



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:40 PM UTC

PDB ID : 8ZDQ / pdb_00008zdq
EMDB ID : EMD-60005
Title : Cryo-EM structure of Mycobacteriophage Douge complete baseplate (gp13, gp17, gp23, gp16, gp18 and gp20)
Authors : Maharana, J.; Wang, C.H.; Tsai, L.A.; Lowary, T.L.; Ho, M.C.
Deposited on : 2024-05-02
Resolution : 3.29 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

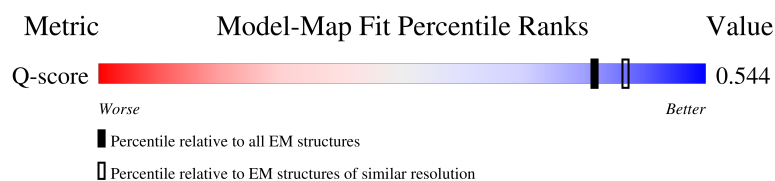
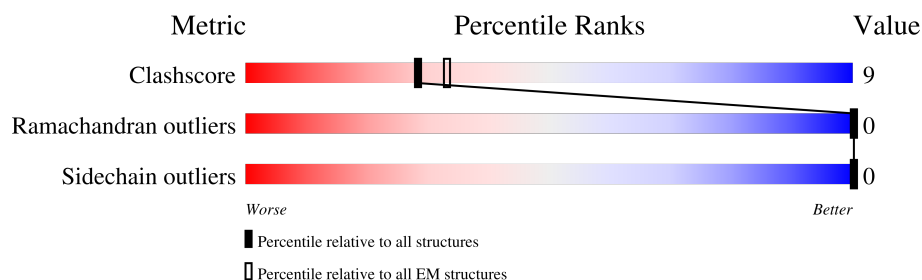
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.29 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14466 (2.79 - 3.79)

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	M	300	18% 82% 18%
1	N	300	18% 81% 19%
1	O	300	18% 81% 19%
1	P	300	18% 84% 16%

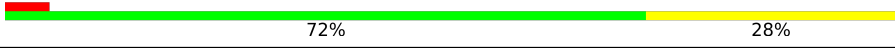
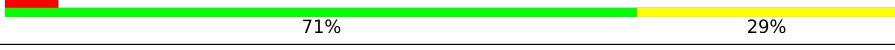
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Mol	Chain	Length	Quality of chain
1	Q	300	18% 81% 18%
1	R	300	18% 80% 20%
2	S	1699	98%
2	T	1699	98%
2	U	1699	98%
3	a	311	5% 85% 15%
3	b	311	84% 16%
3	c	311	82% 18%
3	d	311	82% 18%
3	e	311	5% 81% 19%
3	f	311	80% 20%
3	g	311	84% 16%
3	h	311	79% 21%
3	i	311	6% 83% 17%
3	j	311	82% 18%
3	k	311	83% 17%
3	l	311	80% 20%
4	m	295	75% 23%
4	n	295	70% 28%
4	o	295	75% 23%
4	p	295	74% 24%
4	q	295	74% 24%
4	r	295	74% 24%
5	s	587	77% 23%
5	t	587	77% 23%

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Mol	Chain	Length	Quality of chain
5	u	587	 6% 77% 23%
6	v	878	 6% 70% 30%
6	w	878	 5% 72% 28%
6	x	878	 6% 71% 29%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 90393 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 Tail Tube Protein (gp13).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	M	299	Total	C	N	O	S	0	0
			2256	1438	367	448	3		
1	N	299	Total	C	N	O	S	0	0
			2256	1438	367	448	3		
1	O	299	Total	C	N	O	S	0	0
			2256	1438	367	448	3		
1	P	299	Total	C	N	O	S	0	0
			2256	1438	367	448	3		
1	Q	299	Total	C	N	O	S	0	0
			2256	1438	367	448	3		
1	R	299	Total	C	N	O	S	0	0
			2256	1438	367	448	3		

- Molecule 2 is a protein called Tape Measure Protein (gp16).

Mol	Chain	Residues	Atoms				AltConf	Trace
2	S	42	Total	C	N	O	0	0
			327	201	62	64		
2	T	42	Total	C	N	O	0	0
			327	201	62	64		
2	U	42	Total	C	N	O	0	0
			327	201	62	64		

- Molecule 3 is a protein called Baseplate Upper Protein (gp23).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	b	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	c	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	d	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	e	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	f	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	g	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	h	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	i	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	j	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	k	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		
3	l	311	Total	C	N	O	S	0	0
			2372	1519	388	453	12		

- Molecule 4 is a protein called Distal Tail Protein (gp17).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	m	290	Total	C	N	O	S	0	0
			2343	1497	397	440	9		
4	n	290	Total	C	N	O	S	0	0
			2343	1497	397	440	9		
4	o	290	Total	C	N	O	S	0	0
			2343	1497	397	440	9		
4	p	290	Total	C	N	O	S	0	0
			2343	1497	397	440	9		
4	q	290	Total	C	N	O	S	0	0
			2343	1497	397	440	9		
4	r	290	Total	C	N	O	S	0	0
			2343	1497	397	440	9		

- Molecule 5 is a protein called Baseplate Hub Protein (gp18).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	s	586	Total	C	N	O	S	0	0
			4582	2937	768	863	14		
5	t	586	Total	C	N	O	S	0	0
			4582	2937	768	863	14		
5	u	586	Total	C	N	O	S	0	0
			4582	2937	768	863	14		

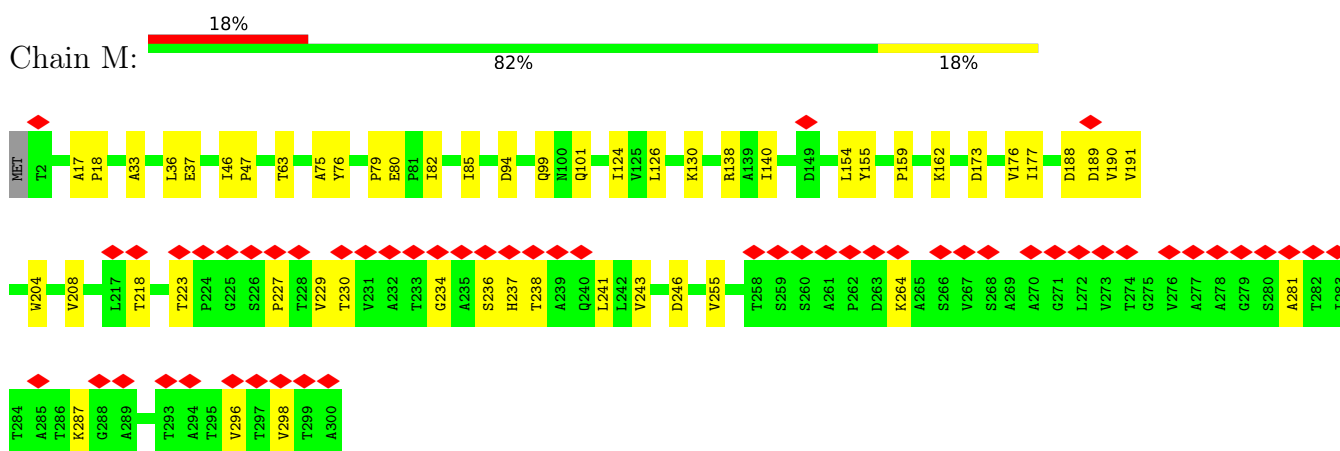
- Molecule 6 is a protein called Central Fiber Protein (gp20).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	v	878	Total	C	N	O	S	0	0
			6536	4125	1095	1298	18		
6	w	878	Total	C	N	O	S	0	0
			6536	4125	1095	1298	18		
6	x	878	Total	C	N	O	S	0	0
			6536	4125	1095	1298	18		

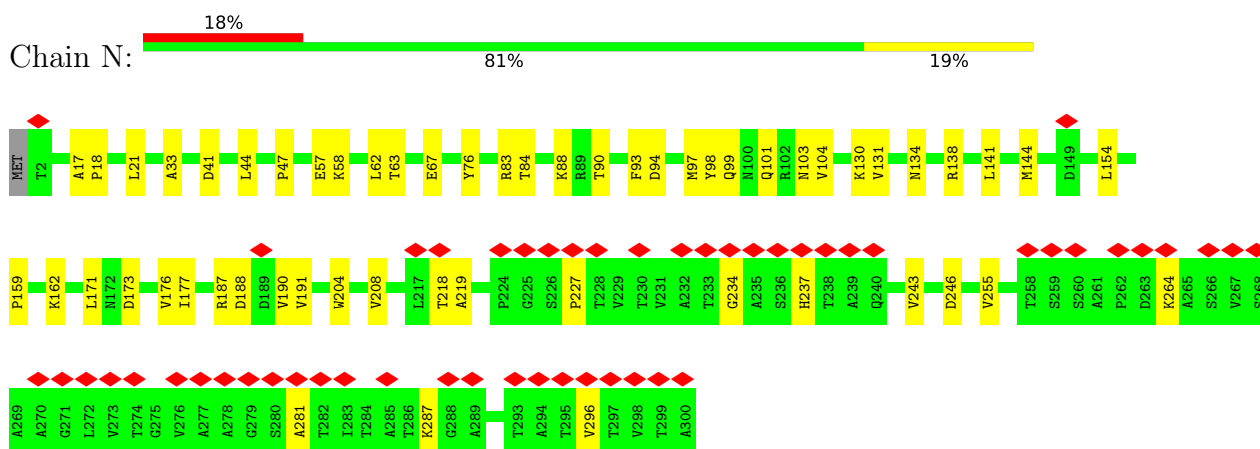
3 Residue-property plots

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.

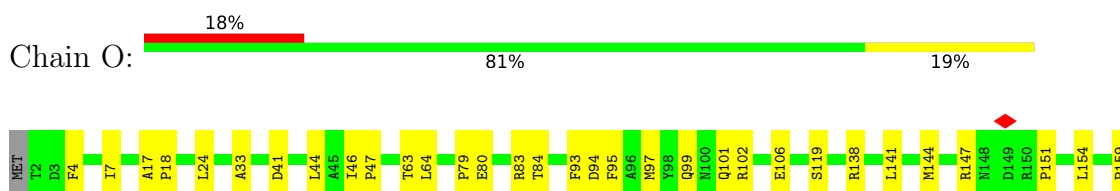
- Molecule 1: Tail Tube Protein (gp13)



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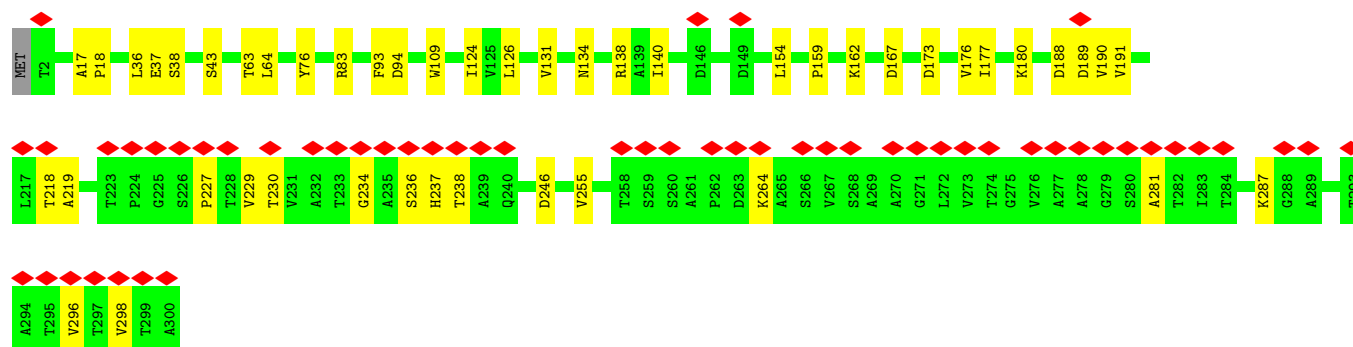
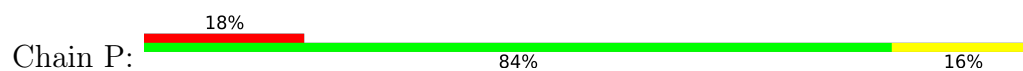


- Molecule 1: Tail Tube Protein (gp13)

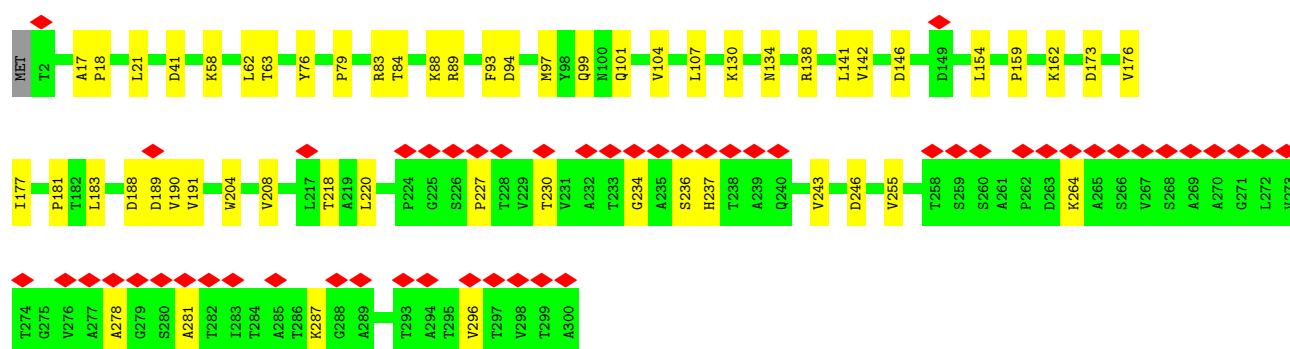
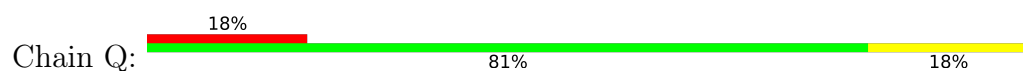




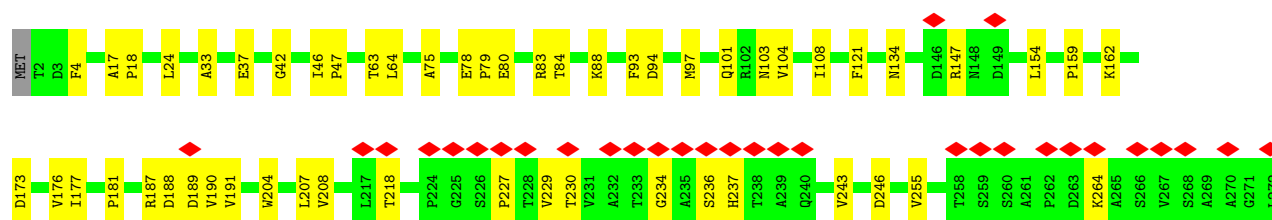
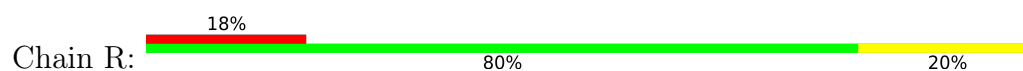
• Molecule 1: Tail Tube Protein (gp13)



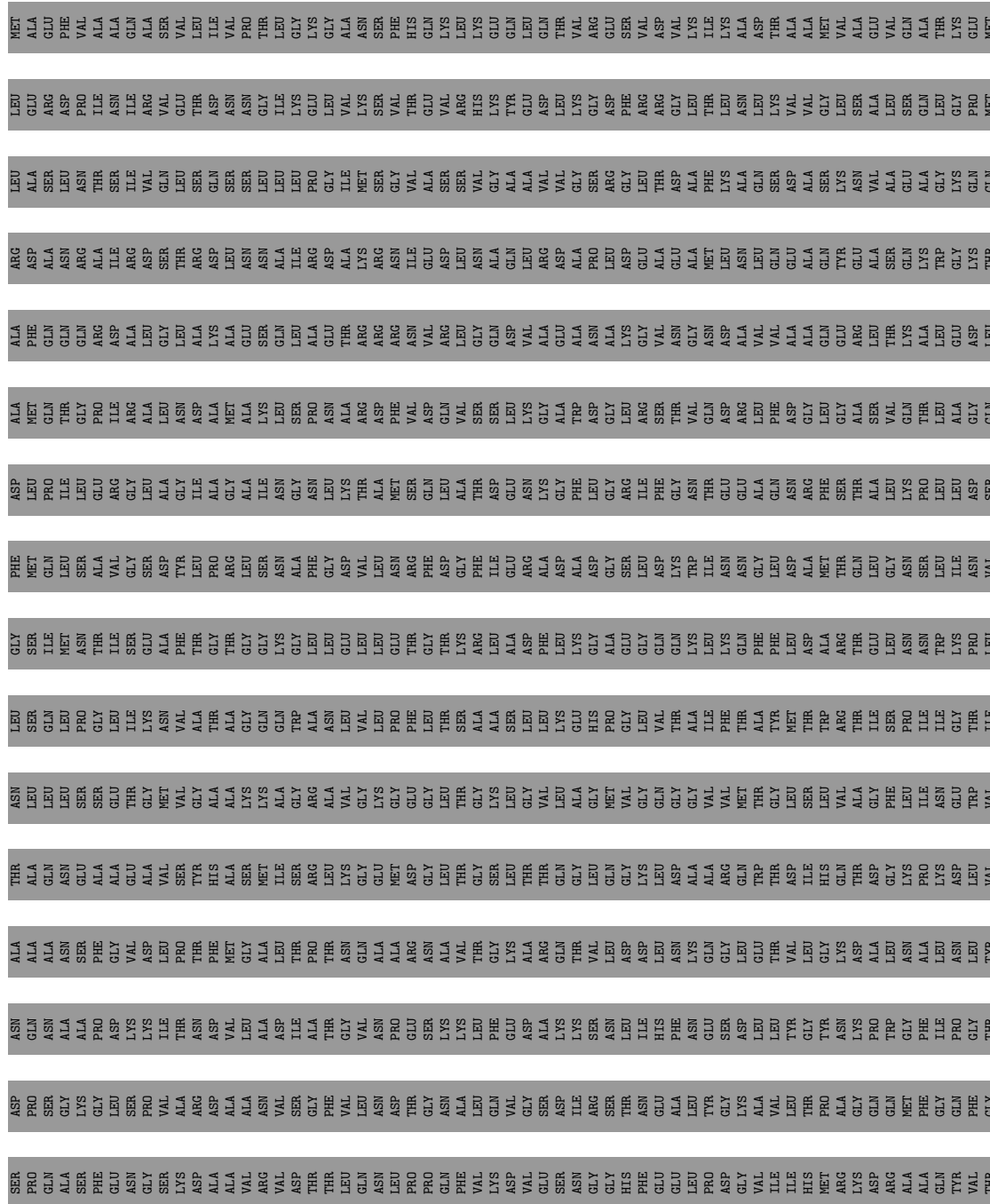
• Molecule 1: Tail Tube Protein (gp13)



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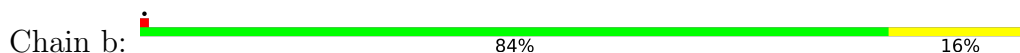


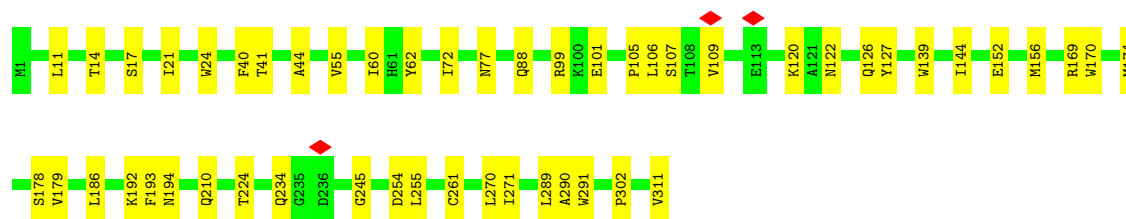




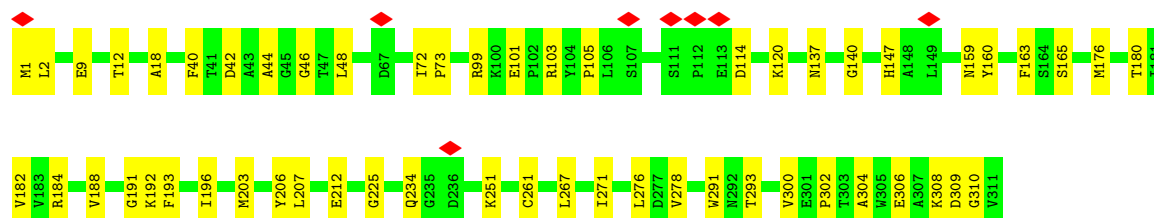
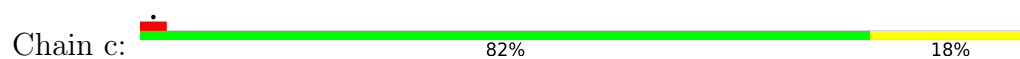
R1699

Chain a:

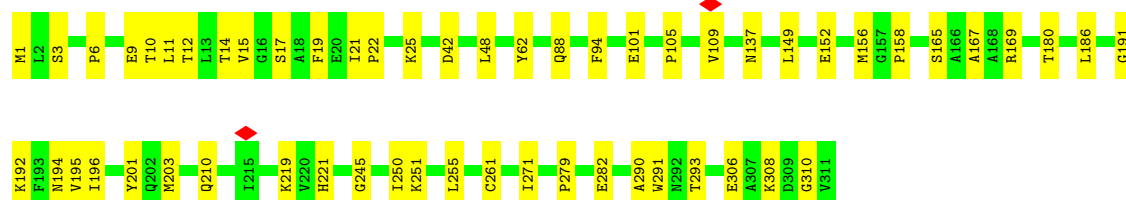
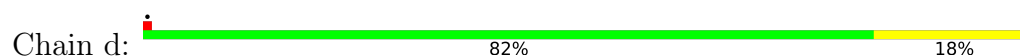




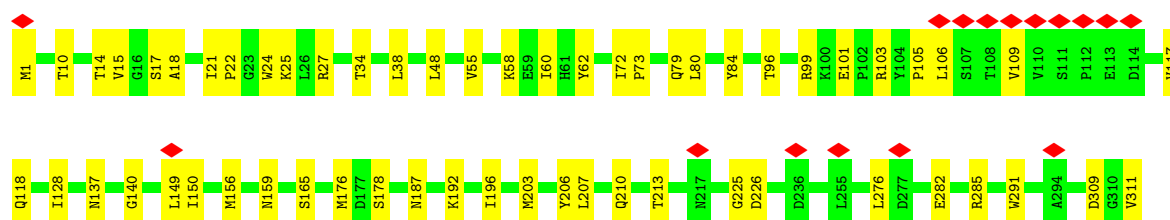
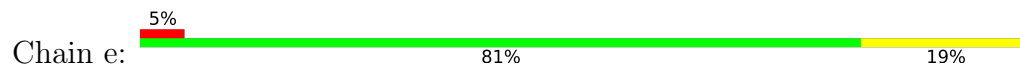
• Molecule 3: Baseplate Upper Protein (gp23)



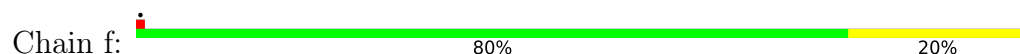
• Molecule 3: Baseplate Upper Protein (gp23)

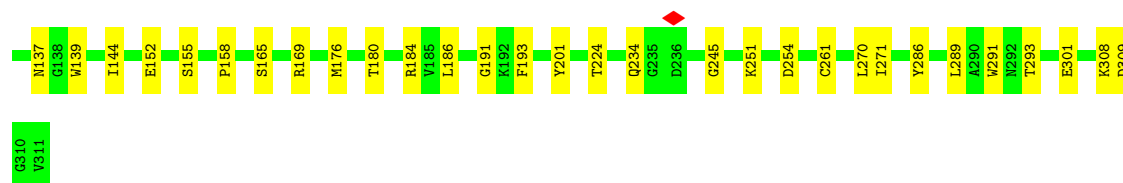


• Molecule 3: Baseplate Upper Protein (gp23)

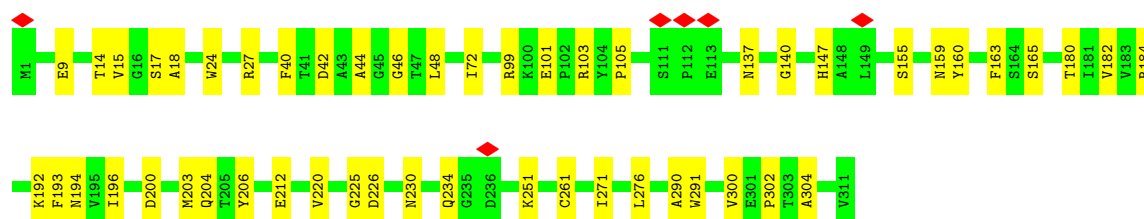
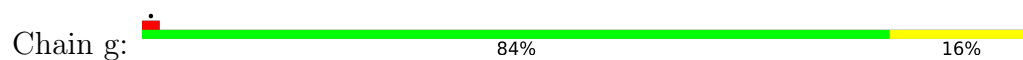


• Molecule 3: Baseplate Upper Protein (gp23)

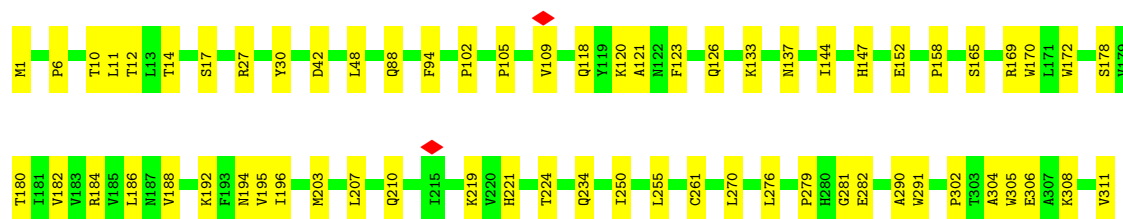
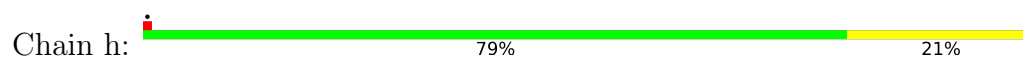




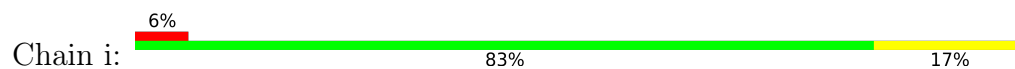
• Molecule 3: Baseplate Upper Protein (gp23)



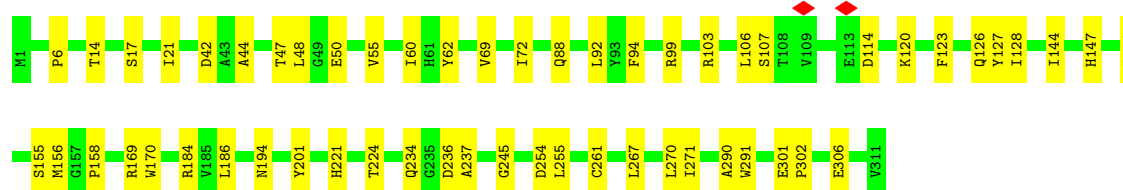
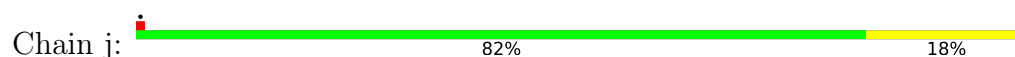
• Molecule 3: Baseplate Upper Protein (gp23)



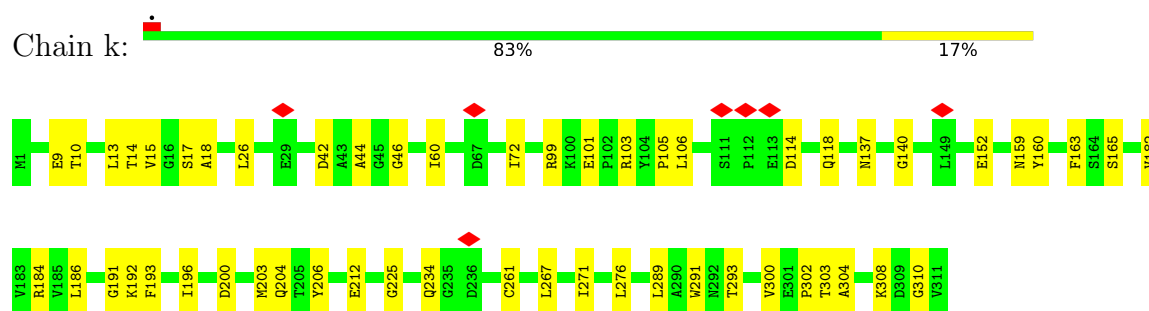
• Molecule 3: Baseplate Upper Protein (gp23)



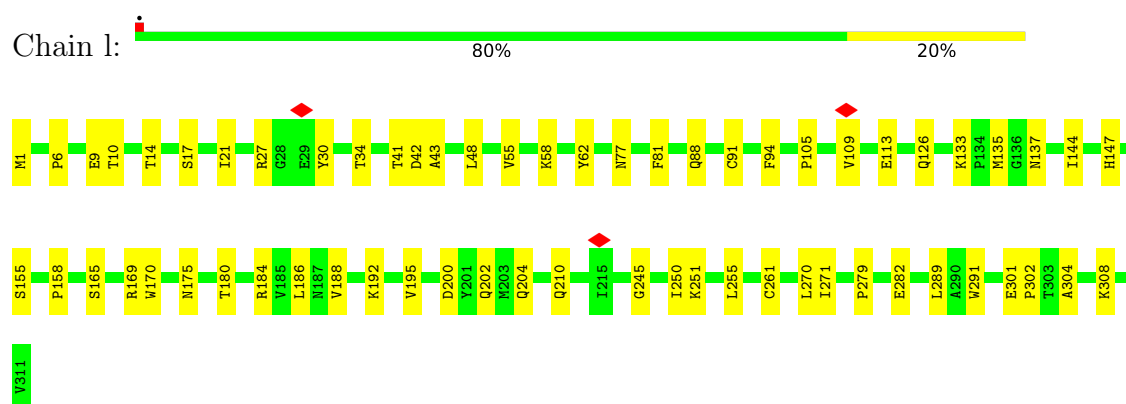
• Molecule 3: Baseplate Upper Protein (gp23)



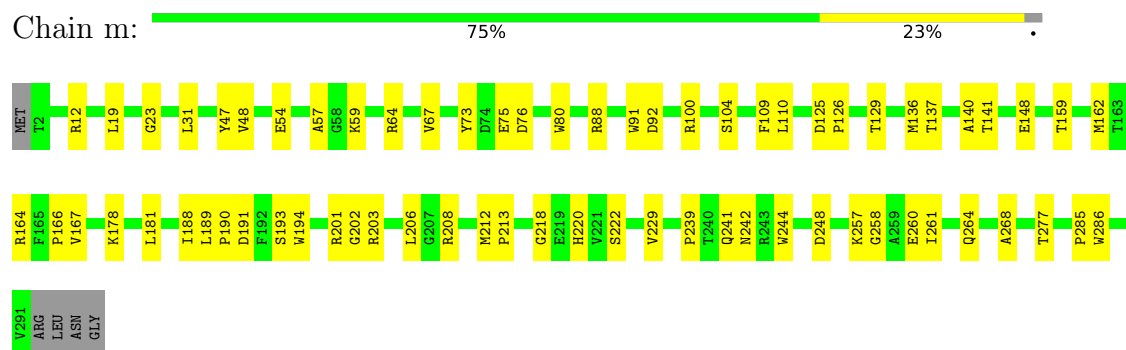
- Molecule 3: Baseplate Upper Protein (gp23)



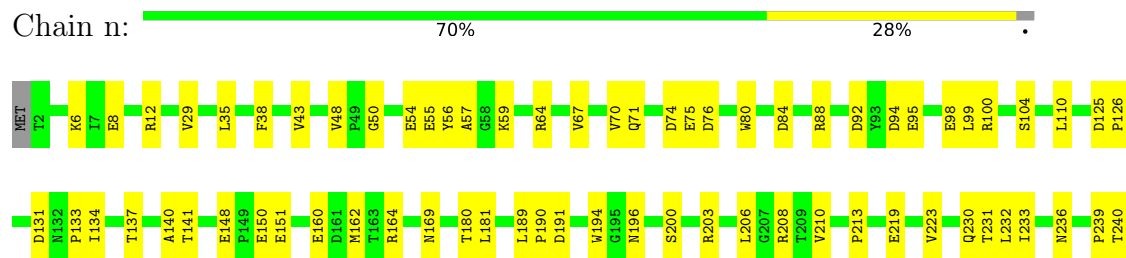
- Molecule 3: Baseplate Upper Protein (gp23)



- Molecule 4: Distal Tail Protein (gp17)



- Molecule 4: Distal Tail Protein (gp17)

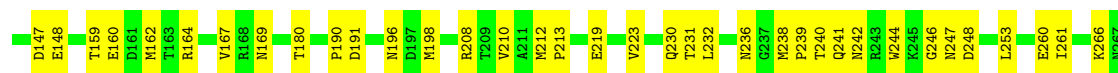
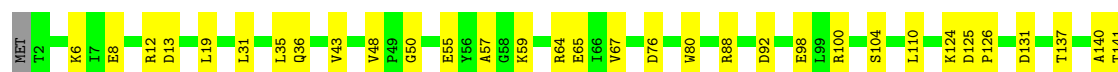




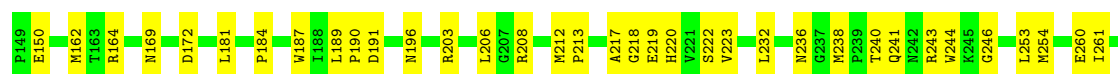
• Molecule 4: Distal Tail Protein (gp17)



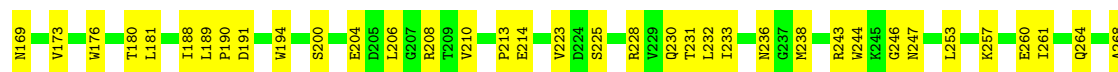
• Molecule 4: Distal Tail Protein (gp17)

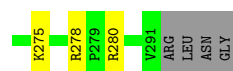


• Molecule 4: Distal Tail Protein (gp17)



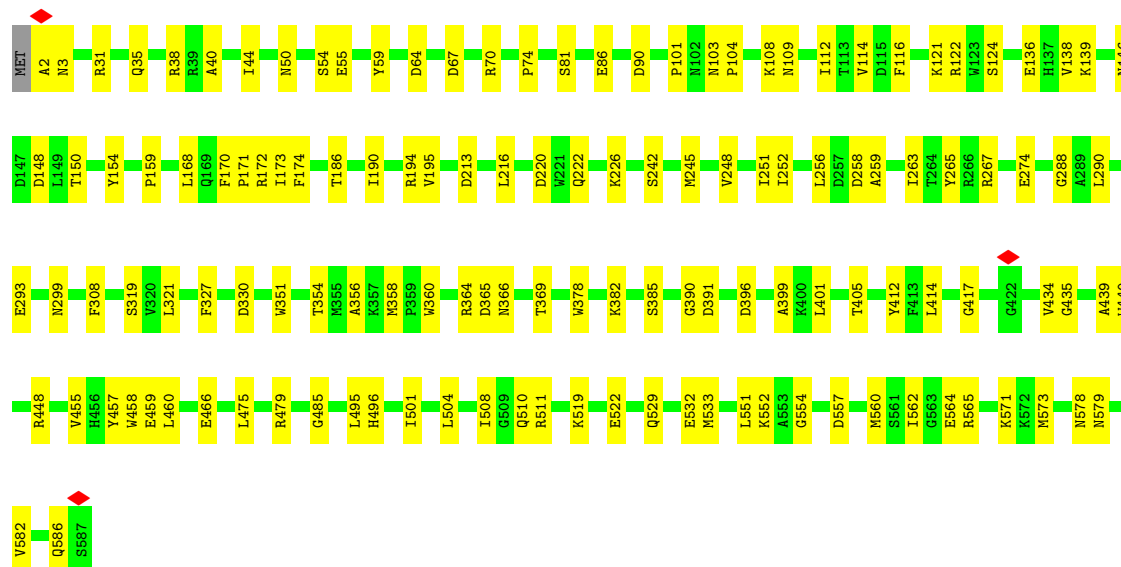
• Molecule 4: Distal Tail Protein (gp17)





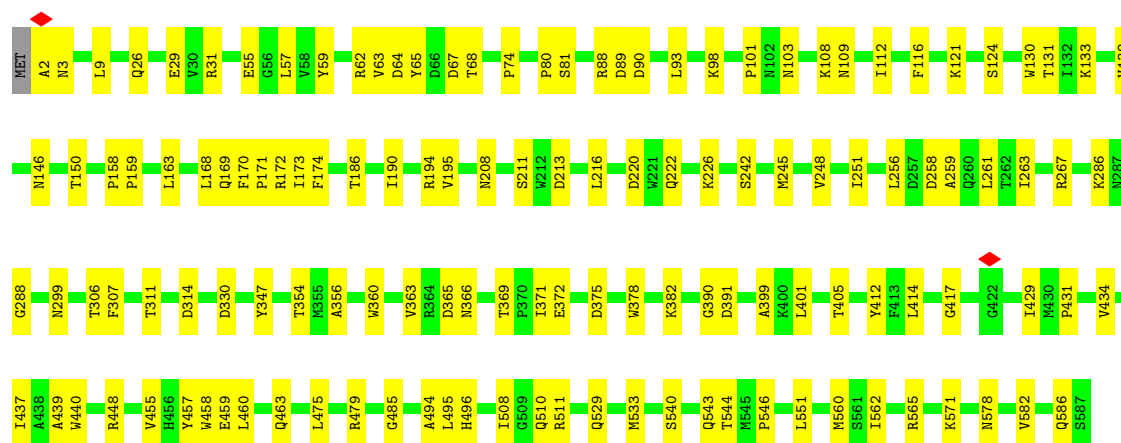
• Molecule 5: Baseplate Hub Protein (gp18)

Chain s: 77% 23%



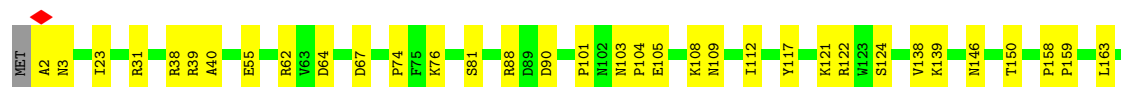
• Molecule 5: Baseplate Hub Protein (gp18)

Chain t: 77% 23%

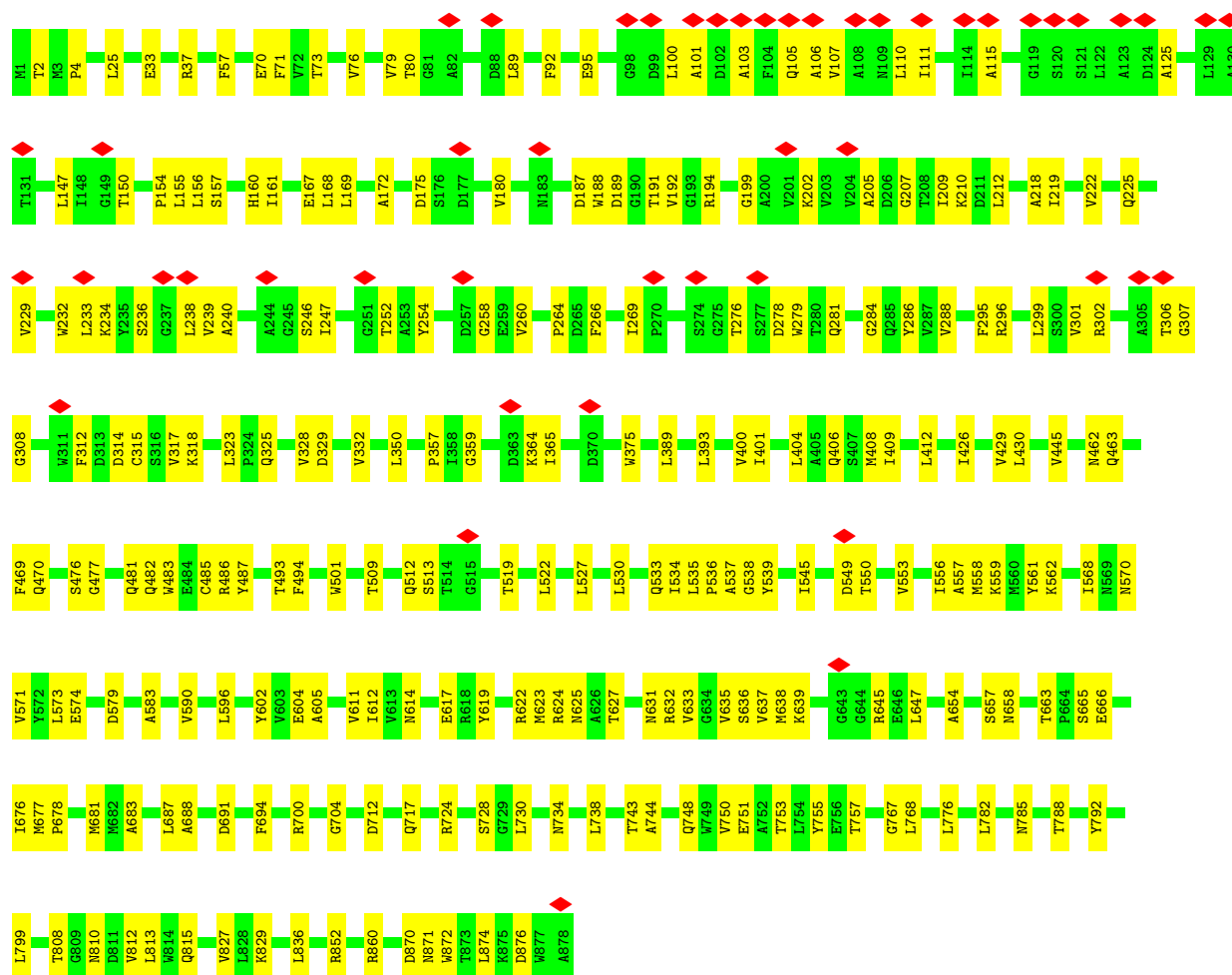


• Molecule 5: Baseplate Hub Protein (gp18)

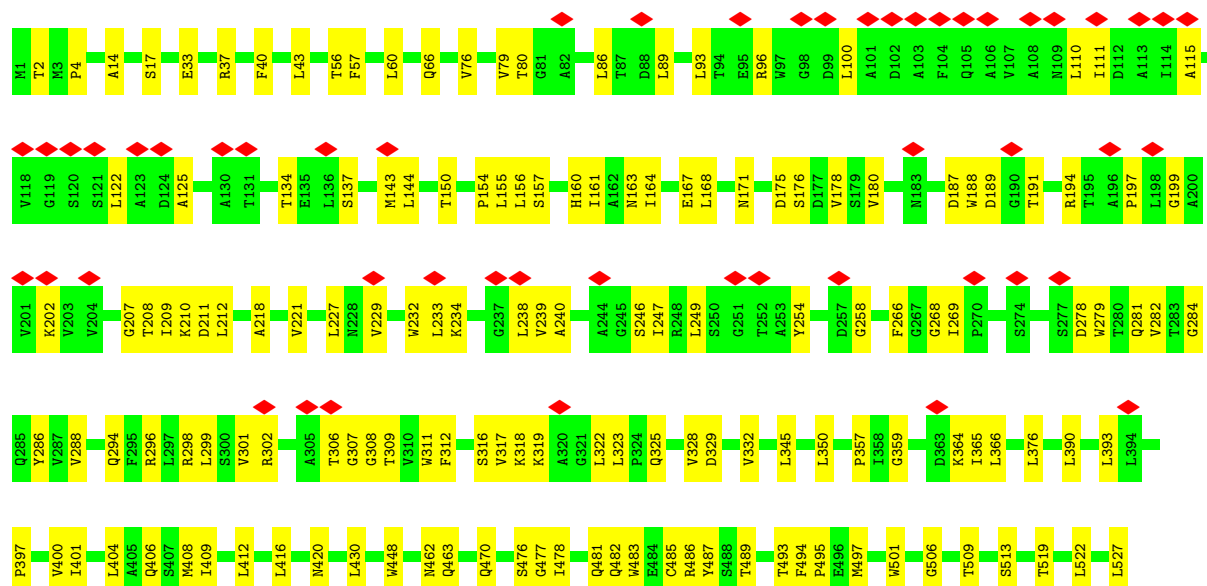
Chain u: 77% 23%

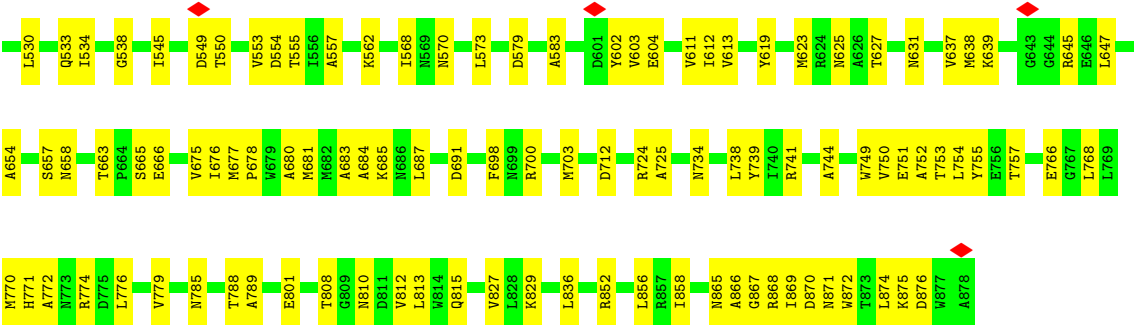






• Molecule 6: Central Fiber Protein (gp20)





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31169	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	430	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.805	Depositor
Minimum map value	0.000	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	636.6, 636.6, 636.6	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	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	M	0.15	0/2306	0.29	0/3159
1	N	0.15	0/2306	0.29	0/3159
1	O	0.15	0/2306	0.29	0/3159
1	P	0.14	0/2306	0.28	0/3159
1	Q	0.14	0/2306	0.28	0/3159
1	R	0.15	0/2306	0.29	0/3159
2	S	0.14	0/334	0.43	0/452
2	T	0.14	0/334	0.42	0/452
2	U	0.13	0/334	0.42	0/452
3	a	0.14	0/2439	0.30	0/3333
3	b	0.14	0/2439	0.28	0/3333
3	c	0.14	0/2439	0.28	0/3333
3	d	0.14	0/2439	0.28	0/3333
3	e	0.14	0/2439	0.29	0/3333
3	f	0.14	0/2439	0.29	0/3333
3	g	0.13	0/2439	0.28	0/3333
3	h	0.14	0/2439	0.29	0/3333
3	i	0.14	0/2439	0.29	0/3333
3	j	0.14	0/2439	0.28	0/3333
3	k	0.13	0/2439	0.28	0/3333
3	l	0.14	0/2439	0.28	0/3333
4	m	0.18	0/2418	0.29	0/3307
4	n	0.17	0/2418	0.31	0/3307
4	o	0.19	0/2418	0.31	0/3307
4	p	0.17	0/2418	0.31	0/3307
4	q	0.17	0/2418	0.30	0/3307
4	r	0.18	0/2418	0.30	0/3307
5	s	0.17	0/4700	0.30	0/6413
5	t	0.17	0/4700	0.30	0/6413
5	u	0.18	0/4700	0.31	0/6413
6	v	0.11	0/6665	0.27	0/9105
6	w	0.11	0/6665	0.27	0/9105
6	x	0.11	0/6665	0.26	0/9105
All	All	0.15	0/92709	0.29	0/126702

There are no bond length outliers.

There are no bond angle outliers.

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	M	2256	0	2233	45	0
1	N	2256	0	2233	48	0
1	O	2256	0	2233	44	0
1	P	2256	0	2233	40	0
1	Q	2256	0	2233	47	0
1	R	2256	0	2233	44	0
2	S	327	0	305	15	0
2	T	327	0	305	11	0
2	U	327	0	305	14	0
3	a	2372	0	2294	34	0
3	b	2372	0	2294	35	0
3	c	2372	0	2294	39	0
3	d	2372	0	2294	42	0
3	e	2372	0	2294	39	0
3	f	2372	0	2294	43	0
3	g	2372	0	2294	35	0
3	h	2372	0	2294	43	0
3	i	2372	0	2294	35	0
3	j	2372	0	2294	40	0
3	k	2372	0	2294	41	0
3	l	2372	0	2294	42	0
4	m	2343	0	2248	49	0
4	n	2343	0	2248	59	0
4	o	2343	0	2248	52	0
4	p	2343	0	2248	54	0
4	q	2343	0	2248	54	0
4	r	2343	0	2248	53	0
5	s	4582	0	4473	111	0
5	t	4582	0	4473	103	0
5	u	4582	0	4473	107	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	v	6536	0	6388	214	0
6	w	6536	0	6388	196	0
6	x	6536	0	6388	207	0
All	All	90393	0	87912	1692	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 9.

The worst 5 of 1692 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:w:207:GLY:HA2	6:w:306:THR:HA	1.54	0.89
6:x:189:ASP:O	6:x:199:GLY:HA2	1.75	0.86
4:p:12:ARG:HD2	4:p:92:ASP:HB2	1.58	0.86
6:w:205:ALA:O	6:w:307:GLY:HA2	1.77	0.84
6:w:189:ASP:O	6:w:199:GLY:HA2	1.78	0.84

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	297/300 (99%)	291 (98%)	6 (2%)	0	100	100
1	N	297/300 (99%)	290 (98%)	7 (2%)	0	100	100
1	O	297/300 (99%)	289 (97%)	8 (3%)	0	100	100
1	P	297/300 (99%)	290 (98%)	7 (2%)	0	100	100
1	Q	297/300 (99%)	290 (98%)	7 (2%)	0	100	100
1	R	297/300 (99%)	290 (98%)	7 (2%)	0	100	100
2	S	40/1699 (2%)	35 (88%)	5 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	T	40/1699 (2%)	35 (88%)	5 (12%)	0	100	100
2	U	40/1699 (2%)	35 (88%)	5 (12%)	0	100	100
3	a	309/311 (99%)	300 (97%)	9 (3%)	0	100	100
3	b	309/311 (99%)	304 (98%)	5 (2%)	0	100	100
3	c	309/311 (99%)	306 (99%)	3 (1%)	0	100	100
3	d	309/311 (99%)	303 (98%)	6 (2%)	0	100	100
3	e	309/311 (99%)	303 (98%)	6 (2%)	0	100	100
3	f	309/311 (99%)	306 (99%)	3 (1%)	0	100	100
3	g	309/311 (99%)	306 (99%)	3 (1%)	0	100	100
3	h	309/311 (99%)	304 (98%)	5 (2%)	0	100	100
3	i	309/311 (99%)	306 (99%)	3 (1%)	0	100	100
3	j	309/311 (99%)	306 (99%)	3 (1%)	0	100	100
3	k	309/311 (99%)	306 (99%)	3 (1%)	0	100	100
3	l	309/311 (99%)	302 (98%)	7 (2%)	0	100	100
4	m	288/295 (98%)	276 (96%)	12 (4%)	0	100	100
4	n	288/295 (98%)	280 (97%)	8 (3%)	0	100	100
4	o	288/295 (98%)	277 (96%)	11 (4%)	0	100	100
4	p	288/295 (98%)	276 (96%)	12 (4%)	0	100	100
4	q	288/295 (98%)	278 (96%)	10 (4%)	0	100	100
4	r	288/295 (98%)	276 (96%)	12 (4%)	0	100	100
5	s	584/587 (100%)	563 (96%)	21 (4%)	0	100	100
5	t	584/587 (100%)	564 (97%)	20 (3%)	0	100	100
5	u	584/587 (100%)	567 (97%)	17 (3%)	0	100	100
6	v	876/878 (100%)	844 (96%)	32 (4%)	0	100	100
6	w	876/878 (100%)	843 (96%)	33 (4%)	0	100	100
6	x	876/878 (100%)	837 (96%)	39 (4%)	0	100	100
All	All	11718/16794 (70%)	11378 (97%)	340 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	M	242/243 (100%)	242 (100%)	0	100	100
1	N	242/243 (100%)	242 (100%)	0	100	100
1	O	242/243 (100%)	242 (100%)	0	100	100
1	P	242/243 (100%)	242 (100%)	0	100	100
1	Q	242/243 (100%)	242 (100%)	0	100	100
1	R	242/243 (100%)	242 (100%)	0	100	100
2	S	33/1284 (3%)	33 (100%)	0	100	100
2	T	33/1284 (3%)	33 (100%)	0	100	100
2	U	33/1284 (3%)	33 (100%)	0	100	100
3	a	253/253 (100%)	253 (100%)	0	100	100
3	b	253/253 (100%)	253 (100%)	0	100	100
3	c	253/253 (100%)	253 (100%)	0	100	100
3	d	253/253 (100%)	253 (100%)	0	100	100
3	e	253/253 (100%)	253 (100%)	0	100	100
3	f	253/253 (100%)	253 (100%)	0	100	100
3	g	253/253 (100%)	253 (100%)	0	100	100
3	h	253/253 (100%)	253 (100%)	0	100	100
3	i	253/253 (100%)	253 (100%)	0	100	100
3	j	253/253 (100%)	253 (100%)	0	100	100
3	k	253/253 (100%)	253 (100%)	0	100	100
3	l	253/253 (100%)	253 (100%)	0	100	100
4	m	254/258 (98%)	254 (100%)	0	100	100
4	n	254/258 (98%)	254 (100%)	0	100	100
4	o	254/258 (98%)	254 (100%)	0	100	100
4	p	254/258 (98%)	254 (100%)	0	100	100
4	q	254/258 (98%)	254 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	r	254/258 (98%)	254 (100%)	0	100	100
5	s	487/488 (100%)	487 (100%)	0	100	100
5	t	487/488 (100%)	487 (100%)	0	100	100
5	u	487/488 (100%)	487 (100%)	0	100	100
6	v	691/691 (100%)	691 (100%)	0	100	100
6	w	691/691 (100%)	691 (100%)	0	100	100
6	x	691/691 (100%)	691 (100%)	0	100	100
All	All	9645/13431 (72%)	9645 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
4	o	36	GLN
6	v	21	ASN
4	p	26	GLN
4	r	236	ASN
6	v	470	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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.

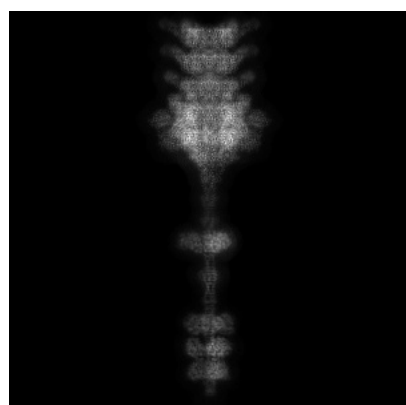
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60005. These allow visual inspection of the internal detail of the map and identification of artifacts.

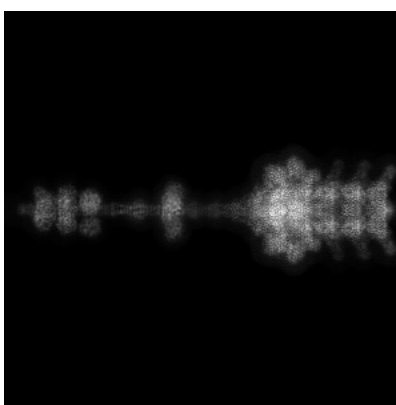
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

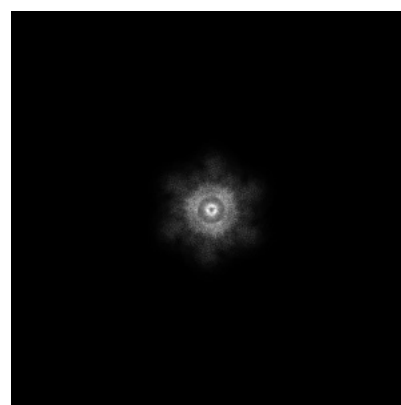
6.1.1 Primary map



X



Y

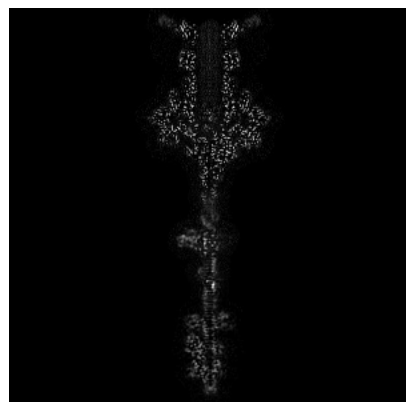


Z

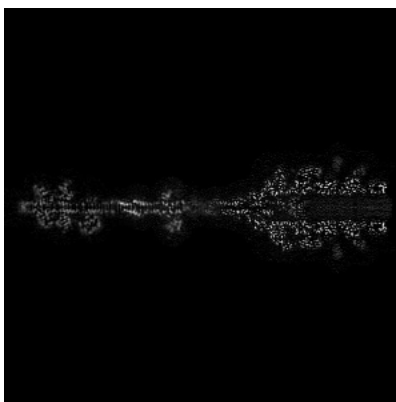
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

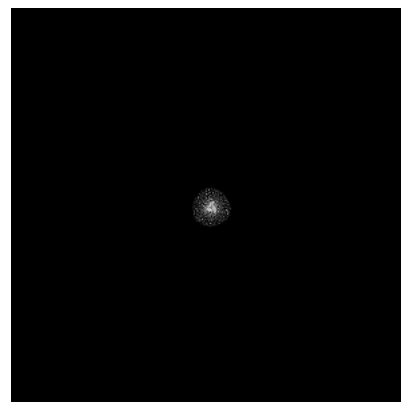
6.2.1 Primary map



X Index: 300



Y Index: 300

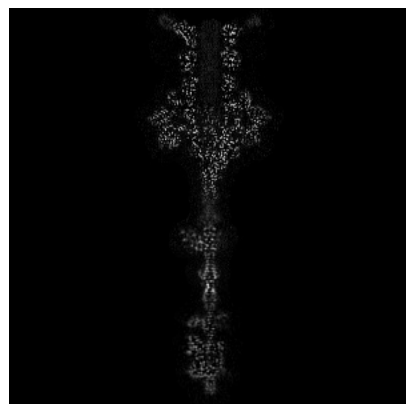


Z Index: 300

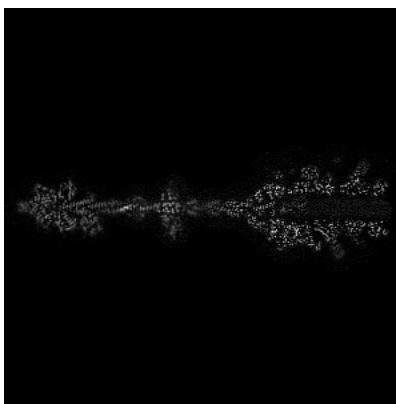
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

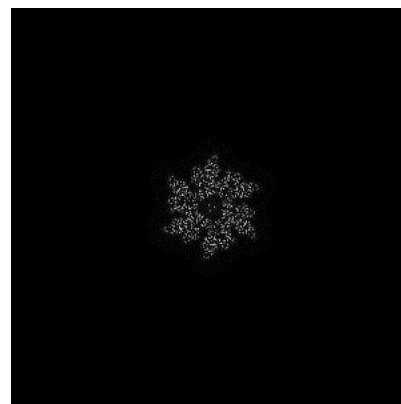
6.3.1 Primary map



X Index: 297



Y Index: 305

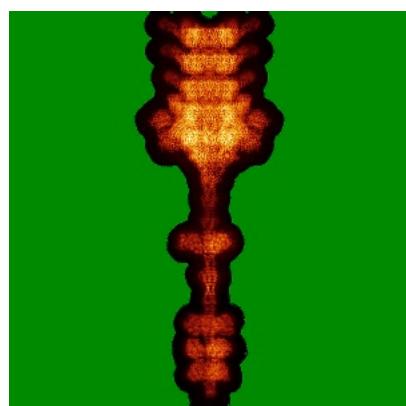


Z Index: 417

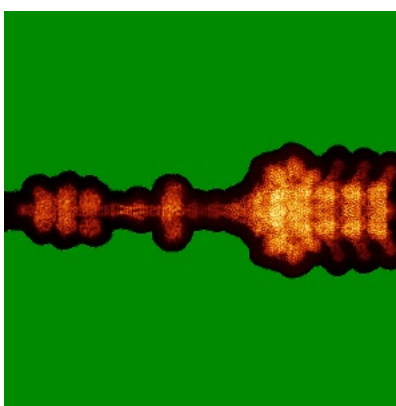
The images above show the largest variance slices of the map in three orthogonal directions.

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

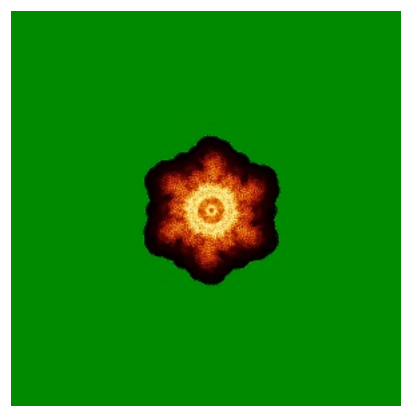
6.4.1 Primary map



X



Y

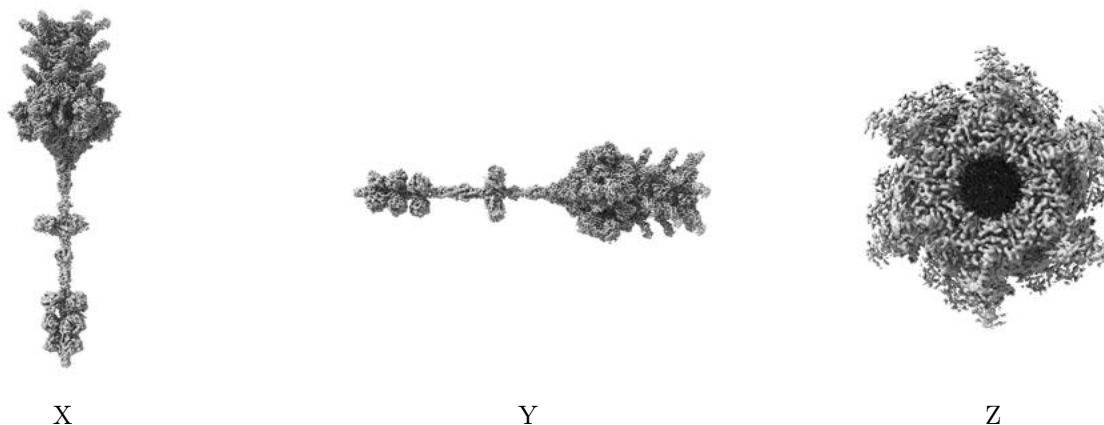


Z

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

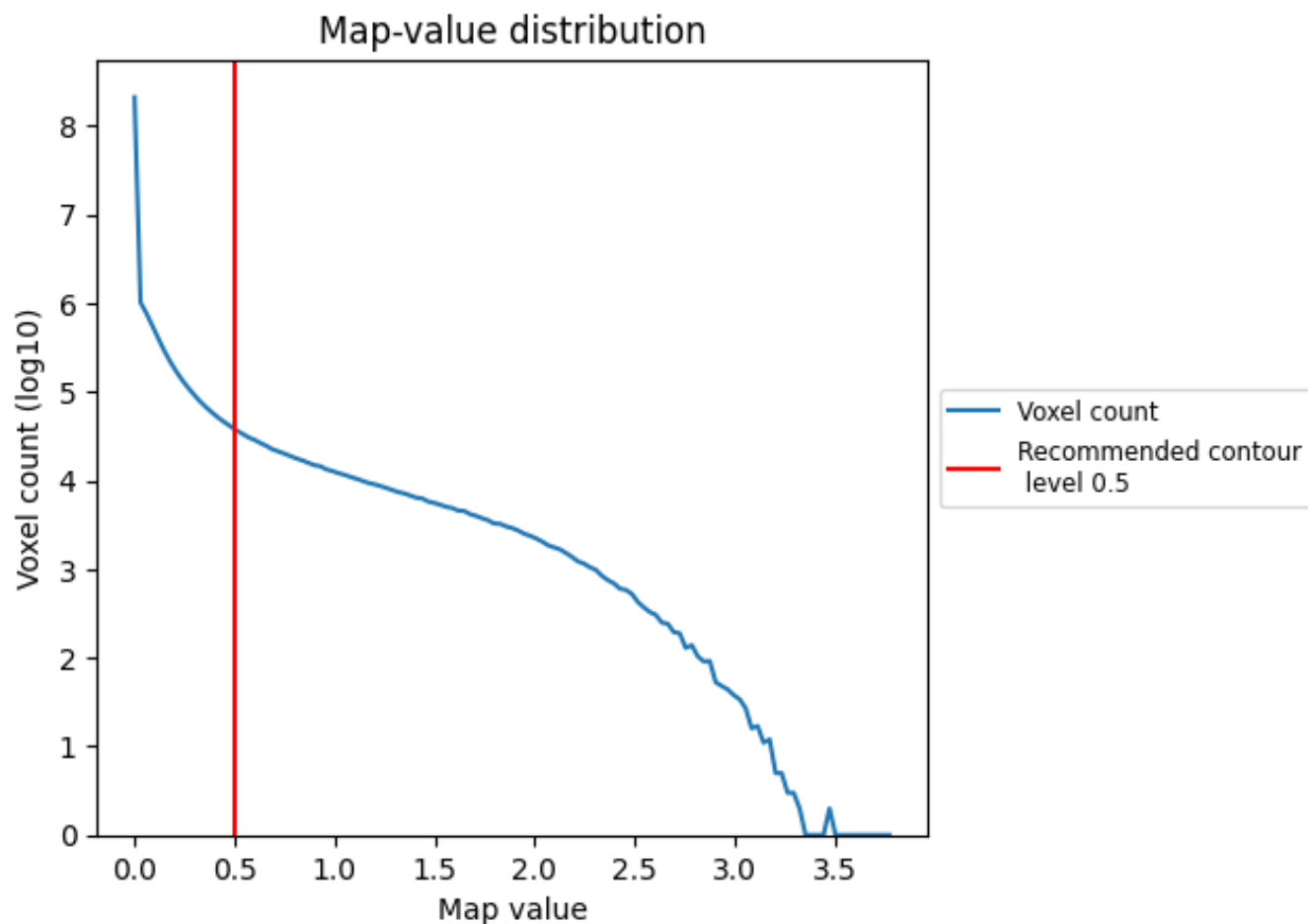
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

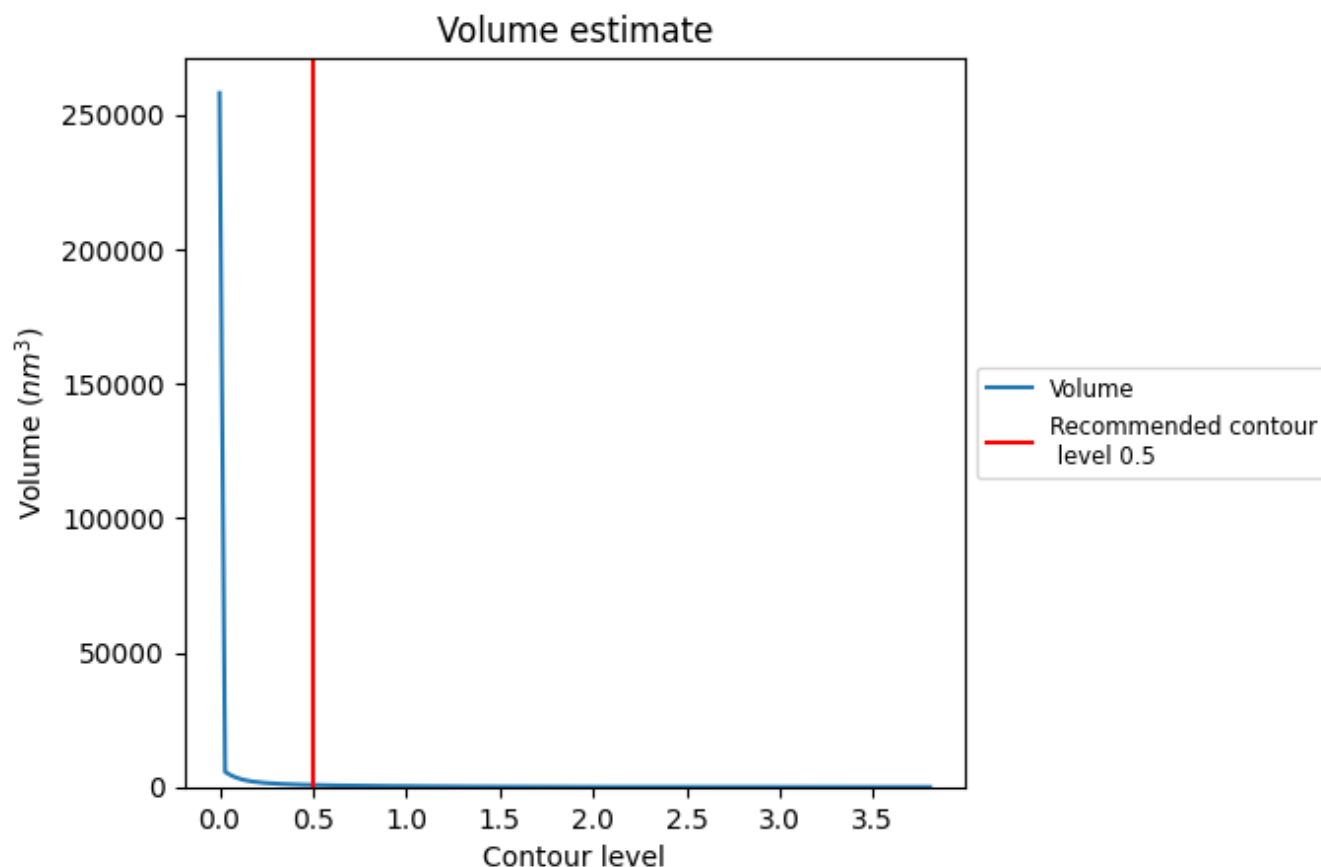
This section contains the results of statistical analysis of the map.

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.

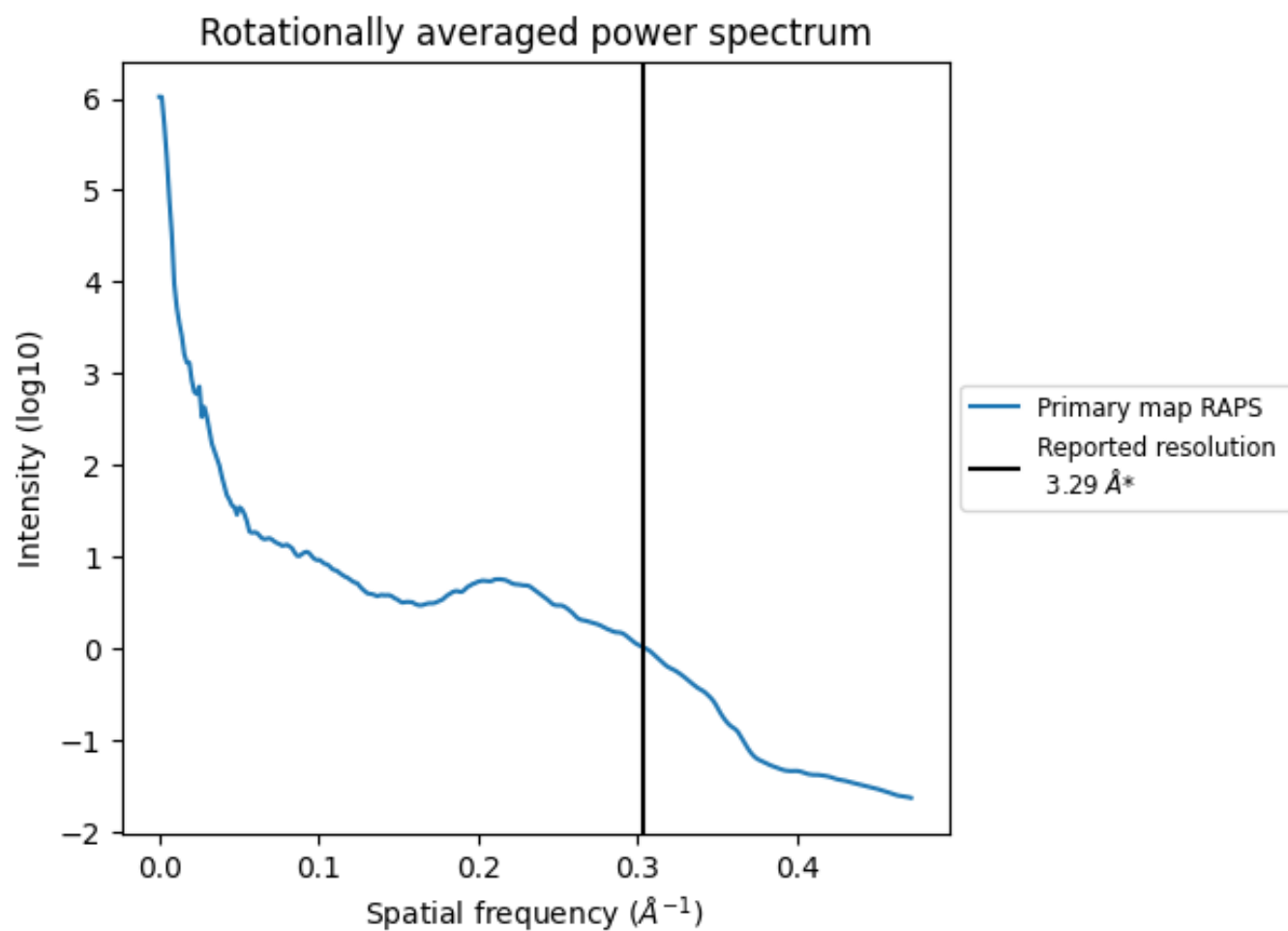
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 730 nm^3 ; this corresponds to an approximate mass of 659 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.304 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

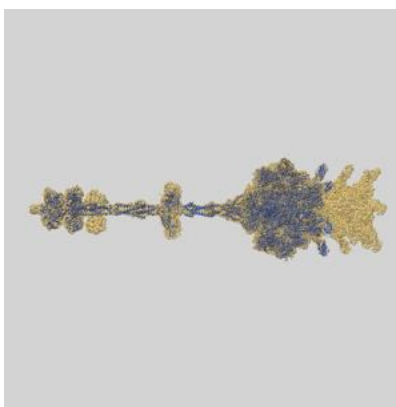
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60005 and PDB model 8ZDQ. Per-residue inclusion information can be found in section [3](#) on page [8](#).

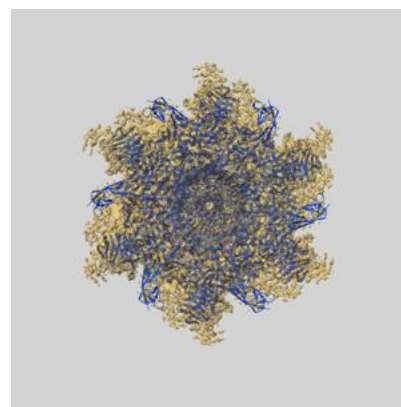
9.1 Map-model overlay [i](#)



X



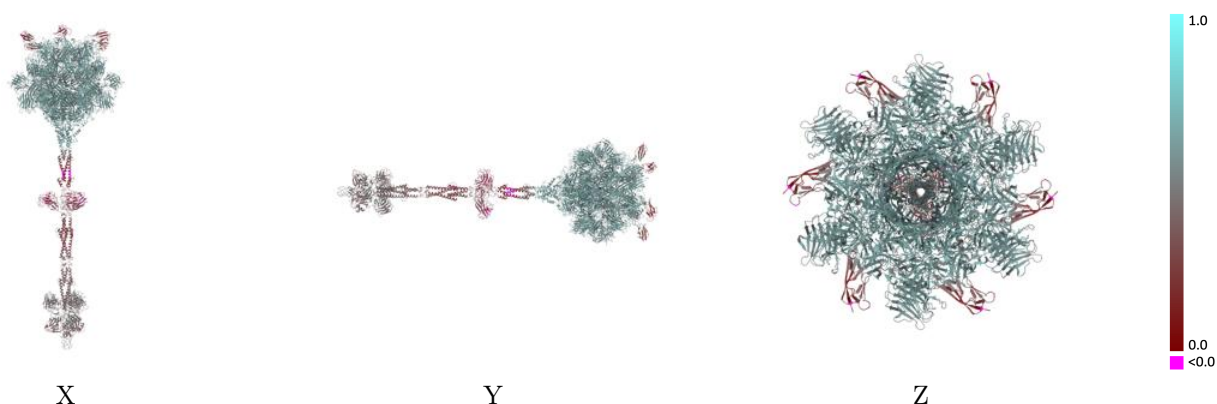
Y



Z

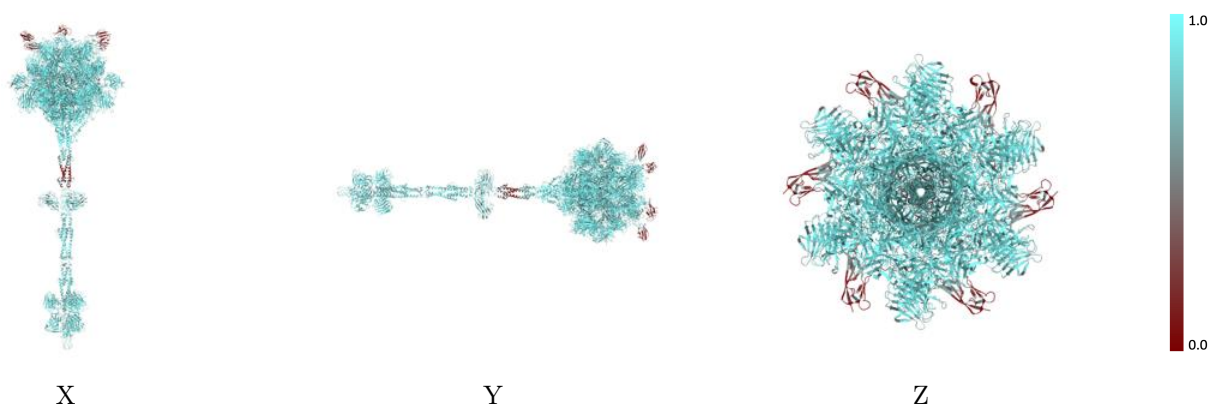
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



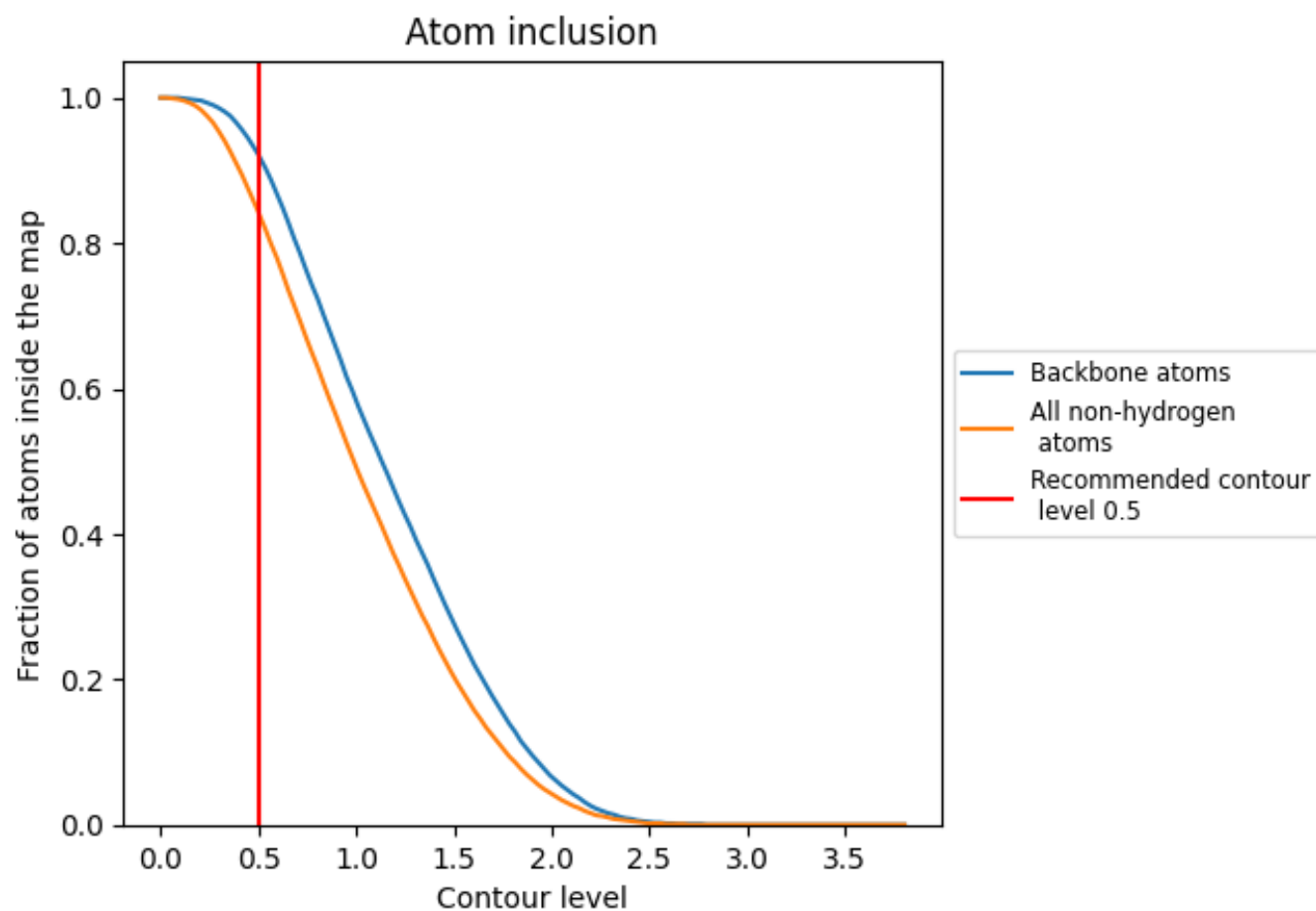
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 84% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8430	 0.5440
M	 0.7530	 0.5390
N	 0.7550	 0.5390
O	 0.7520	 0.5370
P	 0.7510	 0.5370
Q	 0.7560	 0.5370
R	 0.7490	 0.5390
S	 0.7040	 0.4970
T	 0.7110	 0.5100
U	 0.7040	 0.5030
a	 0.8230	 0.5720
b	 0.8720	 0.5920
c	 0.8520	 0.5860
d	 0.8960	 0.6050
e	 0.8240	 0.5710
f	 0.8760	 0.5930
g	 0.8580	 0.5890
h	 0.8950	 0.6050
i	 0.8290	 0.5700
j	 0.8770	 0.5940
k	 0.8520	 0.5860
l	 0.8920	 0.6020
m	 0.9320	 0.6220
n	 0.9320	 0.6200
o	 0.9320	 0.6190
p	 0.9320	 0.6180
q	 0.9350	 0.6250
r	 0.9310	 0.6210
s	 0.9230	 0.6210
t	 0.9230	 0.6200
u	 0.9220	 0.6200
v	 0.7660	 0.3770
w	 0.7660	 0.3790
x	 0.7640	 0.3770

