



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:06 AM UTC

PDB ID : 3U5P / pdb_00003u5p
Title : Crystal structure of the complex of TRIM33 PHD-Bromo and H3(1-28)K9me
3K14acK18acK23ac histone peptide
Authors : Wang, Z.; Patel, D.J.
Deposited on : 2011-10-11
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

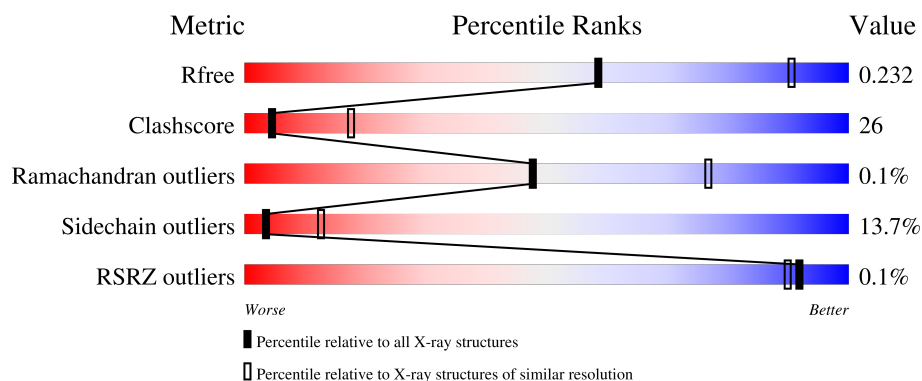
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



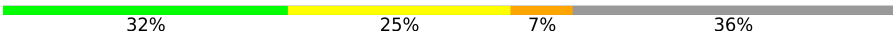
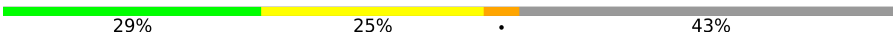
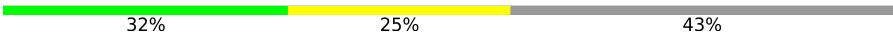
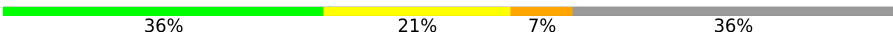
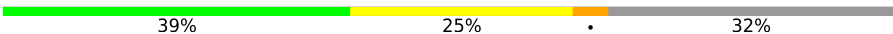
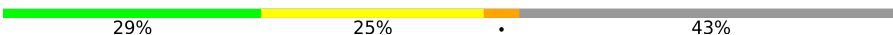
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	207	
1	B	207	
1	C	207	
1	D	207	
1	E	207	

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Mol	Chain	Length	Quality of chain
1	F	207	
1	G	207	
1	H	207	
2	I	28	
2	J	28	
2	K	28	
2	L	28	
2	M	28	
2	N	28	
2	O	28	
2	P	28	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13261 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 E3 ubiquitin-protein ligase TRIM33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1522	973	252	282	15			
1	B	188	Total	C	N	O	S	0	0	0
			1522	973	252	282	15			
1	C	188	Total	C	N	O	S	0	0	0
			1522	973	252	282	15			
1	D	188	Total	C	N	O	S	0	0	0
			1522	973	252	282	15			
1	E	188	Total	C	N	O	S	0	0	0
			1522	973	252	282	15			
1	F	188	Total	C	N	O	S	0	0	0
			1522	973	252	282	15			
1	G	188	Total	C	N	O	S	0	0	0
			1522	973	252	282	15			
1	H	188	Total	C	N	O	S	0	0	0
			1522	973	252	282	15			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	881	SER	-	expression tag	UNP Q9UPN9
B	881	SER	-	expression tag	UNP Q9UPN9
C	881	SER	-	expression tag	UNP Q9UPN9
D	881	SER	-	expression tag	UNP Q9UPN9
E	881	SER	-	expression tag	UNP Q9UPN9
F	881	SER	-	expression tag	UNP Q9UPN9
G	881	SER	-	expression tag	UNP Q9UPN9
H	881	SER	-	expression tag	UNP Q9UPN9

- Molecule 2 is a protein called Histone H3.1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	18	Total	C	N	O	0	0	0
			137	82	31	24			
2	J	16	Total	C	N	O	0	0	0
			128	77	29	22			
2	K	16	Total	C	N	O	0	0	0
			128	77	29	22			
2	L	18	Total	C	N	O	0	0	0
			137	82	31	24			
2	M	19	Total	C	N	O	0	0	0
			146	87	33	26			
2	N	16	Total	C	N	O	0	0	0
			128	77	29	22			
2	O	18	Total	C	N	O	0	0	0
			137	82	31	24			
2	P	16	Total	C	N	O	0	0	0
			128	77	29	22			

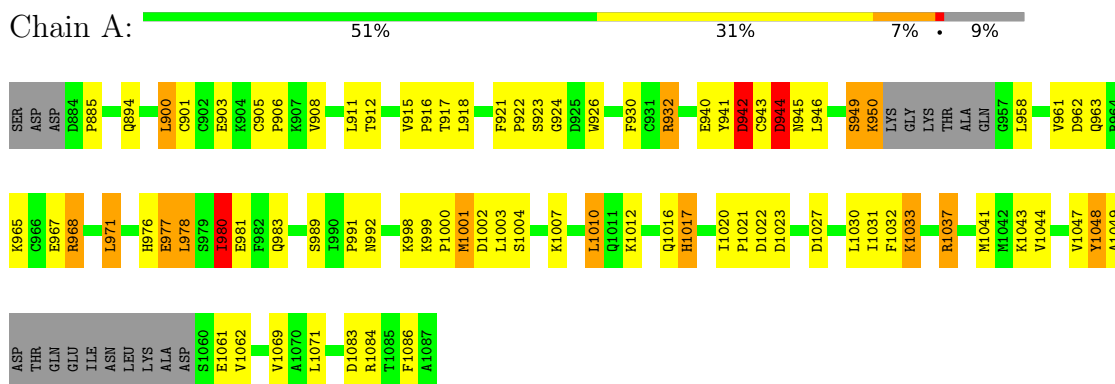
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Zn	0	0
			2	2		
3	B	2	Total	Zn	0	0
			2	2		
3	C	2	Total	Zn	0	0
			2	2		
3	D	2	Total	Zn	0	0
			2	2		
3	E	2	Total	Zn	0	0
			2	2		
3	F	2	Total	Zn	0	0
			2	2		
3	G	2	Total	Zn	0	0
			2	2		
3	H	2	Total	Zn	0	0
			2	2		

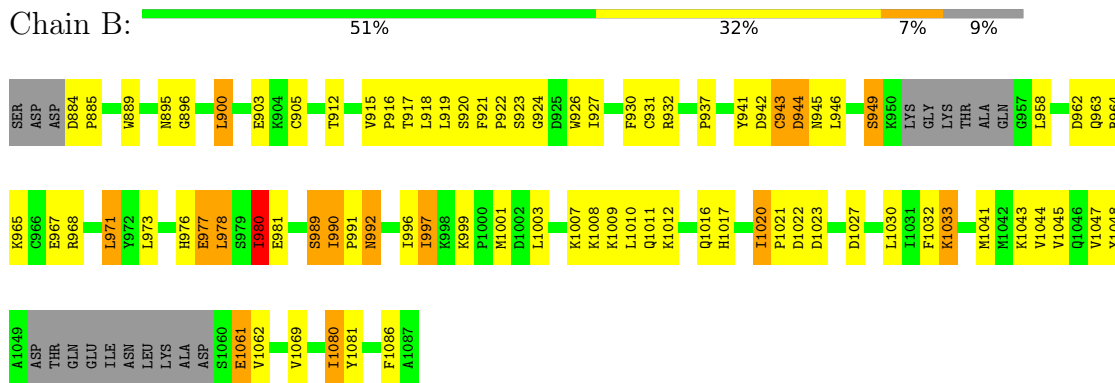
3 Residue-property plots [i](#)

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

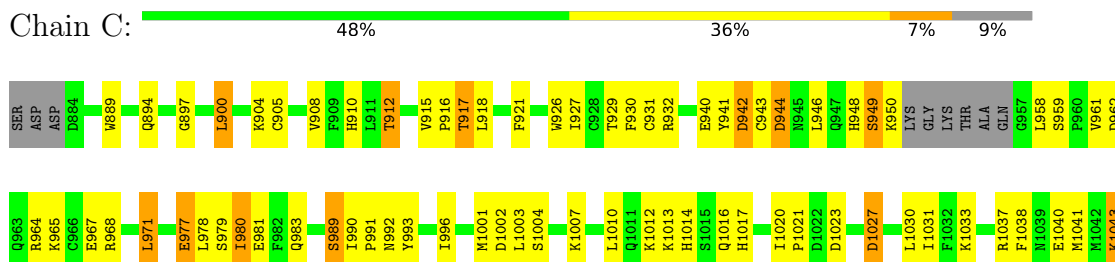
• Molecule 1: E3 ubiquitin-protein ligase TRIM33

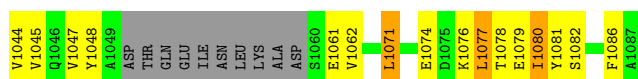


• Molecule 1: E3 ubiquitin-protein ligase TRIM33

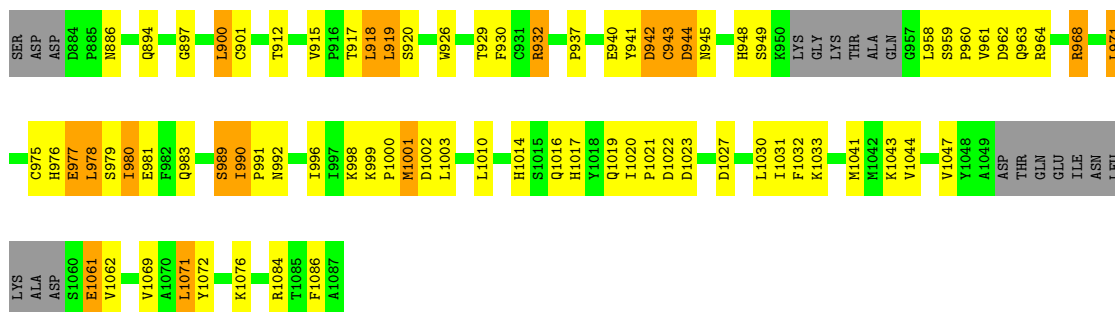


• Molecule 1: E3 ubiquitin-protein ligase TRIM33

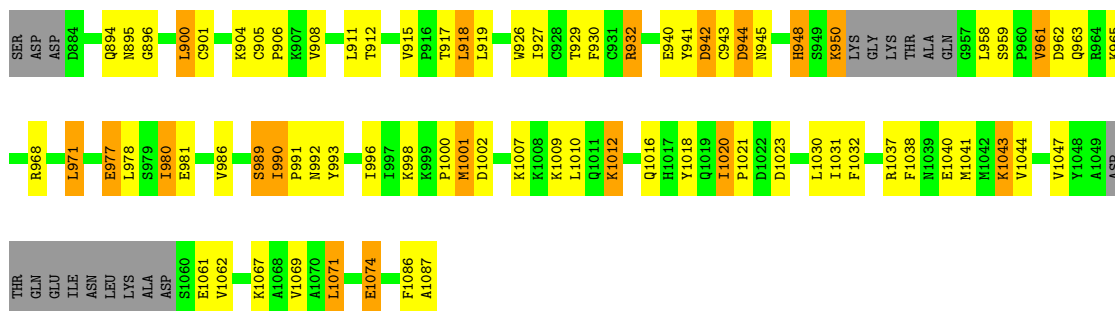




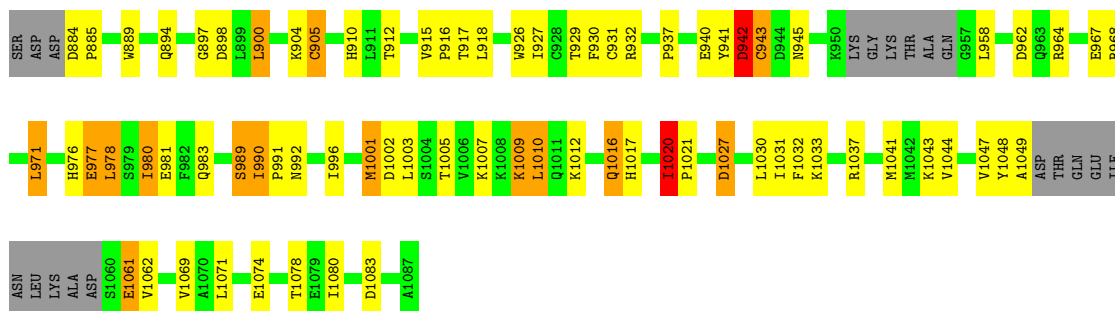
• Molecule 1: E3 ubiquitin-protein ligase TRIM33



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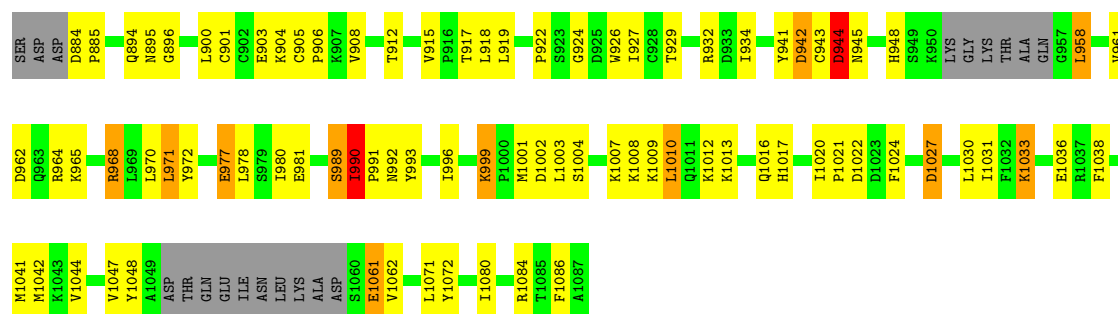
• Molecule 1: E3 ubiquitin-protein ligase TRIM33





• Molecule 1: E3 ubiquitin-protein ligase TRIM33

Chain H: 50% 34% 5% 9%



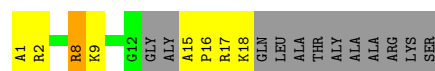
• Molecule 2: Histone H3.1

Chain I: 32% 25% 7% 36%



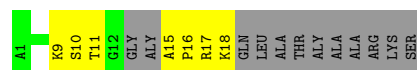
• Molecule 2: Histone H3.1

Chain J: 29% 25% 43%



• Molecule 2: Histone H3.1

Chain K: 32% 25% 43%

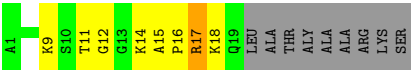


• Molecule 2: Histone H3.1

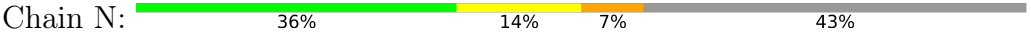
Chain L: 36% 21% 7% 36%



● Molecule 2: Histone H3.1



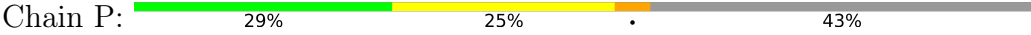
● Molecule 2: Histone H3.1



● Molecule 2: Histone H3.1



● Molecule 2: Histone H3.1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	63.43Å 63.61Å 124.61Å 90.01° 90.04° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 30.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.0 (30.00-2.80) 93.7 (30.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.210 , 0.265 0.212 , 0.232	Depositor DCC
R_{free} test set	2397 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	74.9	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 42.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.478 for k,-h,l 0.478 for -k,h,l 0.480 for h,-k,-l 0.480 for -h,k,-l 0.487 for -h,-k,l 0.479 for k,h,-l 0.480 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13261	wwPDB-VP
Average B, all atoms (Å ²)	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, M3L, ALY

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	0.88	0/1558	1.10	7/2105 (0.3%)
1	B	0.89	0/1558	1.06	7/2105 (0.3%)
1	C	0.96	3/1558 (0.2%)	1.10	2/2105 (0.1%)
1	D	0.93	1/1558 (0.1%)	1.08	4/2105 (0.2%)
1	E	0.94	1/1558 (0.1%)	1.06	4/2105 (0.2%)
1	F	0.93	0/1558	1.09	3/2105 (0.1%)
1	G	0.91	0/1558	1.07	6/2105 (0.3%)
1	H	0.93	0/1558	1.09	7/2105 (0.3%)
2	I	0.58	0/107	0.94	0/140
2	J	0.64	0/103	0.89	0/135
2	K	0.64	0/103	0.71	0/135
2	L	0.58	0/107	0.96	0/140
2	M	0.57	0/115	0.78	0/149
2	N	0.64	0/103	0.99	2/135 (1.5%)
2	O	0.62	0/107	0.89	1/140 (0.7%)
2	P	0.61	0/103	0.87	0/135
All	All	0.91	5/13312 (0.0%)	1.07	43/17949 (0.2%)

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
1	A	0	1
1	D	0	1
1	E	0	1
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	948	HIS	CG-CD2	7.69	1.44	1.35
1	C	948	HIS	CB-CG	5.65	1.58	1.50
1	E	948	HIS	CG-CD2	5.64	1.42	1.35
1	C	948	HIS	ND1-CE1	5.58	1.38	1.32
1	D	948	HIS	CG-CD2	5.35	1.41	1.35

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	942	ASP	N-CA-C	-10.22	94.87	110.10
1	B	944	ASP	N-CA-C	-9.28	101.16	111.28
1	A	999	LYS	CA-C-N	6.73	126.49	119.76
1	A	999	LYS	C-N-CA	6.73	126.49	119.76
1	A	942	ASP	N-CA-C	-6.67	100.36	110.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	932	ARG	Sidechain
1	D	932	ARG	Sidechain
1	E	932	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	1522	0	1486	74	0
1	B	1522	0	1486	84	0
1	C	1522	0	1487	76	0
1	D	1522	0	1486	70	0
1	E	1522	0	1486	72	0
1	F	1522	0	1487	70	0
1	G	1522	0	1486	88	0
1	H	1522	0	1486	74	0
2	I	137	0	149	21	0
2	J	128	0	143	18	0
2	K	128	0	144	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	137	0	150	15	0
2	M	146	0	157	14	0
2	N	128	0	144	9	0
2	O	137	0	150	15	0
2	P	128	0	145	11	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
3	H	2	0	0	0	0
All	All	13261	0	13072	687	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 26.

The worst 5 of 687 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)
2:L:15:ALA:HB1	2:L:16:PRO:CD	1.64	1.25
2:J:15:ALA:CB	2:J:16:PRO:HD3	1.64	1.25
2:I:16:PRO:O	2:I:17:ARG:HD3	1.35	1.24
2:O:15:ALA:HB1	2:O:16:PRO:CD	1.69	1.22
2:O:15:ALA:HB1	2:O:16:PRO:HD3	1.19	1.17

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	182/207 (88%)	170 (93%)	12 (7%)	0	100	100
1	B	182/207 (88%)	174 (96%)	8 (4%)	0	100	100
1	C	182/207 (88%)	177 (97%)	5 (3%)	0	100	100
1	D	182/207 (88%)	174 (96%)	8 (4%)	0	100	100
1	E	182/207 (88%)	175 (96%)	7 (4%)	0	100	100
1	F	182/207 (88%)	177 (97%)	5 (3%)	0	100	100
1	G	182/207 (88%)	171 (94%)	11 (6%)	0	100	100
1	H	182/207 (88%)	170 (93%)	12 (7%)	0	100	100
2	I	14/28 (50%)	14 (100%)	0	0	100	100
2	J	11/28 (39%)	10 (91%)	1 (9%)	0	100	100
2	K	11/28 (39%)	10 (91%)	1 (9%)	0	100	100
2	L	14/28 (50%)	13 (93%)	0	1 (7%)	1	2
2	M	14/28 (50%)	13 (93%)	1 (7%)	0	100	100
2	N	11/28 (39%)	10 (91%)	1 (9%)	0	100	100
2	O	14/28 (50%)	13 (93%)	0	1 (7%)	1	2
2	P	11/28 (39%)	11 (100%)	0	0	100	100
All	All	1556/1880 (83%)	1482 (95%)	72 (5%)	2 (0%)	48	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	O	15	ALA
2	L	15	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	173/189 (92%)	150 (87%)	23 (13%)	4	14
1	B	173/189 (92%)	150 (87%)	23 (13%)	4	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	173/189 (92%)	148 (86%)	25 (14%)	3	11
1	D	173/189 (92%)	148 (86%)	25 (14%)	3	11
1	E	173/189 (92%)	146 (84%)	27 (16%)	2	9
1	F	173/189 (92%)	149 (86%)	24 (14%)	3	12
1	G	173/189 (92%)	147 (85%)	26 (15%)	3	10
1	H	173/189 (92%)	152 (88%)	21 (12%)	5	16
2	I	10/16 (62%)	9 (90%)	1 (10%)	7	24
2	J	10/16 (62%)	9 (90%)	1 (10%)	7	24
2	K	10/16 (62%)	9 (90%)	1 (10%)	7	24
2	L	10/16 (62%)	10 (100%)	0	100	100
2	M	11/16 (69%)	10 (91%)	1 (9%)	9	28
2	N	10/16 (62%)	9 (90%)	1 (10%)	7	24
2	O	10/16 (62%)	9 (90%)	1 (10%)	7	24
2	P	10/16 (62%)	10 (100%)	0	100	100
All	All	1465/1640 (89%)	1265 (86%)	200 (14%)	3	13

5 of 200 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	990	ILE
1	F	1010	LEU
1	H	1072	TYR
1	E	1016	GLN
1	F	929	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	1039	ASN
1	G	1064	GLN
2	O	5	GLN
1	D	1039	ASN
1	E	1019	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

20 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	$\# Z > 2$
2	M3L	O	9	2	10,11,12	0.95	0	9,14,16	1.09	1 (11%)
2	M3L	P	9	2	10,11,12	0.77	0	9,14,16	1.00	0
2	ALY	I	18	2	10,11,12	0.47	0	7,12,14	0.94	0
2	ALY	L	14	2	3,4,12	0.62	0	2,4,14	0.86	0
2	M3L	K	9	2	10,11,12	0.79	0	9,14,16	0.73	0
2	ALY	J	18	2	10,11,12	0.50	0	7,12,14	0.76	0
2	ALY	N	18	2	10,11,12	0.57	0	7,12,14	1.40	2 (28%)
2	ALY	O	18	2	10,11,12	0.65	0	7,12,14	1.01	0
2	ALY	M	18	2	10,11,12	0.57	0	7,12,14	1.06	1 (14%)
2	ALY	L	18	2	10,11,12	0.66	0	7,12,14	1.19	1 (14%)
2	ALY	O	14	2	3,4,12	0.70	0	2,4,14	0.83	0
2	M3L	L	9	2	10,11,12	0.66	0	9,14,16	0.79	0
2	ALY	K	18	2	10,11,12	0.49	0	7,12,14	1.61	3 (42%)
2	ALY	I	14	2	3,4,12	0.68	0	2,4,14	0.64	0
2	M3L	I	9	2	10,11,12	0.73	0	9,14,16	1.24	1 (11%)
2	ALY	P	18	2	10,11,12	0.68	0	7,12,14	1.31	1 (14%)
2	M3L	J	9	2	10,11,12	0.82	0	9,14,16	0.81	0
2	M3L	M	9	2	10,11,12	0.77	0	9,14,16	0.85	0
2	ALY	M	14	2	3,4,12	0.63	0	2,4,14	0.65	0
2	M3L	N	9	2	10,11,12	0.82	0	9,14,16	0.59	0

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
2	M3L	O	9	2	-	4/9/10/12	-
2	M3L	P	9	2	-	5/9/10/12	-
2	ALY	I	18	2	-	6/9/10/12	-
2	ALY	L	14	2	-	0/1/2/12	-
2	M3L	K	9	2	-	1/9/10/12	-
2	ALY	J	18	2	-	4/9/10/12	-
2	ALY	N	18	2	-	4/9/10/12	-
2	ALY	O	18	2	-	4/9/10/12	-
2	ALY	M	18	2	-	5/9/10/12	-
2	ALY	L	18	2	-	4/9/10/12	-
2	ALY	O	14	2	-	0/1/2/12	-
2	M3L	L	9	2	-	2/9/10/12	-
2	ALY	K	18	2	-	5/9/10/12	-
2	ALY	I	14	2	-	0/1/2/12	-
2	M3L	I	9	2	-	4/9/10/12	-
2	ALY	P	18	2	-	7/9/10/12	-
2	M3L	J	9	2	-	6/9/10/12	-
2	M3L	M	9	2	-	4/9/10/12	-
2	ALY	M	14	2	-	0/1/2/12	-
2	M3L	N	9	2	-	1/9/10/12	-

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	18	ALY	CE-NZ-CH	-2.60	118.72	122.56
2	K	18	ALY	CH3-CH-NZ	2.57	120.51	116.12
2	K	18	ALY	OH-CH-CH3	-2.38	117.81	122.05
2	M	18	ALY	CE-NZ-CH	2.37	126.06	122.56
2	O	9	M3L	CD-CE-NZ	-2.37	107.29	115.97

There are no chirality outliers.

5 of 66 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	18	ALY	O-C-CA-CB
2	J	9	M3L	N-CA-CB-CG
2	J	9	M3L	C-CA-CB-CG
2	K	18	ALY	N-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
2	K	18	ALY	C-CA-CB-CG

There are no ring outliers.

13 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	9	M3L	5	0
2	P	9	M3L	2	0
2	K	9	M3L	3	0
2	J	18	ALY	1	0
2	L	18	ALY	1	0
2	L	9	M3L	2	0
2	I	14	ALY	4	0
2	I	9	M3L	2	0
2	P	18	ALY	1	0
2	J	9	M3L	2	0
2	M	9	M3L	4	0
2	M	14	ALY	4	0
2	N	9	M3L	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 16 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 ⓘ

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	188/207 (90%)	-0.75	0	100	100	48, 85, 143, 190	0
1	B	188/207 (90%)	-0.76	0	100	100	49, 86, 148, 215	0
1	C	188/207 (90%)	-0.77	0	100	100	49, 85, 141, 188	0
1	D	188/207 (90%)	-0.74	0	100	100	52, 84, 138, 184	0
1	E	188/207 (90%)	-0.78	0	100	100	49, 86, 144, 206	0
1	F	188/207 (90%)	-0.83	0	100	100	49, 85, 141, 183	0
1	G	188/207 (90%)	-0.81	1 (0%)	87	82	49, 85, 140, 180	0
1	H	188/207 (90%)	-0.81	0	100	100	50, 85, 141, 189	0
2	I	15/28 (53%)	-0.60	0	100	100	84, 108, 188, 190	0
2	J	14/28 (50%)	-0.62	0	100	100	77, 97, 170, 189	0
2	K	14/28 (50%)	-0.71	0	100	100	77, 108, 155, 171	0
2	L	15/28 (53%)	-0.83	0	100	100	76, 101, 169, 188	0
2	M	16/28 (57%)	-0.56	0	100	100	83, 120, 186, 198	0
2	N	14/28 (50%)	-0.83	0	100	100	74, 109, 148, 176	0
2	O	15/28 (53%)	-0.64	0	100	100	80, 105, 187, 190	0
2	P	14/28 (50%)	-0.72	0	100	100	76, 112, 171, 179	0
All	All	1621/1880 (86%)	-0.78	1 (0%)	92	90	48, 87, 150, 215	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	957	GLY	2.2

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
2	ALY	L	14	5/13	0.92	0.10	169,184,191,193	0
2	ALY	O	14	5/13	0.92	0.08	165,190,197,205	0
2	ALY	K	18	12/13	0.95	0.09	49,89,120,127	0
2	ALY	I	18	12/13	0.96	0.09	44,82,129,131	0
2	ALY	M	18	12/13	0.96	0.09	44,84,140,145	0
2	ALY	I	14	5/13	0.96	0.06	169,189,194,194	0
2	ALY	O	18	12/13	0.96	0.10	42,93,128,131	0
2	ALY	N	18	12/13	0.97	0.08	44,83,126,131	0
2	M3L	O	9	12/13	0.97	0.08	68,79,124,127	0
2	ALY	L	18	12/13	0.97	0.10	38,83,116,117	0
2	ALY	J	18	12/13	0.97	0.08	48,90,118,123	0
2	ALY	P	18	12/13	0.97	0.10	50,93,127,130	0
2	M3L	J	9	12/13	0.98	0.06	61,78,119,128	0
2	ALY	M	14	5/13	0.98	0.05	167,190,192,198	0
2	M3L	L	9	12/13	0.98	0.07	62,83,119,121	0
2	M3L	P	9	12/13	0.98	0.05	72,82,119,125	0
2	M3L	I	9	12/13	0.98	0.09	63,78,113,123	0
2	M3L	K	9	12/13	0.99	0.07	69,83,108,111	0
2	M3L	M	9	12/13	0.99	0.04	62,83,117,119	0
2	M3L	N	9	12/13	0.99	0.05	63,77,107,109	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
3	ZN	A	1	1/1	1.00	0.01	66,66,66,66	0
3	ZN	A	2	1/1	1.00	0.01	87,87,87,87	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZN	B	1	1/1	1.00	0.01	61,61,61,61	0
3	ZN	B	2	1/1	1.00	0.01	89,89,89,89	0
3	ZN	C	1	1/1	1.00	0.01	67,67,67,67	0
3	ZN	C	2	1/1	1.00	0.01	89,89,89,89	0
3	ZN	D	1	1/1	1.00	0.01	68,68,68,68	0
3	ZN	D	2	1/1	1.00	0.01	86,86,86,86	0
3	ZN	E	1	1/1	1.00	0.01	69,69,69,69	0
3	ZN	E	2	1/1	1.00	0.02	92,92,92,92	0
3	ZN	F	1	1/1	1.00	0.01	68,68,68,68	0
3	ZN	F	2	1/1	1.00	0.01	88,88,88,88	0
3	ZN	G	1	1/1	1.00	0.01	69,69,69,69	0
3	ZN	G	2	1/1	1.00	0.02	88,88,88,88	0
3	ZN	H	1	1/1	1.00	0.02	68,68,68,68	0
3	ZN	H	2	1/1	1.00	0.01	92,92,92,92	0

6.5 Other polymers [i](#)

There are no such residues in this entry.