



Full wwPDB EM Validation Report ⓘ

Jan 13, 2025 – 11:13 PM JST

PDB ID : 9KMH
EMDB ID : EMD-62433
Title : The Composite Cryo-EM Structure of the Portal Vertex of Bacteriophage FCWL1
Authors : Cai, C.; Wang, Y.; Liu, Y.; Shao, Q.; Wang, A.; Fang, Q.
Deposited on : 2024-11-16
Resolution : 3.50 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

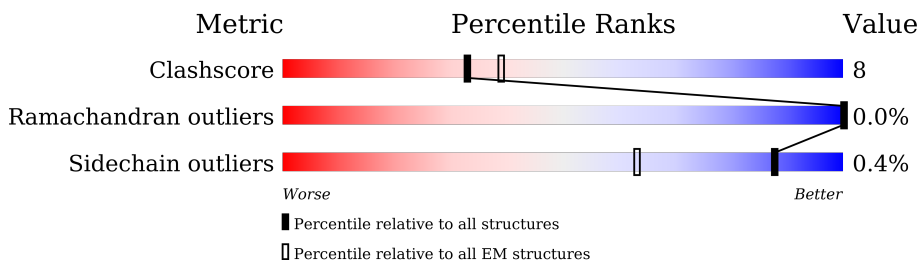
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

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 3.50 Å.

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



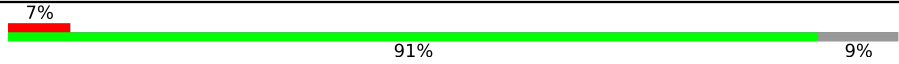
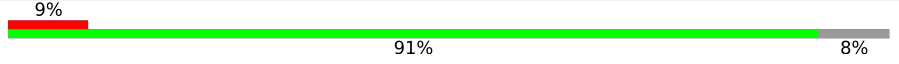
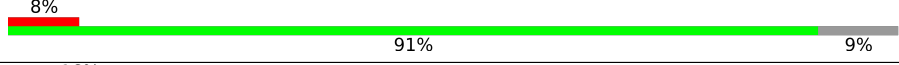
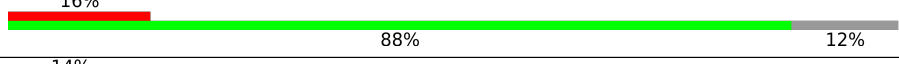
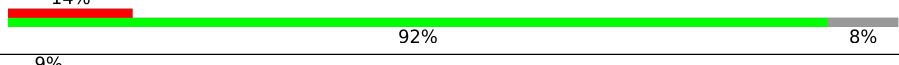
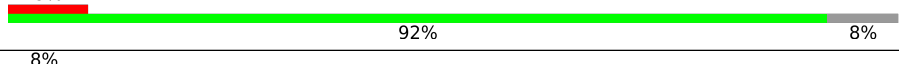
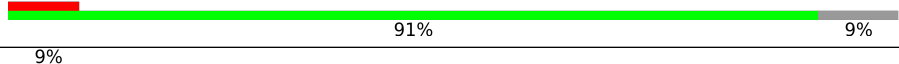
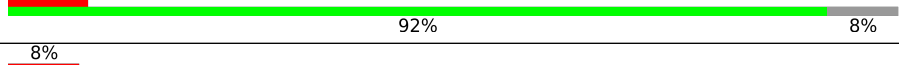
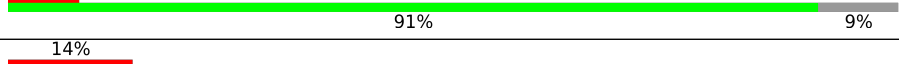
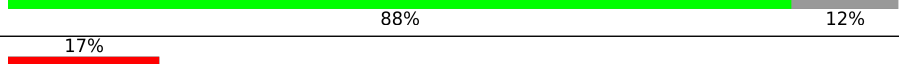
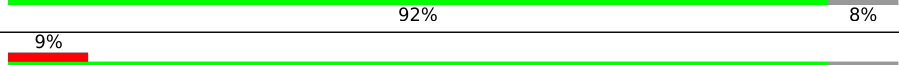
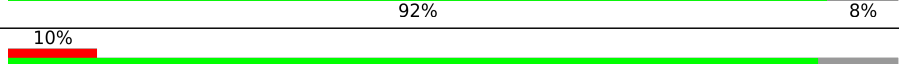

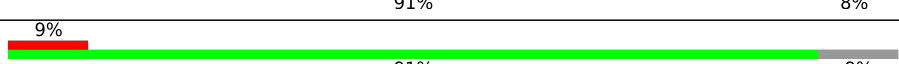
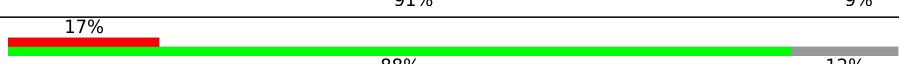
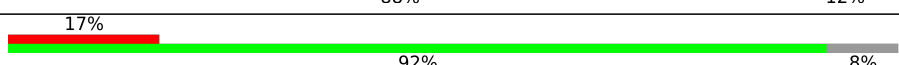
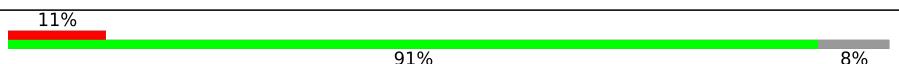
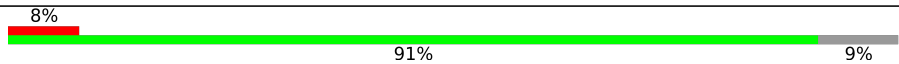
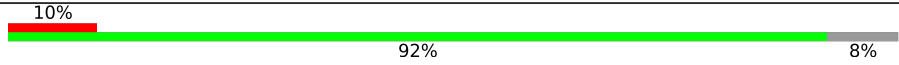
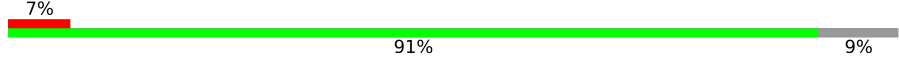

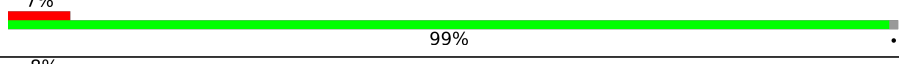
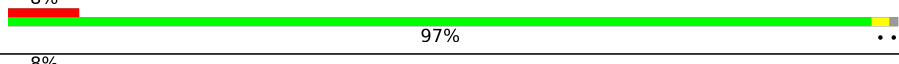
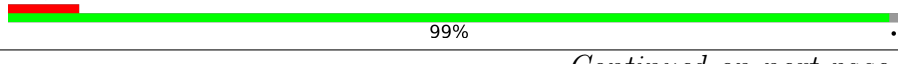

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 $\leq 5\%$. 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	aa	319	
1	af	319	
1	ag	319	
1	ah	319	
1	ai	319	
1	aj	319	
1	an	319	
1	as	319	

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Mol	Chain	Length	Quality of chain
1	at	319	
1	au	319	
1	av	319	
1	aw	319	
1	ba	319	
1	bf	319	
1	bg	319	
1	bh	319	
1	bi	319	
1	bj	319	
1	bn	319	
1	bs	319	
1	bt	319	
1	bu	319	
1	bv	319	
1	bw	319	
1	ca	319	
1	cf	319	
1	cg	319	
1	ch	319	
1	ci	319	
1	cj	319	
2	ab	158	
2	ac	158	
2	ad	158	

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Mol	Chain	Length	Quality of chain
2	ae	158	9% 99%
2	al	158	20% 99%
2	am	158	8% 99%
2	ao	158	9% 98%
2	ap	158	7% 99%
2	aq	158	6% 99%
2	ar	158	8% 99%
2	ay	158	30% 99%
2	az	158	9% 99%
2	bb	158	8% 99%
2	bc	158	9% 99%
2	bd	158	6% 99%
2	be	158	8% 99%
2	bl	158	19% 99%
2	bm	158	8% 99%
2	bo	158	6% 99%
2	bp	158	5% 99%
2	bq	158	6% 99%
2	br	158	8% 99%
2	by	158	28% 99%
2	bz	158	11% 99%
2	cb	158	8% 99%
2	cc	158	8% 99%
2	cd	158	7% 99%
2	ce	158	8% 99%

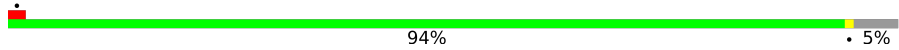
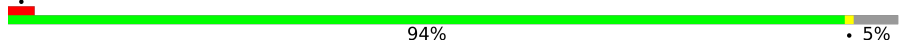
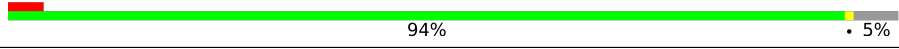
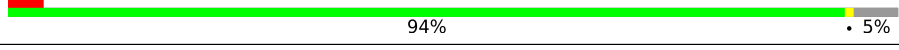
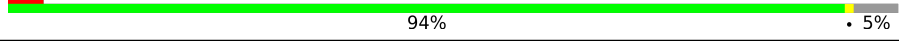
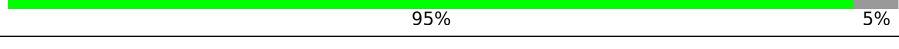
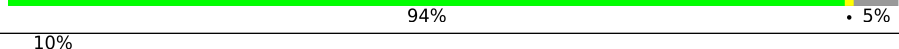
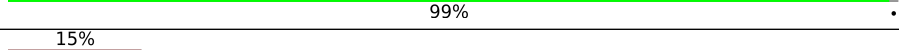
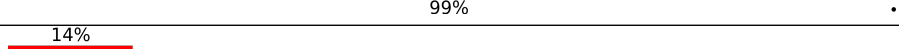
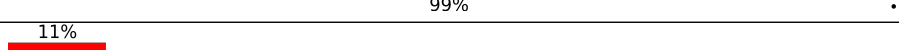
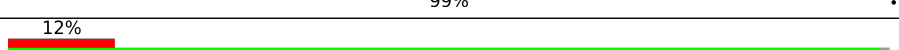
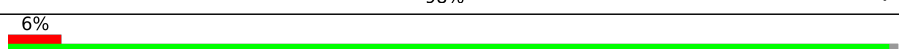

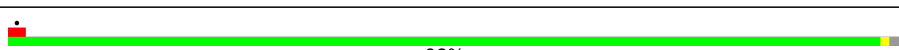
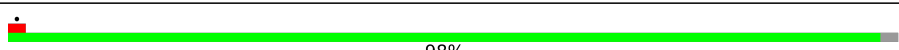
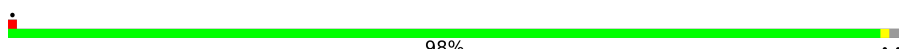

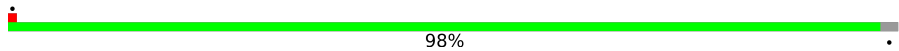


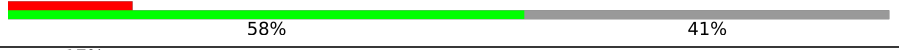



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Mol	Chain	Length	Quality of chain
2	cl	158	22% 99%
2	cm	158	11% 99%
3	cn	444	21% 83% 16%
3	co	444	19% 85% 14%
3	cp	444	17% 83% 16%
3	cq	444	18% 84% 16%
3	cy	444	20% 85% 14%
3	dj	444	21% 83% 16%
3	du	444	20% 86% 14%
3	dy	444	22% 84% 16%
3	dz	444	17% 83% 16%
3	ea	444	18% 86% 14%
3	eb	444	21% 84% 16%
3	ec	444	23% 86% 14%
4	cr	132	100%
4	cs	132	99%
4	ct	132	100%
4	cu	132	100%
4	cv	132	100%
4	cw	132	100%
5	cx	140	95% 5%
5	cz	140	95% 5%
5	da	140	95% 5%
5	db	140	5% 95% 5%
5	dc	140	95% 5%

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Mol	Chain	Length	Quality of chain
5	dd	140	 94% • 5%
5	de	140	 94% • 5%
5	df	140	 94% • 5%
5	dg	140	 94% • 5%
5	dh	140	 94% • 5%
5	di	140	 95% 5%
5	dk	140	 94% • 5%
6	dl	222	 10% 99% •
6	dm	222	 15% 99% •
6	dn	222	 14% 99% •
6	do	222	 11% 99% •
6	dp	222	 12% 98% •
6	dq	222	 6% 99% •
7	dr	123	 98% •
7	ds	123	 98% ••
7	dt	123	 98% •
7	dv	123	 98% ••
7	dw	123	 98% •
7	dx	123	 98% •
8	ak	255	 11% 58% 41%
8	ax	255	 19% 58% 41%
8	bk	255	 14% 58% 41%
8	bx	255	 17% 58% 41%
8	ck	255	 17% 58% 41%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 179175 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	aa	292	2260	1435	376	436	13	0	0
1	af	292	2260	1435	376	436	13	0	0
1	ag	291	2255	1432	375	435	13	0	0
1	ah	292	2260	1435	376	436	13	0	0
1	ai	291	2255	1432	375	435	13	0	0
1	aj	282	2188	1389	364	423	12	0	0
1	an	292	2260	1435	376	436	13	0	0
1	as	292	2260	1435	376	436	13	0	0
1	at	291	2255	1432	375	435	13	0	0
1	au	292	2260	1435	376	436	13	0	0
1	av	291	2255	1432	375	435	13	0	0
1	aw	282	2188	1389	364	423	12	0	0
1	ba	292	2260	1435	376	436	13	0	0
1	bf	292	2260	1435	376	436	13	0	0
1	bg	291	2255	1432	375	435	13	0	0
1	bh	292	2260	1435	376	436	13	0	0
1	bi	291	2255	1432	375	435	13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	bj	282	Total	C	N	O	S	0	0
			2188	1389	364	423	12		
1	bn	292	Total	C	N	O	S	0	0
			2260	1435	376	436	13		
1	bs	292	Total	C	N	O	S	0	0
			2260	1435	376	436	13		
1	bt	291	Total	C	N	O	S	0	0
			2255	1432	375	435	13		
1	bu	292	Total	C	N	O	S	0	0
			2260	1435	376	436	13		
1	bv	291	Total	C	N	O	S	0	0
			2255	1432	375	435	13		
1	bw	282	Total	C	N	O	S	0	0
			2188	1389	364	423	12		
1	ca	292	Total	C	N	O	S	0	0
			2260	1435	376	436	13		
1	cf	292	Total	C	N	O	S	0	0
			2260	1435	376	436	13		
1	cg	291	Total	C	N	O	S	0	0
			2255	1432	375	435	13		
1	ch	292	Total	C	N	O	S	0	0
			2260	1435	376	436	13		
1	ci	291	Total	C	N	O	S	0	0
			2255	1432	375	435	13		
1	cj	282	Total	C	N	O	S	0	0
			2188	1389	364	423	12		

- Molecule 2 is a protein called Decoration protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	ab	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		
2	ac	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		
2	ad	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		
2	ae	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		
2	al	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		
2	am	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	ao	156	1179	738	201	234	6	0	0
2	ap	156	1179	738	201	234	6	0	0
2	aq	156	1179	738	201	234	6	0	0
2	ar	156	1179	738	201	234	6	0	0
2	ay	156	1179	738	201	234	6	0	0
2	az	156	1179	738	201	234	6	0	0
2	bb	156	1179	738	201	234	6	0	0
2	bc	156	1179	738	201	234	6	0	0
2	bd	156	1179	738	201	234	6	0	0
2	be	156	1179	738	201	234	6	0	0
2	bl	156	1179	738	201	234	6	0	0
2	bm	156	1179	738	201	234	6	0	0
2	bo	156	1179	738	201	234	6	0	0
2	bp	156	1179	738	201	234	6	0	0
2	bq	156	1179	738	201	234	6	0	0
2	br	156	1179	738	201	234	6	0	0
2	by	156	1179	738	201	234	6	0	0
2	bz	156	1179	738	201	234	6	0	0
2	cb	156	1179	738	201	234	6	0	0
2	cc	156	1179	738	201	234	6	0	0
2	cd	156	1179	738	201	234	6	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	ce	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		
2	cl	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		
2	cm	156	Total	C	N	O	S	0	0
			1179	738	201	234	6		

- Molecule 3 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	cn	374	Total	C	N	O	S	0	0
			2964	1868	507	580	9		
3	co	383	Total	C	N	O	S	0	0
			3037	1917	517	593	10		
3	cp	371	Total	C	N	O	S	0	0
			2941	1853	504	575	9		
3	cq	374	Total	C	N	O	S	0	0
			2964	1868	507	580	9		
3	cy	383	Total	C	N	O	S	0	0
			3037	1917	517	593	10		
3	dj	373	Total	C	N	O	S	0	0
			2959	1865	506	579	9		
3	du	383	Total	C	N	O	S	0	0
			3037	1917	517	593	10		
3	dy	373	Total	C	N	O	S	0	0
			2959	1865	506	579	9		
3	dz	374	Total	C	N	O	S	0	0
			2964	1868	507	580	9		
3	ea	383	Total	C	N	O	S	0	0
			3037	1917	517	593	10		
3	eb	374	Total	C	N	O	S	0	0
			2964	1868	507	580	9		
3	ec	382	Total	C	N	O	S	0	0
			3031	1914	516	591	10		

- Molecule 4 is a protein called Terminator protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	cr	132	Total	C	N	O	S	0	0
			1070	694	182	188	6		
4	cs	132	Total	C	N	O	S	0	0
			1070	694	182	188	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	ct	132	Total	C	N	O	S	0	0
			1070	694	182	188	6		
4	cu	132	Total	C	N	O	S	0	0
			1070	694	182	188	6		
4	cv	132	Total	C	N	O	S	0	0
			1070	694	182	188	6		
4	cw	132	Total	C	N	O	S	0	0
			1070	694	182	188	6		

- Molecule 5 is a protein called Adaptor protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	cx	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	cz	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	da	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	db	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	dc	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	dd	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	de	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	df	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	dg	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	dh	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	di	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		
5	dk	133	Total	C	N	O	S	0	0
			1063	679	182	194	8		

- Molecule 6 is a protein called Tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	dl	219	Total	C	N	O	S	0	0
			1682	1062	270	341	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	dm	219	Total	C	N	O	S	0	0
			1682	1062	270	341	9		
6	dn	219	Total	C	N	O	S	0	0
			1682	1062	270	341	9		
6	do	219	Total	C	N	O	S	0	0
			1682	1062	270	341	9		
6	dp	219	Total	C	N	O	S	0	0
			1682	1062	270	341	9		
6	dq	219	Total	C	N	O	S	0	0
			1682	1062	270	341	9		

- Molecule 7 is a protein called Connector protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	dr	121	Total	C	N	O	S	0	0
			963	601	174	184	4		
7	ds	121	Total	C	N	O	S	0	0
			963	601	174	184	4		
7	dt	121	Total	C	N	O	S	0	0
			963	601	174	184	4		
7	dv	121	Total	C	N	O	S	0	0
			963	601	174	184	4		
7	dw	121	Total	C	N	O	S	0	0
			963	601	174	184	4		
7	dx	121	Total	C	N	O	S	0	0
			963	601	174	184	4		

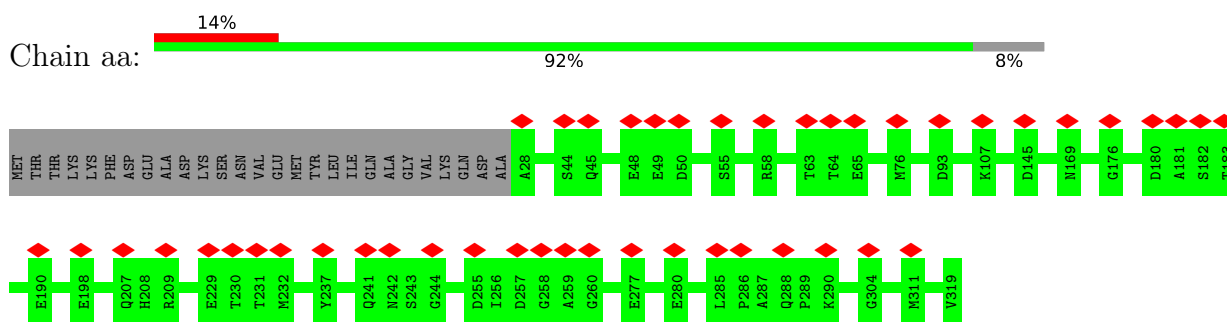
- Molecule 8 is a protein called Decoration protein gp29.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	ak	150	Total	C	N	O	S	0	0
			1095	698	183	211	3		
8	bk	150	Total	C	N	O	S	0	0
			1095	698	183	211	3		
8	bx	150	Total	C	N	O	S	0	0
			1095	698	183	211	3		
8	ck	150	Total	C	N	O	S	0	0
			1095	698	183	211	3		
8	ax	150	Total	C	N	O	S	0	0
			1095	698	183	211	3		

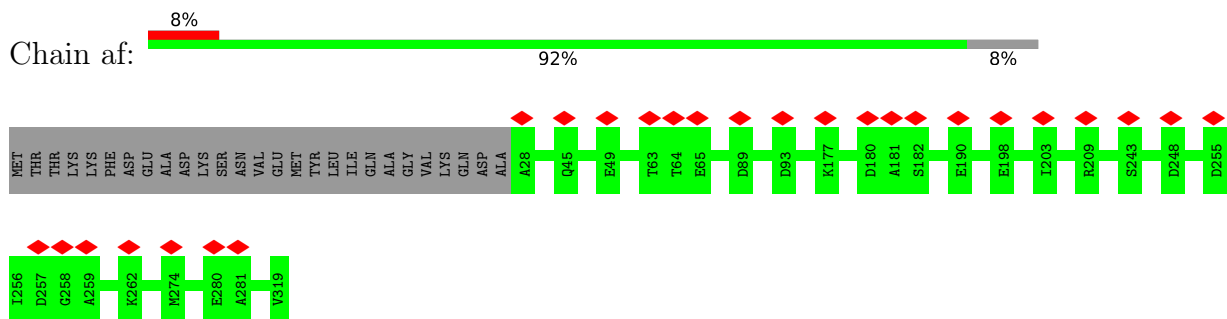
3 Residue-property plots [i](#)

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.

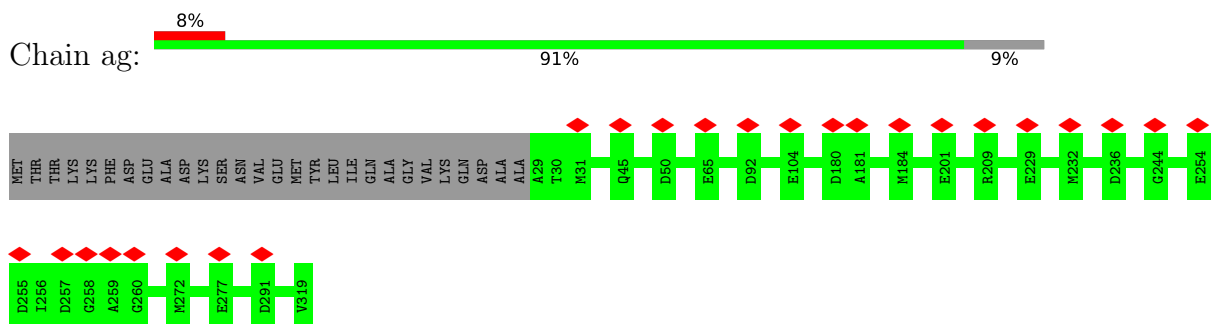
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

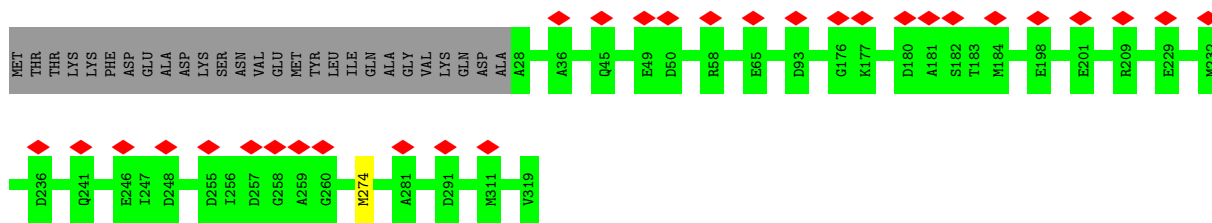


- Molecule 1: Major capsid protein

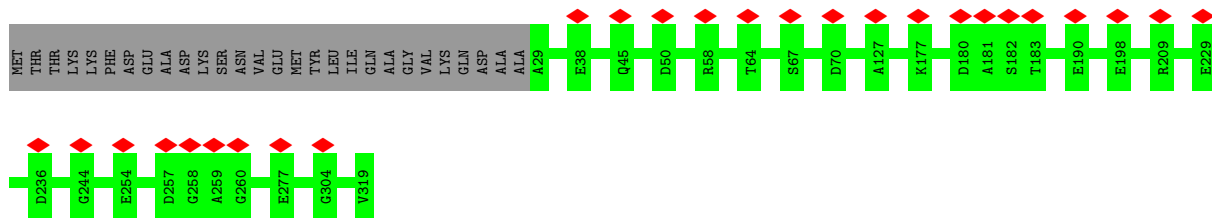


- Molecule 1: Major capsid protein

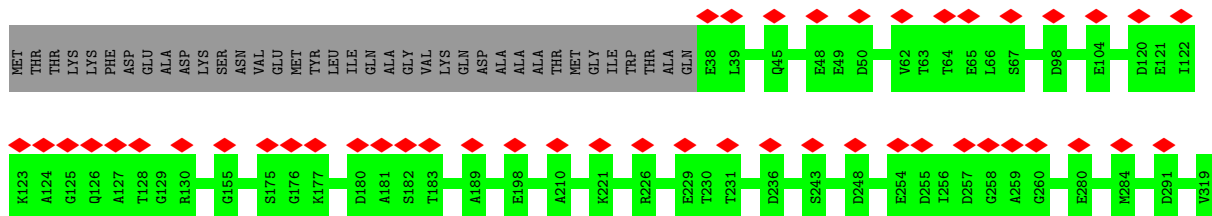
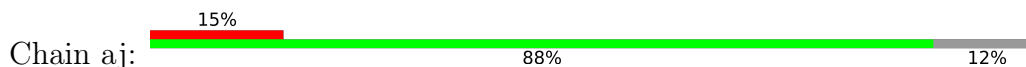




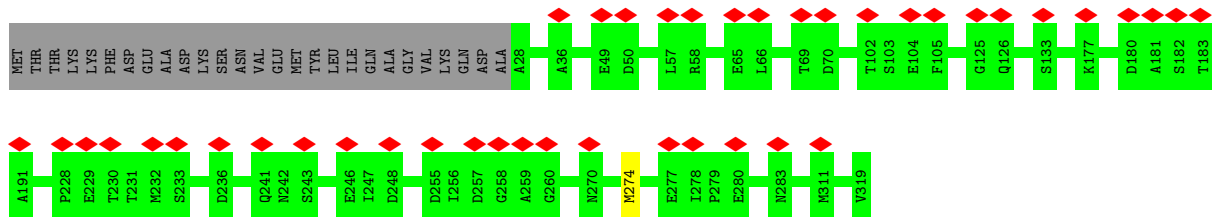
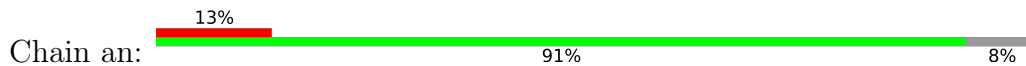
• Molecule 1: Major capsid protein



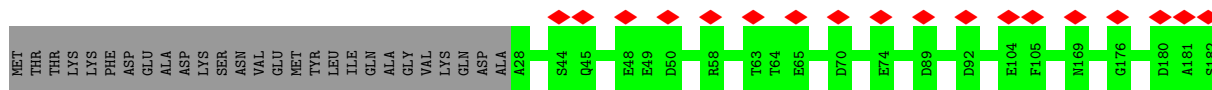
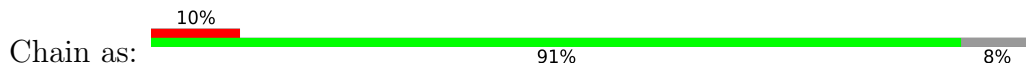
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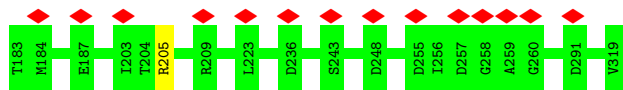


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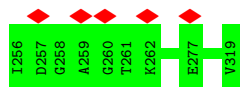
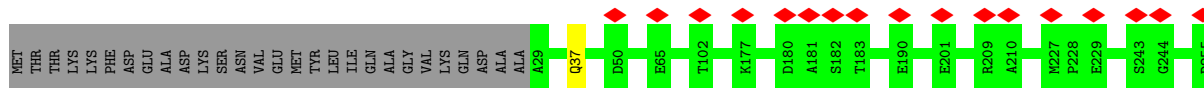
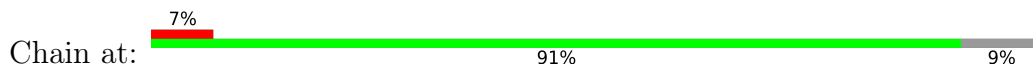


• Molecule 1: Major capsid protein

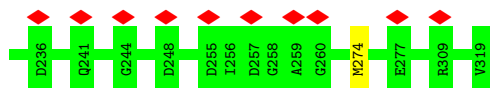
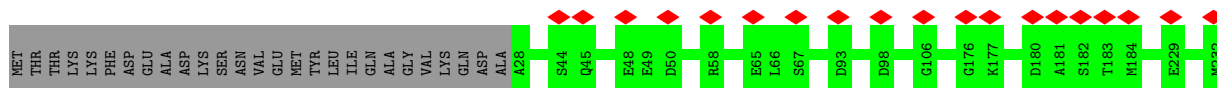
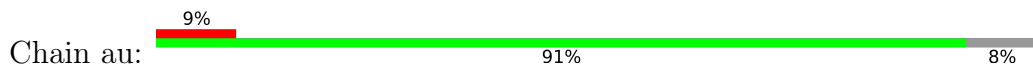




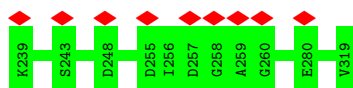
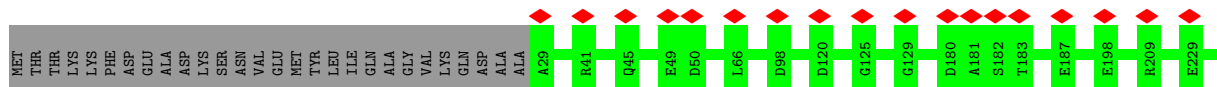
• Molecule 1: Major capsid protein



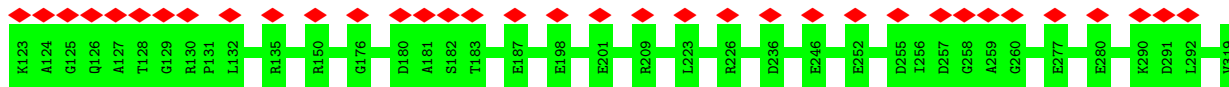
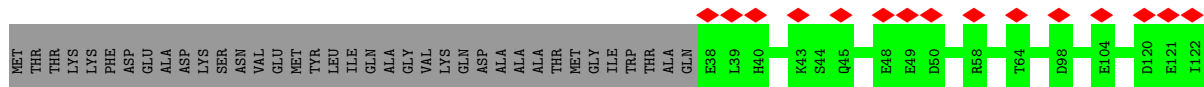
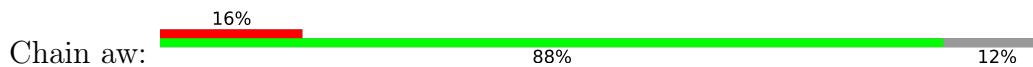
• Molecule 1: Major capsid protein



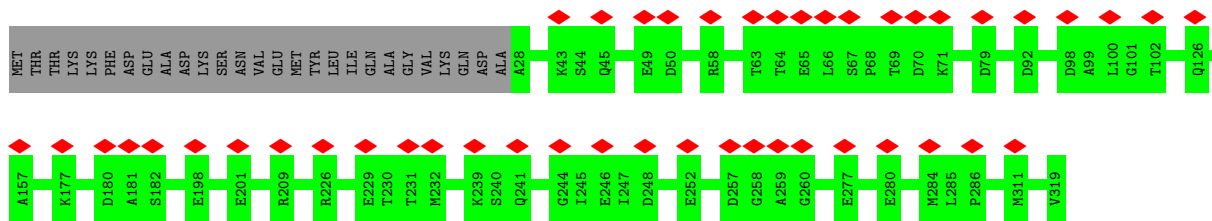
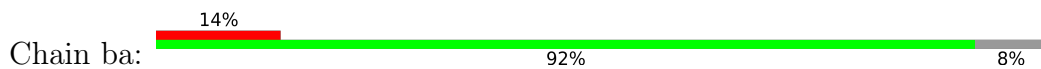
• Molecule 1: Major capsid protein



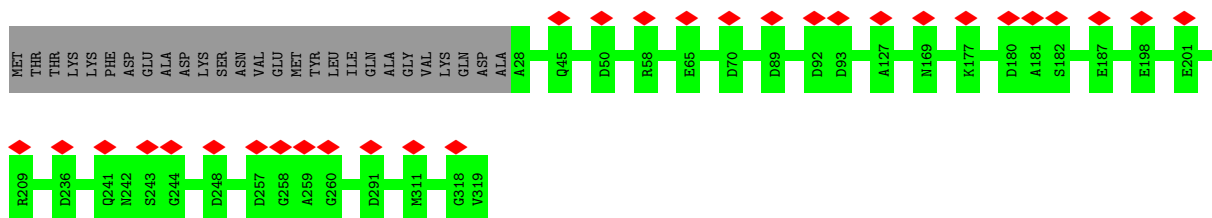
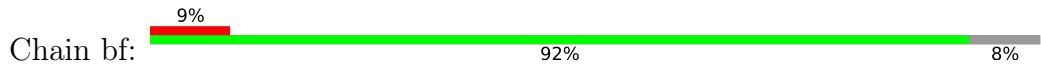
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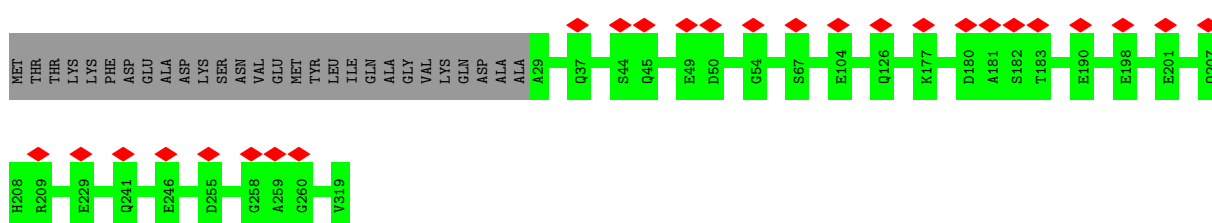
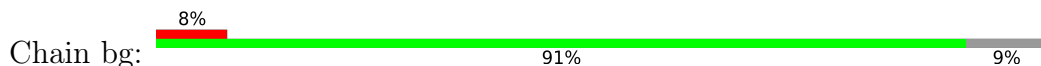
• Molecule 1: Major capsid protein



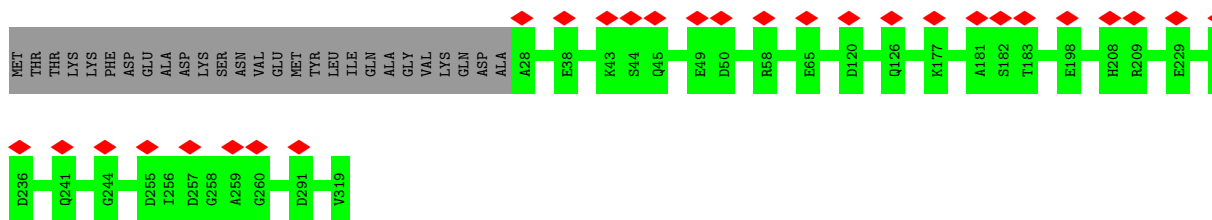
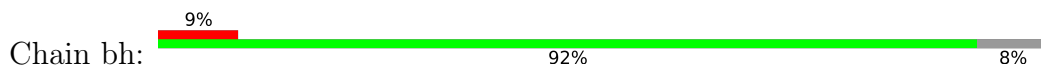
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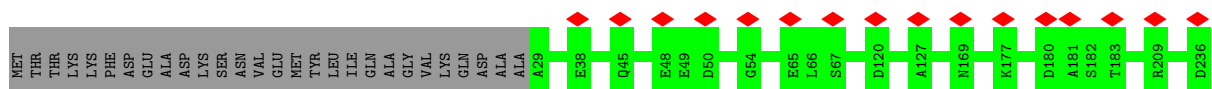
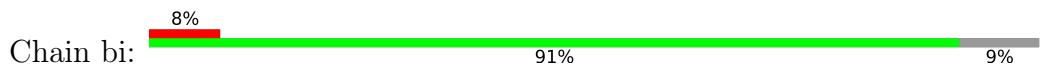
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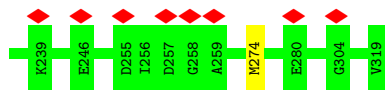


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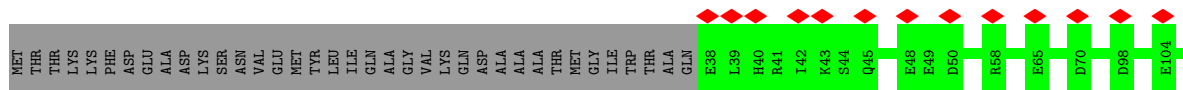
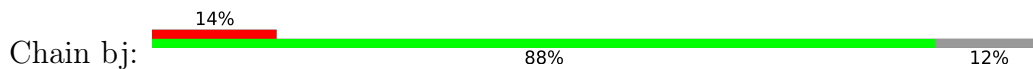


• Molecule 1: Major capsid protein

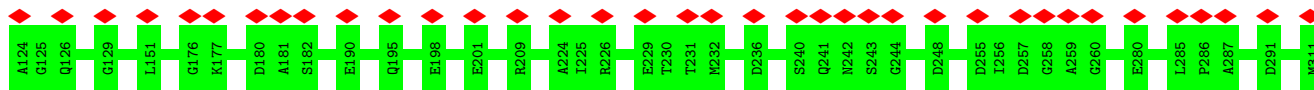




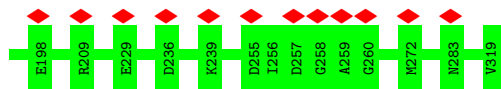
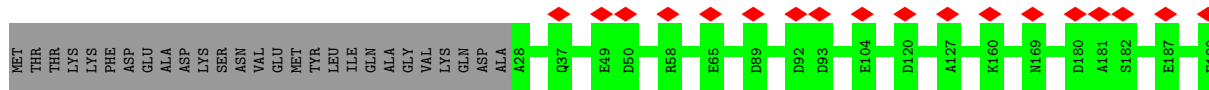
• Molecule 1: Major capsid protein



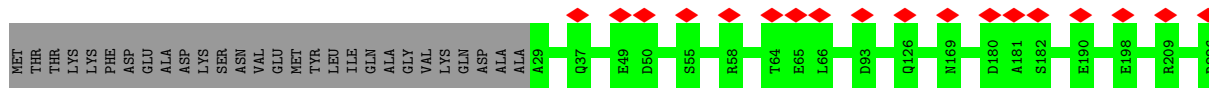
• Molecule 1: Major capsid protein

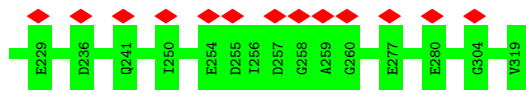


• Molecule 1: Major capsid protein

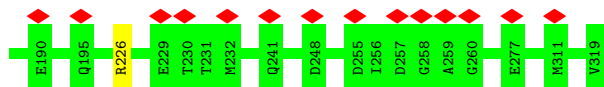
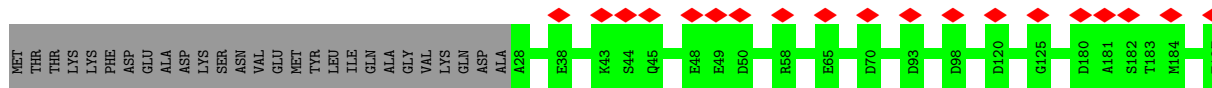


• Molecule 1: Major capsid protein

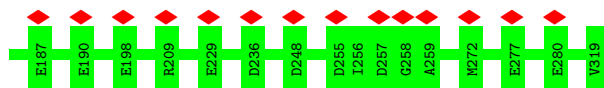
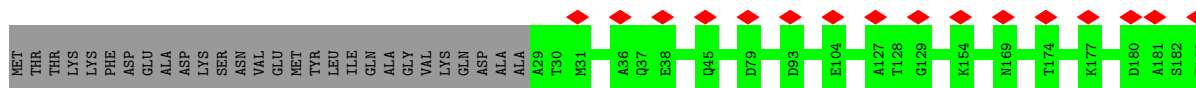
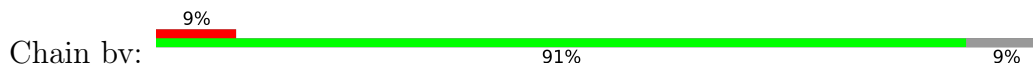




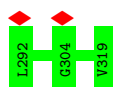
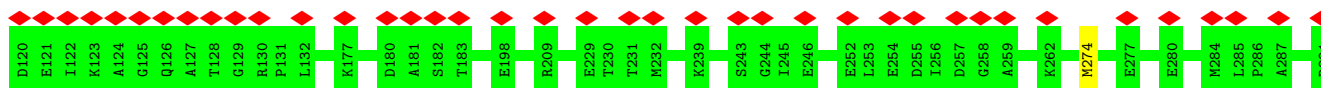
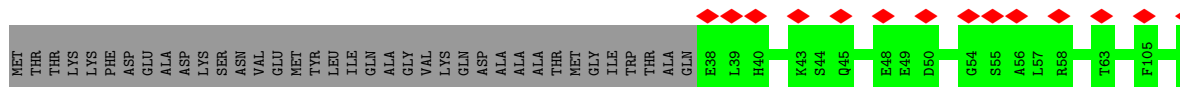
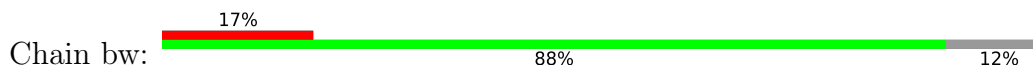
• Molecule 1: Major capsid protein



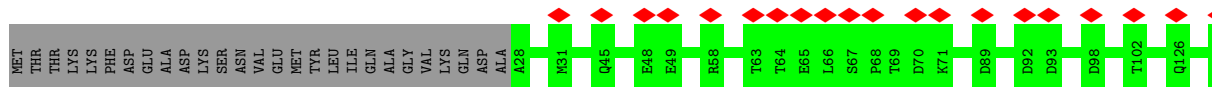
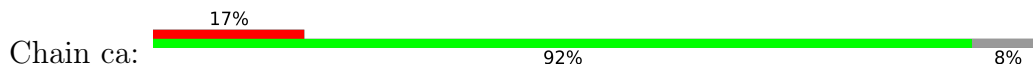
• Molecule 1: Major capsid protein

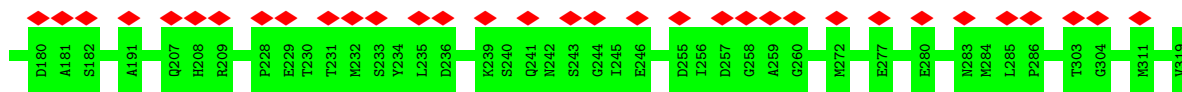


• Molecule 1: Major capsid protein

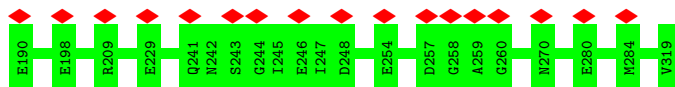
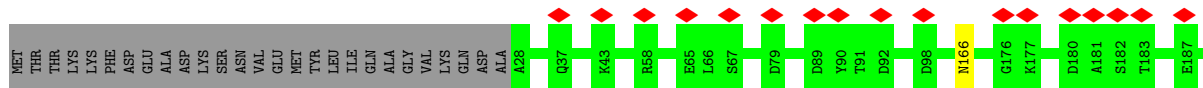
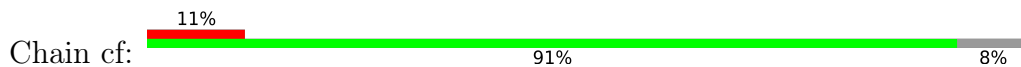


• Molecule 1: Major capsid protein

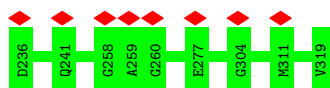
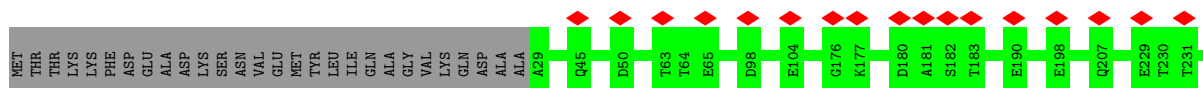




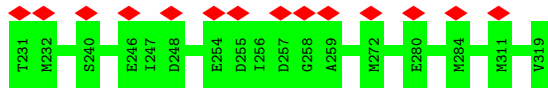
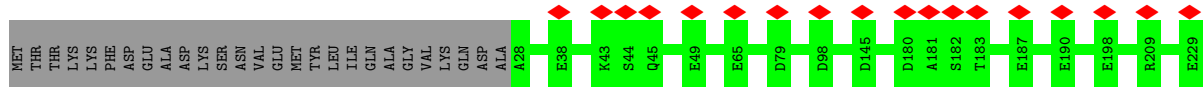
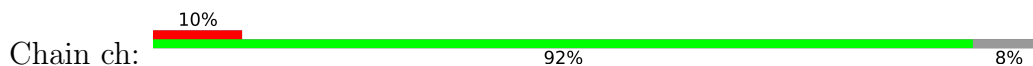
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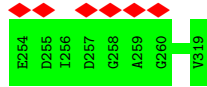
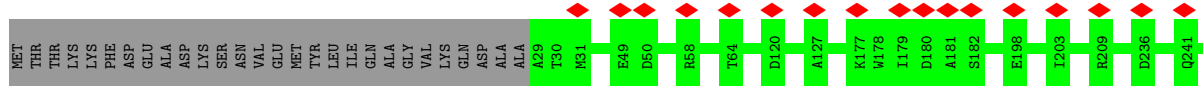
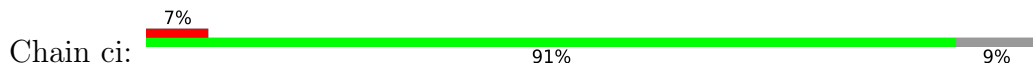
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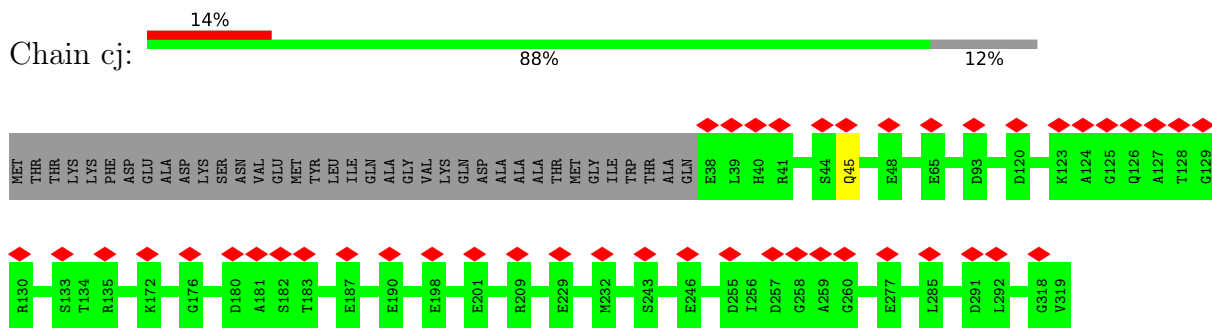
• Molecule 1: Major capsid protein



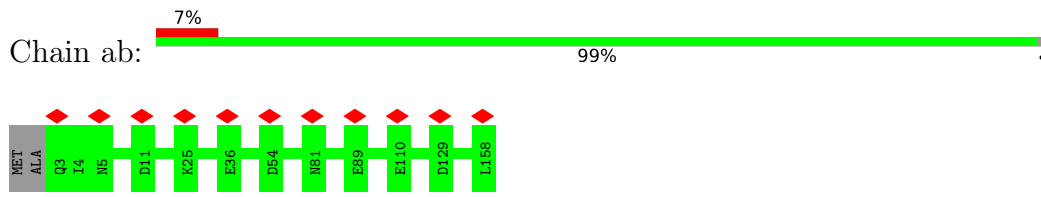
• Molecule 1: Major capsid protein



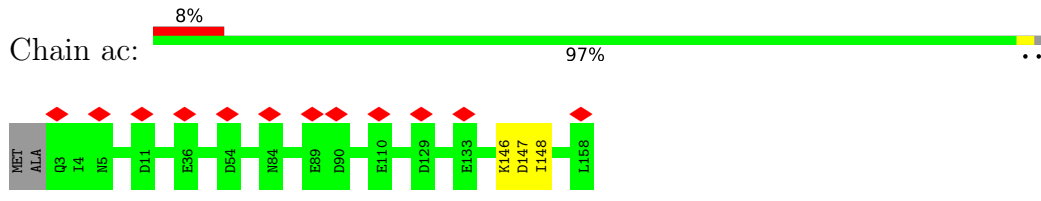
• Molecule 1: Major capsid protein



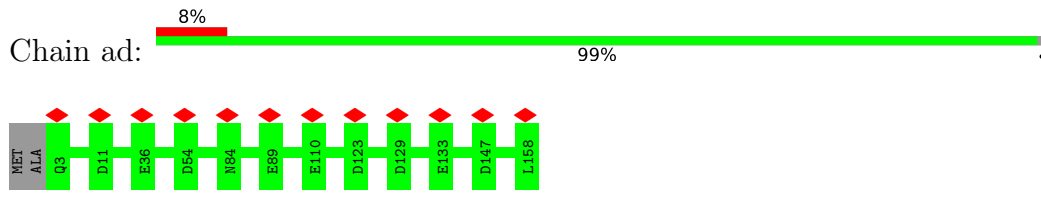
• Molecule 2: Decoration protein



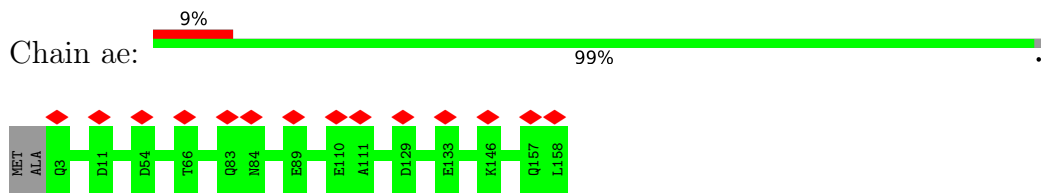
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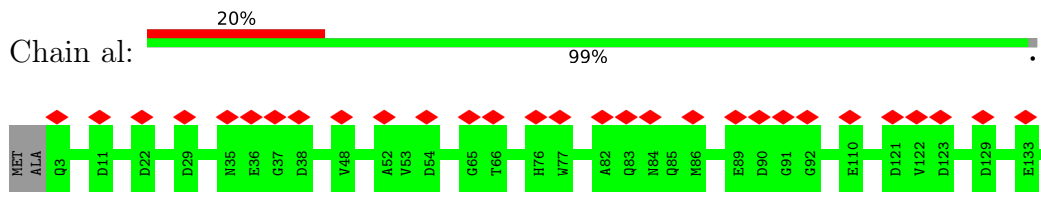
• Molecule 2: Decoration protein



• Molecule 2: Decoration protein

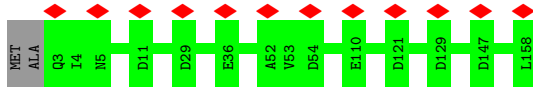


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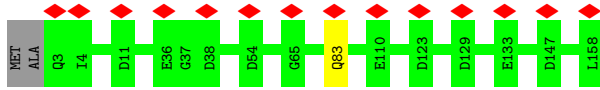


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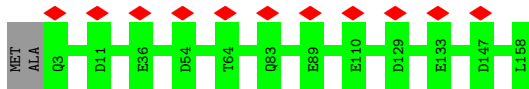




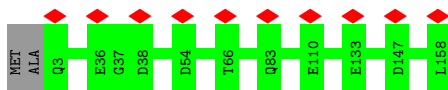
• Molecule 2: Decoration protein



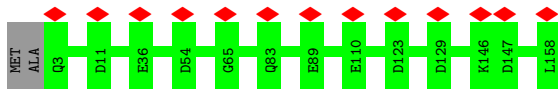
• Molecule 2: Decoration protein



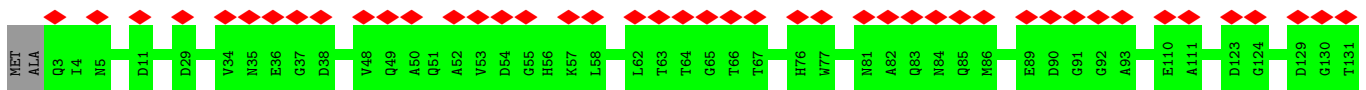
• Molecule 2: Decoration protein



• Molecule 2: Decoration protein

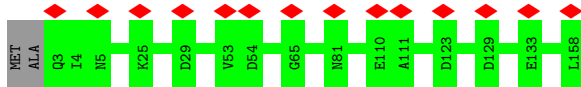


• Molecule 2: Decoration protein

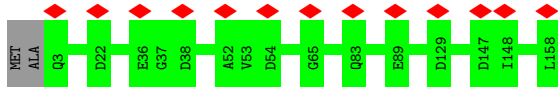


• Molecule 2: Decoration protein

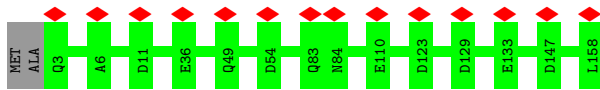




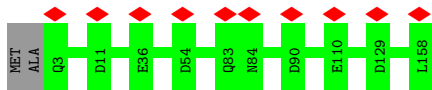
- Molecule 2: Decoration protein



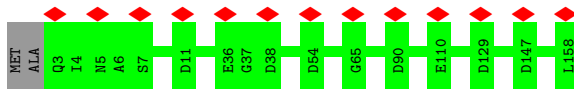
- Molecule 2: Decoration protein



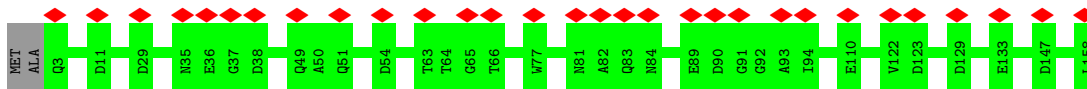
- Molecule 2: Decoration protein



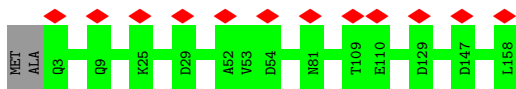
- Molecule 2: Decoration protein



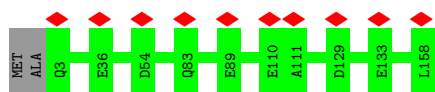
- Molecule 2: Decoration protein



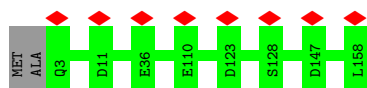
- Molecule 2: Decoration protein



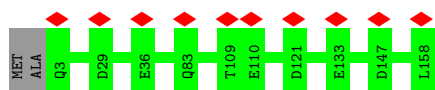
- Molecule 2: Decoration protein



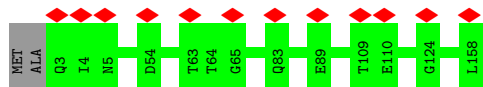
• Molecule 2: Decoration protein



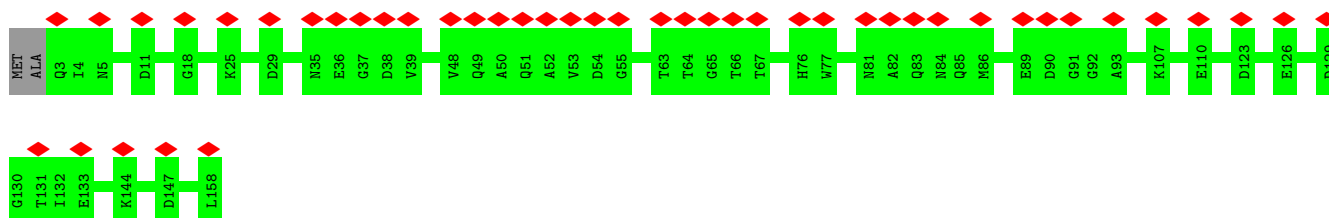
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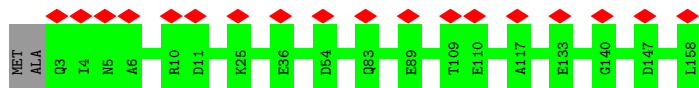
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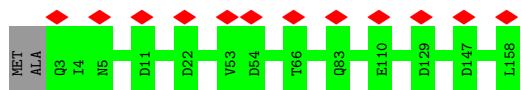
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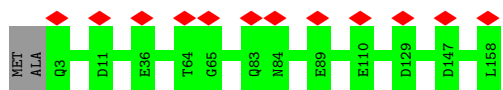
• Molecule 2: Decoration protein



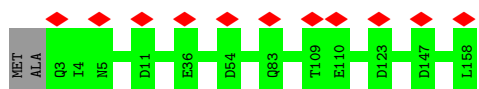
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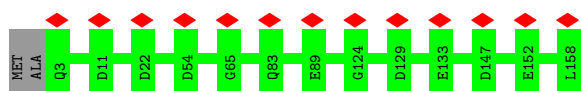
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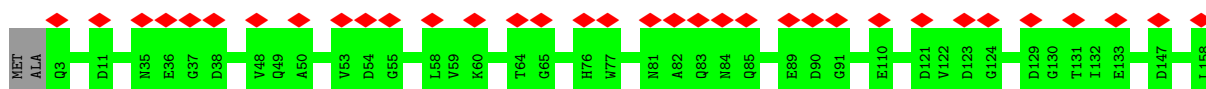
• Molecule 2: Decoration protein



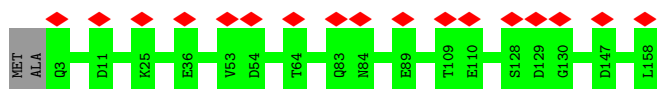
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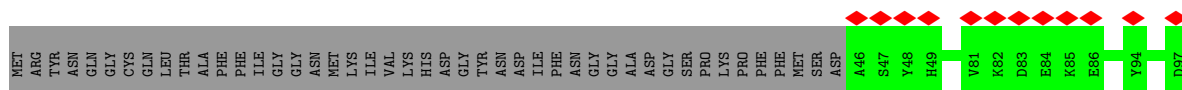
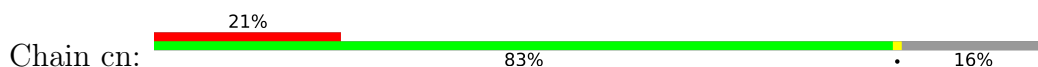
• Molecule 2: Decoration protein

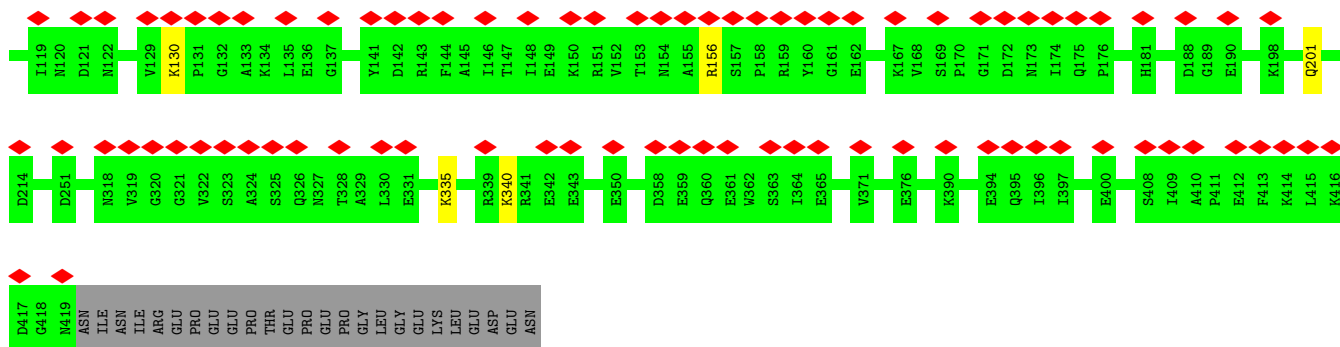


• Molecule 2: Decoration protein

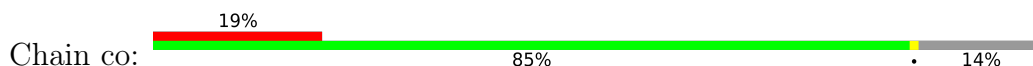


• Molecule 3: Portal protein

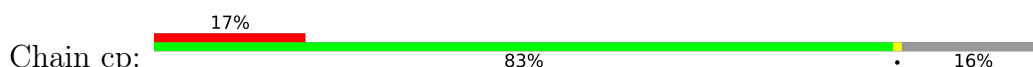




• Molecule 3: Portal protein

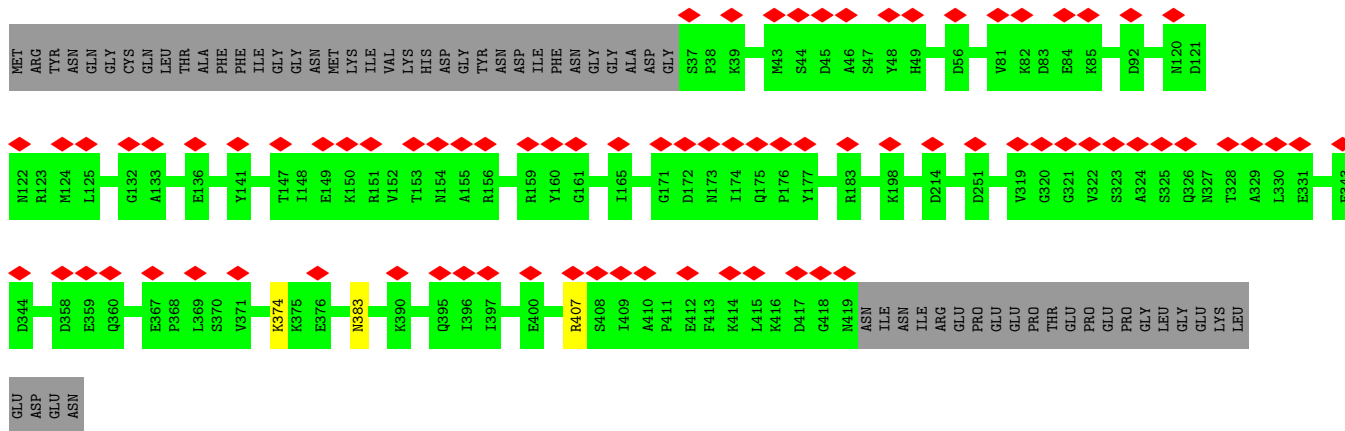
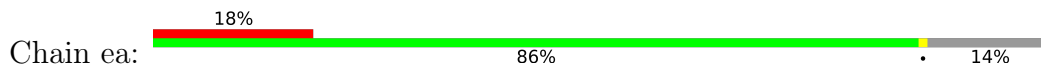


• Molecule 3: Portal protein

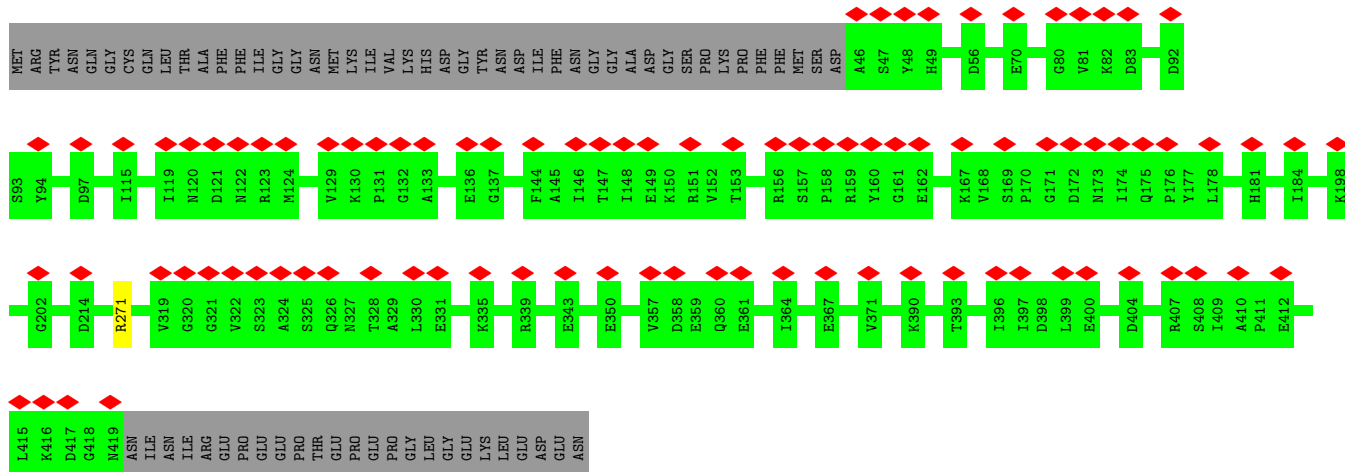
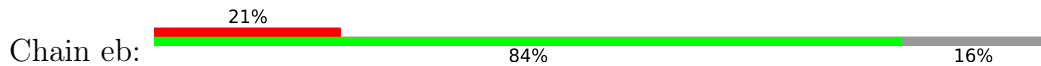


GLU
PRO
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PRO
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LEU
GLY
GLU
LYS
LEU
GLU
GLU
ASP
GLU
ASN

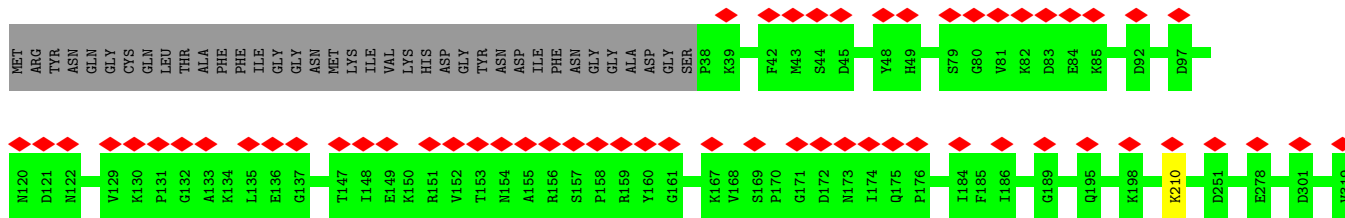
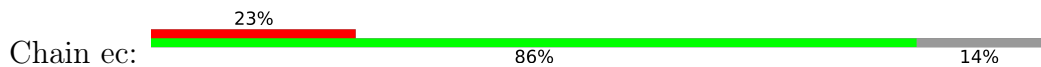
• Molecule 3: Portal protein

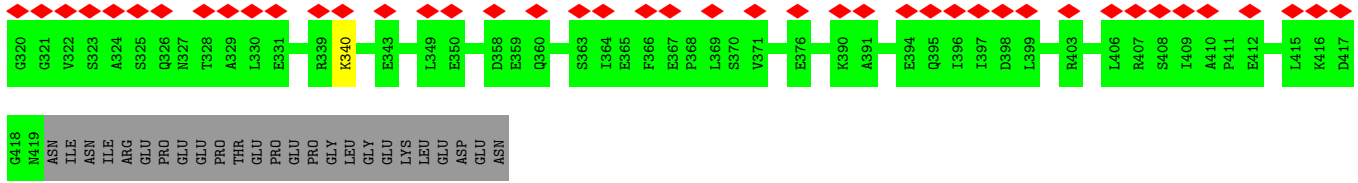


• Molecule 3: Portal protein



• Molecule 3: Portal protein

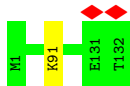




• Molecule 4: Terminator protein



• Molecule 4: Terminator protein



• Molecule 4: Terminator protein



• Molecule 4: Terminator protein



• Molecule 4: Terminator protein

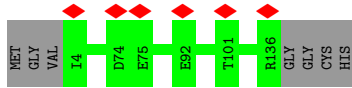


• Molecule 4: Terminator protein

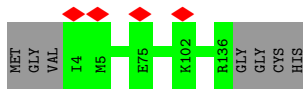




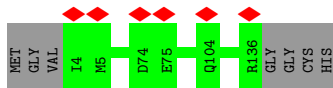
- Molecule 5: Adaptor protein



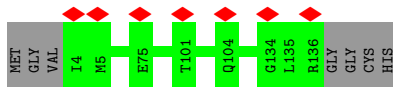
- Molecule 5: Adaptor protein



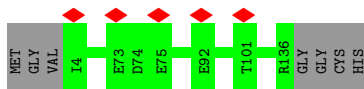
- Molecule 5: Adaptor protein



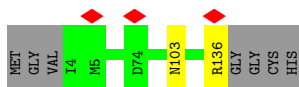
- Molecule 5: Adaptor protein



- Molecule 5: Adaptor protein

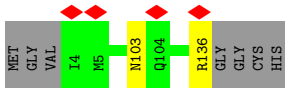


- Molecule 5: Adaptor protein



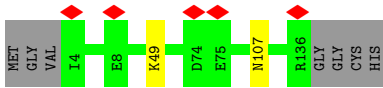
- Molecule 5: Adaptor protein

Chain de:  94% 5%



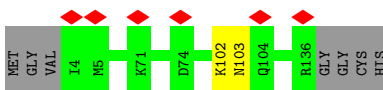
• Molecule 5: Adaptor protein

Chain df:  94% 5%



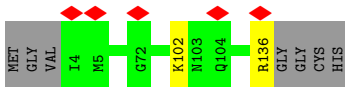
• Molecule 5: Adaptor protein

Chain dg:  94% 5%



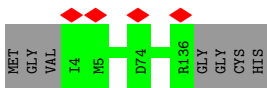
• Molecule 5: Adaptor protein

Chain dh:  94% 5%



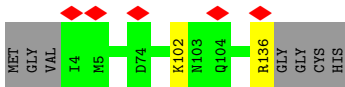
• Molecule 5: Adaptor protein

Chain di:  95% 5%



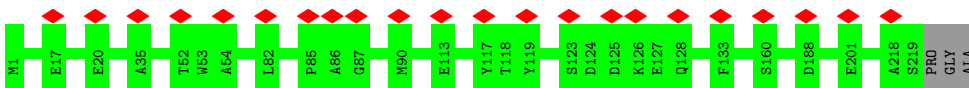
• Molecule 5: Adaptor protein

Chain dk:  94% 5%

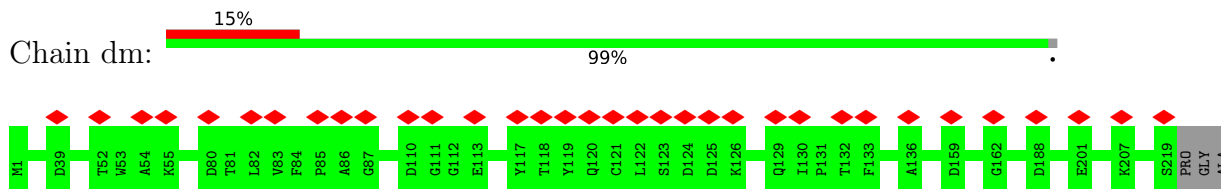


• Molecule 6: Tail tube protein

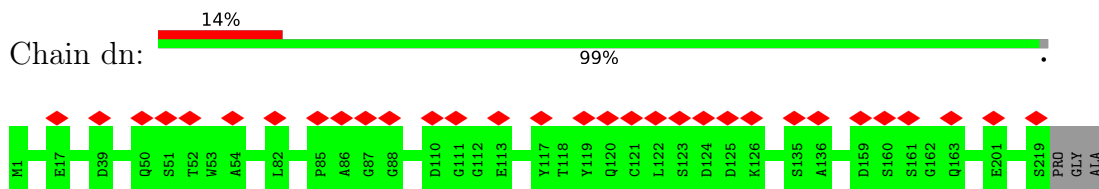
Chain dl:  10% 99%



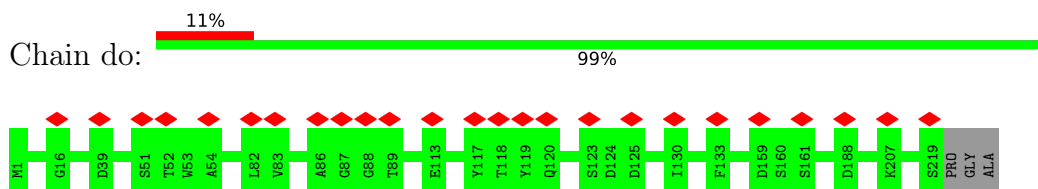
• Molecule 6: Tail tube protein



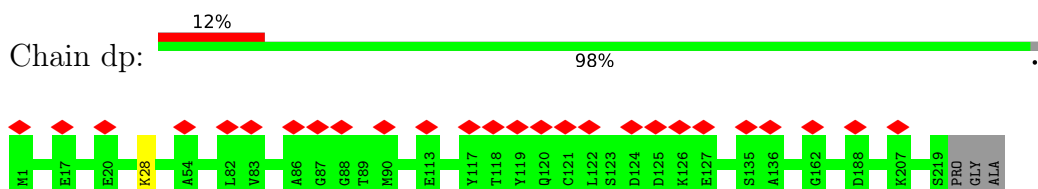
• Molecule 6: Tail tube protein



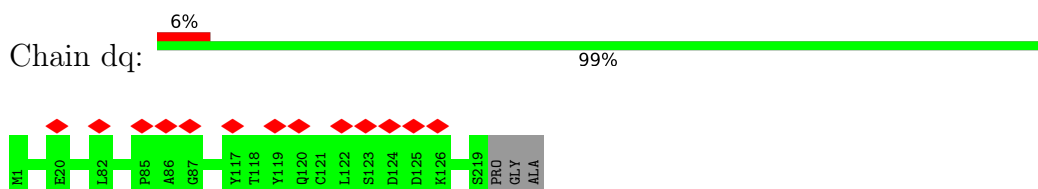
• Molecule 6: Tail tube protein



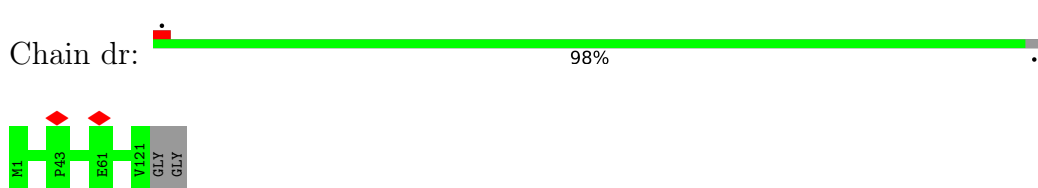
• Molecule 6: Tail tube protein



• Molecule 6: Tail tube protein

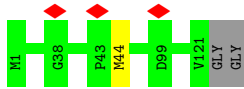


• Molecule 7: Connector protein

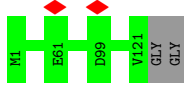


• Molecule 7: Connector protein

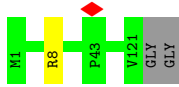




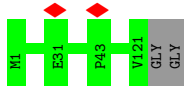
• Molecule 7: Connector protein



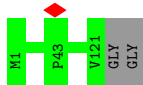
• Molecule 7: Connector protein



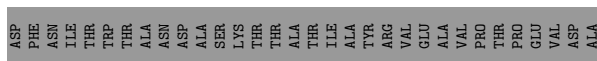
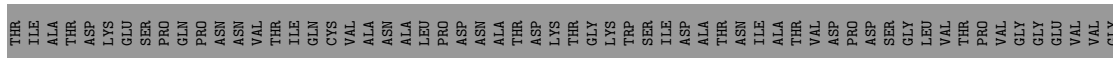
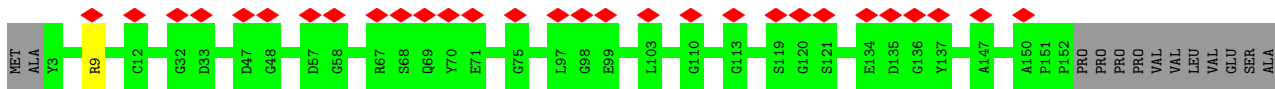
• Molecule 7: Connector protein



• Molecule 7: Connector protein



• Molecule 8: Decoration protein gp29



• Molecule 8: Decoration protein gp29



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	74400	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	17.657	Depositor
Minimum map value	-10.394	Depositor
Average map value	0.007	Depositor
Map value standard deviation	1.076	Depositor
Recommended contour level	3.36	Depositor
Map size (Å)	515.51996, 515.51996, 515.51996	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6109998, 1.6109998, 1.6109998	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	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	aa	0.25	0/2305	0.51	0/3130
1	af	0.25	0/2305	0.50	0/3130
1	ag	0.26	0/2300	0.51	0/3123
1	ah	0.25	0/2305	0.50	0/3130
1	ai	0.26	0/2300	0.52	0/3123
1	aj	0.25	0/2231	0.50	0/3028
1	an	0.25	0/2305	0.51	0/3130
1	as	0.26	0/2305	0.51	0/3130
1	at	0.26	0/2300	0.50	0/3123
1	au	0.25	0/2305	0.51	0/3130
1	av	0.25	0/2300	0.51	0/3123
1	aw	0.25	0/2231	0.51	0/3028
1	ba	0.25	0/2305	0.51	0/3130
1	bf	0.25	0/2305	0.50	0/3130
1	bg	0.25	0/2300	0.50	0/3123
1	bh	0.26	0/2305	0.51	0/3130
1	bi	0.25	0/2300	0.50	0/3123
1	bj	0.26	0/2231	0.51	0/3028
1	bn	0.25	0/2305	0.51	0/3130
1	bs	0.25	0/2305	0.52	0/3130
1	bt	0.25	0/2300	0.50	0/3123
1	bu	0.25	0/2305	0.49	0/3130
1	bv	0.25	0/2300	0.50	0/3123
1	bw	0.25	0/2231	0.50	0/3028
1	ca	0.25	0/2305	0.51	0/3130
1	cf	0.25	0/2305	0.50	0/3130
1	cg	0.25	0/2300	0.49	0/3123
1	ch	0.25	0/2305	0.50	0/3130
1	ci	0.25	0/2300	0.50	0/3123
1	cj	0.25	0/2231	0.51	0/3028
2	ab	0.26	0/1199	0.50	0/1632
2	ac	0.28	0/1199	0.52	0/1632
2	ad	0.25	0/1199	0.49	0/1632
2	ae	0.25	0/1199	0.49	0/1632

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	al	0.25	0/1199	0.49	0/1632
2	am	0.24	0/1199	0.50	0/1632
2	ao	0.25	0/1199	0.49	0/1632
2	ap	0.25	0/1199	0.51	0/1632
2	aq	0.25	0/1199	0.49	0/1632
2	ar	0.25	0/1199	0.48	0/1632
2	ay	0.24	0/1199	0.48	0/1632
2	az	0.25	0/1199	0.49	0/1632
2	bb	0.26	0/1199	0.50	0/1632
2	bc	0.25	0/1199	0.51	0/1632
2	bd	0.25	0/1199	0.49	0/1632
2	be	0.25	0/1199	0.49	0/1632
2	bl	0.24	0/1199	0.49	0/1632
2	bm	0.25	0/1199	0.53	0/1632
2	bo	0.26	0/1199	0.50	0/1632
2	bp	0.25	0/1199	0.49	0/1632
2	bq	0.25	0/1199	0.48	0/1632
2	br	0.25	0/1199	0.49	0/1632
2	by	0.24	0/1199	0.48	0/1632
2	bz	0.24	0/1199	0.49	0/1632
2	cb	0.25	0/1199	0.51	0/1632
2	cc	0.26	0/1199	0.50	0/1632
2	cd	0.25	0/1199	0.49	0/1632
2	ce	0.26	0/1199	0.49	0/1632
2	cl	0.24	0/1199	0.49	0/1632
2	cm	0.25	0/1199	0.49	0/1632
3	cn	0.28	0/3017	0.56	0/4082
3	co	0.28	0/3094	0.57	0/4186
3	cp	0.28	0/2993	0.56	0/4049
3	cq	0.28	0/3017	0.56	0/4082
3	cy	0.28	0/3094	0.56	0/4186
3	dj	0.27	0/3012	0.55	0/4075
3	du	0.27	0/3094	0.57	0/4186
3	dy	0.27	0/3012	0.56	0/4075
3	dz	0.28	0/3017	0.55	0/4082
3	ea	0.29	0/3094	0.60	0/4186
3	eb	0.27	0/3017	0.55	0/4082
3	ec	0.27	0/3088	0.55	0/4177
4	cr	0.29	0/1099	0.53	0/1482
4	cs	0.29	0/1099	0.53	0/1482
4	ct	0.28	0/1099	0.51	0/1482
4	cu	0.29	0/1099	0.53	0/1482
4	cv	0.29	0/1099	0.52	0/1482

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	cw	0.28	0/1099	0.51	0/1482
5	cx	0.27	0/1082	0.53	0/1453
5	cz	0.28	0/1082	0.57	0/1453
5	da	0.27	0/1082	0.57	0/1453
5	db	0.30	0/1082	0.54	0/1453
5	dc	0.28	0/1082	0.56	0/1453
5	dd	0.29	0/1082	0.59	0/1453
5	de	0.28	0/1082	0.57	0/1453
5	df	0.29	0/1082	0.56	0/1453
5	dg	0.27	0/1082	0.54	0/1453
5	dh	0.28	0/1082	0.60	0/1453
5	di	0.28	0/1082	0.56	0/1453
5	dk	0.28	0/1082	0.55	0/1453
6	dl	0.26	0/1713	0.49	0/2329
6	dm	0.26	0/1713	0.51	0/2329
6	dn	0.26	0/1713	0.49	0/2329
6	do	0.26	0/1713	0.51	0/2329
6	dp	0.26	0/1713	0.53	0/2329
6	dq	0.26	0/1713	0.49	0/2329
7	dr	0.27	0/982	0.59	0/1330
7	ds	0.27	0/982	0.60	0/1330
7	dt	0.28	0/982	0.61	0/1330
7	dv	0.26	0/982	0.60	0/1330
7	dw	0.27	0/982	0.58	0/1330
7	dx	0.27	0/982	0.60	0/1330
8	ak	0.42	0/1121	0.57	1/1525 (0.1%)
8	ax	0.42	0/1121	0.58	1/1525 (0.1%)
8	bk	0.43	0/1121	0.57	1/1525 (0.1%)
8	bx	0.42	0/1121	0.57	1/1525 (0.1%)
8	ck	0.43	0/1121	0.58	1/1525 (0.1%)
All	All	0.27	0/182602	0.53	5/247635 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	ax	9	ARG	N-CA-C	6.84	129.47	111.00
8	ck	9	ARG	N-CA-C	6.77	129.27	111.00
8	ak	9	ARG	N-CA-C	6.20	127.74	111.00
8	bx	9	ARG	N-CA-C	6.15	127.61	111.00
8	bk	9	ARG	N-CA-C	6.10	127.46	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	aa	2260	0	2282	0	0
1	af	2260	0	2282	0	0
1	ag	2255	0	2277	0	0
1	ah	2260	0	2282	0	0
1	ai	2255	0	2277	0	0
1	aj	2188	0	2212	0	0
1	an	2260	0	2282	0	0
1	as	2260	0	2282	0	0
1	at	2255	0	2277	0	0
1	au	2260	0	2282	0	0
1	av	2255	0	2277	0	0
1	aw	2188	0	2212	0	0
1	ba	2260	0	2282	0	0
1	bf	2260	0	2282	0	0
1	bg	2255	0	2277	0	0
1	bh	2260	0	2282	0	0
1	bi	2255	0	2277	0	0
1	bj	2188	0	2212	0	0
1	bn	2260	0	2282	0	0
1	bs	2260	0	2282	0	0
1	bt	2255	0	2277	0	0
1	bu	2260	0	2282	0	0
1	bv	2255	0	2277	0	0
1	bw	2188	0	2212	0	0
1	ca	2260	0	2282	0	0
1	cf	2260	0	2282	0	0
1	cg	2255	0	2277	0	0
1	ch	2260	0	2282	0	0
1	ci	2255	0	2277	0	0
1	cj	2188	0	2212	0	0
2	ab	1179	0	1157	0	0
2	ac	1179	0	1157	0	0
2	ad	1179	0	1157	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	ae	1179	0	1157	0	0
2	al	1179	0	1157	0	0
2	am	1179	0	1157	0	0
2	ao	1179	0	1157	0	0
2	ap	1179	0	1157	0	0
2	aq	1179	0	1157	0	0
2	ar	1179	0	1157	0	0
2	ay	1179	0	1157	0	0
2	az	1179	0	1157	0	0
2	bb	1179	0	1157	0	0
2	bc	1179	0	1157	0	0
2	bd	1179	0	1157	0	0
2	be	1179	0	1157	0	0
2	bl	1179	0	1157	0	0
2	bm	1179	0	1157	0	0
2	bo	1179	0	1157	0	0
2	bp	1179	0	1157	0	0
2	bq	1179	0	1157	0	0
2	br	1179	0	1157	0	0
2	by	1179	0	1157	0	0
2	bz	1179	0	1157	0	0
2	cb	1179	0	1157	0	0
2	cc	1179	0	1157	0	0
2	cd	1179	0	1157	0	0
2	ce	1179	0	1157	0	0
2	cl	1179	0	1157	0	0
2	cm	1179	0	1157	0	0
3	cn	2964	0	2945	0	0
3	co	3037	0	3012	0	0
3	cp	2941	0	2925	0	0
3	cq	2964	0	2944	0	0
3	cy	3037	0	3013	0	0
3	dj	2959	0	2939	0	0
3	du	3037	0	3012	0	0
3	dy	2959	0	2939	0	0
3	dz	2964	0	2944	0	0
3	ea	3037	0	3013	0	0
3	eb	2964	0	2944	0	0
3	ec	3031	0	3008	0	0
4	cr	1070	0	1061	0	0
4	cs	1070	0	1061	0	0
4	ct	1070	0	1061	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	cu	1070	0	1061	0	0
4	cv	1070	0	1061	0	0
4	cw	1070	0	1061	0	0
5	cx	1063	0	1074	0	0
5	cz	1063	0	1074	0	0
5	da	1063	0	1074	0	0
5	db	1063	0	1074	0	0
5	dc	1063	0	1074	0	0
5	dd	1063	0	1075	0	0
5	de	1063	0	1074	0	0
5	df	1063	0	1074	0	0
5	dg	1063	0	1075	0	0
5	dh	1063	0	1074	0	0
5	di	1063	0	1074	0	0
5	dk	1063	0	1075	0	0
6	dl	1682	0	1651	0	0
6	dm	1682	0	1651	0	0
6	dn	1682	0	1651	0	0
6	do	1682	0	1651	0	0
6	dp	1682	0	1651	0	0
6	dq	1682	0	1651	0	0
7	dr	963	0	945	0	0
7	ds	963	0	945	0	0
7	dt	963	0	945	0	0
7	dv	963	0	945	0	0
7	dw	963	0	945	0	0
7	dx	963	0	945	0	0
8	ak	1095	0	1059	0	0
8	ax	1095	0	1059	0	0
8	bk	1095	0	1059	0	0
8	bx	1095	0	1059	0	0
8	ck	1095	0	1059	0	0
All	All	179175	0	178536	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	aa	290/319 (91%)	282 (97%)	8 (3%)	0	100	100
1	af	290/319 (91%)	283 (98%)	7 (2%)	0	100	100
1	ag	289/319 (91%)	280 (97%)	9 (3%)	0	100	100
1	ah	290/319 (91%)	284 (98%)	6 (2%)	0	100	100
1	ai	289/319 (91%)	282 (98%)	7 (2%)	0	100	100
1	aj	280/319 (88%)	271 (97%)	9 (3%)	0	100	100
1	an	290/319 (91%)	283 (98%)	7 (2%)	0	100	100
1	as	290/319 (91%)	280 (97%)	10 (3%)	0	100	100
1	at	289/319 (91%)	278 (96%)	11 (4%)	0	100	100
1	au	290/319 (91%)	284 (98%)	6 (2%)	0	100	100
1	av	289/319 (91%)	283 (98%)	6 (2%)	0	100	100
1	aw	280/319 (88%)	272 (97%)	8 (3%)	0	100	100
1	ba	290/319 (91%)	283 (98%)	7 (2%)	0	100	100
1	bf	290/319 (91%)	283 (98%)	7 (2%)	0	100	100
1	bg	289/319 (91%)	277 (96%)	12 (4%)	0	100	100
1	bh	290/319 (91%)	282 (97%)	8 (3%)	0	100	100
1	bi	289/319 (91%)	282 (98%)	7 (2%)	0	100	100
1	bj	280/319 (88%)	274 (98%)	6 (2%)	0	100	100
1	bn	290/319 (91%)	285 (98%)	5 (2%)	0	100	100
1	bs	290/319 (91%)	283 (98%)	7 (2%)	0	100	100
1	bt	289/319 (91%)	280 (97%)	9 (3%)	0	100	100
1	bu	290/319 (91%)	284 (98%)	6 (2%)	0	100	100
1	bv	289/319 (91%)	283 (98%)	6 (2%)	0	100	100
1	bw	280/319 (88%)	273 (98%)	7 (2%)	0	100	100
1	ca	290/319 (91%)	281 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	cf	290/319 (91%)	284 (98%)	6 (2%)	0	100	100
1	cg	289/319 (91%)	278 (96%)	11 (4%)	0	100	100
1	ch	290/319 (91%)	282 (97%)	8 (3%)	0	100	100
1	ci	289/319 (91%)	284 (98%)	5 (2%)	0	100	100
1	cj	280/319 (88%)	274 (98%)	6 (2%)	0	100	100
2	ab	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	ac	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	ad	154/158 (98%)	151 (98%)	3 (2%)	0	100	100
2	ae	154/158 (98%)	151 (98%)	3 (2%)	0	100	100
2	al	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	am	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	ao	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	ap	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	aq	154/158 (98%)	151 (98%)	3 (2%)	0	100	100
2	ar	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	ay	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	az	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	bb	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	bc	154/158 (98%)	148 (96%)	6 (4%)	0	100	100
2	bd	154/158 (98%)	148 (96%)	6 (4%)	0	100	100
2	be	154/158 (98%)	151 (98%)	3 (2%)	0	100	100
2	bl	154/158 (98%)	148 (96%)	6 (4%)	0	100	100
2	bm	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	bo	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	bp	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	bq	154/158 (98%)	151 (98%)	3 (2%)	0	100	100
2	br	154/158 (98%)	153 (99%)	1 (1%)	0	100	100
2	by	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	bz	154/158 (98%)	151 (98%)	3 (2%)	0	100	100
2	cb	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	cc	154/158 (98%)	150 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	cd	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	ce	154/158 (98%)	149 (97%)	5 (3%)	0	100	100
2	cl	154/158 (98%)	150 (97%)	4 (3%)	0	100	100
2	cm	154/158 (98%)	148 (96%)	6 (4%)	0	100	100
3	cn	372/444 (84%)	351 (94%)	21 (6%)	0	100	100
3	co	381/444 (86%)	359 (94%)	22 (6%)	0	100	100
3	cp	369/444 (83%)	347 (94%)	22 (6%)	0	100	100
3	cq	372/444 (84%)	351 (94%)	21 (6%)	0	100	100
3	cy	381/444 (86%)	367 (96%)	14 (4%)	0	100	100
3	dj	371/444 (84%)	353 (95%)	18 (5%)	0	100	100
3	du	381/444 (86%)	356 (93%)	24 (6%)	1 (0%)	37	68
3	dy	371/444 (84%)	348 (94%)	23 (6%)	0	100	100
3	dz	372/444 (84%)	358 (96%)	13 (4%)	1 (0%)	37	68
3	ea	381/444 (86%)	361 (95%)	19 (5%)	1 (0%)	37	68
3	eb	372/444 (84%)	353 (95%)	19 (5%)	0	100	100
3	ec	380/444 (86%)	360 (95%)	20 (5%)	0	100	100
4	cr	130/132 (98%)	123 (95%)	7 (5%)	0	100	100
4	cs	130/132 (98%)	122 (94%)	8 (6%)	0	100	100
4	ct	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
4	cu	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
4	cv	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
4	cw	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
5	cx	131/140 (94%)	122 (93%)	9 (7%)	0	100	100
5	cz	131/140 (94%)	121 (92%)	10 (8%)	0	100	100
5	da	131/140 (94%)	122 (93%)	9 (7%)	0	100	100
5	db	131/140 (94%)	123 (94%)	8 (6%)	0	100	100
5	dc	131/140 (94%)	122 (93%)	9 (7%)	0	100	100
5	dd	131/140 (94%)	122 (93%)	9 (7%)	0	100	100
5	de	131/140 (94%)	121 (92%)	10 (8%)	0	100	100
5	df	131/140 (94%)	121 (92%)	10 (8%)	0	100	100
5	dg	131/140 (94%)	120 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	dh	131/140 (94%)	117 (89%)	14 (11%)	0	100	100
5	di	131/140 (94%)	121 (92%)	10 (8%)	0	100	100
5	dk	131/140 (94%)	121 (92%)	10 (8%)	0	100	100
6	dl	217/222 (98%)	211 (97%)	6 (3%)	0	100	100
6	dm	217/222 (98%)	212 (98%)	5 (2%)	0	100	100
6	dn	217/222 (98%)	212 (98%)	5 (2%)	0	100	100
6	do	217/222 (98%)	211 (97%)	6 (3%)	0	100	100
6	dp	217/222 (98%)	212 (98%)	5 (2%)	0	100	100
6	dq	217/222 (98%)	210 (97%)	7 (3%)	0	100	100
7	dr	119/123 (97%)	100 (84%)	19 (16%)	0	100	100
7	ds	119/123 (97%)	101 (85%)	18 (15%)	0	100	100
7	dt	119/123 (97%)	101 (85%)	18 (15%)	0	100	100
7	dv	119/123 (97%)	99 (83%)	20 (17%)	0	100	100
7	dw	119/123 (97%)	95 (80%)	24 (20%)	0	100	100
7	dx	119/123 (97%)	100 (84%)	19 (16%)	0	100	100
8	ak	148/255 (58%)	145 (98%)	3 (2%)	0	100	100
8	ax	148/255 (58%)	145 (98%)	3 (2%)	0	100	100
8	bk	148/255 (58%)	145 (98%)	3 (2%)	0	100	100
8	bx	148/255 (58%)	146 (99%)	2 (1%)	0	100	100
8	ck	148/255 (58%)	145 (98%)	3 (2%)	0	100	100
All	All	22871/25455 (90%)	21960 (96%)	908 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	du	374	LYS
3	ea	374	LYS
3	dz	374	LYS

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	aa	251/274 (92%)	251 (100%)	0	100	100
1	af	251/274 (92%)	251 (100%)	0	100	100
1	ag	251/274 (92%)	251 (100%)	0	100	100
1	ah	251/274 (92%)	250 (100%)	1 (0%)	89	95
1	ai	251/274 (92%)	251 (100%)	0	100	100
1	aj	245/274 (89%)	245 (100%)	0	100	100
1	an	251/274 (92%)	250 (100%)	1 (0%)	89	95
1	as	251/274 (92%)	250 (100%)	1 (0%)	89	95
1	at	251/274 (92%)	250 (100%)	1 (0%)	89	95
1	au	251/274 (92%)	250 (100%)	1 (0%)	89	95
1	av	251/274 (92%)	251 (100%)	0	100	100
1	aw	245/274 (89%)	245 (100%)	0	100	100
1	ba	251/274 (92%)	251 (100%)	0	100	100
1	bf	251/274 (92%)	251 (100%)	0	100	100
1	bg	251/274 (92%)	251 (100%)	0	100	100
1	bh	251/274 (92%)	251 (100%)	0	100	100
1	bi	251/274 (92%)	250 (100%)	1 (0%)	89	95
1	bj	245/274 (89%)	244 (100%)	1 (0%)	89	95
1	bn	251/274 (92%)	251 (100%)	0	100	100
1	bs	251/274 (92%)	251 (100%)	0	100	100
1	bt	251/274 (92%)	251 (100%)	0	100	100
1	bu	251/274 (92%)	250 (100%)	1 (0%)	89	95
1	bv	251/274 (92%)	251 (100%)	0	100	100
1	bw	245/274 (89%)	244 (100%)	1 (0%)	89	95
1	ca	251/274 (92%)	251 (100%)	0	100	100
1	cf	251/274 (92%)	250 (100%)	1 (0%)	89	95
1	cg	251/274 (92%)	251 (100%)	0	100	100
1	ch	251/274 (92%)	251 (100%)	0	100	100
1	ci	251/274 (92%)	251 (100%)	0	100	100
1	cj	245/274 (89%)	244 (100%)	1 (0%)	89	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	ab	125/126 (99%)	125 (100%)	0	100	100
2	ac	125/126 (99%)	122 (98%)	3 (2%)	44	68
2	ad	125/126 (99%)	125 (100%)	0	100	100
2	ae	125/126 (99%)	125 (100%)	0	100	100
2	al	125/126 (99%)	125 (100%)	0	100	100
2	am	125/126 (99%)	125 (100%)	0	100	100
2	ao	125/126 (99%)	124 (99%)	1 (1%)	79	88
2	ap	125/126 (99%)	125 (100%)	0	100	100
2	aq	125/126 (99%)	125 (100%)	0	100	100
2	ar	125/126 (99%)	125 (100%)	0	100	100
2	ay	125/126 (99%)	125 (100%)	0	100	100
2	az	125/126 (99%)	125 (100%)	0	100	100
2	bb	125/126 (99%)	125 (100%)	0	100	100
2	bc	125/126 (99%)	125 (100%)	0	100	100
2	bd	125/126 (99%)	125 (100%)	0	100	100
2	be	125/126 (99%)	125 (100%)	0	100	100
2	bl	125/126 (99%)	125 (100%)	0	100	100
2	bm	125/126 (99%)	125 (100%)	0	100	100
2	bo	125/126 (99%)	125 (100%)	0	100	100
2	bp	125/126 (99%)	125 (100%)	0	100	100
2	bq	125/126 (99%)	125 (100%)	0	100	100
2	br	125/126 (99%)	125 (100%)	0	100	100
2	by	125/126 (99%)	125 (100%)	0	100	100
2	bz	125/126 (99%)	125 (100%)	0	100	100
2	cb	125/126 (99%)	125 (100%)	0	100	100
2	cc	125/126 (99%)	125 (100%)	0	100	100
2	cd	125/126 (99%)	125 (100%)	0	100	100
2	ce	125/126 (99%)	125 (100%)	0	100	100
2	cl	125/126 (99%)	125 (100%)	0	100	100
2	cm	125/126 (99%)	125 (100%)	0	100	100
3	cn	324/383 (85%)	319 (98%)	5 (2%)	60	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	co	333/383 (87%)	328 (98%)	5 (2%)	60	77
3	cp	322/383 (84%)	319 (99%)	3 (1%)	75	86
3	cq	324/383 (85%)	322 (99%)	2 (1%)	84	91
3	cy	333/383 (87%)	326 (98%)	7 (2%)	48	71
3	dj	324/383 (85%)	320 (99%)	4 (1%)	67	82
3	du	333/383 (87%)	332 (100%)	1 (0%)	91	96
3	dy	324/383 (85%)	322 (99%)	2 (1%)	84	91
3	dz	324/383 (85%)	320 (99%)	4 (1%)	67	82
3	ea	333/383 (87%)	331 (99%)	2 (1%)	84	91
3	eb	324/383 (85%)	323 (100%)	1 (0%)	91	96
3	ec	332/383 (87%)	330 (99%)	2 (1%)	84	91
4	cr	112/112 (100%)	112 (100%)	0	100	100
4	cs	112/112 (100%)	111 (99%)	1 (1%)	75	86
4	ct	112/112 (100%)	112 (100%)	0	100	100
4	cu	112/112 (100%)	112 (100%)	0	100	100
4	cv	112/112 (100%)	112 (100%)	0	100	100
4	cw	112/112 (100%)	112 (100%)	0	100	100
5	cx	112/116 (97%)	112 (100%)	0	100	100
5	cz	112/116 (97%)	112 (100%)	0	100	100
5	da	112/116 (97%)	112 (100%)	0	100	100
5	db	112/116 (97%)	112 (100%)	0	100	100
5	dc	112/116 (97%)	112 (100%)	0	100	100
5	dd	112/116 (97%)	110 (98%)	2 (2%)	54	74
5	de	112/116 (97%)	110 (98%)	2 (2%)	54	74
5	df	112/116 (97%)	110 (98%)	2 (2%)	54	74
5	dg	112/116 (97%)	110 (98%)	2 (2%)	54	74
5	dh	112/116 (97%)	110 (98%)	2 (2%)	54	74
5	di	112/116 (97%)	112 (100%)	0	100	100
5	dk	112/116 (97%)	110 (98%)	2 (2%)	54	74
6	dl	187/188 (100%)	187 (100%)	0	100	100
6	dm	187/188 (100%)	187 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	dn	187/188 (100%)	187 (100%)	0	100	100
6	do	187/188 (100%)	187 (100%)	0	100	100
6	dp	187/188 (100%)	186 (100%)	1 (0%)	86	93
6	dq	187/188 (100%)	187 (100%)	0	100	100
7	dr	104/104 (100%)	104 (100%)	0	100	100
7	ds	104/104 (100%)	103 (99%)	1 (1%)	73	84
7	dt	104/104 (100%)	104 (100%)	0	100	100
7	dv	104/104 (100%)	103 (99%)	1 (1%)	73	84
7	dw	104/104 (100%)	104 (100%)	0	100	100
7	dx	104/104 (100%)	104 (100%)	0	100	100
8	ak	114/200 (57%)	114 (100%)	0	100	100
8	ax	114/200 (57%)	114 (100%)	0	100	100
8	bk	114/200 (57%)	114 (100%)	0	100	100
8	bx	114/200 (57%)	114 (100%)	0	100	100
8	ck	114/200 (57%)	114 (100%)	0	100	100
All	All	19512/21412 (91%)	19443 (100%)	69 (0%)	88	95

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	ac	146	LYS
2	ac	147	ASP
2	ac	148	ILE
1	ah	274	MET
1	an	274	MET
2	ao	83	GLN
1	as	205	ARG
1	at	37	GLN
1	au	274	MET
1	bi	274	MET
1	bj	209	ARG
1	bu	226	ARG
1	bw	274	MET
1	cf	166	ASN
1	cj	45	GLN
3	cn	130	LYS
3	cn	156	ARG

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Mol	Chain	Res	Type
3	cn	201	GLN
3	cn	335	LYS
3	cn	340	LYS
3	co	77	LYS
3	co	156	ARG
3	co	271	ARG
3	co	407	ARG
3	co	416	LYS
3	cp	150	LYS
3	cp	199	GLN
3	cp	271	ARG
3	cq	156	ARG
3	cq	271	ARG
4	cs	91	LYS
3	cy	124	MET
3	cy	150	LYS
3	cy	156	ARG
3	cy	183	ARG
3	cy	241	LYS
3	cy	271	ARG
3	cy	390	LYS
5	dd	103	ASN
5	dd	136	ARG
5	de	103	ASN
5	de	136	ARG
5	df	49	LYS
5	df	107	ASN
5	dg	102	LYS
5	dg	103	ASN
5	dh	102	LYS
5	dh	136	ARG
3	dj	156	ARG
3	dj	191	ARG
3	dj	271	ARG
3	dj	414	LYS
5	dk	102	LYS
5	dk	136	ARG
6	dp	28	LYS
7	ds	44	MET
3	du	156	ARG
7	dv	8	ARG
3	dy	271	ARG

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Mol	Chain	Res	Type
3	dy	407	ARG
3	dz	156	ARG
3	dz	271	ARG
3	dz	326	GLN
3	dz	375	LYS
3	ea	383	ASN
3	ea	407	ARG
3	eb	271	ARG
3	ec	210	LYS
3	ec	340	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
2	ac	157	GLN
1	ah	144	HIS
1	ah	273	ASN
2	am	156	HIS
1	av	146	GLN
2	ay	27	ASN
2	ay	85	GLN
2	az	154	GLN
2	bb	83	GLN
2	be	85	GLN
1	bh	273	ASN
2	bm	51	GLN
1	bw	113	ASN
2	by	27	ASN
2	by	157	GLN
2	cl	27	ASN
2	cm	46	GLN
3	cn	120	ASN
3	cn	310	HIS
3	co	49	HIS
3	co	310	HIS
3	cp	310	HIS
3	cp	318	ASN
3	cq	235	GLN
3	cq	310	HIS
3	cy	316	ASN
3	cy	326	GLN
3	cy	384	ASN

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Mol	Chain	Res	Type
5	cz	95	GLN
5	dc	95	GLN
5	de	103	ASN
3	dj	266	ASN
5	dk	103	ASN
3	du	120	ASN
3	dz	234	GLN
3	ea	326	GLN
3	eb	310	HIS
8	ak	146	ASN
8	bk	72	HIS
8	bx	72	HIS
8	ck	72	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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.

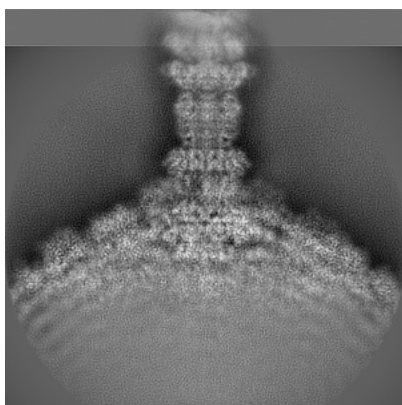
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62433. These allow visual inspection of the internal detail of the map and identification of artifacts.

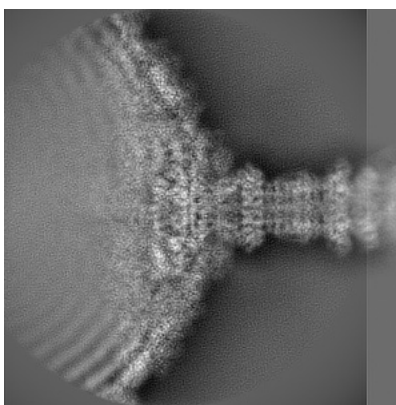
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

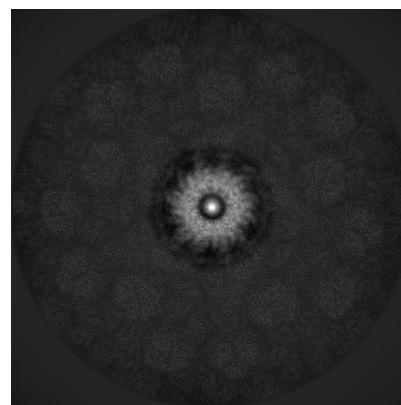
6.1.1 Primary map



X



Y

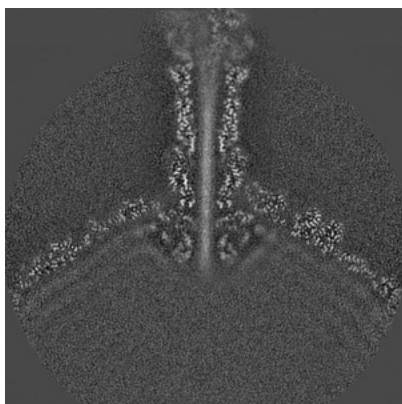


Z

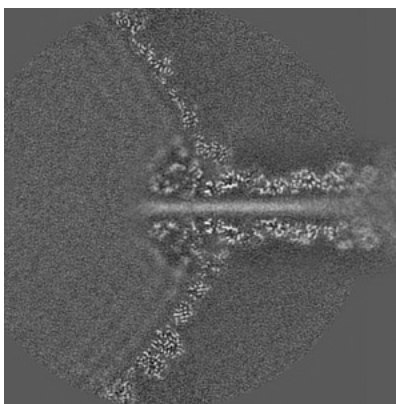
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

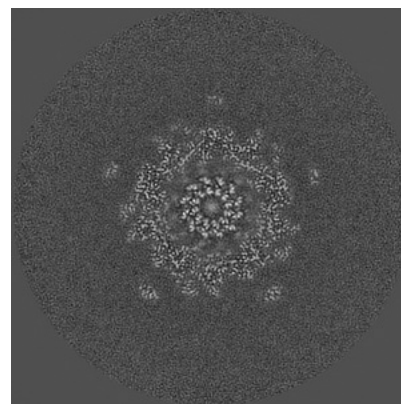
6.2.1 Primary map



X Index: 160



Y Index: 160

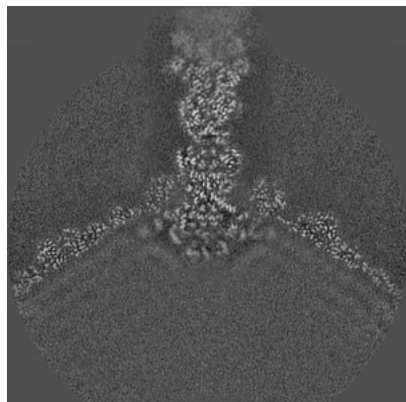


Z Index: 160

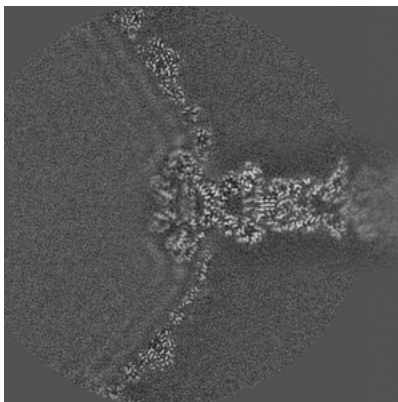
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

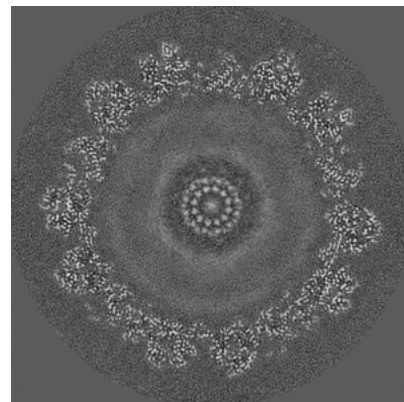
6.3.1 Primary map



X Index: 176



Y Index: 149

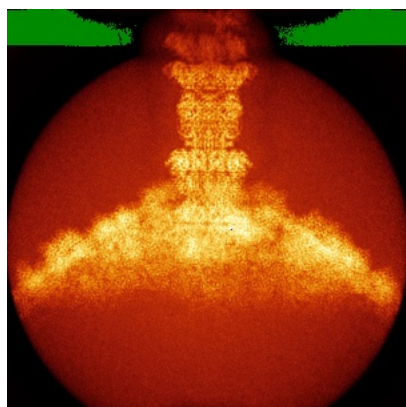


Z Index: 126

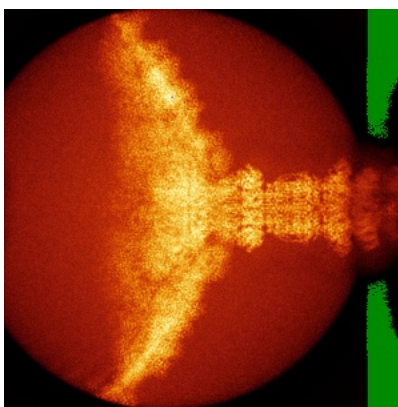
The images above show the largest variance slices of the map in three orthogonal directions.

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

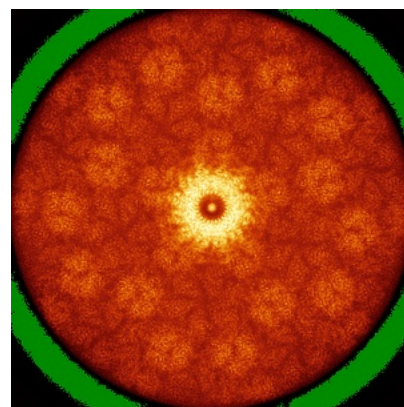
6.4.1 Primary map



X



Y

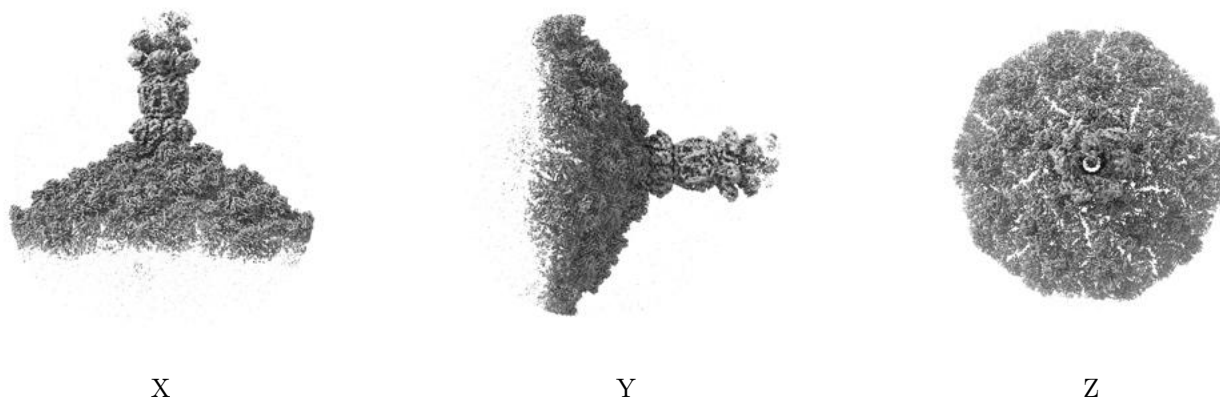


Z

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

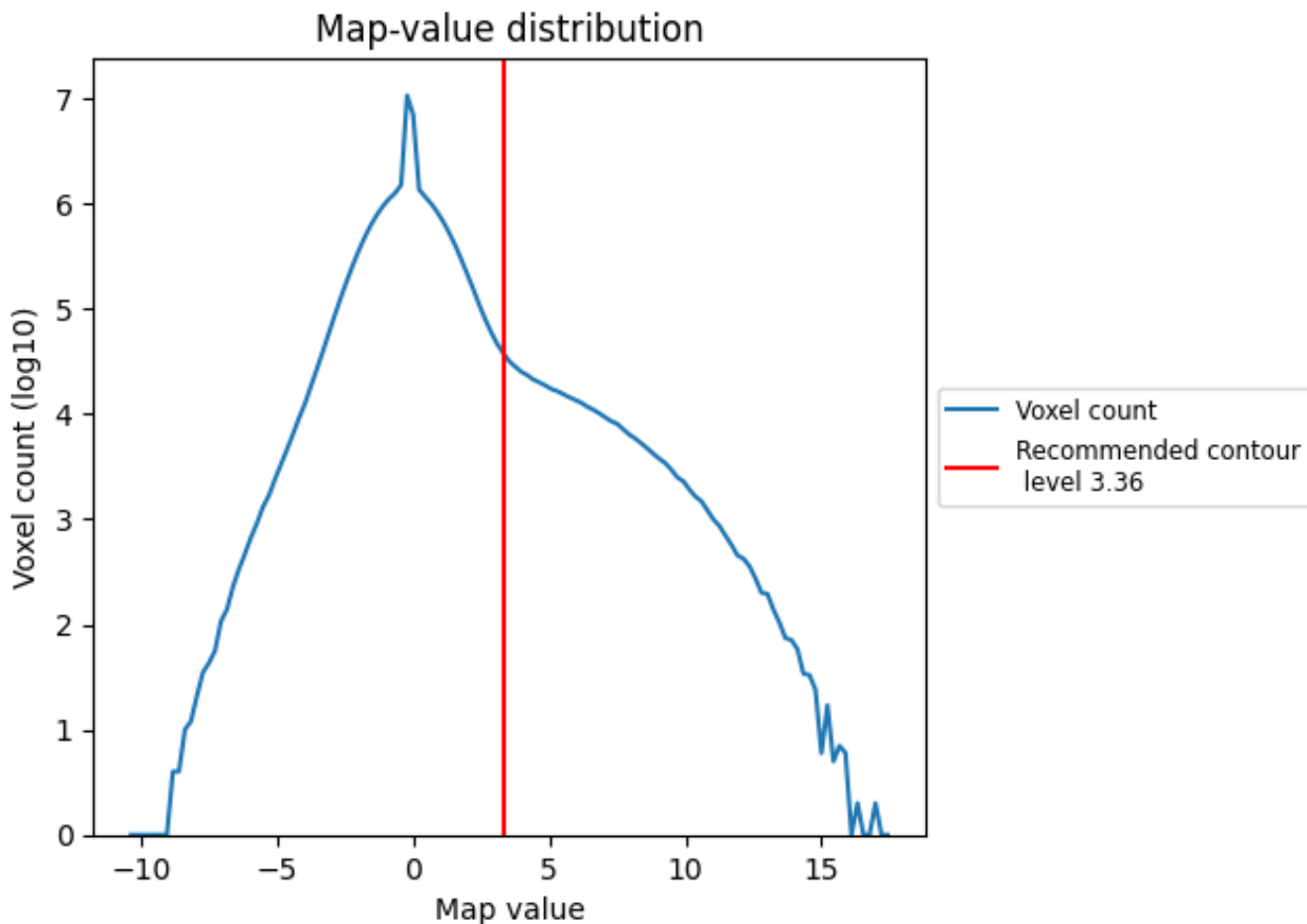
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

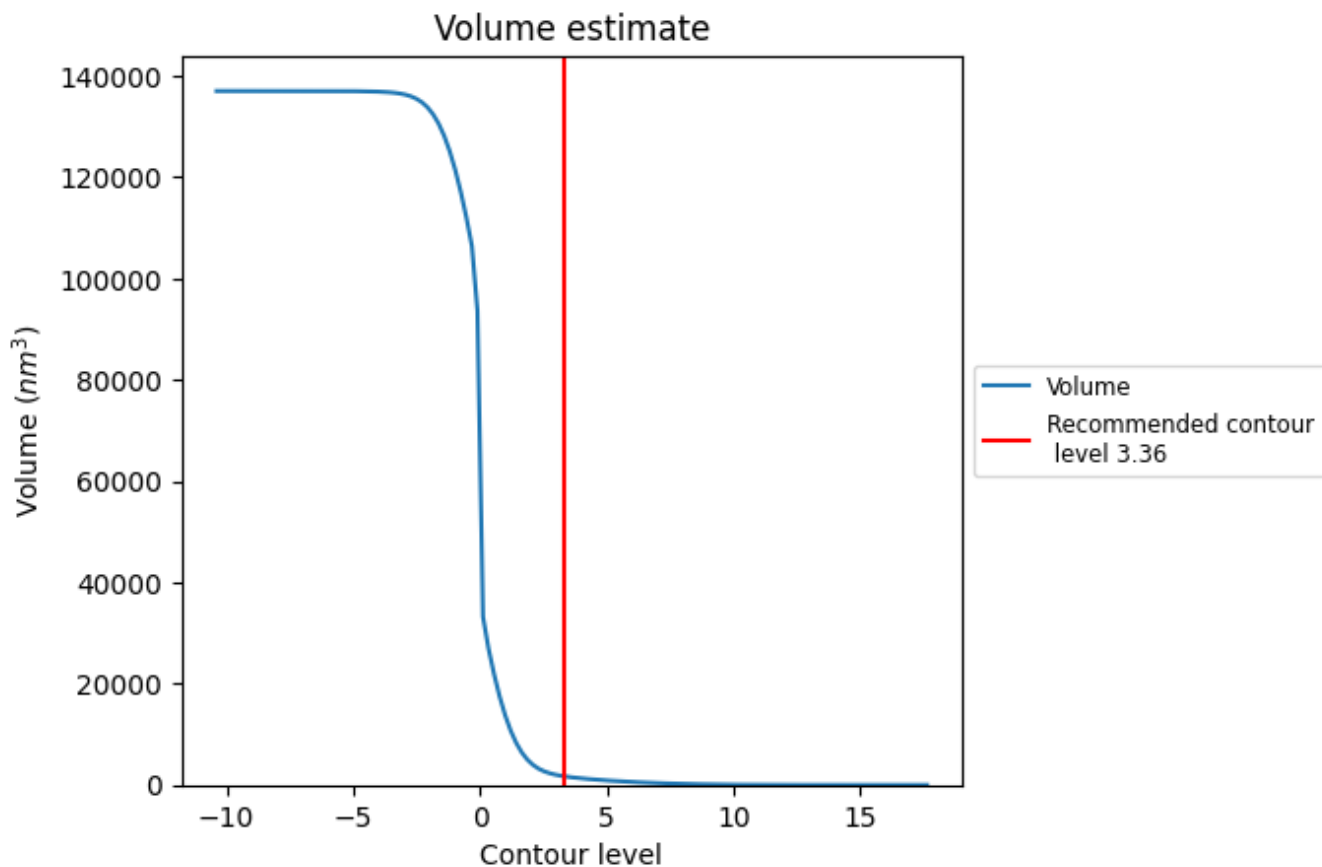
This section contains the results of statistical analysis of the map.

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.

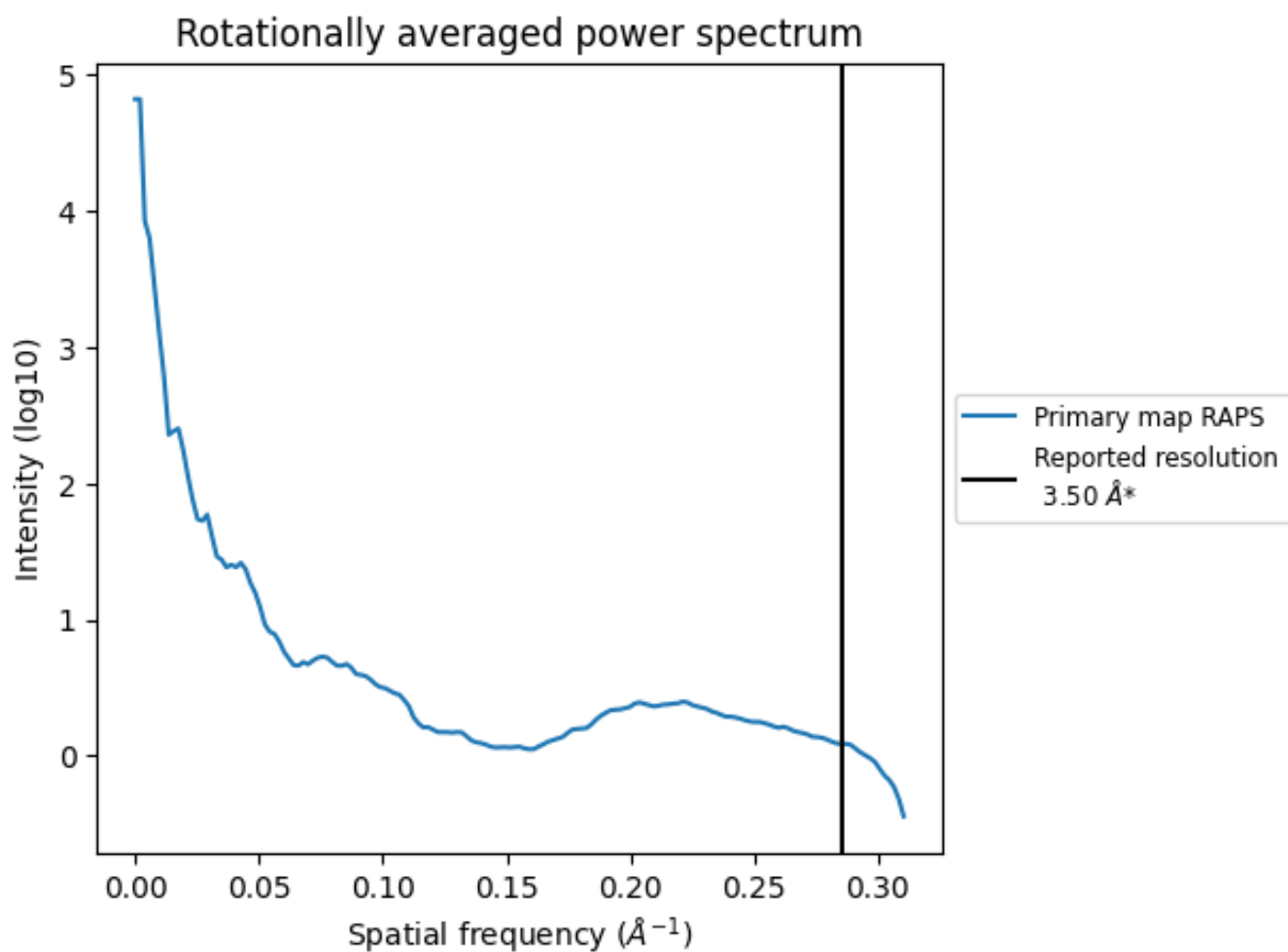
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1690 nm^3 ; this corresponds to an approximate mass of 1526 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 0.286 Å⁻¹

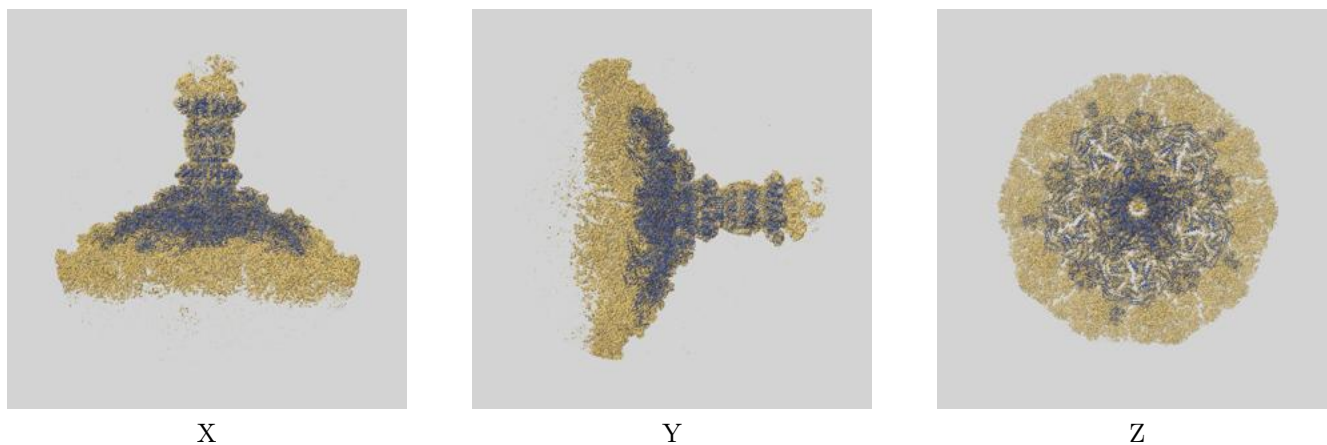
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

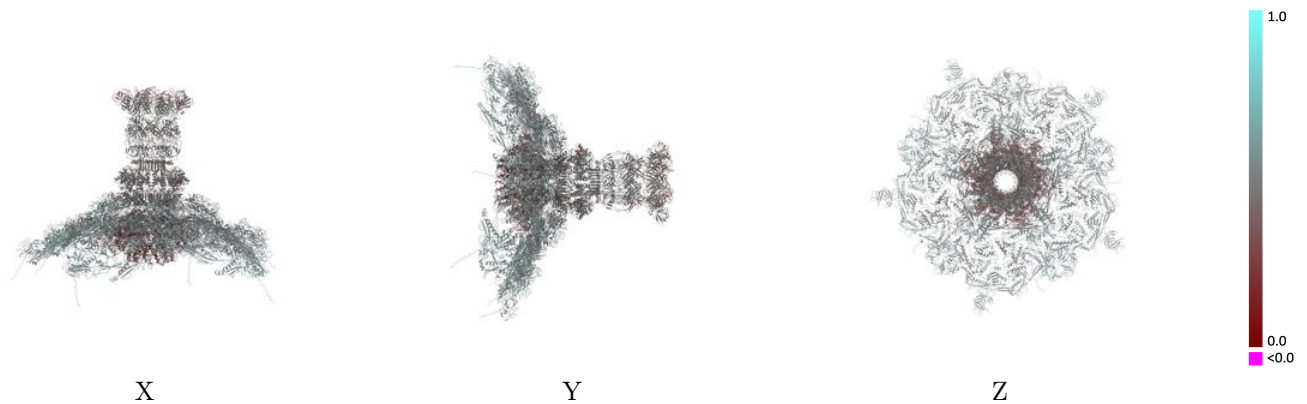
This section contains information regarding the fit between EMDB map EMD-62433 and PDB model 9KMH. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



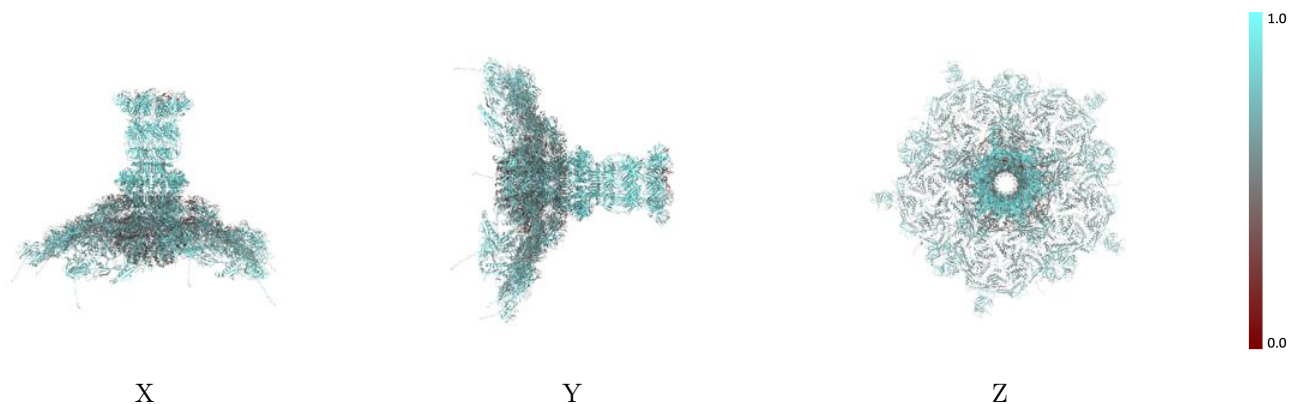
The images above show the 3D surface view of the map at the recommended contour level 3.36 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



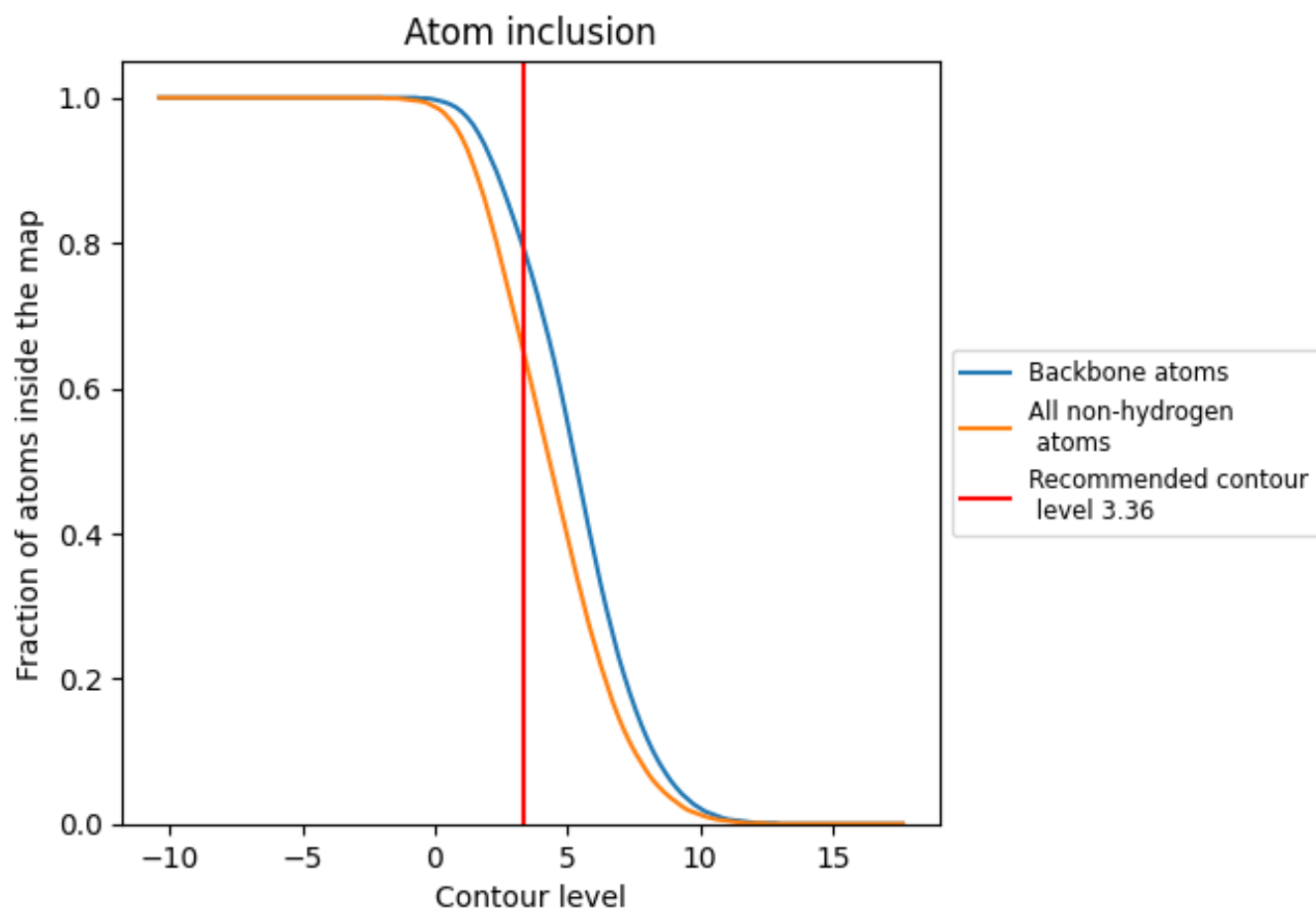
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.36).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (3.36) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6480	 0.4750
aa	 0.6000	 0.5120
ab	 0.6800	 0.5390
ac	 0.6770	 0.5390
ad	 0.6870	 0.5420
ae	 0.6590	 0.5320
af	 0.6290	 0.5230
ag	 0.6460	 0.5240
ah	 0.6380	 0.5260
ai	 0.6370	 0.5300
aj	 0.5970	 0.5180
ak	 0.5340	 0.4730
al	 0.5930	 0.5130
am	 0.6660	 0.5350
an	 0.5950	 0.5110
ao	 0.6840	 0.5390
ap	 0.6890	 0.5370
aq	 0.6780	 0.5360
ar	 0.6720	 0.5350
as	 0.6240	 0.5200
at	 0.6430	 0.5280
au	 0.6380	 0.5220
av	 0.6450	 0.5260
aw	 0.5910	 0.5240
ax	 0.4840	 0.4480
ay	 0.5310	 0.4970
az	 0.6550	 0.5290
ba	 0.5950	 0.5200
bb	 0.6740	 0.5410
bc	 0.6800	 0.5420
bd	 0.6840	 0.5380
be	 0.6730	 0.5390
bf	 0.6370	 0.5250
bg	 0.6460	 0.5270
bh	 0.6360	 0.5230

































































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Chain	Atom inclusion	Q-score
bi	 0.6530	 0.5280
bj	 0.5970	 0.5170
bk	 0.5500	 0.4700
bl	 0.5850	 0.5130
bm	 0.6550	 0.5350
bn	 0.5840	 0.5110
bo	 0.6880	 0.5430
bp	 0.6790	 0.5360
bq	 0.6870	 0.5370
br	 0.6740	 0.5360
bs	 0.6210	 0.5200
bt	 0.6310	 0.5220
bu	 0.6380	 0.5220
bv	 0.6390	 0.5270
bw	 0.5870	 0.5150
bx	 0.5050	 0.4650
by	 0.5310	 0.4990
bz	 0.6530	 0.5270
ca	 0.5800	 0.5110
cb	 0.6800	 0.5410
cc	 0.6980	 0.5420
cd	 0.6830	 0.5330
ce	 0.6710	 0.5330
cf	 0.6280	 0.5190
cg	 0.6370	 0.5290
ch	 0.6310	 0.5200
ci	 0.6430	 0.5290
cj	 0.6030	 0.5170
ck	 0.5350	 0.4630
cl	 0.5610	 0.4990
cm	 0.6510	 0.5340
cn	 0.5660	 0.3690
co	 0.5800	 0.3690
cp	 0.5870	 0.3720
cq	 0.5820	 0.3720
cr	 0.8530	 0.4620
cs	 0.8500	 0.4530
ct	 0.8560	 0.4620
cu	 0.8580	 0.4610
cv	 0.8640	 0.4750
cw	 0.8440	 0.4400
cx	 0.8090	 0.4660

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Chain	Atom inclusion	Q-score
cy	 0.5600	 0.3750
cz	 0.8140	 0.4460
da	 0.8020	 0.4500
db	 0.7900	 0.4550
dc	 0.7990	 0.4510
dd	 0.8040	 0.4510
de	 0.8070	 0.4380
df	 0.8020	 0.4510
dg	 0.8090	 0.4550
dh	 0.8170	 0.4480
di	 0.7990	 0.4410
dj	 0.5680	 0.3720
dk	 0.7880	 0.4480
dl	 0.7280	 0.4070
dm	 0.6680	 0.4000
dn	 0.6830	 0.4040
do	 0.7120	 0.4100
dp	 0.6900	 0.4060
dq	 0.7320	 0.4050
dr	 0.8140	 0.4460
ds	 0.8290	 0.4430
dt	 0.8470	 0.4570
du	 0.5730	 0.3760
dv	 0.8290	 0.4510
dw	 0.8210	 0.4470
dx	 0.8350	 0.4440
dy	 0.5590	 0.3640
dz	 0.5810	 0.3670
ea	 0.5710	 0.3810
eb	 0.5560	 0.3550
ec	 0.5510	 0.3680