



## wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 11:26 PM UTC

PDB ID : 9RDK / pdb\_00009rdk  
EMDB ID : EMD-53937  
Title : Cryo-EM structure of the human SAGA co-activator complex  
Authors : Damilot, M.; Ben-Shem, A.; Papai, G.  
Deposited on : 2025-06-03  
Resolution : 2.41 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](mailto: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>.

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

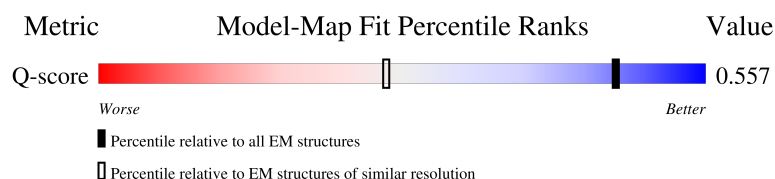
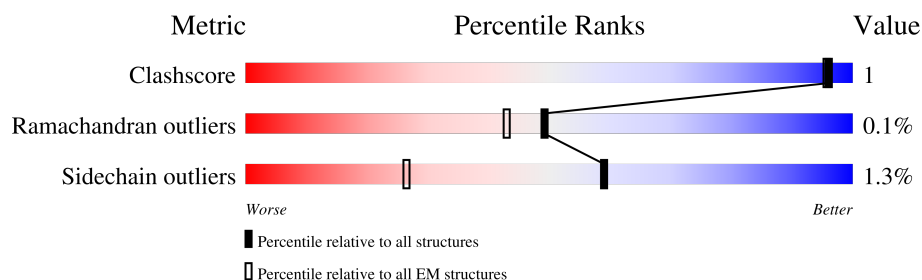
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 2.41 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.





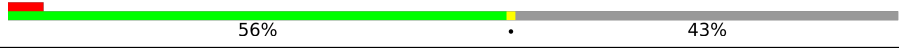



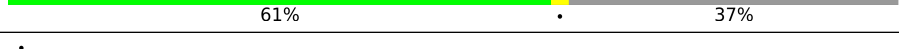

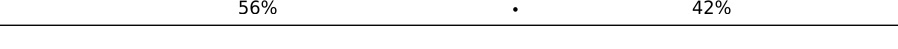
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5662 ( 1.92 - 2.91 )

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  $\geq 3$ , 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	E	251	
2	N	892	
3	L	589	
4	A	1217	

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Mol	Chain	Length	Quality of chain
5	C	3859	
6	D	414	
7	G	161	
8	H	218	
9	I	317	
10	J	335	
11	K	622	
12	M	779	
13	B	86	

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 54084 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 9B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	124	Total	C	N	O	S	0	0
			995	635	175	180	5		

- Molecule 2 is a protein called Ataxin-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	53	Total	C	N	O	S	0	0
			435	274	84	73	4		

- Molecule 3 is a protein called TAF5-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 5L.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	540	Total	C	N	O	S	0	0
			4279	2691	739	828	21		

- Molecule 4 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	1168	Total	C	N	O	S	0	0
			9158	5817	1558	1738	45		

- Molecule 5 is a protein called Transformation/transcription domain-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	3258	Total	C	N	O	S	0	0
			26232	16878	4516	4650	188		

- Molecule 6 is a protein called STAGA complex 65 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	182	Total	C	N	O	S	0	0
			1493	945	268	274	6		

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	91	Total	C	N	O	S	0	0
			744	463	132	145	4		

- Molecule 8 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	99	Total	C	N	O	S	0	0
			784	501	128	151	4		

- Molecule 9 is a protein called Transcription initiation protein SPT3 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	228	Total	C	N	O	S	0	0
			1858	1169	337	338	14		

- Molecule 10 is a protein called Transcriptional adapter 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	181	Total	C	N	O	S	0	0
			1474	927	270	272	5		

- Molecule 11 is a protein called TAF6-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 6L.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	389	Total	C	N	O	S	0	0
			3065	1956	537	559	13		

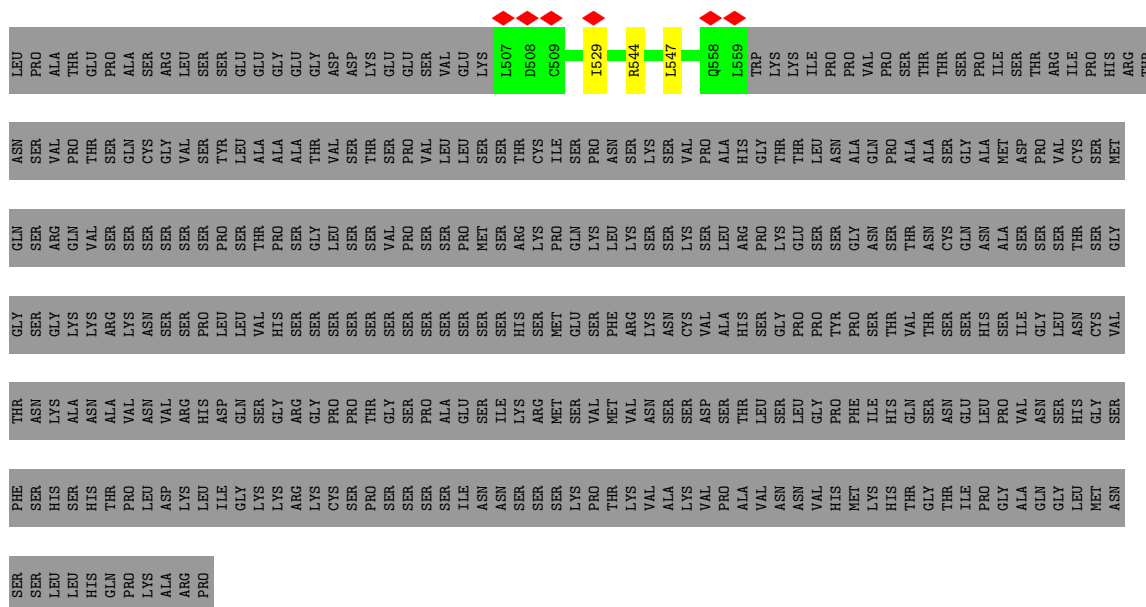
- Molecule 12 is a protein called Transcription factor SPT20 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	388	Total	C	N	O	S	0	0
			3138	1971	548	596	23		

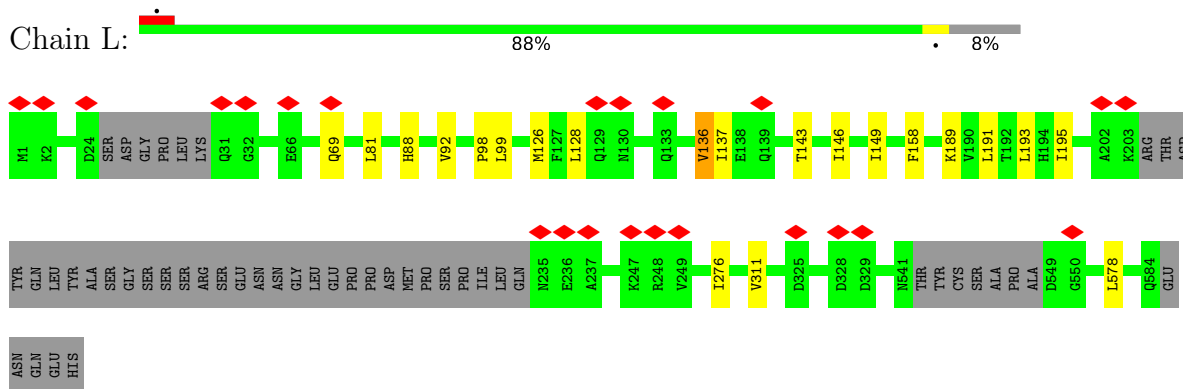
- Molecule 13 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	B	50	Total	C	N	O	S	0	0
			429	275	74	76	4		

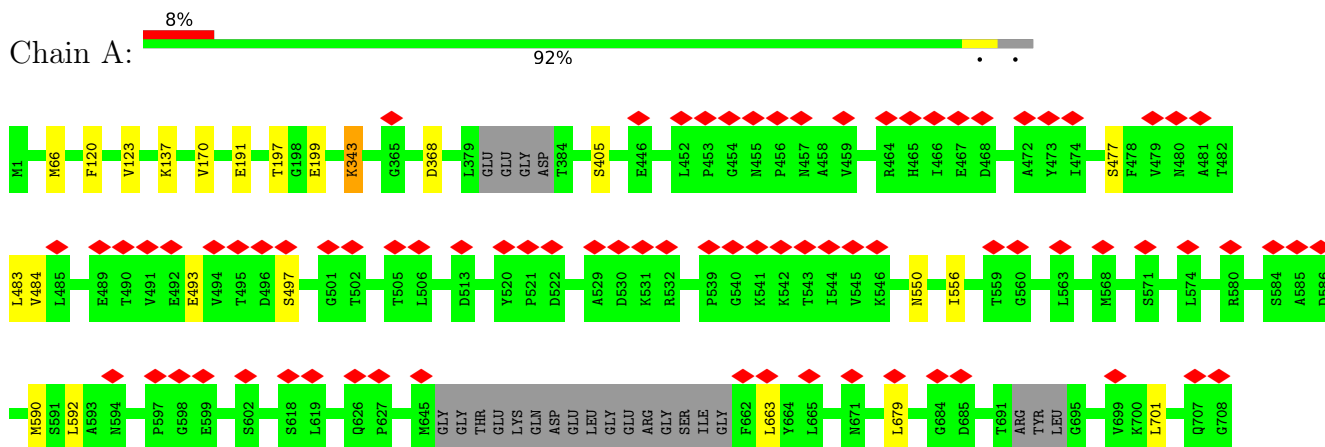


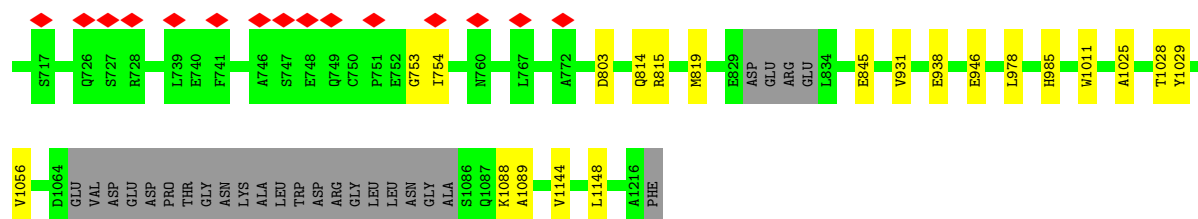


- Molecule 3: TAF5-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 5L



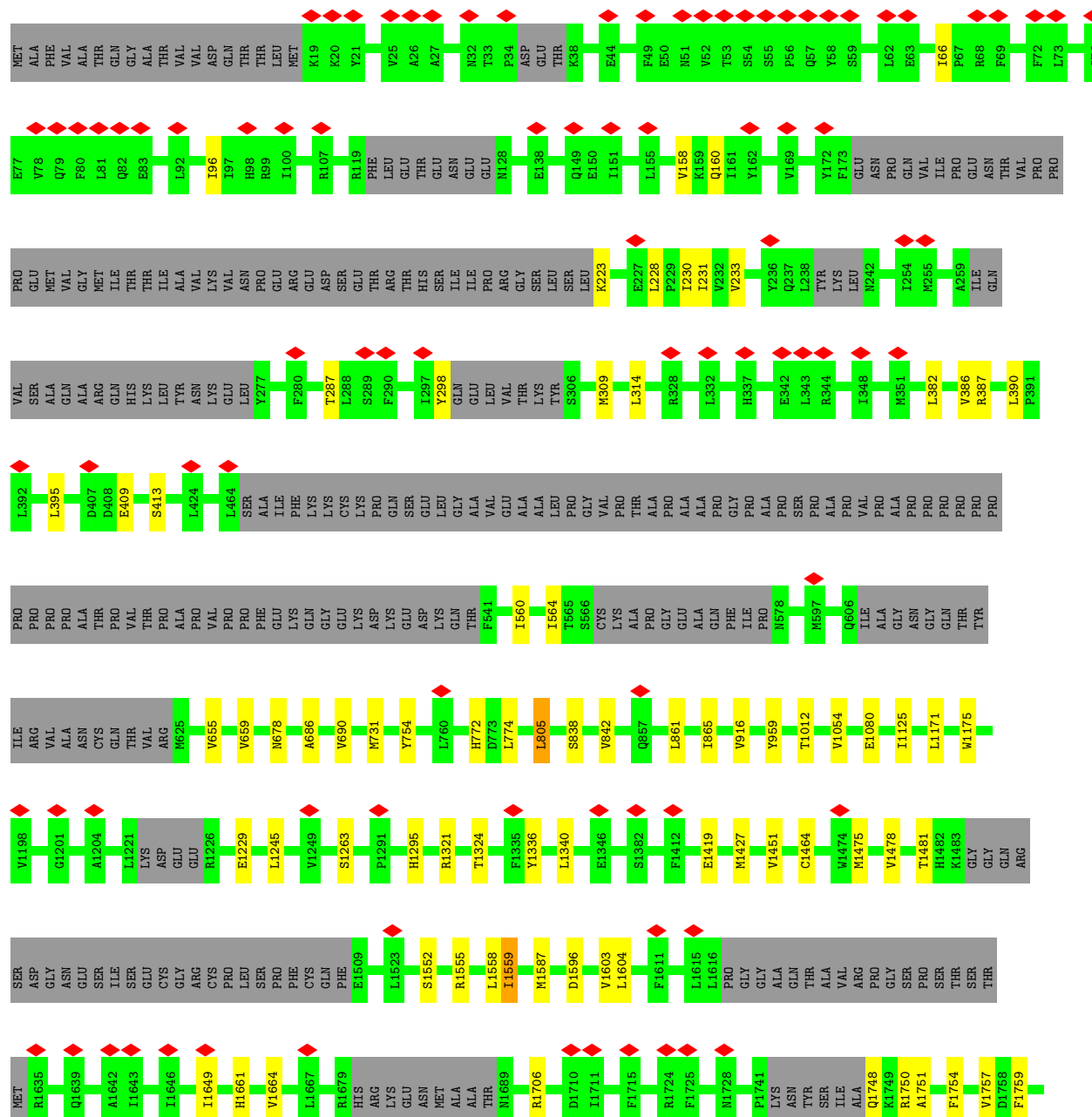
- Molecule 4: Splicing factor 3B subunit 3





• Molecule 5: Transformation/transcription domain-associated protein

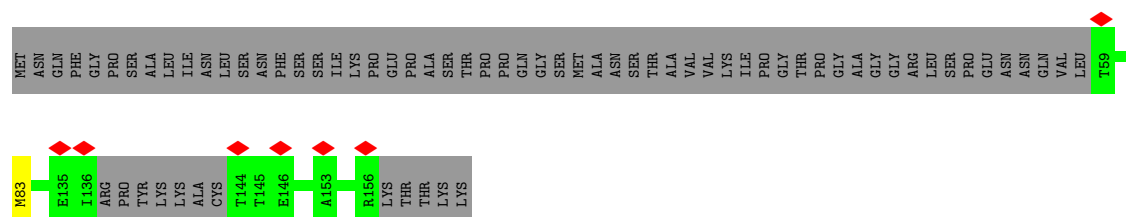
Chain C: 80% 16%



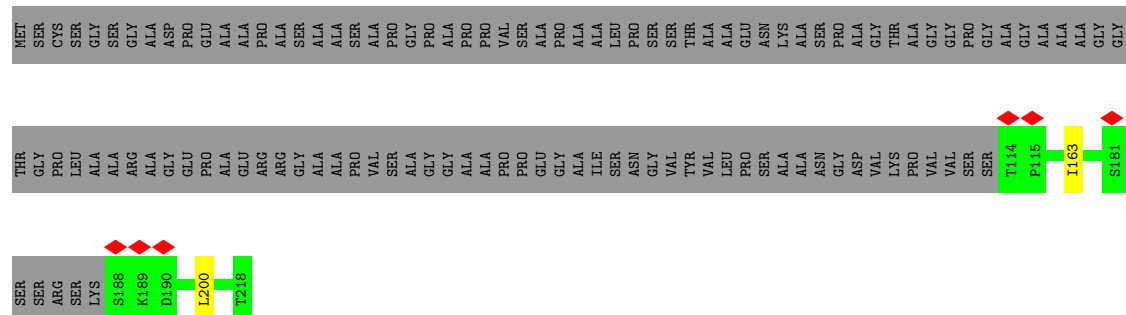
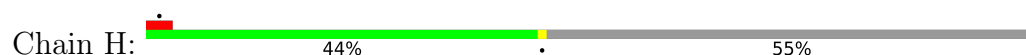




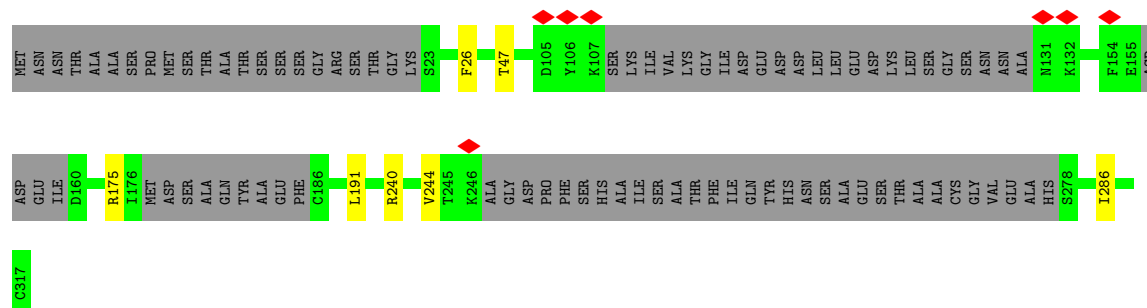
- Molecule 7: Transcription initiation factor TFIID subunit 12



- Molecule 8: Transcription initiation factor TFIID subunit 10

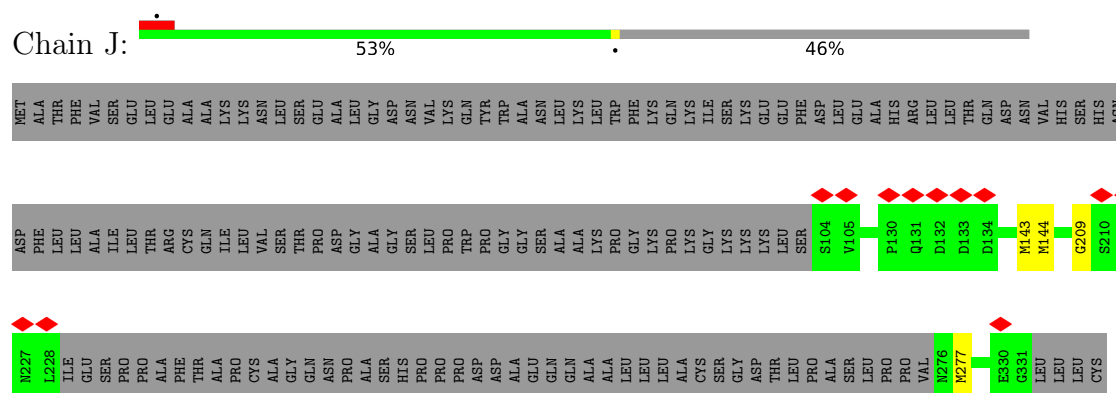


- Molecule 9: Transcription initiation protein SPT3 homolog



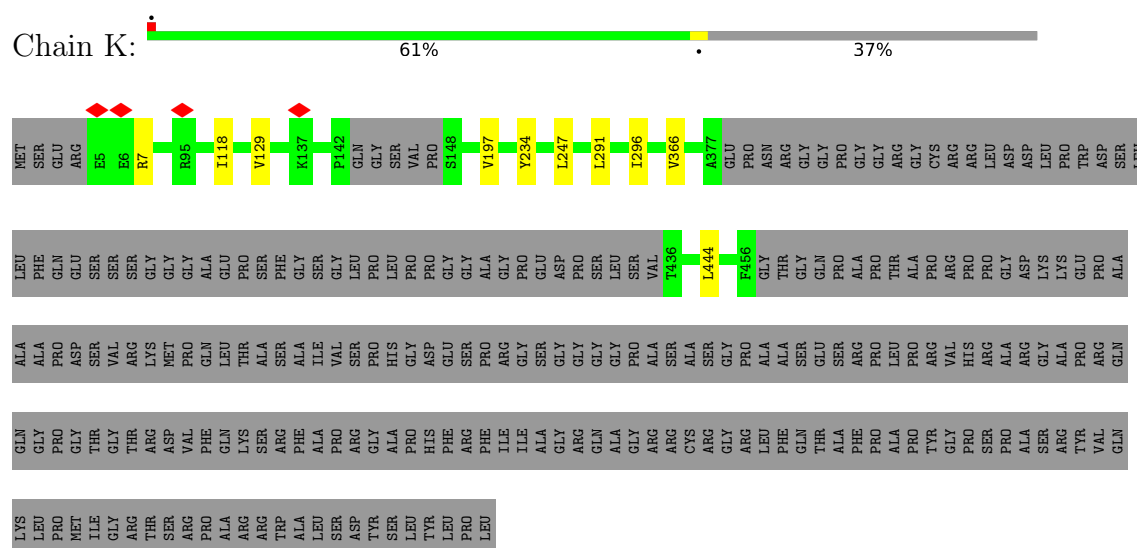
- Molecule 10: Transcriptional adapter 1

Chain J:



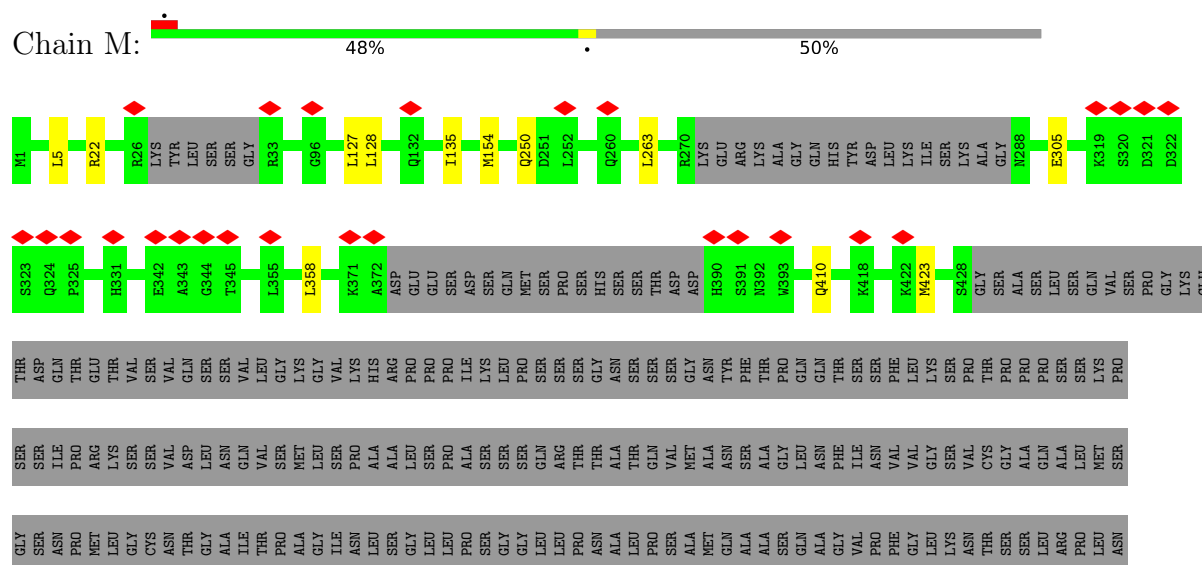
- Molecule 11: TAF6-like RNA polymerase II p300/CBP-associated factor-associated factor 65 kDa subunit 6L

Chain K:



- Molecule 12: Transcription factor SPT20 homolog

Chain M:



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- Molecule 13: Splicing factor 3B subunit 5



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LYS  
PRO  
GLU  
ASN

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	272167	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	29.833	Depositor
Minimum map value	-0.813	Depositor
Average map value	0.056	Depositor
Map value standard deviation	0.638	Depositor
Recommended contour level	3	Depositor
Map size (Å)	408.0, 408.0, 408.0	wwPDB
Map dimensions	408, 408, 408	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	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	E	0.28	0/1018	0.52	0/1384
2	N	0.31	0/448	0.61	0/604
3	L	0.32	0/4366	0.62	0/5920
4	A	0.30	0/9345	0.61	3/12680 (0.0%)
5	C	0.34	0/26775	0.66	12/36210 (0.0%)
6	D	0.30	0/1528	0.58	0/2068
7	G	0.27	0/753	0.52	0/1013
8	H	0.29	0/800	0.57	0/1082
9	I	0.33	0/1881	0.63	0/2518
10	J	0.26	0/1506	0.53	0/2039
11	K	0.30	0/3129	0.59	0/4251
12	M	0.32	0/3196	0.62	2/4316 (0.0%)
13	B	0.31	0/441	0.55	0/594
All	All	0.32	0/55186	0.63	17/74679 (0.0%)

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	E	0	1
4	A	0	1
5	C	0	5
6	D	0	1
9	I	0	1
11	K	0	1
All	All	0	10

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	160	GLN	CA-CB-CG	6.50	127.11	114.10
5	C	2015	LYS	CB-CG-CD	6.03	125.17	111.30
12	M	22	ARG	CA-CB-CG	5.79	125.68	114.10
4	A	343	LYS	CA-C-N	5.60	136.02	125.66
4	A	343	LYS	C-N-CA	5.60	136.02	125.66

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	343	LYS	Peptide
5	C	1759	PHE	Peptide
5	C	2302	ARG	Sidechain
5	C	772	HIS	Peptide
1	E	128	ARG	Peptide

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	995	0	1018	0	0
2	N	435	0	412	2	0
3	L	4279	0	4177	11	0
4	A	9158	0	9102	15	0
5	C	26232	0	26838	55	0
6	D	1493	0	1459	4	0
7	G	744	0	740	1	0
8	H	784	0	781	2	0
9	I	1858	0	1903	2	0
10	J	1474	0	1448	2	0
11	K	3065	0	3081	4	0
12	M	3138	0	3156	6	0
13	B	429	0	407	0	0
All	All	54084	0	54522	97	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 1.

The worst 5 of 97 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)
5:C:1908:LEU:HD11	5:C:1920:VAL:HG22	1.49	0.92
4:A:663:LEU:HD23	4:A:679:LEU:HD12	1.61	0.83
3:L:143:THR:HG21	3:L:149:ILE:HD13	1.74	0.69
5:C:2925:VAL:HG11	5:C:3667:THR:HG21	1.74	0.69
5:C:1427:MET:HE2	5:C:1451:VAL:HG21	1.75	0.67

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	E	122/251 (49%)	118 (97%)	4 (3%)	0	100	100
2	N	51/892 (6%)	47 (92%)	4 (8%)	0	100	100
3	L	532/589 (90%)	507 (95%)	25 (5%)	0	100	100
4	A	1156/1217 (95%)	1086 (94%)	68 (6%)	2 (0%)	43	57
5	C	3188/3859 (83%)	3004 (94%)	178 (6%)	6 (0%)	43	57
6	D	176/414 (42%)	169 (96%)	6 (3%)	1 (1%)	21	30
7	G	87/161 (54%)	83 (95%)	4 (5%)	0	100	100
8	H	95/218 (44%)	93 (98%)	2 (2%)	0	100	100
9	I	218/317 (69%)	205 (94%)	13 (6%)	0	100	100
10	J	177/335 (53%)	168 (95%)	9 (5%)	0	100	100
11	K	383/622 (62%)	375 (98%)	8 (2%)	0	100	100
12	M	380/779 (49%)	361 (95%)	19 (5%)	0	100	100
13	B	48/86 (56%)	47 (98%)	1 (2%)	0	100	100
All	All	6613/9740 (68%)	6263 (95%)	341 (5%)	9 (0%)	49	63

5 of 9 Ramachandran outliers are listed below:



Mol	Chain	Res	Type
4	A	405	SER
5	C	387	ARG
5	C	678	ASN
5	C	1931	VAL
5	C	2195	ARG

### 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	E	110/224 (49%)	109 (99%)	1 (1%)	70	84
2	N	46/779 (6%)	46 (100%)	0	100	100
3	L	478/521 (92%)	474 (99%)	4 (1%)	73	85
4	A	1013/1051 (96%)	1002 (99%)	11 (1%)	65	81
5	C	2916/3423 (85%)	2870 (98%)	46 (2%)	55	74
6	D	165/370 (45%)	163 (99%)	2 (1%)	63	79
7	G	83/141 (59%)	83 (100%)	0	100	100
8	H	86/154 (56%)	86 (100%)	0	100	100
9	I	203/273 (74%)	201 (99%)	2 (1%)	68	82
10	J	161/287 (56%)	159 (99%)	2 (1%)	63	79
11	K	330/505 (65%)	327 (99%)	3 (1%)	70	84
12	M	360/687 (52%)	357 (99%)	3 (1%)	73	85
13	B	46/77 (60%)	44 (96%)	2 (4%)	26	42
All	All	5997/8492 (71%)	5921 (99%)	76 (1%)	59	78

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	C	3251	LEU
12	M	5	LEU
5	C	3462	GLU
9	I	191	LEU
13	B	33	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
5	C	2619	HIS
5	C	3697	GLN
5	C	2646	HIS
5	C	3081	GLN
5	C	3843	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](#)

There are no chain breaks in this entry.

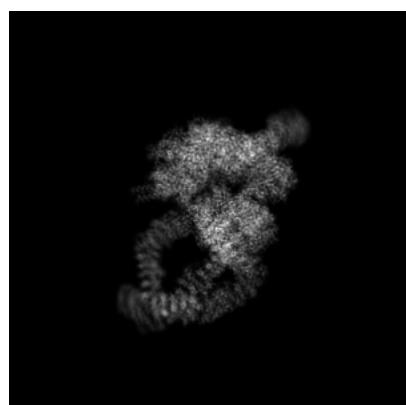
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53937. These allow visual inspection of the internal detail of the map and identification of artifacts.

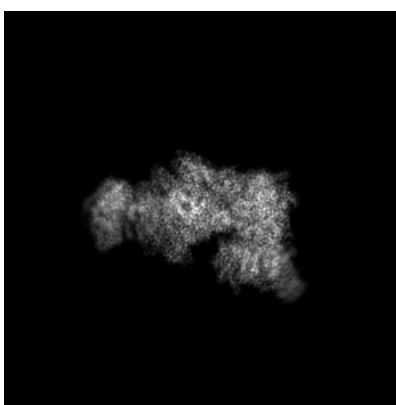
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

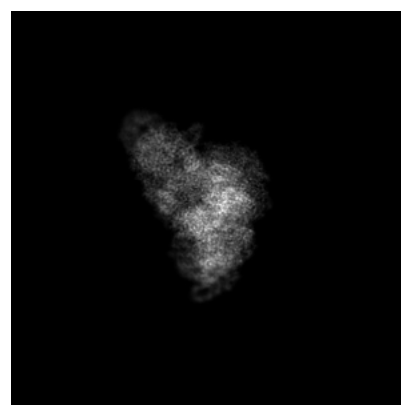
#### 6.1.1 Primary map



X



Y

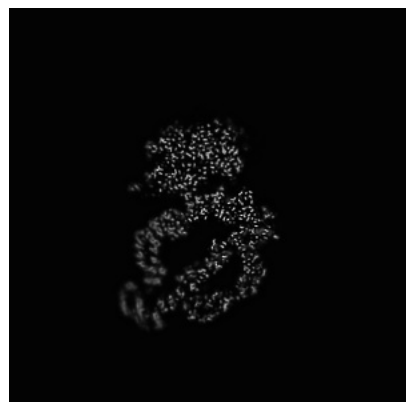


Z

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

### 6.2 Central slices [i](#)

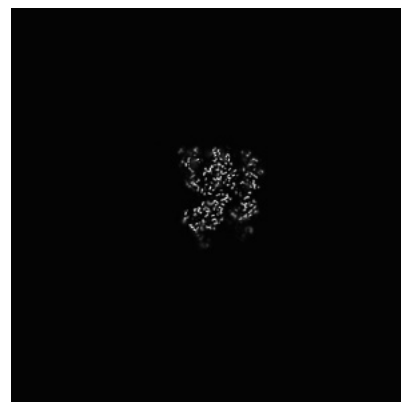
#### 6.2.1 Primary map



X Index: 204



Y Index: 204

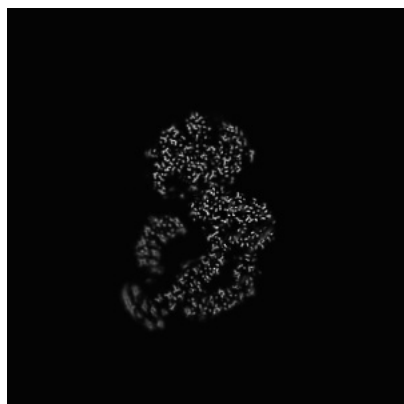


Z Index: 204

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: 211



Y Index: 219

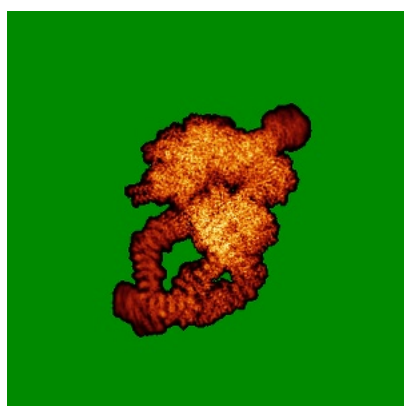


Z Index: 261

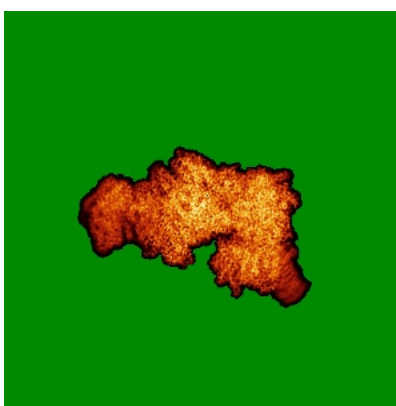
The images above show the largest variance slices of the map in three orthogonal directions.

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

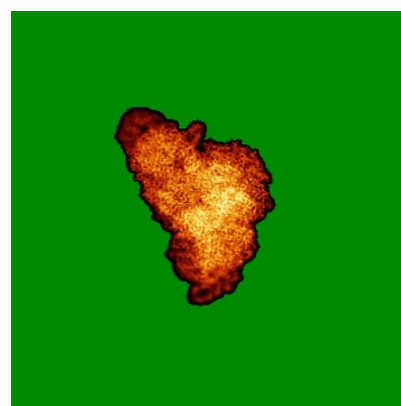
### 6.4.1 Primary map



X



Y

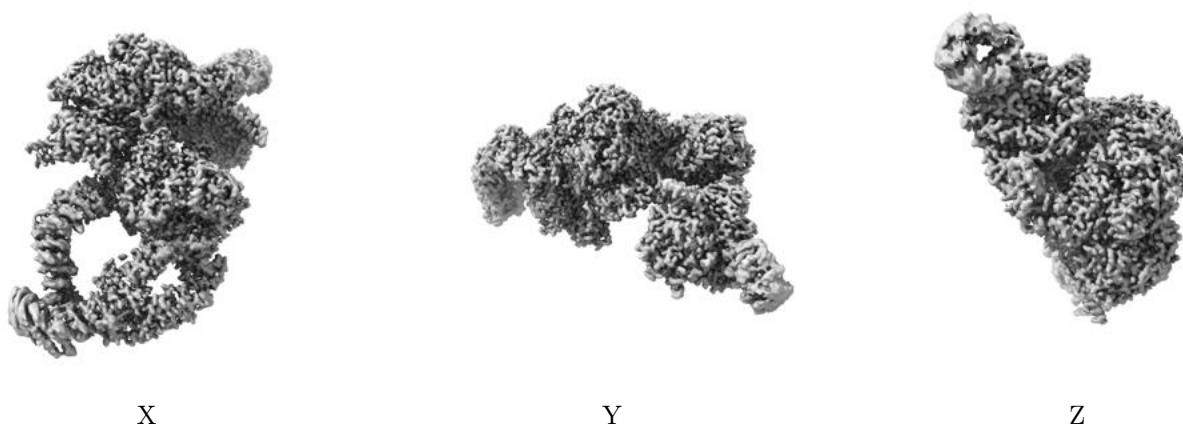


Z

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 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

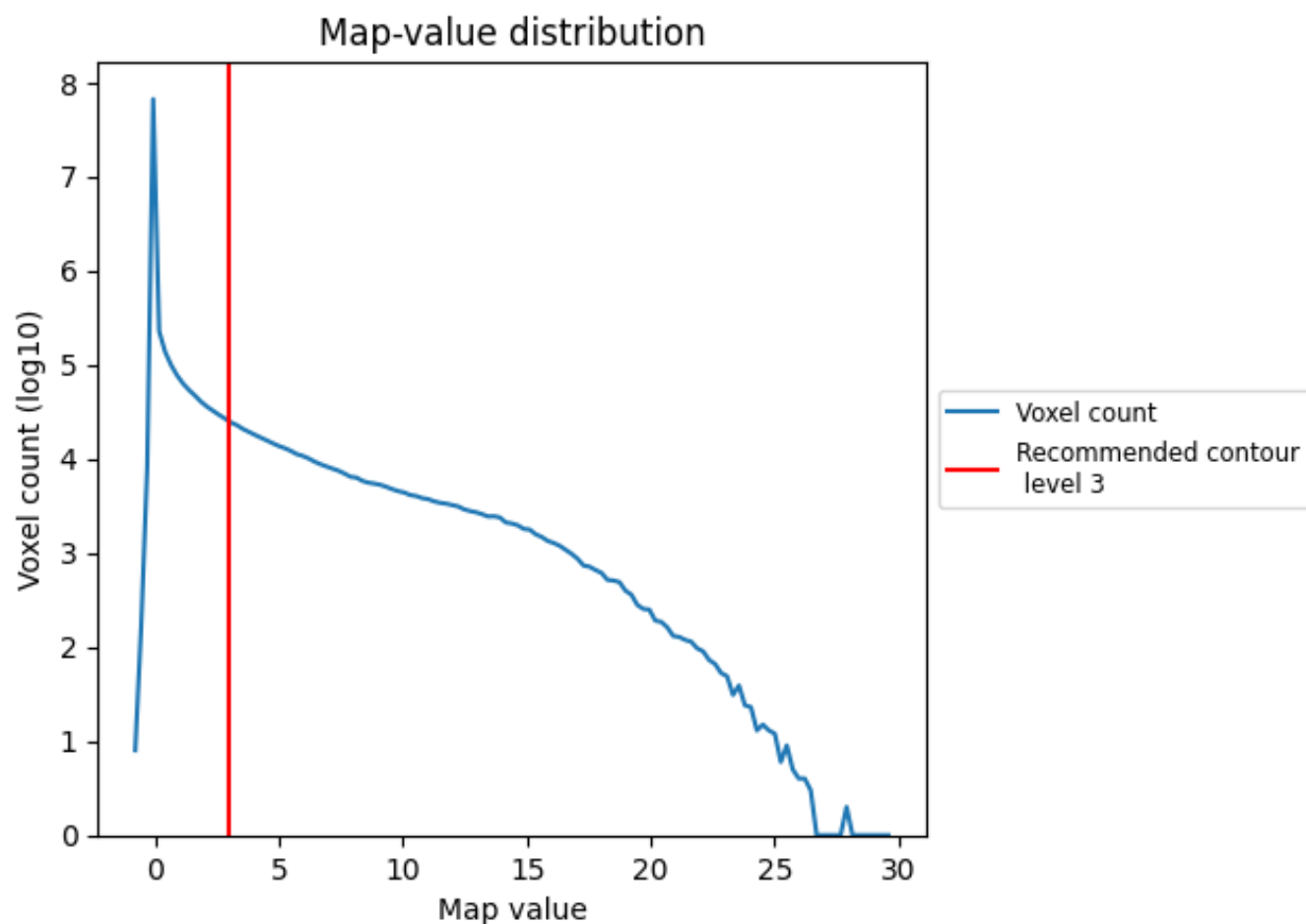
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

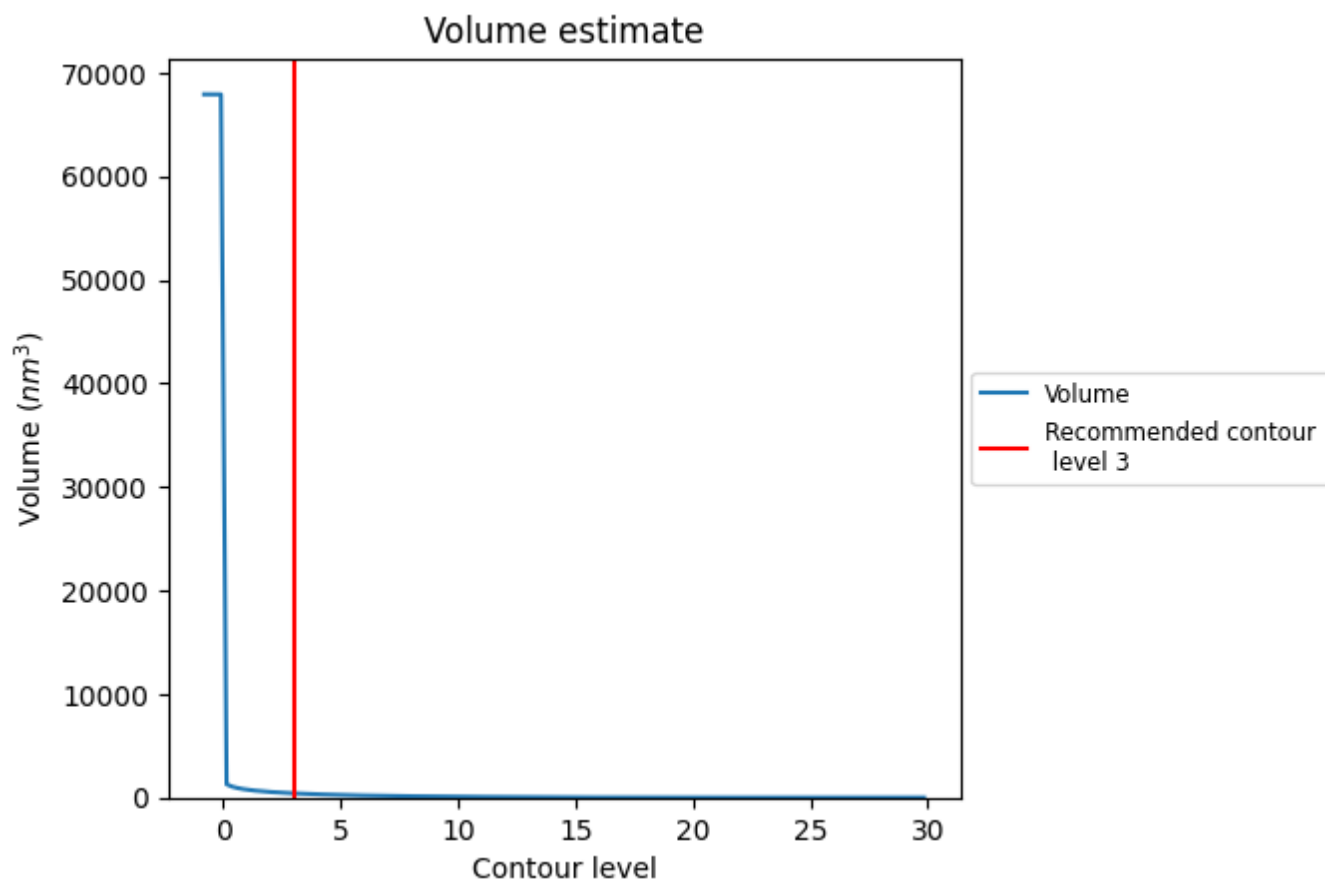
This section contains the results of statistical analysis of the map.

### 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.

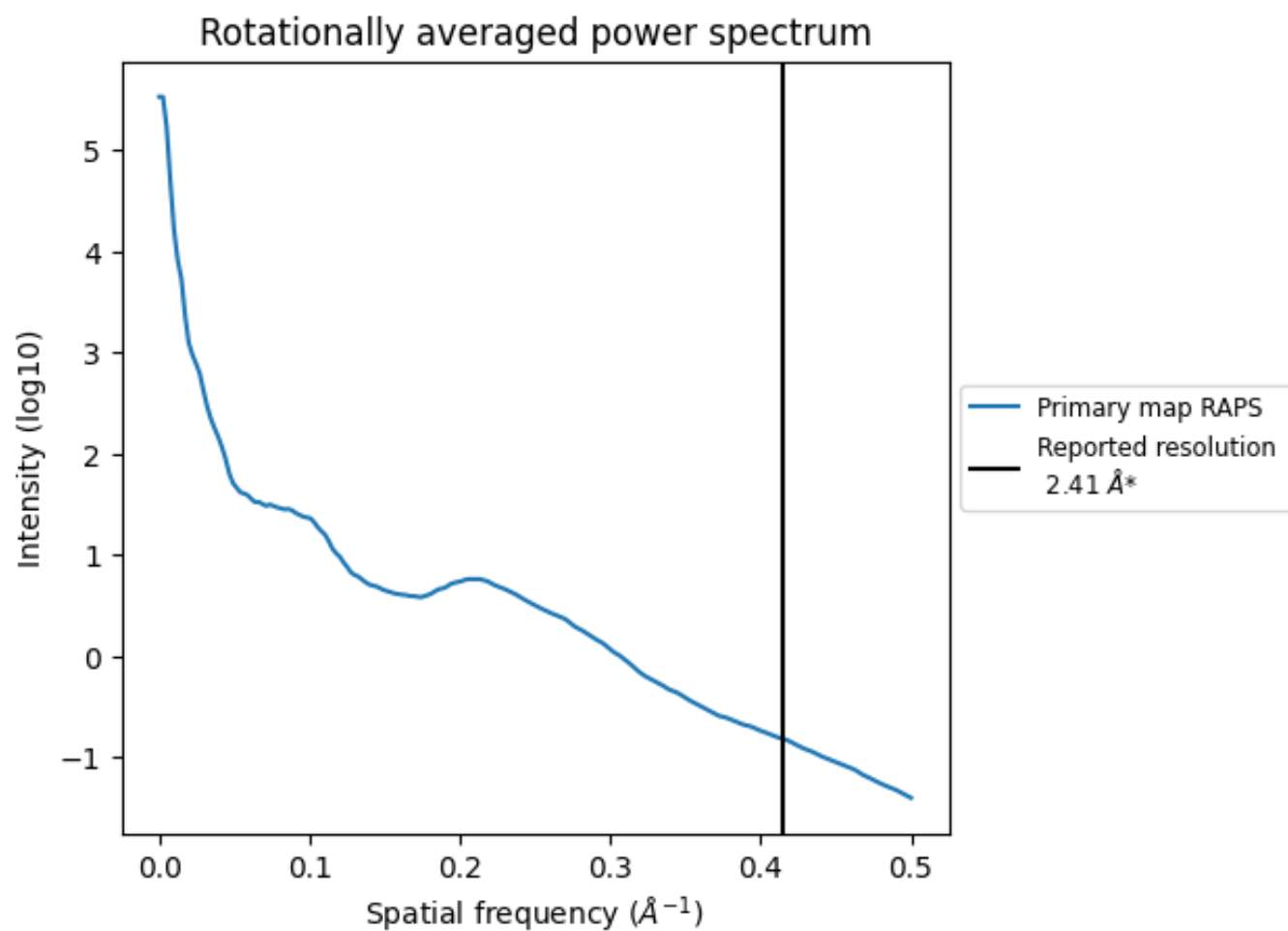
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 409  $\text{nm}^3$ ; this corresponds to an approximate mass of 369 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 0.415 Å<sup>-1</sup>



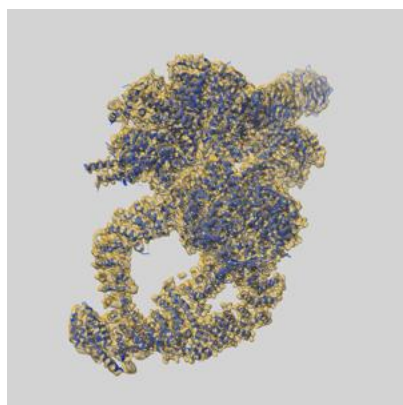
## 8 Fourier-Shell correlation ⓘ

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

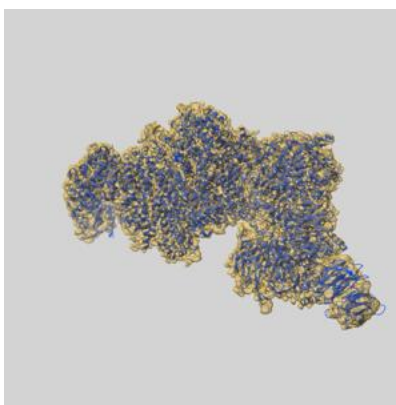
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53937 and PDB model 9RDK. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

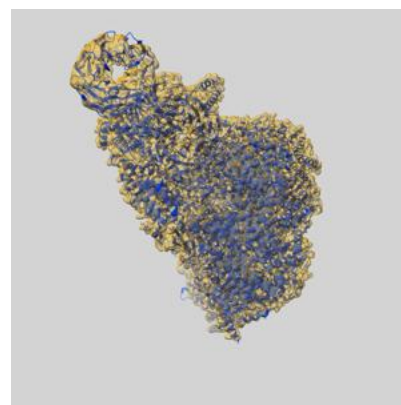
### 9.1 Map-model overlay [i](#)



X



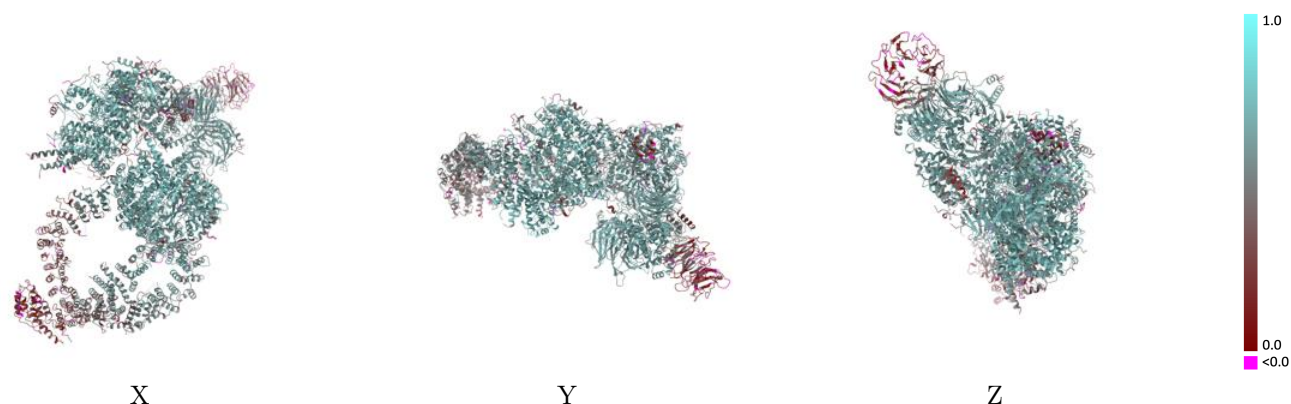
Y



Z

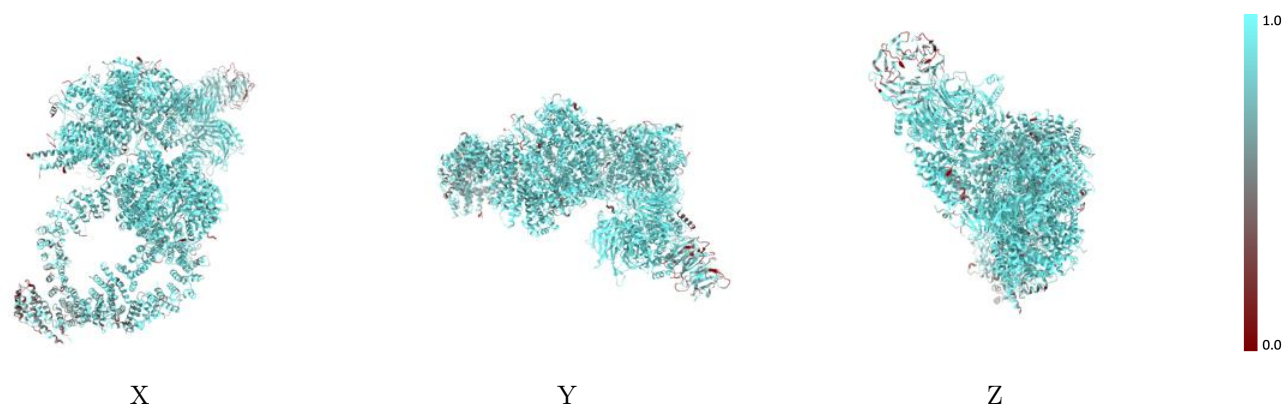
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



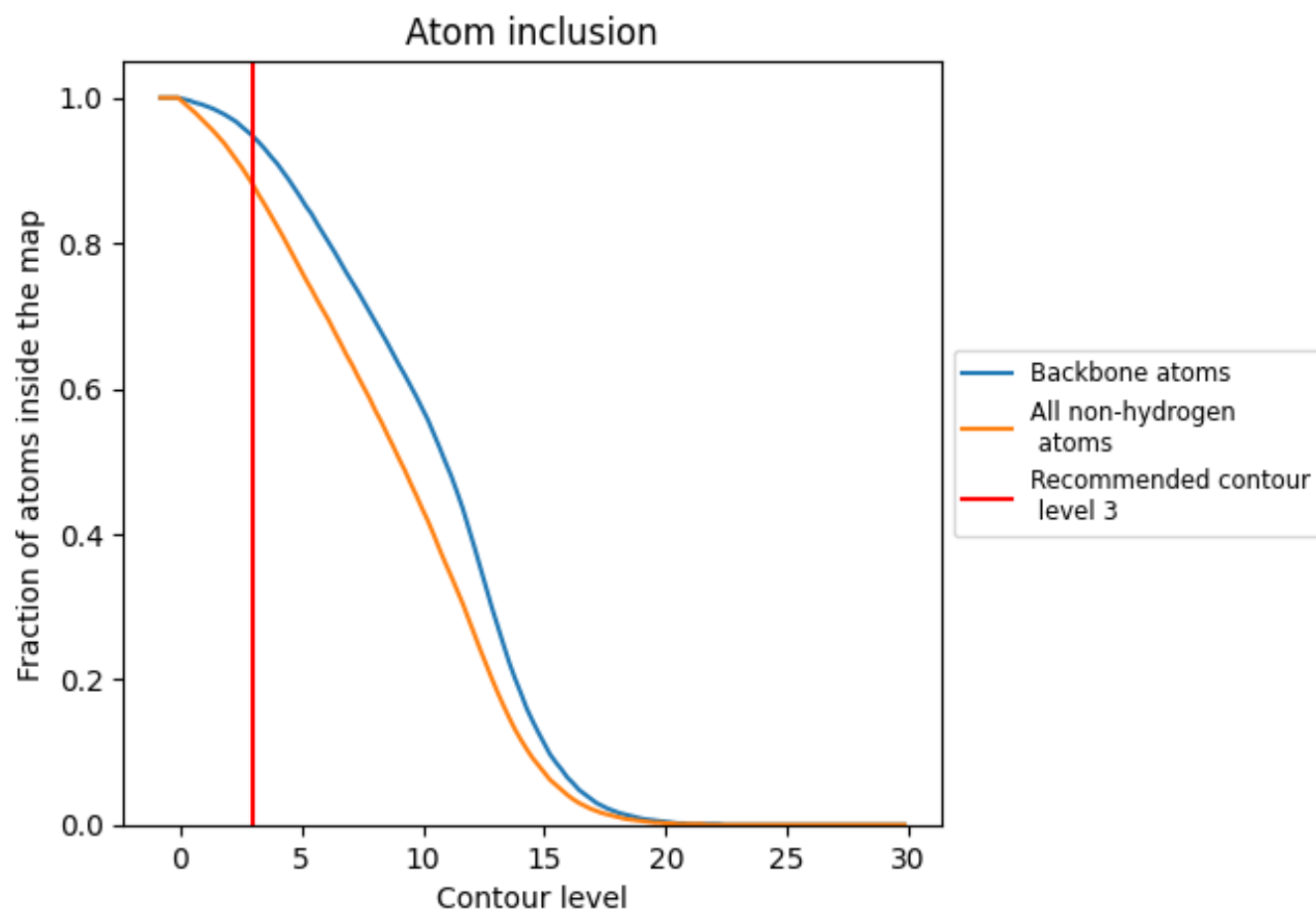
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).





























## 9.4 Atom inclusion ⓘ



At the recommended contour level, 95% of all backbone atoms, 88% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.5570
A	 0.8590	 0.5060
B	 0.9760	 0.6570
C	 0.8690	 0.5500
D	 0.9140	 0.6250
E	 0.9470	 0.6490
G	 0.8860	 0.6180
H	 0.9230	 0.6380
I	 0.9040	 0.5880
J	 0.9110	 0.6200
K	 0.9390	 0.5920
L	 0.9070	 0.5700
M	 0.8580	 0.5580
N	 0.8290	 0.5510

