

# Full wwPDB EM Validation Report (i)

Dec 17, 2022 – 02:05 pm GMT

PDB ID : 6Z9S

EMDB ID : EMD-11090

Title: Transcription termination intermediate complex 4

Authors: Said, N.; Hilal, T.; Loll, B.; Wahl, M.C.

Deposited on : 2020-06-04

Resolution : 4.40 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

EMDB validation analysis : 0.0.1.dev43

Mogul : 1.8.4, CSD as541be (2020)

MolProbity : 4.02b-467 buster-report : 1.1.7 (2018)

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)

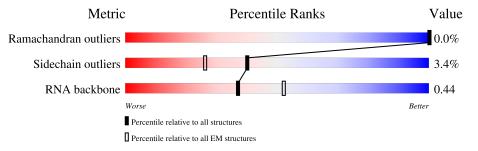
Validation Pipeline (wwPDB-VP) : 2.31.3

### 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 4.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive $(\# \mathrm{Entries})$	${ m EM\ structures} \ (\#{ m Entries})$
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	a	419	7% 92%	7%
1	b	419	92%	7%
1	С	419	92%	7%
1	d	419	92%	7%
1	е	419	92%	7%
1	f	419	92%	7%
2	A	497	60% 99%	•
3	U	329	71%	29%



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Mol	Chain	Length	-	$\mathbf{Q}_{1}$	uality of ch	ain		
3	V	329	13%					
3	V	329		500/	97%			•
				59%				
4	W	91			87%			13%
			7%					
5	X	1342			100%			
			18%	•				
6	Y	1416			96%			•
			10%					
7	K	50		50%	•		48%	
			18%	•				
8	L	50		62%		8%	30%	
			9%					
9	R	99	20%	8%		72%		



# 2 Entry composition (i)

There are 14 unique types of molecules in this entry. The entry contains 51608 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 termination factor Rho.

Mol	Chain	Residues		At	oms			AltConf	Trace
1	f	417	Total	С	N	О	S	0	0
1	1	411	3280	2065	581	617	17	0	0
1	0	417	Total	С	N	О	S	0	0
1	a	417	3280	2065	581	617	17	0	0
1	b	417	Total	С	N	О	S	0	0
1	D	417	3280	2065	581	617	17	0	0
1		417	Total	С	N	О	S	0	0
1	c	417	3280	2065	581	617	17	0	0
1	d	417	Total	С	N	О	S	0	0
1	u	417	3280	2065	581	617	17	0	0
1	0	417	Total	С	N	О	S	0	0
	е	417	3280	2065	581	617	17	U	U

• Molecule 2 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues		At	AltConf	Trace			
2	A	495	Total 3850	C 2395	N 669	O 773	S 13	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP C3SSN7
A	0	ALA	-	expression tag	UNP C3SSN7

• Molecule 3 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace	
2	TT	235	Total	С	N	О	S	0	0	
)	U	233	1825	1135	325	359	6	0	0	
9	V	321	Total	С	N	О	S	0	0	
3	V	321	2504	1566	441	489	8	0	0	



• Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues		At	oms			AltConf	Trace
1	137	79	Total	С	N	О	S	0	0
4	V V	19	627	382	118	126	1	0	

• Molecule 5 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues		A	AltConf	Trace			
5	X	1340	Total 10567	C 6631	N 1841	O 2052	S 43	0	0

• Molecule 6 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues		A	toms			AltConf	Trace
6	Y	1358	Total 10545	C 6620	N 1883	O 1992	S 50	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	1408	LEU	-	expression tag	UNP C3SIA2
Y	1409	GLU	-	expression tag	UNP C3SIA2
Y	1410	VAL	-	expression tag	UNP C3SIA2
Y	1411	HIS	-	expression tag	UNP C3SIA2
Y	1412	HIS	-	expression tag	UNP C3SIA2
Y	1413	HIS	-	expression tag	UNP C3SIA2
Y	1414	HIS	-	expression tag	UNP C3SIA2
Y	1415	HIS	-	expression tag	UNP C3SIA2
Y	1416	HIS	-	expression tag	UNP C3SIA2

• Molecule 7 is a DNA chain called non template strand.

Mol	Chain	Residues		$\mathbf{A}$	toms	AltConf	Trace		
7	К	26	Total 538	C 254	N 103	O 155	P 26	0	0

• Molecule 8 is a DNA chain called template strand.

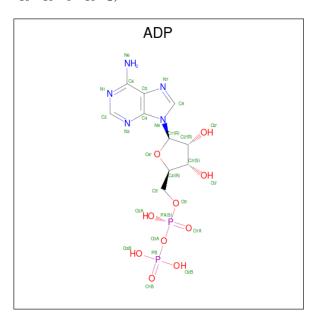
Mol	Chain	Residues		$\mathbf{A}$	toms			AltConf	Trace
8	L	35	Total 704	C 335	N 127	O 208	P 34	0	0

• Molecule 9 is a RNA chain called rut RNA.



Mol	Chain	Residues		$\mathbf{A}^{1}$	toms			AltConf	Trace
9	R	28	Total 590	C 264	N 103	O 195	P 28	0	0

• Molecule 10 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



Mol	Chain	Residues		Ato	oms			AltConf			
10 a	1	Total	С	N	О	Р	0				
	1	27	10	5	10	2	U				
10	b	1	Total	С	N	О	Р	0			
10	D	D	D	10   0	1	27	10	5	10	2	U
10	10	c	1	Total	С	N	О	Р	0		
10		1	27	10	5	10	2	U			
10	d	1	Total	С	N	О	Р	0			
10	u	1	27	10	5	10	2	0			
10	10 e	1	Total	С	N	О	Р	0			
10	e	1	27	10	5	10	2	U			

• Molecule 11 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

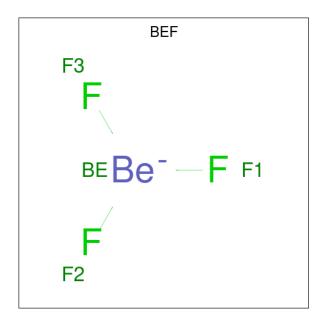
Mol	Chain	Residues	Atoms	AltConf
11	a	1	Total Mg 1 1	0
11	b	1	Total Mg 1 1	0
11	С	1	Total Mg 1 1	0



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Mol	Chain	Residues	Atoms	AltConf
11	d	1	Total Mg 1 1	0
11	е	1	Total Mg 1 1	0
11	Y	1	Total Mg 1 1	0

 $\bullet\,$  Molecule 12 is BERYLLIUM TRIFLUORIDE ION (three-letter code: BEF) (formula: BeF3).



Mol	Chain	Residues	Atoms	AltConf
12	a	1	Total Be F 4 1 3	0
12	b	1	Total Be F 4 1 3	0
12	c	1	Total Be F 4 1 3	0
12	d	1	Total Be F 4 1 3	0
12	e	1	Total Be F 4 1 3	0

• Molecule 13 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
13	Y	2	Total Zn 2 2	0



### • Molecule 14 is water.

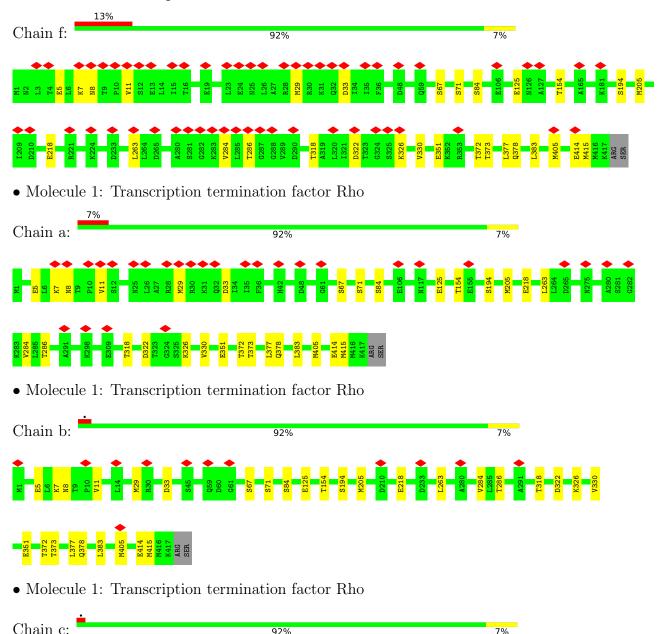
Mol	Chain	Residues	Atoms	AltConf
14	a	3	Total O 3 3	0
14	b	3	Total O 3 3	0
14	c	3	Total O 3 3	0
14	d	3	Total O 3 3	0
14	e	3	Total O 3 3	0



#### 3 Residue-property plots (i)

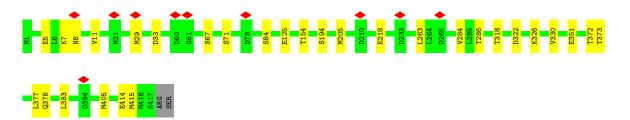
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Transcription termination factor Rho

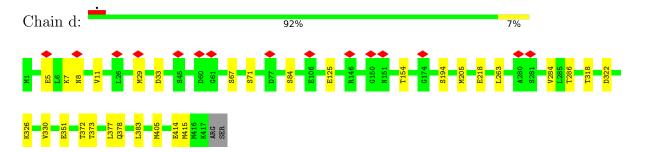




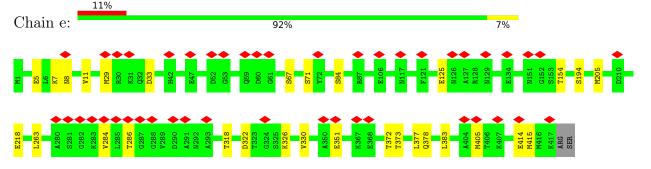
92%



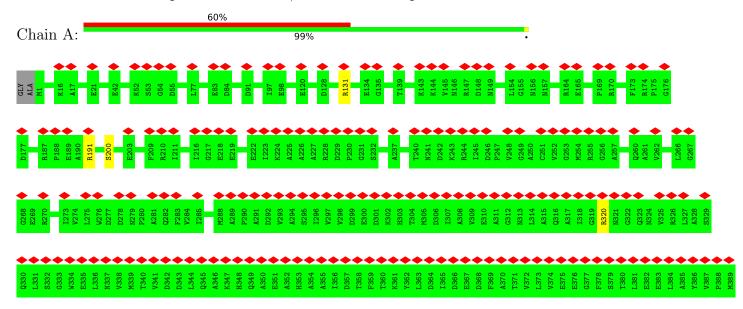
• Molecule 1: Transcription termination factor Rho



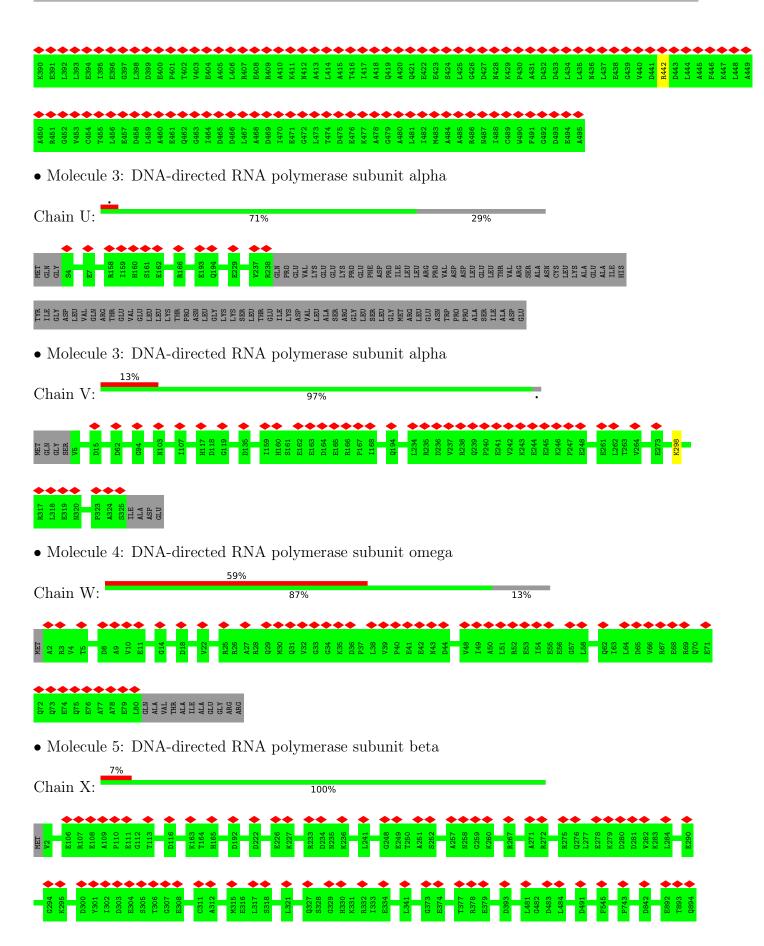
• Molecule 1: Transcription termination factor Rho



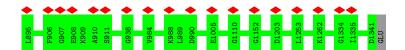
• Molecule 2: Transcription termination/antitermination protein NusA



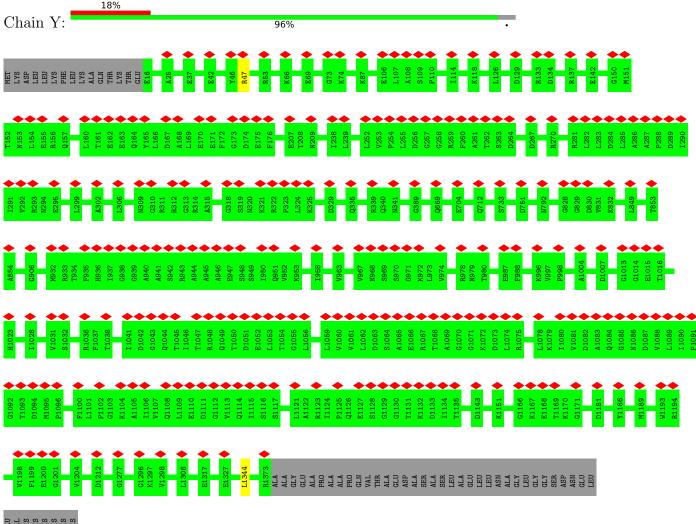






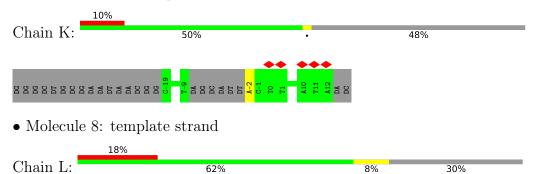


• Molecule 6: DNA-directed RNA polymerase subunit beta'

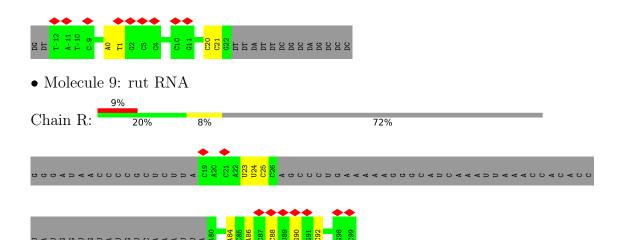


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• Molecule 7: non template strand









# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24950	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.108	Depositor
Minimum map value	-0.958	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	372.0, 372.0, 372.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.24, 1.24, 1.24	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: BEF, MG, ADP, 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	Bo	nd lengths	Bo	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z >5		
1	a	0.25	0/3329	0.43	0/4483		
1	b	0.25	0/3329	0.43	0/4483		
1	С	0.25	0/3329	0.43	0/4483		
1	d	0.25	0/3329	0.43	0/4483		
1	е	0.25	0/3329	0.43	0/4483		
1	f	0.25	0/3329	0.43	0/4483		
2	A	0.24	0/3895	0.44	0/5270		
3	U	0.24	0/1847	0.43	0/2503		
3	V	0.23	0/2538	0.44	0/3441		
4	W	0.23	0/629	0.40	0/847		
5	X	0.24	0/10736	0.42	0/14487		
6	Y	0.24	0/10706	0.42	1/14456 (0.0%)		
7	K	0.61	1/603~(0.2%)	0.88	0/927		
8	L	0.51	0/787	1.09	6/1210 (0.5%)		
9	R	0.18	0/656	0.77	0/1016		
All	All	0.26	$1/52371 \ (0.0\%)$	0.46	7/71055 (0.0%)		

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
7	K	-2	DA	C1'-N9	-5.00	1.40	1.47

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
8	L	0	DA	OP2-P-O3'	-10.74	81.56	105.20
8	L	20	DC	OP2-P-O3'	-10.38	82.37	105.20
8	L	20	DC	OP1-P-O3'	-9.32	84.69	105.20
8	L	0	DA	OP1-P-O3'	-8.19	87.18	105.20
8	L	21	DC	OP1-P-OP2	8.15	131.82	119.60



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Mol	Chain	Res	Type	Atoms	${f Z}$	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
8	L	1	DT	OP1-P-OP2	6.56	129.44	119.60
6	Y	1344	LEU	CA-CB-CG	5.19	127.24	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

### 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	ntiles
1	a	$415/419 \ (99\%)$	402 (97%)	13 (3%)	0	100	100
1	b	415/419~(99%)	402 (97%)	13 (3%)	0	100	100
1	c	415/419 (99%)	401 (97%)	14 (3%)	0	100	100
1	d	415/419 (99%)	401 (97%)	14 (3%)	0	100	100
1	е	415/419 (99%)	402 (97%)	13 (3%)	0	100	100
1	f	415/419 (99%)	401 (97%)	14 (3%)	0	100	100
2	A	493/497 (99%)	449 (91%)	42 (8%)	2 (0%)	34	72
3	U	233/329 (71%)	222 (95%)	11 (5%)	0	100	100
3	V	319/329 (97%)	293 (92%)	26 (8%)	0	100	100
4	W	77/91 (85%)	74 (96%)	3 (4%)	0	100	100
5	X	1338/1342 (100%)	1269 (95%)	69 (5%)	0	100	100
6	Y	1356/1416 (96%)	1295 (96%)	61 (4%)	0	100	100
All	All	6306/6518 (97%)	6011 (95%)	293 (5%)	2 (0%)	100	100



All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	131	ARG
2	A	200	SER

#### 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	Perce	ntiles
1	a	357/359~(99%)	327 (92%)	30 (8%)	11	36
1	b	357/359 (99%)	327 (92%)	30 (8%)	11	36
1	c	357/359~(99%)	327 (92%)	30 (8%)	11	36
1	d	357/359 (99%)	327 (92%)	30 (8%)	11	36
1	e	357/359~(99%)	327 (92%)	30 (8%)	11	36
1	f	357/359 (99%)	327 (92%)	30 (8%)	11	36
2	A	408/409 (100%)	405 (99%)	3 (1%)	84	90
3	U	203/286 (71%)	203 (100%)	0	100	100
3	V	280/286 (98%)	279 (100%)	1 (0%)	91	94
4	W	67/75 (89%)	67 (100%)	0	100	100
5	X	1155/1157 (100%)	1155 (100%)	0	100	100
6	Y	1134/1177 (96%)	1133 (100%)	1 (0%)	93	97
All	All	5389/5544 (97%)	5204 (97%)	185 (3%)	40	61

All (185) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	f	5	GLU
1	f	7	LYS
1	f	8	ASN
1	f	11	VAL
1	f	29	MET
1	f	33	ASP
1	f	67	SER



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Mol	Chain	Res	Type		
1	f	71	SER		
1	f	84	SER		
1	f	125	GLU		
1	f	154	THR		
1	f	194	SER		
1	f	205	MET		
1	f	218	GLU		
1	f	263	LEU		
1	f	284	VAL		
1	f	286	THR		
1	f	318	THR		
1	f	322	ASP		
1	f	326	LYS		
1	f	330	VAL		
1	f	351	GLU		
1	f	372	THR		
1	f	373	THR		
1	f	377	LEU		
1	f	378	GLN		
1	f	383	LEU		
1	f	405	MET		
1	f	414	GLU		
1	f	415	MET		
1	a	5	GLU		
1	a	7	LYS		
1	a	8	ASN		
1	a	11	VAL		
1	a	29	MET		
1	a	33	ASP		
1	a	67	SER		
1	a	71	SER		
1	a	84	SER		
1	a	125	GLU		
1	a	154	THR		
1	a	194	SER		
1	a	205	MET		
1	a	218	GLU		
1	a	263	LEU		
1	a	284	VAL		
1	a	286	THR		
1	a	318	THR		
1	a	322	ASP		



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Mol	Chain	Res	Type		
1	a	326	LYS		
1	a	330	VAL		
1	a	351	GLU		
1	a	372	THR		
1	a	373	THR		
1	a	377	LEU		
1	a	378	GLN		
1	a	383	LEU		
1	a	405	MET		
1	a	414	GLU		
1	a	415	MET		
1	b	5	GLU		
1	b	7	LYS		
1	b	8	ASN		
1	b	11	VAL		
1	b	29	MET		
1	b	33	ASP		
1	b	67	SER		
1	b	71	SER		
1	b	84	SER		
1	b	125	GLU		
1	b	154	THR		
1	b	194	SER		
1	b	205	MET		
1	b	218	GLU		
1	b	263	LEU		
1	b	284	VAL		
1	b	286	THR		
1	b	318	THR		
1	b	322	ASP		
1	b	326	LYS		
1	b	330	VAL		
1	b	351	GLU		
1	b	372	THR		
1	b	373	THR		
1	b	377	LEU		
1	b	378	GLN		
1	b	383	LEU		
1	b	405	MET		
1	b	414	GLU		
1	b	415	MET		
1	С	5	GLU		



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Mol	Chain	Res	Type		
1	С	7	LYS		
1	С	8	ASN		
1	С	11	VAL		
1	С	29	MET		
1	С	33	ASP		
1	С	67	SER		
1	С	71	SER		
1	С	84	SER		
1	С	125	GLU		
1	С	154	THR		
1	С	194	SER		
1	С	205	MET		
1	С	218	GLU		
1	c	263	LEU		
1	С	284	VAL		
1	С	286	THR		
1	С	318	THR		
1	С	322	ASP		
1	С	326	LYS		
1	С	330	VAL		
1	С	351	GLU		
1	С	372	THR		
1	С	373	THR		
1	С	377	LEU		
1	С	378	GLN		
1	С	383	LEU		
1	С	405	MET		
1	С	414	GLU		
1	c	415	MET		
1	d	5	GLU		
1	d	7	LYS		
1	d	8	ASN		
1	d	11	VAL		
1	d	29	MET		
1	d	33	ASP		
1	d	67	SER		
1	d	71	SER		
1	d	84	SER		
1	d	125	GLU		
1	d	154	THR		
1	d	194	SER		
1	d	205	MET		



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Mol	Chain	Res	Type		
1	d	218	GLU		
1	d	263	LEU		
1	d	284	VAL		
1	d	286	THR		
1	d	318	THR		
1	d	322	ASP		
1	d	326	LYS		
1	d	330	VAL		
1	d	351	GLU		
1	d	372	THR		
1	d	373	THR		
1	d	377	LEU		
1	d	378	GLN		
1	d	383	LEU		
1	d	405	MET		
1	d	414	GLU		
1	d	415	MET		
1	е	5	GLU		
1	е	7	LYS		
1	е	8	ASN		
1	е	11	VAL		
1	е	29	MET		
1	е	33	ASP		
1	е	67	SER		
1	е	71	SER		
1	е	84	SER		
1	е	125	GLU		
1	е	154	THR		
1	е	194	SER		
1	е	205	MET		
1	е	218	GLU		
1	е	263	LEU		
1	е	284	VAL		
1	е	286	THR		
1	е	318	THR		
1	е	322	ASP		
1	е	326	LYS		
1	е	330	VAL		
1	е	351	GLU		
1	е	372	THR		
1	е	373	THR		
1	е	377	LEU		



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	J	1	1 0
Mol	Chain	Res	Type
1	е	378	GLN
1	е	383	LEU
1	е	405	MET
1	е	414	GLU
1	е	415	MET
2	A	191	ARG
2	A	320	ARG
2	A	442	ARG
3	V	298	LYS
6	Y	47	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	f	90	ASN
1	f	135	ASN
1	f	199	HIS
1	a	90	ASN
1	a	135	ASN
1	a	199	HIS
1	b	90	ASN
1	b	135	ASN
1	b	199	HIS
1	С	90	ASN
1	c	135	ASN
1	c	199	HIS
1	d	90	ASN
1	d	135	ASN
1	d	199	HIS
1	е	90	ASN
1	е	135	ASN
1	е	199	HIS
2	A	14	ASN
2	A	282	GLN
2	A	303	HIS
2	A A	324	ASN
2	A	412	ASN
3	V	147	GLN
3	V	194	GLN
3	V W	283	GLN
4	W	43	ASN
5	X	519	ASN



Continued from previous page...

Mol	Chain	Res	Type
5	X	580	GLN
5	X	604	HIS
5	X	618	GLN
5	X	808	ASN
5	X	932	GLN
5	X	1009	ASN
5	X	1010	GLN
5	X	1013	GLN
5	X	1017	GLN
5	X	1116	HIS
5	X	1237	HIS
5	X	1268	GLN
6	Y Y	196	GLN
6	Y	365	GLN
6	Y Y Y	488	ASN
6	Y	545	HIS
6	Y	702	GLN
6	Y	739	GLN
6	Y Y	805	GLN
6		1023	HIS
6	Y	1244	GLN

#### 5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	R	26/99~(26%)	8 (30%)	0

All (8) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	R	23	U
9	R	24	U
9	R	25	С
9	R	84	A
9	R	86	A
9	R	88	С
9	R	90	G
9	R	92	С

There are no RNA pucker outliers to report.



#### 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)

Of 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 for Mogul analysis.

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

Mol	Tuna	Chain	Res	Link	Bond lengths				Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
10	ADP	b	1000	1,11	24,29,29	0.95	1 (4%)	29,45,45	1.42	4 (13%)	
10	ADP	a	1000	11	24,29,29	0.96	1 (4%)	29,45,45	1.49	4 (13%)	
10	ADP	е	1000	1,11	24,29,29	0.95	1 (4%)	29,45,45	1.45	4 (13%)	
12	BEF	е	1002	-	0,3,3	-	=	=			
10	ADP	d	1000	1,11	24,29,29	0.95	1 (4%)	29,45,45	1.48	4 (13%)	
12	BEF	b	1002	-	0,3,3	-	-	-			
12	BEF	a	1002	-	0,3,3	-	-	-			
12	BEF	d	1002	-	0,3,3	-	-	-			
10	ADP	c	1000	1,11	24,29,29	0.95	1 (4%)	29,45,45	1.48	4 (13%)	
12	BEF	С	1002	-	0,3,3	-	-	-			

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
10	ADP	b	1000	1,11	-	3/12/32/32	0/3/3/3
10	ADP	a	1000	11	-	0/12/32/32	0/3/3/3
10	ADP	е	1000	1,11	-	2/12/32/32	0/3/3/3



Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	ADP	d	1000	1,11	-	2/12/32/32	0/3/3/3
10	ADP	c	1000	1,11	-	3/12/32/32	0/3/3/3

#### All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
10	a	1000	ADP	C5-C4	2.51	1.47	1.40
10	е	1000	ADP	C5-C4	2.49	1.47	1.40
10	d	1000	ADP	C5-C4	2.48	1.47	1.40
10	b	1000	ADP	C5-C4	2.47	1.47	1.40
10	С	1000	ADP	C5-C4	2.46	1.47	1.40

#### All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^{o})$	$Ideal(^{o})$
10	a	1000	ADP	PA-O3A-PB	-3.68	120.19	132.83
10	d	1000	ADP	C3'-C2'-C1'	3.62	106.43	100.98
10	С	1000	ADP	C3'-C2'-C1'	3.55	106.32	100.98
10	е	1000	ADP	C3'-C2'-C1'	3.49	106.24	100.98
10	С	1000	ADP	PA-O3A-PB	-3.45	120.99	132.83
10	d	1000	ADP	PA-O3A-PB	-3.40	121.14	132.83
10	a	1000	ADP	C3'-C2'-C1'	3.35	106.03	100.98
10	b	1000	ADP	C3'-C2'-C1'	3.29	105.94	100.98
10	С	1000	ADP	N3-C2-N1	-3.21	123.66	128.68
10	d	1000	ADP	N3-C2-N1	-3.19	123.69	128.68
10	е	1000	ADP	PA-O3A-PB	-3.19	121.87	132.83
10	b	1000	ADP	N3-C2-N1	-3.19	123.70	128.68
10	a	1000	ADP	N3-C2-N1	-3.17	123.72	128.68
10	е	1000	ADP	N3-C2-N1	-3.16	123.74	128.68
10	b	1000	ADP	PA-O3A-PB	-3.06	122.33	132.83
10	a	1000	ADP	C4-C5-N7	-2.68	106.61	109.40
10	d	1000	ADP	C4-C5-N7	-2.60	106.69	109.40
10	е	1000	ADP	C4-C5-N7	-2.55	106.74	109.40
10	b	1000	ADP	C4-C5-N7	-2.54	106.75	109.40
10	С	1000	ADP	C4-C5-N7	-2.54	106.75	109.40

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	b	1000	ADP	C5'-O5'-PA-O3A



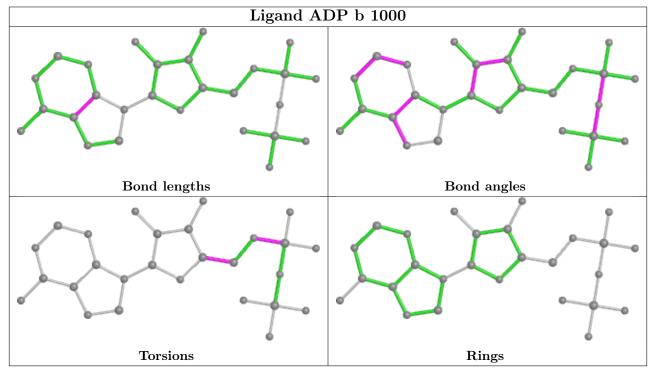
Continued from previous page...

Mol	Chain	Res	Type	Atoms
10	d	1000	ADP	O4'-C4'-C5'-O5'
10	d	1000	ADP	C3'-C4'-C5'-O5'
10	c	1000	ADP	O4'-C4'-C5'-O5'
10	b	1000	ADP	C5'-O5'-PA-O1A
10	c	1000	ADP	C3'-C4'-C5'-O5'
10	е	1000	ADP	O4'-C4'-C5'-O5'
10	b	1000	ADP	O4'-C4'-C5'-O5'
10	c	1000	ADP	C5'-O5'-PA-O1A
10	е	1000	ADP	C5'-O5'-PA-O1A

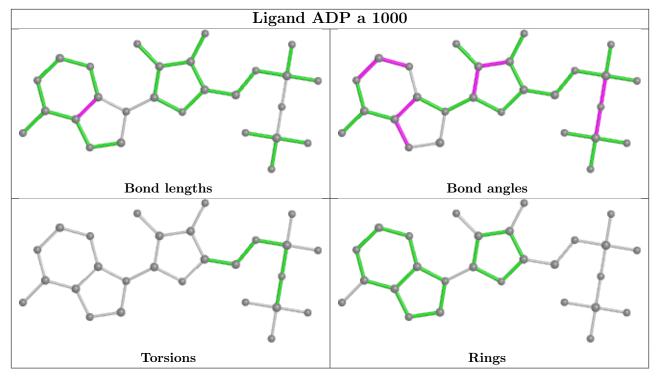
There are no ring outliers.

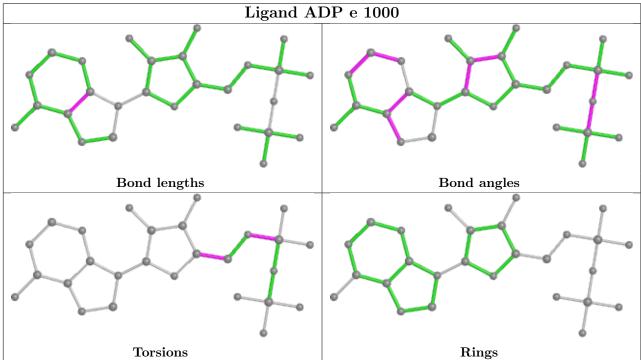
No monomer is involved in short contacts.

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

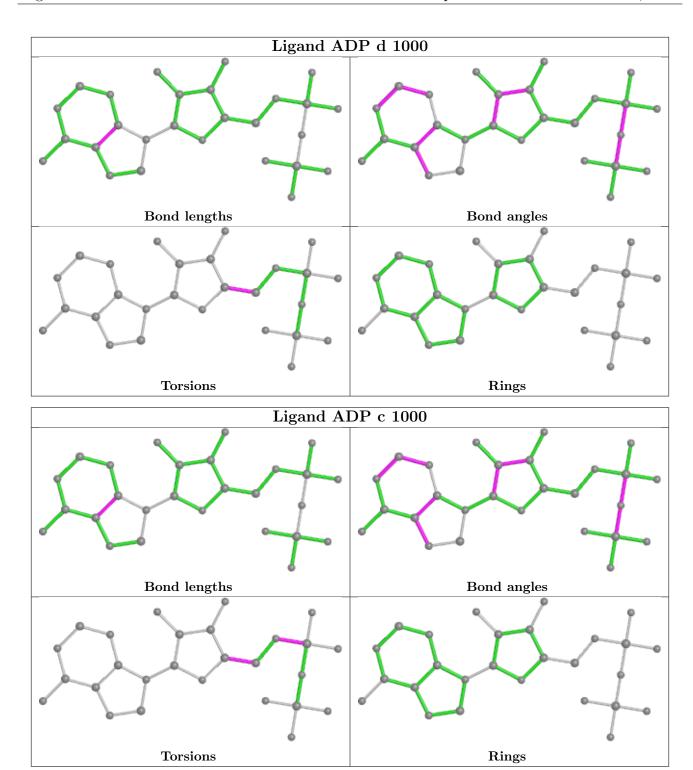












## 5.7 Other polymers (i)

There are no such residues in this entry.



# 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



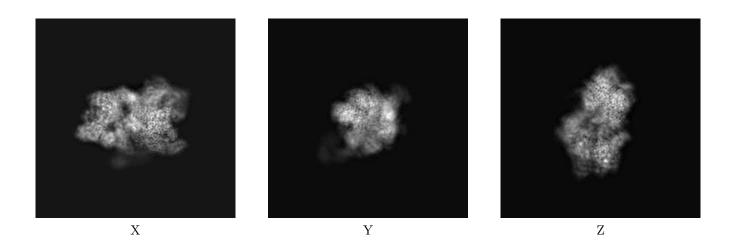
### 6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-11090. 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)

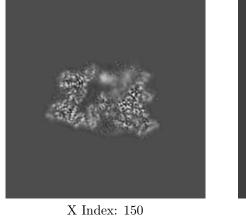
#### 6.1.1 Primary map

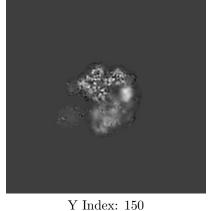


The images above show the map projected in three orthogonal directions.

#### 6.2 Central slices (i)

#### 6.2.1 Primary map







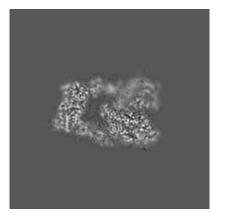
dex: 150 Z Index: 150



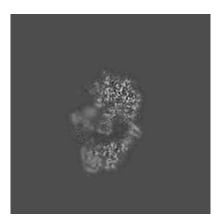
The images above show central slices of the map in three orthogonal directions.

### 6.3 Largest variance slices (i)

#### 6.3.1 Primary map







X Index: 157

Y Index: 173

Z Index: 135

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







 $\mathbf{Z}$ 

The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

Y



# 6.5 Mask visualisation (i)

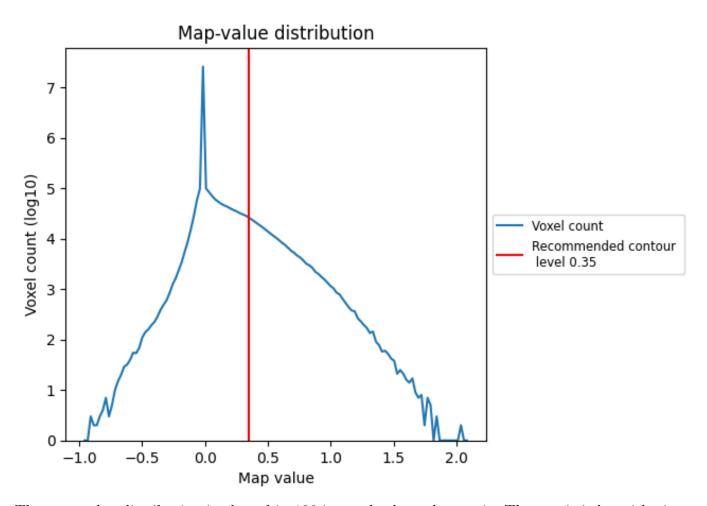
This section was not generated. No masks/segmentation were deposited.



# 7 Map analysis (i)

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

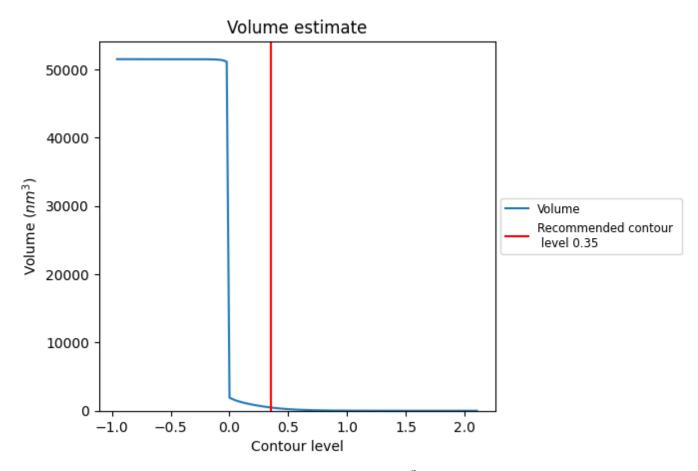
### 7.1 Map-value distribution (i)



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)

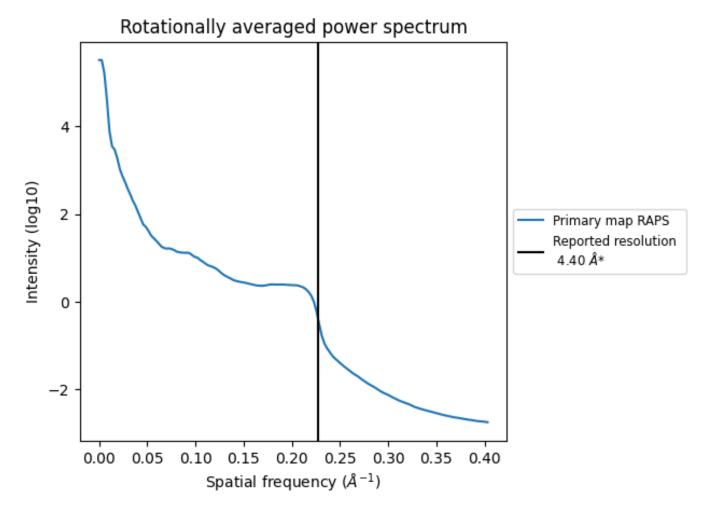


The volume at the recommended contour level is  $483~\mathrm{nm}^3$ ; this corresponds to an approximate mass of  $437~\mathrm{kDa}$ .

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)



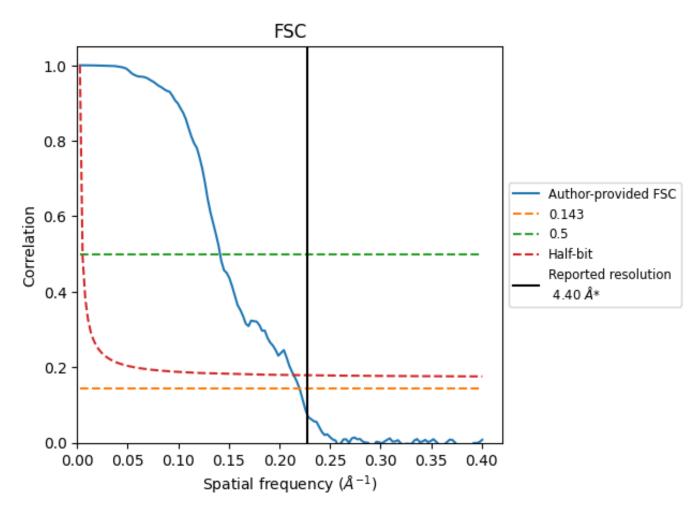
<sup>\*</sup>Reported resolution corresponds to spatial frequency of 0.227  $\rm \mathring{A}^{-1}$ 



### 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 0.227  $\rm \mathring{A}^{-1}$ 



## 8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
resolution estimate (A)	0.143	0.5	Half-bit	
Reported by author	4.40	-	-	
Author-provided FSC curve	4.55	7.08	4.67	
Unmasked-calculated*	-	-	-	

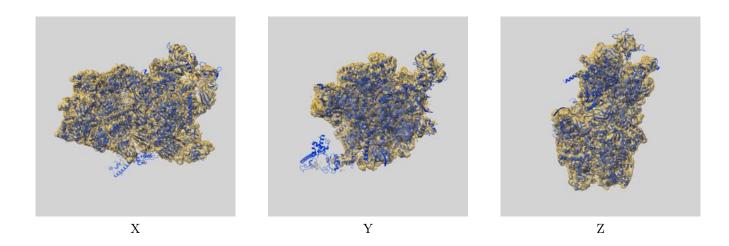
<sup>\*</sup>Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



### 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-11090 and PDB model 6Z9S. Per-residue inclusion information can be found in section 3 on page 9.

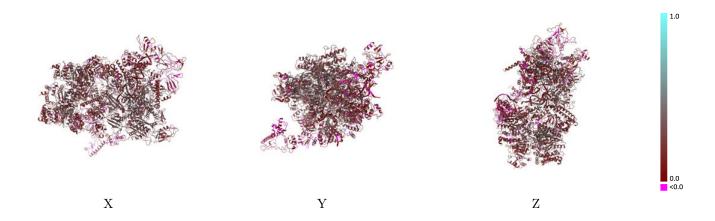
### 9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.35 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.

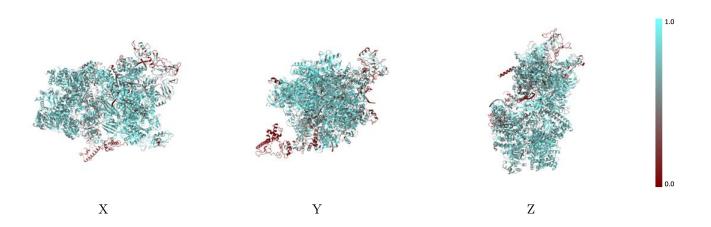


### 9.2 Q-score mapped to coordinate model (i)



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.

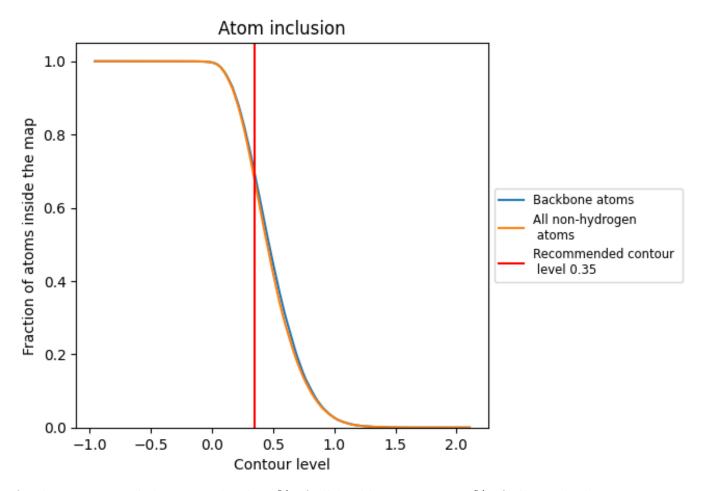
#### 9.3 Atom inclusion mapped to coordinate model (i)



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 (0.35).



### 9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 67% of all non-hydrogen atoms, are inside the map.



## 9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6734	0.2340
A	0.3291	0.1140
K	0.7286	0.1730
L	0.6321	0.1510
R	0.5966	0.1600
U	0.7882	0.3150
V	0.6676	0.2400
W	0.2864	0.2240
X	0.7521	0.2840
Y	0.6612	0.2260
a	0.7360	0.2350
b	0.7622	0.2600
c	0.7800	0.2710
d	0.7489	0.2530
e	0.6645	0.1920
f	0.6702	0.1860



