



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:04 PM UTC

PDB ID : 4Y6V / pdb_00004y6v
Title : Yeast 20S proteasome in complex with Ac-PAE-ep
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-02-13
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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

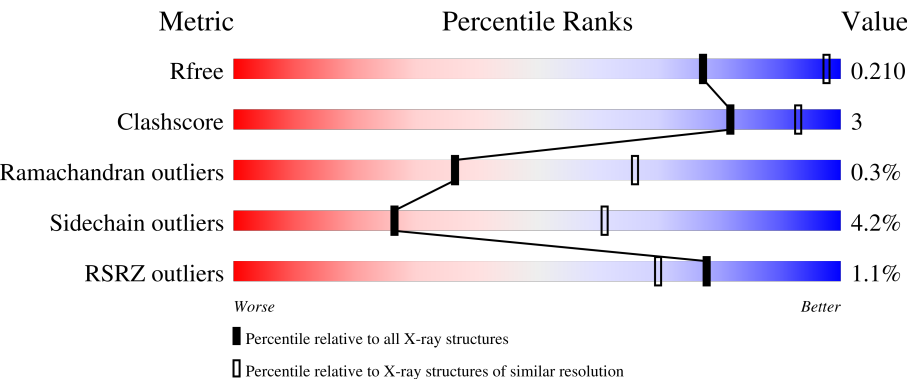
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (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 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

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

Mol	Chain	Length	Quality of chain
1	A	250	0% 96% 0% 0%
1	O	250	0% 96% 0% 0%
2	B	258	2% 83% 10% 5%
2	P	258	5% 84% 9% 5%
3	C	254	3% 83% 9% 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	 3% 84% 8% 6%
4	D	260	 % 83% 7% 10%
4	R	260	 80% 9% 10%
5	E	234	 91% 7%
5	S	234	 2% 89% 9%
6	F	288	 % 79% 6% 16%
6	T	288	 2% 79% 6% 16%
7	G	252	 % 86% 9%
7	U	252	 % 86% 9%
8	H	232	 % 89% 8%
8	V	232	 % 90% 7%
9	I	205	 91% 8%
9	W	205	 92% 8%
10	J	198	 % 88% 10%
10	X	198	 % 87% 10%
11	K	212	 87% 12%
11	Y	212	 88% 10%
12	L	222	 96%
12	Z	222	 95% 5%
13	M	246	 86% 8% 5%
13	a	246	 87% 8% 5%
14	N	196	 % 89% 10%
14	b	196	 % 88% 11%
15	c	4	 75% 25%
15	d	4	 75% 25%

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 49759 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	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			
8	V	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	c	4	Total	C	N	O	0	0	0
			28	18	3	7			
15	d	4	Total	C	N	O	0	0	0
			28	18	3	7			

- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	G	1	Total 1	Mg 1	0	0
16	I	2	Total 2	Mg 2	0	0
16	K	1	Total 1	Mg 1	0	0
16	L	1	Total 1	Mg 1	0	0
16	N	1	Total 1	Mg 1	0	0
16	Z	1	Total 1	Mg 1	0	0

- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	16	Total 16	O 16	0	0
17	B	18	Total 18	O 18	0	0
17	C	18	Total 18	O 18	0	0
17	D	6	Total 6	O 6	0	0
17	E	3	Total 3	O 3	0	0
17	F	10	Total 10	O 10	0	0
17	G	11	Total 11	O 11	0	0
17	H	13	Total 13	O 13	0	0
17	I	12	Total 12	O 12	0	0
17	J	13	Total 13	O 13	0	0
17	K	12	Total 12	O 12	0	0
17	L	15	Total 15	O 15	0	0
17	M	17	Total 17	O 17	0	0

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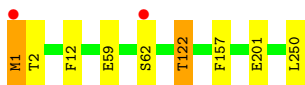
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	N	14	Total 14	O 14	0	0
17	O	1	Total 1	O 1	0	0
17	P	7	Total 7	O 7	0	0
17	Q	12	Total 12	O 12	0	0
17	R	10	Total 10	O 10	0	0
17	S	4	Total 4	O 4	0	0
17	T	8	Total 8	O 8	0	0
17	U	14	Total 14	O 14	0	0
17	V	16	Total 16	O 16	0	0
17	W	8	Total 8	O 8	0	0
17	X	13	Total 13	O 13	0	0
17	Y	15	Total 15	O 15	0	0
17	Z	16	Total 16	O 16	0	0
17	a	15	Total 15	O 15	0	0
17	b	11	Total 11	O 11	0	0
17	d	2	Total 2	O 2	0	0

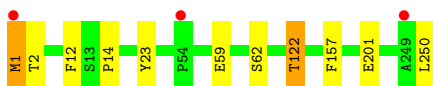
3 Residue-property plots [i](#)

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.

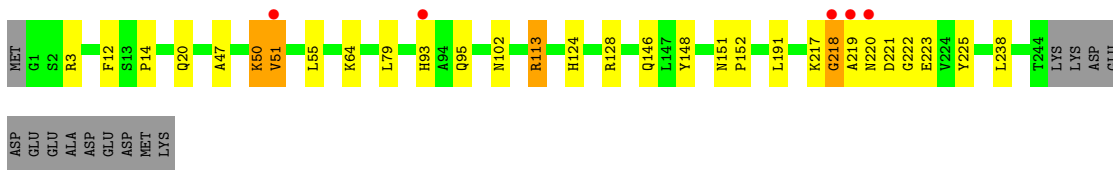
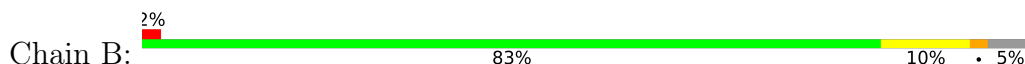
- Molecule 1: Proteasome subunit alpha type-2



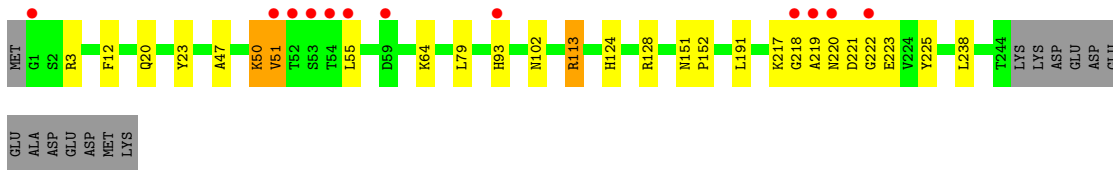
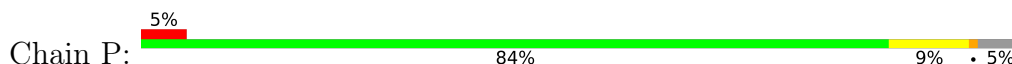
- Molecule 1: Proteasome subunit alpha type-2



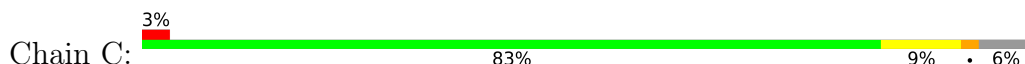
- Molecule 2: Proteasome subunit alpha type-3



- Molecule 2: Proteasome subunit alpha type-3

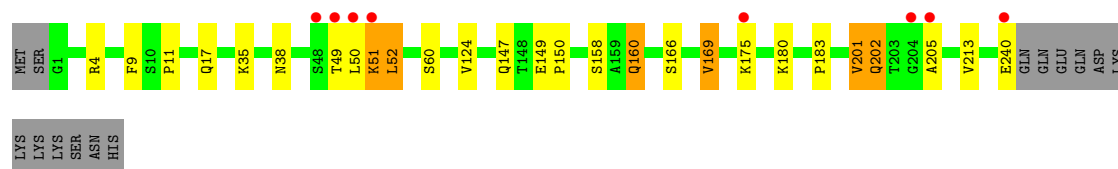
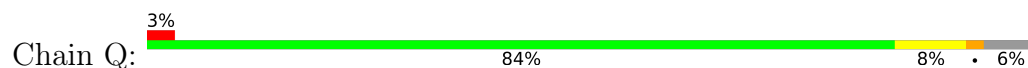


- Molecule 3: Proteasome subunit alpha type-4

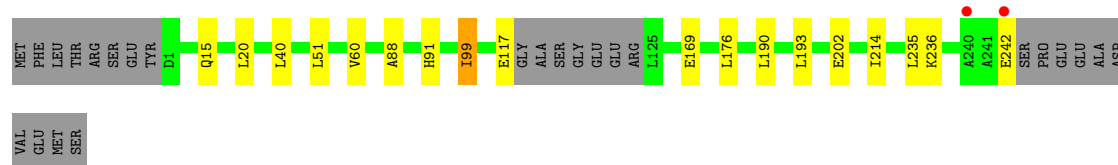
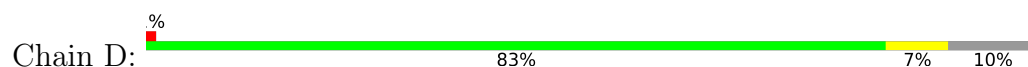




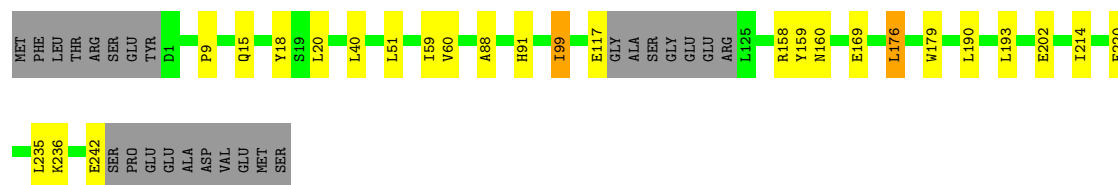
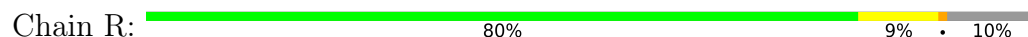
• Molecule 3: Proteasome subunit alpha type-4



• Molecule 4: Proteasome subunit alpha type-5



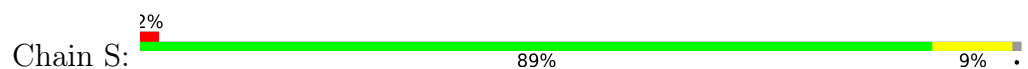
• Molecule 4: Proteasome subunit alpha type-5

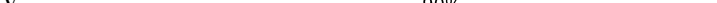


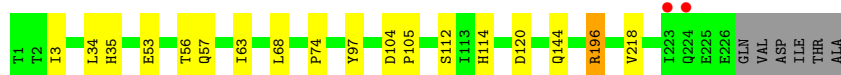
• Molecule 5: Proteasome subunit alpha type-6



• Molecule 5: Proteasome subunit alpha type-6



- Chain V:  90% 7% .



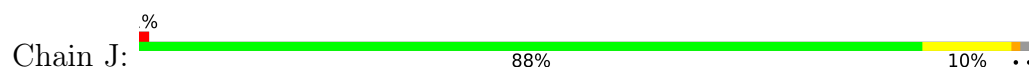
- Molecule 9: Proteasome subunit beta type-3



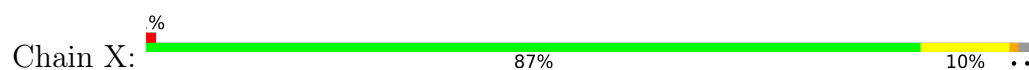
- Molecule 9: Proteasome subunit beta type-3



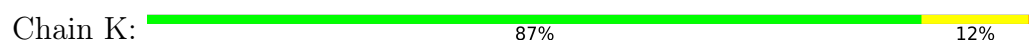
- Molecule 10: Proteasome subunit beta type-4



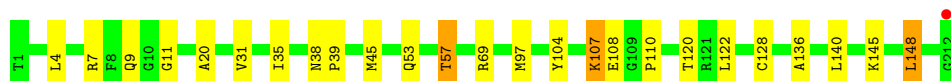
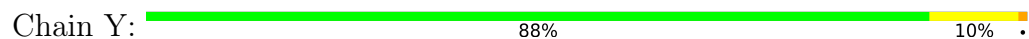
- Molecule 10: Proteasome subunit beta type-4



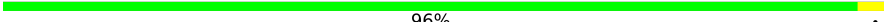
- Molecule 11: Proteasome subunit beta type-5



- Molecule 11: Proteasome subunit beta type-5

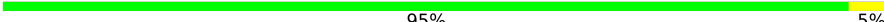


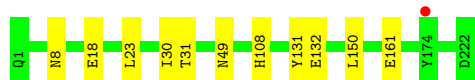
- Molecule 12: Proteasome subunit beta type-6

Chain L:  96% .



- Molecule 12: Proteasome subunit beta type-6

Chain Z:  95% 5% .



- Molecule 13: Proteasome subunit beta type-7

Chain M:  86% 8% 5% .



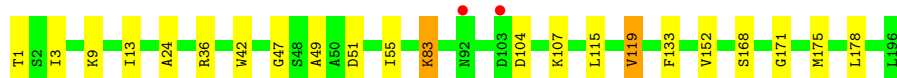
- Molecule 13: Proteasome subunit beta type-7

Chain a:  87% 8% 5% .



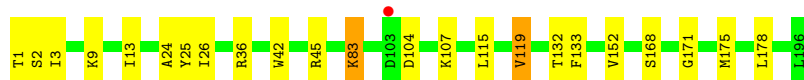
- Molecule 14: Proteasome subunit beta type-1

Chain N:  89% 10% .



- Molecule 14: Proteasome subunit beta type-1

Chain b:  88% 11% .

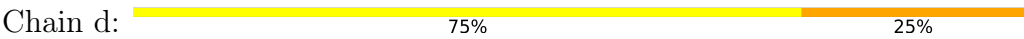


- Molecule 15: Ac-PAE-ep

Chain c:  75% 25% .



- Molecule 15: Ac-PAE-ep



P1
A2
E3
POL4

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.85Å 301.22Å 145.77Å 90.00° 113.15° 90.00°	Depositor
Resolution (Å)	15.00 – 2.80 15.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.2 (15.00-2.80) 97.6 (15.00-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.191 , 0.209 0.193 , 0.210	Depositor DCC
R_{free} test set	12850 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	56.2	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	49759	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.21% 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: POL, GAU, N7P, 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	0.42	0/1952	0.69	0/2642
1	O	0.42	0/1952	0.69	0/2642
2	B	0.43	0/1934	0.70	0/2618
2	P	0.43	0/1934	0.69	0/2618
3	C	0.42	0/1910	0.70	1/2586 (0.0%)
3	Q	0.43	0/1910	0.71	1/2586 (0.0%)
4	D	0.41	0/1837	0.68	0/2475
4	R	0.41	0/1837	0.68	0/2475
5	E	0.42	0/1800	0.66	0/2433
5	S	0.42	0/1800	0.66	0/2433
6	F	0.42	0/1932	0.71	0/2609
6	T	0.42	0/1932	0.70	0/2609
7	G	0.41	0/1945	0.68	0/2634
7	U	0.42	0/1945	0.69	0/2634
8	H	0.52	0/1750	0.68	0/2373
8	V	0.51	1/1750 (0.1%)	0.68	0/2373
9	I	0.42	0/1611	0.68	0/2174
9	W	0.43	0/1611	0.69	1/2174 (0.0%)
10	J	0.44	1/1589 (0.1%)	0.66	0/2142
10	X	0.44	1/1589 (0.1%)	0.66	0/2142
11	K	0.47	0/1681	0.71	0/2274
11	Y	0.46	0/1681	0.69	0/2274
12	L	0.42	0/1795	0.67	0/2420
12	Z	0.45	0/1795	0.68	0/2420
13	M	0.44	0/1855	0.70	1/2514 (0.0%)
13	a	0.45	0/1855	0.71	1/2514 (0.0%)
14	N	0.69	2/1541 (0.1%)	0.70	0/2087
14	b	0.49	0/1541	0.69	0/2087
15	c	0.90	0/4	1.16	0/4
15	d	1.07	0/4	1.30	0/4
All	All	0.45	5/50272 (0.0%)	0.69	5/67970 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	N	47	GLY	C-O	-7.70	1.20	1.24
14	N	49	ALA	C-O	-5.42	1.17	1.24
10	J	2	ASP	CA-C	5.31	1.55	1.52
10	X	2	ASP	CA-C	5.30	1.55	1.52
8	V	3	ILE	C-O	-5.02	1.19	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	a	35	ARG	N-CA-C	8.04	119.82	111.14
13	M	35	ARG	N-CA-C	7.14	118.85	111.14
3	Q	201	VAL	N-CA-C	6.64	116.77	110.53
3	C	201	VAL	N-CA-C	6.53	116.67	110.53
9	W	126	ILE	CB-CA-C	-5.38	105.09	111.65

There are no chirality outliers.

There are no planarity outliers.

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	4	0
1	O	1915	0	1929	5	0
2	B	1904	0	1904	21	0
2	P	1904	0	1904	15	0
3	C	1881	0	1895	13	0
3	Q	1881	0	1895	10	0
4	D	1813	0	1797	5	0
4	R	1813	0	1797	12	0
5	E	1773	0	1775	6	0
5	S	1773	0	1775	10	0
6	F	1892	0	1883	6	0
6	T	1892	0	1883	5	0
7	G	1907	0	1901	11	0
7	U	1907	0	1901	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1719	0	1718	13	0
8	V	1719	0	1719	11	0
9	I	1581	0	1574	12	0
9	W	1581	0	1574	10	0
10	J	1561	0	1569	12	0
10	X	1561	0	1569	15	0
11	K	1644	0	1595	18	0
11	Y	1644	0	1595	17	0
12	L	1757	0	1711	1	0
12	Z	1757	0	1711	5	0
13	M	1824	0	1832	11	0
13	a	1824	0	1832	7	0
14	N	1512	0	1478	14	0
14	b	1512	0	1478	16	0
15	c	28	0	16	5	0
15	d	28	0	16	4	0
16	G	1	0	0	0	0
16	I	2	0	0	0	0
16	K	1	0	0	0	0
16	L	1	0	0	0	0
16	N	1	0	0	0	0
16	Z	1	0	0	0	0
17	A	16	0	0	0	0
17	B	18	0	0	2	0
17	C	18	0	0	0	0
17	D	6	0	0	0	0
17	E	3	0	0	0	0
17	F	10	0	0	0	0
17	G	11	0	0	0	0
17	H	13	0	0	0	0
17	I	12	0	0	0	0
17	J	13	0	0	1	0
17	K	12	0	0	9	0
17	L	15	0	0	0	0
17	M	17	0	0	0	0
17	N	14	0	0	1	0
17	O	1	0	0	0	0
17	P	7	0	0	0	0
17	Q	12	0	0	0	0
17	R	10	0	0	0	0
17	S	4	0	0	0	0
17	T	8	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	U	14	0	0	0	0
17	V	16	0	0	0	0
17	W	8	0	0	0	0
17	X	13	0	0	3	0
17	Y	15	0	0	7	0
17	Z	16	0	0	1	0
17	a	15	0	0	0	0
17	b	11	0	0	0	0
17	d	2	0	0	1	0
All	All	49759	0	49155	249	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 3.

All (249) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:V:112:SER:OG	8:V:120:ASP:OD1	1.59	1.16
10:X:23:ARG:NH1	17:X:201:HOH:O	1.81	1.11
11:Y:45:MET:SD	17:Y:401:HOH:O	2.14	1.06
11:Y:104:TYR:CD2	17:Y:408:HOH:O	2.13	1.01
8:H:88:PHE:O	8:H:91:GLN:NE2	1.94	0.99
11:K:104:TYR:CD2	17:K:411:HOH:O	2.19	0.94
11:K:110:PRO:HB3	17:K:411:HOH:O	1.68	0.93
12:Z:131:TYR:O	12:Z:132:GLU:HG2	1.73	0.88
11:Y:110:PRO:HB3	17:Y:408:HOH:O	1.73	0.87
17:X:201:HOH:O	11:Y:120:THR:OG1	1.94	0.83
12:Z:131:TYR:C	12:Z:132:GLU:HG2	2.04	0.83
15:d:2:ALA:C	15:d:3:GAU:HG2	2.08	0.77
8:H:53:GLU:OE1	8:H:57:GLN:NE2	2.16	0.77
15:c:2:ALA:C	15:c:3:GAU:HG2	2.09	0.76
7:G:68:ARG:HH12	14:N:36:ARG:HH22	1.34	0.73
2:B:12:PHE:H	3:C:17:GLN:HE22	1.37	0.72
14:N:51:ASP:O	14:N:55:ILE:HG13	1.90	0.70
5:E:12:PHE:H	6:F:19:GLN:HE22	1.41	0.68
15:d:2:ALA:O	15:d:3:GAU:HG2	1.93	0.68
11:K:104:TYR:CE2	17:K:411:HOH:O	2.43	0.67
2:B:3:ARG:HB3	5:E:122:TYR:OH	1.94	0.67
11:K:11:GLY:HA2	17:K:411:HOH:O	1.96	0.65
8:V:112:SER:OG	8:V:120:ASP:CG	2.38	0.65
14:N:152:VAL:HA	14:N:175:MET:HE1	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:b:152:VAL:HA	14:b:175:MET:HE1	1.78	0.64
5:S:12:PHE:H	6:T:19:GLN:HE22	1.44	0.64
11:Y:104:TYR:CE2	17:Y:408:HOH:O	2.38	0.63
2:B:218:GLY:O	17:B:301:HOH:O	2.15	0.63
11:K:82:ILE:HB	17:K:401:HOH:O	1.98	0.63
3:C:51:LYS:O	3:C:52:LEU:HB2	1.99	0.63
2:P:221:ASP:O	2:P:223:GLU:N	2.32	0.62
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.00	0.62
7:U:68:ARG:HH12	14:b:36:ARG:HH22	1.47	0.62
11:Y:53:GLN:O	11:Y:57:THR:HG23	2.00	0.62
2:B:221:ASP:O	2:B:223:GLU:N	2.32	0.62
11:K:53:GLN:O	11:K:57:THR:HG23	2.00	0.62
3:Q:9:PHE:H	4:R:15:GLN:HE22	1.47	0.60
17:B:301:HOH:O	8:H:225:GLU:HA	2.02	0.60
2:P:217:LYS:C	2:P:219:ALA:H	2.11	0.59
1:O:122:THR:HG22	2:P:128:ARG:HH21	1.68	0.58
2:B:217:LYS:C	2:B:219:ALA:H	2.10	0.58
14:b:168:SER:O	15:d:4:POL:H33	2.04	0.58
1:O:12:PHE:H	2:P:20:GLN:HE22	1.52	0.57
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.40	0.56
3:Q:160:GLN:HA	3:Q:160:GLN:HE21	1.71	0.56
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.70	0.56
3:C:9:PHE:H	4:D:15:GLN:HE22	1.51	0.55
13:M:35:ARG:HD2	13:M:36:PHE:CE2	2.41	0.55
14:N:168:SER:O	15:c:4:POL:H33	2.07	0.55
1:A:122:THR:HG22	2:B:128:ARG:HH21	1.71	0.55
13:M:35:ARG:HD2	13:M:36:PHE:CZ	2.41	0.55
4:R:176:LEU:HD11	5:S:54:GLU:HB2	1.88	0.55
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	1.88	0.55
10:J:21:VAL:HG11	11:K:122:LEU:HD11	1.89	0.55
4:R:159:TYR:CE2	5:S:56:SER:HB3	2.42	0.54
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.90	0.54
11:Y:45:MET:CE	17:Y:401:HOH:O	2.49	0.54
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.56	0.53
9:I:36:SER:HB2	10:J:126:VAL:HG11	1.89	0.53
3:C:201:VAL:O	3:C:202:GLN:CB	2.56	0.53
11:K:116:ASP:OD2	11:K:118:ASP:HB2	2.08	0.53
10:X:23:ARG:CZ	17:X:201:HOH:O	2.36	0.53
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.90	0.53
8:H:97:TYR:HE2	8:H:114:HIS:CE1	2.28	0.52
14:N:24:ALA:HB3	13:a:146:PHE:HE2	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:47:ALA:HB1	2:P:64:LYS:HD2	1.92	0.52
1:A:12:PHE:H	2:B:20:GLN:HE22	1.57	0.52
4:D:91:HIS:HB3	4:D:99:ILE:HG22	1.92	0.52
4:R:91:HIS:HB3	4:R:99:ILE:HG22	1.92	0.52
8:V:53:GLU:O	8:V:57:GLN:HG2	2.09	0.52
2:B:146:GLN:HG2	3:C:57:ILE:HG21	1.91	0.51
11:Y:110:PRO:CB	17:Y:408:HOH:O	2.44	0.51
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.92	0.51
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.93	0.51
8:V:97:TYR:HE2	8:V:114:HIS:CE1	2.29	0.51
14:b:13:ILE:HG21	14:b:175:MET:HE2	1.93	0.51
15:c:2:ALA:O	15:c:3:GAU:HG2	2.10	0.50
10:J:3:ILE:HG23	10:J:18:SER:HB3	1.93	0.50
10:X:1:MET:HG2	10:X:34:LYS:HE3	1.93	0.50
10:J:25:ILE:O	10:X:139:TYR:OH	2.30	0.50
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.94	0.50
10:X:3:ILE:HG23	10:X:18:SER:HB3	1.94	0.50
11:K:7:ARG:HG2	11:K:110:PRO:HB2	1.94	0.49
14:N:13:ILE:HG21	14:N:175:MET:HE2	1.93	0.49
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.93	0.49
14:N:36:ARG:NH1	17:N:303:HOH:O	2.44	0.49
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.94	0.49
11:Y:128:CYS:SG	11:Y:136:ALA:HB3	2.53	0.49
7:G:23:PHE:O	7:G:26:THR:HB	2.13	0.48
9:I:98:ARG:O	9:I:126:ILE:HD11	2.12	0.48
11:K:128:CYS:SG	11:K:136:ALA:HB3	2.53	0.48
11:Y:7:ARG:HG2	11:Y:110:PRO:HB2	1.95	0.48
10:J:1:MET:HG2	10:J:34:LYS:HE3	1.94	0.48
14:b:83:LYS:HG3	14:b:119:VAL:CG2	2.44	0.48
2:P:12:PHE:H	3:Q:17:GLN:HE22	1.60	0.48
11:Y:107:LYS:HG3	11:Y:108:GLU:HG3	1.95	0.48
11:K:59:LEU:CD1	17:K:401:HOH:O	2.61	0.48
3:C:35:LYS:HG2	3:C:158:SER:O	2.13	0.48
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.13	0.48
11:K:107:LYS:HG3	11:K:108:GLU:HG3	1.95	0.48
7:U:23:PHE:O	7:U:26:THR:HB	2.14	0.48
13:M:146:PHE:HE2	14:b:24:ALA:HB3	1.79	0.47
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.44	0.47
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.44	0.47
2:P:124:HIS:HB3	3:Q:124:VAL:HG12	1.96	0.47
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.43	0.47
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.96	0.47
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	1.95	0.47
11:K:145:LYS:HB2	11:K:148:LEU:HD13	1.96	0.47
2:P:3:ARG:HB3	5:S:122:TYR:OH	2.14	0.47
15:c:2:ALA:C	15:c:3:GAU:CG	2.86	0.47
9:I:101:PRO:HB3	9:I:126:ILE:HD12	1.97	0.47
11:Y:45:MET:CE	11:Y:53:GLN:HG3	2.45	0.47
12:Z:131:TYR:C	12:Z:132:GLU:CG	2.82	0.47
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.96	0.47
13:M:27:LEU:HD21	13:M:34:LEU:HD22	1.97	0.47
11:Y:11:GLY:HA2	17:Y:408:HOH:O	2.15	0.47
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.45	0.46
13:a:27:LEU:HD21	13:a:34:LEU:HD22	1.97	0.46
10:X:1:MET:CB	10:X:34:LYS:HE3	2.46	0.46
3:C:149:GLU:HB2	3:C:150:PRO:HD2	1.98	0.46
10:J:1:MET:CB	10:J:34:LYS:HE3	2.46	0.46
11:K:59:LEU:HD13	17:K:401:HOH:O	2.15	0.46
1:O:1:MET:HG3	6:T:122:TYR:CZ	2.50	0.46
3:Q:149:GLU:HB2	3:Q:150:PRO:HD2	1.98	0.46
6:F:146:MET:HE3	6:F:161:THR:HB	1.98	0.46
7:U:195:GLU:HG3	7:U:235:ARG:HG3	1.97	0.46
15:d:2:ALA:C	15:d:3:GAU:CG	2.86	0.46
10:X:1:MET:HB3	10:X:34:LYS:HE3	1.98	0.45
2:B:217:LYS:C	2:B:219:ALA:N	2.74	0.45
10:J:168:LEU:O	10:J:172:MET:HB2	2.16	0.45
2:P:151:ASN:HB2	2:P:152:PRO:HD2	1.99	0.45
1:A:1:MET:HG3	6:F:122:TYR:CZ	2.51	0.45
2:B:124:HIS:HB3	3:C:124:VAL:HG12	1.99	0.45
13:M:127:LEU:HG	13:M:142:LEU:HD12	1.99	0.45
8:H:50:ALA:CB	9:I:126:ILE:HG23	2.47	0.45
4:R:158:ARG:HB3	5:S:57:SER:HB3	1.98	0.45
7:G:195:GLU:HG3	7:G:235:ARG:HG3	1.98	0.45
9:W:36:SER:HB2	10:X:126:VAL:HG11	1.98	0.45
7:G:63:ILE:HD12	7:G:215:GLU:HG2	1.99	0.45
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.51	0.45
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.97	0.45
8:V:35:HIS:HB3	8:V:56:THR:HG21	1.98	0.45
11:K:110:PRO:CB	17:K:411:HOH:O	2.45	0.45
14:N:171:GLY:HA2	13:a:219:TRP:CH2	2.52	0.45
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:198:LEU:HD12	6:F:243:ILE:HG22	1.98	0.45
8:H:35:HIS:HB3	8:H:56:THR:HG21	1.98	0.45
10:J:1:MET:HB3	10:J:34:LYS:HE3	1.98	0.45
2:P:217:LYS:C	2:P:219:ALA:N	2.74	0.44
6:T:198:LEU:HD12	6:T:243:ILE:HG22	1.98	0.44
14:b:36:ARG:HG3	14:b:42:TRP:CE2	2.52	0.44
2:B:151:ASN:HB2	2:B:152:PRO:HD2	1.99	0.44
7:G:73:VAL:HG12	7:G:133:THR:HB	1.98	0.44
11:K:38:ASN:HB2	11:K:39:PRO:CD	2.47	0.44
11:Y:38:ASN:HB2	11:Y:39:PRO:CD	2.47	0.44
7:U:73:VAL:HG12	7:U:133:THR:HB	1.98	0.44
13:a:127:LEU:HG	13:a:142:LEU:HD12	1.99	0.44
2:B:95:GLN:HE22	9:I:71:ASN:HD22	1.65	0.44
7:U:63:ILE:HD12	7:U:215:GLU:HG2	1.98	0.44
8:H:196:ARG:NH2	9:I:150:GLU:HG3	2.32	0.44
2:P:50:LYS:O	2:P:51:VAL:C	2.60	0.44
17:J:212:HOH:O	10:X:174:MET:SD	2.61	0.43
2:P:219:ALA:HB2	2:P:225:TYR:HB2	1.99	0.43
8:V:104:ASP:HB2	8:V:105:PRO:CD	2.48	0.43
8:H:84:LYS:HA	8:H:113:ILE:HD11	2.00	0.43
11:K:83:LEU:N	17:K:401:HOH:O	2.50	0.43
6:T:146:MET:HE3	6:T:161:THR:HB	1.99	0.43
2:B:50:LYS:O	2:B:51:VAL:C	2.60	0.43
13:M:33:LEU:HD13	14:b:133:PHE:CE1	2.53	0.43
10:X:168:LEU:O	10:X:172:MET:HB2	2.18	0.43
1:O:14:PRO:HA	2:P:23:TYR:CD1	2.53	0.43
8:H:196:ARG:NH2	9:I:150:GLU:O	2.51	0.43
10:J:139:TYR:OH	10:X:25:ILE:O	2.37	0.43
3:Q:11:PRO:HA	4:R:18:TYR:CD1	2.54	0.43
8:H:104:ASP:HB2	8:H:105:PRO:CD	2.48	0.43
2:B:219:ALA:HB2	2:B:225:TYR:HB2	2.00	0.43
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.54	0.43
5:S:9:THR:HG21	5:S:119:THR:HA	2.00	0.43
2:B:148:TYR:OH	3:C:57:ILE:HB	2.19	0.43
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.54	0.43
5:S:230:ALA:HA	5:S:233:ILE:HD12	2.01	0.43
10:X:119:ILE:HG12	10:X:125:LYS:HG3	2.00	0.43
14:b:45:ARG:NH2	17:d:101:HOH:O	2.39	0.42
10:J:119:ILE:HG12	10:J:125:LYS:HG3	2.01	0.42
15:c:3:GAU:HA	15:c:4:POL:H32	1.77	0.42
9:I:141:ALA:HB2	9:I:177:ASP:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:187:ARG:HA	14:b:26:ILE:HB	2.01	0.42
4:R:9:PRO:HA	5:S:23:TYR:CD1	2.54	0.42
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	2.02	0.42
7:G:165:LYS:HD2	7:G:205:LEU:HD22	2.02	0.42
13:M:187:ARG:HG3	14:b:25:TYR:CE1	2.54	0.42
2:B:14:PRO:HA	3:C:20:TYR:CD1	2.54	0.42
13:M:219:TRP:CH2	14:b:171:GLY:HA2	2.55	0.42
7:U:165:LYS:HD2	7:U:205:LEU:HD22	2.01	0.42
4:D:88:ALA:HA	4:D:99:ILE:HG21	2.02	0.42
5:E:9:THR:HG21	5:E:119:THR:HA	2.00	0.42
3:Q:166:SER:HA	3:Q:169:VAL:HG13	2.02	0.42
7:G:34:LEU:C	7:G:34:LEU:HD23	2.45	0.42
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.02	0.42
5:E:230:ALA:HA	5:E:233:ILE:HD12	2.01	0.42
14:N:1:THR:CG2	14:N:3:ILE:HG23	2.50	0.42
14:N:83:LYS:HG3	14:N:119:VAL:HG22	2.01	0.42
4:R:91:HIS:CD2	4:R:99:ILE:HG22	2.55	0.42
2:B:14:PRO:HA	3:C:20:TYR:CE1	2.55	0.41
9:I:20:VAL:HG13	9:I:118:PRO:HB3	2.02	0.41
7:U:34:LEU:C	7:U:34:LEU:HD23	2.45	0.41
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.41
11:K:20:ALA:HB2	11:K:31:VAL:HG21	2.02	0.41
12:Z:108:HIS:CE1	17:Z:402:HOH:O	2.73	0.41
10:J:126:VAL:HG12	10:J:128:LEU:HG	2.02	0.41
12:L:8:ASN:HA	12:L:30:ILE:O	2.20	0.41
9:W:141:ALA:HB2	9:W:177:ASP:HB2	2.02	0.41
9:W:170:LEU:C	9:W:170:LEU:HD23	2.45	0.41
6:F:122:TYR:CE1	7:G:125:MET:HE3	2.56	0.41
6:T:216:SER:HB3	6:T:219:GLU:HB2	2.02	0.41
8:V:218:VAL:CG2	9:W:196:LYS:HB2	2.51	0.41
6:F:216:SER:HB3	6:F:219:GLU:HB2	2.02	0.41
4:D:91:HIS:CD2	4:D:99:ILE:HG22	2.56	0.41
7:G:78:ILE:N	7:G:79:PRO:CD	2.83	0.41
8:V:63:ILE:HG23	8:V:74:PRO:HB3	2.03	0.41
9:W:20:VAL:HG23	9:W:189:ILE:HB	2.03	0.41
10:X:126:VAL:HG12	10:X:128:LEU:HG	2.03	0.41
12:Z:8:ASN:HA	12:Z:30:ILE:O	2.19	0.41
7:G:149:ASP:HB2	7:G:150:PRO:CD	2.51	0.41
8:H:53:GLU:O	8:H:53:GLU:HG3	2.20	0.41
8:V:196:ARG:NH2	9:W:150:GLU:O	2.54	0.41
14:b:1:THR:CG2	14:b:3:ILE:HG23	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:b:83:LYS:HG3	14:b:119:VAL:HG22	2.02	0.41
2:P:93:HIS:CE1	2:P:113:ARG:HG2	2.56	0.41
13:a:97:ALA:HA	13:a:130:VAL:HG21	2.03	0.40
14:b:1:THR:HG22	14:b:2:SER:N	2.36	0.40
14:N:133:PHE:CE1	13:a:33:LEU:HD13	2.55	0.40
14:N:133:PHE:HA	14:b:132:THR:O	2.21	0.40
2:B:93:HIS:CE1	2:B:113:ARG:HG2	2.57	0.40
3:C:166:SER:HA	3:C:169:VAL:HG13	2.02	0.40
7:G:187:GLU:HG2	7:G:192:LYS:HB2	2.04	0.40
13:M:96:LEU:O	13:M:100:MET:HG2	2.21	0.40
13:M:97:ALA:HA	13:M:130:VAL:HG21	2.03	0.40
7:U:187:GLU:HG2	7:U:192:LYS:HB2	2.04	0.40
8:V:196:ARG:NH2	9:W:150:GLU:HG3	2.36	0.40
13:a:96:LEU:O	13:a:100:MET:HG2	2.21	0.40
8:H:63:ILE:HG23	8:H:74:PRO:HB3	2.02	0.40
9:I:170:LEU:C	9:I:170:LEU:HD23	2.46	0.40
4:R:59:ILE:HG22	4:R:220:PHE:HZ	1.87	0.40
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.57	0.40
1:A:122:THR:CG2	2:B:128:ARG:HH21	2.34	0.40
9:W:20:VAL:HG13	9:W:118:PRO:HB3	2.02	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%)	6 (2%)	1 (0%)	30	60
1	O	248/250 (99%)	240 (97%)	7 (3%)	1 (0%)	30	60
2	B	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	7	25
2	P	242/258 (94%)	234 (97%)	4 (2%)	4 (2%)	7	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	238/254 (94%)	231 (97%)	4 (2%)	3 (1%)	9	31
3	Q	238/254 (94%)	231 (97%)	4 (2%)	3 (1%)	9	31
4	D	231/260 (89%)	229 (99%)	2 (1%)	0	100	100
4	R	231/260 (89%)	229 (99%)	2 (1%)	0	100	100
5	E	229/234 (98%)	221 (96%)	8 (4%)	0	100	100
5	S	229/234 (98%)	221 (96%)	8 (4%)	0	100	100
6	F	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
6	T	241/288 (84%)	238 (99%)	3 (1%)	0	100	100
7	G	239/252 (95%)	239 (100%)	0	0	100	100
7	U	239/252 (95%)	239 (100%)	0	0	100	100
8	H	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
8	V	224/232 (97%)	218 (97%)	6 (3%)	0	100	100
9	I	202/205 (98%)	197 (98%)	5 (2%)	0	100	100
9	W	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
10	J	193/198 (98%)	189 (98%)	3 (2%)	1 (0%)	24	55
10	X	193/198 (98%)	188 (97%)	4 (2%)	1 (0%)	24	55
11	K	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
11	Y	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
12	L	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
12	Z	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
13	M	231/246 (94%)	223 (96%)	7 (3%)	1 (0%)	30	60
13	a	231/246 (94%)	223 (96%)	7 (3%)	1 (0%)	30	60
14	N	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
14	b	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
15	c	1/4 (25%)	1 (100%)	0	0	100	100
15	d	1/4 (25%)	1 (100%)	0	0	100	100
All	All	6286/6622 (95%)	6143 (98%)	123 (2%)	20 (0%)	36	66

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
2	B	222	GLY

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Mol	Chain	Res	Type
3	C	202	GLN
2	P	51	VAL
2	P	222	GLY
3	Q	202	GLN
1	A	2	THR
3	C	205	ALA
1	O	2	THR
3	Q	205	ALA
2	B	218	GLY
2	B	220	ASN
2	P	218	GLY
2	P	220	ASN
3	C	183	PRO
10	J	24	GLY
3	Q	183	PRO
10	X	24	GLY
13	M	229	GLY
13	a	229	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	209/209 (100%)	202 (97%)	7 (3%)	33	69
1	O	209/209 (100%)	202 (97%)	7 (3%)	33	69
2	B	203/216 (94%)	196 (97%)	7 (3%)	32	68
2	P	203/216 (94%)	196 (97%)	7 (3%)	32	68
3	C	212/226 (94%)	198 (93%)	14 (7%)	15	43
3	Q	212/226 (94%)	198 (93%)	14 (7%)	15	43
4	D	194/215 (90%)	179 (92%)	15 (8%)	12	36
4	R	194/215 (90%)	179 (92%)	15 (8%)	12	36
5	E	190/193 (98%)	181 (95%)	9 (5%)	23	57
5	S	190/193 (98%)	181 (95%)	9 (5%)	23	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	201/239 (84%)	193 (96%)	8 (4%)	28	63
6	T	201/239 (84%)	193 (96%)	8 (4%)	28	63
7	G	206/210 (98%)	197 (96%)	9 (4%)	25	59
7	U	206/210 (98%)	197 (96%)	9 (4%)	25	59
8	H	185/190 (97%)	180 (97%)	5 (3%)	39	74
8	V	185/190 (97%)	181 (98%)	4 (2%)	45	78
9	I	172/173 (99%)	168 (98%)	4 (2%)	44	78
9	W	172/173 (99%)	169 (98%)	3 (2%)	53	83
10	J	173/175 (99%)	168 (97%)	5 (3%)	37	73
10	X	173/175 (99%)	168 (97%)	5 (3%)	37	73
11	K	169/169 (100%)	160 (95%)	9 (5%)	20	52
11	Y	169/169 (100%)	160 (95%)	9 (5%)	20	52
12	L	185/185 (100%)	178 (96%)	7 (4%)	29	64
12	Z	185/185 (100%)	179 (97%)	6 (3%)	34	70
13	M	199/208 (96%)	191 (96%)	8 (4%)	28	63
13	a	199/208 (96%)	192 (96%)	7 (4%)	32	67
14	N	162/162 (100%)	155 (96%)	7 (4%)	26	60
14	b	162/162 (100%)	155 (96%)	7 (4%)	26	60
All	All	5320/5540 (96%)	5096 (96%)	224 (4%)	26	61

All (224) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	59	GLU
1	A	62	SER
1	A	122	THR
1	A	157	PHE
1	A	201	GLU
1	A	250	LEU
2	B	50	LYS
2	B	55	LEU
2	B	79	LEU
2	B	102	ASN
2	B	113	ARG
2	B	191	LEU

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Mol	Chain	Res	Type
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	49	THR
3	C	50	LEU
3	C	51	LYS
3	C	52	LEU
3	C	60	SER
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	175	LYS
3	C	180	LYS
3	C	213	VAL
3	C	240	GLU
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU
4	D	60	VAL
4	D	99	ILE
4	D	117	GLU
4	D	169	GLU
4	D	176	LEU
4	D	190	LEU
4	D	193	LEU
4	D	202	GLU
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	55	LEU
5	E	71	LEU
5	E	92	ASN
5	E	188	LEU
5	E	207	VAL
5	E	208	ASP
5	E	231	LYS
6	F	68	ARG
6	F	123	ASN
6	F	172	LEU

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Mol	Chain	Res	Type
6	F	181	GLU
6	F	201	GLU
6	F	207	ASP
6	F	221	ASN
6	F	240	GLN
7	G	13	GLU
7	G	26	THR
7	G	75	ASN
7	G	83	ASN
7	G	115	LEU
7	G	122	ARG
7	G	125	MET
7	G	235	ARG
7	G	236	LEU
8	H	34	LEU
8	H	53	GLU
8	H	68	LEU
8	H	144	GLN
8	H	196	ARG
9	I	37	ASN
9	I	126	ILE
9	I	171	LEU
9	I	192	ASP
10	J	3	ILE
10	J	23	ARG
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
11	K	4	LEU
11	K	9	GLN
11	K	35	ILE
11	K	57	THR
11	K	69	ARG
11	K	97	MET
11	K	107	LYS
11	K	140	LEU
11	K	148	LEU
12	L	18	GLU
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	132	GLU

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Mol	Chain	Res	Type
12	L	150	LEU
12	L	161	GLU
13	M	2	GLN
13	M	35	ARG
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	187	ARG
13	M	212	LEU
13	M	224	ASP
14	N	9	LYS
14	N	83	LYS
14	N	104	ASP
14	N	107	LYS
14	N	115	LEU
14	N	119	VAL
14	N	178	LEU
1	O	1	MET
1	O	59	GLU
1	O	62	SER
1	O	122	THR
1	O	157	PHE
1	O	201	GLU
1	O	250	LEU
2	P	50	LYS
2	P	55	LEU
2	P	79	LEU
2	P	102	ASN
2	P	113	ARG
2	P	191	LEU
2	P	238	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	49	THR
3	Q	50	LEU
3	Q	51	LYS
3	Q	52	LEU
3	Q	60	SER
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	175	LYS

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Mol	Chain	Res	Type
3	Q	180	LYS
3	Q	213	VAL
3	Q	240	GLU
4	R	20	LEU
4	R	40	LEU
4	R	51	LEU
4	R	60	VAL
4	R	99	ILE
4	R	117	GLU
4	R	169	GLU
4	R	176	LEU
4	R	190	LEU
4	R	193	LEU
4	R	202	GLU
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	55	LEU
5	S	71	LEU
5	S	92	ASN
5	S	188	LEU
5	S	207	VAL
5	S	208	ASP
5	S	231	LYS
6	T	68	ARG
6	T	123	ASN
6	T	172	LEU
6	T	181	GLU
6	T	201	GLU
6	T	207	ASP
6	T	221	ASN
6	T	240	GLN
7	U	13	GLU
7	U	26	THR
7	U	75	ASN
7	U	83	ASN
7	U	115	LEU
7	U	122	ARG
7	U	125	MET

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Mol	Chain	Res	Type
7	U	235	ARG
7	U	236	LEU
8	V	34	LEU
8	V	68	LEU
8	V	144	GLN
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU
9	W	192	ASP
10	X	3	ILE
10	X	23	ARG
10	X	35	THR
10	X	90	LYS
10	X	99	GLN
11	Y	4	LEU
11	Y	9	GLN
11	Y	35	ILE
11	Y	57	THR
11	Y	69	ARG
11	Y	97	MET
11	Y	107	LYS
11	Y	140	LEU
11	Y	148	LEU
12	Z	18	GLU
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	150	LEU
12	Z	161	GLU
13	a	2	GLN
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	187	ARG
13	a	212	LEU
13	a	224	ASP
14	b	9	LYS
14	b	83	LYS
14	b	104	ASP
14	b	107	LYS
14	b	115	LEU
14	b	119	VAL

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Mol	Chain	Res	Type
14	b	178	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (161) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
2	B	20	GLN
2	B	95	GLN
2	B	119	GLN
2	B	123	GLN
2	B	124	HIS
2	B	146	GLN
2	B	176	GLN
2	B	232	GLN
3	C	17	GLN
3	C	115	GLN
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	100	ASN
4	D	146	GLN
4	D	225	ASN
5	E	68	HIS
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	240	GLN
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	166	GLN

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Mol	Chain	Res	Type
7	G	167	GLN
7	G	175	ASN
8	H	66	HIS
8	H	86	HIS
8	H	165	ASN
8	H	194	ASN
8	H	219	ASN
9	I	37	ASN
9	I	88	GLN
9	I	203	GLN
10	J	10	GLN
10	J	37	GLN
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	85	ASN
11	K	143	ASN
11	K	176	ASN
11	K	208	ASN
12	L	1	GLN
12	L	3	ASN
12	L	49	ASN
12	L	70	ASN
12	L	79	HIS
12	L	80	ASN
12	L	153	GLN
12	L	155	ASN
12	L	158	ASN
12	L	197	GLN
13	M	48	ASN
13	M	102	GLN
13	M	108	ASN
13	M	149	HIS
13	M	194	ASN
13	M	213	GLN
14	N	38	HIS
14	N	69	GLN
14	N	141	ASN
14	N	161	GLN

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Mol	Chain	Res	Type
2	P	20	GLN
2	P	93	HIS
2	P	95	GLN
2	P	119	GLN
2	P	123	GLN
2	P	124	HIS
2	P	146	GLN
2	P	176	GLN
2	P	232	GLN
3	Q	17	GLN
3	Q	115	GLN
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
4	R	106	GLN
4	R	146	GLN
4	R	160	ASN
4	R	225	ASN
5	S	59	GLN
5	S	68	HIS
5	S	99	ASN
5	S	118	ASN
5	S	120	GLN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
6	T	240	GLN
7	U	30	ASN
7	U	83	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	167	GLN
7	U	172	ASN

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Mol	Chain	Res	Type
7	U	175	ASN
8	V	35	HIS
8	V	66	HIS
8	V	86	HIS
8	V	194	ASN
8	V	219	ASN
9	W	37	ASN
9	W	63	ASN
9	W	88	GLN
9	W	203	GLN
10	X	10	GLN
10	X	37	GLN
10	X	55	GLN
10	X	63	ASN
10	X	146	HIS
10	X	147	HIS
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	49	ASN
12	Z	70	ASN
12	Z	80	ASN
12	Z	153	GLN
12	Z	155	ASN
12	Z	158	ASN
12	Z	197	GLN
13	a	18	ASN
13	a	48	ASN
13	a	102	GLN
13	a	108	ASN
13	a	149	HIS
13	a	194	ASN
13	a	213	GLN
14	b	38	HIS
14	b	69	GLN
14	b	141	ASN
14	b	161	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	GAU	d	3	14,15	8,8,8	1.50	2 (25%)	8,9,9	1.76	2 (25%)
15	N7P	d	1	15	9,10,11	1.78	2 (22%)	9,13,15	2.18	3 (33%)
15	N7P	c	1	15	9,10,11	1.68	2 (22%)	9,13,15	2.24	4 (44%)
15	GAU	c	3	14,15	8,8,8	1.65	2 (25%)	8,9,9	1.35	1 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	GAU	d	3	14,15	-	2/7/7/7	-
15	N7P	d	1	15	-	0/4/16/18	0/1/1/1
15	N7P	c	1	15	-	0/4/16/18	0/1/1/1
15	GAU	c	3	14,15	-	2/7/7/7	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	c	3	GAU	C-CA	3.71	1.58	1.52
15	c	1	N7P	CB-CA	-3.33	1.46	1.53
15	d	1	N7P	CB-CA	-3.21	1.46	1.53
15	d	1	N7P	CA-N	-2.91	1.45	1.48
15	c	1	N7P	CG-CD	-2.80	1.42	1.51
15	d	3	GAU	C-CA	2.71	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	c	3	GAU	OE2-CD	-2.53	1.22	1.30
15	d	3	GAU	OE2-CD	-2.30	1.23	1.30

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	d	1	N7P	CB-CA-C	-3.88	107.34	112.66
15	c	1	N7P	CB-CA-C	-3.70	107.58	112.66
15	d	1	N7P	O1-C1-N	3.46	124.45	120.45
15	c	1	N7P	O1-C1-N	3.38	124.35	120.45
15	c	1	N7P	CA-N-C1	3.32	127.49	120.82
15	d	3	GAU	CG-CB-CA	-3.02	106.42	112.87
15	d	3	GAU	CB-CA-N	-3.00	100.05	109.16
15	d	1	N7P	CA-N-C1	2.65	126.15	120.82
15	c	3	GAU	CB-CA-N	-2.51	101.53	109.16
15	c	1	N7P	CB-CG-CD	-2.26	98.60	104.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	c	3	GAU	O-C-CA-N
15	c	3	GAU	O-C-CA-CB
15	d	3	GAU	O-C-CA-CB
15	d	3	GAU	O-C-CA-N

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	d	3	GAU	3	0
15	c	3	GAU	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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 [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%)	-0.38	2 (0%) 82 75	39, 50, 82, 120	0
1	O	250/250 (100%)	-0.28	3 (1%) 76 68	42, 58, 99, 128	0
2	B	244/258 (94%)	-0.22	5 (2%) 65 56	38, 56, 94, 143	0
2	P	244/258 (94%)	-0.05	12 (4%) 35 27	44, 60, 105, 149	0
3	C	240/254 (94%)	-0.15	7 (2%) 53 43	40, 62, 116, 140	0
3	Q	240/254 (94%)	0.00	8 (3%) 49 39	41, 68, 144, 163	0
4	D	235/260 (90%)	-0.24	2 (0%) 81 74	43, 62, 95, 133	0
4	R	235/260 (90%)	-0.21	0 100 100	43, 64, 103, 137	0
5	E	231/234 (98%)	-0.18	1 (0%) 88 84	46, 66, 101, 148	0
5	S	231/234 (98%)	-0.02	4 (1%) 69 60	48, 72, 113, 161	0
6	F	243/288 (84%)	-0.30	2 (0%) 82 75	41, 57, 104, 132	0
6	T	243/288 (84%)	-0.09	5 (2%) 63 54	44, 67, 118, 148	0
7	G	241/252 (95%)	-0.37	2 (0%) 82 75	34, 52, 83, 132	0
7	U	241/252 (95%)	-0.26	3 (1%) 76 68	40, 56, 85, 129	0
8	H	226/232 (97%)	-0.26	2 (0%) 81 74	32, 48, 79, 143	0
8	V	226/232 (97%)	-0.24	2 (0%) 81 74	40, 52, 82, 157	0
9	I	204/205 (99%)	-0.54	0 100 100	36, 47, 73, 96	0
9	W	204/205 (99%)	-0.52	0 100 100	38, 49, 75, 101	0
10	J	195/198 (98%)	-0.40	1 (0%) 87 82	38, 51, 75, 132	0
10	X	195/198 (98%)	-0.42	1 (0%) 87 82	36, 51, 75, 137	0
11	K	212/212 (100%)	-0.38	1 (0%) 87 82	36, 52, 72, 95	0
11	Y	212/212 (100%)	-0.38	1 (0%) 87 82	40, 51, 73, 94	0
12	L	222/222 (100%)	-0.43	1 (0%) 87 82	38, 53, 79, 114	0
12	Z	222/222 (100%)	-0.41	1 (0%) 87 82	38, 51, 78, 112	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	M	233/246 (94%)	-0.47	1 (0%) 88 84	35, 50, 71, 89	0
13	a	233/246 (94%)	-0.46	1 (0%) 88 84	35, 49, 68, 85	0
14	N	196/196 (100%)	-0.32	2 (1%) 79 72	35, 46, 71, 101	0
14	b	196/196 (100%)	-0.39	1 (0%) 87 82	36, 47, 72, 106	0
15	c	1/4 (25%)	0.90	0 100 100	65, 65, 65, 65	0
15	d	1/4 (25%)	0.05	0 100 100	61, 61, 61, 61	0
All	All	6346/6622 (95%)	-0.29	71 (1%) 78 70	32, 55, 98, 163	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	X	1	MET	6.9
10	J	1	MET	4.6
2	B	219	ALA	4.6
8	V	223	ILE	4.6
3	Q	50	LEU	4.2
14	b	103	ASP	4.0
3	Q	205	ALA	4.0
2	B	218	GLY	3.8
2	P	219	ALA	3.7
13	a	1	THR	3.6
8	H	223	ILE	3.5
3	C	205	ALA	3.5
4	D	240	ALA	3.4
2	P	218	GLY	3.3
5	S	52	ALA	3.1
3	Q	49	THR	3.1
2	P	52	THR	3.0
3	Q	204	GLY	2.9
2	B	51	VAL	2.9
6	F	215	CYS	2.9
12	L	174	TYR	2.9
1	O	249	ALA	2.9
1	O	1	MET	2.8
3	Q	240	GLU	2.8
6	T	178	HIS	2.8
3	C	51	LYS	2.7
5	E	122	TYR	2.7
6	T	244	ASN	2.7
3	C	50	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
2	P	53	SER	2.7
2	P	51	VAL	2.6
2	P	220	ASN	2.6
7	G	242	GLN	2.6
6	T	215	CYS	2.5
2	P	222	GLY	2.5
8	H	224	GLN	2.5
3	C	240	GLU	2.4
3	Q	175	LYS	2.4
7	U	242	GLN	2.4
3	C	204	GLY	2.4
13	M	1	THR	2.4
6	T	206	LYS	2.4
1	A	62	SER	2.4
7	G	68	ARG	2.3
2	P	1	GLY	2.3
2	B	220	ASN	2.3
14	N	92	ASN	2.3
8	V	224	GLN	2.3
6	F	202	ASP	2.2
2	B	93	HIS	2.2
12	Z	174	TYR	2.2
1	A	1	MET	2.2
2	P	54	THR	2.2
6	T	203	ASN	2.2
3	Q	48	SER	2.2
11	K	116	ASP	2.1
3	C	201	VAL	2.1
3	C	49	THR	2.1
14	N	103	ASP	2.1
4	D	242	GLU	2.1
3	Q	51	LYS	2.1
11	Y	212	GLY	2.1
7	U	3	TYR	2.1
2	P	55	LEU	2.0
7	U	68	ARG	2.0
2	P	93	HIS	2.0
1	O	54	PRO	2.0
2	P	59	ASP	2.0
5	S	203	GLU	2.0
5	S	58	TYR	2.0
5	S	122	TYR	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	GAU	c	3	9/9	0.89	0.14	62,72,75,77	0
15	GAU	d	3	9/9	0.89	0.12	53,62,64,69	0
15	N7P	d	1	10/11	0.94	0.10	42,58,67,74	0
15	N7P	c	1	10/11	0.95	0.09	53,63,71,78	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
16	MG	Z	301	1/1	0.91	0.08	57,57,57,57	0
16	MG	I	301	1/1	0.95	0.14	70,70,70,70	0
16	MG	K	301	1/1	0.97	0.06	49,49,49,49	0
16	MG	L	301	1/1	0.98	0.11	58,58,58,58	0
16	MG	N	201	1/1	0.98	0.03	45,45,45,45	0
16	MG	I	302	1/1	0.98	0.10	51,51,51,51	0
16	MG	G	301	1/1	0.99	0.08	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.