



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 08:53 AM UTC

PDB ID : 9WMS / pdb_00009wms
EMDB ID : EMD-66103
Title : Co-transcriptional histone H3K36 methylation complex containing RNA polymerase II elongation complex, Set2, and the upstream nucleosome. (temp115, type B)
Authors : Kujirai, T.; Ehara, H.; Ito, T.; Henmi, M.; Sekine, S.; Kurumizaka, H.
Deposited on : 2025-09-03
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

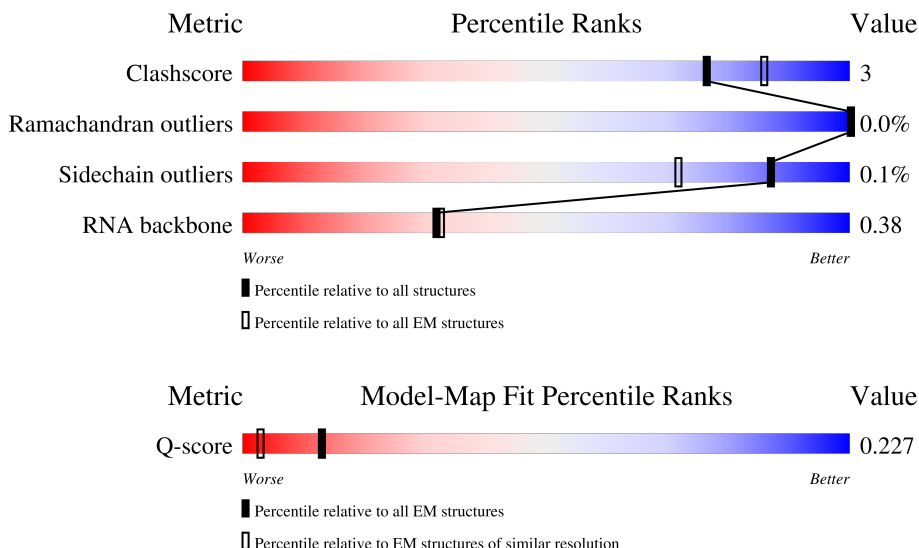
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1743	
2	B	1227	
3	C	304	

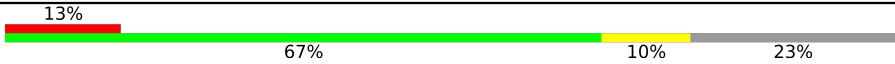
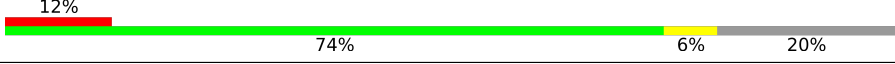
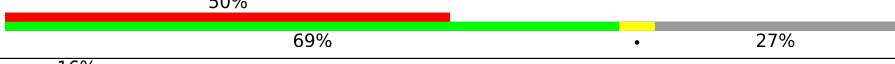
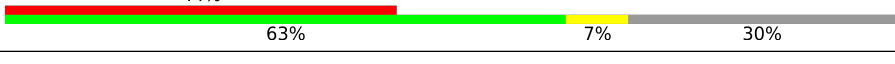
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Mol	Chain	Length	Quality of chain
4	D	186	
5	E	214	
6	F	155	
7	G	171	
8	H	145	
9	I	115	
10	J	72	
11	K	118	
12	L	72	
13	M	113	
14	N	198	
15	P	20	
16	T	198	
17	V	108	
18	W	911	
19	m	1503	
20	n	417	
21	q	1084	
22	r	544	
23	s	725	
24	u	459	
25	v	396	
26	x	395	
27	a	139	
27	e	139	

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Mol	Chain	Length	Quality of chain
28	b	106	
28	f	106	
29	c	133	
29	g	133	
30	d	129	
30	h	129	

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 78450 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1404	Total	C	N	O	S	0	0
			11064	6975	1930	2089	70		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1164	Total	C	N	O	S	0	0
			9284	5848	1639	1739	58		

- Molecule 3 is a protein called RNA polymerase II third largest subunit B44, part of central core.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	263	Total	C	N	O	S	0	0
			2098	1319	354	413	12		

- Molecule 4 is a protein called RNA polymerase II subunit B32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	174	Total	C	N	O	S	0	0
			1349	828	244	274	3		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	213	Total	C	N	O	S	0	0
			1741	1094	312	325	10		

- Molecule 6 is a protein called RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			677	429	114	131	3		

- Molecule 7 is a protein called RNA polymerase II subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	171	Total	C	N	O	S	0	0
			1325	858	214	248	5		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	133	Total	C	N	O	S	0	0
			1053	671	169	209	4		

- Molecule 9 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	111	Total	C	N	O	S	0	0
			917	565	161	180	11		

- Molecule 10 is a protein called RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	67	Total	C	N	O	S	0	0
			554	355	97	96	6		

- Molecule 11 is a protein called RNA polymerase II subunit B12.5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	113	Total	C	N	O	S	0	0
			932	599	160	169	4		

- Molecule 12 is a protein called RNA polymerase subunit ABC10-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			359	221	72	61	5		

- Molecule 13 is a protein called Transcription elongation factor 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	64	Total	C	N	O	S	0	0
			505	318	82	99	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-2	GLY	-	expression tag	UNP C4QZ45
M	-1	PRO	-	expression tag	UNP C4QZ45
M	0	GLY	-	expression tag	UNP C4QZ45

- Molecule 14 is a DNA chain called DNA (198-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	118	Total	C	N	O	P	0	0
			2420	1152	405	745	118		

- Molecule 15 is a RNA chain called RNA (5'-R(P*GP*CP*UP*UP*GP*UP*GP*CP*UP*GP*UP*CP*UP*UP*CP*GP*UP*CP*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	20	Total	C	N	O	P	0	0
			417	186	64	147	20		

- Molecule 16 is a DNA chain called DNA (198-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	129	Total	C	N	O	P	0	0
			2649	1247	541	732	129		

- Molecule 17 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	V	106	Total	C	N	O	S	0	0
			824	512	150	155	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	7	MET	-	initiating methionine	UNP C4R0E6

- Molecule 18 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	W	535	Total	C	N	O	S	0	0
			4250	2680	754	814	2		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	-2	GLY	-	expression tag	UNP C4R370
W	-1	PRO	-	expression tag	UNP C4R370
W	0	GLY	-	expression tag	UNP C4R370

- Molecule 19 is a protein called Transcription elongation factor Spt6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	1178	Total	C	N	O	S	0	0
			9653	6112	1648	1866	27		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	-2	GLY	-	expression tag	UNP C4R7H2
m	-1	PRO	-	expression tag	UNP C4R7H2
m	0	GLY	-	expression tag	UNP C4R7H2

- Molecule 20 is a protein called Protein that interacts with Spt6p and copurifies with Spt5p and RNA polymerase II.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	n	139	Total	C	N	O	S	0	0
			1115	716	193	202	4		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	-2	GLY	-	expression tag	UNP C4R7L8
n	-1	PRO	-	expression tag	UNP C4R7L8
n	0	GLY	-	expression tag	UNP C4R7L8

- Molecule 21 is a protein called Component of the Paf1p complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	q	930	Total	C	N	O	S	0	0
			7552	4805	1283	1439	25		

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
q	-39	MET	-	initiating methionine	UNP C4R6B2
q	-38	LYS	-	expression tag	UNP C4R6B2
q	-37	ASP	-	expression tag	UNP C4R6B2
q	-36	HIS	-	expression tag	UNP C4R6B2
q	-35	LEU	-	expression tag	UNP C4R6B2
q	-34	ILE	-	expression tag	UNP C4R6B2
q	-33	HIS	-	expression tag	UNP C4R6B2
q	-32	ASN	-	expression tag	UNP C4R6B2
q	-31	HIS	-	expression tag	UNP C4R6B2
q	-30	HIS	-	expression tag	UNP C4R6B2
q	-29	LYS	-	expression tag	UNP C4R6B2
q	-28	HIS	-	expression tag	UNP C4R6B2
q	-27	GLU	-	expression tag	UNP C4R6B2
q	-26	HIS	-	expression tag	UNP C4R6B2
q	-25	ALA	-	expression tag	UNP C4R6B2
q	-24	HIS	-	expression tag	UNP C4R6B2
q	-23	ALA	-	expression tag	UNP C4R6B2
q	-22	GLU	-	expression tag	UNP C4R6B2
q	-21	HIS	-	expression tag	UNP C4R6B2
q	-20	ASP	-	expression tag	UNP C4R6B2
q	-19	TYR	-	expression tag	UNP C4R6B2
q	-18	LYS	-	expression tag	UNP C4R6B2
q	-17	ASP	-	expression tag	UNP C4R6B2
q	-16	ASP	-	expression tag	UNP C4R6B2
q	-15	ASP	-	expression tag	UNP C4R6B2
q	-14	ASP	-	expression tag	UNP C4R6B2
q	-13	LYS	-	expression tag	UNP C4R6B2
q	-12	GLU	-	expression tag	UNP C4R6B2
q	-11	HIS	-	expression tag	UNP C4R6B2
q	-10	LEU	-	expression tag	UNP C4R6B2
q	-9	TYR	-	expression tag	UNP C4R6B2
q	-8	PHE	-	expression tag	UNP C4R6B2
q	-7	GLN	-	expression tag	UNP C4R6B2
q	-6	GLY	-	expression tag	UNP C4R6B2
q	-5	SER	-	expression tag	UNP C4R6B2
q	-4	SER	-	expression tag	UNP C4R6B2
q	-3	GLY	-	expression tag	UNP C4R6B2
q	-2	SER	-	expression tag	UNP C4R6B2
q	-1	SER	-	expression tag	UNP C4R6B2
q	0	GLY	-	expression tag	UNP C4R6B2

- Molecule 22 is a protein called RNAPII-associated chromatin remodeling Paf1 complex sub-

unit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	r	266	Total	C	N	O	S	0	0
			2139	1342	374	412	11		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	-29	MET	-	initiating methionine	UNP F2QQ42
r	-28	LYS	-	expression tag	UNP F2QQ42
r	-27	ASP	-	expression tag	UNP F2QQ42
r	-26	HIS	-	expression tag	UNP F2QQ42
r	-25	LEU	-	expression tag	UNP F2QQ42
r	-24	ILE	-	expression tag	UNP F2QQ42
r	-23	HIS	-	expression tag	UNP F2QQ42
r	-22	ASN	-	expression tag	UNP F2QQ42
r	-21	HIS	-	expression tag	UNP F2QQ42
r	-20	HIS	-	expression tag	UNP F2QQ42
r	-19	LYS	-	expression tag	UNP F2QQ42
r	-18	HIS	-	expression tag	UNP F2QQ42
r	-17	GLU	-	expression tag	UNP F2QQ42
r	-16	HIS	-	expression tag	UNP F2QQ42
r	-15	ALA	-	expression tag	UNP F2QQ42
r	-14	HIS	-	expression tag	UNP F2QQ42
r	-13	ALA	-	expression tag	UNP F2QQ42
r	-12	GLU	-	expression tag	UNP F2QQ42
r	-11	HIS	-	expression tag	UNP F2QQ42
r	-10	LEU	-	expression tag	UNP F2QQ42
r	-9	TYR	-	expression tag	UNP F2QQ42
r	-8	PHE	-	expression tag	UNP F2QQ42
r	-7	GLN	-	expression tag	UNP F2QQ42
r	-6	GLY	-	expression tag	UNP F2QQ42
r	-5	SER	-	expression tag	UNP F2QQ42
r	-4	SER	-	expression tag	UNP F2QQ42
r	-3	GLY	-	expression tag	UNP F2QQ42
r	-2	SER	-	expression tag	UNP F2QQ42
r	-1	SER	-	expression tag	UNP F2QQ42
r	0	GLY	-	expression tag	UNP F2QQ42

- Molecule 23 is a protein called Histone-lysine N-methyltransferase, H3 lysine-36 specific.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	s	430	Total	C	N	O	S	0	0
			3415	2124	592	676	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	-2	GLY	-	expression tag	UNP C4QY01
s	-1	PRO	-	expression tag	UNP C4QY01
s	0	GLY	-	expression tag	UNP C4QY01

- Molecule 24 is a protein called Leo1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	208	Total	C	N	O	S	0	0
			1707	1063	304	337	3		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	-29	MET	-	initiating methionine	UNP C4R3K1
u	-28	LYS	-	expression tag	UNP C4R3K1
u	-27	ASP	-	expression tag	UNP C4R3K1
u	-26	HIS	-	expression tag	UNP C4R3K1
u	-25	LEU	-	expression tag	UNP C4R3K1
u	-24	ILE	-	expression tag	UNP C4R3K1
u	-23	HIS	-	expression tag	UNP C4R3K1
u	-22	ASN	-	expression tag	UNP C4R3K1
u	-21	HIS	-	expression tag	UNP C4R3K1
u	-20	HIS	-	expression tag	UNP C4R3K1
u	-19	LYS	-	expression tag	UNP C4R3K1
u	-18	HIS	-	expression tag	UNP C4R3K1
u	-17	GLU	-	expression tag	UNP C4R3K1
u	-16	HIS	-	expression tag	UNP C4R3K1
u	-15	ALA	-	expression tag	UNP C4R3K1
u	-14	HIS	-	expression tag	UNP C4R3K1
u	-13	ALA	-	expression tag	UNP C4R3K1
u	-12	GLU	-	expression tag	UNP C4R3K1
u	-11	HIS	-	expression tag	UNP C4R3K1
u	-10	LEU	-	expression tag	UNP C4R3K1
u	-9	TYR	-	expression tag	UNP C4R3K1
u	-8	PHE	-	expression tag	UNP C4R3K1
u	-7	GLN	-	expression tag	UNP C4R3K1
u	-6	GLY	-	expression tag	UNP C4R3K1
u	-5	SER	-	expression tag	UNP C4R3K1
u	-4	SER	-	expression tag	UNP C4R3K1
u	-3	GLY	-	expression tag	UNP C4R3K1
u	-2	SER	-	expression tag	UNP C4R3K1

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Chain	Residue	Modelled	Actual	Comment	Reference
u	-1	SER	-	expression tag	UNP C4R3K1
u	0	GLY	-	expression tag	UNP C4R3K1

- Molecule 25 is a protein called RNAP II-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	v	349	Total	C	N	O	S	0	0
			2878	1835	510	528	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	-2	GLY	-	expression tag	UNP C4R997
v	-1	SER	-	expression tag	UNP C4R997
v	0	ALA	-	expression tag	UNP C4R997

- Molecule 26 is a protein called Constituent of Paf1 complex with RNA polymerase II, Paf1p, Hpr1p, Ctr9, Leo1, Rtf1 and Ccr4p.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	x	205	Total	C	N	O	S	0	0
			1682	1086	287	307	2		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	-29	MET	-	initiating methionine	UNP C4R1E6
x	-28	LYS	-	expression tag	UNP C4R1E6
x	-27	ASP	-	expression tag	UNP C4R1E6
x	-26	HIS	-	expression tag	UNP C4R1E6
x	-25	LEU	-	expression tag	UNP C4R1E6
x	-24	ILE	-	expression tag	UNP C4R1E6
x	-23	HIS	-	expression tag	UNP C4R1E6
x	-22	ASN	-	expression tag	UNP C4R1E6
x	-21	HIS	-	expression tag	UNP C4R1E6
x	-20	HIS	-	expression tag	UNP C4R1E6
x	-19	LYS	-	expression tag	UNP C4R1E6
x	-18	HIS	-	expression tag	UNP C4R1E6
x	-17	GLU	-	expression tag	UNP C4R1E6
x	-16	HIS	-	expression tag	UNP C4R1E6
x	-15	ALA	-	expression tag	UNP C4R1E6
x	-14	HIS	-	expression tag	UNP C4R1E6

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Chain	Residue	Modelled	Actual	Comment	Reference
x	-13	ALA	-	expression tag	UNP C4R1E6
x	-12	GLU	-	expression tag	UNP C4R1E6
x	-11	HIS	-	expression tag	UNP C4R1E6
x	-10	LEU	-	expression tag	UNP C4R1E6
x	-9	TYR	-	expression tag	UNP C4R1E6
x	-8	PHE	-	expression tag	UNP C4R1E6
x	-7	GLN	-	expression tag	UNP C4R1E6
x	-6	GLY	-	expression tag	UNP C4R1E6
x	-5	SER	-	expression tag	UNP C4R1E6
x	-4	SER	-	expression tag	UNP C4R1E6
x	-3	GLY	-	expression tag	UNP C4R1E6
x	-2	SER	-	expression tag	UNP C4R1E6
x	-1	SER	-	expression tag	UNP C4R1E6
x	0	GLY	-	expression tag	UNP C4R1E6

- Molecule 27 is a protein called Histone H3.3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	91	Total	C	N	O	S	0	0
			739	466	141	130	2		
27	e	104	Total	C	N	O	S	0	0
			841	530	163	145	3		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	-3	GLY	-	expression tag	UNP P84243
a	-2	SER	-	expression tag	UNP P84243
a	-1	HIS	-	expression tag	UNP P84243
a	36	MET	LYS	variant	UNP P84243
e	-3	GLY	-	expression tag	UNP P84243
e	-2	SER	-	expression tag	UNP P84243
e	-1	HIS	-	expression tag	UNP P84243
e	36	MET	LYS	variant	UNP P84243

- Molecule 28 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	82	Total	C	N	O	S	0	0
			653	412	127	113	1		
28	f	78	Total	C	N	O	S	0	0
			619	391	120	107	1		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	-3	GLY	-	expression tag	UNP P62805
b	-2	SER	-	expression tag	UNP P62805
b	-1	HIS	-	expression tag	UNP P62805
f	-3	GLY	-	expression tag	UNP P62805
f	-2	SER	-	expression tag	UNP P62805
f	-1	HIS	-	expression tag	UNP P62805

- Molecule 29 is a protein called Histone H2A type 1-B/E.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	c	106	Total	C	N	O	0	0
			819	517	160	142		
29	g	97	Total	C	N	O	0	0
			752	472	148	132		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	-3	GLY	-	expression tag	UNP P04908
c	-2	SER	-	expression tag	UNP P04908
c	-1	HIS	-	expression tag	UNP P04908
g	-3	GLY	-	expression tag	UNP P04908
g	-2	SER	-	expression tag	UNP P04908
g	-1	HIS	-	expression tag	UNP P04908

- Molecule 30 is a protein called Histone H2B type 1-J.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	94	Total	C	N	O	S	0	0
			732	459	131	139	3		
30	h	90	Total	C	N	O	S	0	0
			696	438	122	133	3		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
d	-3	GLY	-	expression tag	UNP P06899
d	-2	SER	-	expression tag	UNP P06899
d	-1	HIS	-	expression tag	UNP P06899
d	120	CYS	LYS	engineered mutation	UNP P06899
h	-3	GLY	-	expression tag	UNP P06899

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Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
h	-2	SER	-	expression tag	UNP P06899
h	-1	HIS	-	expression tag	UNP P06899
h	120	CYS	LYS	engineered mutation	UNP P06899

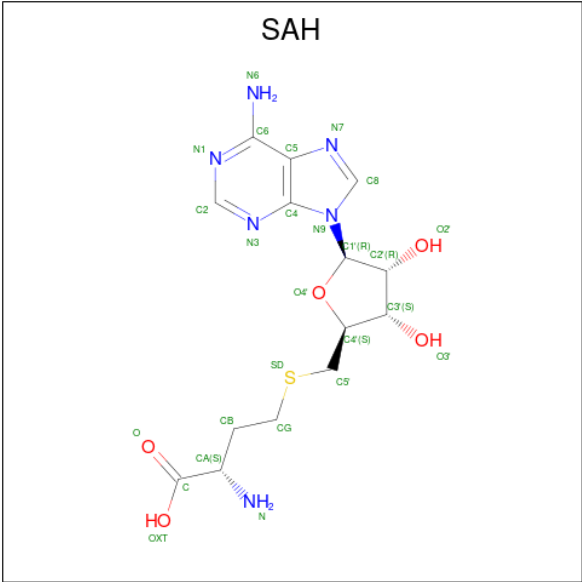
- Molecule 31 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
31	A	2	Total 2	Zn 2	0
31	B	1	Total 1	Zn 1	0
31	C	1	Total 1	Zn 1	0
31	I	2	Total 2	Zn 2	0
31	J	1	Total 1	Zn 1	0
31	L	1	Total 1	Zn 1	0
31	M	1	Total 1	Zn 1	0
31	V	1	Total 1	Zn 1	0
31	s	3	Total 3	Zn 3	0

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
32	A	1	Total 1	Mg 1	0

- Molecule 33 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).

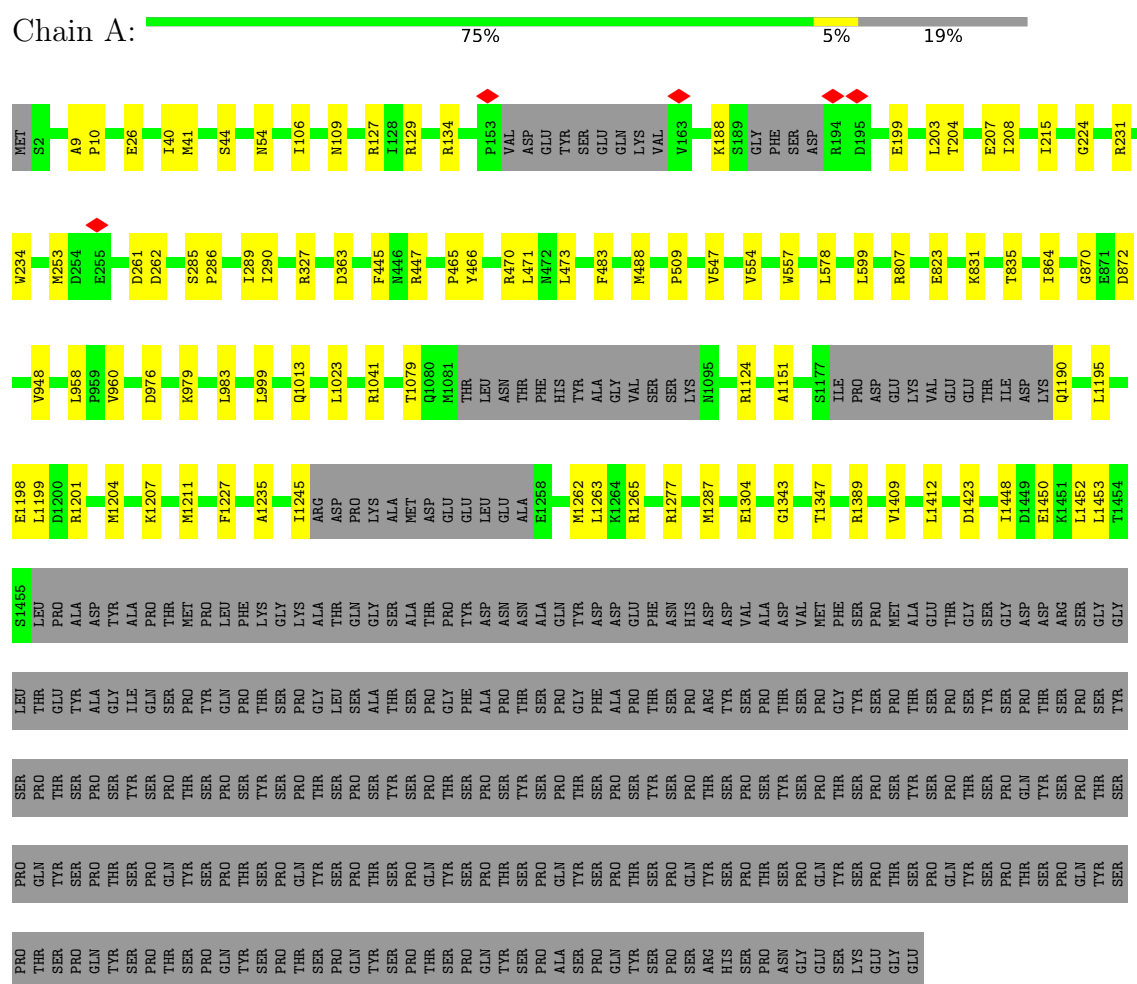


Mol	Chain	Residues	Atoms					AltConf
33	s	1	Total	C	N	O	S	0
			26	14	6	5	1	

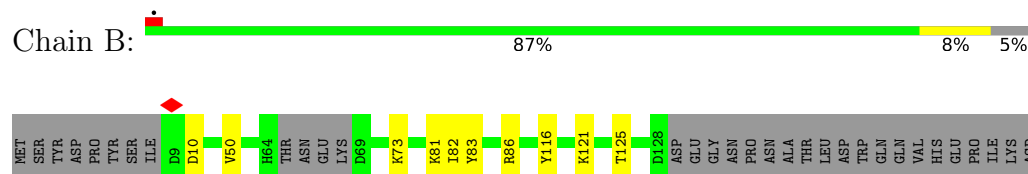
3 Residue-property plots [i](#)

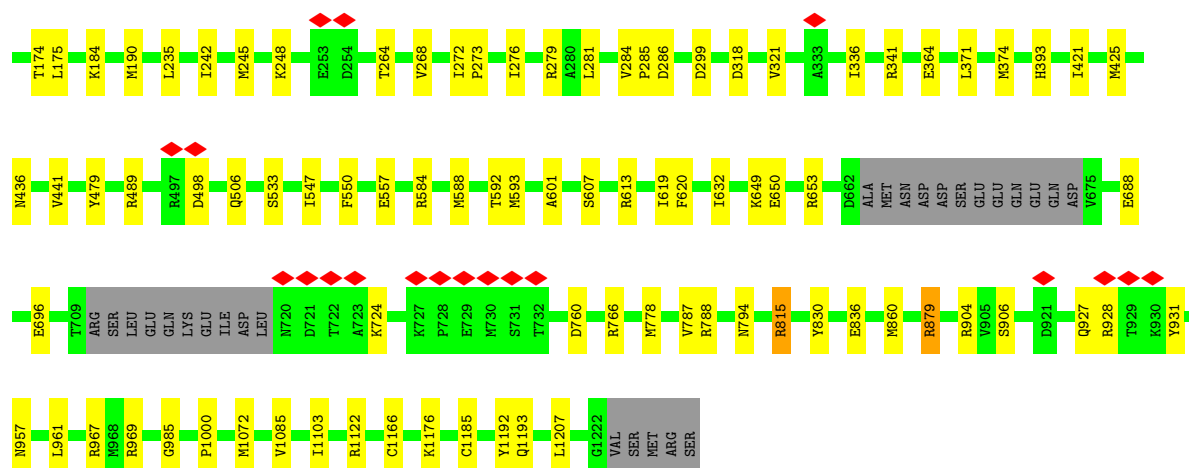
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: DNA-directed RNA polymerase subunit



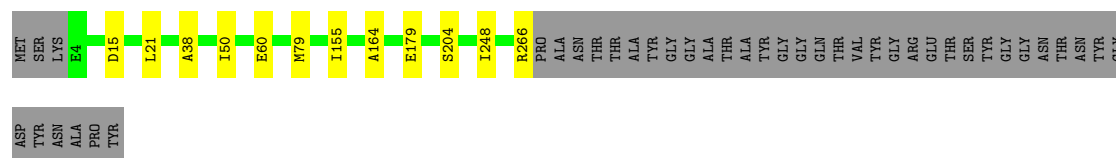
• Molecule 2: DNA-directed RNA polymerase subunit beta





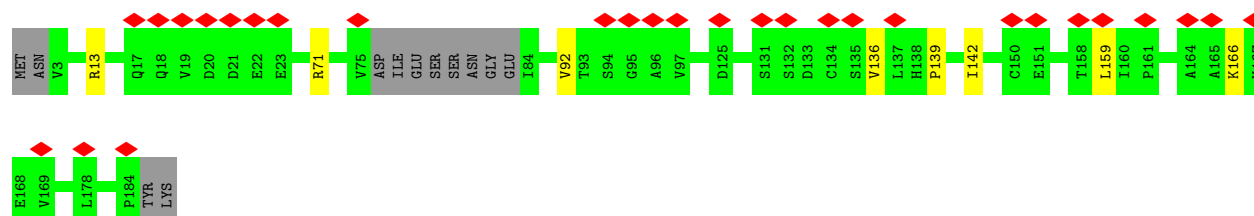
- Molecule 3: RNA polymerase II third largest subunit B44, part of central core

Chain C: 83% 13%



- Molecule 4: RNA polymerase II subunit B32

Chain D: 16% 89% 6%



- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 92% 7%



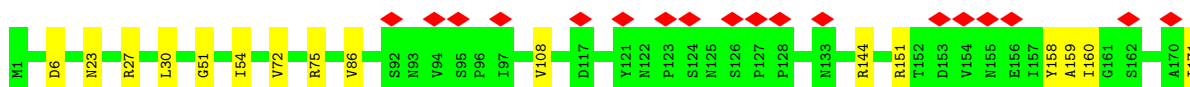
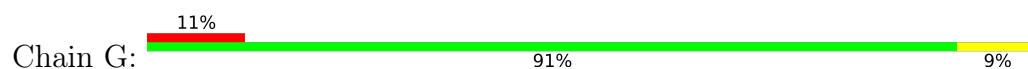
- Molecule 6: RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III

Chain F: 53% 46%

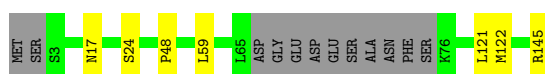




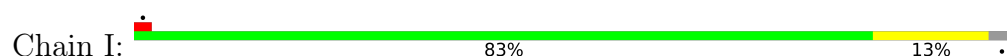
- Molecule 7: RNA polymerase II subunit



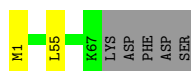
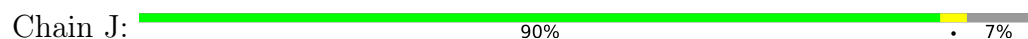
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



- Molecule 9: DNA-directed RNA polymerase subunit



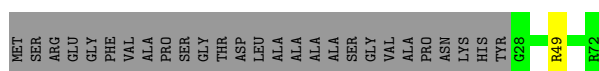
- Molecule 10: RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III



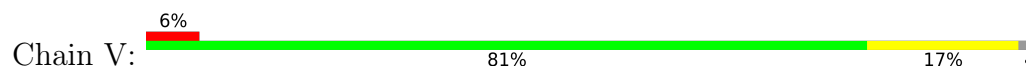
- Molecule 11: RNA polymerase II subunit B12.5

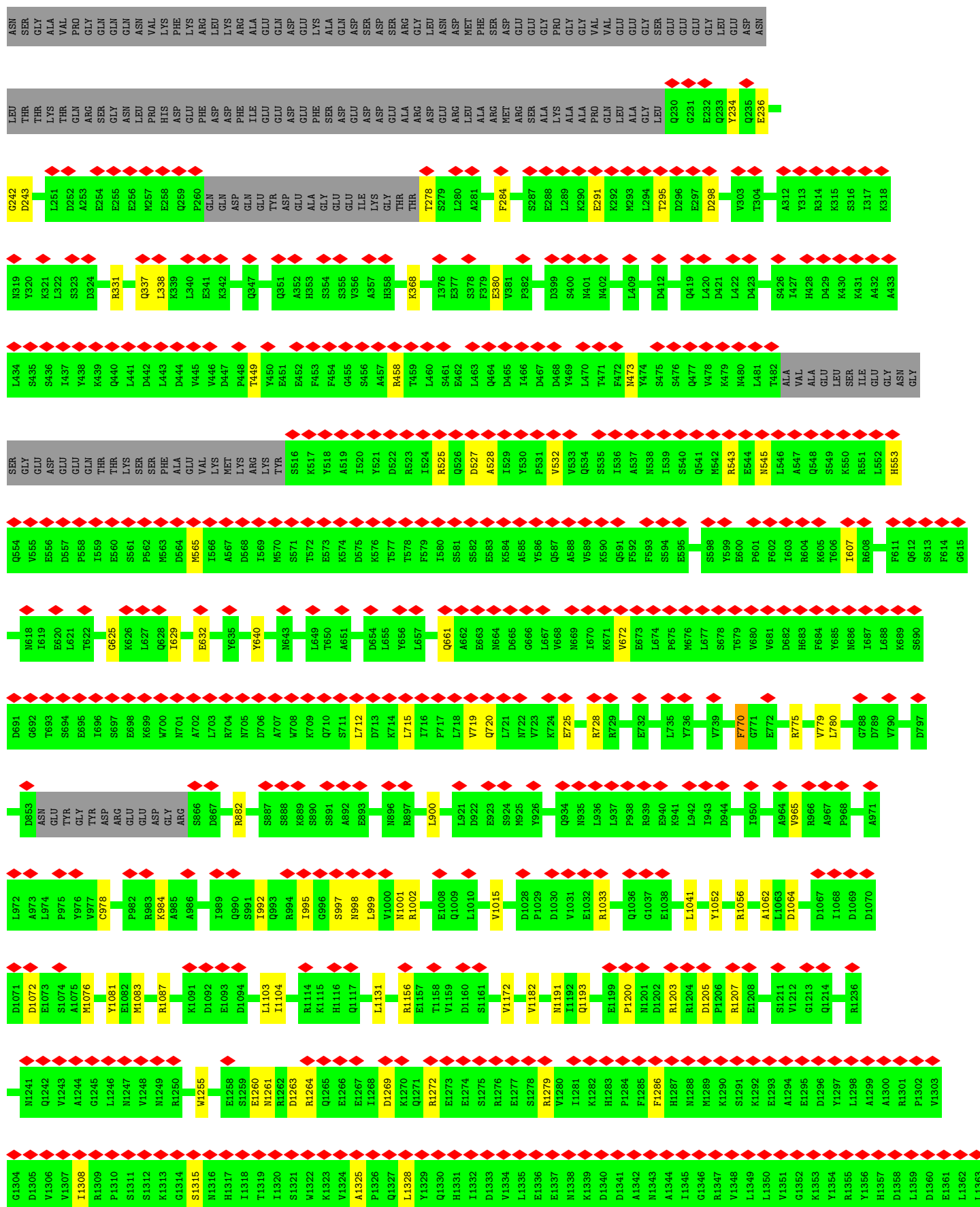


- Molecule 12: RNA polymerase subunit ABC10-alpha



- Molecule 13: Transcription elongation factor 1 homolog

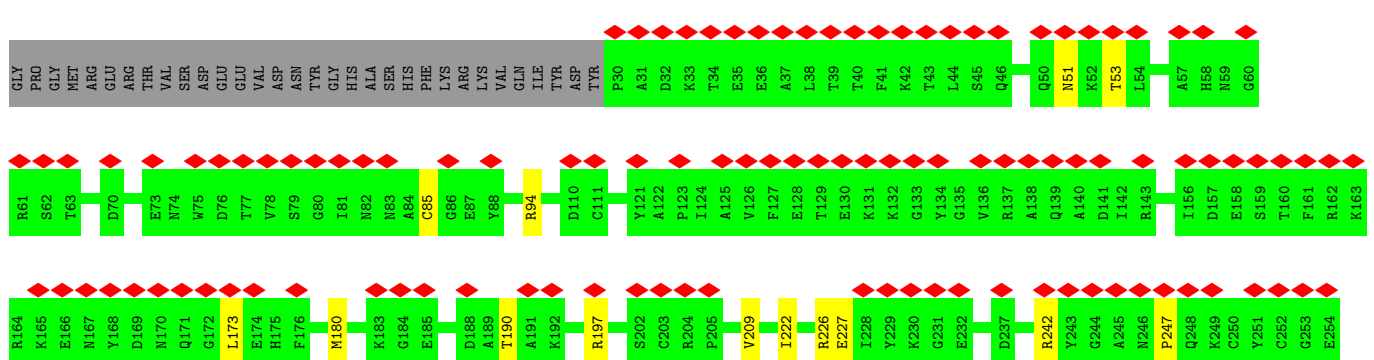
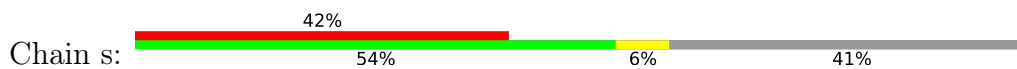






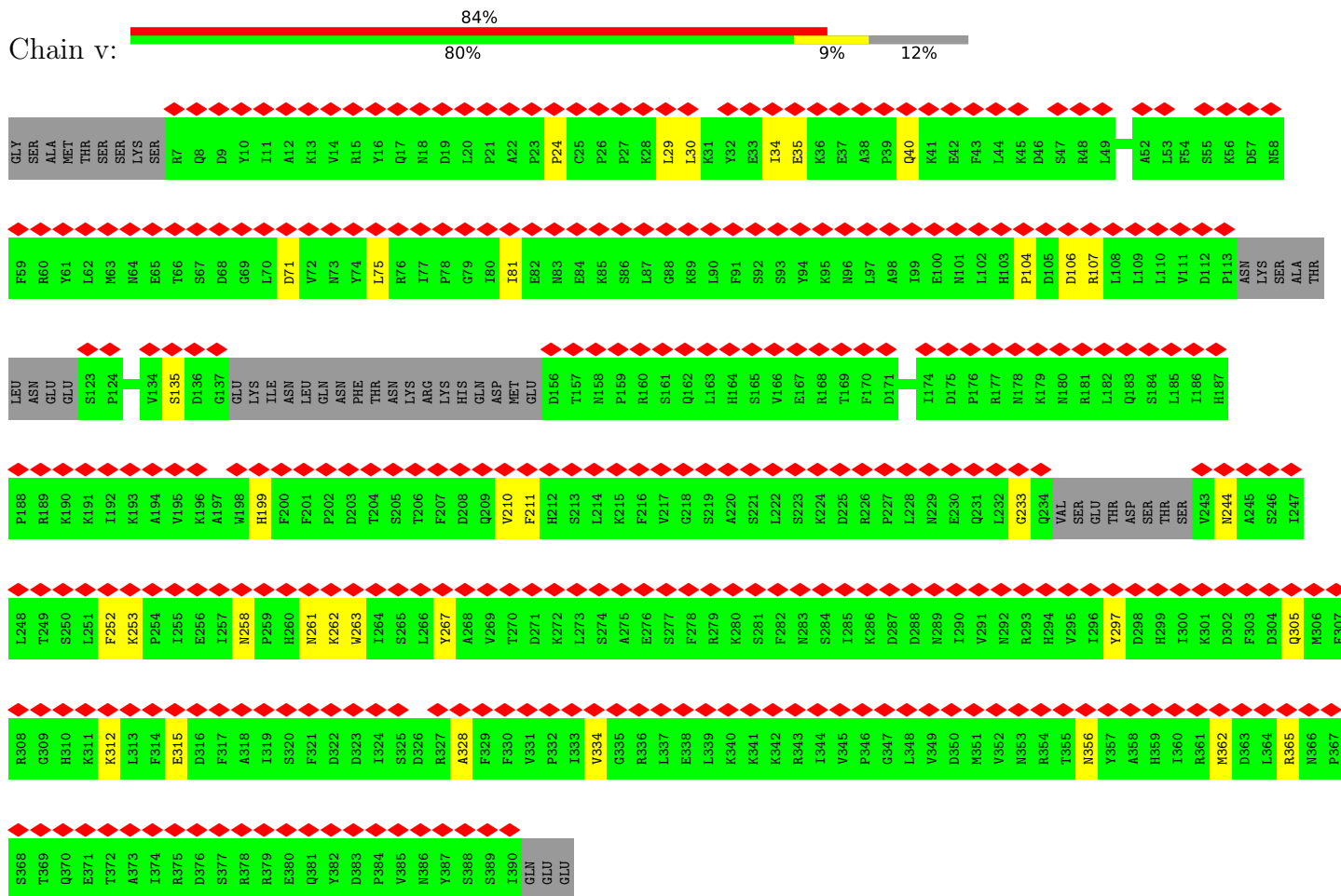
L201	Y202	Q203	K204	A205	L206	L207	L208	N209	P210	L211	I212	V213	P214	D215	P216	R217	L218	G219	I220	G221	L222	C223	F224	V225	H226	L227	N228	N229	K230	Q231	L232	V237	H238	N239	S240	L241	K242	V243	H244	P245	Q246	N247	N248	L249	N250	T251	K252	I253	L254	I255	C256	L257	A258	K259	F260					
D261	Y262	C263	F264	N265	E266	S267	K268	D269	A270	D270	D271	E272	F273	T274	A275	L276	Y277	R278	E279	S280	L281	E282	F283	L284	H285	S286	C287	L288	K289	E290	D291	A292	K293	H294	P295	L296	L297	L298	M299	V300	L301	A302	S303	Y304	Y305	F306	S307	K308	E309	E312	K313	V314	I253	L254	I255	C256	L257	A258	K259	F260
L322	K323	E324	N325	S326	R327	N328	A329	A330	F331	V332	S333	A334	S335	H336	F337	V338	L339	A340	R341	V342	A343	Y344	H345	K346	E347	D348	I349	V350	Q351	A352	Q353	K354	K357	Q358	A359	E360	D361	S362	Q363	N364	S365	N366	T367	L368	A369	K370	L371	G372	Y373	L377	I378	A379	R380	L317	C318	E382	N319	L320	V321	
D385	A386	T387	I388	Y389	L390	E391	K392	F393	F394	K395	E396	N397	Q398	D399	S400	K401	L402	S403	E404	M405	L406	L407	L408	L409	G410	I411	I412	Y413	Q415	S416	G417	K418	S419	Y420	Y421	D422	A423	I424	I425	F426	L427	E428	K429	Y430	V431	A432	V433	Q434	Q435	E436	E437	N438	Y439	P440	I441	L442	P443	E444		
A445	V446	L447	V448	L449	S450	R451	V452	V453	A454	N455	K456	D457	L458	N459	V460	A461	L462	D463	Y464	L465	M466	K467	A468	M469	D470	I471	L472	G473	D474	K475	A476	M477	V478	Y479	V480	L481	N482	M483	L484	G485	I486	V487	H488	F489	F490	R491	N492	N493	V494	S495	Q496	S497	S498	D499	F500	F501	A502	Q503	S504	
L505	E506	A507	L508	N509	N510	V511	S512	P513	Q514	N515	K516	E517	A518	L519	S520	L521	T522	L523	H524	Y525	N526	K527	A528	R529	V530	E531	E532	V533	S534	N535	Q536	S537	E538	A539	E540	K541	L542	Y543	S544	K545	L546	M547	E548	K549	C550	P551	G552	Y553	T554	S555	N556	R559	Y560	I561	Y562	L563	L564	A565		
L566	K567	S568	N569	G570	N571	N572	Y573	A574	D575	V576	Q577	Q578	L579	L580	D581	D582	F583	P584	S585	D586	L587	E588	V589	R590	S591	F592	Y593	G594	W595	F596	L597	K598	R599	Y600	G601	R602	K603	N604	G605	L606	K607	Q608	D609	L610	E611	S612	Q613	H614	H615	K616	D617	T618	L619	L620	N621	Y622	D623	K624	H625	
D626	C627	Y628	A629	L630	L631	S632	L633	G634	N635	L636	Y637	A638	T639	L640	A641	R642	E643	M644	K645	V646	T647	D648	Q649	K650	Q651	N652	E653	L654	K655	R656	Q657	Q658	Y659	L660	R661	A662	A663	Q664	F665	Y666	H667	K668	V669	L670	S671	D672	D673	P674	K675	H676	L677	Y678	A679	A680	Q681	G682	L683	A684	L685	
L686	F687	S688	D689	K690	E691	R692	T693	G694	L695	A696	L697	E698	T699	F700	K701	K702	W703	R704	D705	T706	V707	Q708	D709	L710	G711	T712	F713	L714	N715	L716	G717	H718	C719	F720	N721	E722	A723	K724	Q725	F726	G727	K728	A729	L730	E731	S732	Y733	T734	L735	A736	E738	K739	F740	S741	N742	G743	H744	D745		
S746	K747	L748	L749	V750	L751	L752	A755	W756	Y757	V758	R759	G760	F761	Y762	E763	K764	S765	W766	D767	A768	Y769	K770	K771	A772	L773	E774	V775	S776	E777	Q778	A779	Y780	Q781	L782	S783	K784	L785	F786	A787	L788	R789	F790	N791	L792	Y793	F794	L795	Q796	F797	Q798	Y799	A800	D801	F802	V803	K804	S805	L806		
P807	N808	T809	Q810	R811	D812	L813	T814	T815	L816	E817	N818	A819	L820	S821	G822	L823	Q824	D825	A826	L827	E828	K829	S829	L830	L831	K832	L833	A834	E835	L836	E837	Q838	P839	P840	Y841	P842	S843	E844	D845	R847	A848	R849	A850	T851	H852	G853	S854	H855	T856	L857	R858	N859	Q860	L861	E862	R863	K864	L865	Q866	
D867	Q868	Q869	D870	Y871	E872	H873	S874	L875	Q876	E877	R880	R883	R884	K885	Q886	Q887	L888	D889	E890	E891	K892	R893	L894	E895	Q896	E897	Q898	R899	R900	E901	E902	E903	A904	R905	K906	R907	Q908	E909	A910	E911	L912	L913	L914	R915	L918	L919	K920	Q921	E922	E923	E924	Y925	N926	K927	H928	D929				
I930	ASP	ALA	ASN	TYR	ASP	GLU	ASN	ASP	ASP	VAL	LEU	GLU	ASN	SER	LYS	GLU	ASP	ASN	GLY	GLN	GLY	GLY	GLN	ASN	THR	THR	THR	ALA	PRO	ASP	LEU	ARG	GLN	LYS	ILE	ARG	GLU	GLU	GLY	ASN	ASN	THR	GLU	ASP	ASP	PRO	ILE	LEU	ASP	ASN	GLU									
GLU	GLU	ALA	ASN	TYR	ASP	GLU	ASN	ASP	ASP	VAL	LEU	GLU	ASN	SER	LYS	GLU	ASP	ASN	GLY	GLN	GLY	GLY	GLN	ASN	THR	THR	THR	ALA	PRO	ASP	LEU	ARG	GLN	LYS	ILE	ARG	GLU	GLU	GLY	ASN	ASN	THR	GLU	ASP	ASP	PRO	ILE	LEU	ASP	ASN	GLU									

Chain r:

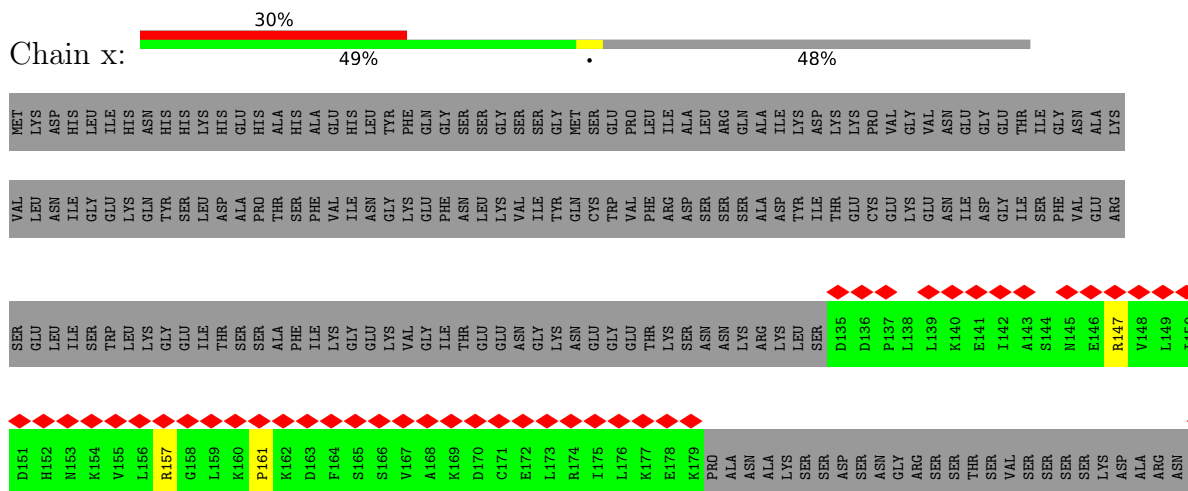


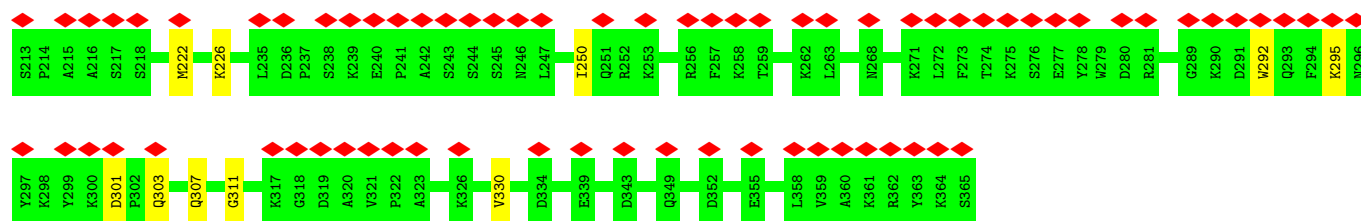


- Molecule 25: RNAP II-associated protein

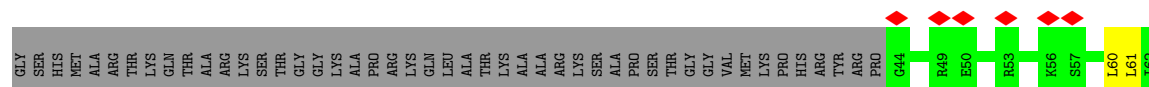


- Molecule 26: Constituent of Paf1 complex with RNA polymerase II, Paf1p, Hpr1p, Ctr9, Leo1, Rtf1 and Ccr4p

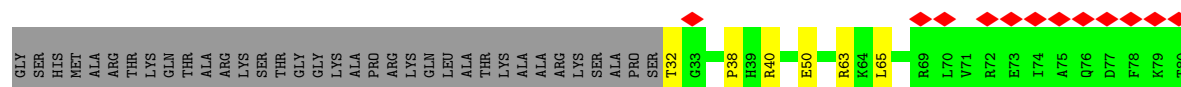




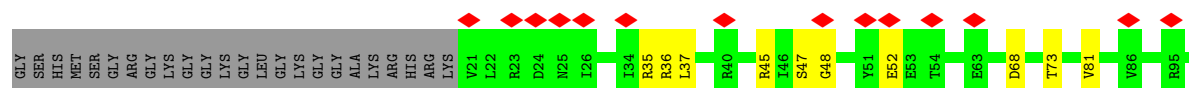
• Molecule 27: Histone H3.3



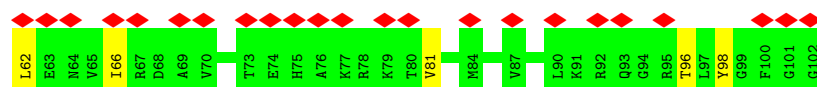
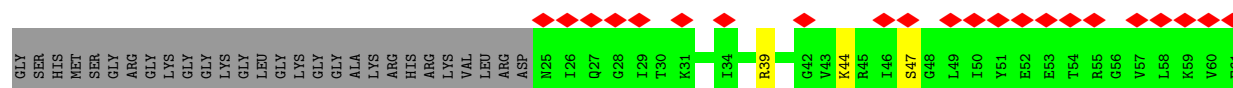
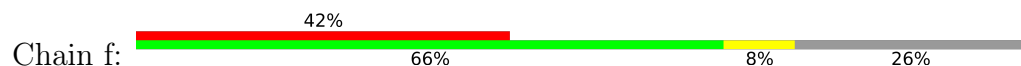
• Molecule 27: Histone H3.3



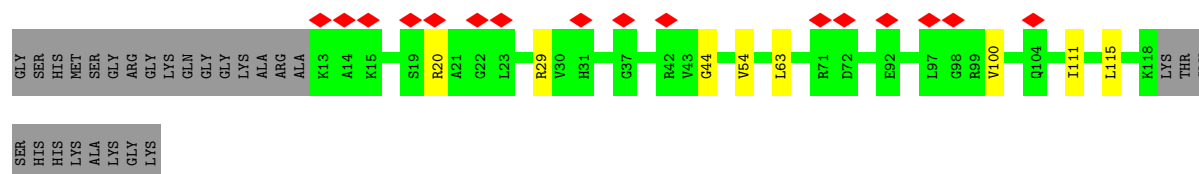
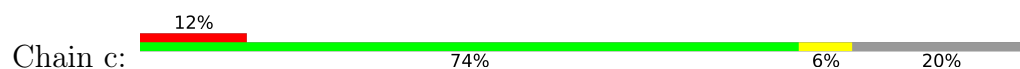
• Molecule 28: Histone H4



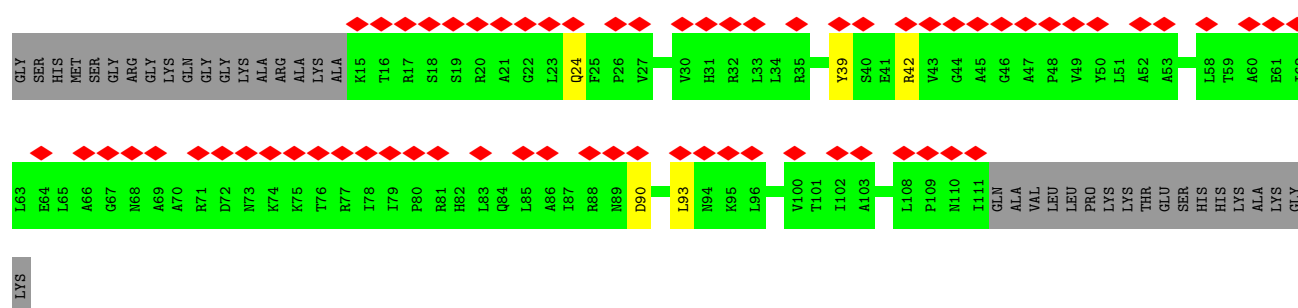
• Molecule 28: Histone H4



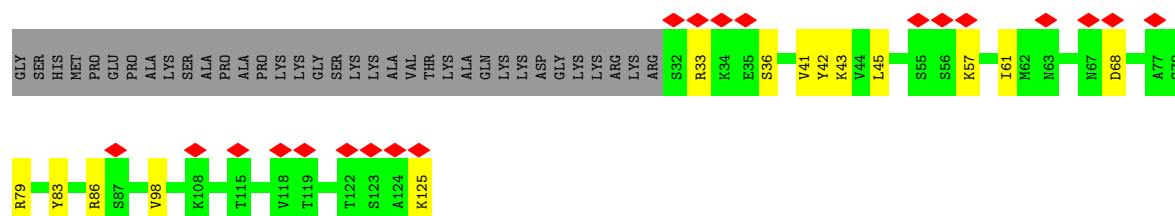
- Molecule 29: Histone H2A type 1-B/E



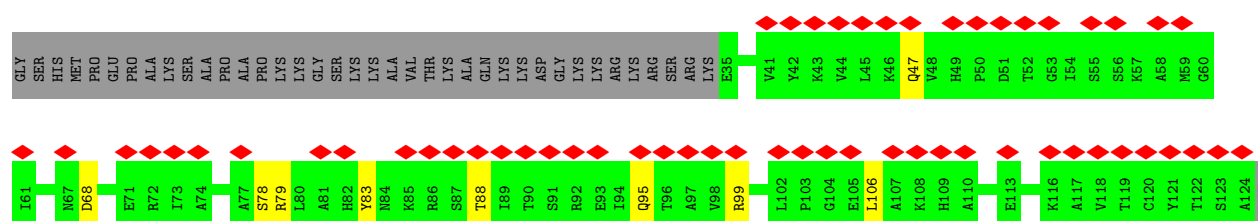
- Molecule 29: Histone H2A type 1-B/E



- Molecule 30: Histone H2B type 1-J



- Molecule 30: Histone H2B type 1-J



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	59019	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.167	Depositor
Minimum map value	-0.063	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	398.25, 398.25, 398.25	wwPDB
Map dimensions	270, 270, 270	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.475, 1.475, 1.475	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SAH, 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	0.21	0/11267	0.42	0/15222
2	B	0.21	0/9464	0.42	0/12763
3	C	0.21	0/2139	0.41	0/2895
4	D	0.15	0/1361	0.33	0/1837
5	E	0.20	0/1773	0.43	0/2385
6	F	0.19	0/687	0.38	0/931
7	G	0.15	0/1354	0.33	0/1837
8	H	0.21	0/1070	0.38	0/1444
9	I	0.12	0/934	0.29	0/1257
10	J	0.19	0/563	0.41	0/753
11	K	0.21	0/953	0.41	0/1291
12	L	0.20	0/365	0.45	0/484
13	M	0.16	0/513	0.37	0/693
14	N	0.36	0/2701	0.64	0/4171
15	P	0.26	0/462	0.59	0/716
16	T	0.34	0/2986	0.56	0/4600
17	V	0.15	0/840	0.33	0/1140
18	W	0.17	0/4319	0.42	1/5838 (0.0%)
19	m	0.17	0/9847	0.38	0/13321
20	n	0.18	0/1132	0.38	0/1526
21	q	0.16	0/7689	0.33	0/10368
22	r	0.17	0/2169	0.35	0/2901
23	s	0.19	0/3469	0.44	0/4670
24	u	0.15	0/1740	0.31	0/2347
25	v	0.16	0/2944	0.33	0/3973
26	x	0.14	0/1716	0.31	0/2310
27	a	0.27	0/747	0.56	0/1001
27	e	0.28	0/853	0.55	0/1144
28	b	0.26	0/660	0.58	0/883
28	f	0.28	0/626	0.54	0/837
29	c	0.24	0/829	0.58	0/1118
29	g	0.22	0/761	0.52	0/1026

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	d	0.25	0/743	0.58	0/998
30	h	0.27	0/707	0.61	0/954
All	All	0.21	0/80383	0.43	1/109634 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
18	W	435	LEU	N-CA-C	5.13	117.18	109.23

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	11064	0	11090	61	0
2	B	9284	0	9282	64	0
3	C	2098	0	2057	9	0
4	D	1349	0	1345	5	0
5	E	1741	0	1754	11	0
6	F	677	0	693	2	0
7	G	1325	0	1342	10	0
8	H	1053	0	1050	4	0
9	I	917	0	864	10	0
10	J	554	0	573	1	0
11	K	932	0	944	9	0
12	L	359	0	358	1	0
13	M	505	0	495	3	0
14	N	2420	0	1343	17	0
15	P	417	0	213	1	0
16	T	2649	0	1426	17	0
17	V	824	0	795	11	0
18	W	4250	0	4296	55	0
19	m	9653	0	9500	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	n	1115	0	1186	15	0
21	q	7552	0	7545	44	0
22	r	2139	0	2155	18	0
23	s	3415	0	3351	25	0
24	u	1707	0	1676	21	0
25	v	2878	0	2873	25	0
26	x	1682	0	1731	8	0
27	a	739	0	778	6	0
27	e	841	0	883	10	0
28	b	653	0	696	10	0
28	f	619	0	659	8	0
29	c	819	0	879	10	0
29	g	752	0	797	4	0
30	d	732	0	750	12	0
30	h	696	0	706	7	0
31	A	2	0	0	0	0
31	B	1	0	0	0	0
31	C	1	0	0	0	0
31	I	2	0	0	0	0
31	J	1	0	0	0	0
31	L	1	0	0	0	0
31	M	1	0	0	0	0
31	V	1	0	0	0	0
31	s	3	0	0	0	0
32	A	1	0	0	0	0
33	s	26	0	19	0	0
All	All	78450	0	76104	464	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 (464) 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)
1:A:445:PHE:CE2	1:A:471:LEU:HD21	2.24	0.72
16:T:56:DC:H4'	30:d:33:ARG:HD2	1.73	0.71
18:W:461:LEU:HD13	19:m:278:THR:HA	1.74	0.70
14:N:10:DG:H5''	27:e:65:LEU:HB3	1.73	0.69
18:W:218:ILE:CD1	20:n:289:MET:HE1	2.22	0.68
18:W:444:LEU:HG	19:m:284:PHE:CE1	2.28	0.68
16:T:15:DA:H5'	28:b:45:ARG:HH21	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:W:444:LEU:HD12	19:m:284:PHE:CD2	2.29	0.67
1:A:445:PHE:HE2	1:A:471:LEU:HD21	1.60	0.67
2:B:1166:CYS:HB3	2:B:1185:CYS:SG	2.35	0.67
1:A:483:PHE:CD2	2:B:836:GLU:HB2	2.29	0.67
18:W:487:ILE:HD11	18:W:531:ARG:HB2	1.79	0.65
19:m:337:GLN:HG2	19:m:458:ARG:HH22	1.62	0.65
14:N:3:DC:H5'	27:e:40:ARG:HG2	1.80	0.64
18:W:352:LEU:HD11	18:W:435:LEU:HD11	1.79	0.64
1:A:285:SER:HB2	1:A:290:ILE:HD11	1.80	0.63
30:h:79:ARG:NH1	30:h:83:TYR:OH	2.32	0.62
14:N:-60:DT:OP1	30:d:42:TYR:OH	2.18	0.62
19:m:473:ASN:HA	19:m:525:ARG:HH22	1.64	0.62
19:m:331:ARG:HH21	19:m:368:LYS:HB3	1.65	0.62
3:C:266:ARG:HH12	11:K:82:ARG:HH22	1.48	0.61
1:A:1211:MET:SD	1:A:1211:MET:N	2.73	0.61
18:W:444:LEU:HB2	19:m:284:PHE:CE2	2.35	0.61
29:g:39:TYR:HB3	30:h:78:SER:HB2	1.83	0.61
1:A:831:LYS:NZ	1:A:1079:THR:O	2.34	0.60
16:T:-7:DG:O3'	27:e:63:ARG:NH2	2.33	0.60
23:s:426:LYS:NZ	23:s:440:ASN:OD1	2.32	0.60
2:B:1103:ILE:O	2:B:1122:ARG:NH1	2.34	0.60
9:I:33:ASP:OD1	24:u:75:HIS:N	2.35	0.60
14:N:9:DT:H1'	14:N:10:DG:C8	2.37	0.60
2:B:969:ARG:NH1	3:C:60:GLU:OE1	2.35	0.59
21:q:922:ALA:O	21:q:926:ASN:ND2	2.35	0.59
21:q:793:VAL:HG11	21:q:830:LEU:HG	1.83	0.59
19:m:1072:ASP:OD2	23:s:366:ARG:NH1	2.35	0.59
21:q:569:ASN:O	21:q:603:LYS:NZ	2.36	0.59
17:V:15:CYS:HB3	17:V:32:CYS:SG	2.42	0.59
23:s:320:MET:HE3	23:s:347:LYS:HB3	1.84	0.59
18:W:327:ARG:HB3	18:W:436:ILE:HD12	1.84	0.59
2:B:73:LYS:HG2	2:B:125:THR:HG22	1.85	0.59
2:B:778:MET:HE3	2:B:794:ASN:HB3	1.84	0.59
21:q:169:ASP:OD1	21:q:185:LYS:NZ	2.35	0.58
27:a:68:GLN:HE21	27:a:72:ARG:HH21	1.49	0.58
1:A:1262:MET:SD	1:A:1265:ARG:NH2	2.76	0.58
7:G:27:ARG:NH1	7:G:54:ILE:O	2.36	0.58
17:V:57:LEU:HD11	17:V:81:LEU:HD22	1.85	0.58
20:n:206:SER:O	20:n:210:ASN:ND2	2.35	0.58
21:q:253:ILE:HG12	21:q:297:LEU:HD21	1.84	0.58
29:c:20:ARG:NH1	30:d:125:LYS:OXT	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1176:LYS:HD2	18:W:598:LEU:HD23	1.86	0.58
19:m:672:VAL:O	19:m:720:GLN:NE2	2.37	0.58
2:B:436:ASN:ND2	24:u:264:LEU:HD22	2.19	0.57
8:H:48:PRO:O	8:H:145:ARG:NH1	2.37	0.57
22:r:269:ASP:HB3	22:r:349:LEU:HD21	1.85	0.57
18:W:616:GLN:OE1	18:W:619:SER:OG	2.23	0.57
2:B:436:ASN:HD22	24:u:264:LEU:HD22	1.69	0.57
4:D:71:ARG:HE	4:D:92:VAL:HG13	1.70	0.57
18:W:218:ILE:HG13	20:n:289:MET:HE1	1.86	0.57
10:J:1:MET:HA	10:J:55:LEU:HB2	1.86	0.57
18:W:444:LEU:HG	19:m:284:PHE:CZ	2.39	0.57
2:B:815:ARG:HD2	25:v:135:SER:HB3	1.86	0.57
2:B:50:VAL:HG21	2:B:82:ILE:HD11	1.86	0.56
2:B:489:ARG:NH2	2:B:533:SER:O	2.37	0.56
1:A:127:ARG:O	1:A:129:ARG:NH1	2.38	0.56
25:v:233:GLY:O	25:v:244:ASN:ND2	2.38	0.56
8:H:59:LEU:HD21	8:H:122:MET:HE1	1.87	0.56
13:M:49:CYS:SG	13:M:52:CYS:HB2	2.45	0.56
14:N:3:DC:C5'	27:e:40:ARG:HG2	2.35	0.56
19:m:1261:ASN:OD1	19:m:1264:ARG:NH2	2.39	0.56
2:B:879:ARG:HG3	15:P:3:G:H8	1.70	0.56
16:T:22:DC:H2''	16:T:23:DA:C8	2.40	0.56
9:I:73:LYS:NZ	9:I:112:ASP:OD2	2.39	0.56
1:A:1207:LYS:O	1:A:1277:ARG:NH2	2.39	0.56
21:q:531:GLU:O	21:q:535:ASN:N	2.37	0.56
23:s:180:MET:HB3	27:e:38:PRO:HD3	1.88	0.56
25:v:267:TYR:HB3	25:v:297:TYR:HB3	1.87	0.56
27:a:60:LEU:HD22	27:a:93:GLN:HE21	1.71	0.56
1:A:1124:ARG:NH2	1:A:1304:GLU:OE2	2.39	0.55
24:u:121:PHE:HB3	24:u:153:ARG:HB3	1.86	0.55
1:A:473:LEU:HD23	2:B:836:GLU:HG3	1.88	0.55
1:A:1201:ARG:NH2	1:A:1235:ALA:O	2.39	0.55
2:B:421:ILE:HD11	2:B:441:VAL:HG22	1.89	0.55
9:I:20:LYS:O	9:I:23:GLN:NE2	2.39	0.55
23:s:190:THR:O	23:s:197:ARG:NH2	2.40	0.55
22:r:200:ASP:HB3	22:r:319:VAL:HG11	1.88	0.55
3:C:248:ILE:HG21	11:K:102:ASP:HB2	1.88	0.55
5:E:126:VAL:HG11	5:E:131:ILE:HG12	1.88	0.55
21:q:793:VAL:HG13	21:q:826:ALA:HB1	1.87	0.55
22:r:490:VAL:HG22	22:r:495:ARG:HE	1.72	0.55
2:B:927:GLN:HB2	2:B:931:TYR:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:W:524:GLU:O	20:n:232:GLN:NE2	2.40	0.54
23:s:280:ALA:O	23:s:351:ARG:NH1	2.39	0.54
19:m:1056:ARG:HB3	19:m:1076:MET:HB3	1.88	0.54
23:s:268:ASP:OD1	23:s:296:LYS:NZ	2.40	0.54
19:m:607:ILE:HG22	19:m:719:VAL:HG11	1.89	0.54
21:q:157:LYS:NZ	25:v:71:ASP:OD1	2.40	0.54
4:D:159:LEU:HD22	7:G:86:VAL:HG11	1.90	0.54
2:B:281:LEU:HD12	2:B:364:GLU:HB2	1.88	0.54
24:u:209:LEU:HB2	25:v:252:PHE:HB2	1.88	0.54
9:I:100:PHE:HE1	9:I:111:ARG:HE	1.56	0.54
21:q:155:TYR:HB2	21:q:164:ALA:HB2	1.90	0.54
2:B:557:GLU:OE2	2:B:584:ARG:NH1	2.40	0.53
27:e:120:MET:SD	28:f:47:SER:OG	2.65	0.53
17:V:89:ARG:NH1	17:V:109:ASP:OD2	2.41	0.53
26:x:292:TRP:HA	26:x:295:LYS:HE2	1.89	0.53
13:M:33:SER:HA	13:M:50:LYS:HE2	1.91	0.53
24:u:199:LEU:HD11	25:v:211:PHE:HB3	1.91	0.53
1:A:40:ILE:HG23	1:A:54:ASN:HD22	1.72	0.53
18:W:327:ARG:NH1	18:W:335:GLY:O	2.38	0.53
2:B:393:HIS:NE2	2:B:696:GLU:OE2	2.42	0.53
2:B:906:SER:OG	18:W:781:GLU:OE1	2.27	0.53
9:I:45:ARG:NH2	9:I:47:GLU:OE2	2.42	0.52
14:N:9:DT:H4'	14:N:10:DG:OP1	2.08	0.52
19:m:1083:MET:HE1	19:m:1131:LEU:HD23	1.91	0.52
27:a:106:ASP:OD2	27:a:131:ARG:NH1	2.40	0.52
9:I:14:LEU:HB3	9:I:27:TYR:HB3	1.92	0.52
19:m:532:VAL:HG22	19:m:565:MET:HE2	1.91	0.52
2:B:235:LEU:HD23	2:B:242:ILE:HG13	1.91	0.52
7:G:6:ASP:OD1	7:G:75:ARG:NH1	2.43	0.52
19:m:725:GLU:OE2	19:m:728:ARG:NH2	2.36	0.52
21:q:59:ALA:HB1	21:q:63:LEU:HD12	1.91	0.52
23:s:85:CYS:O	23:s:94:ARG:NH1	2.43	0.52
19:m:236:GLU:OE2	20:n:252:ARG:NH2	2.43	0.52
26:x:157:ARG:HB3	26:x:161:PRO:HB3	1.91	0.52
23:s:378:THR:HG23	23:s:382:LEU:HD12	1.91	0.52
24:u:145:ILE:O	24:u:149:THR:OG1	2.21	0.52
1:A:976:ASP:O	1:A:979:LYS:NZ	2.42	0.52
1:A:1423:ASP:OD1	1:A:1423:ASP:N	2.41	0.52
16:T:14:DA:OP1	28:b:48:GLY:N	2.29	0.52
18:W:232:ARG:HH12	18:W:235:LYS:HE3	1.73	0.52
29:g:42:ARG:HB2	30:h:88:THR:HG22	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:q:215:ASP:OD1	21:q:217:ARG:NH1	2.43	0.52
21:q:451:ARG:NH1	25:v:35:GLU:OE1	2.43	0.52
21:q:578:GLN:NE2	21:q:582:ASP:OD1	2.43	0.52
29:c:115:LEU:HD11	28:f:44:LYS:HB2	1.91	0.52
19:m:1426:LEU:HD13	19:m:1469:ARG:HH21	1.74	0.51
21:q:766:MET:HG3	21:q:770:LYS:HE3	1.92	0.51
21:q:830:LEU:HD22	21:q:846:LEU:HB3	1.91	0.51
5:E:60:LEU:O	21:q:915:ARG:NH1	2.39	0.51
21:q:357:LYS:NZ	21:q:361:ASP:OD1	2.43	0.51
21:q:239:ASN:HA	21:q:242:LYS:HD2	1.92	0.51
1:A:999:LEU:O	1:A:1013:GLN:NE2	2.38	0.51
14:N:-54:DC:H2"	14:N:-53:DT:C5	2.45	0.51
19:m:1033:ARG:HH12	19:m:1087:ARG:HH12	1.58	0.51
2:B:10:ASP:HB3	2:B:649:LYS:HG3	1.93	0.51
11:K:25:SER:O	26:x:307:GLN:NE2	2.41	0.51
24:u:114:LEU:HD11	24:u:150:VAL:HG23	1.92	0.51
18:W:229:VAL:HG21	18:W:286:LEU:HD11	1.92	0.51
19:m:1200:PRO:O	19:m:1203:ARG:NH1	2.43	0.51
23:s:247:PRO:HG3	23:s:266:GLN:HB3	1.91	0.51
28:b:73:THR:HG21	28:b:81:VAL:HG22	1.91	0.51
14:N:-49:DG:OP1	29:c:20:ARG:NH2	2.44	0.50
1:A:447:ARG:HB2	1:A:488:MET:HE3	1.93	0.50
19:m:1002:ARG:HH11	19:m:1052:TYR:HH	1.57	0.50
1:A:1195:LEU:HB2	1:A:1263:LEU:HD21	1.93	0.50
20:n:260:MET:HG3	20:n:284:TRP:HZ3	1.76	0.50
26:x:226:LYS:HG3	26:x:250:ILE:HG22	1.93	0.50
18:W:356:PRO:HG2	18:W:394:PHE:HB2	1.92	0.50
18:W:218:ILE:CG1	20:n:289:MET:HE1	2.42	0.50
18:W:666:GLU:HG2	18:W:705:VAL:HG12	1.93	0.50
19:m:1255:TRP:NE1	19:m:1260:GLU:OE1	2.42	0.50
21:q:250:ASN:HA	21:q:253:ILE:HD12	1.93	0.50
23:s:226:ARG:NH1	23:s:227:GLU:O	2.45	0.50
19:m:1191:ASN:OD1	19:m:1193:GLN:NE2	2.42	0.50
18:W:666:GLU:HA	18:W:705:VAL:HA	1.94	0.50
20:n:207:ILE:HG23	20:n:212:LEU:HB3	1.92	0.50
20:n:216:VAL:HG13	20:n:237:LEU:HD13	1.94	0.49
1:A:286:PRO:HG2	1:A:289:ILE:HD12	1.93	0.49
18:W:328:VAL:HA	18:W:435:LEU:HD23	1.94	0.49
23:s:51:ASN:OD1	23:s:53:THR:OG1	2.24	0.49
24:u:191:THR:HG22	24:u:219:VAL:HG22	1.94	0.49
2:B:190:MET:SD	2:B:190:MET:N	2.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:245:MET:HE1	2:B:371:LEU:HD21	1.93	0.49
18:W:704:ARG:NH1	19:m:632:GLU:OE2	2.46	0.49
14:N:7:DC:H1'	14:N:8:DG:H5'	1.94	0.49
20:n:163:LEU:HD11	20:n:194:VAL:HG22	1.94	0.49
1:A:9:ALA:O	2:B:1193:GLN:NE2	2.44	0.49
1:A:1190:GLN:HA	1:A:1245:ILE:HA	1.95	0.49
16:T:45:DC:H5''	29:c:44:GLY:HA2	1.95	0.49
17:V:9:GLU:HA	17:V:20:PRO:HA	1.95	0.49
26:x:311:GLY:HA3	26:x:330:VAL:HG12	1.95	0.49
18:W:327:ARG:NH2	18:W:441:ASN:O	2.46	0.49
18:W:351:ARG:HA	18:W:429:THR:HA	1.94	0.49
3:C:38:ALA:HA	3:C:164:ALA:HB3	1.95	0.49
18:W:640:LYS:NZ	18:W:641:LEU:O	2.46	0.49
17:V:10:ARG:HA	17:V:52:SER:HA	1.95	0.49
19:m:1041:LEU:HD11	19:m:1081:TYR:HD2	1.77	0.49
30:d:79:ARG:NH1	30:d:83:TYR:OH	2.41	0.49
2:B:248:LYS:NZ	2:B:264:THR:OG1	2.46	0.48
2:B:336:ILE:O	2:B:341:ARG:NH1	2.46	0.48
19:m:1172:VAL:HA	19:m:1182:VAL:HG12	1.93	0.48
19:m:1425:LYS:HE3	19:m:1428:PRO:HA	1.94	0.48
21:q:31:LYS:HB2	21:q:57:GLU:HA	1.94	0.48
2:B:613:ARG:HH21	9:I:62:ILE:HD11	1.76	0.48
21:q:390:LEU:HB3	21:q:409:LEU:HD21	1.96	0.48
21:q:479:TYR:HD1	25:v:30:LEU:HB3	1.78	0.48
25:v:210:VAL:HG13	25:v:334:VAL:HG21	1.95	0.48
29:c:63:LEU:HD13	30:d:45:LEU:HB2	1.94	0.48
1:A:106:ILE:HD13	1:A:215:ILE:HD11	1.96	0.48
2:B:601:ALA:HA	24:u:239:SER:HB3	1.96	0.48
11:K:14:ASP:N	11:K:14:ASP:OD1	2.47	0.48
23:s:247:PRO:HD3	23:s:266:GLN:CD	2.39	0.48
24:u:173:TRP:NE1	24:u:179:SER:OG	2.37	0.48
2:B:279:ARG:NH2	2:B:286:ASP:OD1	2.46	0.48
18:W:317:ASP:O	18:W:318:VAL:C	2.55	0.48
19:m:998:ASN:HD22	19:m:999:LEU:N	2.12	0.48
19:m:1269:ASP:OD1	19:m:1272:ARG:NH1	2.46	0.48
2:B:268:VAL:HG11	2:B:272:ILE:HD11	1.95	0.48
21:q:65:LEU:HD13	25:v:81:ILE:HG12	1.95	0.48
24:u:80:TYR:CZ	25:v:356:ASN:HB2	2.49	0.48
1:A:204:THR:OG1	1:A:207:GLU:OE1	2.31	0.47
23:s:242:ARG:NH1	23:s:264:ARG:O	2.47	0.47
1:A:599:LEU:O	8:H:121:LEU:HD12	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1199:LEU:HD13	1:A:1204:MET:HG3	1.96	0.47
18:W:465:ALA:HA	18:W:468:LEU:HD12	1.95	0.47
18:W:494:LEU:HD21	20:n:183:PRO:HG3	1.96	0.47
21:q:559:ARG:NH2	25:v:24:PRO:O	2.47	0.47
22:r:223:VAL:HG22	22:r:325:GLN:HG2	1.95	0.47
2:B:550:PHE:HB3	2:B:593:MET:HE1	1.96	0.47
27:a:133:GLU:OE1	27:a:133:GLU:N	2.47	0.47
1:A:363:ASP:OD1	1:A:363:ASP:N	2.45	0.47
14:N:13:DT:H5'	14:N:13:DT:C6	2.50	0.47
19:m:882:ARG:HH22	19:m:1156:ARG:HH21	1.62	0.47
21:q:72:VAL:HG21	25:v:75:LEU:HD13	1.97	0.47
23:s:173:LEU:O	27:e:32:THR:OG1	2.32	0.47
1:A:1227:PHE:HB2	1:A:1245:ILE:HD11	1.97	0.47
24:u:108:VAL:HG22	24:u:219:VAL:HB	1.96	0.47
22:r:493:ASN:HB2	22:r:502:ILE:HD11	1.96	0.47
19:m:780:LEU:HD12	19:m:900:LEU:HB3	1.97	0.47
1:A:1450:GLU:OE2	7:G:23:ASN:ND2	2.47	0.47
23:s:339:THR:HG22	23:s:341:ASP:H	1.80	0.47
17:V:78:GLN:O	17:V:82:TYR:OH	2.23	0.47
16:T:14:DA:H5''	28:b:47:SER:HA	1.96	0.46
21:q:708:GLN:OE1	21:q:739:LYS:NZ	2.48	0.46
29:c:29:ARG:NH1	30:d:36:SER:O	2.46	0.46
19:m:1279:ARG:NH1	19:m:1315:SER:O	2.48	0.46
5:E:49:MET:SD	5:E:49:MET:N	2.76	0.46
14:N:-21:DG:H2''	14:N:-20:DC:C5	2.51	0.46
18:W:326:VAL:HA	18:W:440:ILE:HD13	1.97	0.46
25:v:263:TRP:HE1	25:v:356:ASN:HD21	1.61	0.46
1:A:10:PRO:HG2	2:B:1192:TYR:HD1	1.80	0.46
1:A:870:GLY:C	1:A:872:ASP:H	2.24	0.46
11:K:29:ASN:ND2	11:K:78:GLU:O	2.49	0.46
19:m:625:GLY:O	19:m:629:ILE:HG12	2.14	0.46
1:A:1452:LEU:HD22	6:F:131:PRO:HB3	1.98	0.46
11:K:45:LEU:HG	11:K:94:ILE:HD13	1.98	0.46
27:e:50:GLU:HG3	28:f:39:ARG:HG2	1.96	0.46
1:A:261:ASP:OD1	1:A:262:ASP:N	2.48	0.46
7:G:160:ILE:HD12	18:W:553:LEU:HD12	1.97	0.46
17:V:66:SER:HB2	18:W:260:TYR:HB3	1.98	0.46
22:r:211:MET:HB3	22:r:286:LEU:HD23	1.97	0.46
18:W:215:ARG:NH2	19:m:234:TYR:CE1	2.85	0.45
19:m:1104:ILE:HD12	23:s:456:PRO:HB2	1.98	0.45
21:q:189:LEU:HD22	21:q:194:LYS:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:g:90:ASP:HB3	29:g:93:LEU:HB2	1.96	0.45
1:A:864:ILE:HD12	5:E:169:LEU:HD11	1.99	0.45
7:G:151:ARG:HB3	7:G:158:TYR:HB2	1.98	0.45
6:F:110:ASP:OD1	6:F:110:ASP:N	2.38	0.45
18:W:546:LYS:NZ	19:m:291:GLU:OE1	2.48	0.45
22:r:276:PHE:HB2	22:r:279:GLN:HB2	1.99	0.45
1:A:215:ILE:O	1:A:231:ARG:NH2	2.47	0.45
2:B:86:ARG:NH2	22:r:369:GLU:OE1	2.50	0.45
18:W:215:ARG:NH1	19:m:234:TYR:CE1	2.84	0.45
23:s:395:THR:HA	23:s:398:VAL:HG12	1.98	0.45
1:A:1151:ALA:O	1:A:1198:GLU:N	2.47	0.45
13:M:46:LEU:HD11	13:M:55:SER:HB3	1.99	0.45
17:V:58:VAL:N	17:V:82:TYR:O	2.45	0.45
19:m:640:TYR:OH	19:m:1263:ASP:OD2	2.32	0.45
19:m:984:LYS:HE2	19:m:1015:VAL:HG21	1.99	0.45
16:T:-11:DG:H2"	16:T:-10:DC:C6	2.52	0.45
22:r:244:LYS:NZ	22:r:305:GLU:OE2	2.46	0.45
23:s:342:TYR:CZ	23:s:346:ARG:HD2	2.51	0.45
29:g:24:GLN:HE21	30:h:47:GLN:HE21	1.63	0.45
1:A:807:ARG:NH1	2:B:724:LYS:O	2.43	0.45
1:A:835:THR:HG21	1:A:1079:THR:HA	1.99	0.45
12:L:49:ARG:HD3	22:r:339:VAL:HG11	1.98	0.45
19:m:1002:ARG:NH1	19:m:1052:TYR:OH	2.43	0.45
29:c:100:VAL:HG12	28:f:96:THR:HB	1.97	0.45
5:E:34:MET:HE2	5:E:34:MET:HB2	1.80	0.45
21:q:210:PRO:O	21:q:217:ARG:NH2	2.39	0.45
2:B:588:MET:HE3	2:B:588:MET:HB3	1.88	0.45
18:W:527:THR:HA	18:W:530:LEU:HD12	1.99	0.45
25:v:258:ASN:OD1	25:v:261:ASN:N	2.44	0.45
1:A:599:LEU:HD12	1:A:599:LEU:HA	1.73	0.44
2:B:498:ASP:HB3	14:N:42:DA:C4	2.53	0.44
5:E:89:ILE:HD13	5:E:118:SER:HB2	1.98	0.44
18:W:444:LEU:HD12	19:m:284:PHE:CG	2.52	0.44
18:W:638:TYR:CZ	19:m:882:ARG:HG3	2.52	0.44
19:m:712:LEU:HA	19:m:715:LEU:HB2	1.98	0.44
19:m:1064:ASP:OD1	23:s:457:LYS:NZ	2.46	0.44
21:q:320:LEU:HD13	22:r:514:LEU:HD11	1.99	0.44
14:N:56:DG:C2	16:T:-55:DG:C2	3.05	0.44
18:W:751:THR:HG23	18:W:798:ILE:HG12	1.99	0.44
1:A:231:ARG:HB3	1:A:234:TRP:CD2	2.53	0.44
1:A:466:TYR:HB2	1:A:470:ARG:NH2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:948:VAL:O	5:E:200:ARG:NH1	2.50	0.44
1:A:1343:GLY:O	1:A:1347:THR:OG1	2.29	0.44
5:E:21:MET:HE2	5:E:186:TYR:HA	2.00	0.44
18:W:628:LYS:HE3	19:m:661:GLN:HE22	1.82	0.44
19:m:992:ILE:HG22	19:m:997:SER:HA	1.99	0.44
23:s:345:LEU:HD13	23:s:376:ILE:HG23	1.99	0.44
24:u:90:LEU:HB2	25:v:362:MET:HE1	1.99	0.44
25:v:34:ILE:O	25:v:40:GLN:NE2	2.38	0.44
1:A:41:MET:HG2	1:A:44:SER:HA	1.98	0.44
19:m:527:ASP:OD1	19:m:528:ALA:N	2.47	0.44
19:m:1365:GLU:O	19:m:1369:ASN:ND2	2.49	0.44
2:B:284:VAL:N	2:B:285:PRO:HD2	2.32	0.44
4:D:139:PRO:HA	4:D:142:ILE:HD12	1.99	0.44
19:m:1062:ALA:HB2	19:m:1103:LEU:HD11	1.99	0.44
21:q:737:LEU:O	21:q:742:ASN:N	2.47	0.44
25:v:312:LYS:HB3	25:v:315:GLU:HG2	1.99	0.44
28:b:52:GLU:OE1	28:b:52:GLU:N	2.48	0.44
1:A:134:ARG:HH21	1:A:224:GLY:HA2	1.82	0.44
2:B:273:PRO:HG2	2:B:276:ILE:HD12	2.00	0.44
3:C:15:ASP:OD1	3:C:15:ASP:N	2.44	0.44
4:D:136:VAL:O	4:D:166:LYS:NZ	2.50	0.44
14:N:13:DT:O4	16:T:-14:DA:N6	2.50	0.44
23:s:209:VAL:HG22	23:s:222:ILE:HG12	1.99	0.44
3:C:179:GLU:OE2	3:C:204:SER:OG	2.36	0.44
19:m:1426:LEU:HD21	19:m:1465:MET:HE2	1.99	0.44
2:B:650:GLU:OE1	2:B:653:ARG:NH2	2.49	0.44
19:m:770:PHE:HB3	19:m:779:VAL:HG22	2.00	0.44
21:q:568:SER:O	21:q:571:ASN:ND2	2.50	0.44
22:r:230:ARG:NH1	22:r:292:SER:OG	2.45	0.44
22:r:366:GLU:HG2	24:u:252:VAL:HG22	1.99	0.44
25:v:262:LYS:HD3	25:v:305:GLN:HE21	1.81	0.44
28:b:68:ASP:N	28:b:68:ASP:OD1	2.50	0.44
7:G:144:ARG:HB2	7:G:171:ILE:HD13	1.99	0.43
23:s:417:GLN:O	23:s:420:SER:OG	2.31	0.43
28:b:98:TYR:OH	30:h:68:ASP:OD2	2.33	0.43
17:V:67:TRP:NE1	18:W:217:LEU:O	2.51	0.43
23:s:264:ARG:O	23:s:265:THR:C	2.60	0.43
26:x:222:MET:HE3	26:x:222:MET:HB3	1.85	0.43
1:A:465:PRO:O	1:A:470:ARG:NH2	2.52	0.43
1:A:958:LEU:HD13	1:A:1023:LEU:HD22	2.01	0.43
2:B:547:ILE:HG21	2:B:619:ILE:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:T:-6:DA:P	27:e:63:ARG:HH21	2.41	0.43
18:W:534:PHE:HB3	18:W:554:ILE:HD13	2.00	0.43
21:q:617:ASP:OD1	21:q:621:ASN:ND2	2.51	0.43
21:q:641:ALA:HB1	21:q:655:LYS:HG3	2.00	0.43
18:W:472:ALA:O	18:W:476:VAL:HG23	2.18	0.43
25:v:104:PRO:HA	25:v:107:ARG:HD3	2.00	0.43
30:d:68:ASP:OD2	28:f:98:TYR:OH	2.33	0.43
1:A:1389:ARG:NH2	16:T:-44:DT:O2	2.50	0.43
2:B:374:MET:HE2	2:B:374:MET:HB3	1.84	0.43
22:r:245:VAL:HG23	22:r:298:GLU:HG2	2.01	0.43
29:c:63:LEU:HD11	30:d:41:VAL:HG13	1.99	0.43
1:A:1448:ILE:HD11	1:A:1453:LEU:HD11	2.01	0.43
1:A:188:LYS:HE3	1:A:199:GLU:HB2	2.01	0.43
9:I:23:GLN:O	9:I:24:ARG:NE	2.51	0.43
17:V:59:ALA:HB1	18:W:244:LEU:HD13	2.01	0.43
18:W:344:LEU:HD12	18:W:349:GLU:HB2	2.01	0.43
19:m:242:GLY:HA3	20:n:258:LYS:HG2	2.00	0.43
9:I:62:ILE:HD12	9:I:62:ILE:HA	1.93	0.43
1:A:327:ARG:HG3	1:A:1409:VAL:HG21	2.01	0.42
2:B:788:ARG:O	2:B:967:ARG:NH1	2.52	0.42
2:B:860:MET:HE3	2:B:860:MET:HB3	1.84	0.42
7:G:30:LEU:HD22	7:G:72:VAL:HG11	2.00	0.42
21:q:520:SER:O	21:q:524:HIS:ND1	2.48	0.42
1:A:547:VAL:HG22	1:A:578:LEU:HD21	2.01	0.42
8:H:17:ASN:OD1	8:H:24:SER:OG	2.31	0.42
18:W:508:SER:HA	18:W:524:GLU:HA	1.99	0.42
30:d:57:LYS:O	30:d:61:ILE:HG13	2.19	0.42
16:T:32:DA:H2''	16:T:33:DC:C5	2.54	0.42
19:m:1205:ASP:OD1	19:m:1207:ARG:NE	2.48	0.42
21:q:162:ASP:OD1	21:q:192:ARG:NH2	2.51	0.42
2:B:928:ARG:NH2	19:m:775:ARG:O	2.52	0.42
21:q:155:TYR:HB3	21:q:160:ARG:HB2	2.01	0.42
23:s:296:LYS:HB2	23:s:302:ILE:HD13	2.01	0.42
24:u:200:VAL:HA	24:u:211:THR:HA	2.00	0.42
24:u:208:ILE:HG22	25:v:253:LYS:HG3	2.01	0.42
26:x:301:ASP:OD1	26:x:303:GLN:NE2	2.53	0.42
14:N:-20:DC:OP1	28:b:36:ARG:NH2	2.52	0.42
29:c:111:ILE:HG23	29:c:115:LEU:HD23	2.00	0.42
1:A:983:LEU:HD13	1:A:1041:ARG:HA	2.01	0.42
1:A:1287:MET:HE3	1:A:1287:MET:HB2	1.96	0.42
2:B:83:TYR:HB2	2:B:116:TYR:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:W:752:LEU:HD23	18:W:770:VAL:HG12	1.99	0.42
19:m:545:ASN:ND2	19:m:553:HIS:O	2.53	0.42
19:m:992:ILE:HA	19:m:995:ILE:HG12	2.02	0.42
20:n:217:ARG:HG3	20:n:259:VAL:HG21	2.02	0.42
21:q:9:TYR:OH	25:v:106:ASP:OD2	2.28	0.42
21:q:766:MET:HE1	21:q:799:ILE:HG23	2.02	0.42
22:r:277:PRO:HB2	22:r:305:GLU:HB3	2.01	0.42
2:B:299:ASP:OD1	2:B:299:ASP:N	2.52	0.42
14:N:-16:DT:H2''	14:N:-15:DT:H5''	2.02	0.42
18:W:315:SER:O	18:W:316:SER:C	2.61	0.42
1:A:203:LEU:HB3	1:A:208:ILE:HD11	2.01	0.42
2:B:607:SER:HB2	2:B:620:PHE:HB2	2.02	0.42
19:m:1325:ALA:HB3	19:m:1328:LEU:HB3	2.02	0.42
21:q:780:TYR:O	21:q:784:LYS:N	2.50	0.42
28:f:62:LEU:HD23	28:f:62:LEU:HA	1.81	0.42
11:K:55:ASP:OD1	11:K:55:ASP:N	2.41	0.42
18:W:336:ASP:OD2	18:W:357:ARG:NE	2.47	0.42
18:W:461:LEU:HD12	19:m:278:THR:HG23	2.01	0.42
21:q:737:LEU:HD12	21:q:741:SER:HB2	2.01	0.42
2:B:632:ILE:HD11	2:B:688:GLU:HB3	2.01	0.41
2:B:830:TYR:CZ	2:B:1000:PRO:HD3	2.55	0.41
5:E:81:PHE:HE1	5:E:110:ILE:HD13	1.84	0.41
17:V:63:ASN:HB3	17:V:75:ASP:HA	2.01	0.41
29:c:54:VAL:HG21	30:d:98:VAL:HG21	2.01	0.41
1:A:1412:LEU:HD13	2:B:1207:LEU:HD21	2.02	0.41
16:T:52:DG:H2''	16:T:53:DA:C8	2.55	0.41
18:W:334:LYS:HB3	18:W:388:ARG:HH12	1.84	0.41
19:m:380:GLU:HB3	19:m:978:CYS:SG	2.60	0.41
30:h:106:LEU:HD23	30:h:106:LEU:HA	1.95	0.41
14:N:-34:DT:H2''	14:N:-33:DG:C8	2.56	0.41
24:u:268:GLU:HA	24:u:271:ARG:HG2	2.03	0.41
1:A:253:MET:SD	16:T:-31:DA:H2''	2.60	0.41
2:B:957:ASN:OD1	2:B:961:LEU:N	2.53	0.41
22:r:263:SER:OG	22:r:264:LYS:N	2.53	0.41
1:A:823:GLU:OE2	2:B:506:GLN:NE2	2.53	0.41
2:B:81:LYS:NZ	24:u:247:TYR:O	2.43	0.41
2:B:592:THR:HA	24:u:226:PHE:HZ	1.85	0.41
7:G:108:VAL:HG22	7:G:159:ALA:HB3	2.02	0.41
21:q:41:PHE:CG	21:q:70:VAL:HG11	2.55	0.41
21:q:710:LEU:HD13	21:q:740:PHE:HB2	2.01	0.41
30:d:43:LYS:HB2	30:d:43:LYS:HE3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:ASP:HB3	1:A:509:PRO:HD3	2.03	0.41
2:B:318:ASP:HB3	2:B:321:VAL:HG22	2.02	0.41
5:E:27:TYR:HA	5:E:63:PRO:HA	2.03	0.41
18:W:250:ARG:NH2	18:W:284:ASP:OD2	2.53	0.41
18:W:551:THR:HG21	18:W:586:SER:HA	2.03	0.41
11:K:65:HIS:HB3	11:K:68:PHE:HD2	1.86	0.41
16:T:15:DA:OP2	28:b:35:ARG:NH2	2.53	0.41
18:W:648:GLN:NE2	18:W:679:VAL:H	2.18	0.41
25:v:29:LEU:N	26:x:147:ARG:O	2.52	0.41
28:f:66:ILE:HD13	28:f:66:ILE:HA	1.93	0.41
2:B:174:THR:O	2:B:175:LEU:C	2.64	0.41
3:C:50:ILE:HG12	3:C:155:ILE:HG22	2.03	0.41
3:C:79:MET:HE2	3:C:79:MET:HB3	1.87	0.41
19:m:449:THR:HG21	19:m:543:ARG:HD2	2.03	0.41
19:m:1001:ASN:OD1	19:m:1002:ARG:N	2.54	0.41
21:q:710:LEU:HD11	21:q:748:LEU:HD11	2.03	0.41
22:r:206:PHE:H	22:r:229:LEU:HD21	1.84	0.41
22:r:208:ARG:N	22:r:291:ASP:OD1	2.52	0.41
27:a:61:LEU:HD12	28:b:37:LEU:HD23	2.02	0.41
30:h:95:GLN:O	30:h:99:ARG:HG3	2.21	0.41
9:I:17:LYS:N	9:I:26:LEU:O	2.50	0.41
27:a:122:LYS:H	27:a:122:LYS:HG2	1.70	0.41
1:A:109:ASN:HD21	20:n:199:LEU:HB3	1.85	0.40
2:B:184:LYS:HB3	2:B:787:VAL:HG21	2.03	0.40
2:B:479:TYR:CE2	2:B:778:MET:HG2	2.56	0.40
3:C:21:LEU:HD22	11:K:101:LEU:HD11	2.03	0.40
5:E:63:PRO:HB3	5:E:74:LEU:HD23	2.03	0.40
19:m:338:LEU:HD23	19:m:338:LEU:HA	1.86	0.40
24:u:89:SER:HB3	25:v:365:ARG:HE	1.86	0.40
30:d:86:ARG:HD3	30:d:86:ARG:HA	1.99	0.40
27:e:82:LEU:HD22	28:f:81:VAL:HG23	2.03	0.40
16:T:-9:DA:H2''	16:T:-8:DC:O4'	2.21	0.40
19:m:1286:PHE:HA	19:m:1308:ILE:HB	2.03	0.40
1:A:554:VAL:HB	1:A:557:TRP:HB2	2.04	0.40
2:B:121:LYS:HE2	2:B:121:LYS:HB3	1.88	0.40
2:B:760:ASP:OD1	2:B:760:ASP:N	2.48	0.40
2:B:766:ARG:NH2	2:B:985:GLY:O	2.53	0.40
2:B:1072:MET:HG3	2:B:1085:VAL:HB	2.04	0.40
19:m:243:ASP:OD1	19:m:243:ASP:N	2.55	0.40
19:m:295:THR:OG1	19:m:298:ASP:OD2	2.37	0.40
19:m:965:VAL:HG21	19:m:992:ILE:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:q:98:ALA:HB1	21:q:140:LEU:HB3	2.03	0.40
1:A:26:GLU:OE2	4:D:13:ARG:NH1	2.54	0.40
2:B:81:LYS:HE3	2:B:81:LYS:HB3	1.77	0.40
7:G:51:GLY:HA2	7:G:54:ILE:HD11	2.03	0.40
18:W:524:GLU:HB2	20:n:232:GLN:HE22	1.87	0.40
25:v:199:HIS:O	25:v:328:ALA:N	2.54	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 PDB entries followed by that with respect to all EM entries.

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	1392/1743 (80%)	1356 (97%)	35 (2%)	1 (0%)	48	78
2	B	1154/1227 (94%)	1127 (98%)	27 (2%)	0	100	100
3	C	261/304 (86%)	259 (99%)	2 (1%)	0	100	100
4	D	170/186 (91%)	168 (99%)	2 (1%)	0	100	100
5	E	211/214 (99%)	207 (98%)	4 (2%)	0	100	100
6	F	82/155 (53%)	79 (96%)	3 (4%)	0	100	100
7	G	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
8	H	129/145 (89%)	125 (97%)	4 (3%)	0	100	100
9	I	109/115 (95%)	105 (96%)	4 (4%)	0	100	100
10	J	65/72 (90%)	65 (100%)	0	0	100	100
11	K	111/118 (94%)	109 (98%)	2 (2%)	0	100	100
12	L	43/72 (60%)	41 (95%)	2 (5%)	0	100	100
13	M	62/113 (55%)	61 (98%)	1 (2%)	0	100	100
17	V	104/108 (96%)	102 (98%)	2 (2%)	0	100	100
18	W	529/911 (58%)	505 (96%)	24 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	m	1170/1503 (78%)	1152 (98%)	18 (2%)	0	100	100
20	n	137/417 (33%)	136 (99%)	1 (1%)	0	100	100
21	q	928/1084 (86%)	923 (100%)	5 (0%)	0	100	100
22	r	260/544 (48%)	254 (98%)	6 (2%)	0	100	100
23	s	428/725 (59%)	414 (97%)	14 (3%)	0	100	100
24	u	206/459 (45%)	206 (100%)	0	0	100	100
25	v	341/396 (86%)	330 (97%)	11 (3%)	0	100	100
26	x	201/395 (51%)	200 (100%)	1 (0%)	0	100	100
27	a	89/139 (64%)	89 (100%)	0	0	100	100
27	e	102/139 (73%)	100 (98%)	2 (2%)	0	100	100
28	b	80/106 (76%)	77 (96%)	3 (4%)	0	100	100
28	f	76/106 (72%)	74 (97%)	2 (3%)	0	100	100
29	c	104/133 (78%)	101 (97%)	3 (3%)	0	100	100
29	g	95/133 (71%)	93 (98%)	2 (2%)	0	100	100
30	d	92/129 (71%)	91 (99%)	1 (1%)	0	100	100
30	h	88/129 (68%)	85 (97%)	3 (3%)	0	100	100
All	All	8988/12191 (74%)	8800 (98%)	187 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	960	VAL

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 PDB entries followed by that with respect to all EM entries.

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	1219/1528 (80%)	1219 (100%)	0	100	100
2	B	1018/1077 (94%)	1014 (100%)	4 (0%)	84	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	236/264 (89%)	236 (100%)	0	100	100
4	D	149/160 (93%)	149 (100%)	0	100	100
5	E	196/197 (100%)	196 (100%)	0	100	100
6	F	75/137 (55%)	75 (100%)	0	100	100
7	G	148/148 (100%)	148 (100%)	0	100	100
8	H	120/130 (92%)	120 (100%)	0	100	100
9	I	106/109 (97%)	106 (100%)	0	100	100
10	J	61/66 (92%)	61 (100%)	0	100	100
11	K	104/109 (95%)	104 (100%)	0	100	100
12	L	38/56 (68%)	38 (100%)	0	100	100
13	M	61/99 (62%)	61 (100%)	0	100	100
17	V	90/92 (98%)	90 (100%)	0	100	100
18	W	482/796 (61%)	482 (100%)	0	100	100
19	m	1079/1354 (80%)	1078 (100%)	1 (0%)	88	89
20	n	125/361 (35%)	125 (100%)	0	100	100
21	q	824/962 (86%)	824 (100%)	0	100	100
22	r	239/485 (49%)	239 (100%)	0	100	100
23	s	380/649 (59%)	380 (100%)	0	100	100
24	u	192/406 (47%)	192 (100%)	0	100	100
25	v	325/369 (88%)	325 (100%)	0	100	100
26	x	190/354 (54%)	190 (100%)	0	100	100
27	a	77/112 (69%)	77 (100%)	0	100	100
27	e	87/112 (78%)	87 (100%)	0	100	100
28	b	67/81 (83%)	67 (100%)	0	100	100
28	f	63/81 (78%)	63 (100%)	0	100	100
29	c	84/102 (82%)	84 (100%)	0	100	100
29	g	77/102 (76%)	77 (100%)	0	100	100
30	d	80/107 (75%)	80 (100%)	0	100	100
30	h	76/107 (71%)	76 (100%)	0	100	100
All	All	8068/10712 (75%)	8063 (100%)	5 (0%)	87	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	425	MET
2	B	815	ARG
2	B	879	ARG
2	B	904	ARG
19	m	770	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	276	ASN
1	A	278	GLN
1	A	288	HIS
1	A	291	ASN
1	A	387	HIS
1	A	661	ASN
1	A	690	GLN
1	A	1080	GLN
2	B	157	HIS
2	B	477	ASN
2	B	492	ASN
2	B	524	GLN
2	B	549	ASN
2	B	794	ASN
2	B	996	HIS
2	B	1179	GLN
3	C	8	ASN
3	C	13	GLN
3	C	25	ASN
4	D	46	HIS
4	D	130	ASN
4	D	170	ASN
5	E	53	GLN
5	E	162	GLN
6	F	104	ASN
6	F	119	GLN
6	F	127	GLN
7	G	122	ASN
8	H	43	ASN
9	I	23	GLN
12	L	55	HIS
13	M	65	GLN
18	W	283	ASN

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Mol	Chain	Res	Type
18	W	558	ASN
18	W	786	ASN
19	m	353	HIS
19	m	428	HIS
19	m	661	GLN
19	m	819	ASN
19	m	869	HIS
19	m	886	HIS
19	m	899	GLN
19	m	998	ASN
19	m	1191	ASN
19	m	1193	GLN
19	m	1242	GLN
19	m	1288	ASN
19	m	1338	ASN
19	m	1436	ASN
20	n	156	GLN
20	n	232	GLN
21	q	58	ASN
21	q	132	ASN
21	q	147	ASN
21	q	187	GLN
21	q	319	ASN
21	q	397	ASN
21	q	398	GLN
21	q	503	GLN
21	q	526	ASN
21	q	615	HIS
21	q	625	HIS
22	r	279	GLN
22	r	493	ASN
23	s	83	ASN
23	s	171	GLN
23	s	248	GLN
23	s	311	ASN
24	u	93	HIS
24	u	103	GLN
24	u	138	GLN
24	u	172	GLN
24	u	261	GLN
25	v	64	ASN
25	v	199	HIS

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Mol	Chain	Res	Type
25	v	283	ASN
25	v	381	GLN
26	x	246	ASN
26	x	251	GLN
27	a	68	GLN
27	a	108	ASN
28	b	75	HIS
29	c	31	HIS
29	c	94	ASN
30	d	84	ASN
30	d	95	GLN
27	e	39	HIS
27	e	55	GLN
28	f	64	ASN
29	g	24	GLN
29	g	84	GLN
30	h	67	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	P	19/20 (95%)	8 (42%)	0

All (8) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
15	P	-6	C
15	P	-5	U
15	P	-4	U
15	P	-3	G
15	P	-2	U
15	P	-1	G
15	P	0	C
15	P	1	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 14 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
33	SAH	s	1904	-	27,28,28	1.12	3 (11%)	36,40,40	2.11	10 (27%)

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
33	SAH	s	1904	-	-	1/15/31/31	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	s	1904	SAH	C2-N3	2.70	1.38	1.33
33	s	1904	SAH	C2-N1	2.56	1.38	1.33
33	s	1904	SAH	OXT-C	-2.32	1.23	1.30

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	s	1904	SAH	N3-C2-N1	-5.63	120.07	128.58
33	s	1904	SAH	C5-C4-N3	-4.63	120.35	126.72
33	s	1904	SAH	N9-C8-N7	-3.82	108.52	113.94
33	s	1904	SAH	C5'-SD-CG	-3.56	91.69	102.26
33	s	1904	SAH	C2-N3-C4	3.46	120.28	111.83
33	s	1904	SAH	C5-N7-C8	3.34	108.70	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	s	1904	SAH	N3-C4-N9	3.21	132.63	127.17
33	s	1904	SAH	OXT-C-O	-2.67	118.03	124.08
33	s	1904	SAH	C2'-C1'-N9	-2.53	107.02	113.30
33	s	1904	SAH	C4-C5-N7	-2.23	108.03	110.58

There are no chirality outliers.

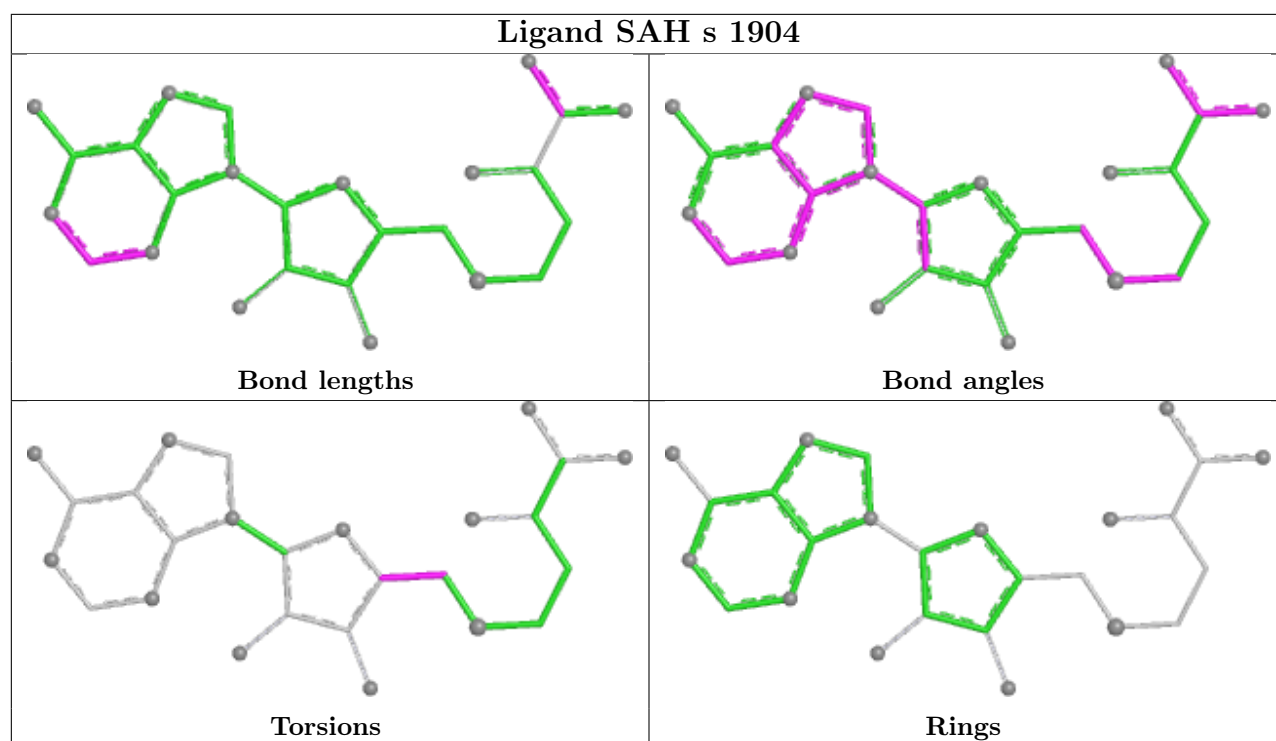
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
33	s	1904	SAH	C3'-C4'-C5'-SD

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

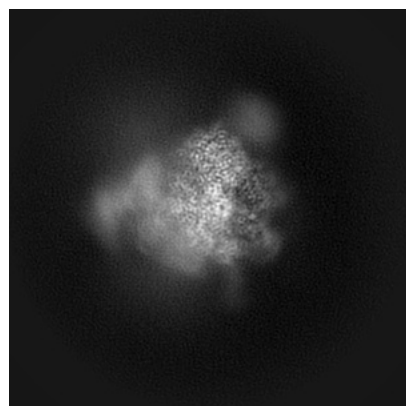
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66103. These allow visual inspection of the internal detail of the map and identification of artifacts.

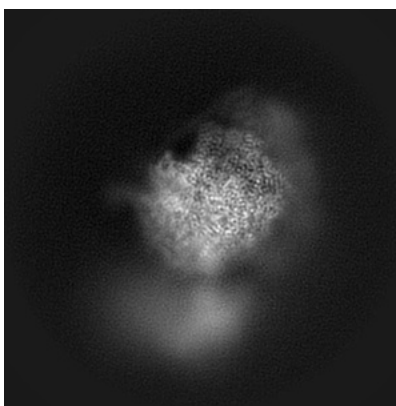
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

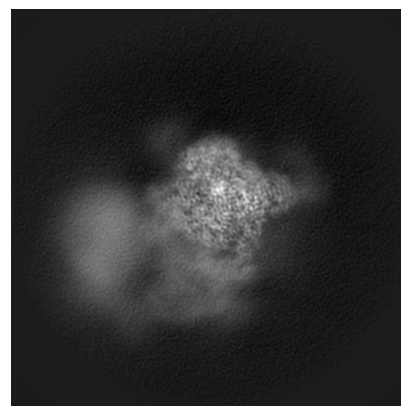
6.1.1 Primary map



X

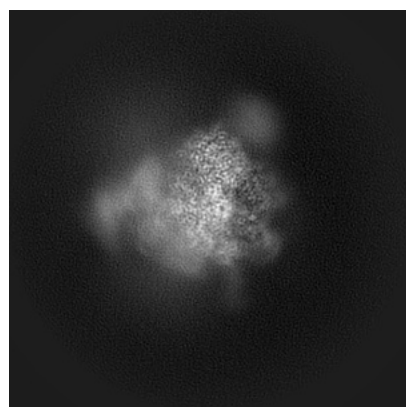


Y

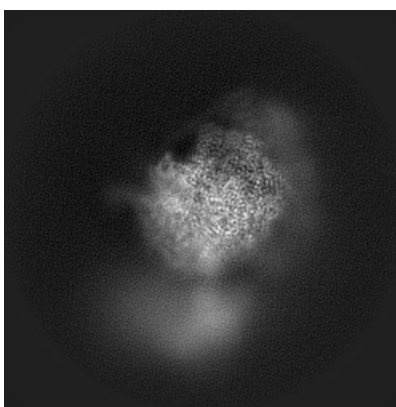


Z

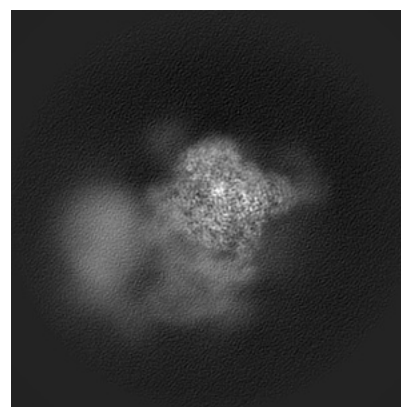
6.1.2 Raw map



X



Y

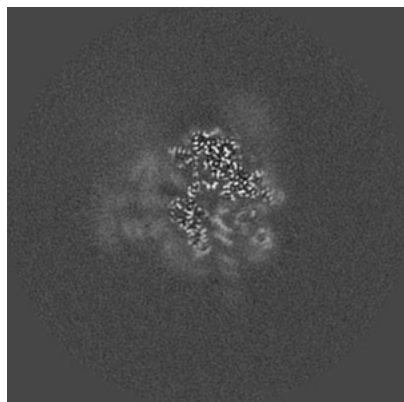


Z

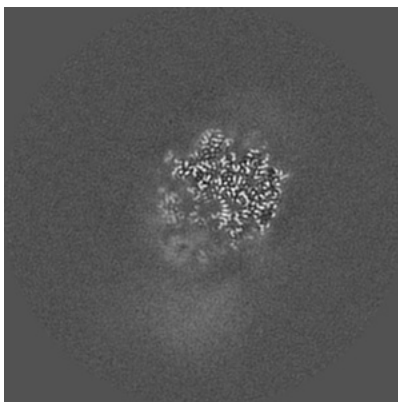
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

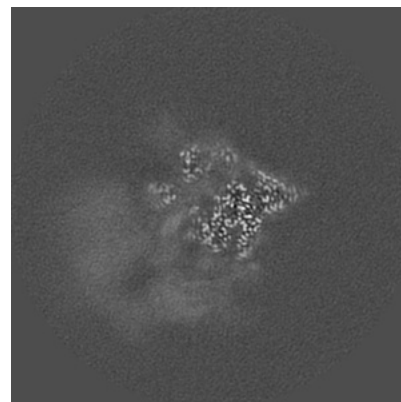
6.2.1 Primary map



X Index: 135

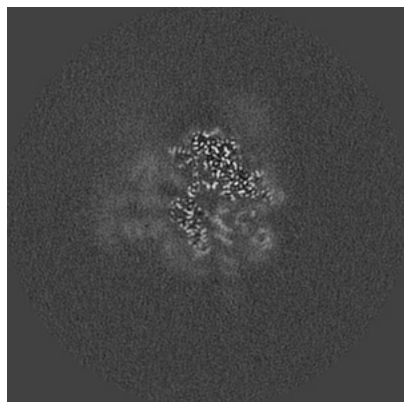


Y Index: 135

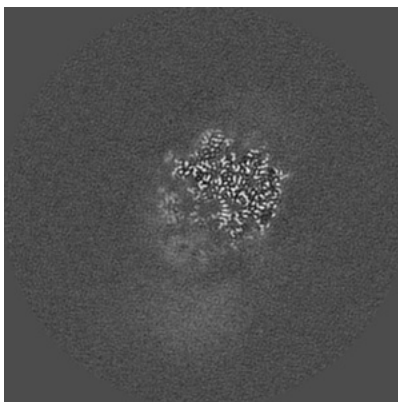


Z Index: 135

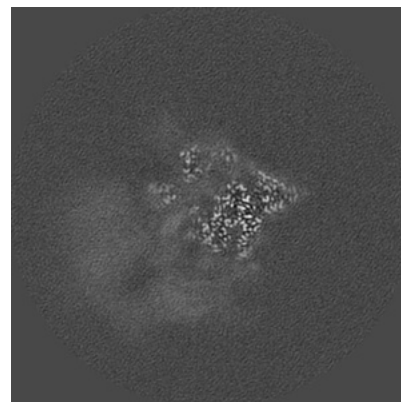
6.2.2 Raw map



X Index: 135



Y Index: 135

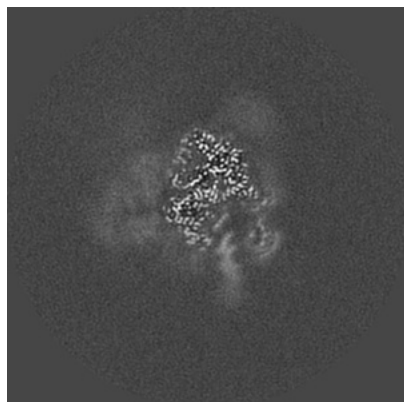


Z Index: 135

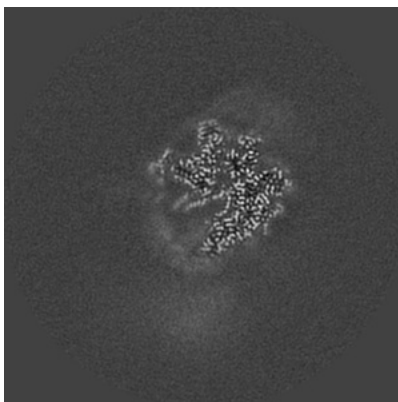
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

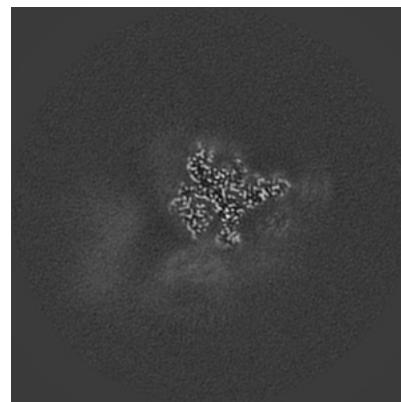
6.3.1 Primary map



X Index: 141

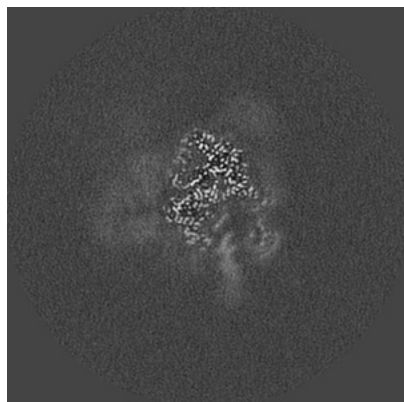


Y Index: 141

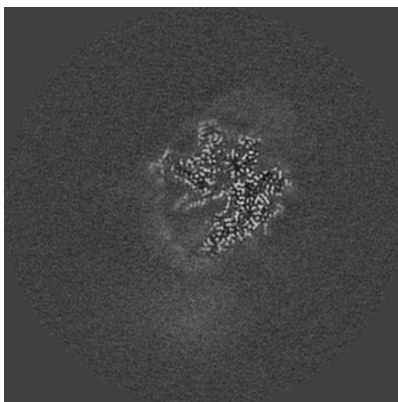


Z Index: 157

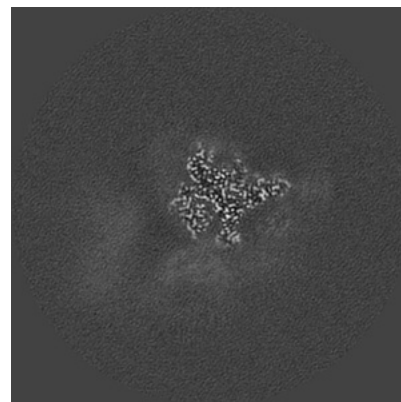
6.3.2 Raw map



X Index: 141



Y Index: 141

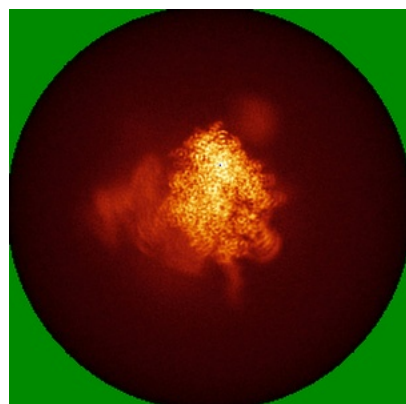


Z Index: 157

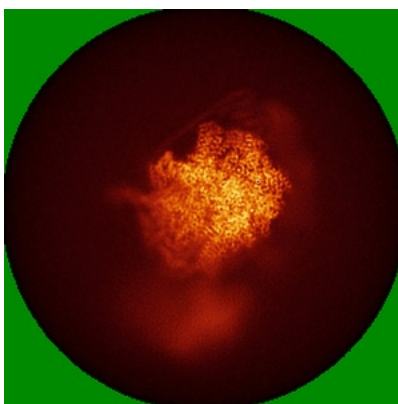
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

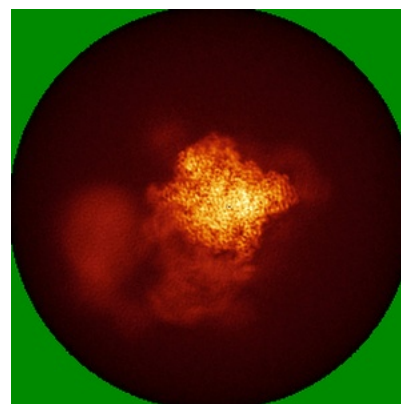
6.4.1 Primary map



X

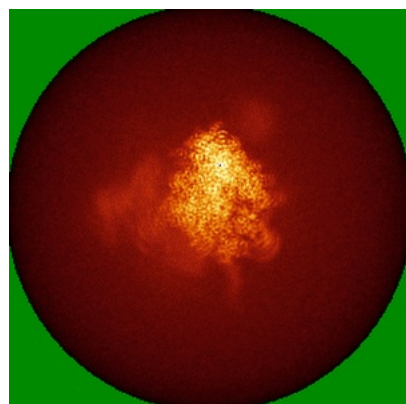


Y

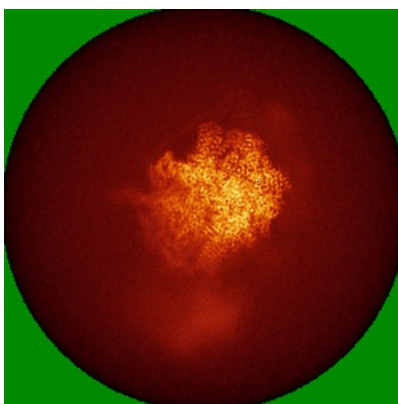


Z

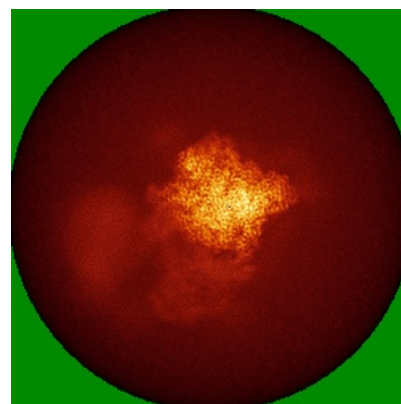
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

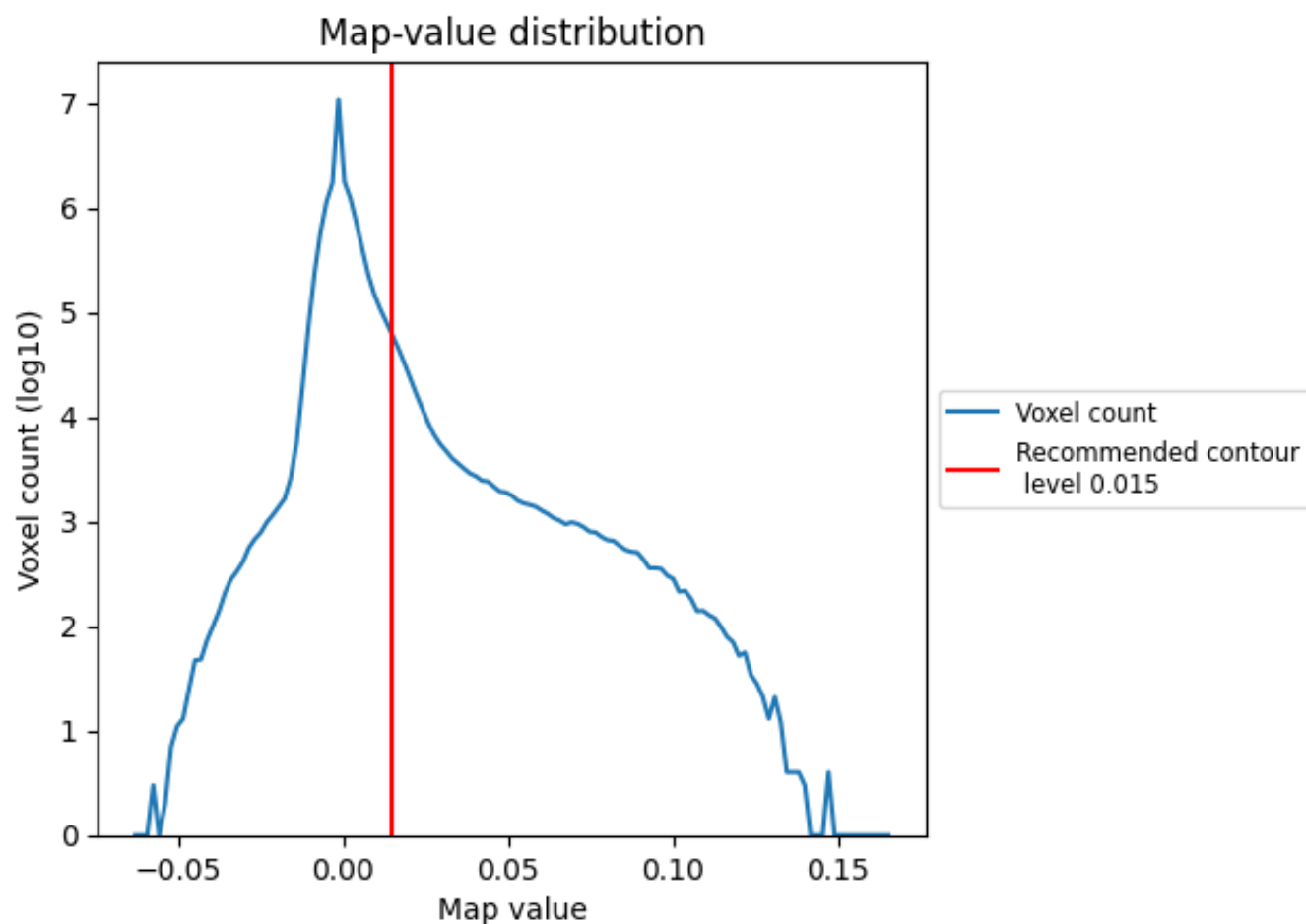
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

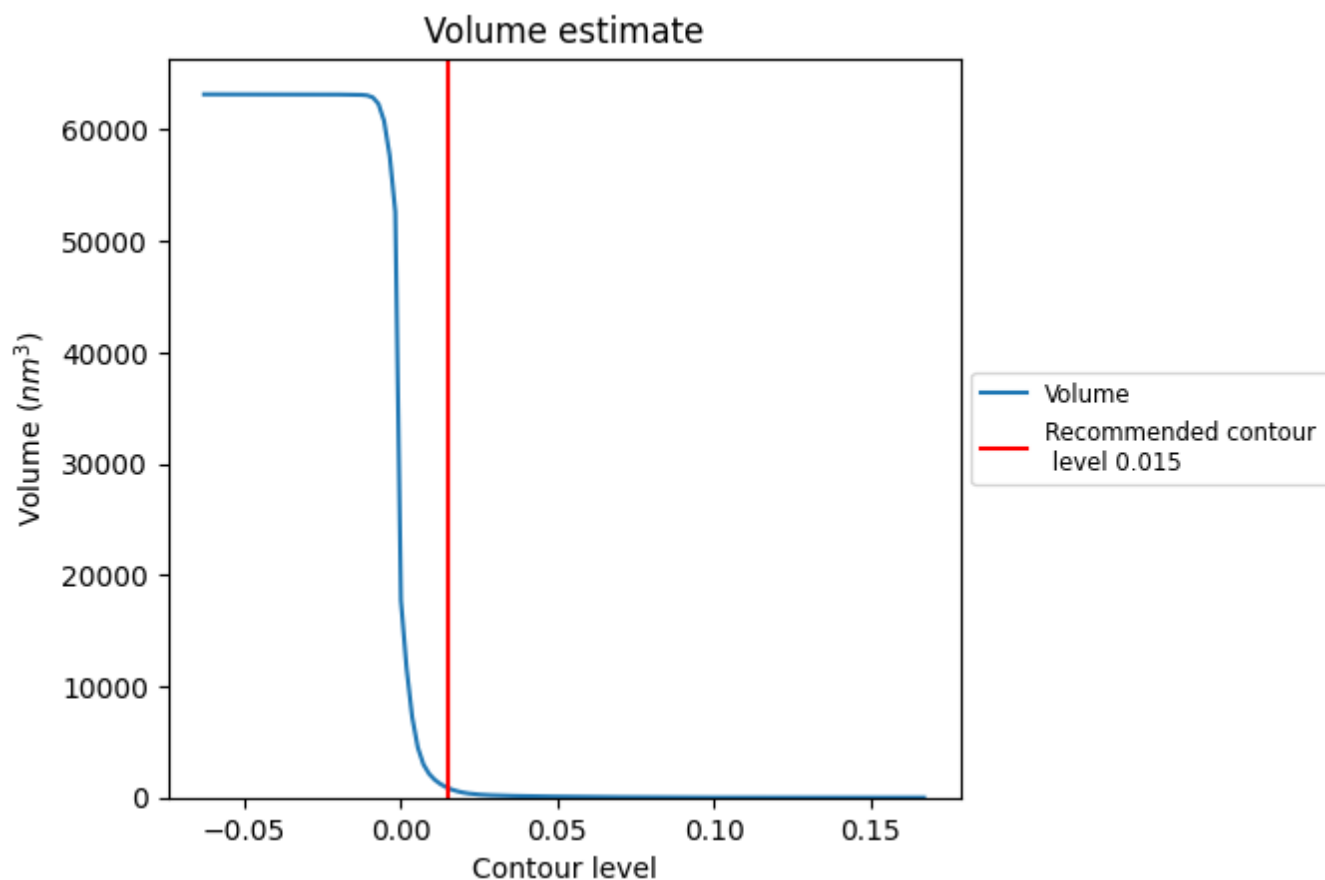
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

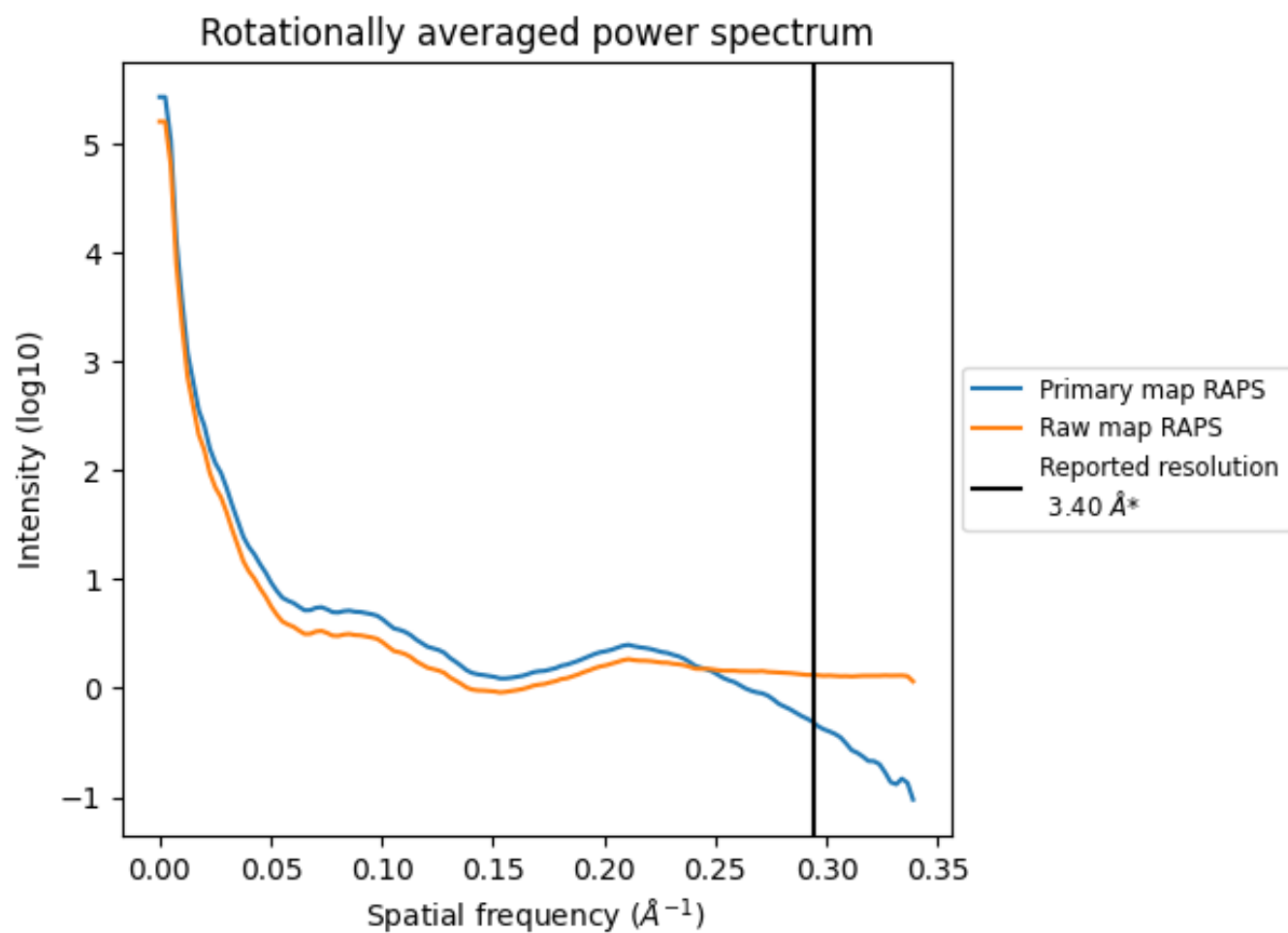
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 867 nm³; this corresponds to an approximate mass of 783 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

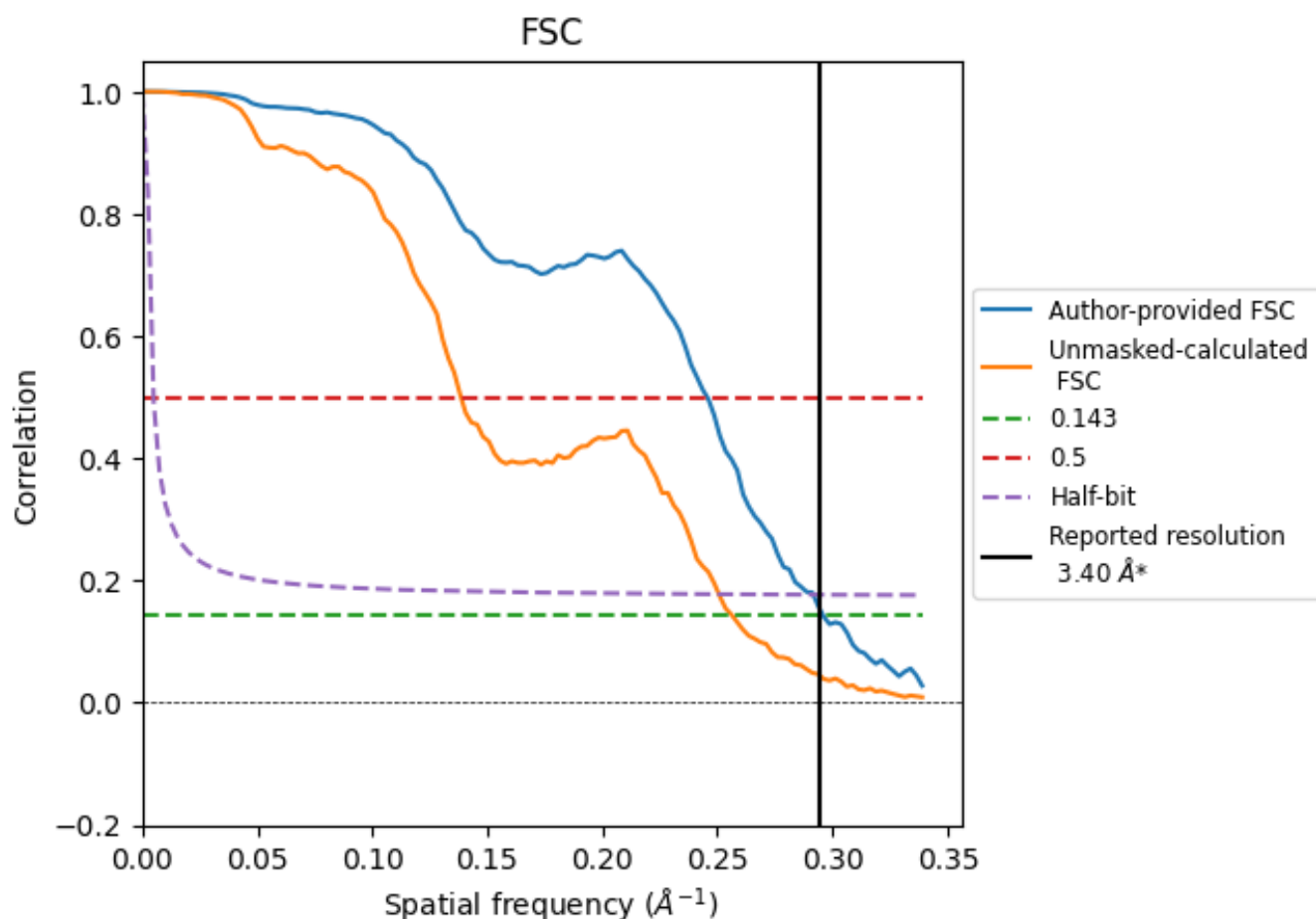


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates

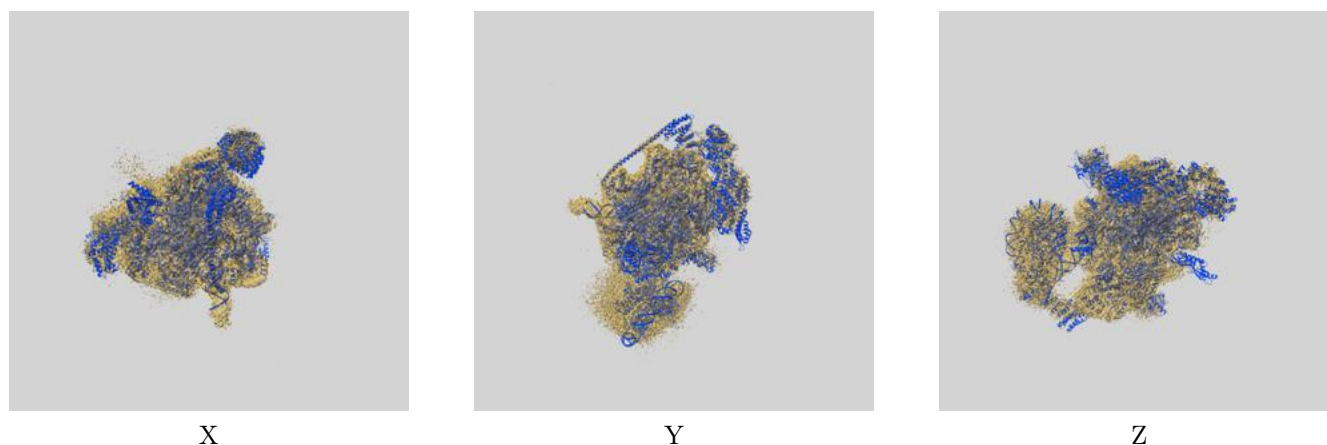
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.38	4.07	3.43
Unmasked-calculated*	3.90	7.22	3.99

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.90 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-66103 and PDB model 9WMS. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)

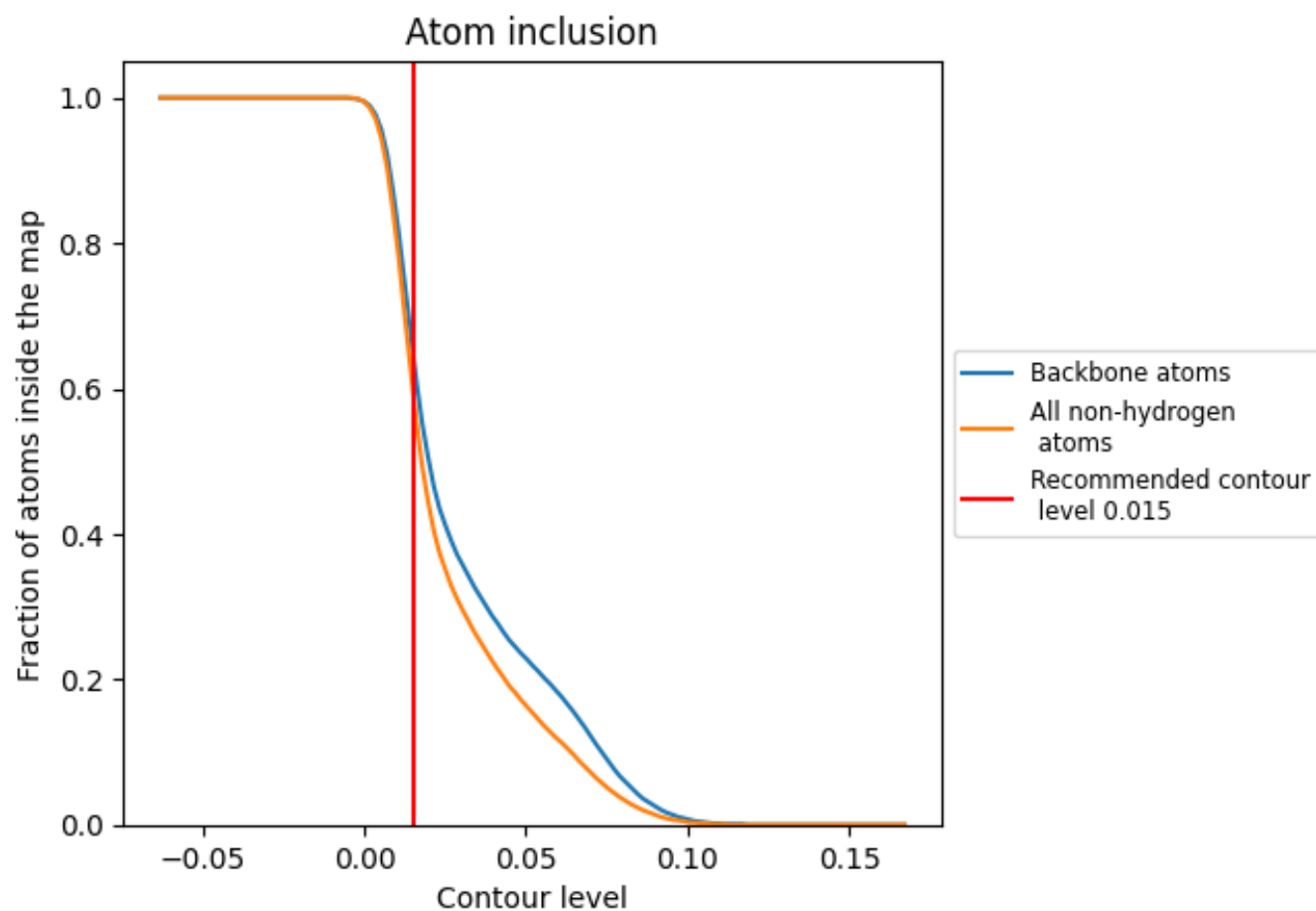


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6000	 0.2270
A	 0.9510	 0.4830
B	 0.9410	 0.4870
C	 0.9610	 0.5200
D	 0.7050	 0.1770
E	 0.9690	 0.4640
F	 0.9680	 0.5140
G	 0.7880	 0.2830
H	 0.9800	 0.5060
I	 0.9210	 0.3510
J	 0.9650	 0.5310
K	 0.9650	 0.5250
L	 0.9600	 0.4780
M	 0.8070	 0.1740
N	 0.4500	 0.0550
P	 0.8630	 0.3200
T	 0.5070	 0.1120
V	 0.8080	 0.0580
W	 0.6700	 0.1570
a	 0.5510	 -0.0070
b	 0.6170	 0.0310
c	 0.6930	 -0.0280
d	 0.6420	 0.0090
e	 0.5700	 0.0050
f	 0.3920	 -0.0290
g	 0.3160	 -0.0040
h	 0.3170	 0.0020
m	 0.4410	 0.0460
n	 0.7100	 0.1410
q	 0.1060	 0.0450
r	 0.1230	 0.1070
s	 0.2780	 0.0250
u	 0.1140	 0.0950
v	 0.0690	 0.0420
x	 0.3420	 0.2400

