

# Full wwPDB EM Validation Report (i)

Feb 4, 2023 – 08:19 AM EST

PDB ID : 7TQU

EMDB ID : EMD-26072

Title: Coxsackievirus A21 capsid subdomain in complex with mouse polyclonal an-

tibody pAbC-1

Authors : Antanasijevic, A.; Ward, A.B.

Deposited on : 2022-01-27

Resolution : 3.80 Å(reported)

Based on initial model : 1Z7S

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 (i)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43

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)

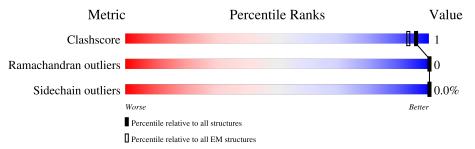
Validation Pipeline (wwPDB-VP) : 2.32.1

# 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 3.80 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 $(\# \mathrm{Entries})$	${ m EM~structures} \ (\#{ m Entries})$
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	Н	112	96%	
2	L	102	94%	6%
3	a	298	91%	• 5%
3	e	298	91%	• 5%
3	i	298	92%	• 5%
4	b	272	94%	
4	f	272	95%	
4	j	272	94%	

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Mol	Chain	Length	Quality of chain	
			12%	
5	$^{\mathrm{c}}$	240	95%	
			9%	
5	g	240	95%	• •
			11%	
5	k	240	96%	
			51%	
6	d	69	99%	•
			41%	
6	h	69	99%	•
			36%	
6	l	69	97%	••



# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 20891 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 pAbC-1 heavy chain.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
1	Н	112	Total 560	C 336	N 112	O 112	0	0

• Molecule 2 is a protein called pAbC-1 light chain.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
2	L	102	Total 510	C 306	N 102	O 102	0	0

• Molecule 3 is a protein called VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0	283	Total	С	N	О	S	0	0
)	a	200	2226	1410	380	426	10	0	0
3	0	282	Total	С	N	О	S	0	0
3	е	202	2219	1405	379	425	10	0	U
3	;	283	Total	С	N	О	S	0	0
0	1	200	2226	1410	380	426	10	U	U

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue Modelled Actua		Actual	Comment	Reference
a	290	ALA	THR	conflict	UNP Q7T7N6
е	290	ALA	THR	conflict	UNP Q7T7N6
i	290	ALA	THR	conflict	UNP Q7T7N6

• Molecule 4 is a protein called VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	h	263	Total	С	N	О	S	0	0
	D	203	2043	1300	345	386	12	0	
4	f	965	Total	С	N	О	S	0	0
4	4   t	265	2057	1308	347	391	11	0	U

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	j	261	Total 2029	C 1293	N 342	O 383	S 11	0	0

• Molecule 5 is a protein called VP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	233	Total 1801	C 1148	N 297	O 336	S 20	0	0
5	g	234	Total 1810	C 1154		O 337	S 20	0	0
5	k	236	Total 1826	C 1166	N 301	O 339	S 20	0	0

There are 3 discrepancies between the modelled and reference sequences:

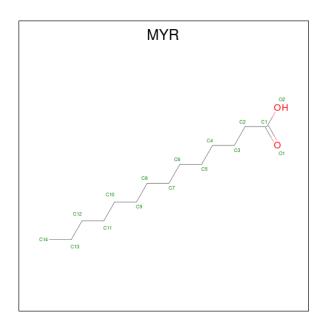
Chain	Residue	Modelled	Actual	Comment	Reference
С	225	ARG	LYS	conflict	UNP Q7T7N6
g	225	ARG	LYS	conflict	UNP Q7T7N6
k	225	ARG	LYS	conflict	UNP Q7T7N6

• Molecule 6 is a protein called VP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d	68	Total 512	C 311		O 110	S 1	0	0
6	h	68	Total 512	C 311		O 110	S 1	0	0
6	1	68	Total 512	C 311	N 90	O 110	S 1	0	0

 $\bullet$  Molecule 7 is MYRISTIC ACID (three-letter code: MYR) (formula:  $\mathrm{C}_{14}\mathrm{H}_{28}\mathrm{O}_2).$ 





Mol	Chain	Residues	Atoms	AltConf
7	0	1	Total C O	0
'	7 a	1	$16 \qquad 14  2$	
7	е	1	Total C O	0
'	е	1	$16 \qquad 14  2$	0
7	į	1	Total C O	0
(	1	1 1	16   14   2	0

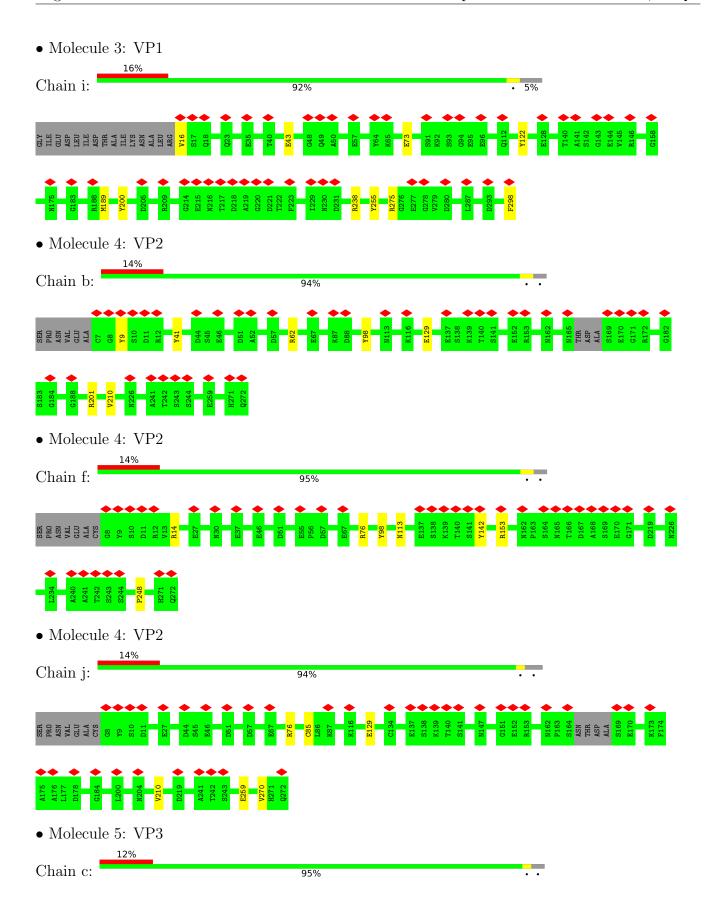


# 3 Residue-property plots (i)

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.

• Molecule 1: pAbC-1 heavy chain Chain H: 96% • Molecule 2: pAbC-1 light chain Chain L: 6% • Molecule 3: VP1 Chain a: 91% • 5% • Molecule 3: VP1 Chain e: • 5% 91% 3LV 3LU ASP ASP CEU ILLE ALA ALA ALA ALA ALA ALA ALA ALA











# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19748	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.028	Depositor
Minimum map value	-0.018	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	292.59998, 292.59998, 292.59998	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	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: MYR

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	Во	ond lengths	В	ond angles
Mol	Chain	RMSZ	# Z  > 5	RMSZ	# Z >5
3	a	1.16	8/2288 (0.3%)	0.92	5/3121 (0.2%)
3	е	1.19	$10/2281 \ (0.4\%)$	0.95	4/3111 (0.1%)
3	i	1.16	$9/2288 \; (0.4\%)$	0.92	4/3121 (0.1%)
4	b	1.16	2/2099~(0.1%)	0.98	7/2870 (0.2%)
4	f	1.14	2/2114 (0.1%)	0.95	6/2893 (0.2%)
4	j	1.22	7/2085 (0.3%)	0.91	2/2851 (0.1%)
5	c	1.03	$2/1850 \ (0.1\%)$	0.91	2/2520 (0.1%)
5	g	1.06	5/1859~(0.3%)	0.92	2/2531 (0.1%)
5	k	1.05	2/1875~(0.1%)	0.97	5/2553~(0.2%)
6	d	0.95	0/519	0.80	0/705
6	h	0.97	0/519	0.83	0/705
6	1	0.93	0/519	0.87	1/705~(0.1%)
All	All	1.12	47/20296 (0.2%)	0.93	38/27686 (0.1%)

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
4	j	85	CYS	CB-SG	-9.26	1.66	1.82
3	е	43	GLU	CG-CD	-8.46	1.39	1.51
4	j	129	GLU	CG-CD	-8.44	1.39	1.51
3	е	100	PHE	CB-CG	-7.67	1.38	1.51
3	i	298	PHE	CG-CD2	7.26	1.49	1.38
3	е	298	PHE	CG-CD2	6.99	1.49	1.38
3	е	298	PHE	CG-CD1	6.98	1.49	1.38
4	j	129	GLU	CD-OE2	-6.97	1.18	1.25
3	i	298	PHE	CG-CD1	6.87	1.49	1.38
5	g	62	VAL	CB-CG2	-6.86	1.38	1.52
3	a	298	PHE	CG-CD1	6.62	1.48	1.38
3	a	298	PHE	CG-CD2	6.56	1.48	1.38
3	е	264	TRP	CB-CG	-6.34	1.38	1.50
5	c	105	TYR	CB-CG	-6.19	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(A)
5	g	219	PHE	CB-CG	-5.86	1.41	1.51
5	С	62	VAL	CB-CG2	-5.84	1.40	1.52
4	b	129	GLU	CG-CD	-5.84	1.43	1.51
3	i	73	GLU	CD-OE2	-5.82	1.19	1.25
4	j	270	VAL	CB-CG2	-5.78	1.40	1.52
4	f	248	PRO	N-CD	-5.62	1.40	1.47
3	i	43	GLU	CG-CD	-5.62	1.43	1.51
3	е	43	GLU	CD-OE2	-5.57	1.19	1.25
3	a	122	TYR	CB-CG	-5.57	1.43	1.51
4	j	210	VAL	CB-CG1	-5.54	1.41	1.52
3	i	122	TYR	CB-CG	-5.51	1.43	1.51
4	f	113	ASN	CB-CG	-5.50	1.38	1.51
3	a	43	GLU	CG-CD	-5.49	1.43	1.51
3	i	122	TYR	CG-CD2	-5.45	1.32	1.39
3	е	298	PHE	CE2-CZ	5.38	1.47	1.37
3	е	57	GLU	CD-OE1	-5.37	1.19	1.25
3	i	298	PHE	CE2-CZ	5.36	1.47	1.37
4	j	259	GLU	CD-OE1	-5.35	1.19	1.25
5	k	185	GLU	CD-OE2	-5.30	1.19	1.25
4	b	210	VAL	CB-CG1	-5.29	1.41	1.52
3	a	270	ARG	CG-CD	-5.26	1.38	1.51
5	g	105	TYR	CG-CD1	-5.25	1.32	1.39
3	i	16	VAL	CB-CG1	5.21	1.63	1.52
4	j	259	GLU	CD-OE2	-5.17	1.20	1.25
3	е	122	TYR	CB-CG	-5.15	1.44	1.51
3	a	165	TRP	CB-CG	-5.13	1.41	1.50
5	g	105	TYR	CB-CG	-5.13	1.44	1.51
3	i	255	TYR	CB-CG	-5.12	1.44	1.51
3	a	298	PHE	CE2-CZ	5.11	1.47	1.37
3	е	96	GLU	CD-OE2	-5.08	1.20	1.25
3	a	193	TYR	CE2-CZ	-5.07	1.31	1.38
5	g	185	GLU	CD-OE1	-5.02	1.20	1.25
5	k	236	ILE	CB-CG1	5.01	1.68	1.54

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
4	b	201	ARG	NE-CZ-NH2	-9.28	115.66	120.30
4	b	201	ARG	NE-CZ-NH1	8.13	124.36	120.30
4	j	76	ARG	NE-CZ-NH2	-8.12	116.24	120.30
4	f	153	ARG	NE-CZ-NH2	-7.61	116.50	120.30
5	k	93	ARG	NE-CZ-NH1	7.49	124.04	120.30

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
5	k	196	ARG	NE-CZ-NH2	-7.37	116.62	120.30
4	f	76	ARG	NE-CZ-NH1	7.22	123.91	120.30
4	j	76	ARG	NE-CZ-NH1	7.14	123.87	120.30
3	е	275	ARG	NE-CZ-NH2	-6.79	116.91	120.30
3	е	67	ARG	NE-CZ-NH1	6.50	123.55	120.30
4	b	62	ARG	NE-CZ-NH1	6.46	123.53	120.30
3	i	122	TYR	CB-CG-CD2	-6.17	117.30	121.00
5	g	114	ARG	NE-CZ-NH2	-6.16	117.22	120.30
3	i	200	TYR	CB-CG-CD1	-6.08	117.35	121.00
3	a	67	ARG	NE-CZ-NH2	-6.07	117.27	120.30
3	a	115	ARG	NE-CZ-NH2	6.06	123.33	120.30
5	С	114	ARG	NE-CZ-NH2	-5.90	117.35	120.30
4	b	9	TYR	CB-CG-CD1	-5.89	117.47	121.00
3	i	275	ARG	NE-CZ-NH2	-5.84	117.38	120.30
5	k	114	ARG	NE-CZ-NH2	-5.83	117.39	120.30
4	f	98	TYR	CB-CG-CD2	-5.83	117.50	121.00
5	g	105	TYR	CB-CG-CD1	-5.81	117.51	121.00
4	b	41	TYR	CB-CG-CD2	-5.76	117.55	121.00
4	f	76	ARG	NE-CZ-NH2	-5.75	117.42	120.30
3	a	114	ARG	NE-CZ-NH2	5.65	123.12	120.30
3	i	238	ARG	NE-CZ-NH2	-5.60	117.50	120.30
3	е	188	ARG	CB-CG-CD	-5.60	97.05	111.60
4	f	142	TYR	CB-CG-CD1	-5.53	117.68	121.00
4	b	62	ARG	NE-CZ-NH2	-5.39	117.60	120.30
3	a	200	TYR	CB-CG-CD1	-5.30	117.82	121.00
5	С	156	ASP	CB-CG-OD2	5.26	123.03	118.30
4	b	98	TYR	CB-CG-CD2	-5.15	117.91	121.00
4	f	14	ARG	NE-CZ-NH1	5.14	122.87	120.30
6	1	32	TYR	CB-CG-CD1	-5.12	117.93	121.00
3	е	114	ARG	NE-CZ-NH2	5.06	122.83	120.30
3	a	126	ASP	CB-CG-OD1	5.04	122.83	118.30
5	k	93	ARG	NE-CZ-NH2	-5.04	117.78	120.30
5	k	221	VAL	N-CA-C	5.01	124.52	111.00

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	Н	560	0	144	2	0
2	L	510	0	123	3	0
3	a	2226	0	2146	0	0
3	е	2219	0	2137	0	0
3	i	2226	0	2146	0	0
4	b	2043	0	1966	0	0
4	f	2057	0	1978	0	0
4	j	2029	0	1955	0	0
5	С	1801	0	1778	0	0
5	g	1810	0	1791	0	0
5	k	1826	0	1813	0	0
6	d	512	0	493	0	0
6	h	512	0	493	0	0
6	1	512	0	493	0	0
7	a	16	0	27	0	0
7	е	16	0	27	0	0
7	i	16	0	27	0	0
All	All	20891	0	19537	5	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (5) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:H:28:UNK:C	1:H:30:UNK:N	2.70	0.54
2:L:27:UNK:O	2:L:28:UNK:C	2.56	0.53
2:L:49:UNK:O	2:L:50:UNK:C	2.63	0.42
1:H:39:UNK:O	1:H:40:UNK:C	2.63	0.42
2:L:92:UNK:O	2:L:93:UNK:C	2.67	0.41

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	ntiles
3	a	281/298 (94%)	275 (98%)	6 (2%)	0	100	100
3	e	280/298 (94%)	276 (99%)	4 (1%)	0	100	100
3	i	281/298 (94%)	276 (98%)	5 (2%)	0	100	100
4	b	259/272~(95%)	252 (97%)	7 (3%)	0	100	100
4	f	263/272 (97%)	256 (97%)	7 (3%)	0	100	100
4	j	257/272 (94%)	247 (96%)	10 (4%)	0	100	100
5	c	231/240 (96%)	227 (98%)	4 (2%)	0	100	100
5	g	232/240 (97%)	228 (98%)	4 (2%)	0	100	100
5	k	234/240 (98%)	231 (99%)	3 (1%)	0	100	100
6	d	66/69~(96%)	65 (98%)	1 (2%)	0	100	100
6	h	66/69~(96%)	65 (98%)	1 (2%)	0	100	100
6	1	66/69~(96%)	66 (100%)	0	0	100	100
All	All	$2516/2637\ (95\%)$	2464 (98%)	52 (2%)	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 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
3	a	248/260~(95%)	248 (100%)	0	100	100
3	e	247/260~(95%)	247 (100%)	0	100	100
3	i	248/260 (95%)	247 (100%)	1 (0%)	91	95
4	b	223/230~(97%)	223 (100%)	0	100	100
4	f	224/230 (97%)	224 (100%)	0	100	100
4	j	$221/230\ (96\%)$	221 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Perce	$\mathbf{ntiles}$
5	c	$207/213\ (97\%)$	207 (100%)	0	100	100
5	g	208/213 (98%)	208 (100%)	0	100	100
5	k	210/213 (99%)	210 (100%)	0	100	100
6	d	57/58 (98%)	57 (100%)	0	100	100
6	h	57/58 (98%)	57 (100%)	0	100	100
6	1	57/58 (98%)	57 (100%)	0	100	100
All	All	2207/2283 (97%)	2206 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	i	189	MET

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

Mol	Chain	Res	Type
4	b	118	HIS
4	f	113	ASN
4	f	203	ASN

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

# 5.4 Non-standard residues in protein, DNA, RNA chains i

There are no non-standard protein/DNA/RNA residues in this entry.

# 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

# 5.6 Ligand geometry (i)

3 ligands 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	Trme	Chain	Des	Res Link Bond lengths			В	ond ang	les	
MIOI	Type	Chain	Res	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	MYR	a	300	-	15,15,15	1.37	2 (13%)	15,15,15	1.13	2 (13%)
7	MYR	i	300	-	15,15,15	1.41	2 (13%)	15,15,15	1.20	2 (13%)
7	MYR	е	300	-	15,15,15	1.41	2 (13%)	15,15,15	1.32	2 (13%)

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
7	MYR	a	300	-	-	5/13/13/13	-
7	MYR	i	300	-	-	4/13/13/13	-
7	MYR	е	300	-	-	6/13/13/13	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
7	a	300	MYR	O2-C1	-3.23	1.19	1.30
7	i	300	MYR	O2-C1	-3.13	1.20	1.30
7	е	300	MYR	O2-C1	-3.11	1.20	1.30
7	a	300	MYR	O1-C1	2.95	1.31	1.22
7	е	300	MYR	O1-C1	2.93	1.31	1.22
7	i	300	MYR	O1-C1	2.87	1.31	1.22

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
7	е	300	MYR	O2-C1-O1	-3.88	113.63	123.30
7	i	300	MYR	O2-C1-O1	-3.26	115.18	123.30
7	е	300	MYR	O2-C1-C2	3.14	124.12	114.03
7	a	300	MYR	O2-C1-O1	-3.09	115.61	123.30
7	i	300	MYR	O2-C1-C2	3.03	123.76	114.03
7	a	300	MYR	O2-C1-C2	2.58	122.33	114.03



There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	е	300	MYR	C1-C2-C3-C4
7	i	300	MYR	C7-C8-C9-C10
7	i	300	MYR	C6-C7-C8-C9
7	i	300	MYR	C2-C3-C4-C5
7	i	300	MYR	C1-C2-C3-C4
7	a	300	MYR	C3-C4-C5-C6
7	е	300	MYR	C2-C3-C4-C5
7	a	300	MYR	C7-C8-C9-C10
7	е	300	MYR	C5-C6-C7-C8
7	a	300	MYR	C5-C6-C7-C8
7	е	300	MYR	O2-C1-C2-C3
7	a	300	MYR	O2-C1-C2-C3
7	е	300	MYR	O1-C1-C2-C3
7	a	300	MYR	O1-C1-C2-C3
7	е	300	MYR	C11-C12-C13-C14

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.



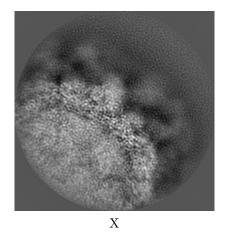
# 6 Map visualisation (i)

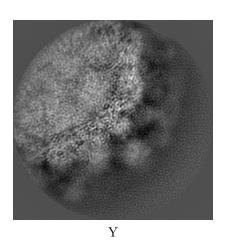
This section contains visualisations of the EMDB entry EMD-26072. These allow visual inspection of the internal detail of the map and identification of artifacts.

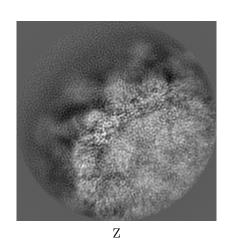
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections (i)

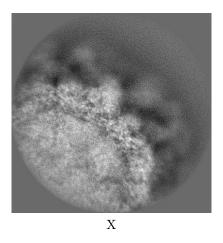
#### 6.1.1 Primary map

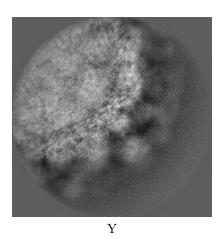


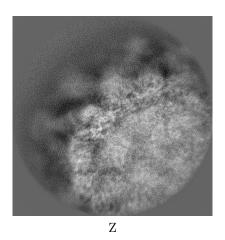




#### 6.1.2 Raw map





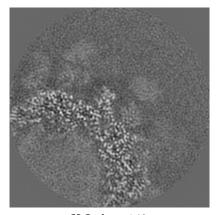


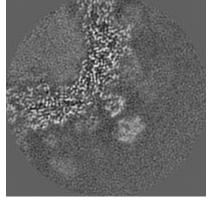
The images above show the map projected in three orthogonal directions.

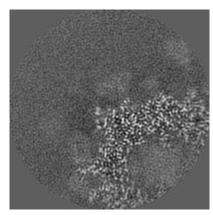


# 6.2 Central slices (i)

# 6.2.1 Primary map





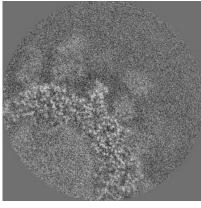


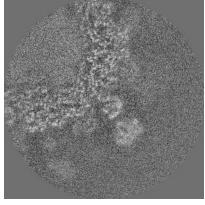
X Index: 140

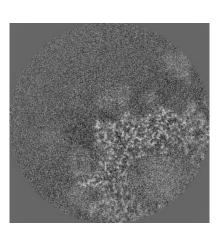
Y Index: 140

Z Index: 140

#### 6.2.2 Raw map







X Index: 140

Y Index: 140

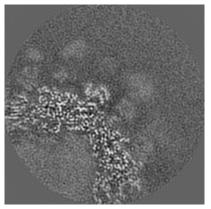
Z Index: 140

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

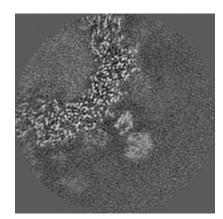


# 6.3 Largest variance slices (i)

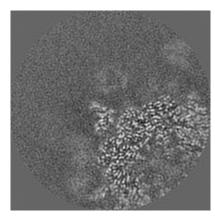
#### 6.3.1 Primary map





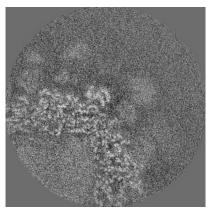


Y Index: 142

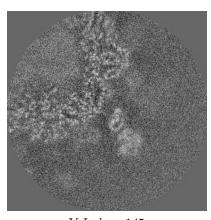


Z Index: 146

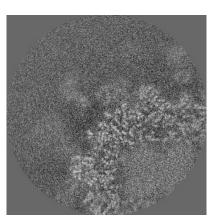
### 6.3.2 Raw map



X Index: 134



Y Index: 145



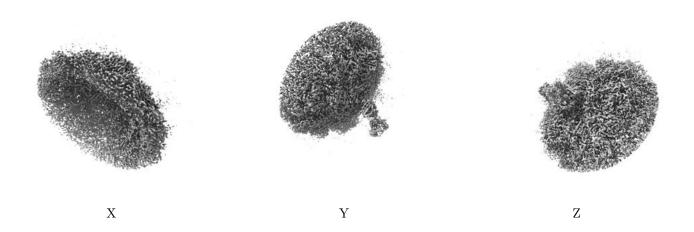
Z Index: 133

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



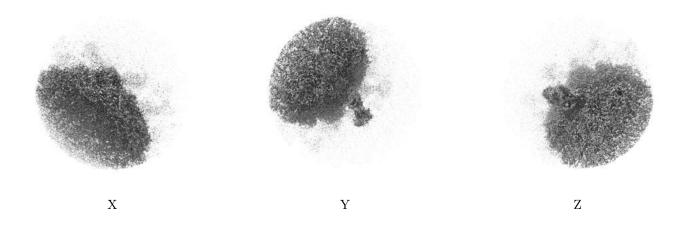
# 6.4 Orthogonal surface views (i)

#### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

#### 6.4.2 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.



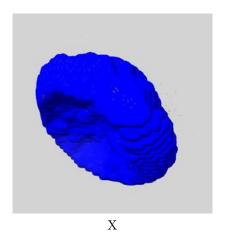
### 6.5 Mask visualisation (i)

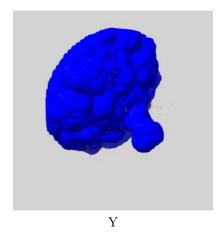
This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

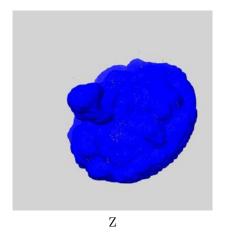
A mask typically either:

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

### $6.5.1 \quad \mathrm{emd} \, \underline{\hspace{0.1cm}} 26072 \, \underline{\hspace{0.1cm}} \mathrm{msk} \, \underline{\hspace{0.1cm}} 1.\mathrm{map} \, \, \underline{\hspace{0.1cm}} \underline{\hspace{0.1cm}} \underline{\hspace{0.1cm}}$



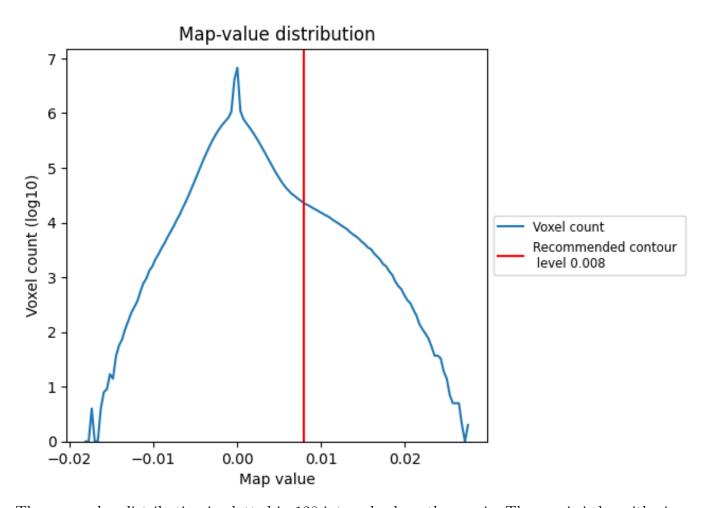




# 7 Map analysis (i)

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

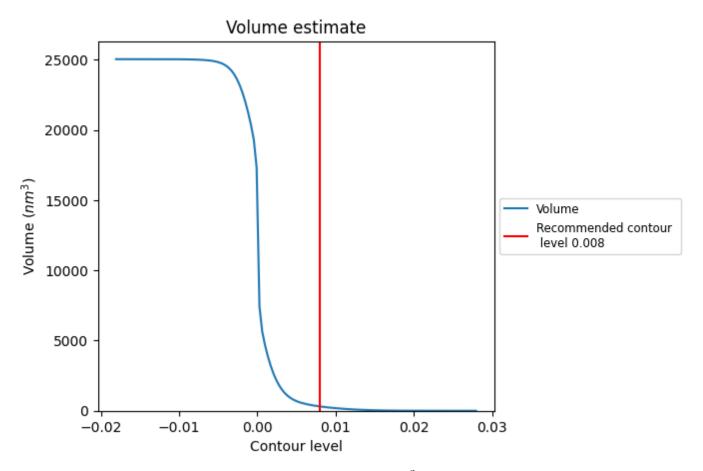
## 7.1 Map-value distribution (i)



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)

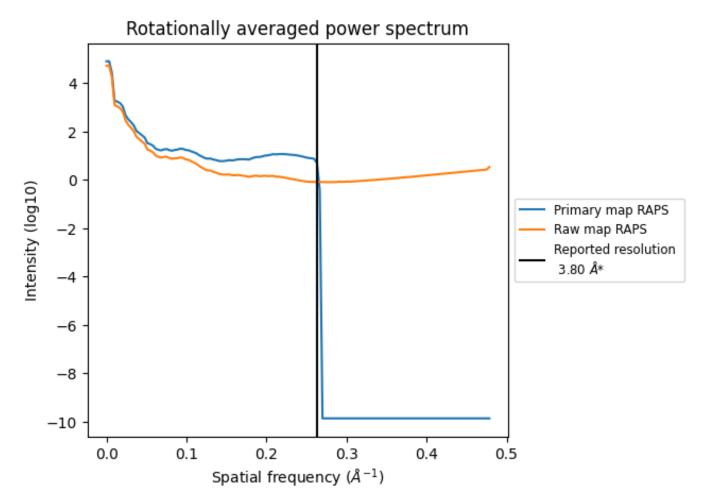


The volume at the recommended contour level is  $308~\mathrm{nm}^3$ ; this corresponds to an approximate mass of  $279~\mathrm{kDa}$ .

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)



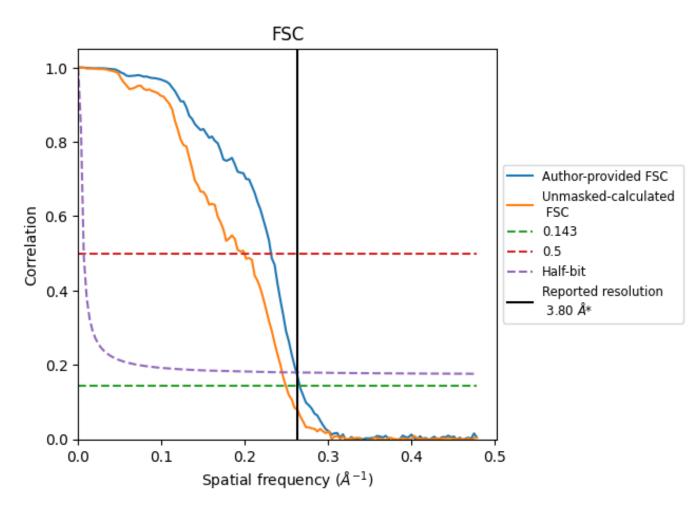
<sup>\*</sup>Reported resolution corresponds to spatial frequency of 0.263  $\rm \mathring{A}^{-1}$ 



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



# 8.2 Resolution estimates (i)

Resolution estimate (Å)	Estim	Estimation criterion (FSC cut-off)			
rtesolution estimate (A)	0.143	0.5	Half-bit		
Reported by author	3.80	-	-		
Author-provided FSC curve	3.76	4.32	3.82		
Unmasked-calculated*	4.01	5.02	4.09		

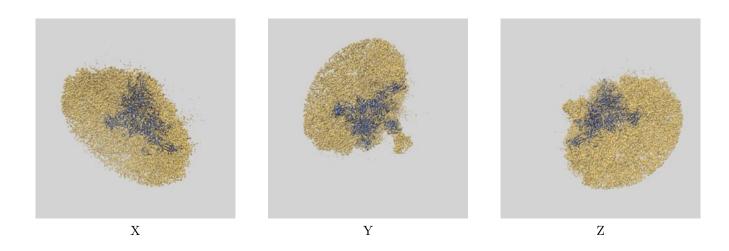
<sup>\*</sup>Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-26072 and PDB model 7TQU. Per-residue inclusion information can be found in section 3 on page 7.

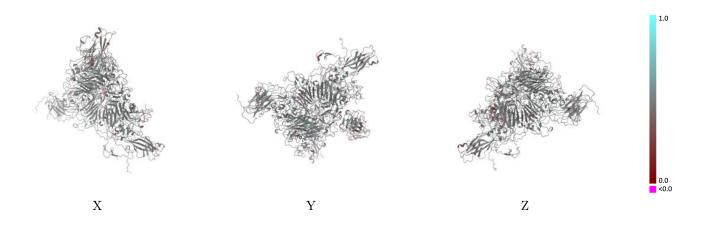
# 9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.008 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.

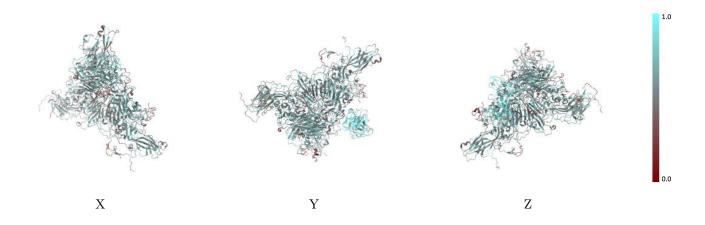


## 9.2 Q-score mapped to coordinate model (i)



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.

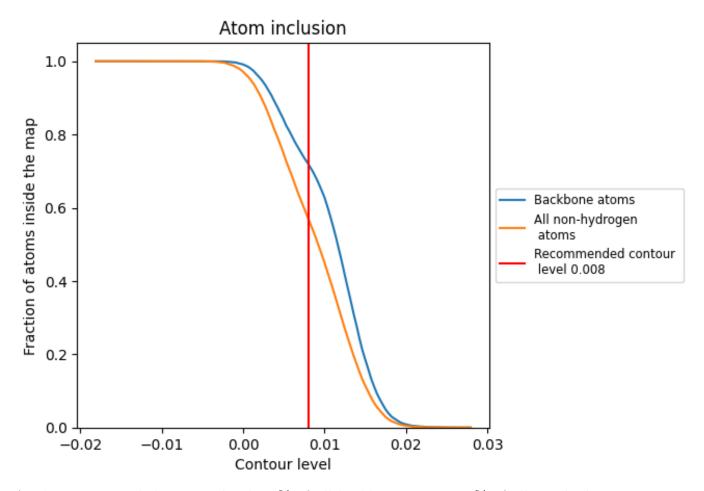
## 9.3 Atom inclusion mapped to coordinate model (i)



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 (0.008).



# 9.4 Atom inclusion (i)



At the recommended contour level, 72% of all backbone atoms, 57% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5697	0.4720
Н	0.7839	0.4460
L	0.7196	0.4210
a	0.5450	0.4670
b	0.5751	0.4770
С	0.5750	0.4820
d	0.4103	0.4430
e	0.5614	0.4780
f	0.5810	0.4770
g	0.5967	0.4800
h	0.4458	0.4420
i	0.5473	0.4730
j	0.5806	0.4840
k	0.5814	0.4760
1	0.4418	0.4550



