



# Full wwPDB EM Validation Report (i)

Oct 3, 2023 – 12:42 PM JST

PDB ID : 8KD6  
EMDB ID : EMD-37126  
Title : Rpd3S in complex with nucleosome with H3K36MLA modification and 187bp DNA, class3  
Authors : Dong, S.; Li, H.; Wang, M.; Rasheed, N.; Zou, B.; Gao, X.; Guan, J.; Li, W.; Zhang, J.; Wang, C.; Zhou, N.; Shi, X.; Li, M.; Zhou, M.; Huang, J.; Li, H.; Zhang, Y.; Wong, K.H.; Zhang, X.; Chao, W.C.H.; He, J.  
Deposited on : 2023-08-09  
Resolution : 3.07 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](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 (i) 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 \(i\)](#)) were used in the production of this report:

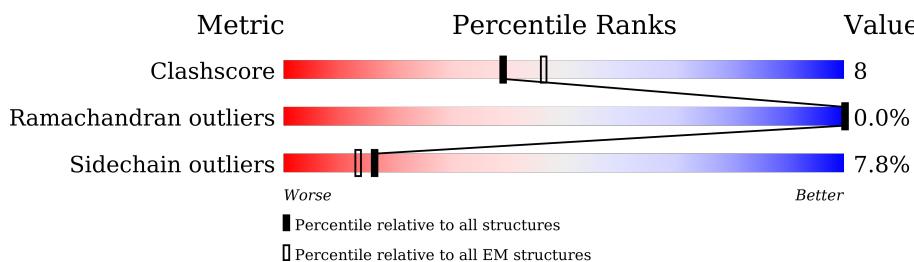
EMDB validation analysis : 0.0.1.dev50  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
**ELECTRON MICROSCOPY**

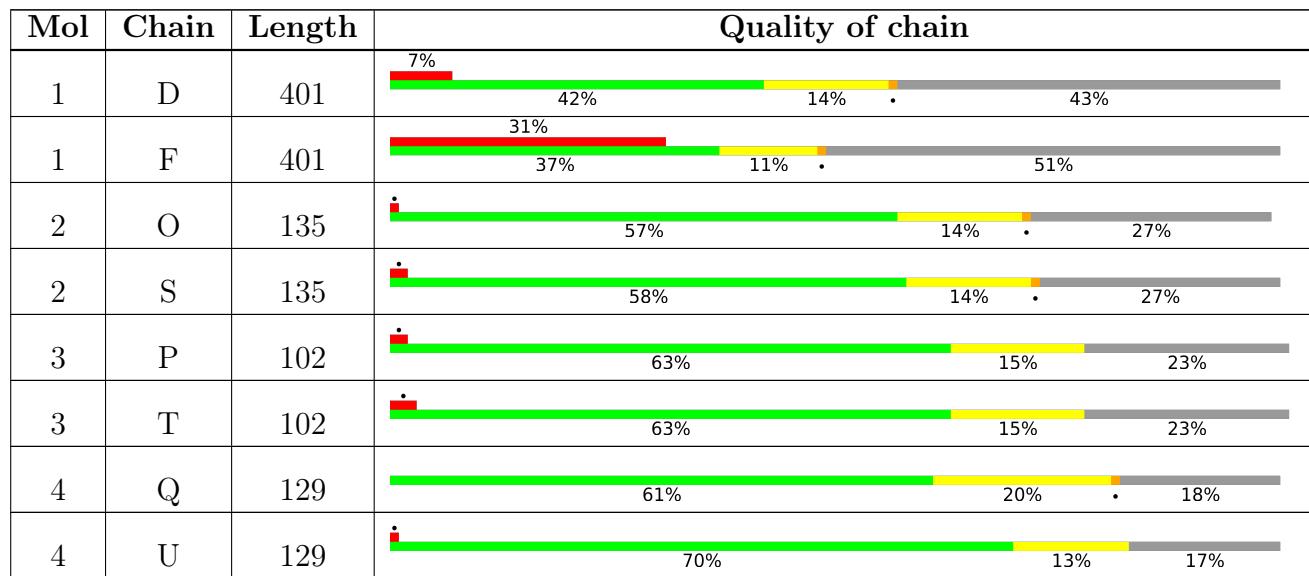
The reported resolution of this entry is 3.07 Å.

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.



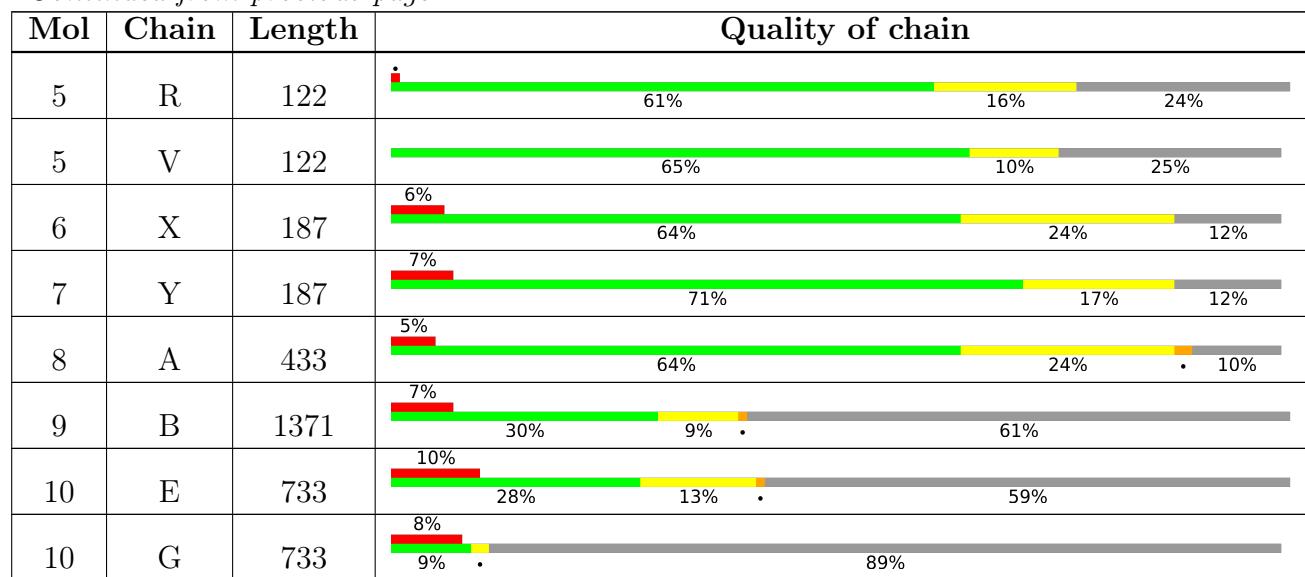
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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.



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## 2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 26982 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 Chromatin modification-related protein EAF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	D	230	1875	1200	311	353	11	0	0
1	F	198	1627	1048	270	298	11	0	0

- Molecule 2 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	O	98	811	515	155	139	2	0	0
2	S	98	811	515	155	139	2	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	110	ALA	CYS	engineered mutation	UNP A0A310TTQ1
S	110	ALA	CYS	engineered mutation	UNP A0A310TTQ1

- Molecule 3 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	P	79	637	403	124	109	1	0	0
3	T	79	637	403	124	109	1	0	0

- Molecule 4 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O			
4	Q	106	818	514	162	142		0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	U	107	Total	C	N	O	0	0
			825	519	163	143		

- Molecule 5 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	R	93	Total	C	N	O	S	0
			730	460	131	137	2	0
5	V	91	Total	C	N	O	S	0
			715	451	128	134	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	29	THR	SER	engineered mutation	UNP P02281
V	29	THR	SER	engineered mutation	UNP P02281

- Molecule 6 is a DNA chain called 187bp DNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	X	164	Total	C	N	O	P	0
			3384	1599	639	982	164	0

- Molecule 7 is a DNA chain called 187bp DNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	Y	164	Total	C	N	O	P	0
			3340	1585	605	986	164	0

- Molecule 8 is a protein called Histone deacetylase RPD3.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	A	388	Total	C	N	O	S	0
			3073	1945	521	582	25	0

- Molecule 9 is a protein called Transcriptional regulatory protein SIN3.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	B	537	Total	C	N	O	S	0
			4505	2899	756	835	15	0

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	166	MET	-	initiating methionine	UNP P22579
B	167	HIS	-	expression tag	UNP P22579
B	168	HIS	-	expression tag	UNP P22579
B	169	HIS	-	expression tag	UNP P22579
B	170	HIS	-	expression tag	UNP P22579
B	171	HIS	-	expression tag	UNP P22579
B	172	HIS	-	expression tag	UNP P22579
B	173	HIS	-	expression tag	UNP P22579
B	174	HIS	-	expression tag	UNP P22579
B	175	PRO	-	expression tag	UNP P22579
B	176	GLN	-	expression tag	UNP P22579
B	177	LEU	-	expression tag	UNP P22579
B	178	ALA	-	expression tag	UNP P22579
B	179	MET	-	expression tag	UNP P22579
B	180	TRP	-	expression tag	UNP P22579
B	181	SER	-	expression tag	UNP P22579
B	182	HIS	-	expression tag	UNP P22579
B	183	PRO	-	expression tag	UNP P22579
B	184	GLN	-	expression tag	UNP P22579
B	185	PHE	-	expression tag	UNP P22579
B	186	GLU	-	expression tag	UNP P22579
B	187	LYS	-	expression tag	UNP P22579
B	188	GLY	-	expression tag	UNP P22579
B	189	GLY	-	expression tag	UNP P22579
B	190	GLY	-	expression tag	UNP P22579
B	191	SER	-	expression tag	UNP P22579
B	192	GLY	-	expression tag	UNP P22579
B	193	GLY	-	expression tag	UNP P22579
B	194	GLY	-	expression tag	UNP P22579
B	195	SER	-	expression tag	UNP P22579
B	196	GLY	-	expression tag	UNP P22579
B	197	GLY	-	expression tag	UNP P22579
B	198	GLY	-	expression tag	UNP P22579
B	199	SER	-	expression tag	UNP P22579
B	200	TRP	-	expression tag	UNP P22579
B	201	SER	-	expression tag	UNP P22579
B	202	HIS	-	expression tag	UNP P22579
B	203	PRO	-	expression tag	UNP P22579
B	204	GLN	-	expression tag	UNP P22579
B	205	PHE	-	expression tag	UNP P22579
B	206	GLU	-	expression tag	UNP P22579
B	207	LYS	-	expression tag	UNP P22579

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Chain	Residue	Modelled	Actual	Comment	Reference
B	208	GLU	-	expression tag	UNP P22579
B	209	ASN	-	expression tag	UNP P22579
B	210	LEU	-	expression tag	UNP P22579
B	211	TYR	-	expression tag	UNP P22579
B	212	PHE	-	expression tag	UNP P22579
B	213	GLN	-	expression tag	UNP P22579
B	214	SER	-	expression tag	UNP P22579

- Molecule 10 is a protein called Transcriptional regulatory protein RCO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	301	Total	C	N	O	S	0	0
			2475	1572	433	453	17		
10	G	84	Total	C	N	O	S	0	0
			718	470	120	125	3		

There are 98 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	685	MET	-	expression tag	UNP Q04779
E	686	HIS	-	expression tag	UNP Q04779
E	687	HIS	-	expression tag	UNP Q04779
E	688	HIS	-	expression tag	UNP Q04779
E	689	HIS	-	expression tag	UNP Q04779
E	690	HIS	-	expression tag	UNP Q04779
E	691	HIS	-	expression tag	UNP Q04779
E	692	HIS	-	expression tag	UNP Q04779
E	693	HIS	-	expression tag	UNP Q04779
E	694	PRO	-	expression tag	UNP Q04779
E	695	GLN	-	expression tag	UNP Q04779
E	696	LEU	-	expression tag	UNP Q04779
E	697	ALA	-	expression tag	UNP Q04779
E	698	MET	-	expression tag	UNP Q04779
E	699	TRP	-	expression tag	UNP Q04779
E	700	SER	-	expression tag	UNP Q04779
E	701	HIS	-	expression tag	UNP Q04779
E	702	PRO	-	expression tag	UNP Q04779
E	703	GLN	-	expression tag	UNP Q04779
E	704	PHE	-	expression tag	UNP Q04779
E	705	GLU	-	expression tag	UNP Q04779
E	706	LYS	-	expression tag	UNP Q04779
E	707	GLY	-	expression tag	UNP Q04779

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Chain	Residue	Modelled	Actual	Comment	Reference
E	708	GLY	-	expression tag	UNP Q04779
E	709	GLY	-	expression tag	UNP Q04779
E	710	SER	-	expression tag	UNP Q04779
E	711	GLY	-	expression tag	UNP Q04779
E	712	GLY	-	expression tag	UNP Q04779
E	713	GLY	-	expression tag	UNP Q04779
E	714	SER	-	expression tag	UNP Q04779
E	715	GLY	-	expression tag	UNP Q04779
E	716	GLY	-	expression tag	UNP Q04779
E	717	GLY	-	expression tag	UNP Q04779
E	718	SER	-	expression tag	UNP Q04779
E	719	TRP	-	expression tag	UNP Q04779
E	720	SER	-	expression tag	UNP Q04779
E	721	HIS	-	expression tag	UNP Q04779
E	722	PRO	-	expression tag	UNP Q04779
E	723	GLN	-	expression tag	UNP Q04779
E	724	PHE	-	expression tag	UNP Q04779
E	725	GLU	-	expression tag	UNP Q04779
E	726	LYS	-	expression tag	UNP Q04779
E	727	GLU	-	expression tag	UNP Q04779
E	728	ASN	-	expression tag	UNP Q04779
E	729	LEU	-	expression tag	UNP Q04779
E	730	TYR	-	expression tag	UNP Q04779
E	731	PHE	-	expression tag	UNP Q04779
E	732	GLN	-	expression tag	UNP Q04779
E	733	SER	-	expression tag	UNP Q04779
G	685	MET	-	expression tag	UNP Q04779
G	686	HIS	-	expression tag	UNP Q04779
G	687	HIS	-	expression tag	UNP Q04779
G	688	HIS	-	expression tag	UNP Q04779
G	689	HIS	-	expression tag	UNP Q04779
G	690	HIS	-	expression tag	UNP Q04779
G	691	HIS	-	expression tag	UNP Q04779
G	692	HIS	-	expression tag	UNP Q04779
G	693	HIS	-	expression tag	UNP Q04779
G	694	PRO	-	expression tag	UNP Q04779
G	695	GLN	-	expression tag	UNP Q04779
G	696	LEU	-	expression tag	UNP Q04779
G	697	ALA	-	expression tag	UNP Q04779
G	698	MET	-	expression tag	UNP Q04779
G	699	TRP	-	expression tag	UNP Q04779
G	700	SER	-	expression tag	UNP Q04779

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Chain	Residue	Modelled	Actual	Comment	Reference
G	701	HIS	-	expression tag	UNP Q04779
G	702	PRO	-	expression tag	UNP Q04779
G	703	GLN	-	expression tag	UNP Q04779
G	704	PHE	-	expression tag	UNP Q04779
G	705	GLU	-	expression tag	UNP Q04779
G	706	LYS	-	expression tag	UNP Q04779
G	707	GLY	-	expression tag	UNP Q04779
G	708	GLY	-	expression tag	UNP Q04779
G	709	GLY	-	expression tag	UNP Q04779
G	710	SER	-	expression tag	UNP Q04779
G	711	GLY	-	expression tag	UNP Q04779
G	712	GLY	-	expression tag	UNP Q04779
G	713	GLY	-	expression tag	UNP Q04779
G	714	SER	-	expression tag	UNP Q04779
G	715	GLY	-	expression tag	UNP Q04779
G	716	GLY	-	expression tag	UNP Q04779
G	717	GLY	-	expression tag	UNP Q04779
G	718	SER	-	expression tag	UNP Q04779
G	719	TRP	-	expression tag	UNP Q04779
G	720	SER	-	expression tag	UNP Q04779
G	721	HIS	-	expression tag	UNP Q04779
G	722	PRO	-	expression tag	UNP Q04779
G	723	GLN	-	expression tag	UNP Q04779
G	724	PHE	-	expression tag	UNP Q04779
G	725	GLU	-	expression tag	UNP Q04779
G	726	LYS	-	expression tag	UNP Q04779
G	727	GLU	-	expression tag	UNP Q04779
G	728	ASN	-	expression tag	UNP Q04779
G	729	LEU	-	expression tag	UNP Q04779
G	730	TYR	-	expression tag	UNP Q04779
G	731	PHE	-	expression tag	UNP Q04779
G	732	GLN	-	expression tag	UNP Q04779
G	733	SER	-	expression tag	UNP Q04779

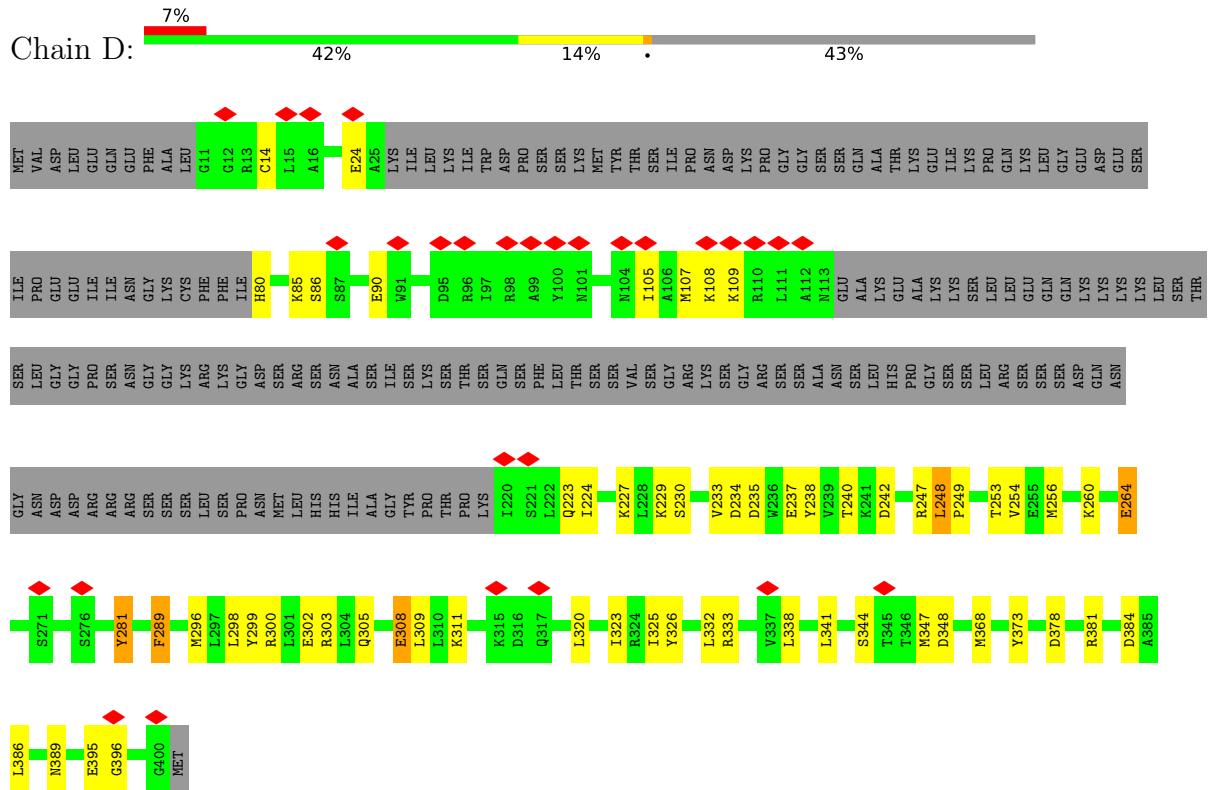
- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
11	A	1	Total 1      1	0

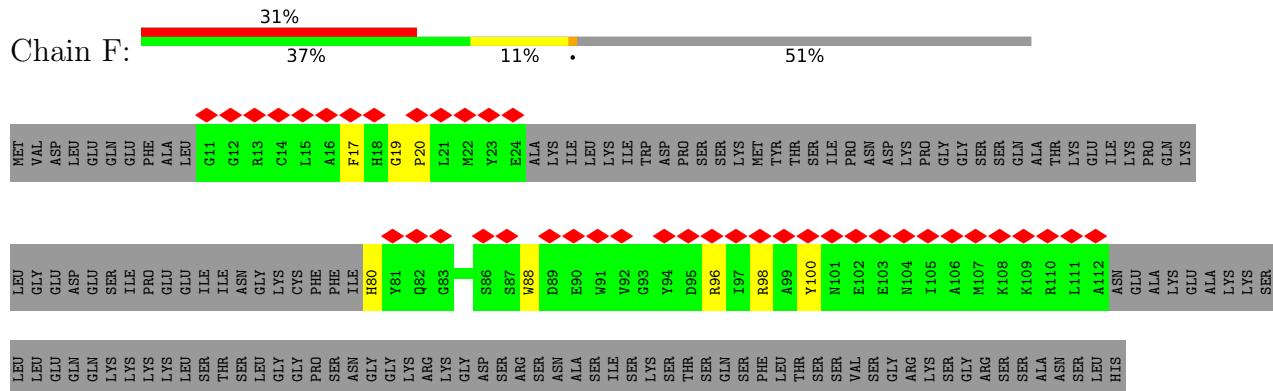
### 3 Residue-property plots

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: Chromatin modification-related protein EAF3



- Molecule 1: Chromatin modification-related protein EAF3





- Molecule 2: Histone H3

Chain O: 

- Molecule 2: Histone H3

Chain S: 

- Molecule 3: Histone H4

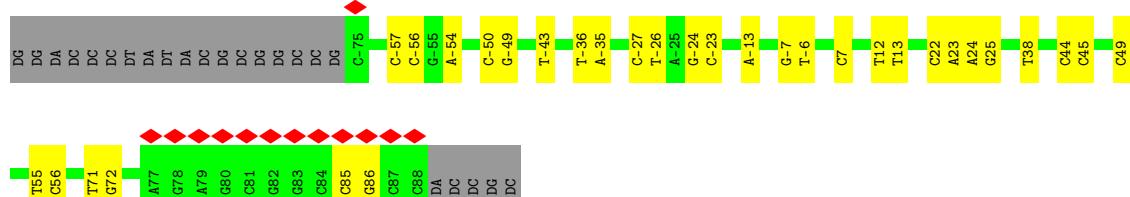
Chain P: 

- Molecule 3: Histone H4

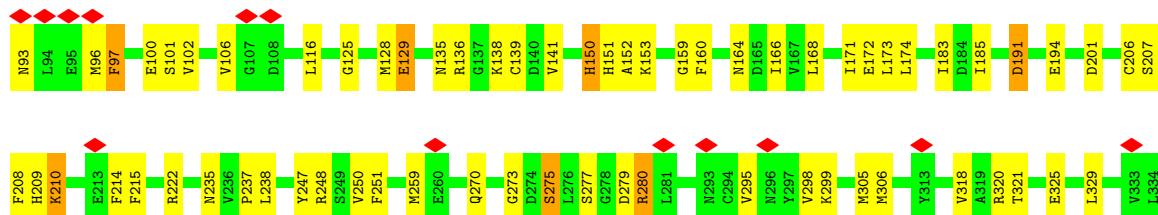
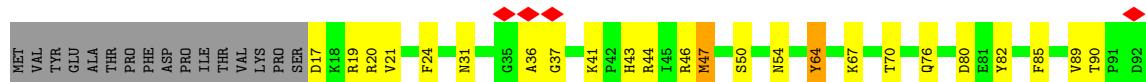
Chain T: 

- Molecule 4: Histone H2A

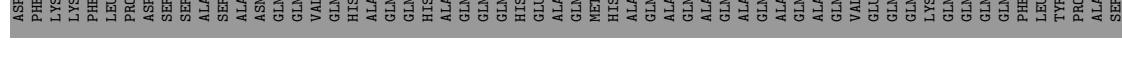
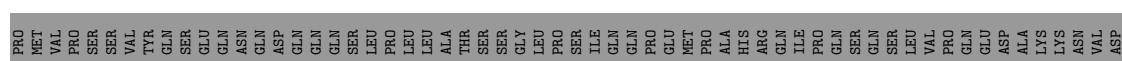
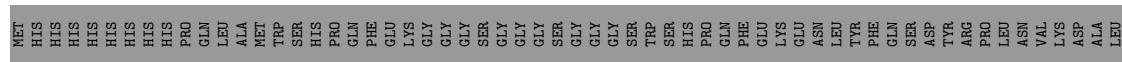


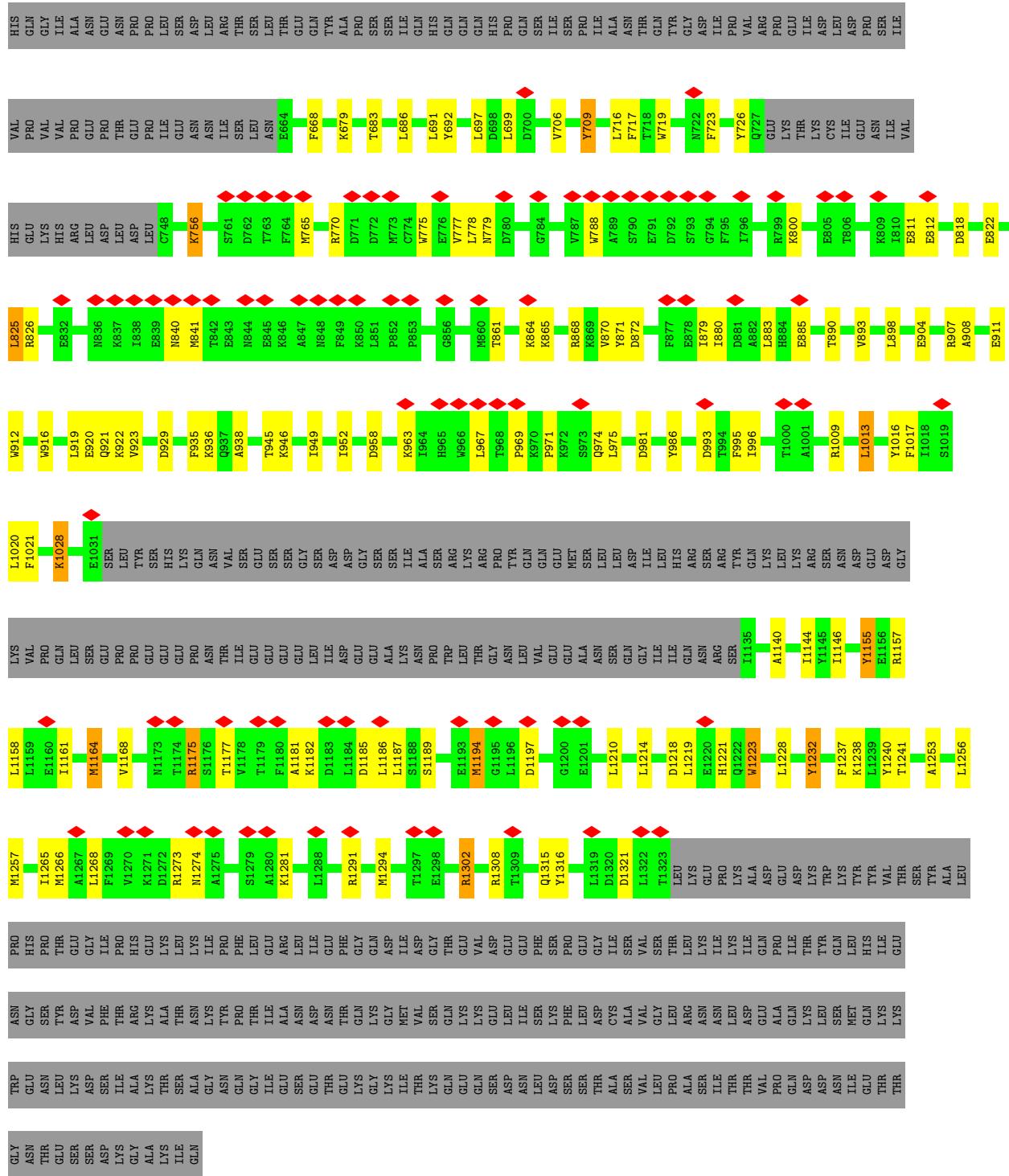


- Molecule 8: Histone deacetylase RPD3



- Molecule 9: Transcriptional regulatory protein SIN3

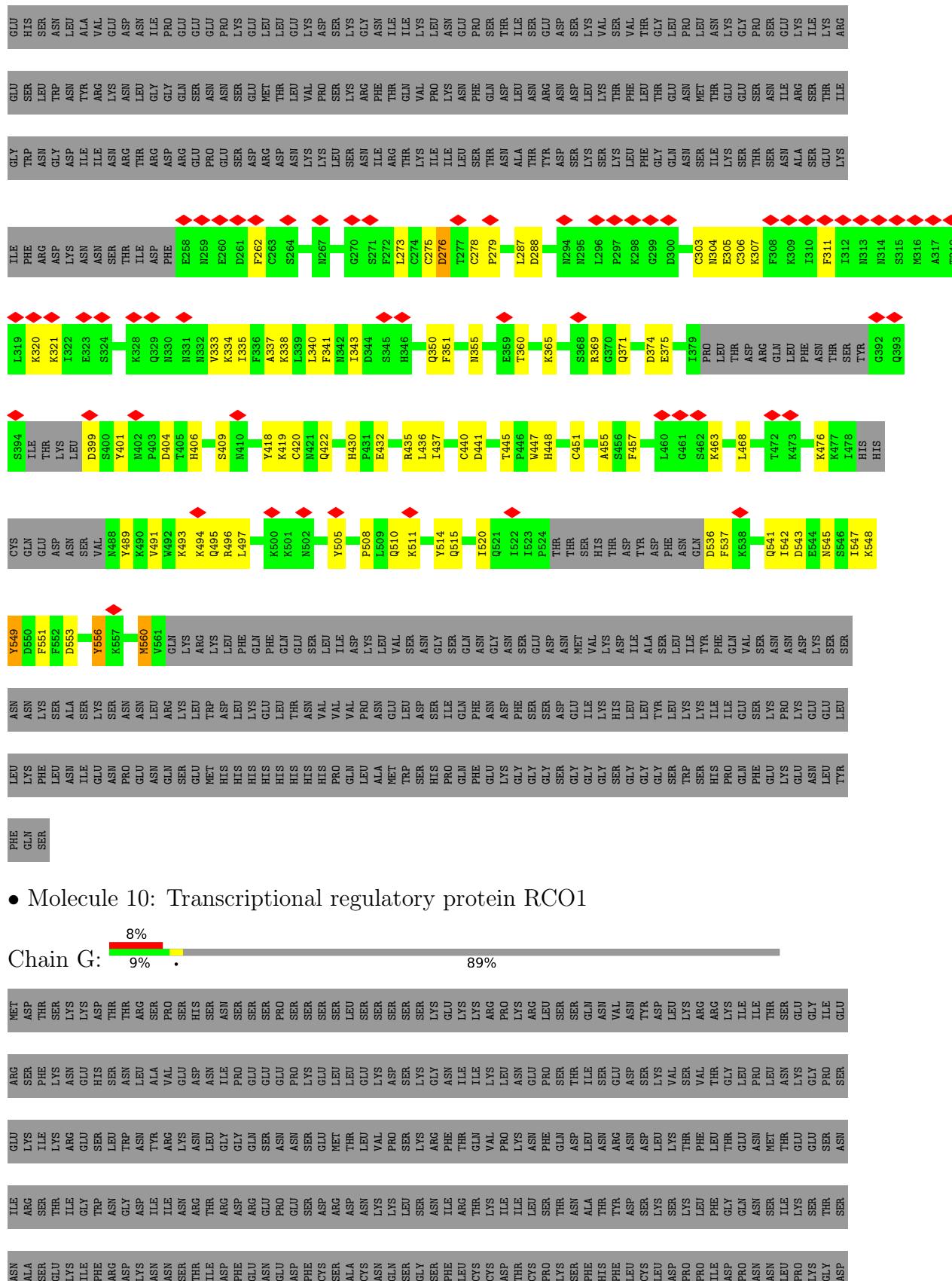




- Molecule 10: Transcriptional regulatory protein RCO1

A horizontal progress bar for 'Chain E' with a total length of 100%. The bar is divided into segments: a red segment at 0% labeled '10%', a green segment at 28%, a yellow segment at 13%, a small orange segment at 14%, a grey segment at 59%, and a black segment at 100% labeled with a dot. The segments are separated by thin white lines.





- Molecule 10: Transcriptional regulatory protein RCO1



ARG	MET	ASP	SER	ILE	LYS	GLU
SER	ASP	THR	PHE	LYS	GLN	GLU
SER	SER	LYS	ILE	ASN	GLU	GLU






## 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68388	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.543	Depositor
Minimum map value	-0.049	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	383.4, 383.4, 383.4	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.71, 0.71, 0.71	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

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	D	0.29	0/1913	0.67	3/2584 (0.1%)
1	F	0.28	0/1660	0.84	6/2239 (0.3%)
2	O	0.25	0/812	0.61	1/1092 (0.1%)
2	S	0.25	0/812	0.57	0/1092
3	P	0.24	0/644	0.57	0/863
3	T	0.24	0/644	0.60	0/863
4	Q	0.24	0/827	0.53	0/1115
4	U	0.27	0/835	0.56	0/1127
5	R	0.24	0/741	0.49	0/997
5	V	0.26	0/726	0.50	0/978
6	X	0.54	0/3801	0.90	0/5870
7	Y	0.52	0/3741	0.89	0/5766
8	A	0.27	0/3147	0.56	0/4250
9	B	0.27	0/4607	0.62	6/6211 (0.1%)
10	E	0.31	0/2533	0.65	3/3403 (0.1%)
10	G	0.31	0/732	0.57	1/975 (0.1%)
All	All	0.36	0/28175	0.71	20/39425 (0.1%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	F	296	MET	N-CA-C	15.49	152.82	111.00
10	E	279	PRO	CA-N-CD	-11.99	94.72	111.50
1	F	296	MET	CB-CA-C	-10.61	89.19	110.40
1	F	297	LEU	N-CA-CB	-10.52	89.36	110.40
9	B	1185	ASP	CB-CG-OD1	8.35	125.81	118.30
9	B	825	LEU	CA-CB-CG	7.25	131.97	115.30
1	F	304	LEU	CA-CB-CG	7.25	131.97	115.30
10	E	279	PRO	N-CD-CG	-7.00	92.70	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	334	LEU	CA-CB-CG	6.86	131.09	115.30
9	B	975	LEU	CA-CB-CG	6.63	130.54	115.30
9	B	1013	LEU	CA-CB-CG	6.61	130.51	115.30
1	D	235	ASP	CB-CG-OD1	6.02	123.72	118.30
1	F	287	LEU	CA-CB-CG	5.94	128.96	115.30
9	B	1164	MET	CB-CG-SD	5.78	129.75	112.40
1	D	248	LEU	CA-CB-CG	5.66	128.33	115.30
1	D	234	ASP	CB-CG-OD2	5.41	123.17	118.30
10	E	47	ASP	CB-CG-OD2	5.21	122.99	118.30
10	G	560	MET	CA-CB-CG	5.16	122.08	113.30
2	O	90	MET	CB-CG-SD	5.06	127.57	112.40
9	B	1266	MET	CB-CG-SD	5.01	127.43	112.40

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	D	1875	0	1868	55	0
1	F	1627	0	1646	25	0
2	O	811	0	861	15	0
2	S	811	0	861	13	0
3	P	637	0	681	11	0
3	T	637	0	681	15	0
4	Q	818	0	875	46	0
4	U	825	0	882	11	0
5	R	730	0	755	15	0
5	V	715	0	737	8	0
6	X	3384	0	1838	28	0
7	Y	3340	0	1840	21	0
8	A	3073	0	2937	72	0
9	B	4505	0	4466	71	0
10	E	2475	0	2439	77	0
10	G	718	0	734	13	0
11	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	26982	0	24101	397	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 8.

All (397) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:36:ALA:HB1	10:E:48:LEU:CD2	1.41	1.49
8:A:36:ALA:CB	10:E:48:LEU:HD23	1.54	1.35
1:D:240:THR:CG2	10:E:371:GLN:HB2	1.58	1.30
4:Q:23:LEU:HD22	4:Q:56:GLU:OE1	1.35	1.24
8:A:36:ALA:CB	10:E:48:LEU:CD2	2.11	1.21
4:Q:23:LEU:CD2	4:Q:56:GLU:OE1	1.89	1.20
4:Q:115:LEU:CD1	3:T:44:LYS:HD3	1.71	1.19
1:D:240:THR:HG21	10:E:371:GLN:HB2	1.22	1.17
4:Q:115:LEU:HG	2:S:48:LEU:HD21	1.30	1.11
1:D:240:THR:HG21	10:E:371:GLN:CB	1.81	1.10
4:Q:30:VAL:HG13	4:Q:51:LEU:HD23	1.36	1.07
4:Q:111:ILE:HG23	4:Q:115:LEU:HD23	1.36	1.06
4:Q:51:LEU:HD21	5:R:67:PHE:CE1	1.90	1.05
4:Q:115:LEU:HD11	3:T:44:LYS:HD3	1.30	1.05
4:Q:111:ILE:CG2	4:Q:115:LEU:HD23	1.86	1.04
4:Q:30:VAL:CG1	4:Q:51:LEU:HD23	1.92	0.98
1:D:298:LEU:HG	1:D:303:ARG:CD	1.95	0.96
1:D:240:THR:HG21	10:E:371:GLN:CA	1.95	0.95
9:B:883:LEU:HD23	9:B:890:THR:OG1	1.69	0.92
8:A:36:ALA:HB1	10:E:48:LEU:HD21	1.51	0.92
4:Q:115:LEU:HD12	3:T:44:LYS:HD3	1.51	0.89
1:D:240:THR:HG22	10:E:371:GLN:HB2	1.55	0.87
4:Q:107:VAL:HG12	4:Q:108:LEU:N	1.90	0.85
1:D:298:LEU:HG	1:D:303:ARG:HD2	1.57	0.85
4:Q:107:VAL:HG12	4:Q:108:LEU:H	1.40	0.85
1:D:240:THR:HG21	10:E:371:GLN:HA	1.57	0.84
10:E:494:LYS:HG2	10:E:495:GLN:H	1.40	0.84
8:A:36:ALA:HB1	10:E:48:LEU:HD23	0.82	0.81
1:D:298:LEU:CG	1:D:303:ARG:HD2	2.10	0.81
1:D:298:LEU:HG	1:D:303:ARG:HD3	1.60	0.81
8:A:36:ALA:HB3	10:E:48:LEU:CD2	2.14	0.78
10:G:309:LYS:HG3	10:G:313:ASN:HB3	1.69	0.75
4:Q:115:LEU:HD11	3:T:44:LYS:CD	2.12	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:298:LEU:CD2	1:D:303:ARG:HD2	2.17	0.74
4:Q:107:VAL:CG1	4:Q:108:LEU:H	1.99	0.74
1:D:240:THR:CG2	10:E:371:GLN:CB	2.46	0.73
10:E:491:VAL:CG1	10:E:493:LYS:HD3	2.20	0.71
10:G:309:LYS:HA	10:G:313:ASN:HB2	1.72	0.71
1:D:298:LEU:CD2	1:D:303:ARG:CD	2.70	0.69
9:B:883:LEU:CD2	9:B:890:THR:OG1	2.40	0.69
4:Q:51:LEU:CD2	5:R:67:PHE:CE1	2.72	0.68
8:A:404:VAL:HG12	8:A:406:GLU:H	1.58	0.68
4:Q:107:VAL:CG1	4:Q:108:LEU:N	2.56	0.67
4:Q:115:LEU:CG	2:S:48:LEU:HD21	2.18	0.67
1:D:298:LEU:CG	1:D:303:ARG:CD	2.67	0.66
8:A:101:SER:HB3	8:A:106:VAL:O	1.95	0.66
10:E:508:PRO:HB3	10:E:541:GLN:HB2	1.79	0.64
10:E:491:VAL:HG12	10:E:493:LYS:CD	2.28	0.64
1:D:298:LEU:HD21	1:D:303:ARG:HD2	1.79	0.64
8:A:37:GLY:N	10:E:48:LEU:HD21	2.13	0.63
1:D:248:LEU:HD23	1:D:305:GLN:HE21	1.62	0.63
2:S:40:ARG:HH22	6:X:-8:DG:H21	1.47	0.63
8:A:36:ALA:C	10:E:48:LEU:HD21	2.18	0.62
10:E:447:TRP:HE1	10:E:468:LEU:HD11	1.62	0.62
8:A:70:THR:HG21	8:A:404:VAL:N	2.15	0.62
1:F:258:LEU:HD22	1:F:261:TYR:HE1	1.65	0.62
8:A:210:LYS:HA	8:A:238:LEU:H	1.65	0.62
4:Q:51:LEU:HD21	5:R:67:PHE:CD1	2.34	0.62
8:A:41:LYS:NZ	9:B:812:GLU:OE2	2.32	0.62
8:A:365:THR:HG21	10:E:435:ARG:CD	2.30	0.62
9:B:1177:THR:HB	9:B:1182:LYS:HE2	1.80	0.61
8:A:125:GLY:O	8:A:129:GLU:HB2	2.00	0.61
8:A:405:GLU:HG3	8:A:408:SER:OG	2.01	0.61
3:T:32:PRO:HA	3:T:35:ARG:HB3	1.81	0.60
2:O:56:LYS:NZ	6:X:-64:DA:OP2	2.34	0.60
4:Q:111:ILE:HG23	4:Q:115:LEU:CD2	2.23	0.60
1:D:298:LEU:HD12	1:D:302:GLU:HB2	1.84	0.59
8:A:20:ARG:HG3	8:A:139:CYS:HA	1.84	0.59
9:B:770:ARG:HH12	9:B:778:LEU:HD12	1.67	0.59
1:D:248:LEU:HD23	1:D:305:GLN:NE2	2.18	0.59
10:E:491:VAL:HG11	10:E:493:LYS:HD3	1.83	0.59
8:A:43:HIS:NE2	9:B:822:GLU:OE2	2.35	0.59
8:A:365:THR:HG21	10:E:435:ARG:HD2	1.85	0.58
10:E:42:GLN:O	10:E:51:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:11:ARG:HH21	6:X:44:DT:H1'	1.68	0.58
8:A:36:ALA:CB	10:E:48:LEU:HD21	2.17	0.58
1:D:238:TYR:HA	1:D:242:ASP:HB2	1.84	0.58
2:O:79:LYS:HD3	2:O:82:LEU:HD13	1.85	0.58
10:E:419:LYS:HD3	10:E:451:CYS:HB3	1.85	0.58
2:O:85:GLN:HA	7:Y:-24:DG:H5"	1.84	0.58
2:O:128:ARG:HE	2:O:133:GLU:HB2	1.68	0.58
9:B:1197:ASP:OD1	9:B:1197:ASP:N	2.37	0.58
1:D:298:LEU:CD1	1:D:302:GLU:HB2	2.34	0.57
1:F:229:LYS:HD3	1:F:232:LEU:HD21	1.86	0.57
9:B:1302:ARG:HB3	9:B:1315:GLN:HB3	1.86	0.57
9:B:706:VAL:HA	9:B:709:TYR:HB2	1.86	0.57
4:Q:115:LEU:HG	2:S:48:LEU:CD2	2.21	0.56
1:D:229:LYS:HD3	10:E:360:THR:HG21	1.87	0.56
5:R:52:SER:HA	7:Y:-54:DA:H5"	1.88	0.56
8:A:90:THR:OG1	8:A:93:ASN:OD1	2.23	0.56
8:A:191:ASP:OD1	8:A:191:ASP:N	2.36	0.56
8:A:171:ILE:HA	8:A:174:LEU:HD12	1.87	0.56
9:B:1157:ARG:HG2	9:B:1238:LYS:HB3	1.87	0.55
4:Q:42:ARG:HE	5:R:85:THR:HB	1.71	0.55
10:E:303:CYS:SG	10:E:306:CYS:N	2.74	0.55
10:E:520:ILE:HD12	10:E:542:ILE:HG21	1.88	0.55
1:D:384:ASP:OD1	1:D:384:ASP:N	2.40	0.55
8:A:349:PRO:HB3	9:B:921:GLN:HG2	1.88	0.55
10:E:340:LEU:HA	10:E:343:ILE:HD12	1.88	0.55
1:D:260:LYS:O	1:D:264:GLU:HB2	2.07	0.55
8:A:41:LYS:O	8:A:44:ARG:NH1	2.39	0.55
1:F:228:LEU:HD22	1:F:367:LEU:HD23	1.89	0.55
3:T:39:ARG:NH1	3:T:43:VAL:O	2.40	0.54
8:A:152:ALA:HB3	8:A:164:ASN:HB2	1.88	0.54
10:E:511:LYS:HD2	10:G:334:LYS:HD2	1.89	0.54
6:X:65:DA:H2"	6:X:66:DT:C2	2.42	0.54
10:E:337:ALA:HA	10:E:340:LEU:HG	1.88	0.54
4:Q:30:VAL:HG13	4:Q:51:LEU:CD2	2.23	0.54
4:Q:16:THR:HA	7:Y:-43:DT:H5"	1.90	0.54
10:E:491:VAL:HG12	10:E:493:LYS:HD3	1.87	0.54
10:E:60:GLU:H	10:E:61:ARG:HH21	1.56	0.54
1:D:80:HIS:HE1	1:D:86:SER:HA	1.73	0.53
2:S:61:LEU:HD12	3:T:37:LEU:HD23	1.88	0.53
6:X:-47:DC:H2"	6:X:-46:DT:C5	2.44	0.53
10:E:333:VAL:HG23	10:E:337:ALA:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:288:ASP:OD2	10:E:304:ASN:ND2	2.41	0.53
4:Q:54:VAL:HG21	5:R:95:VAL:HG11	1.89	0.53
2:S:116:ARG:HD3	6:X:-3:DA:H3'	1.90	0.53
1:D:298:LEU:CD2	1:D:303:ARG:NE	2.72	0.53
8:A:21:VAL:HG22	8:A:141:VAL:HB	1.89	0.53
1:D:308:GLU:HA	1:D:311:LYS:HG2	1.91	0.53
9:B:945:THR:HG23	9:B:1146:ILE:HD13	1.90	0.53
1:D:253:THR:OG1	1:D:323:ILE:O	2.26	0.52
3:P:39:ARG:NH1	3:P:43:VAL:O	2.41	0.52
4:U:12:ALA:HB3	6:X:-42:DG:H4'	1.91	0.52
8:A:273:GLY:HA3	8:A:318:VAL:HB	1.90	0.52
9:B:686:LEU:HD22	10:E:547:ILE:HG21	1.92	0.52
1:F:316:ASP:N	1:F:316:ASP:OD1	2.42	0.52
8:A:337:ASP:OD1	8:A:352:LYS:NZ	2.43	0.52
1:F:338:LEU:HG	1:F:342:ILE:HD11	1.91	0.52
4:Q:81:ARG:HH22	4:Q:109:PRO:HD3	1.75	0.52
8:A:19:ARG:HD3	8:A:299:LYS:HD3	1.91	0.52
4:U:41:GLU:OE2	4:U:41:GLU:N	2.34	0.51
10:E:355:ASN:OD1	10:E:355:ASN:N	2.43	0.51
8:A:80:ASP:H	9:B:765:MET:HE1	1.74	0.51
8:A:31:ASN:O	9:B:865:LYS:NZ	2.37	0.51
8:A:405:GLU:O	8:A:408:SER:N	2.42	0.51
10:E:307:LYS:HA	10:E:311:PHE:HD2	1.76	0.51
4:Q:90:ASP:HB3	4:Q:93:LEU:HB2	1.92	0.51
2:S:72:ARG:HH21	2:S:84:PHE:HB2	1.75	0.51
3:T:92:ARG:HH22	5:V:98:LEU:HD23	1.76	0.51
7:Y:24:DA:H2”	7:Y:25:DG:C8	2.45	0.51
1:D:105:ILE:HG13	1:D:108:LYS:HA	1.92	0.51
4:U:80:PRO:HB3	5:V:58:ILE:HD12	1.92	0.51
9:B:920:GLU:HA	9:B:923:VAL:HG12	1.92	0.51
1:D:237:GLU:OE1	10:E:496:ARG:NH2	2.43	0.51
9:B:840:ASN:OD1	9:B:840:ASN:N	2.44	0.51
1:F:339:PRO:HA	1:F:342:ILE:HG12	1.92	0.50
3:T:36:ARG:NH1	6:X:-13:DA:OP1	2.44	0.50
2:O:87:SER:HA	2:O:90:MET:HB2	1.93	0.50
2:O:109:LEU:HA	2:O:112:ILE:HD12	1.92	0.50
2:S:60:LEU:HD13	2:S:93:GLN:HG2	1.94	0.50
8:A:76:GLN:O	9:B:770:ARG:NH1	2.41	0.50
9:B:1168:VAL:HG21	9:B:1232:TYR:CD2	2.46	0.50
9:B:1291:ARG:HD2	9:B:1321:ASP:HB2	1.93	0.50
8:A:159:GLY:HA2	8:A:215:PHE:HE2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:15:LYS:HD3	4:Q:20:ARG:HD3	1.92	0.50
1:D:298:LEU:HD11	1:D:302:GLU:C	2.31	0.50
4:U:54:VAL:HG21	5:V:95:VAL:HG21	1.94	0.50
1:F:17:PHE:HB2	1:F:96:ARG:HB3	1.92	0.50
4:U:90:ASP:HB3	4:U:93:LEU:HB2	1.93	0.50
8:A:405:GLU:O	8:A:406:GLU:C	2.49	0.50
9:B:864:LYS:HG2	9:B:880:ILE:HG12	1.93	0.50
10:E:440:CYS:HB3	10:E:445:THR:H	1.76	0.50
1:D:298:LEU:HD23	1:D:303:ARG:NE	2.26	0.50
8:A:194:GLU:OE2	8:A:235:ASN:ND2	2.45	0.50
10:E:404:ASP:OD1	10:E:404:ASP:N	2.45	0.50
3:P:91:LYS:HA	3:P:96:THR:HG22	1.93	0.49
4:Q:51:LEU:HD21	5:R:67:PHE:HE1	1.65	0.49
2:S:108:ASN:ND2	3:T:42:GLY:O	2.45	0.49
7:Y:-50:DC:H2"	7:Y:-49:DG:H5"	1.93	0.49
9:B:963:LYS:HE3	9:B:971:PRO:HD3	1.92	0.49
10:E:432:GLU:O	10:E:435:ARG:NH1	2.40	0.49
1:F:254:VAL:O	1:F:258:LEU:HB2	2.13	0.49
3:P:97:LEU:HD11	4:U:103:ALA:HB2	1.94	0.49
1:F:80:HIS:NE2	7:Y:12:DT:OP1	2.44	0.49
3:P:64:ASN:OD1	3:P:67:ARG:NH2	2.46	0.49
1:F:267:GLN:HE21	10:G:561:VAL:HB	1.78	0.49
4:Q:79:ILE:HG22	4:Q:81:ARG:H	1.77	0.49
2:S:63:ARG:HB2	2:S:66:PRO:HD2	1.95	0.49
10:G:310:ILE:HD12	10:G:314:ASN:ND2	2.28	0.49
2:O:61:LEU:HD22	3:P:36:ARG:HB3	1.95	0.49
4:U:79:ILE:HG22	4:U:81:ARG:H	1.76	0.49
6:X:31:DT:H2"	6:X:32:DG:H5"	1.94	0.49
1:F:256:MET:SD	1:F:257:VAL:N	2.86	0.49
8:A:185:ILE:HA	8:A:208:PHE:HB2	1.95	0.49
1:F:300:ARG:O	1:F:304:LEU:HD12	2.13	0.48
4:U:54:VAL:HG22	5:V:107:ALA:HB1	1.95	0.48
8:A:89:VAL:HG21	8:A:116:LEU:HD23	1.95	0.48
9:B:1228:LEU:HD12	9:B:1240:TYR:HE1	1.78	0.48
9:B:963:LYS:O	9:B:967:LEU:N	2.46	0.48
1:F:239:VAL:HA	1:F:243:LYS:HA	1.95	0.48
4:Q:30:VAL:HG13	5:R:67:PHE:HE1	1.77	0.48
6:X:-37:DG:N2	7:Y:38:DT:O2	2.46	0.48
9:B:870:VAL:HG13	9:B:871:TYR:HD2	1.79	0.48
1:D:299:TYR:HA	10:E:350:GLN:HB2	1.95	0.48
9:B:1253:ALA:HA	9:B:1256:LEU:HD23	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:323:GLU:OE2	10:G:323:GLU:N	2.45	0.48
1:D:230:SER:HA	1:D:233:VAL:HG22	1.96	0.48
8:A:183:ILE:HG13	8:A:206:CYS:HB3	1.96	0.48
9:B:952:ILE:HG13	9:B:1316:TYR:HB2	1.96	0.48
9:B:967:LEU:HG	9:B:969:PRO:HD2	1.95	0.48
1:D:348:ASP:OD1	10:E:338:LYS:NZ	2.46	0.48
1:D:300:ARG:HA	1:D:303:ARG:HG2	1.96	0.48
4:Q:76:THR:O	5:R:49:THR:OG1	2.31	0.48
6:X:-6:DG:H2"	6:X:-5:DG:N7	2.29	0.47
8:A:136:ARG:HG2	8:A:138:LYS:HG2	1.96	0.47
9:B:777:VAL:HG23	9:B:778:LEU:HG	1.97	0.47
2:S:128:ARG:HE	2:S:133:GLU:HG3	1.79	0.47
9:B:1158:LEU:HA	9:B:1161:ILE:HG22	1.97	0.47
1:D:85:LYS:HE2	1:D:85:LYS:HB2	1.77	0.47
2:O:106:ASP:OD1	2:O:131:ARG:NH1	2.47	0.47
7:Y:85:DC:H2"	7:Y:86:DG:C8	2.50	0.47
9:B:1194:MET:HE1	9:B:1223:TRP:HE1	1.79	0.47
1:D:320:LEU:HD21	1:D:325:ILE:HD13	1.97	0.47
8:A:298:VAL:HG13	8:A:305:MET:HE1	1.96	0.47
10:G:344:ASP:OD1	10:G:344:ASP:N	2.43	0.47
1:D:24:GLU:O	1:D:80:HIS:N	2.47	0.47
4:Q:51:LEU:CD2	5:R:67:PHE:HE1	2.22	0.47
1:D:227:LYS:HG3	10:E:537:PHE:HE1	1.80	0.47
10:E:494:LYS:HG2	10:E:495:GLN:N	2.20	0.47
2:O:62:ILE:HD11	3:P:37:LEU:HD11	1.97	0.47
4:Q:23:LEU:HD23	4:Q:56:GLU:OE1	2.04	0.47
1:F:355:LEU:O	1:F:359:THR:HG23	2.14	0.46
2:O:40:ARG:HD2	2:O:40:ARG:HA	1.80	0.46
5:V:53:SER:N	6:X:-54:DC:OP1	2.48	0.46
8:A:335:ASP:N	8:A:335:ASP:OD1	2.48	0.46
9:B:1020:LEU:O	9:B:1273:ARG:NH2	2.48	0.46
9:B:1168:VAL:HG21	9:B:1232:TYR:HD2	1.79	0.46
10:E:491:VAL:HG12	10:E:493:LYS:HD2	1.96	0.46
3:T:87:VAL:HG21	3:T:100:PHE:HD1	1.80	0.46
9:B:699:LEU:HD13	9:B:726:TYR:HD1	1.81	0.46
8:A:150:HIS:HB3	8:A:166:ILE:HD12	1.97	0.46
10:E:510:GLN:HB3	10:E:514:TYR:HD1	1.80	0.46
8:A:97:PHE:CE1	8:A:100:GLU:HB2	2.51	0.46
10:E:545:ASN:O	10:E:549:TYR:HB2	2.15	0.46
1:D:298:LEU:HD11	1:D:302:GLU:O	2.16	0.46
8:A:44:ARG:HA	8:A:47:MET:HE3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:320:ARG:HD2	8:A:353:LEU:HA	1.97	0.46
9:B:908:ALA:HA	9:B:911:GLU:HG2	1.97	0.46
8:A:237:PRO:HB2	10:E:455:ALA:HB2	1.98	0.46
9:B:1265:ILE:HA	9:B:1268:LEU:HG	1.97	0.46
7:Y:12:DT:H2"	7:Y:13:DT:C5	2.50	0.46
9:B:779:ASN:OD1	9:B:779:ASN:N	2.49	0.46
8:A:405:GLU:O	8:A:407:ASP:N	2.50	0.45
10:E:36:PRO:HB2	10:E:46:TYR:OH	2.16	0.45
10:G:355:ASN:N	10:G:355:ASN:OD1	2.49	0.45
2:S:79:LYS:HD3	2:S:82:LEU:HD13	1.96	0.45
8:A:207:SER:OG	8:A:209:HIS:ND1	2.46	0.45
7:Y:22:DC:H2"	7:Y:23:DA:H5"	1.98	0.45
8:A:247:TYR:HA	8:A:250:VAL:HG12	1.99	0.45
9:B:993:ASP:HA	9:B:996:ILE:HG12	1.97	0.45
9:B:1182:LYS:HA	9:B:1182:LYS:HD3	1.83	0.45
3:P:36:ARG:NH1	7:Y:-13:DA:OP2	2.45	0.45
7:Y:-7:DC:H2"	7:Y:-6:DT:C5	2.50	0.45
4:Q:29:ARG:NH2	5:R:37:TYR:OH	2.50	0.45
5:V:48:ASP:OD1	5:V:48:ASP:N	2.45	0.45
8:A:414:THR:HG22	8:A:415:LYS:N	2.31	0.45
9:B:963:LYS:HD3	9:B:963:LYS:HA	1.74	0.45
10:E:545:ASN:HA	10:E:548:LYS:HE2	1.99	0.45
8:A:350:ASP:OD1	8:A:350:ASP:N	2.46	0.45
8:A:370:ASP:O	8:A:374:THR:HG23	2.16	0.45
8:A:24:PHE:HE1	8:A:64:TYR:HD1	1.64	0.45
8:A:37:GLY:HA2	9:B:812:GLU:HG3	1.99	0.45
4:Q:107:VAL:HG11	2:S:105:GLU:OE1	2.17	0.44
9:B:986:TYR:HE2	9:B:1028:LYS:H	1.65	0.44
10:E:436:LEU:HD13	10:E:457:PHE:HE1	1.82	0.44
1:D:389:ASN:HB3	9:B:756:LYS:HE2	1.99	0.44
6:X:-40:DC:C6	6:X:-39:DT:H72	2.52	0.44
7:Y:-36:DT:H2"	7:Y:-35:DA:N7	2.33	0.44
1:D:247:ARG:HG2	1:D:249:PRO:HD2	1.99	0.44
10:E:556:TYR:HE1	10:G:558:SER:HB3	1.83	0.44
9:B:919:LEU:HD22	9:B:922:LYS:HE2	1.99	0.44
10:G:309:LYS:HA	10:G:313:ASN:CB	2.43	0.44
1:D:308:GLU:HA	1:D:311:LYS:HE2	1.99	0.44
2:O:72:ARG:NH1	7:Y:-23:DC:OP1	2.50	0.44
10:E:543:ASP:OD1	10:E:543:ASP:N	2.48	0.44
9:B:904:GLU:HG3	10:E:43:ASN:HD22	1.82	0.44
9:B:699:LEU:HD23	9:B:699:LEU:HA	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:548:LYS:HG3	10:G:551:PHE:HE2	1.83	0.44
4:Q:63:LEU:HD22	5:R:42:LEU:HD13	1.98	0.44
4:U:29:ARG:NH2	7:Y:49:DC:OP1	2.51	0.44
9:B:883:LEU:HD23	9:B:890:THR:HG1	1.79	0.43
10:E:420:CYS:SG	10:E:448:HIS:ND1	2.90	0.43
1:D:248:LEU:HD22	1:D:309:LEU:HD21	1.98	0.43
9:B:692:TYR:HA	9:B:697:LEU:HB2	2.00	0.43
9:B:893:VAL:HG21	10:E:62:SER:HB3	2.00	0.43
4:Q:88:ARG:HA	4:Q:88:ARG:HD3	1.92	0.43
9:B:1181:ALA:HB1	9:B:1186:LEU:HB2	2.00	0.43
10:E:399:ASP:OD1	10:E:399:ASP:N	2.51	0.43
4:Q:95:LYS:HG2	5:R:100:PRO:HG3	2.01	0.43
7:Y:55:DT:H2"	7:Y:56:DC:C5	2.54	0.43
9:B:1175:ARG:HA	9:B:1175:ARG:HH11	1.83	0.43
9:B:861:THR:HG22	9:B:864:LYS:HD2	2.00	0.43
9:B:1020:LEU:HD11	9:B:1273:ARG:HG3	2.00	0.43
1:D:395:GLU:HG3	9:B:788:TRP:HE1	1.84	0.43
4:U:17:ARG:HB2	4:U:27:VAL:HB	2.01	0.43
9:B:958:ASP:HB3	10:E:422:GLN:HG2	2.01	0.43
1:D:254:VAL:HG11	1:D:289:PHE:HE2	1.84	0.43
4:Q:29:ARG:HE	4:Q:29:ARG:HB2	1.63	0.43
9:B:936:LYS:HA	9:B:936:LYS:HD3	1.75	0.43
4:Q:63:LEU:HD13	5:R:42:LEU:HB2	2.00	0.43
9:B:879:ILE:O	9:B:883:LEU:HG	2.17	0.43
10:G:562:GLN:HA	10:G:565:LYS:HD3	2.00	0.43
9:B:981:ASP:O	9:B:1155:TYR:OH	2.34	0.43
9:B:1218:ASP:OD1	9:B:1218:ASP:N	2.51	0.43
10:E:494:LYS:CG	10:E:495:GLN:H	2.18	0.43
1:F:260:LYS:HZ1	1:F:261:TYR:HD2	1.66	0.43
3:P:44:LYS:HD2	4:U:115:LEU:HG	2.00	0.43
5:V:95:VAL:HG13	5:V:99:LEU:HD12	2.01	0.43
6:X:67:DT:H2"	6:X:68:DC:C5	2.54	0.43
8:A:405:GLU:O	8:A:408:SER:OG	2.27	0.43
2:O:63:ARG:HD3	6:X:17:DA:H4'	2.00	0.42
7:Y:-57:DC:H2"	7:Y:-56:DC:C5	2.54	0.42
1:F:332:LEU:HA	1:F:335:ILE:HG12	2.00	0.42
6:X:-63:DT:H2"	6:X:-62:DA:H8	1.84	0.42
10:E:275:CYS:HB3	10:E:278:CYS:HB3	2.00	0.42
1:F:98:ARG:HD2	1:F:100:TYR:H	1.85	0.42
8:A:275:SER:O	8:A:275:SER:OG	2.37	0.42
1:F:244:LYS:HD3	1:F:244:LYS:HA	1.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Q:111:ILE:HG22	4:Q:115:LEU:HD23	1.85	0.42
6:X:24:DC:H2"	6:X:25:DT:C5	2.54	0.42
6:X:46:DG:H2"	6:X:47:DA:N7	2.34	0.42
6:X:61:DC:H2"	6:X:62:DG:H5"	2.01	0.42
1:D:396:GLY:O	8:A:102:VAL:HB	2.20	0.42
3:T:79:LYS:HA	3:T:79:LYS:HD3	1.78	0.42
6:X:-17:DT:H2"	6:X:-16:DT:C5	2.54	0.42
9:B:935:PHE:HA	9:B:938:ALA:HB3	2.01	0.42
8:A:135:ASN:HD21	8:A:173:LEU:HA	1.83	0.42
10:E:406:HIS:HA	10:E:437:ILE:HD11	2.01	0.42
1:D:224:ILE:HB	1:D:229:LYS:HE3	2.02	0.42
3:P:38:ALA:HB1	3:P:43:VAL:HB	2.02	0.42
9:B:716:LEU:HD12	9:B:719:TRP:HD1	1.85	0.42
9:B:1140:ALA:HB1	9:B:1144:ILE:HG23	2.01	0.42
9:B:1274:ASN:OD1	9:B:1274:ASN:N	2.52	0.42
10:G:557:LYS:O	10:G:561:VAL:HG12	2.20	0.42
7:Y:44:DC:H2"	7:Y:45:DC:C5	2.55	0.41
8:A:36:ALA:HB3	10:E:48:LEU:HD22	1.98	0.41
9:B:936:LYS:HD3	9:B:1241:THR:HG22	2.02	0.41
1:D:378:ASP:H	10:E:489:TYR:HE2	1.68	0.41
7:Y:-27:DC:H2"	7:Y:-26:DT:C5	2.54	0.41
1:D:333:ARG:HB3	10:E:351:PHE:CE1	2.54	0.41
1:D:338:LEU:HD23	1:D:338:LEU:HA	1.94	0.41
6:X:-86:DC:H2"	6:X:-85:DG:C8	2.55	0.41
6:X:27:DG:H2"	6:X:28:DA:N7	2.35	0.41
6:X:28:DA:H2"	6:X:29:DG:H5"	2.01	0.41
10:E:275:CYS:SG	10:E:276:ASP:N	2.93	0.41
6:X:-63:DT:H2"	6:X:-62:DA:C8	2.55	0.41
1:F:321:VAL:HG12	1:F:323:ILE:H	1.85	0.41
7:Y:71:DT:H2"	7:Y:72:DG:C8	2.55	0.41
1:D:332:LEU:HD23	1:D:332:LEU:HA	1.87	0.41
2:O:108:ASN:ND2	3:P:42:GLY:O	2.54	0.41
4:Q:115:LEU:CD1	3:T:44:LYS:HB2	2.50	0.41
5:R:87:THR:OG1	5:R:90:GLU:OE1	2.37	0.41
5:V:54:LYS:HA	5:V:54:LYS:HD3	1.70	0.41
6:X:13:DT:H2"	6:X:14:DT:C5	2.56	0.41
8:A:280:ARG:HE	8:A:280:ARG:HB2	1.63	0.41
1:D:281:TYR:HA	10:E:335:ILE:HD11	2.02	0.41
6:X:-61:DT:H2"	6:X:-60:DA:C8	2.56	0.41
9:B:679:LYS:O	9:B:683:THR:HG23	2.21	0.41
1:F:19:GLY:HA2	1:F:20:PRO:HD3	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:226:ILE:HG23	1:F:229:LYS:HG3	2.03	0.41
3:T:47:SER:HA	7:Y:7:DC:H5"	2.03	0.41
8:A:135:ASN:ND2	8:A:172:GLU:O	2.53	0.41
8:A:151:HIS:CG	8:A:159:GLY:HA3	2.56	0.41
8:A:168:LEU:HA	8:A:171:ILE:HG12	2.03	0.41
9:B:949:ILE:HA	9:B:952:ILE:HG22	2.03	0.41
9:B:1175:ARG:HA	9:B:1175:ARG:NH1	2.36	0.41
9:B:1210:LEU:HD22	9:B:1219:LEU:HD21	2.03	0.41
10:E:374:ASP:OD1	10:E:374:ASP:N	2.50	0.41
10:E:476:LYS:HE3	10:E:476:LYS:HB2	1.96	0.41
1:D:227:LYS:HZ2	10:E:536:ASP:N	2.18	0.41
3:T:38:ALA:HB1	3:T:43:VAL:HB	2.03	0.41
9:B:826:ARG:HE	9:B:826:ARG:HB3	1.64	0.41
10:E:560:MET:SD	10:E:560:MET:N	2.88	0.41
4:Q:114:VAL:O	4:Q:114:VAL:HG12	2.21	0.40
1:D:303:ARG:NH2	10:E:287:LEU:O	2.54	0.40
6:X:-30:DA:H2'	6:X:-29:DT:H71	2.02	0.40
8:A:405:GLU:C	8:A:407:ASP:N	2.74	0.40
9:B:870:VAL:HG11	9:B:898:LEU:HD21	2.04	0.40
10:E:441:ASP:HB3	10:E:463:LYS:HE3	2.02	0.40
2:O:63:ARG:HB2	2:O:66:PRO:HD2	2.03	0.40
2:O:119:ILE:HD12	3:P:50:ILE:HG12	2.04	0.40
8:A:50:SER:O	8:A:54:ASN:ND2	2.44	0.40
8:A:141:VAL:HG11	8:A:329:LEU:HD22	2.02	0.40
10:E:320:LYS:HD2	10:E:320:LYS:HA	1.81	0.40
1:F:228:LEU:HD12	1:F:228:LEU:HA	1.90	0.40
1:F:330:HIS:O	1:F:334:LEU:HD23	2.21	0.40
6:X:37:DC:H2"	6:X:38:DG:C8	2.57	0.40
8:A:43:HIS:CD2	8:A:46:ARG:HH21	2.40	0.40
8:A:321:THR:O	8:A:325:GLU:HG2	2.20	0.40
1:F:227:LYS:HG2	1:F:367:LEU:HD11	2.03	0.40
1:F:330:HIS:O	1:F:333:ARG:HG3	2.22	0.40
4:Q:13:LYS:HD2	4:Q:13:LYS:HA	1.97	0.40
8:A:247:TYR:O	8:A:251:PHE:HB2	2.21	0.40
8:A:295:VAL:HA	8:A:298:VAL:HG12	2.03	0.40
9:B:691:LEU:HD23	9:B:691:LEU:HA	1.82	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	D	224/401 (56%)	212 (95%)	12 (5%)	0	100 100
1	F	192/401 (48%)	182 (95%)	10 (5%)	0	100 100
2	O	96/135 (71%)	94 (98%)	2 (2%)	0	100 100
2	S	96/135 (71%)	95 (99%)	1 (1%)	0	100 100
3	P	77/102 (76%)	76 (99%)	1 (1%)	0	100 100
3	T	77/102 (76%)	75 (97%)	2 (3%)	0	100 100
4	Q	104/129 (81%)	103 (99%)	1 (1%)	0	100 100
4	U	105/129 (81%)	104 (99%)	1 (1%)	0	100 100
5	R	91/122 (75%)	90 (99%)	1 (1%)	0	100 100
5	V	89/122 (73%)	89 (100%)	0	0	100 100
8	A	384/433 (89%)	364 (95%)	19 (5%)	1 (0%)	41 71
9	B	531/1371 (39%)	513 (97%)	18 (3%)	0	100 100
10	E	289/733 (39%)	252 (87%)	37 (13%)	0	100 100
10	G	80/733 (11%)	76 (95%)	4 (5%)	0	100 100
All	All	2435/5048 (48%)	2325 (96%)	109 (4%)	1 (0%)	100 100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	A	406	GLU

### 5.3.2 Protein sidechains (i)

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	D	209/359 (58%)	190 (91%)	19 (9%)	9	31
1	F	182/359 (51%)	166 (91%)	16 (9%)	10	34
2	O	84/108 (78%)	82 (98%)	2 (2%)	49	74
2	S	84/108 (78%)	79 (94%)	5 (6%)	19	48
3	P	66/78 (85%)	64 (97%)	2 (3%)	41	70
3	T	66/78 (85%)	65 (98%)	1 (2%)	65	84
4	Q	83/101 (82%)	81 (98%)	2 (2%)	49	74
4	U	84/101 (83%)	80 (95%)	4 (5%)	25	57
5	R	80/102 (78%)	71 (89%)	9 (11%)	6	22
5	V	78/102 (76%)	74 (95%)	4 (5%)	24	54
8	A	326/367 (89%)	293 (90%)	33 (10%)	7	26
9	B	499/1247 (40%)	456 (91%)	43 (9%)	10	36
10	E	284/692 (41%)	256 (90%)	28 (10%)	8	27
10	G	82/692 (12%)	77 (94%)	5 (6%)	18	48
All	All	2207/4494 (49%)	2034 (92%)	173 (8%)	16	39

All (173) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	14	CYS
1	D	90	GLU
1	D	107	MET
1	D	109	LYS
1	D	223	GLN
1	D	256	MET
1	D	264	GLU
1	D	281	TYR
1	D	289	PHE
1	D	296	MET
1	D	308	GLU
1	D	326	TYR
1	D	341	LEU
1	D	344	SER
1	D	347	MET
1	D	368	MET
1	D	373	TYR

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Mol	Chain	Res	Type
1	D	381	ARG
1	D	386	LEU
1	F	88	TRP
1	F	238	TYR
1	F	241	LYS
1	F	247	ARG
1	F	256	MET
1	F	260	LYS
1	F	261	TYR
1	F	287	LEU
1	F	288	TYR
1	F	289	PHE
1	F	296	MET
1	F	312	LYS
1	F	326	TYR
1	F	334	LEU
1	F	347	MET
1	F	353	GLN
2	O	37	LYS
2	O	109	LEU
3	P	52	GLU
3	P	84	MET
4	Q	38	ASN
4	Q	81	ARG
5	R	31	LYS
5	R	33	SER
5	R	53	SER
5	R	88	SER
5	R	89	ARG
5	R	105	LYS
5	R	109	SER
5	R	113	LYS
5	R	120	SER
2	S	41	TYR
2	S	42	ARG
2	S	53	ARG
2	S	59	GLU
2	S	63	ARG
3	T	84	MET
4	U	36	LYS
4	U	75	LYS
4	U	95	LYS

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Mol	Chain	Res	Type
4	U	104	GLN
5	V	32	GLU
5	V	81	ASN
5	V	102	GLU
5	V	105	LYS
8	A	17	ASP
8	A	47	MET
8	A	64	TYR
8	A	67	LYS
8	A	82	TYR
8	A	85	PHE
8	A	96	MET
8	A	97	PHE
8	A	128	MET
8	A	129	GLU
8	A	150	HIS
8	A	153	LYS
8	A	160	PHE
8	A	191	ASP
8	A	201	ASP
8	A	210	LYS
8	A	214	PHE
8	A	222	ARG
8	A	248	ARG
8	A	259	MET
8	A	270	GLN
8	A	275	SER
8	A	277	SER
8	A	279	ASP
8	A	280	ARG
8	A	306	MET
8	A	336	LYS
8	A	340	TYR
8	A	344	TYR
8	A	345	GLU
8	A	360	MET
8	A	381	GLU
8	A	422	ARG
9	B	668	PHE
9	B	709	TYR
9	B	717	PHE
9	B	723	PHE

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Mol	Chain	Res	Type
9	B	756	LYS
9	B	775	TRP
9	B	800	LYS
9	B	811	GLU
9	B	818	ASP
9	B	825	LEU
9	B	841	MET
9	B	868	ARG
9	B	872	ASP
9	B	885	GLU
9	B	907	ARG
9	B	912	TRP
9	B	916	TRP
9	B	929	ASP
9	B	946	LYS
9	B	974	GLN
9	B	995	PHE
9	B	1009	ARG
9	B	1013	LEU
9	B	1016	TYR
9	B	1017	PHE
9	B	1021	PHE
9	B	1028	LYS
9	B	1155	TYR
9	B	1164	MET
9	B	1175	ARG
9	B	1187	LEU
9	B	1189	SER
9	B	1194	MET
9	B	1214	LEU
9	B	1221	HIS
9	B	1223	TRP
9	B	1232	TYR
9	B	1237	PHE
9	B	1257	MET
9	B	1281	LYS
9	B	1294	MET
9	B	1302	ARG
9	B	1308	ARG
10	E	34	LYS
10	E	37	LYS
10	E	38	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
10	E	41	SER
10	E	51	ARG
10	E	61	ARG
10	E	262	PHE
10	E	273	LEU
10	E	276	ASP
10	E	305	GLU
10	E	321	LYS
10	E	334	LYS
10	E	341	PHE
10	E	365	LYS
10	E	369	ARG
10	E	375	GLU
10	E	401	TYR
10	E	409	SER
10	E	418	TYR
10	E	430	HIS
10	E	497	LEU
10	E	505	TYR
10	E	515	GLN
10	E	549	TYR
10	E	551	PHE
10	E	553	ASP
10	E	556	TYR
10	E	560	MET
10	G	304	ASN
10	G	316	MET
10	G	346	HIS
10	G	551	PHE
10	G	556	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	305	GLN
1	F	259	ASN
9	B	1293	HIS

### 5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	M3L	O	36	2	10,11,12	0.52	0	9,14,16	0.49	0
2	M3L	S	36	2	10,11,12	0.51	0	9,14,16	0.48	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	M3L	O	36	2	-	3/9/10/12	-
2	M3L	S	36	2	-	1/9/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	O	36	M3L	O-C-CA-CB
2	O	36	M3L	CA-CB-CG-CD
2	O	36	M3L	N-CA-CB-CG
2	S	36	M3L	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [\(i\)](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

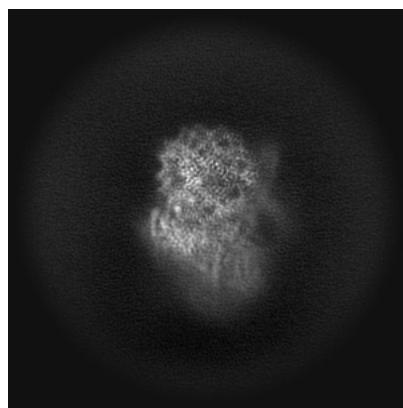
## 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-37126. These allow visual inspection of the internal detail of the map and identification of artifacts.

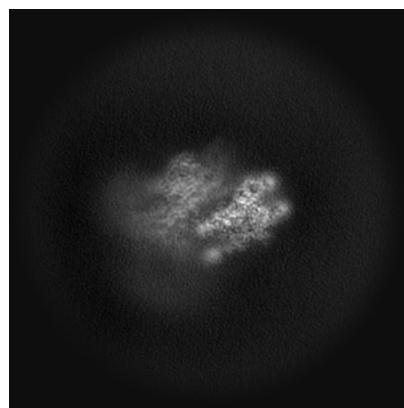
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections (i)

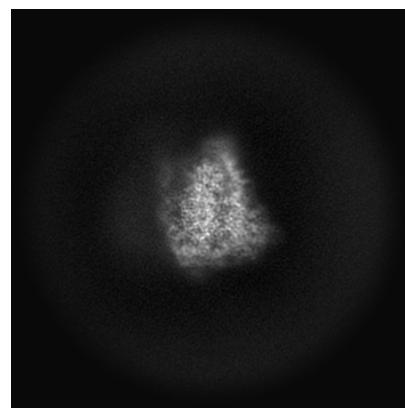
#### 6.1.1 Primary map



X

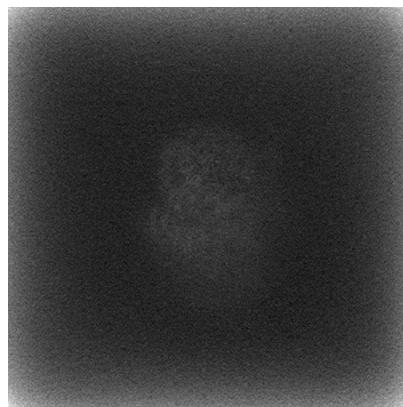


Y



Z

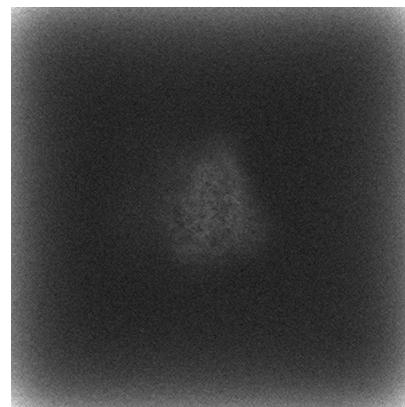
#### 6.1.2 Raw map



X



Y

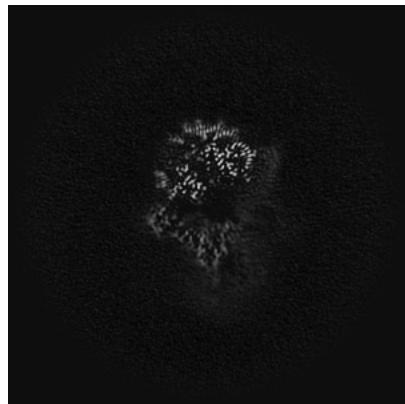


Z

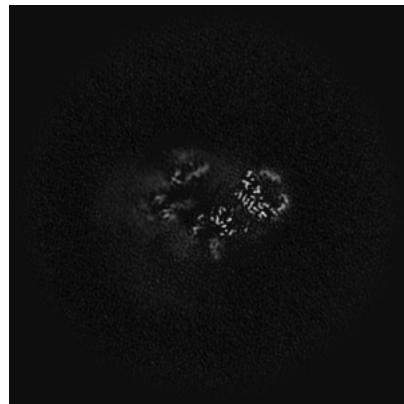
The images above show the map projected in three orthogonal directions.

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

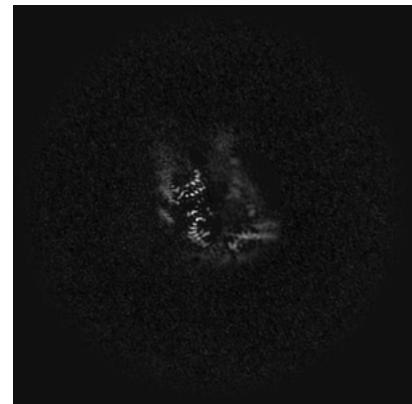
### 6.2.1 Primary map



X Index: 270

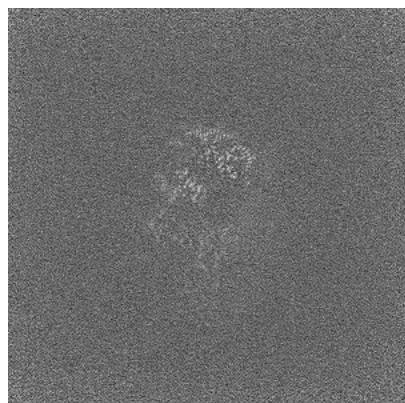


Y Index: 270

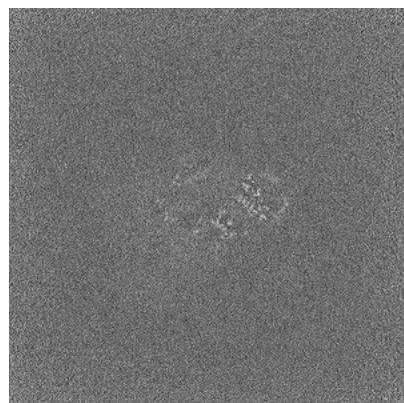


Z Index: 270

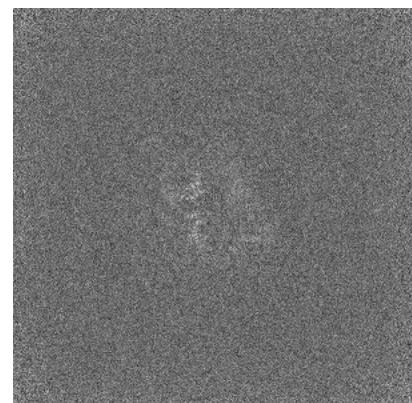
### 6.2.2 Raw map



X Index: 270



Y Index: 270

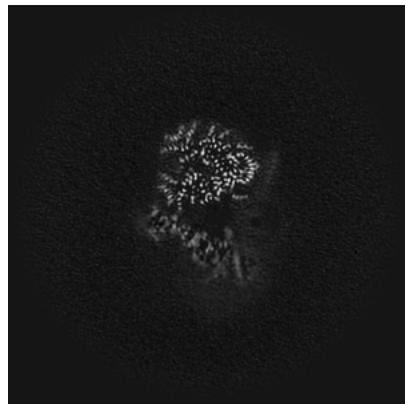


Z Index: 270

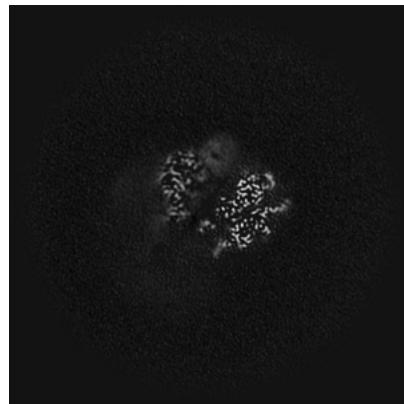
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [\(i\)](#)

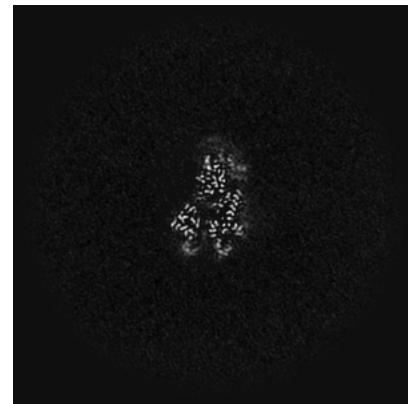
### 6.3.1 Primary map



X Index: 261

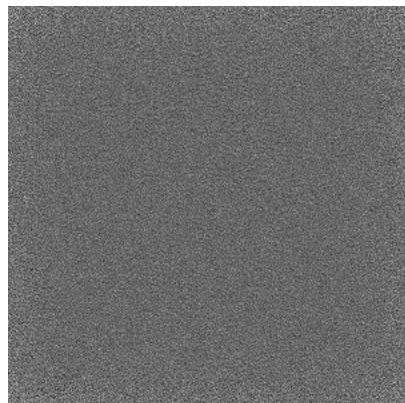


Y Index: 242

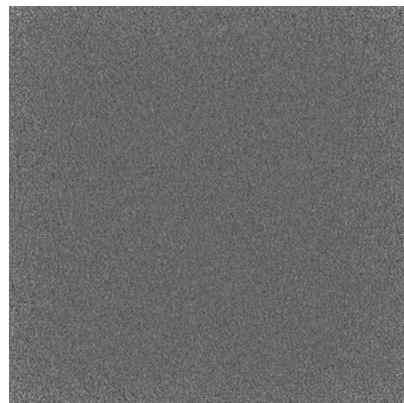


Z Index: 318

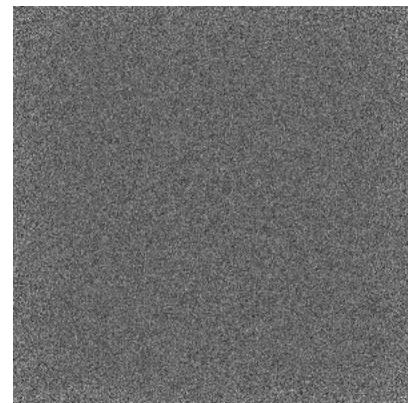
### 6.3.2 Raw map



X Index: 0



Y Index: 0

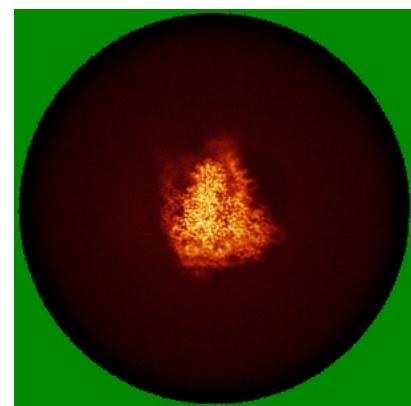
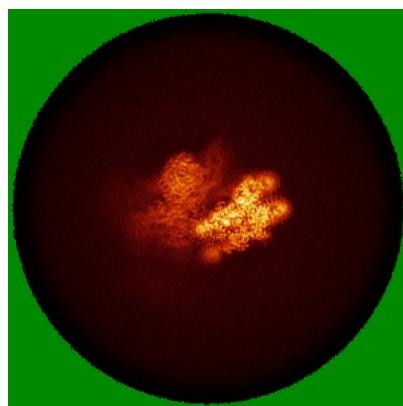
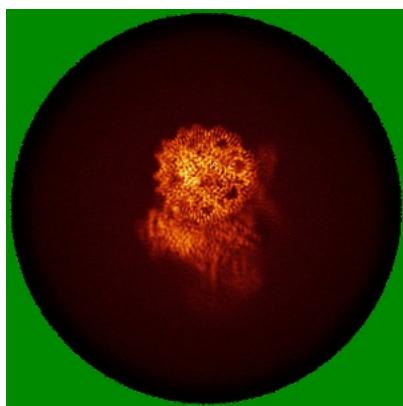


Z Index: 0

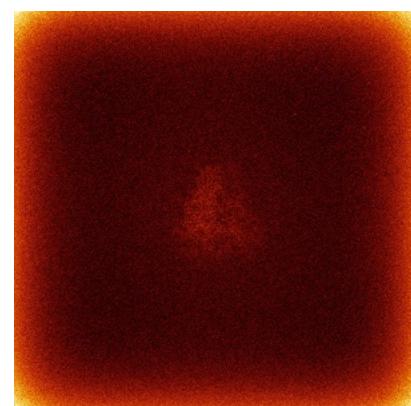
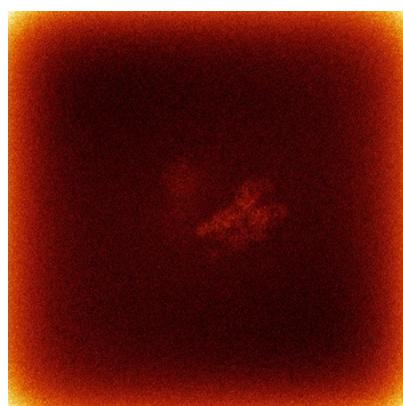
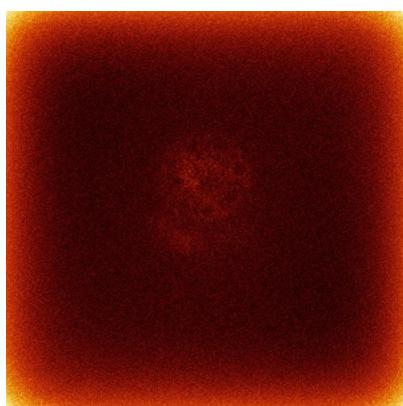
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



### 6.4.2 Raw map



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.

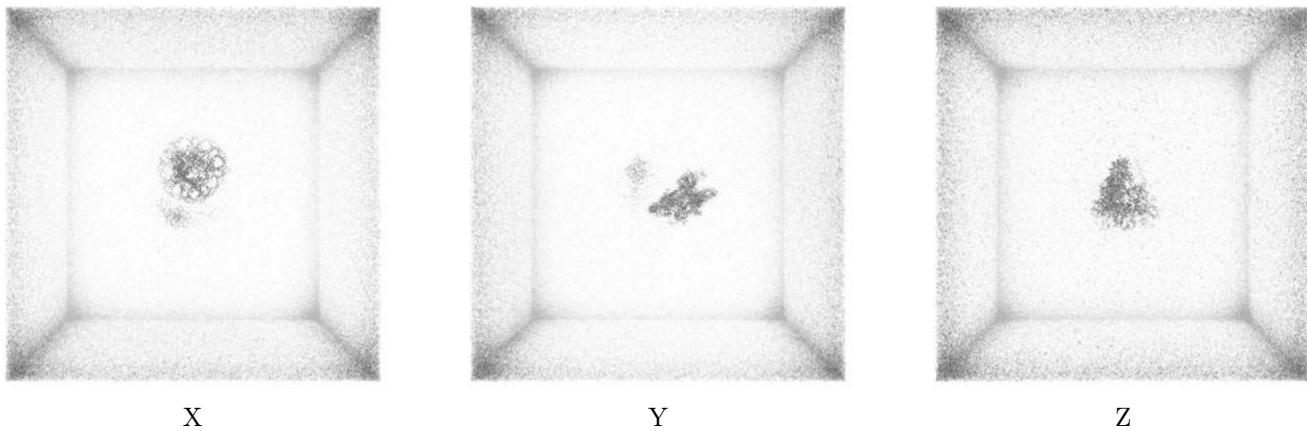
## 6.5 Orthogonal surface views [\(i\)](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

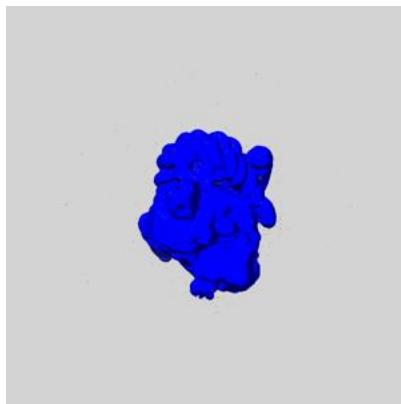
## 6.6 Mask visualisation [\(i\)](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

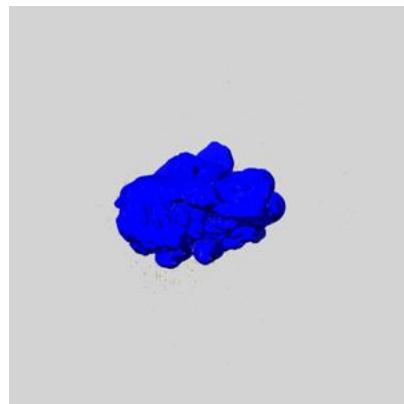
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

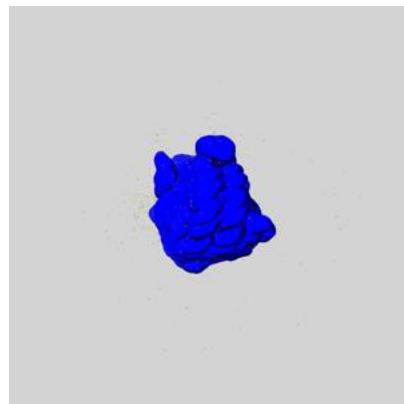
### 6.6.1 emd\_37126\_msk\_1.map [\(i\)](#)



X



Y

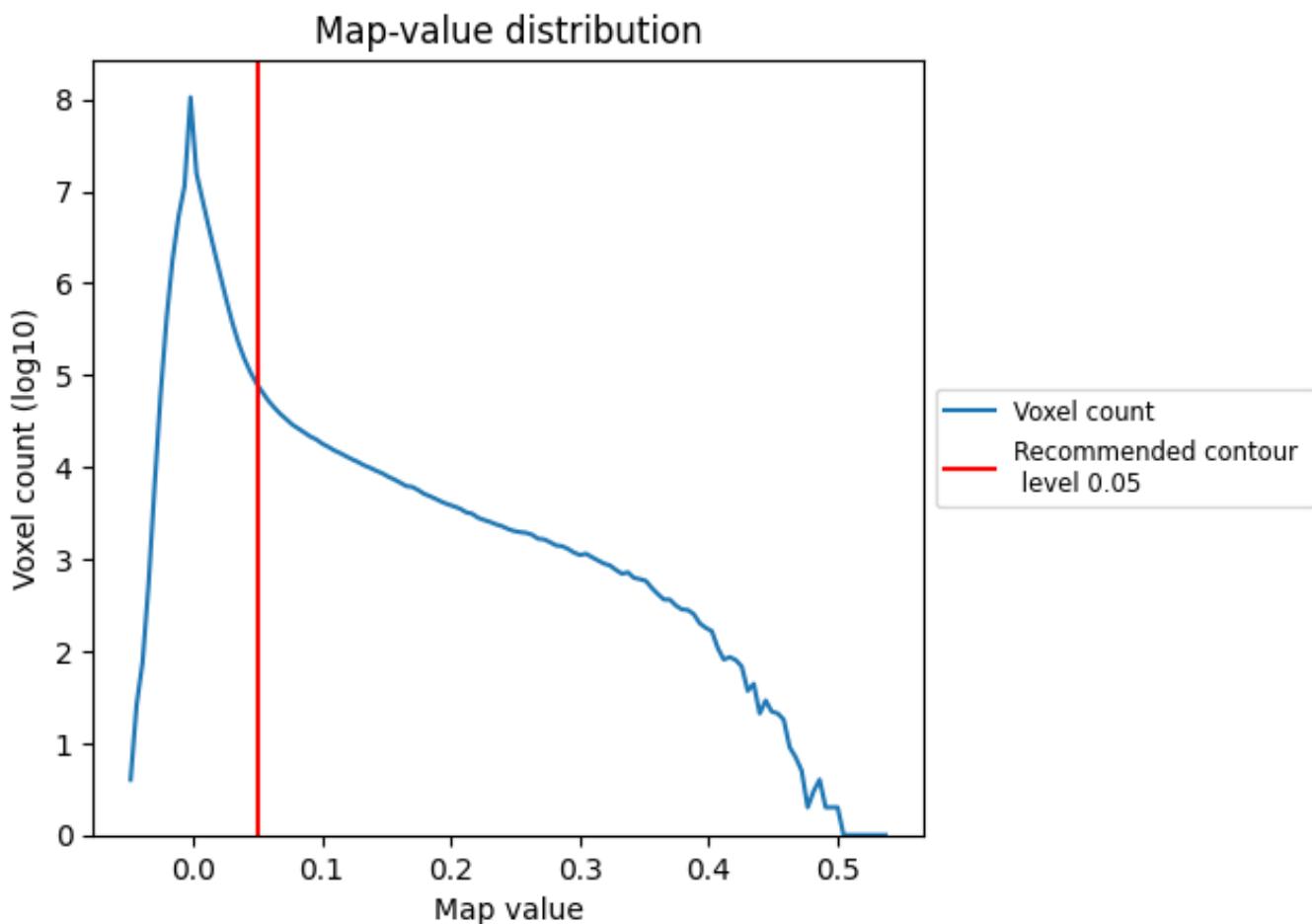


Z

## 7 Map analysis (i)

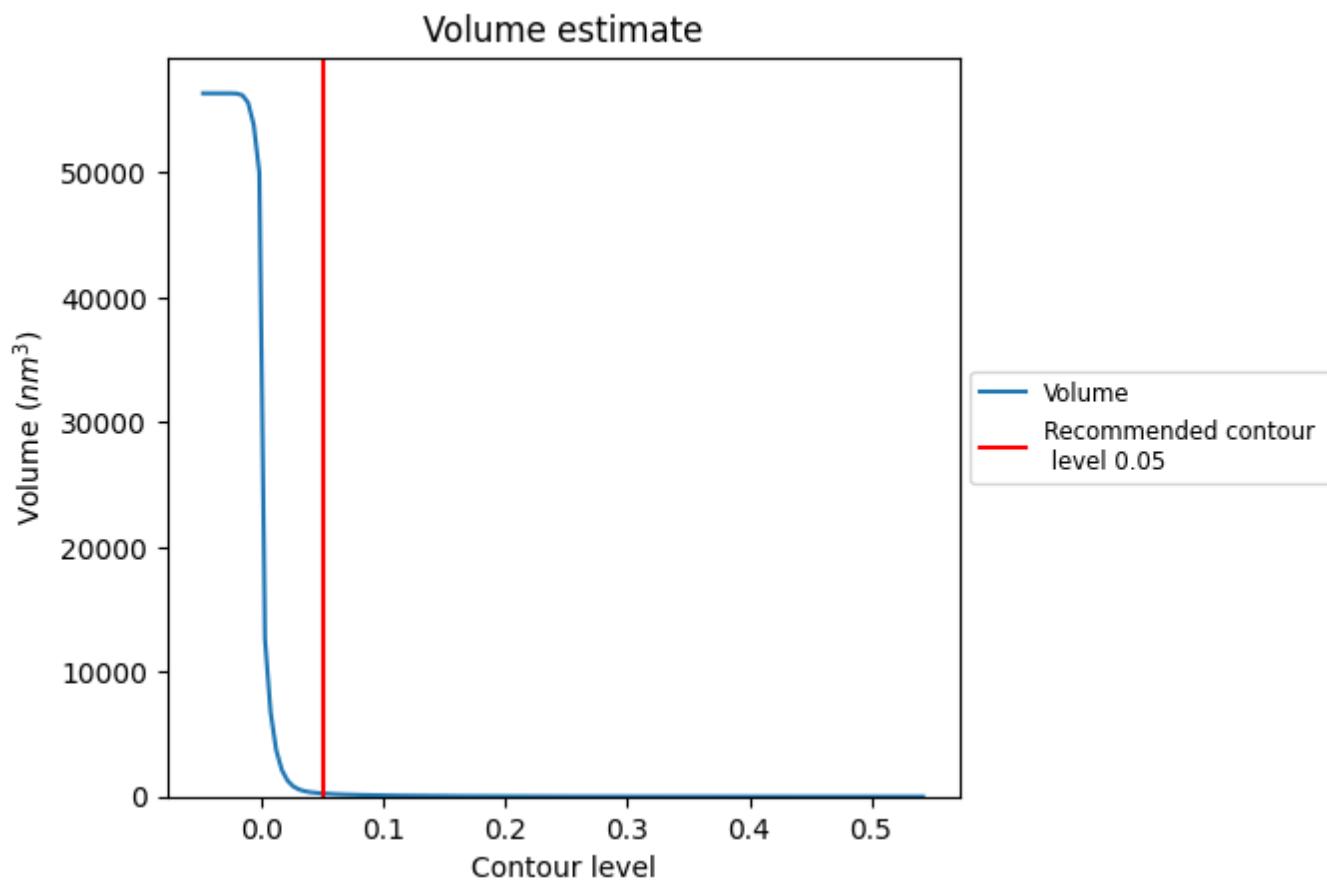
This section contains the results of statistical analysis of the map.

### 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.

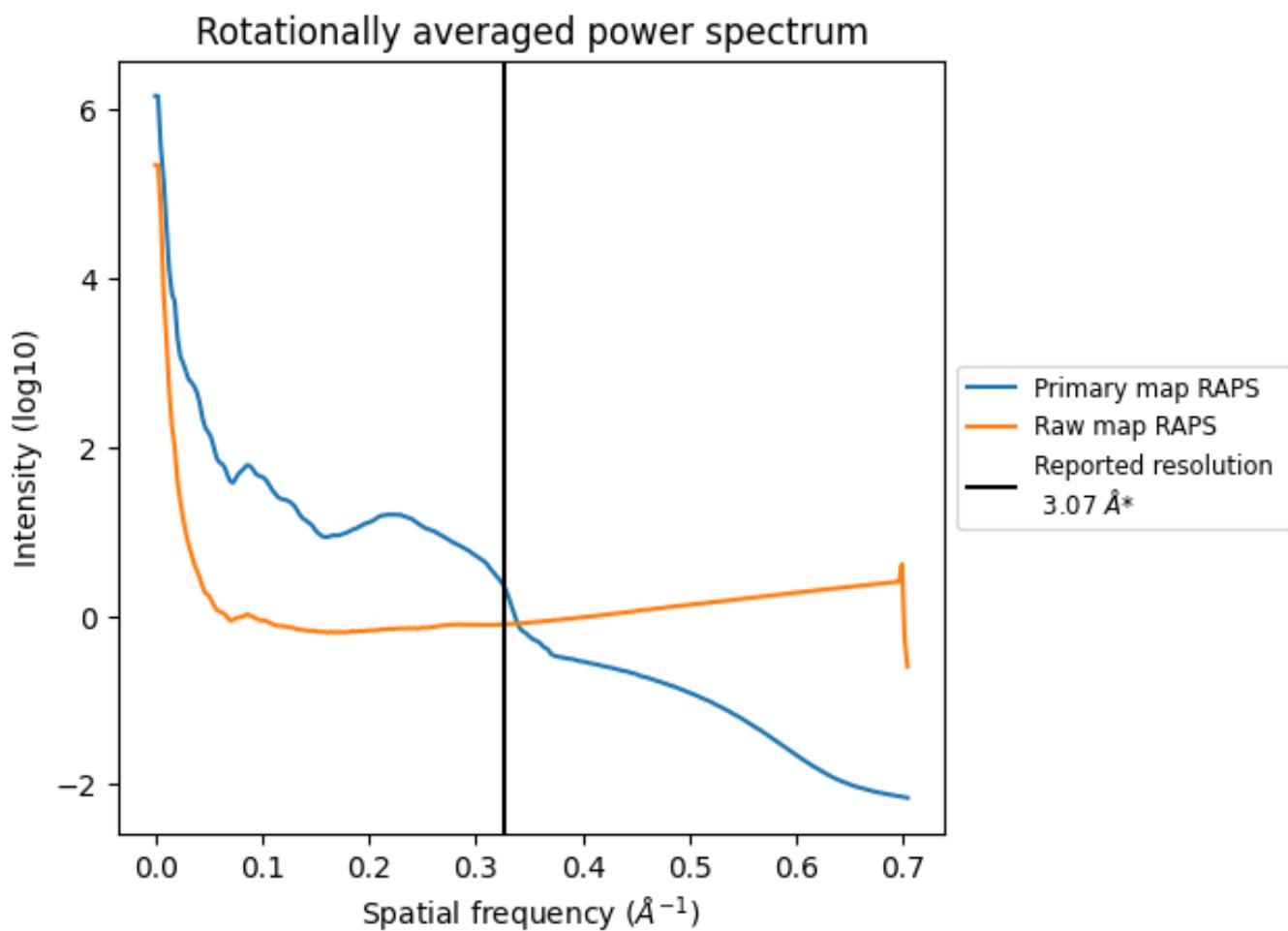
## 7.2 Volume estimate (i)



The volume at the recommended contour level is 244 nm<sup>3</sup>; this corresponds to an approximate mass of 221 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 [\(i\)](#)

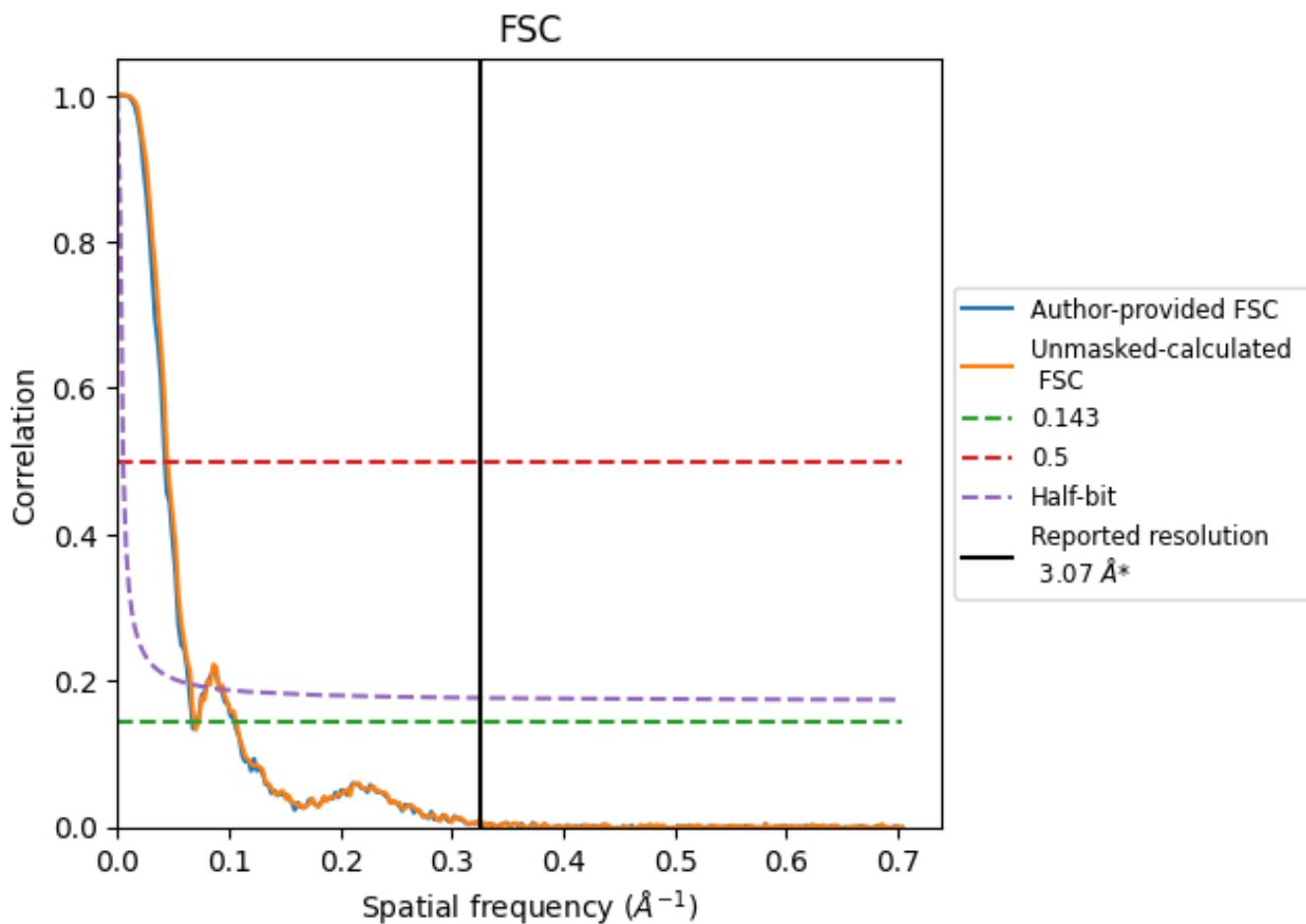


\*Reported resolution corresponds to spatial frequency of  $0.326 \text{ \AA}^{-1}$

## 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  $0.326 \text{\AA}^{-1}$

## 8.2 Resolution estimates [\(i\)](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.07	-	-
Author-provided FSC curve	14.86	23.36	15.62
Unmasked-calculated*	14.43	22.27	15.15

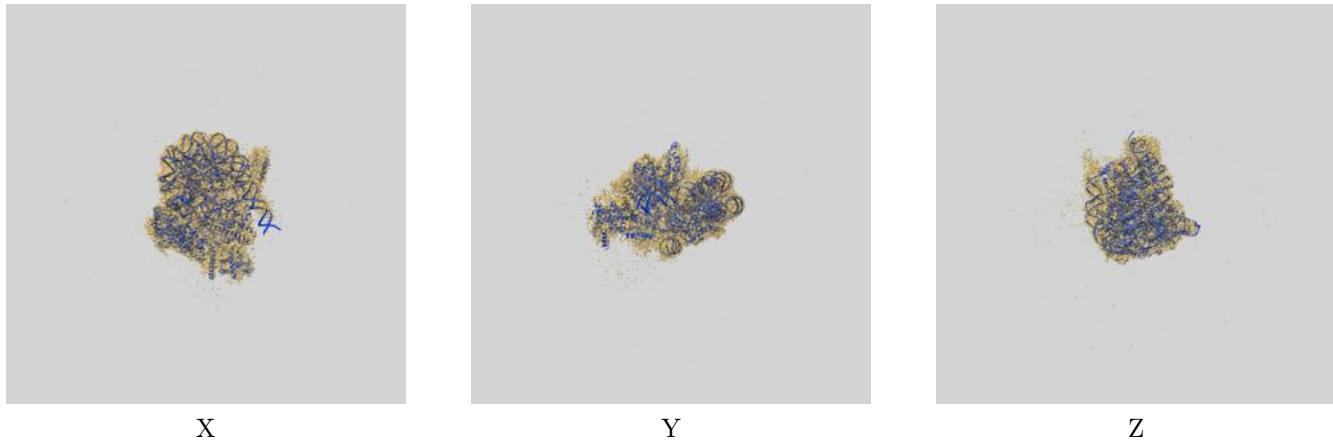
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 14.86 differs from the reported value 3.07 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 14.43 differs from the reported value 3.07 by more than 10 %

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

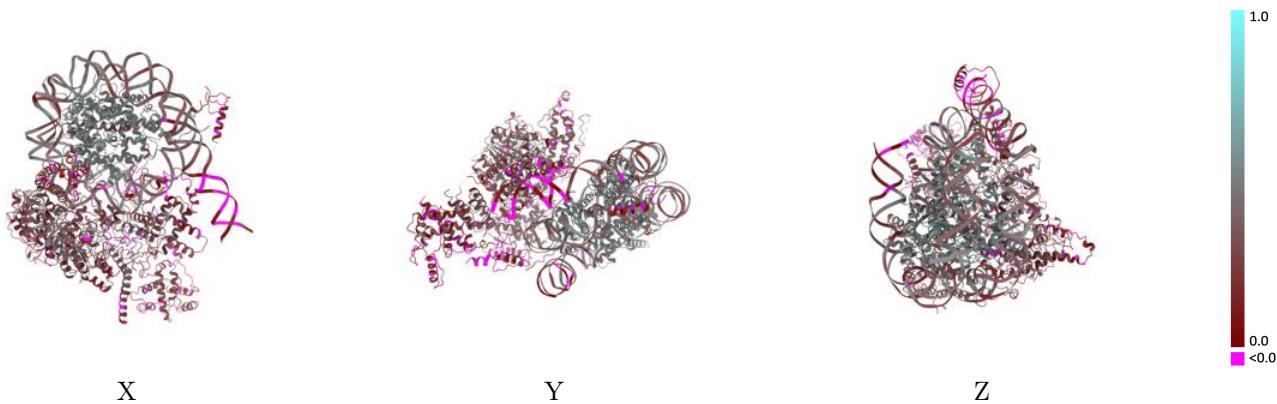
This section contains information regarding the fit between EMDB map EMD-37126 and PDB model 8KD6. Per-residue inclusion information can be found in section 3 on page 10.

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



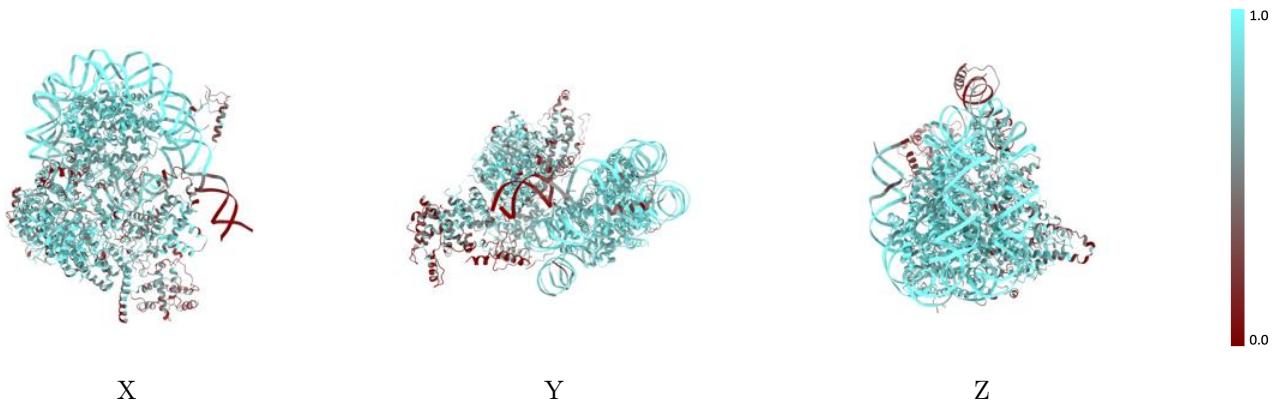
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



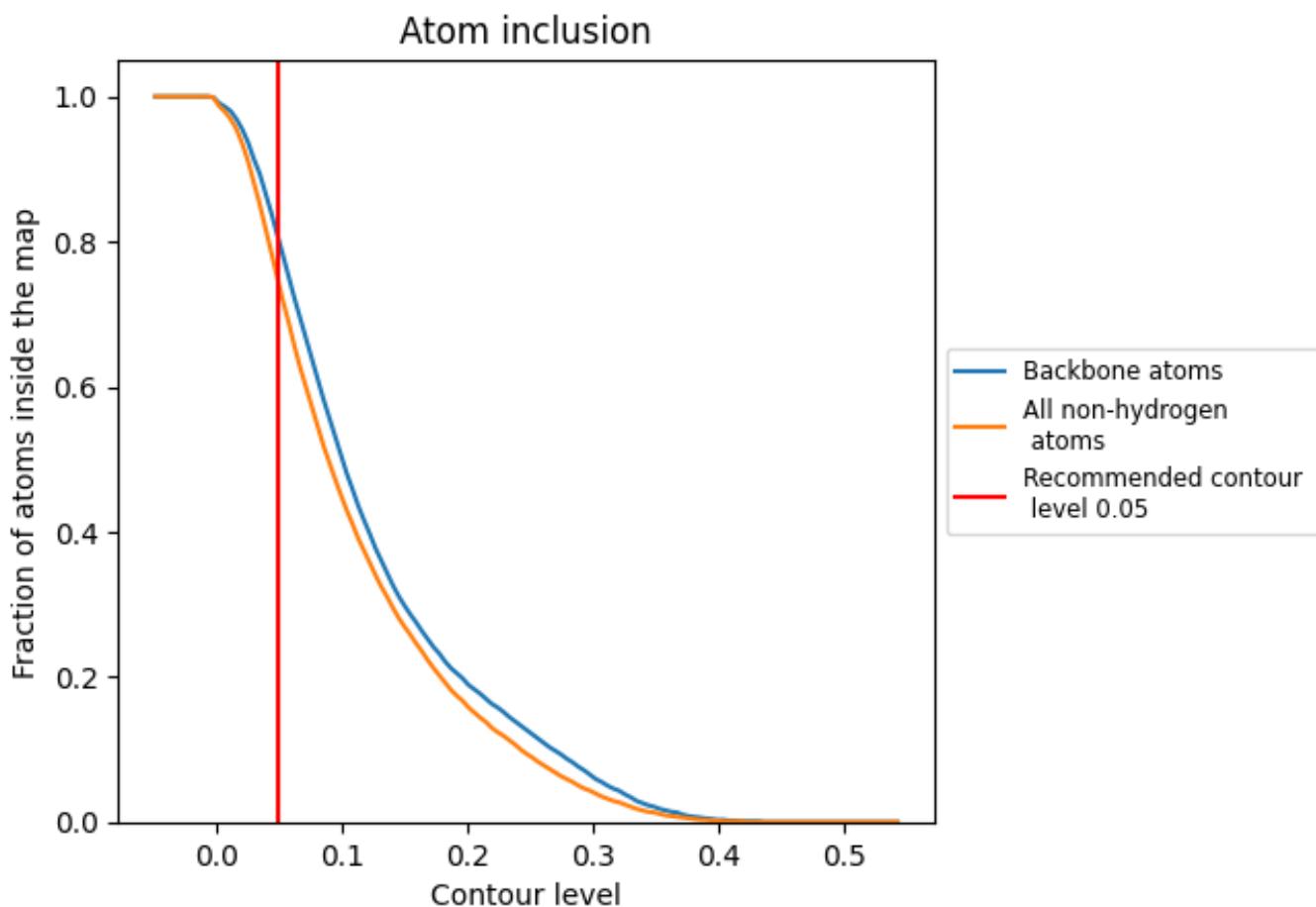
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

## 9.4 Atom inclusion [\(i\)](#)



At the recommended contour level, 80% of all backbone atoms, 74% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7410	0.3110
A	0.7960	0.3070
B	0.6780	0.2470
D	0.7120	0.2690
E	0.6140	0.2290
F	0.3150	0.1090
G	0.2550	0.0640
O	0.8870	0.4730
P	0.9310	0.5080
Q	0.8990	0.4670
R	0.9310	0.4980
S	0.8760	0.4520
T	0.8970	0.5090
U	0.9030	0.4710
V	0.9230	0.4870
X	0.8230	0.3240
Y	0.8240	0.3240

