	9	LYS
14	b	22	THR
14	b	36	ARG

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Mol	Chain	Res	Type
14	b	119	VAL
14	b	141	ASN
14	b	143	ARG
14	b	144	GLU
14	b	178	LEU
14	b	191	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (101) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	93	HIS
2	B	119	GLN
2	B	123	GLN
2	B	124	HIS
2	B	232	GLN
3	C	38	ASN
3	C	116	GLN
3	C	120	GLN
3	C	147	GLN
3	C	160	GLN
3	C	233	GLN
4	D	15	GLN
4	D	91	HIS
4	D	100	ASN
4	D	106	GLN
4	D	180	HIS
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	120	GLN
5	E	151	ASN
5	E	184	ASN
6	F	86	ASN
6	F	123	ASN
7	G	30	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN
7	G	175	ASN
8	H	30	ASN
8	H	189	ASN

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Mol	Chain	Res	Type
9	I	63	ASN
10	J	55	GLN
10	J	61	GLN
10	J	63	ASN
10	J	146	HIS
10	J	147	HIS
11	K	9	GLN
11	K	62	GLN
11	K	85	ASN
11	K	143	ASN
11	K	176	ASN
11	K	208	ASN
12	L	3	ASN
12	L	70	ASN
12	L	94	GLN
12	L	197	GLN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN
13	M	149	HIS
14	N	38	HIS
2	P	93	HIS
2	P	119	GLN
2	P	123	GLN
2	P	124	HIS
2	P	232	GLN
3	Q	38	ASN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
3	Q	233	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	120	GLN
5	S	151	ASN
5	S	165	GLN
5	S	184	ASN

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Mol	Chain	Res	Type
6	T	86	ASN
6	T	123	ASN
7	U	30	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
8	V	30	ASN
8	V	189	ASN
9	W	63	ASN
10	X	55	GLN
10	X	63	ASN
11	Y	9	GLN
11	Y	85	ASN
11	Y	143	ASN
11	Y	176	ASN
11	Y	208	ASN
12	Z	3	ASN
12	Z	70	ASN
12	Z	94	GLN
13	a	2	GLN
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	149	HIS
13	a	213	GLN
14	b	38	HIS
14	b	141	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/250 (100%)	-0.24	3 (1%) 76 69	38, 54, 96, 150	0
1	O	250/250 (100%)	-0.24	2 (0%) 82 77	45, 62, 109, 155	0
2	B	244/258 (94%)	-0.11	6 (2%) 58 48	40, 62, 113, 170	0
2	P	244/258 (94%)	-0.12	5 (2%) 65 56	44, 64, 110, 164	0
3	C	240/254 (94%)	-0.16	4 (1%) 69 61	41, 65, 130, 165	0
3	Q	240/254 (94%)	0.16	13 (5%) 31 24	51, 82, 166, 194	0
4	D	235/260 (90%)	-0.21	2 (0%) 81 75	45, 67, 102, 141	0
4	R	235/260 (90%)	-0.09	2 (0%) 81 75	52, 73, 115, 169	0
5	E	231/234 (98%)	-0.21	0 100 100	44, 69, 109, 148	0
5	S	231/234 (98%)	0.02	3 (1%) 75 67	50, 79, 129, 167	0
6	F	243/288 (84%)	-0.31	1 (0%) 88 85	40, 63, 109, 139	0
6	T	243/288 (84%)	-0.14	2 (0%) 82 77	45, 73, 131, 167	0
7	G	241/252 (95%)	-0.34	0 100 100	38, 56, 94, 141	0
7	U	241/252 (95%)	-0.28	1 (0%) 88 85	35, 61, 97, 142	0
8	H	222/232 (95%)	-0.37	0 100 100	37, 52, 87, 122	0
8	V	222/232 (95%)	-0.39	0 100 100	40, 56, 85, 128	0
9	I	204/205 (99%)	-0.51	0 100 100	34, 51, 78, 101	0
9	W	204/205 (99%)	-0.40	0 100 100	36, 54, 87, 114	0
10	J	195/198 (98%)	-0.36	1 (0%) 87 83	34, 55, 83, 122	0
10	X	195/198 (98%)	-0.33	2 (1%) 79 73	37, 58, 85, 142	0
11	K	212/212 (100%)	-0.18	3 (1%) 73 65	39, 55, 82, 103	0
11	Y	212/212 (100%)	-0.25	1 (0%) 87 83	43, 55, 81, 104	0
12	L	222/222 (100%)	-0.08	16 (7%) 21 17	32, 59, 111, 141	0
12	Z	222/222 (100%)	-0.04	14 (6%) 26 20	36, 58, 111, 148	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.31	3 (1%) 75 67	34, 58, 85, 103	0
13	a	233/246 (94%)	-0.28	4 (1%) 69 61	35, 60, 85, 105	0
14	N	191/215 (88%)	-0.23	3 (1%) 70 62	33, 57, 94, 139	0
14	b	191/215 (88%)	-0.18	2 (1%) 79 73	32, 58, 94, 138	0
All	All	6326/6652 (95%)	-0.22	93 (1%) 72 64	32, 61, 111, 194	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	219	ALA	5.1
3	Q	50	LEU	4.9
12	Z	163	GLY	4.6
12	L	166	GLY	4.4
12	L	174	TYR	4.4
10	X	1	MET	4.4
4	D	240	ALA	4.3
12	Z	174	TYR	4.3
1	O	1	MET	4.2
12	L	163	GLY	4.2
12	Z	170	LYS	4.1
1	A	1	MET	4.1
13	a	1	THR	4.0
2	P	219	ALA	3.9
12	Z	166	GLY	3.9
13	a	69	ASP	3.8
12	L	170	LYS	3.5
3	Q	49	THR	3.4
3	Q	51	LYS	3.4
2	P	1	GLY	3.3
12	L	162	PRO	3.2
5	S	209	ASN	3.2
1	A	2	THR	3.2
3	Q	52	LEU	3.1
12	Z	162	PRO	3.1
5	S	52	ALA	3.0
13	M	35	ARG	2.9
4	R	241	ALA	2.9
7	U	242	GLN	2.9
1	O	53	SER	2.9
10	J	1	MET	2.8
2	B	51	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
13	a	35	ARG	2.8
12	Z	173	LYS	2.8
12	Z	165	ASN	2.8
11	K	118	ASP	2.8
12	Z	167	LYS	2.6
14	N	196	LEU	2.6
12	Z	160	TYR	2.6
12	L	168	VAL	2.6
2	B	1	GLY	2.6
3	Q	206	LYS	2.6
12	Z	164	THR	2.6
14	N	141	ASN	2.6
13	a	31	GLY	2.6
3	Q	234	ILE	2.6
12	Z	156	PHE	2.5
2	B	220	ASN	2.5
6	T	178	HIS	2.5
3	C	240	GLU	2.5
12	L	173	LYS	2.5
14	N	157	HIS	2.4
12	L	159	GLN	2.4
11	K	212	GLY	2.4
3	C	205	ALA	2.4
3	Q	205	ALA	2.4
12	L	156	PHE	2.4
10	X	150	PRO	2.4
3	Q	231	VAL	2.3
13	M	69	ASP	2.3
12	L	172	LEU	2.3
3	Q	3	ASP	2.3
3	C	203	THR	2.3
11	K	209	ASN	2.3
3	Q	208	ILE	2.3
12	L	171	PRO	2.3
2	P	218	GLY	2.3
14	b	141	ASN	2.3
11	Y	118	ASP	2.3
3	Q	203	THR	2.3
1	A	249	ALA	2.2
2	B	93	HIS	2.2
3	Q	230	TYR	2.2
3	C	206	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
4	D	241	ALA	2.2
12	Z	159	GLN	2.2
2	P	52	THR	2.2
13	M	1	THR	2.2
5	S	190	LYS	2.2
12	Z	161	GLU	2.2
12	L	165	ASN	2.1
12	Z	168	VAL	2.1
12	L	169	LYS	2.1
2	B	55	LEU	2.1
2	P	93	HIS	2.1
14	b	143	ARG	2.1
3	Q	189	CYS	2.1
12	L	164	THR	2.1
6	F	215	CYS	2.1
12	L	106	TYR	2.1
12	L	167	LYS	2.0
4	R	240	ALA	2.0
6	T	201	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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($\text{\AA}^2$)	Q<0.9
15	MG	N	201	1/1	0.93	0.18	49,49,49,49	0
15	MG	Z	301	1/1	0.94	0.08	63,63,63,63	0
15	MG	I	301	1/1	0.97	0.04	59,59,59,59	0
15	MG	V	301	1/1	0.98	0.12	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
15	MG	Y	301	1/1	0.98	0.10	52,52,52,52	0
15	MG	G	301	1/1	0.98	0.04	49,49,49,49	0
16	CL	N	202	1/1	0.98	0.08	53,53,53,53	0
16	CL	U	301	1/1	0.98	0.08	56,56,56,56	0
16	CL	b	201	1/1	0.98	0.07	59,59,59,59	0
15	MG	G	302	1/1	0.99	0.14	35,35,35,35	0
15	MG	K	301	1/1	0.99	0.06	43,43,43,43	0
16	CL	G	303	1/1	0.99	0.07	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.