

# wwPDB EM Validation Summary Report (i)

Jul 29, 2021 – 06:04 am BST

PDB ID	:	7OH9
EMDB ID	:	EMD-12897
$\operatorname{Title}$	:	Nucleosome with TBP and TFIIA bound at SHL -6
Authors	:	Wang, H.; Cramer, P.
Deposited on	:	2021-05-09
Resolution	:	3.00  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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

EMDB validation analysis	:	$0.0.0\mathrm{dev84}$
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.22

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.00 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.



Motrio	Whole archive	EM structures	
wietric	$(\# { m Entries})$	$(\# { m Entries})$	
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.

Mol	Chain	Length	Quality of chain							
1	А	135	<b>•</b> 57%	15%	28%					
1	Е	135	<b>●</b> 66%	7%	27%					
2	В	102	<b>•</b> 59%	21%	• 20%					
2	F	102	<b>•</b> 69%	9%	• 22%					
3	С	129	75%		9% • 16%					
3	G	129	• 74%		8% 18%					
4	D	122	<b>6</b> 6%	14%	20%					
4	Н	122	<b>•</b> 68%	10%	22%					



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Mol	Chain	Length	Quality of chain								
5	Ι	145	·	95%		5%					
6	J	145	•	85%		15%					
7	Κ	240	<b>8%</b> 58%		17%	25%					
8	L	171	29%	18%	4	14%					
9	М	122	39% 57%	_	28%	• 15%					



# 2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 15099 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Δ	07	Total	С	Ν	Ο	S	0	0
	Л	31	802	506	155	138	3	0	0
1	F	08	Total	С	Ν	Ο	$\mathbf{S}$	0	0
		30	811	512	157	139	3		

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	102	ALA	GLY	$\operatorname{conflict}$	UNP P84233
Е	102	ALA	GLY	conflict	UNP P84233

• Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	В	80	Total	С	Ν	Ο	$\mathbf{S}$	0	0
	2 D	02	653	412	127	113	1	0	0
9	Б	80	Total	С	Ν	Ο	$\mathbf{S}$	0	0
	Ľ		638	401	125	111	1		0

• Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues		Ato	$\mathbf{ms}$	AltConf	Trace	
3	С	109	Total 843	С 531	N 167	О 145	0	0
3	G	106	Total 818	C 516	N 160	O 142	0	0

• Molecule 4 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	97	Total 767	C 481	N 142	0 142	${ m S} { m 2}$	0	0



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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Н	95	Total 745	C 469	N 134	O 140	S 2	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	29	THR	SER	$\operatorname{conflict}$	UNP P02281
Н	29	THR	SER	conflict	UNP P02281

• Molecule 5 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ι	145	Total 2955	C 1404	N 537	O 869	Р 145	0	0

• Molecule 6 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	145	Total 2990	C 1416	N 558	0 871	Р 145	0	0

• Molecule 7 is a protein called TATA-binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace	
7	К	180	Total 1439	C 936	N 246	0 251	${ m S}{ m 6}$	3	0

• Molecule 8 is a protein called Transcription initiation factor IIA large subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace	
8	L	96	Total 823	С 516	N 138	O 166	${ m S} { m 3}$	3	0

There are 115 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	?	-	ASN	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	GLY	deletion	UNP P32773
L	?	-	LEU	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773



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Chain	Residue	Modelled	Actual	Comment	Reference
L	?	-	LEU	deletion	UNP P32773
L	?	-	PRO	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	SER	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773

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L	?	-	LEU	deletion	UNP P32773
L	?	-	PRO	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	SER	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	PRO	deletion	UNP P32773
L	?	-	HIS	deletion	UNP P32773
L	?	-	SER	deletion	UNP P32773
L	?	-	GLY	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	VAL	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	ALA	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	SER	deletion	UNP P32773
L	?	-	GLY	deletion	UNP P32773
L	?	-	ALA	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	LEU	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	_	SER	deletion	UNP P32773
L	?		GLY	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773



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	JIOIN	$p_{1}c_{0}c_{0}a_{0}$	puyc

Chain	Residue	Modelled	Actual	Comment	Reference
L	?	-	ALA	deletion	UNP P32773
L	?	-	ASP	deletion	UNP P32773
L	?	-	VAL	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	SER	deletion	UNP P32773
L	?	-	GLN	deletion	UNP P32773
L	?	-	PRO	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	VAL	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	PRO	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	LEU	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ALA	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	_	ILE	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	VAL	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	ASN	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	ASP	deletion	UNP P32773
L	?	-	ASP	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	SER	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	ASP	deletion	UNP P32773
L	?	-	ASP	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	_	LYS	deletion	UNP P32773



Chain	Residue	Modelled	Actual	Comment	Reference
L	?	_	GLU	deletion	UNP P32773
L	?	_	GLU	deletion	UNP P32773
L	?	-	ASP	deletion	UNP P32773
L	?	-	VAL	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	THR	deletion	UNP P32773
L	?	-	ARG	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	GLN	deletion	UNP P32773
L	?	-	ILE	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	GLN	deletion	UNP P32773
L	?	-	VAL	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	LEU	deletion	UNP P32773
L	?	-	GLN	deletion	UNP P32773
L	?	-	ALA	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	GLU	deletion	UNP P32773
L	?	-	LYS	deletion	UNP P32773
L	?	-	ARG	deletion	UNP P32773

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• Molecule 9 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace	
9	М	104	Total 815	C 512	N 136	O 163	$\frac{S}{4}$	1	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Chain A: 57% 15% 28% • Molecule 1: Histone H3.2 Chain E: 66% 27% 7% • Molecule 2: Histone H4 Chain B: 59% 21% 20% 721 222 223 • Molecule 2: Histone H4 Chain F: 69% 9% 22%
- Molecule 1: Histone H3.2

• Molecule 3: Histone H2A

Chain C:	75%	9% •	16%
SER GLY ARG GLY GLY GLY GLY CLY THR THR THR	S19 R29 R32 V54 V100 D90 V100 V100 L115 L115	K118 THR THR GLU SER SER K1A ALA LYS SER SER	2
• Molecule 3: Hist	cone H2A		
Chain G:	74%	8%	18%
SER 6LY ARG 6LY 6LY 6LV 6LV 6LX ARG ALA ALA	T16 S19 E41 E41 E41 E41 E62 L63 L63 L63 L63 L63 L63 L63 L63 C1102 L13 C1102 L13 T104	GLU SER SER ALA LYS SER LYS SER LYS LYS LYS SER LYS	
• Molecule 4: Hist	cone H2B 1.1		
Chain D:	66%	14%	20%
ALA ALA ALA ALA ALA ALA ALA ALA ALA ALA	ALA VALA THR THR THR CITY CITY CITY ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	158 158 158 158 158 158 158 158 158 158	R89 E90 793 194 198 198 198 198 198 198 198
• Molecule 4: Hist	cone H2B 1.1		
Chain H:	68%	10%	22%
ALA ALA SER ALA ALA ALA PRO PRO PRO CYS SER SER SER SER SER SER SER SER SER SE	ALA VIL THR THR THR CIN CIN CIN CIN CIN CIN CIN CIN CIN CIN	L58 M659 M659 R73 R76 S84 R89	V95 L98 K122
• Molecule 5: DN	A (145-MER)		
Chain I:	95%		5%
69 69 69 69 69 69 69 69 69 69	467 TT2 = 1 →		
• Molecule 6: DN	A (145-MER)		
Chain J:	85%		15%
A-72 	A-43 -43 -43 -43 -43 -43 -43 -43		
• Molecule 7: TAT	[A-binding protein		
Chain K:	58%	17%	25%
MET ALA ALA ASP ASP GLU GLU CYS GLU CYS GLU CYS	LYNS LYNS TILR VALL PRO ASP ASP ASP ASP ASP ASA ASC ASP ASA ASP ASP ASP ASP ASP ASP ASP ASP	ALA THR THR PHE GLN GLN GLU GLU GLU GLU CLU CLU ASP ASG	ALA ALA PRO GLU GLU GLU GLU CYS ASP ALA ALLA









# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	85777	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	41.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.076	Depositor
Minimum map value	-0.029	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0125	Depositor
Map size (Å)	209.99998, 209.99998, 209.99998	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor



# 5 Model quality (i)

## 5.1 Standard geometry (i)

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).

Mal	Chain	Bond	Bond lengths		ond angles
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.40	0/814	0.64	0/1092
1	Е	0.39	0/823	0.62	0/1104
2	В	0.39	0/660	0.63	0/883
2	F	0.39	0/645	0.62	0/862
3	С	0.37	0/853	0.65	1/1149~(0.1%)
3	G	0.34	0/828	0.56	0/1117
4	D	0.37	0/778	0.56	1/1043~(0.1%)
4	Н	0.34	0/756	0.54	0/1015
5	Ι	0.70	0/3311	0.94	0/5103
6	J	0.73	0/3357	0.93	0/5184
7	K	0.28	0/1466	0.61	0/1972
8	L	0.35	0/832	0.74	0/1120
9	М	0.32	0/822	0.82	3/1111~(0.3%)
All	All	0.53	0/15945	0.79	5/22755~(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
7	Κ	0	1
8	L	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	С	90	ASP	CB-CG-OD1	6.53	124.18	118.30
9	М	19	LEU	CA-CB-CG	6.36	129.93	115.30
9	М	41	LEU	CA-CB-CG	6.06	129.23	115.30



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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
9	М	19	LEU	CB-CG-CD1	5.33	120.06	111.00
4	D	65	ASP	CB-CG-OD1	5.08	122.87	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	Κ	186	GLU	Peptide
8	L	19	ASN	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	А	802	0	841	15	0
1	Е	811	0	853	10	0
2	В	653	0	696	16	0
2	F	638	0	676	10	0
3	С	843	0	908	10	0
3	G	818	0	877	10	0
4	D	767	0	799	14	0
4	Н	745	0	773	11	0
5	Ι	2955	0	1628	7	0
6	J	2990	0	1629	16	0
7	K	1439	0	1519	26	0
8	L	823	0	799	21	0
9	М	815	0	817	25	0
All	All	15099	0	12815	140	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 5.

The worst 5 of 140 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1 Atom-2		Interatomic distance (Å)	$egin{array}{clash} { m overlap} \ ({ m \AA}) \end{array}$	
7:K:85:VAL:HG23	7:K:146:ILE:HG13	1.74	0.69	



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:LEU:HD12	2:B:36:ARG:HB3	1.79	0.65
8:L:32:GLU:OE1	8:L:36:GLN:NE2	2.29	0.64
3:G:16:THR:HA	6:J:-43:DA:H5"	1.80	0.64
4:H:73:GLU:OE1	4:H:76:ARG:NH2	2.32	0.61

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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	Perce	$\mathbf{ntiles}$
1	А	95/135~(70%)	93~(98%)	2(2%)	0	100	100
1	Е	96/135~(71%)	96 (100%)	0	0	100	100
2	В	80/102~(78%)	78~(98%)	2(2%)	0	100	100
2	F	78/102~(76%)	77~(99%)	1 (1%)	0	100	100
3	С	107/129~(83%)	105~(98%)	2(2%)	0	100	100
3	G	104/129~(81%)	102~(98%)	2(2%)	0	100	100
4	D	95/122~(78%)	94 (99%)	1 (1%)	0	100	100
4	Н	93/122~(76%)	90~(97%)	3 (3%)	0	100	100
7	K	181/240~(75%)	176 (97%)	5(3%)	0	100	100
8	L	93/171~(54%)	85~(91%)	8 (9%)	0	100	100
9	М	101/122 (83%)	97~(96%)	4 (4%)	0	100	100
All	All	1123/1509~(74%)	1093~(97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.



#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Perce	ntiles
1	А	85/110~(77%)	84~(99%)	1 (1%)	71	90
1	Ε	86/110~(78%)	86 (100%)	0	100	100
2	В	67/78~(86%)	66~(98%)	1 (2%)	65	87
2	F	65/78~(83%)	64~(98%)	1 (2%)	65	87
3	С	86/101~(85%)	85~(99%)	1 (1%)	71	90
3	G	84/101~(83%)	84 (100%)	0	100	100
4	D	83/102~(81%)	83~(100%)	0	100	100
4	Н	81/102~(79%)	80~(99%)	1 (1%)	71	90
7	K	155/205~(76%)	155~(100%)	0	100	100
8	L	91/154~(59%)	89~(98%)	2 (2%)	52	81
9	М	93/108~(86%)	92~(99%)	1 (1%)	73	90
All	All	976/1249~(78%)	968 (99%)	8 (1%)	82	93

5 of 8 residues with a non-rotameric side chain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
9	М	53	LYS
8	L	263	LYS
4	Н	60	ASN
2	F	92	ARG
8	L	250	LYS

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

Mol	Chain	Res	Type
3	С	73	ASN
1	Е	68	GLN
3	G	104	GLN



#### 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 monosaccharides 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-12897. 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



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

### 6.2 Central slices (i)

#### 6.2.1 Primary map



X Index: 100



Y Index: 100



Z Index: 100



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: 110

Y Index: 112

Z Index: 118

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

### 6.4 Orthogonal surface views (i)

#### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0125. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



## 6.5 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  $118 \text{ nm}^3$ ; this corresponds to an approximate mass of 106 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 0.333  ${\rm \AA^{-1}}$ 



# 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 0.333  ${\rm \AA}^{-1}$ 



## 8.2 Resolution estimates (i)

$\mathbf{Besolution estimate}(\mathbf{\hat{\lambda}})$	Estimation criterion (FSC cut-off)		
rtesolution estimate (A)	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.93	3.19	2.98
$Calculated^*$	-	-	_

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-12897 and PDB model 7OH9. Per-residue inclusion information can be found in section 3 on page 9.

## 9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.0125 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 Atom inclusion (i)



At the recommended contour level, 93% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

