

Full wwPDB EM Validation Report (i)

Mar 20, 2024 – 07:48 AM JST

PDB ID : 7BR7

EMDB ID : EMD-30158

Title: Epstein-Barr virus, C1 portal-proximal penton vertex, CATC binding

Authors : Li, Z.; Yu, X. Deposited on : 2020-03-26

Resolution : 4.30 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.dev70

MolProbity : 4.02b-467

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $MapQ \quad : \quad 1.9.13$

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

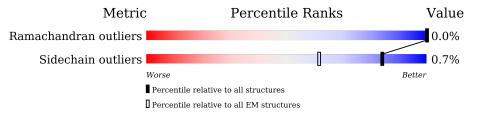
Validation Pipeline (wwPDB-VP) : 2.36

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 4.30 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

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	G	570	14%		85%	
1	K	570	12%	8	38%	
2	С	507	33%	66%		32%
3	В	3149	•	99%		
3	О	3149		99%		
4	2	176	32% 40%	·	58%	
4	Y	176	25%		58%	
4	Z	176	27%		58%	
4	m	176	38% 38%		60%	



Mol	Chain	Length	Quality of chain	
4	У	176	41% . 58%	
5	S	1381	15%	
5	Т	1381	94%	• 6%
5	W	1381	96%	
5	1	1381	90%	9%
5	X	1381	95%	
6	5	364	85%	• 14%
6	e	364	87% 53%	• 12%
7	6	301	99%	
7	7	301	93%	• 5%
7	f	301	96%	•
7	g	301	95%	



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 73138 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 Capsid vertex component 2.

\mathbf{Mol}	Chain	Residues	${f Atoms}$			AltConf	Trace		
1	К	68	Total 563				0	0	
1	G	84	Total 675				0	0	

• Molecule 2 is a protein called Capsid vertex component 1.

Mol	Chain	Residues		At	oms			AltConf	Trace
2	С	346	Total 2705	C 1733	N 482	O 478	S 12	0	0

• Molecule 3 is a protein called Large tegument protein deneddylase.

Mol	Chain	Residues	Atoms			AltConf	Trace	
2	D	35	Total	С	N	О	0	0
3	Б	39	301	192	61	48	0	U
9	0	29	Total	С	N	О	0	0
3		29	252	163	49	40	0	U

• Molecule 4 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues		At	oms			AltConf	Trace
4	m	71	Total	С	N	О	S	0	0
4	m	7.1	600	381	111	107	1	0	U
4	V	74	Total	С	N	О	S	0	0
4	1	74	621	394	114	112	1	0	U
4	Z	74	Total	С	N	О	S	0	0
4	L	74	621	394	114	112	1	0	0
4	2	74	Total	С	N	О	S	0	0
4	<u> </u>	74	621	394	114	112	1	0	U
4	77	74	Total	С	N	О	S	0	0
4	У	74	621	394	114	112	1	0	U



• Molecule 5 is a protein called Major capsid protein.

Mol	Chain	Residues		A	toms			AltConf	Trace
5	S	1327	Total	С	N	О	S	0	0
9	B	1327	10455	6644	1812	1940	59	0	
5	Т	1305	Total	С	N	О	S	0	0
9	1	1303	10257	6513	1780	1905	59	0	
5	W	1331	Total	С	N	О	S	0	0
9	V V	1551	10463	6650	1810	1944	59	0	
5	X	1325	Total	С	N	О	S	0	0
9	A	1323	10404	6607	1803	1935	59	0	
5	1	1250	Total	С	N	О	S	0	0
		1290	9872	6274	1716	1823	59		

• Molecule 6 is a protein called Triplex capsid protein 1.

Mol	Chain	Residues	Atoms			AltConf	Trace		
6	e	319	Total 2505		- '	O 446	S 7	0	0
6	5	313		C 1576		O 440	S 6	0	0

 \bullet Molecule 7 is a protein called Triplex capsid protein 2.

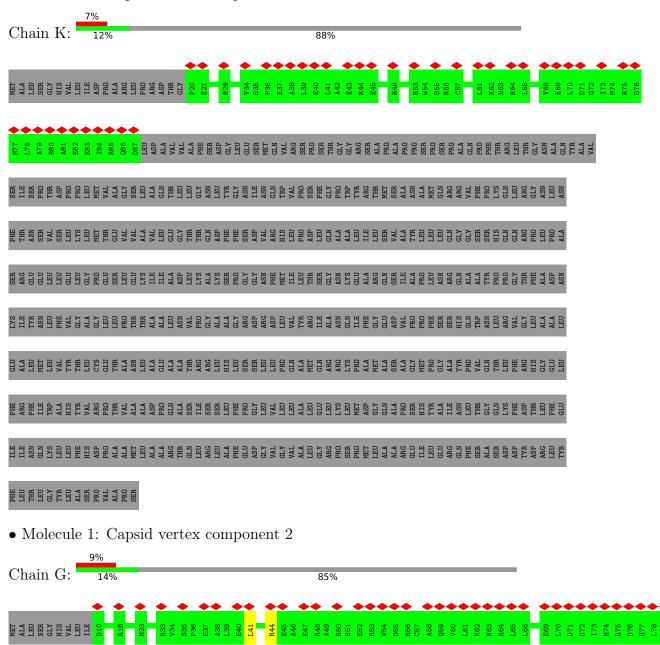
Mol	Chain	Residues		$\mathbf{A}\mathbf{t}$	oms			AltConf	Trace
7	f	290	Total	С	N	О	S	0	0
'	1	290	2279	1466	378	419	16	0	U
7	œ	290	Total	С	N	О	S	0	0
'	g	290	2272	1464	376	414	18	0	U
7	6	297	Total	С	N	О	S	0	0
'	U	291	2329	1496	385	430	18	0	U
7	7	287	Total	С	N	О	S	0	0
	1	201	2262	1452	375	417	18		U



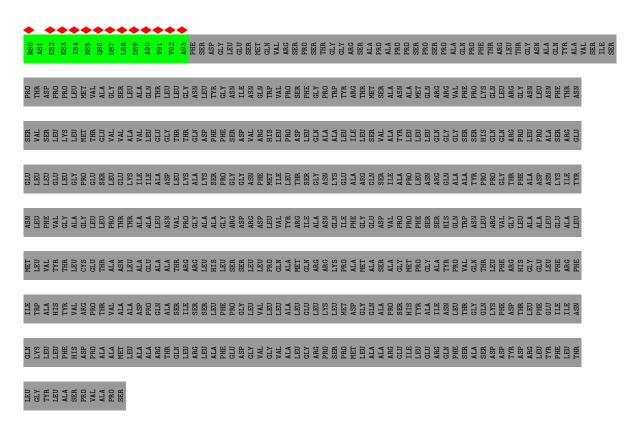
3 Residue-property plots (i)

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.

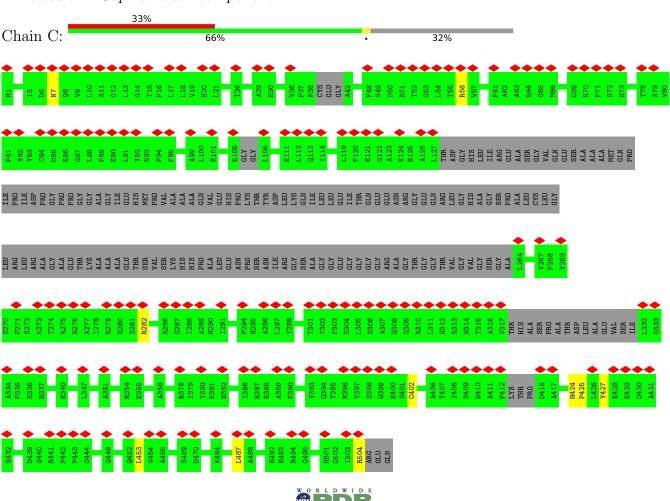
• Molecule 1: Capsid vertex component 2



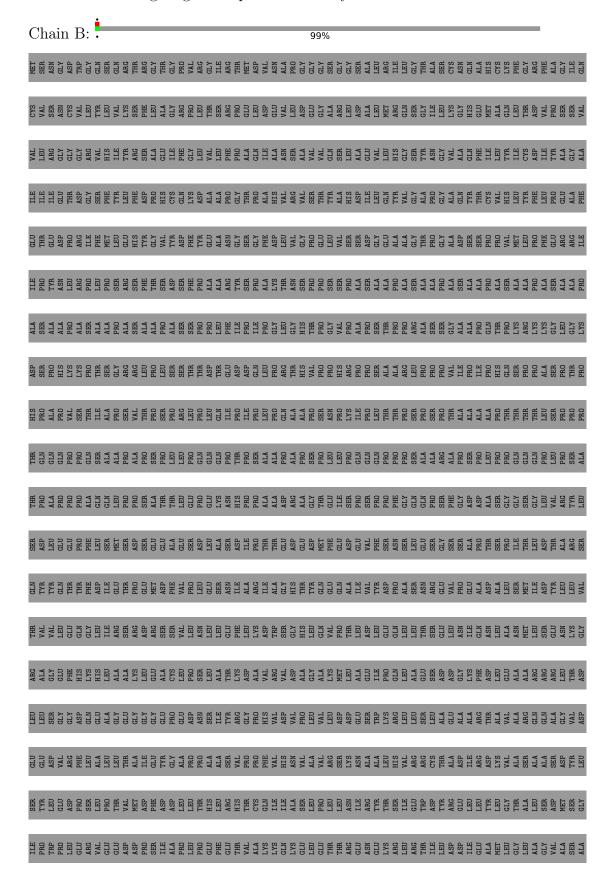




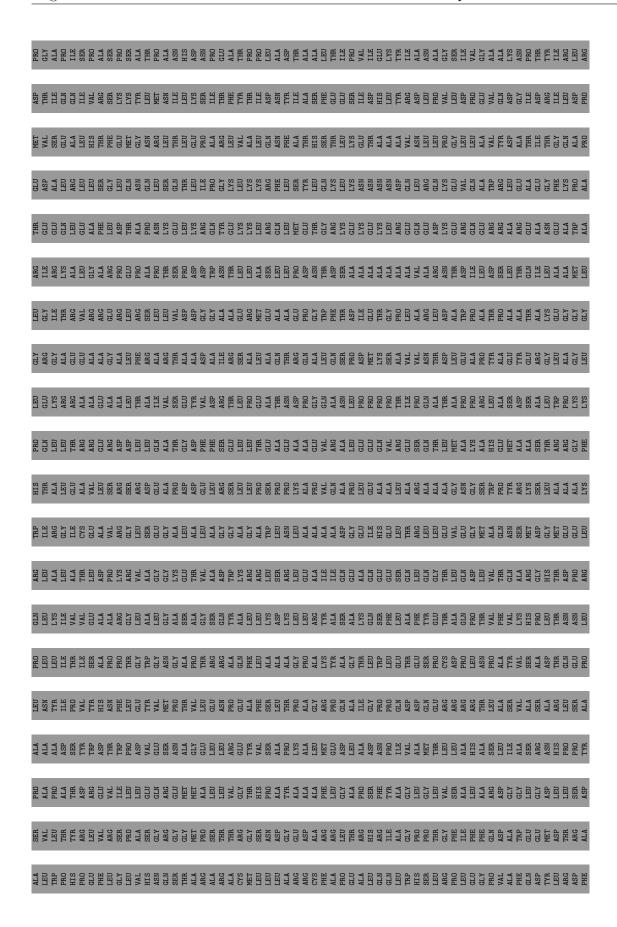
• Molecule 2: Capsid vertex component 1



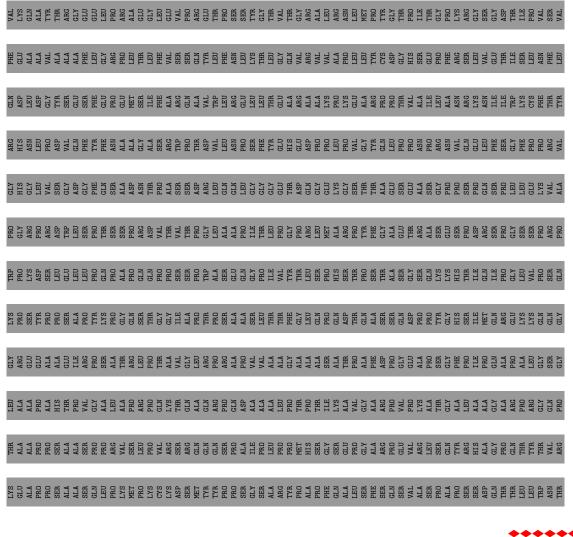
• Molecule 3: Large tegument protein deneddylase









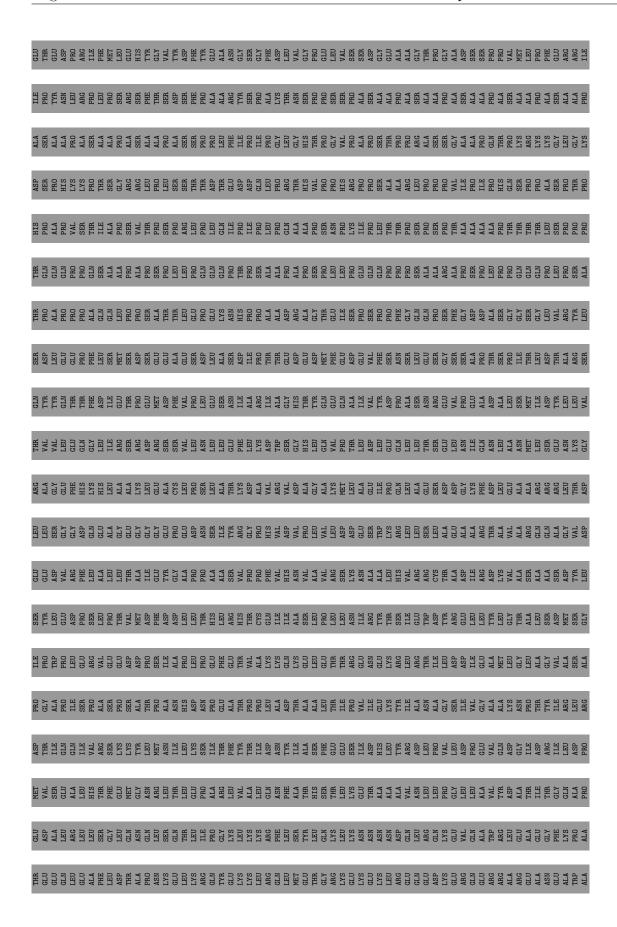


F3122 V3123 S3124 Q3125 Q3125 Q3126 R3127 R3128 K3129 E3131 F3134 F3136 F3136 F3136 F3136 F3136 F3141 F3141

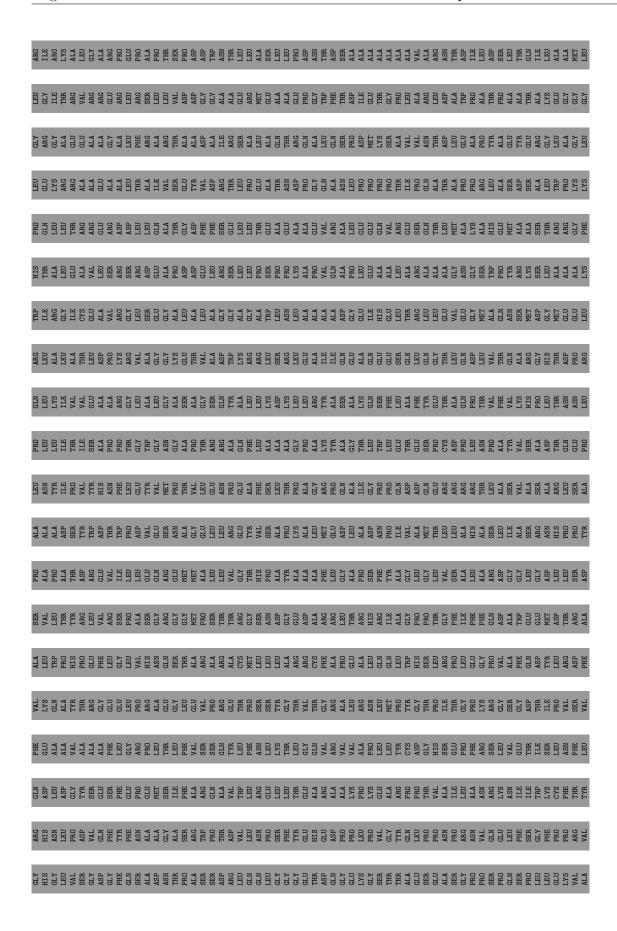
• Molecule 3: Large tegument protein deneddylase

Chain O:

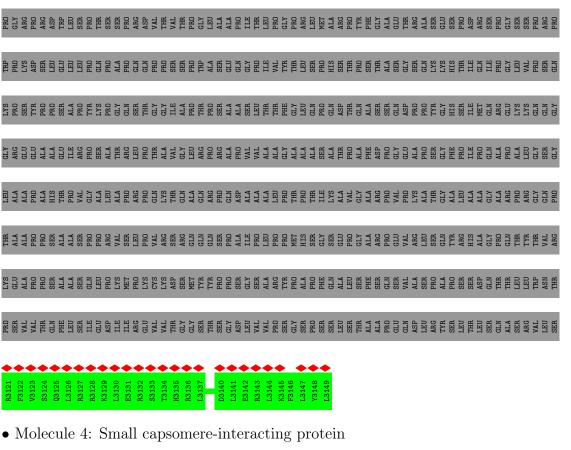


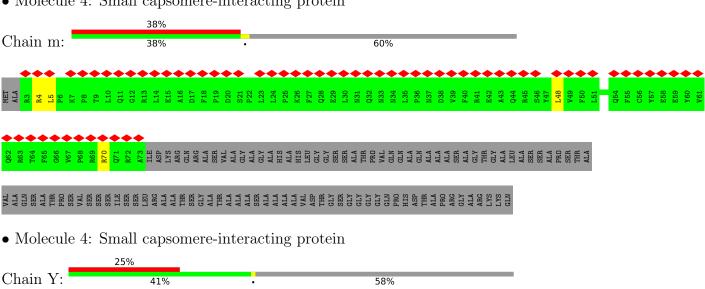






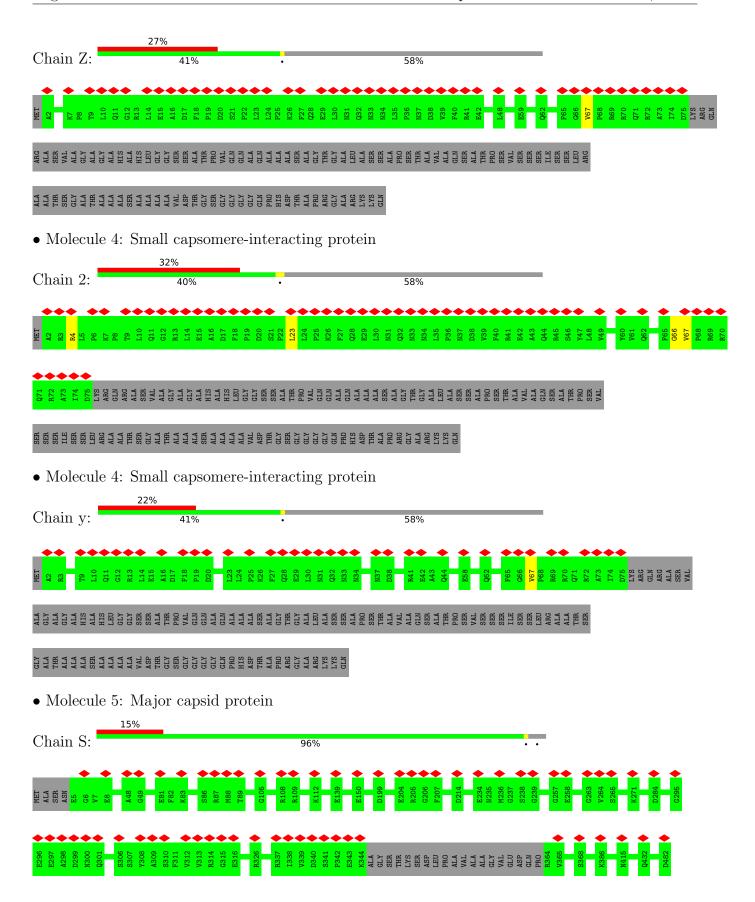




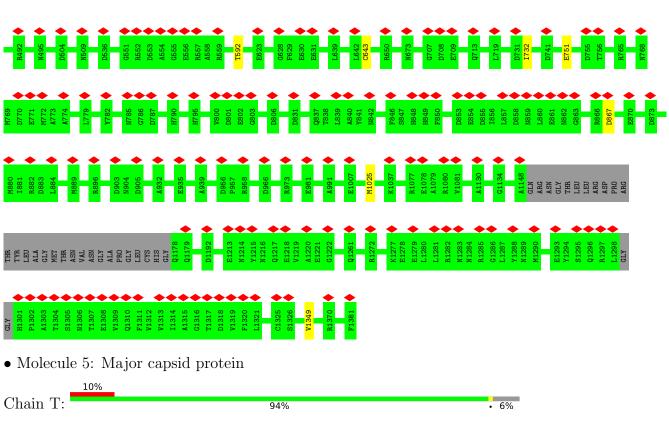


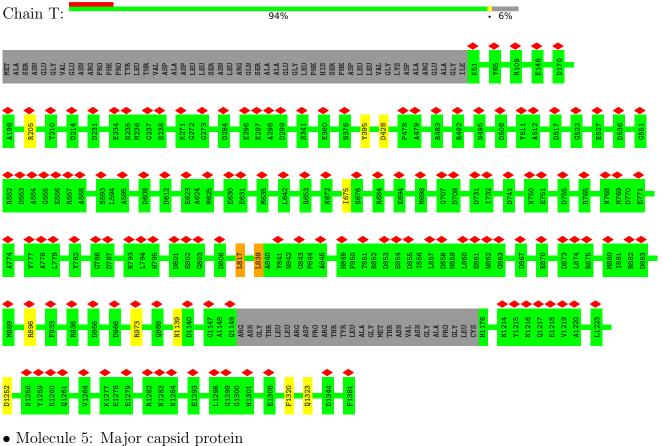
• Molecule 4: Small capsomere-interacting protein





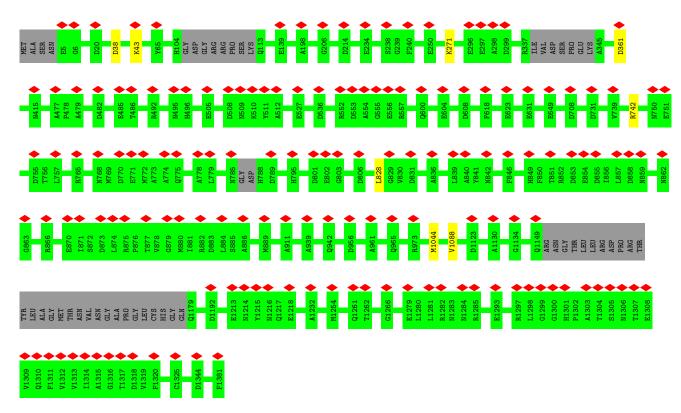




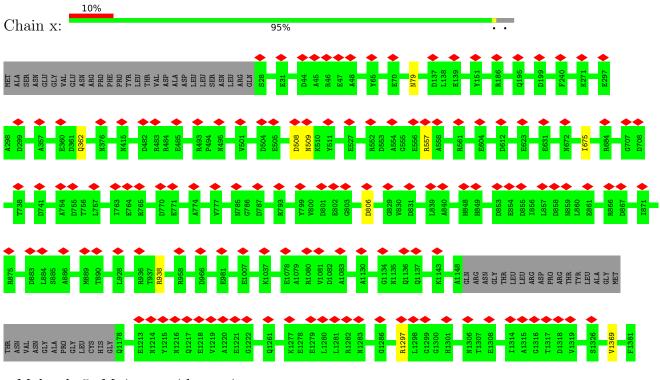


Chain W: 96%





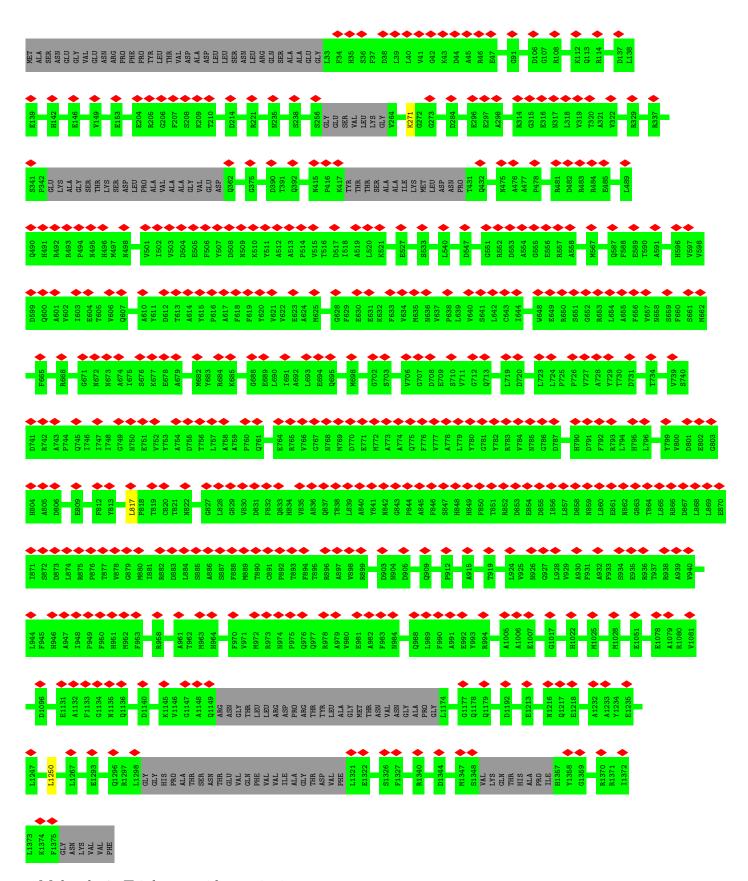
• Molecule 5: Major capsid protein



• Molecule 5: Major capsid protein

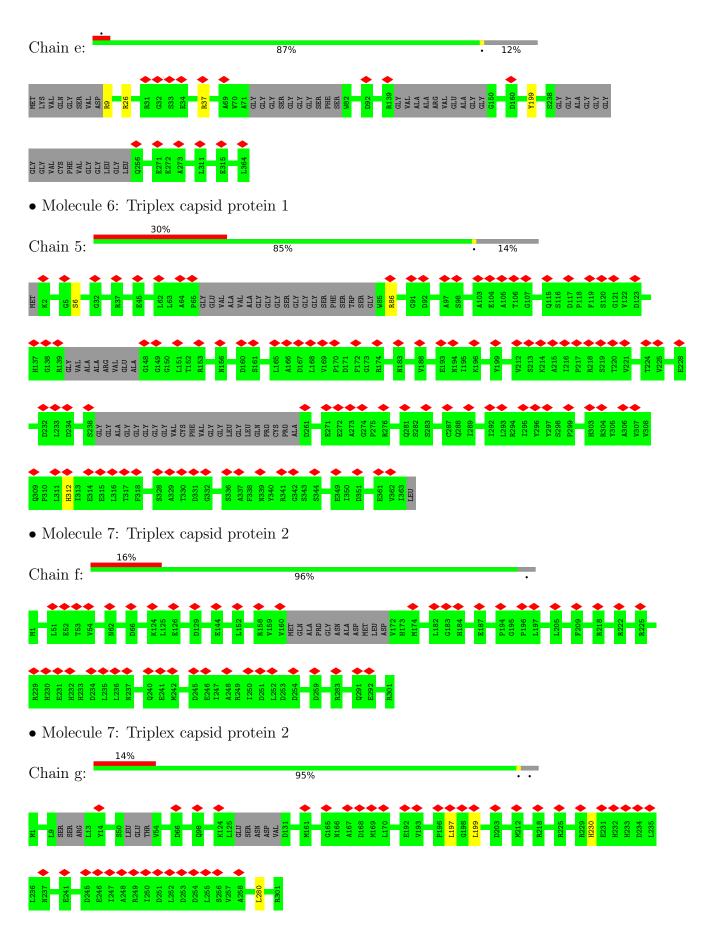
Chain l: 90% 9%





 \bullet Molecule 6: Triplex capsid protein 1



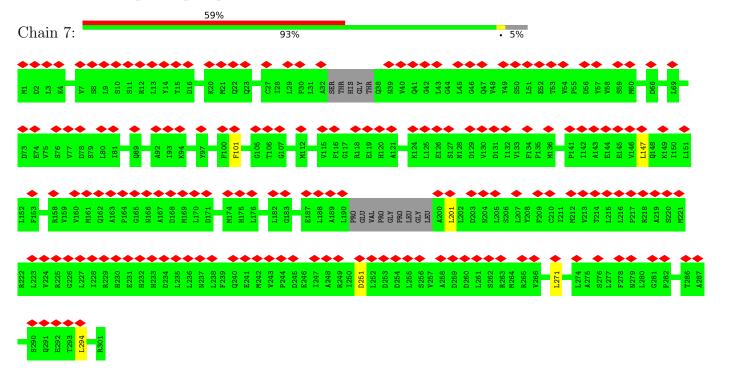




• Molecule 7: Triplex capsid protein 2



• Molecule 7: Triplex capsid protein 2





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	93334	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 $(e^-/\text{Å}^2)$	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.086	Depositor
Minimum map value	-0.040	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	392.99997, 392.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	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).

Mol	Chain	Во	nd lengths	E	Bond angles
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5
1	G	0.37	0/684	0.59	0/924
1	K	0.27	0/570	0.59	0/765
2	С	0.46	$2/2770 \ (0.1\%)$	0.61	$2/3763 \; (0.1\%)$
3	В	0.25	0/304	0.46	0/404
3	О	0.28	0/255	0.66	0/339
4	2	0.34	0/636	0.67	2/861 (0.2%)
4	Y	0.31	0/636	0.61	1/861 (0.1%)
4	Z	0.31	0/636	0.54	0/861
4	m	0.34	0/615	0.59	1/832 (0.1%)
4	у	0.34	0/636	0.60	0/861
5	S	0.37	1/10699~(0.0%)	0.54	1/14537~(0.0%)
5	Т	0.38	1/10499 (0.0%)	0.55	$4/14270 \ (0.0\%)$
5	W	0.37	0/10706	0.54	3/14549~(0.0%)
5	1	0.34	0/10102	0.54	1/13718 (0.0%)
5	X	0.40	1/10648 (0.0%)	0.55	1/14471 (0.0%)
6	5	0.32	0/2523	0.53	0/3431
6	е	0.36	0/2572	0.53	0/3503
7	6	0.32	0/2377	0.58	0/3236
7	7	0.31	0/2306	0.65	4/3135 (0.1%)
7	f	0.33	0/2327	0.54	0/3169
7	g	0.33	0/2319	0.60	1/3155~(0.0%)
All	All	0.37	5/74820 (0.0%)	0.56	21/101645 (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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	2	0	1
5	Т	0	1
6	5	0	1
7	g	0	1



Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	Ideal(Å)
2	С	425	PRO	N-CA	13.35	1.70	1.47
5	X	362	GLN	C-N	8.97	1.51	1.34
5	Т	1323	GLN	C-N	8.89	1.51	1.34
2	С	424	HIS	C-N	5.91	1.45	1.34
5	S	1025	MET	C-N	-5.24	1.22	1.34

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
5	W	361	ASP	CB-CG-OD1	8.72	126.15	118.30
5	Т	817	LEU	CA-CB-CG	8.15	134.05	115.30
2	С	425	PRO	CA-N-CD	-7.99	100.32	111.50
7	7	271	LEU	CA-CB-CG	7.04	131.48	115.30
5	X	806	ASP	CB-CG-OD1	6.88	124.49	118.30
4	Y	23	LEU	CA-CB-CG	6.63	130.55	115.30
4	2	23	LEU	CA-CB-CG	6.51	130.28	115.30
5	1	817	LEU	CA-CB-CG	6.32	129.83	115.30
7	g	199	LEU	CA-CB-CG	6.15	129.45	115.30
5	S	732	ILE	CG1-CB-CG2	-6.09	98.00	111.40
2	С	487	LEU	CA-CB-CG	5.98	129.06	115.30
4	2	4	ARG	C-N-CA	5.56	135.60	121.70
7	7	201	LEU	CA-CB-CG	5.49	127.92	115.30
7	7	294	LEU	CA-CB-CG	5.41	127.75	115.30
5	Т	428	ASP	CB-CG-OD2	5.19	122.97	118.30
5	W	38	ASP	CB-CG-OD2	5.19	122.97	118.30
7	7	147	LEU	CA-CB-CG	5.17	127.19	115.30
5	W	828	LEU	CA-CB-CG	5.06	126.95	115.30
5	Т	839	LEU	CB-CG-CD2	-5.06	102.40	111.00
4	m	48	LEU	CA-CB-CG	5.05	126.91	115.30
5	Т	1252	ASP	CB-CG-OD1	5.03	122.83	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	2	66	GLY	Peptide



Mol	Chain	Res	Type	Group
6	5	312	HIS	Peptide
5	Т	817	LEU	Peptide
7	g	230	HIS	Peptide

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	G	82/570~(14%)	74 (90%)	8 (10%)	0	100	100
1	K	$66/570\ (12\%)$	65 (98%)	1 (2%)	0	100	100
2	С	334/507 (66%)	318 (95%)	16 (5%)	0	100	100
3	В	33/3149 (1%)	33 (100%)	0	0	100	100
3	О	27/3149 (1%)	26 (96%)	1 (4%)	0	100	100
4	2	72/176 (41%)	61 (85%)	11 (15%)	0	100	100
4	Y	72/176 (41%)	66 (92%)	6 (8%)	0	100	100
4	Z	72/176 (41%)	67 (93%)	5 (7%)	0	100	100
4	m	69/176 (39%)	66 (96%)	3 (4%)	0	100	100
4	У	72/176 (41%)	62 (86%)	10 (14%)	0	100	100
5	S	1319/1381 (96%)	1236 (94%)	83 (6%)	0	100	100
5	Т	1301/1381 (94%)	1201 (92%)	100 (8%)	0	100	100
5	W	1321/1381 (96%)	1226 (93%)	95 (7%)	0	100	100
5	1	1236/1381 (90%)	1162 (94%)	74 (6%)	0	100	100
5	X	1321/1381 (96%)	1227 (93%)	94 (7%)	0	100	100
6	5	305/364 (84%)	288 (94%)	17 (6%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
6	e	311/364~(85%)	291 (94%)	20 (6%)	0	100	100
7	6	293/301~(97%)	280 (96%)	13 (4%)	0	100	100
7	7	$281/301\ (93\%)$	254 (90%)	26 (9%)	1 (0%)	34	72
7	f	$286/301\ (95\%)$	272 (95%)	14 (5%)	0	100	100
7	g	$282/301 \ (94\%)$	259 (92%)	23 (8%)	0	100	100
All	All	9155/17662~(52%)	8534 (93%)	620 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	7	101	PHE

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	G	70/465~(15%)	68 (97%)	2 (3%)	42	64
1	K	59/465~(13%)	59 (100%)	0	100	100
2	С	288/400~(72%)	281 (98%)	7 (2%)	49	69
3	В	33/2539~(1%)	33 (100%)	0	100	100
3	O	27/2539~(1%)	27 (100%)	0	100	100
4	2	68/128~(53%)	67 (98%)	1 (2%)	65	80
4	Y	68/128~(53%)	68 (100%)	0	100	100
4	Z	68/128~(53%)	67 (98%)	1 (2%)	65	80
4	m	66/128~(52%)	63 (96%)	3 (4%)	27	54
4	У	68/128~(53%)	67 (98%)	1 (2%)	65	80
5	S	1133/1171~(97%)	1128 (100%)	5 (0%)	91	94
5	Т	1111/1171~(95%)	1103 (99%)	8 (1%)	84	90
5	W	1132/1171 (97%)	1127 (100%)	5 (0%)	91	94



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
5	1	1069/1171 (91%)	1067 (100%)	2 (0%)	93	96
5	X	1125/1171 (96%)	1117 (99%)	8 (1%)	84	90
6	5	264/289 (91%)	262 (99%)	2 (1%)	81	89
6	e	$268/289 \ (93\%)$	264 (98%)	4 (2%)	65	80
7	6	$264/267 \ (99\%)$	264 (100%)	0	100	100
7	7	256/267~(96%)	255 (100%)	1 (0%)	91	94
7	f	259/267~(97%)	259 (100%)	0	100	100
7	g	256/267~(96%)	254 (99%)	2 (1%)	81	89
All	All	7952/14549 (55%)	7900 (99%)	52 (1%)	84	90

All (52) residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	G	41	LEU
1	G	44 7	ARG
2	С		ASN
2	С	56	ARG
2	С	282	ARG
2	С	402	CYS
2 2 2 2 2 2 2 2 4 4	G G C C C C C C C	427	ARG CYS TYR
2	С	453	LEU
2	С	504	ARG
4	m	4	ARG ARG LEU
4	m	5	LEU
4	m	70	ARG
4 4	Z	67	ARG VAL VAL
	2 S	67	VAL
5	S	592	THR CYS GLU
5	S	643	CYS
5	S	751	GLU
5	S	867	ASP VAL ARG
5	S	1349	VAL
5	Т	205	ARG
5	Т	395	TYR ILE LEU
5	Т	675	ILE
5 5	S S T T T T T T T	839	LEU
5	Т	896	ARG
5	Т	973	ARG
5	Т	1139	ASN



Continued from previous page...

Mol	Chain	Res	Type
5	Т	1320	PHE
5	T W W	43	LYS
5	W	271	LYS
5	W	742	ARG
5	W	1044	MET
5	W	1088	VAL
5	X	79	ASN
5	X	508	ASP
5	X	509	ASN
5	X	557	ARG
5	X	675	ILE
5	X	938	ARG
5	X	1297	ARG
5	X	1369	VAL
4	У	67	VAL
6	е	9	ARG
6	е	26	ARG
6	e	37	ARG
6	е	199	TYR
7	g	197	LEU
7	g l	280	LEU
5		271	LYS
5	l	1250	LEU
6	5	6	SER
6	5	86	ARG
7	7	251	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (123) such sidechains are listed below:

Mol	Chain	Res	Type
1	K	63	ASN
1	G	30	ASN
1	G	63	ASN
1	G	86	GLN
2	С	7	ASN
2	С	20	HIS
2	С	34	ASN
2	С	38	ASN
2	С	410	ASN
4	2	11	GLN
5	S	24	ASN
5	S	64	GLN



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Mol	Chain	Res	Type
5	S	333	HIS
5	S S	442	ASN
5	S	465	HIS
5	S	495	ASN ASN
5	S	498	ASN
5	S	531	HIS
5	S	534	ASN
5	S	543	HIS HIS
5	S	564	HIS
5	S	596	HIS
5	S	636	ASN
5	S	750	ASN ASN
5	S	842	ASN
5	S	1089	HIS
5	S	1139	ASN
5	S	1241	ASN
5	S	1289	ASN HIS
5	S	1353	HIS
5	Т	94	GLN
5	Т	242	GLN
5	S S T T T T T T T T T T T T T T T T T T	398	ASN GLN
5	Т	432	GLN
5	Т	475	ASN HIS
5	Т	531	
5	Т	534	ASN
5	Т	543	HIS
5	Т	570	ASN ASN
5	Т	750	
5	Т	842	ASN
5	Т	904	ASN
5	Т	997	HIS
5	Т	1073	ASN
5	T T T	1089	HIS
5	Т	1139	ASN
5	Т	1261	GLN
5	T W	1276	ASN
5	W	142	HIS
5	W	472	ASN
5	W	498	ASN
5	W	564	HIS
5	W	596	HIS
5	W	607	GLN

5 | W | 607 | GLN | Continued on next page...



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			ous page
Mol	Chain	Res	Type
5	W	669	HIS
5	W	750	ASN
5	W	824	HIS
5	W	964	HIS
5	W	984	ASN
5	W	1139	ASN
5	W	1197	GLN
5	W	1329	GLN
5	X	113	GLN
5	X	126	HIS
5	X	389	ASN
5	X	415	ASN
5	X	509	ASN
5	X	531	HIS
5	X	534	ASN
5	X	543	HIS
5	X	570	ASN
5	X	581	GLN
5	X	722	ASN
5	X	750	ASN
5	X	822	ASN
5	X	824	HIS
5	X	842	ASN
5	X	1056	ASN
5	X	1089	HIS
5	X	1122	GLN
5	X	1139	ASN
5	X	1200	ASN
5	X	1216	ASN
5	X	1283	ASN
5	X	1310	GLN
5	X	1351	GLN
4	у	37	ASN
6	e	46	HIS
6	е	136	ASN
6	е	227	GLN
6	е	288	GLN
6	е	291	ASN
6	е	303	HIS
7	f	41	GLN
7	f	120	HIS
7	f	128	ASN



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Mol	Chain	Res	$oxed{\mathbf{Type}}$
7	f	175	HIS
7	f	240	GLN
7	g	62	ASN
7		148	GLN
5	g l	195	GLN
5	l	402	GLN
5	l	490	GLN
5	l	509	ASN
5	1	636	ASN
5	l	673	ASN
5	l	750	ASN
5	l	768	ASN
5	1	785	ASN
5	l	926	ASN
5	l	997	HIS
5	l	1039	HIS
5	1	1056	ASN
6	5	102	ASN
6	5	156	ASN
6	5	208	HIS
6	5	288	GLN
6	5	291	ASN
6	5	356	ASN
7	6	204	ASN
7	7	62	ASN
7	7	204	ASN
7	7	240	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.



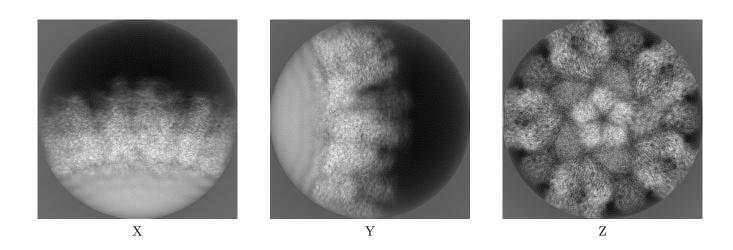
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-30158. 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)

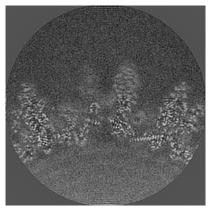
6.1.1 Primary map



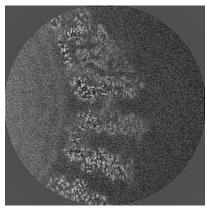
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

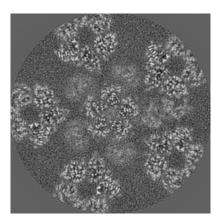
6.2.1 Primary map



X Index: 150



Y Index: 150



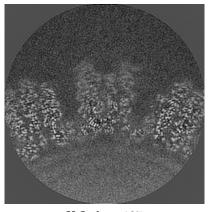
Z Index: 150

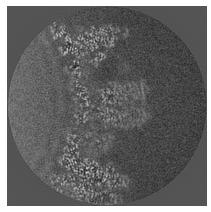


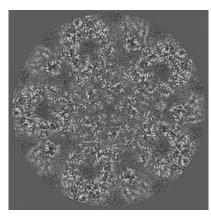
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map







X Index: 137

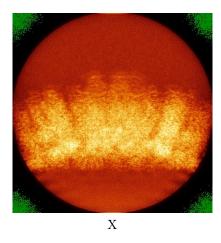
Y Index: 122

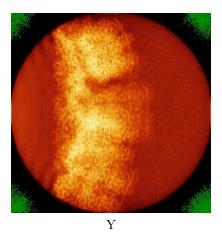
Z Index: 107

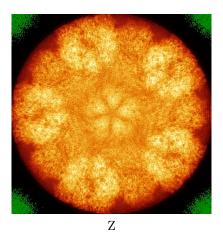
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map





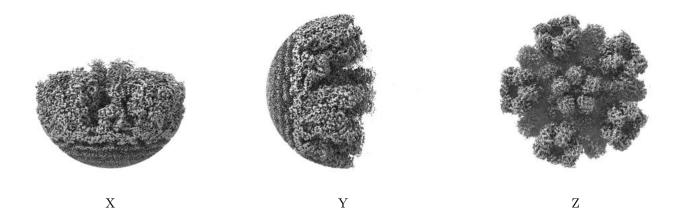


The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



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

6.6 Mask visualisation (i)

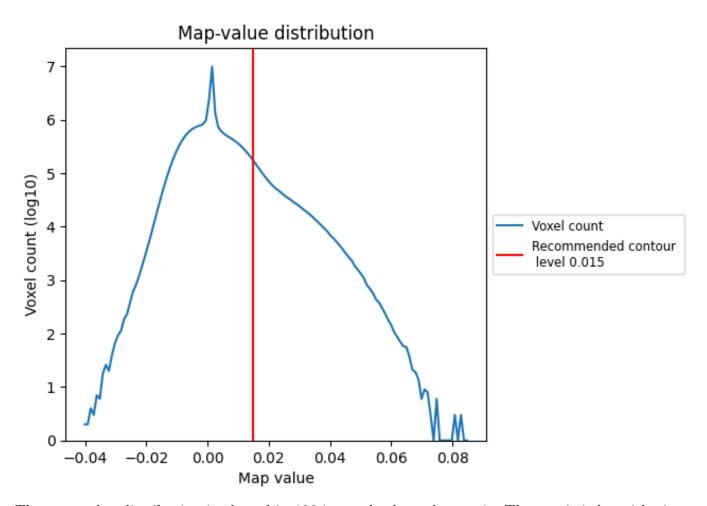
This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

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

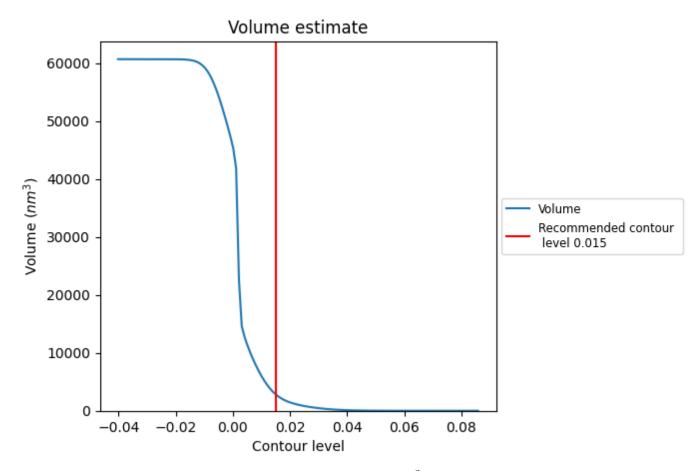
7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



7.2 Volume estimate (i)

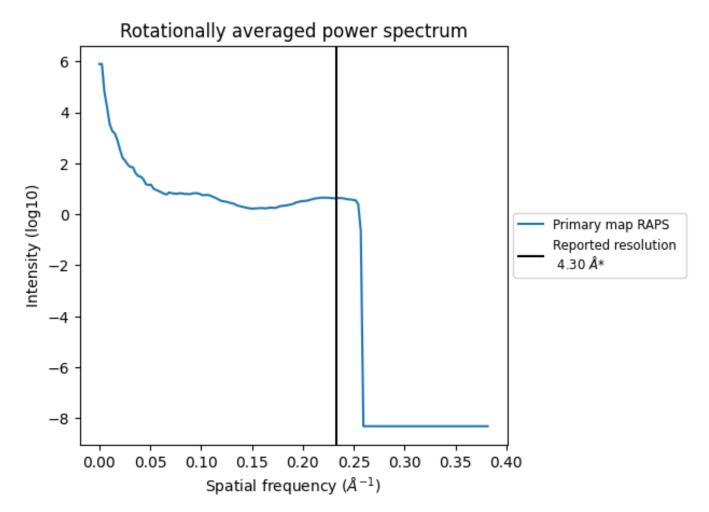


The volume at the recommended contour level is $2834~\mathrm{nm}^3$; this corresponds to an approximate mass of $2560~\mathrm{kDa}$.

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)



^{*}Reported resolution corresponds to spatial frequency of 0.233 $\rm \mathring{A}^{-1}$



8 Fourier-Shell correlation (i)

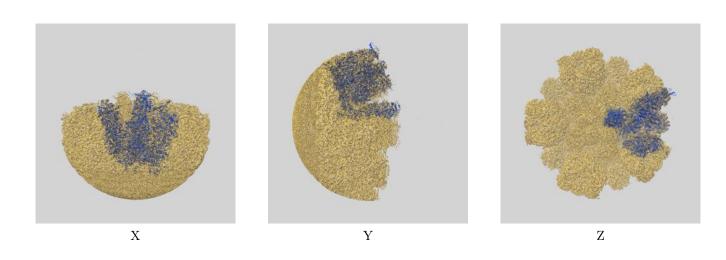
This section was not generated. No FSC curve or half-maps provided.



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-30158 and PDB model 7BR7. Per-residue inclusion information can be found in section 3 on page 6.

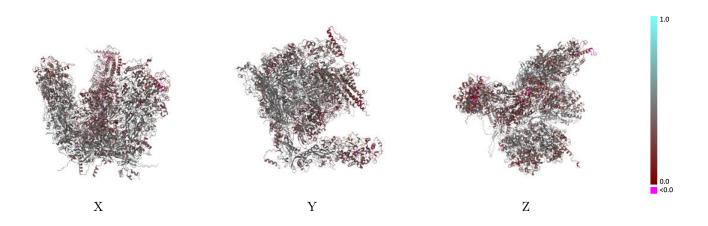
9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.015 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.

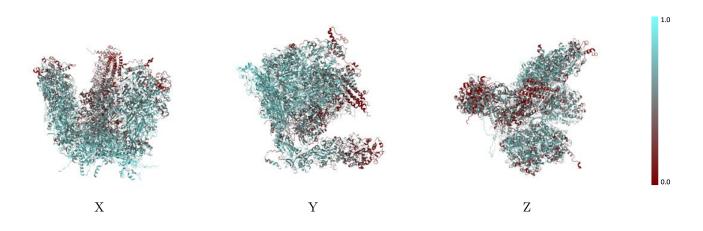


9.2 Q-score mapped to coordinate model (i)



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.

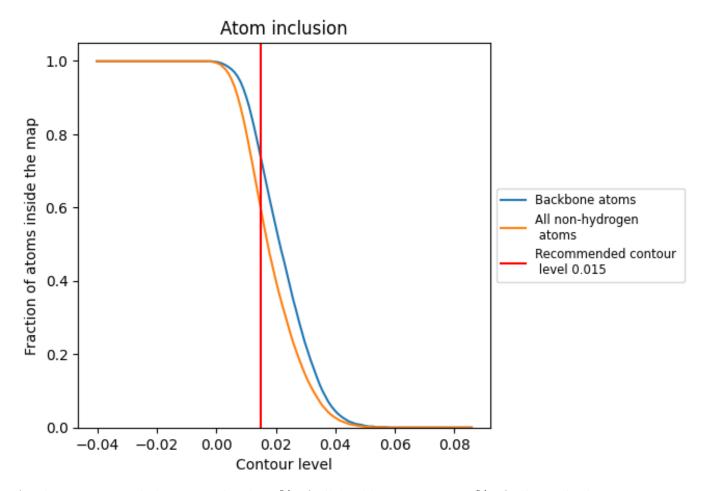
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.015).



9.4 Atom inclusion (i)



At the recommended contour level, 73% of all backbone atoms, 59% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5910	0.4010
2	0.2020	0.1920
5	0.5120	0.3760
6	0.3890	0.3170
7	0.3490	0.2900
В	0.1190	0.2240
С	0.4190	0.3250
G	0.3320	0.3020
K	0.3780	0.3370
О	0.1660	0.2240
S	0.6400	0.4260
Т	0.6870	0.4350
W	0.6850	0.4260
Y	0.3530	0.3450
Z	0.3430	0.3240
e	0.7250	0.4360
f	0.6330	0.3990
g	0.6470	0.4090
l	0.5110	0.3890
m	0.1140	0.2250
X	0.6800	0.4410
У	0.4080	0.3350



