



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 02:48 PM UTC

PDB ID : 6MZL / pdb_00006mzl
EMDB ID : EMD-9305
Title : Human TFIID canonical state
Authors : Patel, A.B.; Louder, R.K.; Greber, B.J.; Grunberg, S.; Luo, J.; Fang, J.; Liu, Y.; Ranish, J.; Hahn, S.; Nogales, E.
Deposited on : 2018-11-05
Resolution : 23.00 Å(reported)

This is a wwPDB EM 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/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
MolProbity : 4-5-2 with Phenix2.0
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

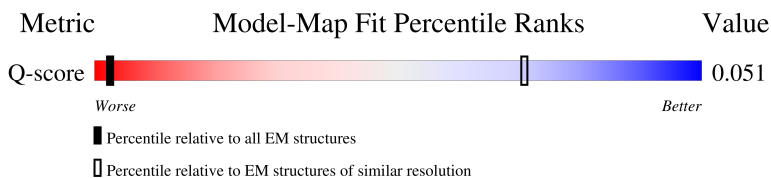
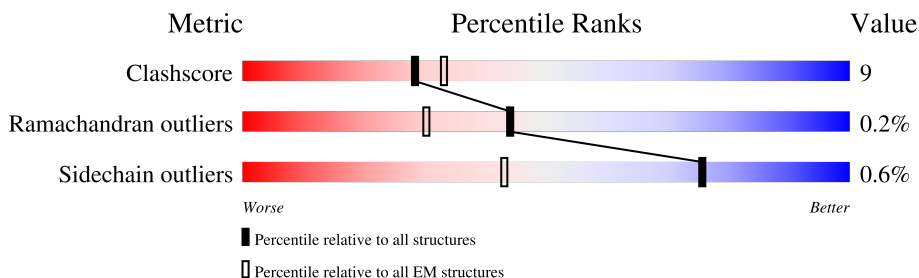
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 23.00 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.



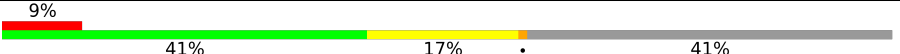
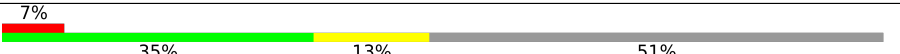
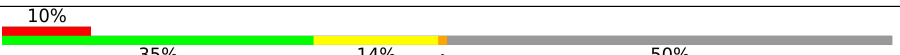
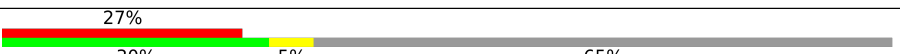
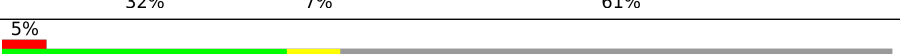
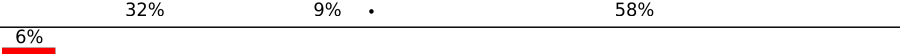
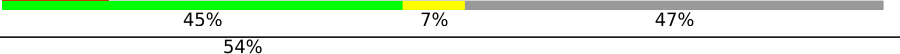
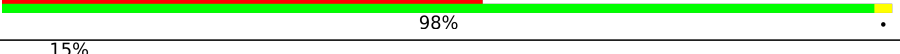
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	17 (22.90 - 23.50)

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	1872	14% 22% 75%
2	B	1199	16% 52% 28% 19%
3	C	929	9% 90%
4	D	1085	9% 91%

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Mol	Chain	Length	Quality of chain
4	E	1085	
5	F	800	
5	G	800	
6	H	677	
7	I	677	
8	J	349	
9	K	310	
10	L	264	
10	M	264	
11	N	218	
11	O	218	
12	P	211	
13	Q	161	
13	R	161	
14	S	124	
15	T	339	
16	Y	96	
17	Z	238	

2 Entry composition [i](#)

There are 17 unique types of molecules in this entry. The entry contains 36618 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 Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	472	Total	C	N	O	S	0	0
			3772	2397	659	693	23		

- Molecule 2 is a protein called Transcription initiation factor TFIID subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	968	Total	C	N	O	S	0	0
			7832	5031	1322	1421	58		

- Molecule 3 is a protein called Transcription initiation factor TFIID subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	93	Total	C	N	O	S	0	0
			742	467	128	141	6		

- Molecule 4 is a protein called Transcription initiation factor TFIID subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	102	Total	C	N	O	0	0
			686	423	130	133		
4	E	102	Total	C	N	O	0	0
			686	423	130	133		

- Molecule 5 is a protein called Transcription initiation factor TFIID subunit 5, TAF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	473	Total	C	N	O	S	0	0
			3646	2314	638	679	15		
5	G	473	Total	C	N	O	S	0	0
			3646	2314	638	679	15		

- Molecule 6 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	329	Total	C	N	O	S	0	0
			2494	1575	439	464	16		

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	339	Total	C	N	O	S	0	0
			2520	1585	445	474	16		

- Molecule 8 is a protein called Transcription initiation factor TFIID subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	123	Total	C	N	O	S	0	0
			998	638	184	172	4		

- Molecule 9 is a protein called Transcription initiation factor TFIID subunit 8,TAF8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	202	Total	C	N	O	S	0	0
			1449	906	260	278	5		

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 9, TAF9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	104	Total	C	N	O	S	0	0
			732	456	129	142	5		
10	M	104	Total	C	N	O	S	0	0
			732	456	129	142	5		

- Molecule 11 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	82	Total	C	N	O	S	0	0
			645	413	102	126	4		
11	O	82	Total	C	N	O	S	0	0
			645	413	102	126	4		

- Molecule 12 is a protein called Transcription initiation factor TFIID subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	89	Total	C	N	O	S	0	0
			707	447	127	128	5		

- Molecule 13 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	74	Total	C	N	O	S	0	0
			611	381	107	120	3		
13	R	74	Total	C	N	O	S	0	0
			611	381	107	120	3		

- Molecule 14 is a protein called Transcription initiation factor TFIID subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	45	Total	C	N	O	S	0	0
			365	233	54	73	5		

- Molecule 15 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	180	Total	C	N	O	S	0	0
			1429	927	252	243	7		

- Molecule 16 is a protein called poly(UNK).

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Y	96	Total	C	N	O	0	0
			480	288	96	96		

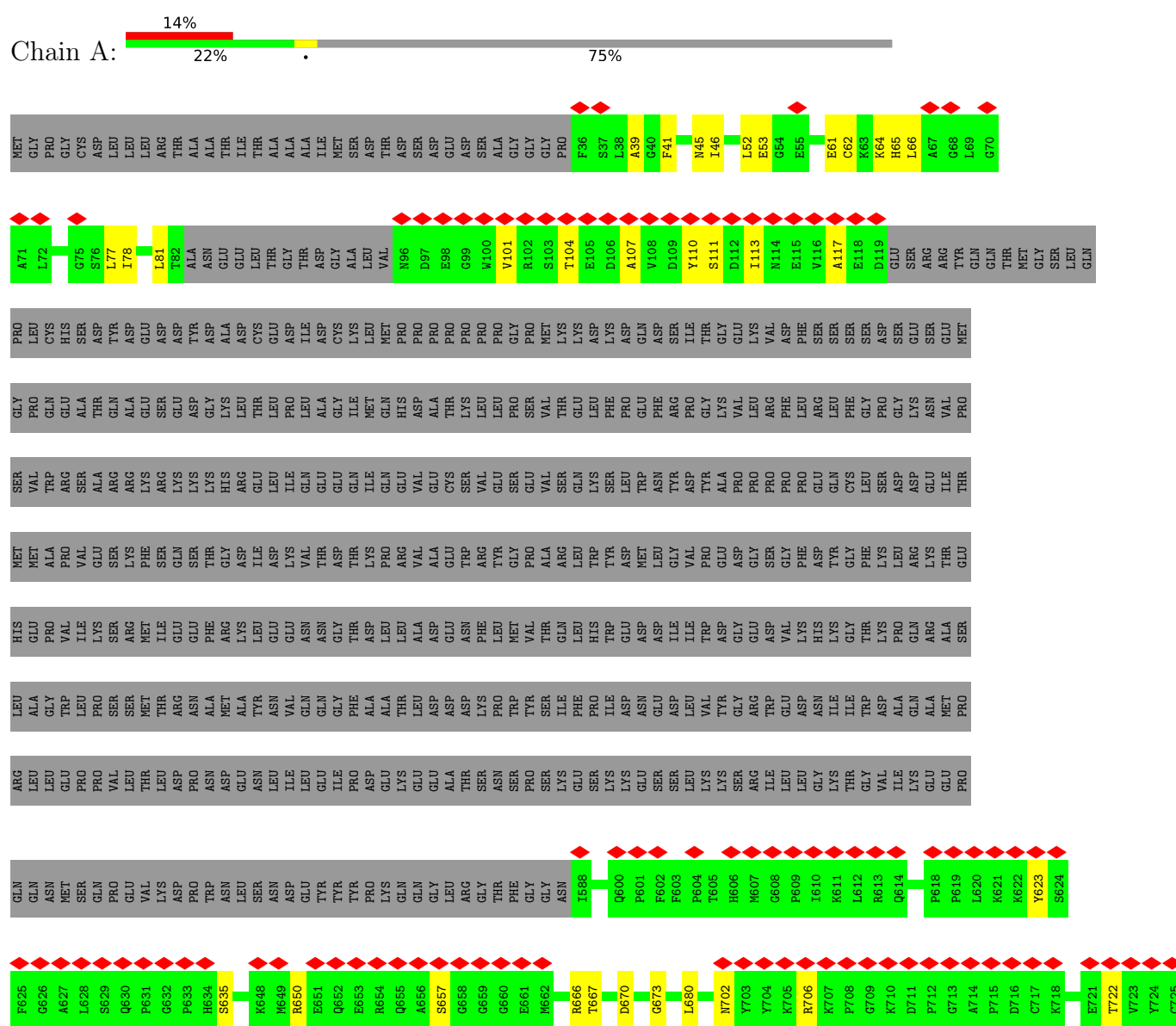
- Molecule 17 is a protein called poly(UNK).

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Z	238	Total	C	N	O	0	0
			1190	714	238	238		

3 Residue-property plots

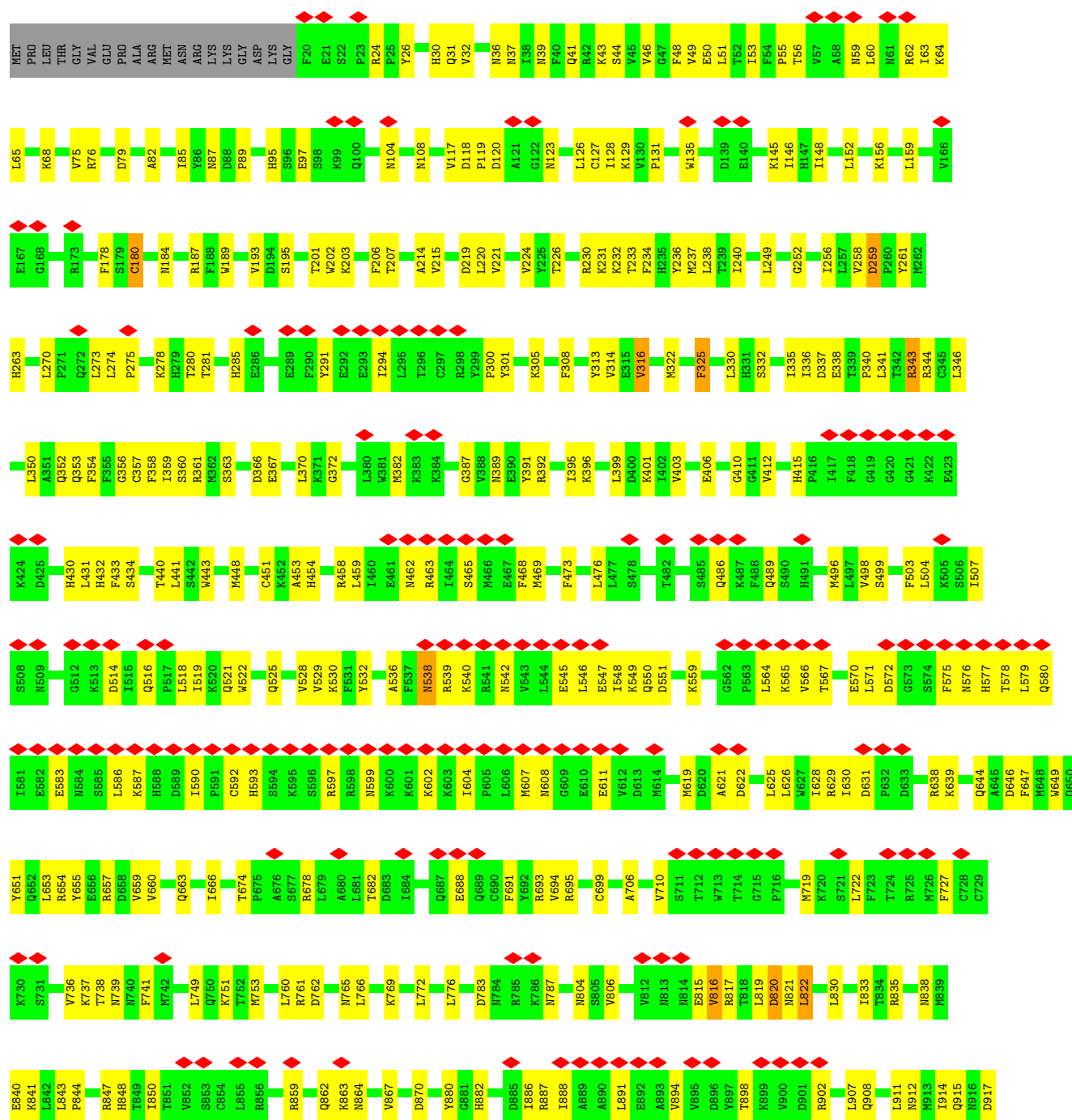
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Transcription initiation factor TFIID subunit 1





- Molecule 2: Transcription initiation factor TFIID subunit 2



MET	GLN	TRP	PHE	CYS	PRO	LYS	CYS	ALA	ASN	LYS	LYS	LYS	ASP	LYS	HIS	LYS	ARG	LYS	HIS	ALA	HIS																											
ARG	SER	VAL	THR	VAL	GLU	THR	VAL	SER	THR	TYR	VAL	ILE	ARG	ASP	GLU	GLY	ASN	GLN	ILE	TRP	CYS	PRO	GLY	CYS	ASN	LYS	PRO	ASP	ASP	GLY	SER	MET	ILE	GLY	CYS	ASP	CYS	ASP	ASP	TRP	TYR	THR	HIS	TRP	PRO	PRO	PRO	GLU

- Molecule 4: Transcription initiation factor TFIID subunit 4



Y934	ALA	GLN	VAL	LEU	LEU	SER	GLN	HIS	SER	LEU	ALA	PRO	GLY	PRO	PRO	HIS	MET
E935	VAL	ILE	SER	LEU	ALA	THR	ARG	ALA	GLN	ALA	ALA	PRO	PHE	GLY	ALA	VAL	ALA
Q936	ASN	GLN	THR	ARG	LEU	ILE	LYS	PRO	GLN	ARG	GLN	VAL	GLY	PRO	ALA	GLY	SER
A937	LEU	ASN	GLN	GLN	LEU	VAL	VAL	THR	GLN	ALA	GLY	ALA	ALA	PRO	LEU	SER	ASP
S938	SER	PRO	PRO	GLN	LEU	ALA	LEU	THR	THR	LEU	PRO	ALA	ALA	GLY	ARG	PRO	LEU
D939	GLU	LEU	THR	THR	THR	ALA	ALA	THR	THR	THR	THR	THR	ALA	LYS	PRO	ALA	LEU
I953	ALA	VAL	LYS	PHE	ALA	THR	THR	THR	THR	PRO	SER	THR	ALA	LYS	PRO	ALA	LEU
E954	ARG	VAL	VAL	SER	GLY	VAL	VAL	ARG	PRO	VAL	SER	ALA	ALA	GLY	ALA	ALA	PHE
K955	ILE	VAL	GLY	ALA	SER	GLY	GLY	ALA	PRO	ALA	ALA	PRO	ALA	PRO	GLY	ALA	PHE
Q956	LEU	VAL	GLN	ILE	GLU	THR	ALA	PRO	ARG	ILE	VAL	PRO	ALA	ALA	GLY	GLY	ASN
R957	ALA	VAL	GLN	THR	THR	THR	ALA	THR	THR	THR	GLY	ALA	SER	GLN	PRO	GLY	SER
K958	ASN	PRO	PRO	GLN	GLN	THR	ALA	SER	SER	PRO	PRO	ALA	ALA	SER	ALA	ALA	GLY
D959	SER	ALA	GLN	GLN	ALA	ALA	GLN	ALA	GLN	THR	ALA	PRO	PRO	CYS	ALA	VAL	VAL
E960	GLU	VAL	THR	SER	ASN	ALA	THR	PRO	PRO	MET	ALA	ALA	ALA	ASN	PRO	PRO	ASP
Q961	LEU	LEU	PRO	GLN	VAL	ASN	VAL	PRO	PRO	GLN	GLY	ALA	ALA	ASN	VAL	GLU	LYS
E962	VAL	GLY	PRO	GLN	GLN	LYS	VAL	VAL	VAL	GLY	GLY	PRO	PRO	SER	VAL	ALA	VAL
R963	THR	THR	VAL	VAL	VAL	GLU	GLY	GLN	GLN	ALA	ALA	ALA	ALA	ALA	ALA	ALA	SER
E964	LEU	LYS	ILE	ILE	PRO	LEU	THR	ILE	ILE	THR	PRO	ALA	ALA	ALA	ALA	GLY	ASP
R965	THR	ALA	GLN	GLN	PRO	VAL	THR	SER	THR	THR	SER	VAL	ALA	LEU	ALA	ALA	LEU
I966	ARG	LEU	PRO	THR	GLN	GLN	GLN	THR	THR	ASN	SER	VAL	VAL	LEU	ALA	ALA	VAL
L966	SER	ALA	PRO	SER	LEU	ASN	LEU	GLN	GLN	ILE	GLN	SER	ALA	ASN	ALA	PRO	GLY
M967	CYS	VAL	VAL	LYS	GLN	GLN	GLN	ALA	ALA	ALA	ASN	ALA	GLN	HIS	ALA	GLU	SER
R968	LYS	VAL	VAL	VAL	LYS	ASP	THR	PRO	PRO	GLY	PHE	VAL	VAL	GLY	PRO	PRO	LEU
	ASP	SER	PRO	ALA	THR	GLY	GLY	GLY	GLY	GLN	GLN	PRO	PRO	ALA	PRO	PRO	GLU
E970	E970	ALA	GLN	ALA	LEU	LYS	THR	THR	THR	LEU	LEU	PRO	PRO	ALA	ALA	ALA	SER
K971	L873	GLN	GLN	ILE	ILE	ILE	GLU	ILE	ILE	GLN	ALA	ALA	PRO	PRO	ALA	GLY	GLY
SER	E884	LYS	GLN	VAL	VAL	PHE	GLN	ARG	VAL	THR	THR	ALA	ALA	SER	GLY	GLY	SER
ARG	T885	ASN	VAL	VAL	LEU	THR	VAL	THR	VAL	VAL	THR	ALA	THR	LEU	ALA	GLY	ALA
GLN	Q886	ASN	VAL	LEU	SER	THR	GLY	THR	GLY	GLY	GLY	ALA	ALA	VAL	ALA	ALA	ARG
GLU	K887	LYS	THR	SER	SER	SER	ALA	THR	ARG	THR	ALA	ALA	THR	ASN	LYS	GLY	HIS
ASP	K888	LEU	THR	LEU	ARG	THR	THR	PRO	SER	LEU	PRO	PRO	LEU	ASN	PRO	GLY	HIS
PRO	H889	LYS	THR	SER	SER	LEU	THR	THR	THR	GLY	ALA	ALA	ALA	ALA	GLY	GLY	HIS
GLU		GLU	GLN	VAL	TYR	THR	THR	THR	ASN	LYS	VAL	ARG	ARG	PRO	PRO	PRO	HIS
GLN	T892	PRO	PRO	GLN	ARG	THR	THR	ILE	THR	GLY	LYS	PRO	ALA	ALA	GLN	GLN	LEU
LEU	E893	GLY	PRO	ARG	GLU	GLU	SER	ILE	GLN	GLY	LYS	PRO	PRO	ALA	ALA	ARG	ARG
LEU	L894	GLY	THR	THR	LEU	LEU	ALA	GLN	GLY	ALA	GLY	GLY	GLY	LEU	LEU	GLY	ARG
ARG																	
LEU	V899	GLY	VAL	ALA	ASN	SER	THR	VAL	THR	ALA	PRO	PRO	ALA	PRO	ALA	PRO	THR
LYS		SER	LEU	LEU	SER	SER	THR	THR	ILE	MET	LYS	ALA	ALA	PRO	ALA	PRO	THR
GLN		PHE	LEU	ARG	SER	PRO	GLU	SER	THR	VAL	ARG	LYS	PRO	LEU	ALA	PRO	THR
LYS	H904	ARG	THR	THR	THR	PRO	THR	GLN	GLN	THR	THR	THR	PRO	LEU	ALA	PRO	GLU
ALA		ASP	GLN	ALA	GLN	GLN	MET	ALA	GLN	GLN	VAL	VAL	PRO	LYS	ALA	PRO	GLY
LYS	Q907	ASP	PRO	PRO	ALA	ALA	GLU	GLN	GLN	SER	SER	THR	PRO	PRO	ARG	ARG	ARG
GLU	Q908	GLY	HIS	ASN	THR	THR	TYR	THR	ALA	ALA	GLN	GLN	THR	ALA	PRO	ARG	ALA
MET		ASP	ASP	VAL	VAL	VAL	VAL	THR	SER	SER	GLN	GLN	ALA	ALA	PRO	ALA	ALA
GLN	Q911	ILE	ARG	THR	THR	THR	VAL	THR	VAL	ALA	SER	ARG	ALA	PRO	PRO	LEU	ALA
GLN		ASN	ILE	SER	THR	THR	ILE	GLN	VAL	ALA	ALA	THR	ALA	PRO	GLY	VAL	ALA
GLN	V914	ASP	ASP	ILE	ALA	PHE	ALA	PRO	GLN	MET	GLN	PRO	ALA	GLY	VAL	PRO	ALA
LEU		VAL	VAL	LEU	LEU	LEU	LEU	SER	THR	THR	THR	THR	VAL	THR	GLY	ALA	ALA
LEU	K929	ALA	THR	GLN	GLN	LYS	ASN	ALA	ALA	ALA	ALA	THR	ALA	ILE	PRO	GLY	LEU
ALA	D930	THR	THR	PRO	PRO	SER	PHE	THR	THR	THR	THR	THR	THR	THR	PRO	PRO	ASN



ARG	LVS	ARG	VAL	ASP	CYS	PRO	GLY	GLY	SER	SER	GLY	ALA	GLU	GLY	SER	GLY	VAL	VAL	PRO	GLY	SER	SER	GLY	VAL	GLY	THR	THR	ARG	ARG	GLN	PHE	THR	ARG	ASN	LEU	ARG	ASP	LEU	TLE	ILE	THR	ARG	VAL	ASN	LEU	ARG	CYS	PHE	TYR	THR	GLU	ASN	GLU	THR	STR																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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- Molecule 5: Transcription initiation factor TFIID subunit 5, TAF5



NET	ALA	ALA	LEU	ALA	GLU	GLN	THR	GLU	VAL	ALA	VAL	LYS	LEU	GLU	PRO	PRO	THR	THR	LEU	LEU	PRO	PRO	GLN	GLY	GLY	ASP	GLY	ALA	ALA	GLY	GLY	GLY	SER	GLY	GLY	THR	THR	ASN	ASN	GLY	ASN	PRO	ASN	GLY	GLY	GLY	GLY	ASN	VAL	ALA	ALA	SER	SER	SER	THR	GLY	GLY	ASP
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GLY	GLY	THR	PRO	LYS	PRO	THR	VAL	ALA	ALA	SER	ALA	ALA	ALA	ALA	ALA	PRO	PRO	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ASP	ASP	GLN	THR	LEU	LEU	ALA	ALA	VAL	VAL	LEU	GLN	PHE	LEU	LEU	ARG	GLN	GLN	SER	LYS	LEU	LEU	ARG	ARG	ARG	GLU	ALA
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GLY	LEU	LEU	GLU	GLU	ALA	VAL	VAL	ALA	GLY	SER	GLY	ALA	ALA	PRO	PRO	GLY	GLY	THR	THR	VAL	VAL	SER	GLY	SER	SER	ALA	ALA	SER	GLY
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PRO ALA ALA PRO GLY LYS VAL GLY SER VAL VAL GLU ASP GLN PRO ASP VAL SER ALA VAL LEU SER ALA TYR ASN GLN GLN GLY	D2 I10	S219 G220 L221 K222 H223 F224 I225 E226 C227 S228 L229 D230 C231 H232 H233 A234 E235 L236 T237 Q238 L239 F240 Y241 L251 A260 V266	
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F267	H268	G269	D270	Q271	E272		D277	T286	K287	L288	T302	I309	S310	R311	D312	S313	Y314	Q315	L316	L317	R318	R319	H320	L321	Q322	E323	K324	N327	T332	V333	Q334	E335	H336	L337	V338	I339	D340	I341	F342	D343	GLY	MET	PRO	ARG	SER	LYS	GLN	ILE	ASP	ALA	VAL	PHE	THR	ASN	TRP	NET
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VAL	GLY	SER	LEU	ALA	GLY	GLU	ALA	LYS	ARG	GLU	ALA	ASN	LYS	SER	LYS	VAL	PHE	PHE	GLY	LEU	LEU	LYS	GLU	PRO	PRO	LEU	ASP	ASP	GLU	ASP	GLU	GLU	GLU	GLY	LYS	PRO	LYS	LYS	LYS	LYS	PRO	LYS	LYS	LYS	ASP	SER	GLY	ILE	GLY	SER	LYS	SER	LYS	LYS
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LYS	GLN	ASP	PRO	ASN	ALA	PRO	PRO	GLN	ASN	ARG	ILE	PRO	LEU	PRO	GLU	LEU	LYS	ASP	SER	ASP	LYS	LEU	LEU	LYS	ILE	ILE	MET	ASN	MET	LYS	GLU	THR	THR	LYS	ARG	VAL	ARG	LEU	GLY	PRO	ASP	CYS	L458	L461	N468	Q471	Q472	A475	T479	D491	X496	K499	F490
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X501	X502	X503	X504	X505	X506	X507	X508	X509	X510	X511	X512	X513	X514	X515	X516	X517	X518	X519	X520	X521	X522	X523	X524	X525	X526	X527	X528	X529	X530	X531	X532	X533	X534	X535	X536	X537	X538	X539	X540	X541	X542	X543	X544	X545	X546	X547	X548	X549	X550	X551	X552	X553	X554	X555	X556	X557	X558	X559	X560	X561	X562	X563	X564	X565	X566	X567	X568	X569	X570	X571	X572	X573	X574	X575	X576	X577	X578	X579	X580	X581	X582	X583	X584	X585	X586	X587	X588	X589	X590	X591	X592	X593	X594	X595	X596	X597	X598	X599	X600	X601	X602	X603	X604	X605	X606	X607	X608	X609	X610	X611	X612	X613	X614	X615	X616	X617	X618	X619	X620	X621	X622	X623	X624	X625	X626	X627	X628	X629	X630	X631	X632	X633	X634	X635	X636	X637	X638	X639	X640	X641	X642	X643	X644	X645	X646	X647	X648	X649	X650	X651	X652	X653	X654	X655	X656	X657	X658	X659	X660	X661	X662	X663	X664	X665	X666	X667	X668	X669	X670	X671	X672	X673	X674	X675	X676	X677	X678	X679	X680	X681	X682	X683	X684	X685	X686	X687	X688	X689	X690	X691	X692	X693	X694	X695	X696	X697	X698	X699	X700	X701	X702	X703	X704	X705	X706	X707	X708	X709	X710	X711	X712	X713	X714	X715	X716	X717	X718	X719	X720	X721	X722	X723	X724	X725	X726	X727	X728	X729	X730	X731	X732	X733	X734	X735	X736	X737	X738	X739	X740	X741	X742	X743	X744	X745	X746	X747	X748	X749	X750	X751	X752	X753	X754	X755	X756	X757	X758	X759	X760	X761	X762	X763	X764	X765	X766	X767	X768	X769	X770	X771	X772	X773	X774	X775	X776	X777	X778	X779	X780	X781	X782	X783	X784	X785	X786	X787	X788	X789	X790	X791	X792	X793	X794	X795	X796	X797	X798	X799	X800	X801	X802	X803	X804	X805	X806	X807	X808	X809	X810	X811	X812	X813	X814	X815	X816	X817	X818	X819	X820	X821	X822	X823	X824	X825	X826	X827	X828	X829	X830	X831	X832	X833	X834	X835	X836	X837	X838	X839	X840	X841	X842	X843	X844	X845	X846	X847	X848	X849	X850	X851	X852	X853	X854	X855	X856	X857	X858	X859	X860	X861	X862	X863	X864	X865	X866	X867	X868	X869	X870	X871	X872	X873	X874	X875	X876	X877	X878	X879	X880	X881	X882	X883	X884	X885	X886	X887	X888	X889	X890	X891	X892	X893	X894	X895	X896	X897	X898	X899	X900	X901	X902	X903	X904	X905	X906	X907	X908	X909	X910	X911	X912	X913	X914	X915	X916	X917	X918	X919	X920	X921	X922	X923	X924	X925	X926	X927	X928	X929	X930	X931	X932	X933	X934	X935	X936	X937	X938	X939	X940	X941	X942	X943	X944	X945	X946	X947	X948	X949	X950	X951	X952	X953	X954	X955	X956	X957	X958	X959	X960	X961	X962	X963	X964	X965	X966	X967	X968	X969	X970	X971	X972	X973	X974	X975	X976	X977	X978	X979	X980	X981	X982	X983	X984	X985	X986	X987	X988	X989	X990	X991	X992	X993	X994	X995	X996	X997	X998	X999	X1000
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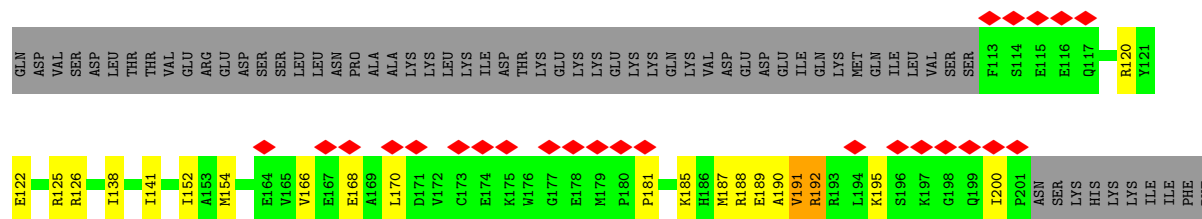
[illegible]

PRO	GLN
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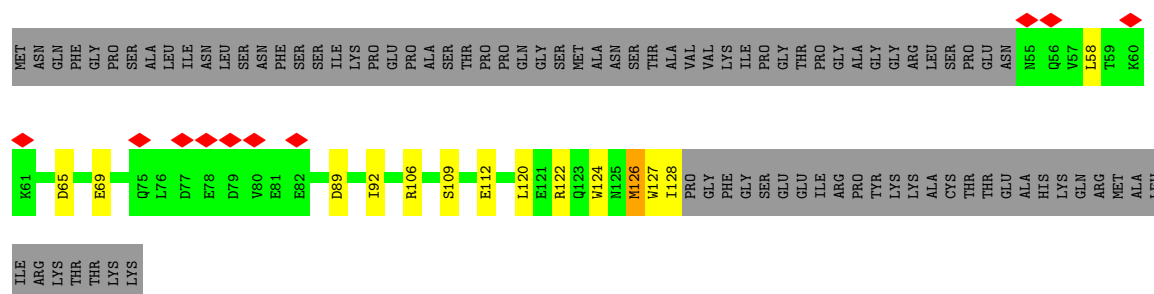
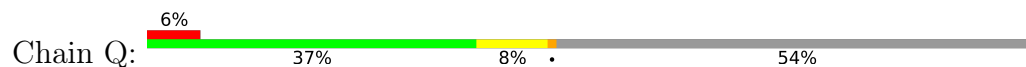
- Molecule 5: Transcription initiation factor TFIID subunit 5, TAF5



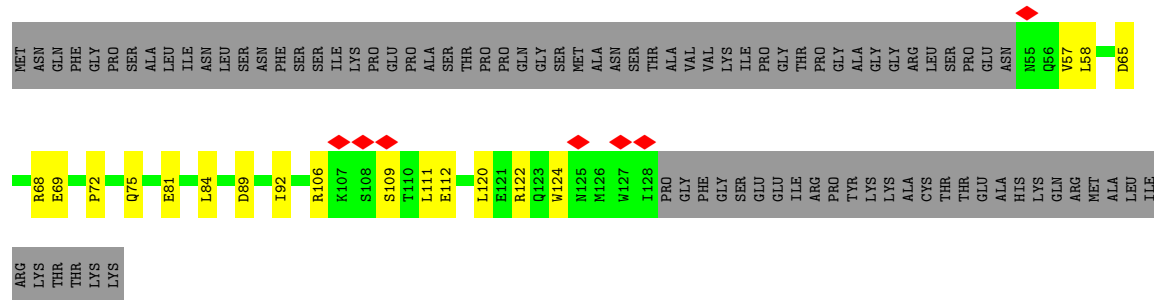
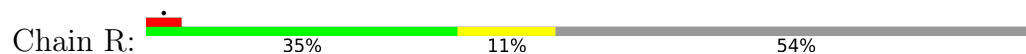
MET	ALA	ALA	LEU	ALA	GLU	GLN	THR	GLU	VAL	ALA	VAL	LYS	LEU	GLU	PRO	GLY	PRO	LEU	LEU	PRO	PRO	GLN	ALA	GLY	ASP	GLY	ALA	GLY	GLY	SER	GLY	GLY	THR	THR	ASN	ASN	GLY	PRO	ASN	GLY	GLY	GLY	GLY	VAL	ALA	ALA	SER	SER	THR	GLY	GLY	ASP
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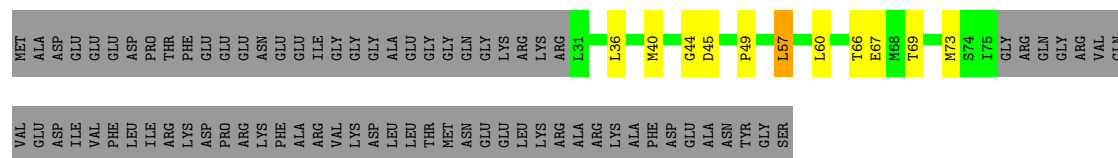
• Molecule 13: Transcription initiation factor TFIID subunit 12



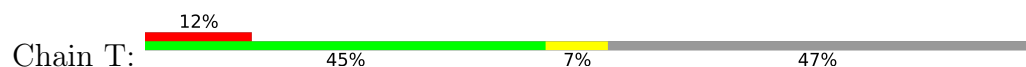
• Molecule 13: Transcription initiation factor TFIID subunit 12

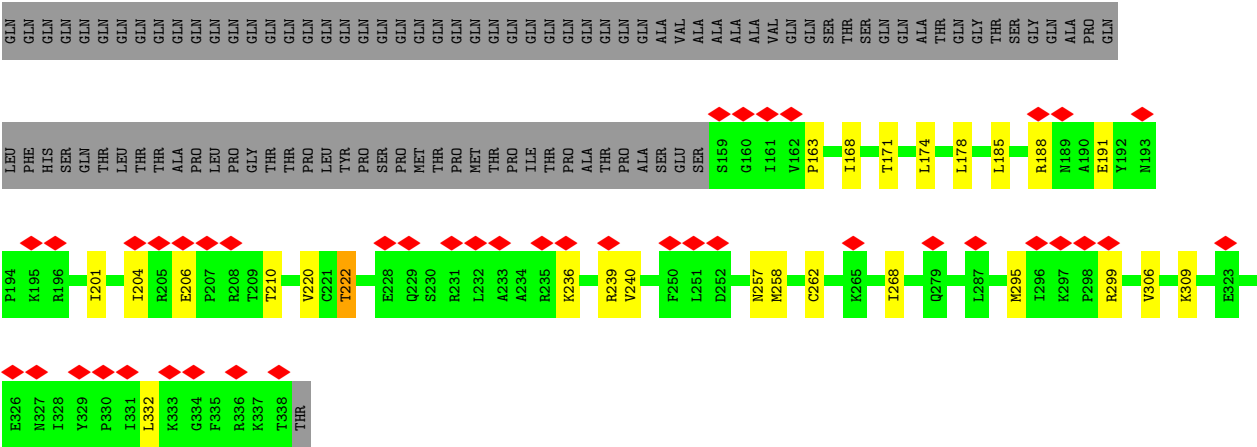


• Molecule 14: Transcription initiation factor TFIID subunit 13

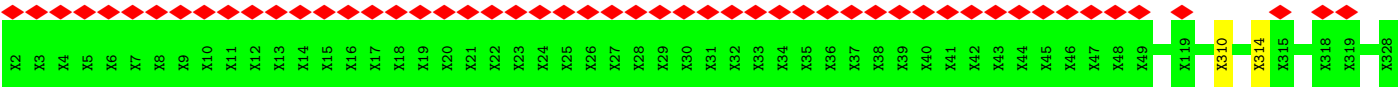


• Molecule 15: TATA-box-binding protein

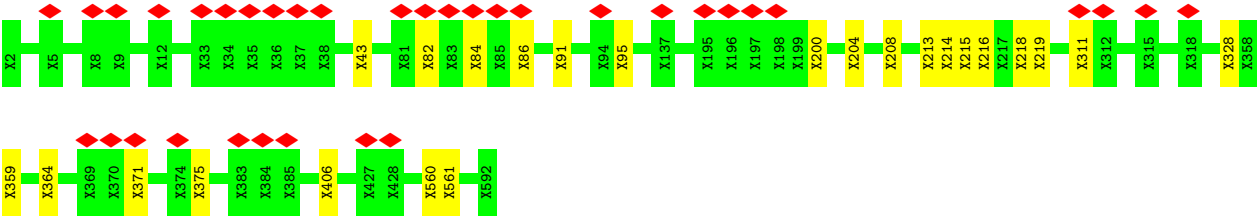
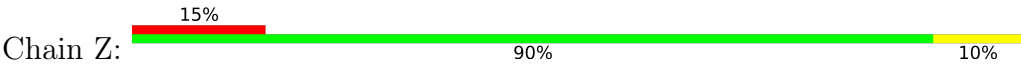




● Molecule 16: poly(UNK)



● Molecule 17: poly(UNK)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	107900	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.065	Depositor
Minimum map value	-0.017	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	380.16, 380.16, 380.16	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.64, 2.64, 2.64	Depositor

5 Model quality

5.1 Standard geometry

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	0.19	0/3858	0.51	3/5193 (0.1%)
2	B	0.53	0/8029	0.85	7/10882 (0.1%)
3	C	0.24	0/757	0.53	0/1027
4	D	0.31	0/692	0.70	3/945 (0.3%)
4	E	0.29	0/692	0.52	0/945
5	F	0.22	0/3537	0.59	0/4802
5	G	0.50	0/3537	0.81	4/4802 (0.1%)
6	H	0.46	0/2533	0.75	1/3439 (0.0%)
7	I	0.42	0/2506	0.77	3/3402 (0.1%)
8	J	0.23	0/1017	0.52	0/1370
9	K	0.41	0/1212	0.65	0/1640
10	L	0.18	0/705	0.50	0/955
10	M	0.32	0/705	0.69	0/955
11	N	0.21	0/657	0.48	0/891
11	O	0.32	0/657	0.55	0/891
12	P	0.34	0/719	0.89	3/965 (0.3%)
13	Q	0.26	0/618	0.65	1/835 (0.1%)
13	R	0.27	0/618	0.59	0/835
14	S	0.24	0/371	0.68	0/498
15	T	0.28	0/1455	0.59	0/1958
All	All	0.39	0/34875	0.71	25/47230 (0.1%)

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
2	B	0	17
5	F	0	3
5	G	0	8
6	H	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	I	0	4
9	K	0	2
10	M	0	1
17	Z	0	1
All	All	0	43

There are no bond length outliers.

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	908	GLN	CB-CG-CD	7.70	125.69	112.60
7	I	261	THR	CA-C-N	-7.45	109.75	122.56
7	I	261	THR	C-N-CA	-7.45	109.75	122.56
1	A	657	SER	N-CA-C	6.79	120.81	111.71
12	P	192	ARG	CB-CG-CD	-6.25	96.92	111.30

There are no chirality outliers.

5 of 43 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	949	GLU	Peptide
2	B	193	VAL	Peptide
2	B	259	ASP	Peptide
2	B	316	VAL	Peptide
2	B	325	PHE	Peptide

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	3772	0	3742	43	0
2	B	7832	0	7789	223	0
3	C	742	0	719	8	0
4	D	686	0	572	8	0
4	E	686	0	572	13	0
5	F	3646	0	3312	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	3646	0	3312	94	0
6	H	2494	0	2474	58	0
7	I	2520	0	2422	65	0
8	J	998	0	1055	12	0
9	K	1449	0	1281	34	0
10	L	732	0	624	6	0
10	M	732	0	624	13	0
11	N	645	0	640	7	0
11	O	645	0	640	15	0
12	P	707	0	730	26	0
13	Q	611	0	610	16	0
13	R	611	0	610	16	0
14	S	365	0	351	12	0
15	T	1429	0	1521	19	0
16	Y	480	0	112	1	0
17	Z	1190	0	280	17	0
All	All	36618	0	33992	667	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 9.

The worst 5 of 667 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:874:GLU:HG2	2:B:468:PHE:HZ	1.27	0.99
2:B:566:VAL:O	2:B:577:HIS:HA	1.64	0.97
2:B:532:TYR:O	2:B:551:ASP:HB2	1.67	0.94
2:B:50:GLU:HA	2:B:146:ILE:O	1.70	0.92
1:A:874:GLU:HG2	2:B:468:PHE:CZ	2.04	0.91

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	462/1872 (25%)	454 (98%)	7 (2%)	1 (0%)	43	78
2	B	966/1199 (81%)	781 (81%)	183 (19%)	2 (0%)	43	78
3	C	91/929 (10%)	89 (98%)	2 (2%)	0	100	100
4	D	100/1085 (9%)	93 (93%)	7 (7%)	0	100	100
4	E	100/1085 (9%)	94 (94%)	6 (6%)	0	100	100
5	F	429/800 (54%)	382 (89%)	47 (11%)	0	100	100
5	G	429/800 (54%)	352 (82%)	77 (18%)	0	100	100
6	H	325/677 (48%)	293 (90%)	31 (10%)	1 (0%)	36	72
7	I	326/677 (48%)	292 (90%)	32 (10%)	2 (1%)	21	59
8	J	119/349 (34%)	117 (98%)	2 (2%)	0	100	100
9	K	149/310 (48%)	133 (89%)	15 (10%)	1 (1%)	18	56
10	L	96/264 (36%)	93 (97%)	3 (3%)	0	100	100
10	M	96/264 (36%)	89 (93%)	7 (7%)	0	100	100
11	N	78/218 (36%)	75 (96%)	3 (4%)	0	100	100
11	O	78/218 (36%)	74 (95%)	4 (5%)	0	100	100
12	P	87/211 (41%)	86 (99%)	1 (1%)	0	100	100
13	Q	72/161 (45%)	71 (99%)	1 (1%)	0	100	100
13	R	72/161 (45%)	68 (94%)	4 (6%)	0	100	100
14	S	43/124 (35%)	43 (100%)	0	0	100	100
15	T	178/339 (52%)	177 (99%)	1 (1%)	0	100	100
All	All	4296/11743 (37%)	3856 (90%)	433 (10%)	7 (0%)	44	78

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	950	VAL
7	I	256	LEU
6	H	321	PRO
7	I	257	PRO
9	K	218	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	407/1665 (24%)	407 (100%)	0	100	100
2	B	879/1083 (81%)	874 (99%)	5 (1%)	78	83
3	C	83/833 (10%)	82 (99%)	1 (1%)	63	75
4	D	52/815 (6%)	51 (98%)	1 (2%)	50	67
4	E	52/815 (6%)	52 (100%)	0	100	100
5	F	367/619 (59%)	366 (100%)	1 (0%)	86	86
5	G	367/619 (59%)	360 (98%)	7 (2%)	50	67
6	H	260/574 (45%)	259 (100%)	1 (0%)	84	84
7	I	252/564 (45%)	251 (100%)	1 (0%)	84	84
8	J	113/322 (35%)	113 (100%)	0	100	100
9	K	132/223 (59%)	132 (100%)	0	100	100
10	L	61/229 (27%)	60 (98%)	1 (2%)	55	70
10	M	61/229 (27%)	60 (98%)	1 (2%)	55	70
11	N	71/154 (46%)	71 (100%)	0	100	100
11	O	71/154 (46%)	71 (100%)	0	100	100
12	P	78/182 (43%)	77 (99%)	1 (1%)	61	74
13	Q	70/141 (50%)	70 (100%)	0	100	100
13	R	70/141 (50%)	70 (100%)	0	100	100
14	S	42/106 (40%)	41 (98%)	1 (2%)	43	64
15	T	155/293 (53%)	154 (99%)	1 (1%)	78	83
All	All	3643/9761 (37%)	3621 (99%)	22 (1%)	76	83

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	G	780	VAL
10	L	73	LEU
7	I	347	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	M	73	LEU
4	D	908	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
5	G	636	HIS
9	K	30	HIS
5	G	784	HIS
7	I	64	GLN
10	M	37	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
17	Z	8
16	Y	2

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Z	95:UNK	C	119:UNK	N	129.81
1	Z	52:UNK	C	81:UNK	N	116.40
1	Z	143:UNK	C	195:UNK	N	95.92
1	Z	223:UNK	C	309:UNK	N	54.56
1	Y	143:UNK	C	309:UNK	N	54.12

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9305. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary 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: 72



Y Index: 72



Z Index: 72

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: 79



Y Index: 62

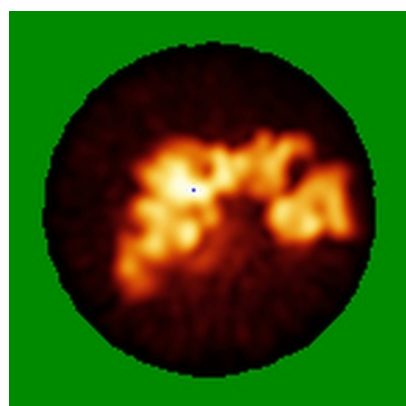


Z Index: 80

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

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

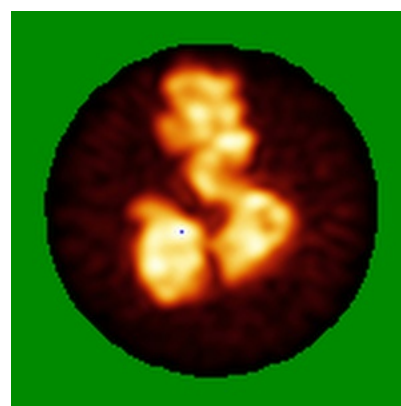
6.4.1 Primary map



X



Y

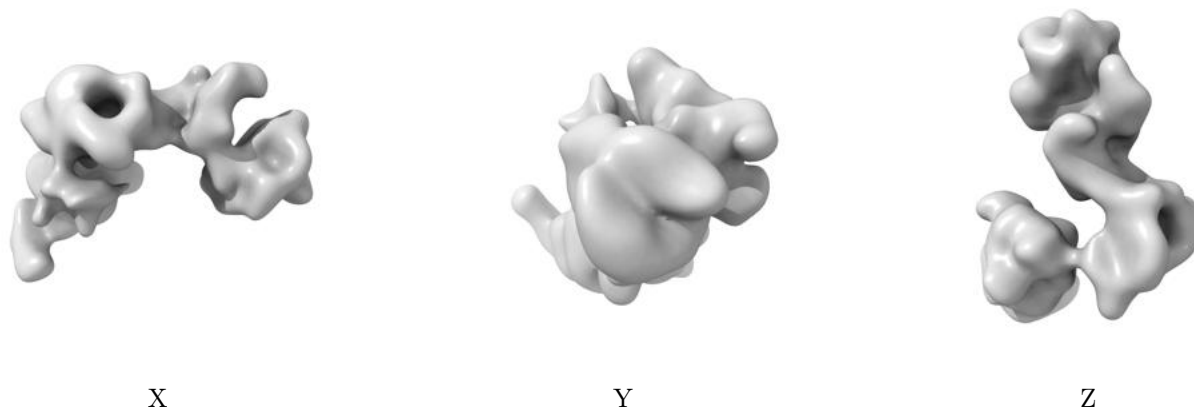


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

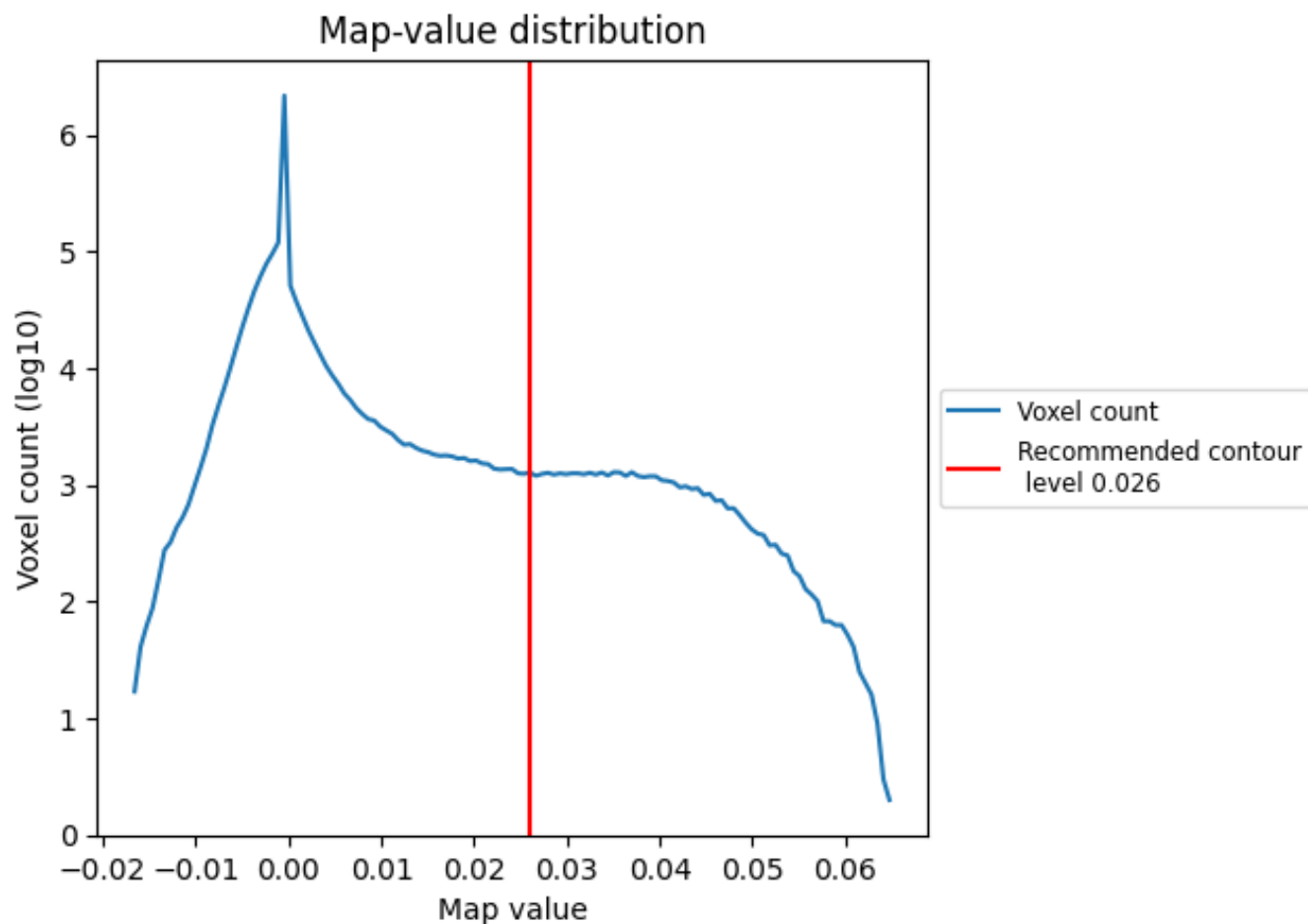
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

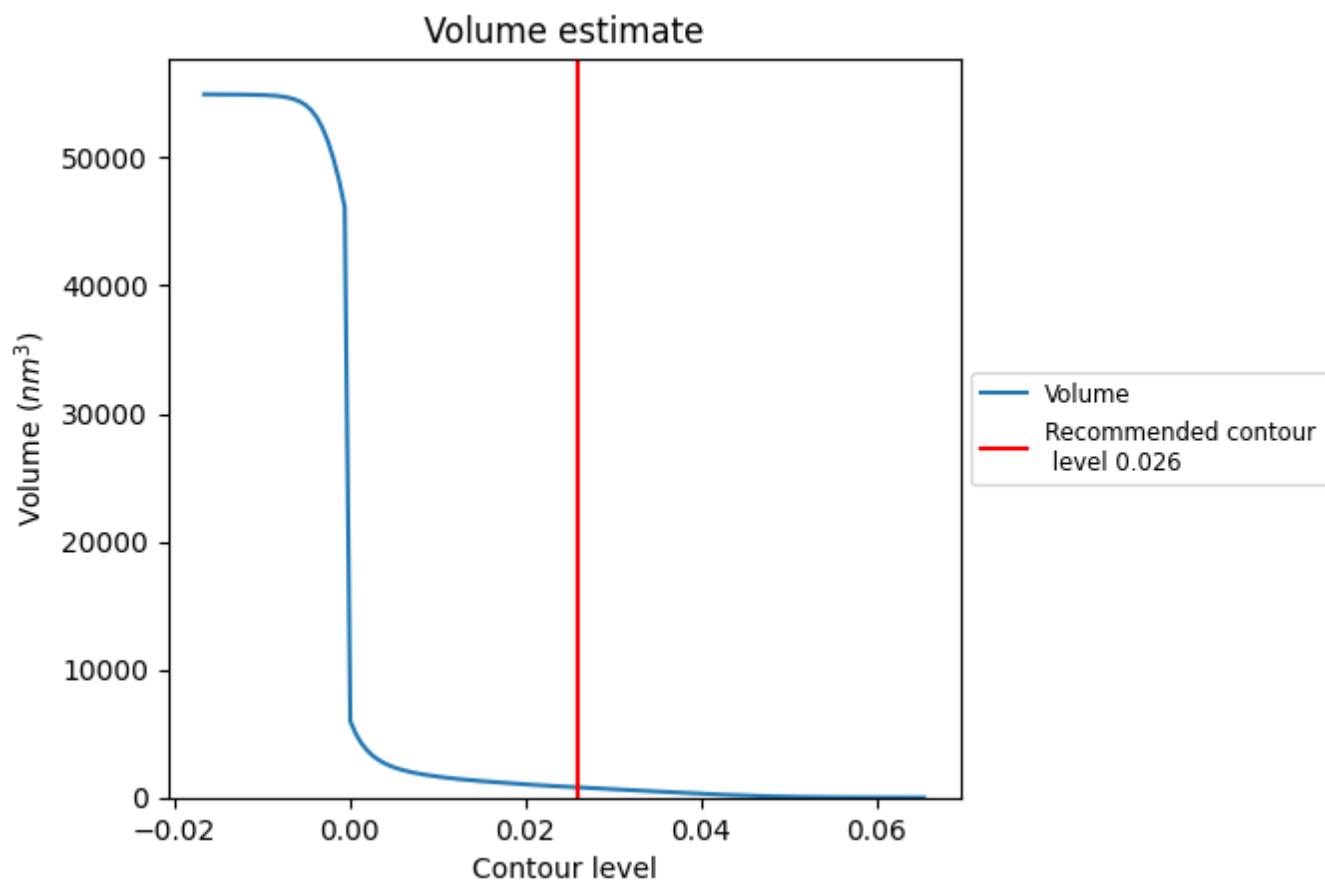
This section contains the results of statistical analysis of the map.

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.

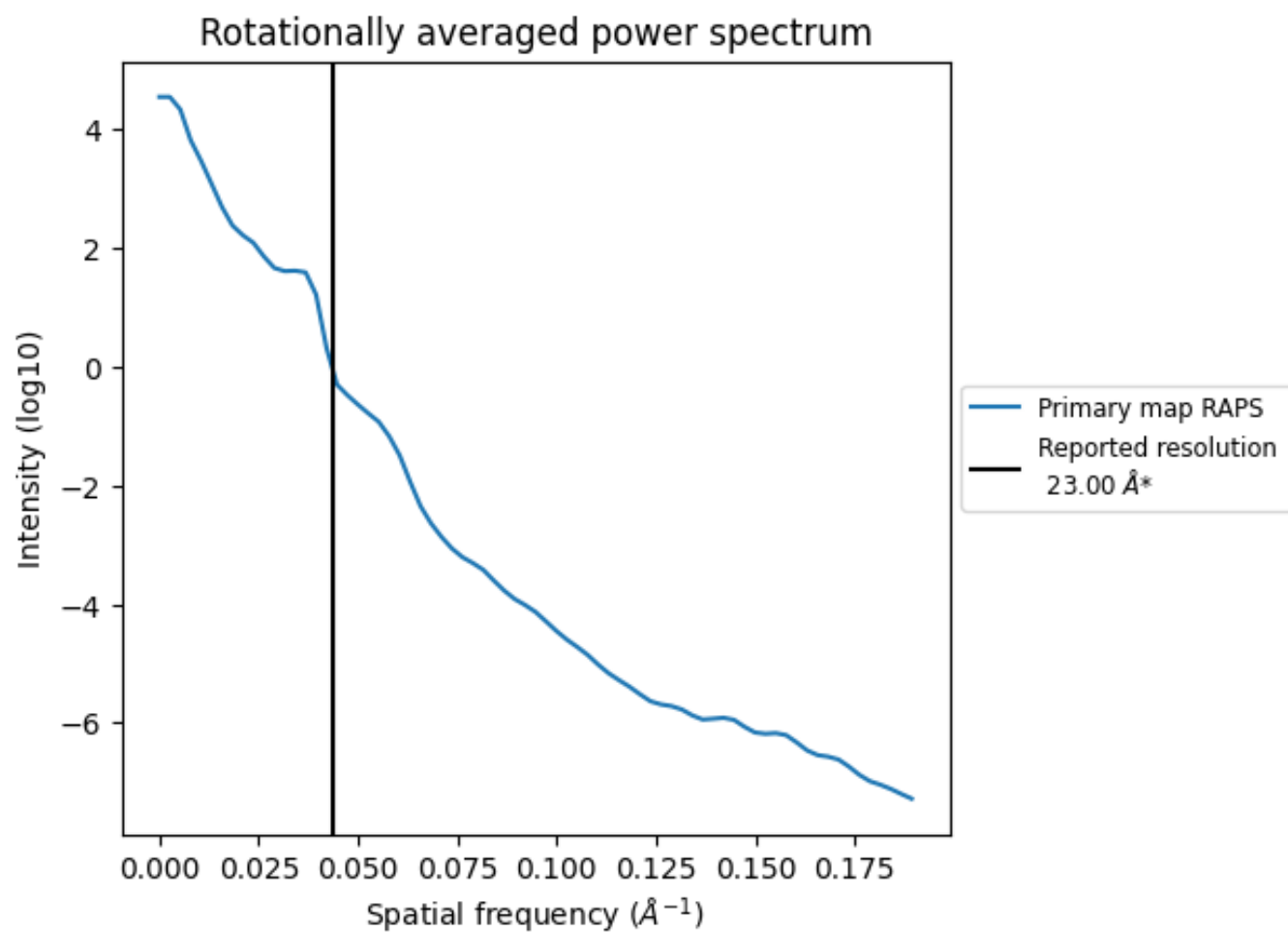
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 794 nm³; this corresponds to an approximate mass of 717 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 0.043 Å⁻¹

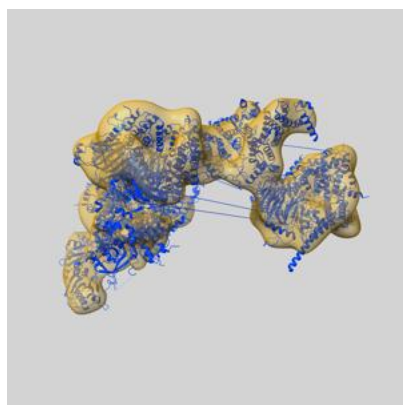
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

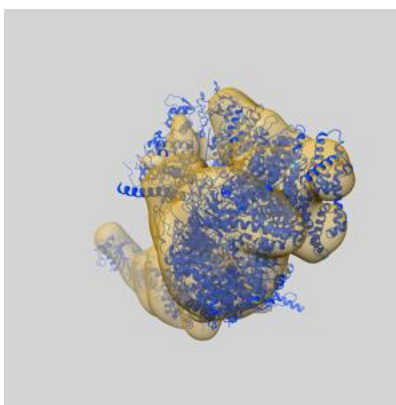
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9305 and PDB model 6MZL. Per-residue inclusion information can be found in section 3 on page 7.

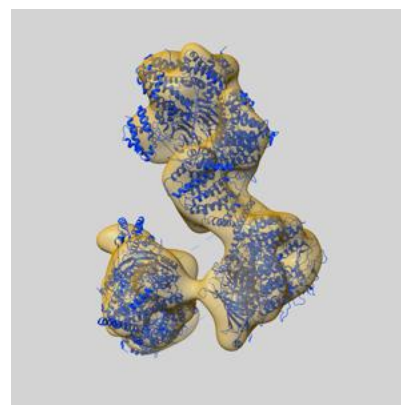
9.1 Map-model overlay [i](#)



X



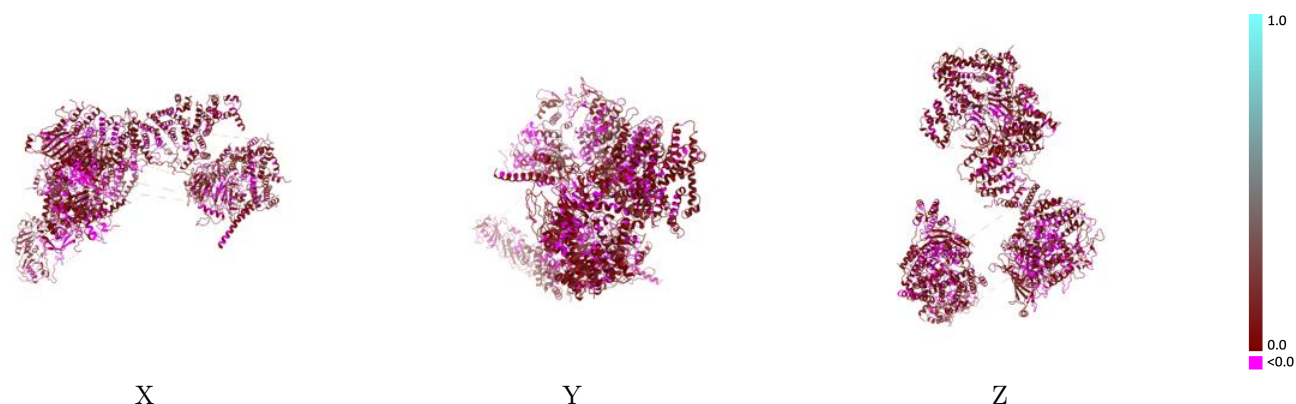
Y



Z

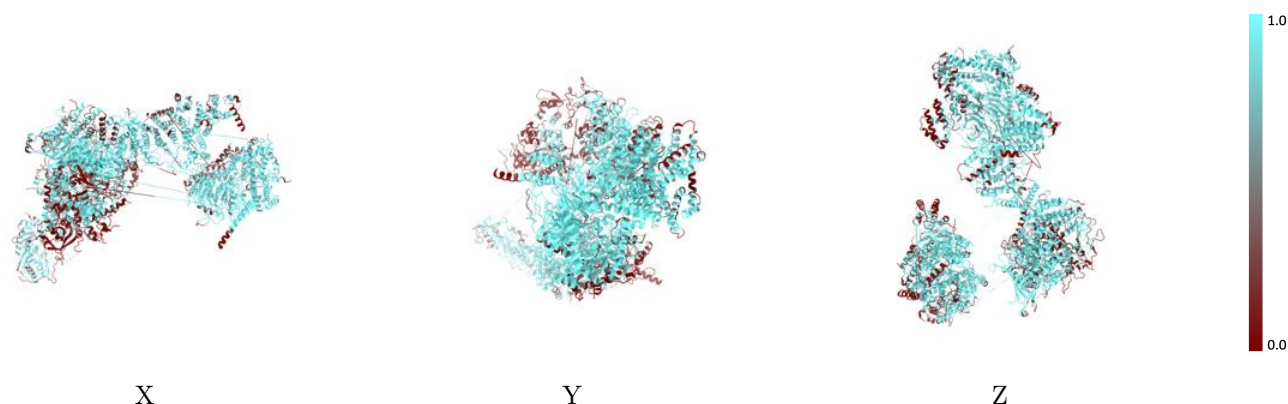
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



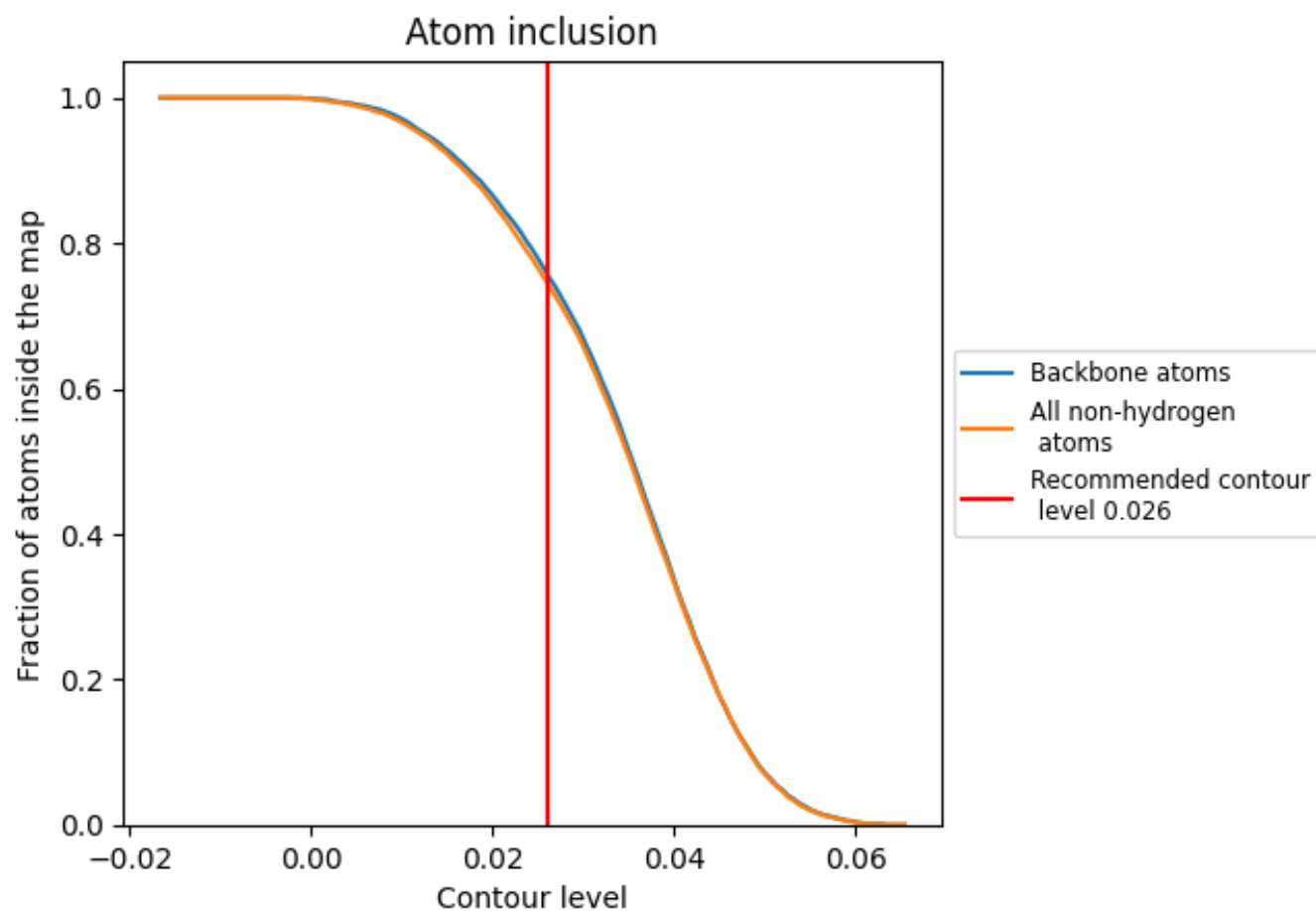
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 75% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7460	 0.0510
A	 0.4130	 0.0390
B	 0.7830	 0.0480
C	 0.9420	 0.0820
D	 0.6920	 0.0730
E	 0.7920	 0.0700
F	 0.7470	 0.0340
G	 0.8160	 0.0530
H	 0.8450	 0.0500
I	 0.8020	 0.0650
J	 0.2060	 0.0100
K	 0.9390	 0.0760
L	 0.9360	 0.0420
M	 0.7170	 0.0580
N	 0.8630	 0.0590
O	 0.9430	 0.0750
P	 0.6940	 0.0320
Q	 0.8170	 0.0450
R	 0.8400	 0.0710
S	 0.9670	 0.0990
T	 0.7180	 0.0690
Y	 0.4790	 0.0320
Z	 0.8570	 0.0550

