wwPDB EM Validation Summary Report (i)

Nov 19, 2022 – 09:20 AM EST

PDB ID	:	2FL8
EMDB ID	:	EMD-1048
Title	:	Fitting of the gp10 trimer structure into the cryoEM map of the bacteriophage T4 baseplate in the hexagonal conformation.
Authors	:	Leiman, P.G.; Shneider, M.M.; Mesyanzhinov, V.V.; Rossmann, M.G.
Deposited on	:	2006-01-05
Resolution	:	12.00 Å(reported)
Based on initial models	:	1S2E, 2FKK

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 (i) symbol.

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

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

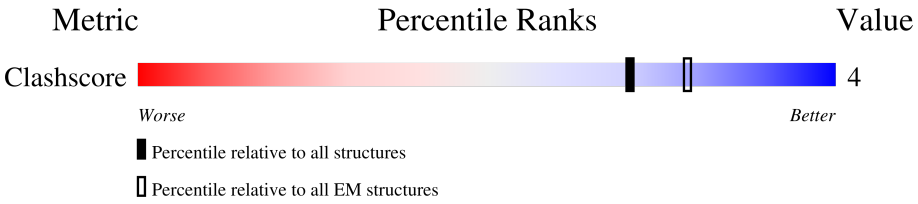
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 12.00 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	158937	4297

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	602	5% 57% 43%
1	B	602	5% 57% 43%
1	C	602	6% 57% 43%
1	D	602	6% 57% 43%
1	E	602	5% 56% 43%
1	F	602	6% 56% 43%
1	G	602	6% 57% 43%
1	H	602	5% 57% 43%
1	I	602	6% 57% 43%
1	J	602	5% 57% 43%

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Mol	Chain	Length	Quality of chain
1	K	602	5% 57% 43%
1	L	602	6% 57% 43%
1	M	602	6% 57% 43%
1	N	602	5% 56% 43%
1	O	602	6% 57% 43%
1	P	602	6% 57% 43%
1	Q	602	5% 57% 43%
1	R	602	6% 56% 43%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 6192 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 Baseplate structural protein Gp10.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	344	Total C 344 344	0	344
1	B	344	Total C 344 344	0	344
1	C	344	Total C 344 344	0	344
1	D	344	Total C 344 344	0	344
1	E	344	Total C 344 344	0	344
1	F	344	Total C 344 344	0	344
1	G	344	Total C 344 344	0	344
1	H	344	Total C 344 344	0	344
1	I	344	Total C 344 344	0	344
1	J	344	Total C 344 344	0	344
1	K	344	Total C 344 344	0	344
1	L	344	Total C 344 344	0	344
1	M	344	Total C 344 344	0	344
1	N	344	Total C 344 344	0	344
1	O	344	Total C 344 344	0	344
1	P	344	Total C 344 344	0	344
1	Q	344	Total C 344 344	0	344

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Mol	Chain	Residues	Atoms		AltConf	Trace
1	R	344	Total 344	C 344	0	344

There are 36 discrepancies between the modelled and reference sequences:

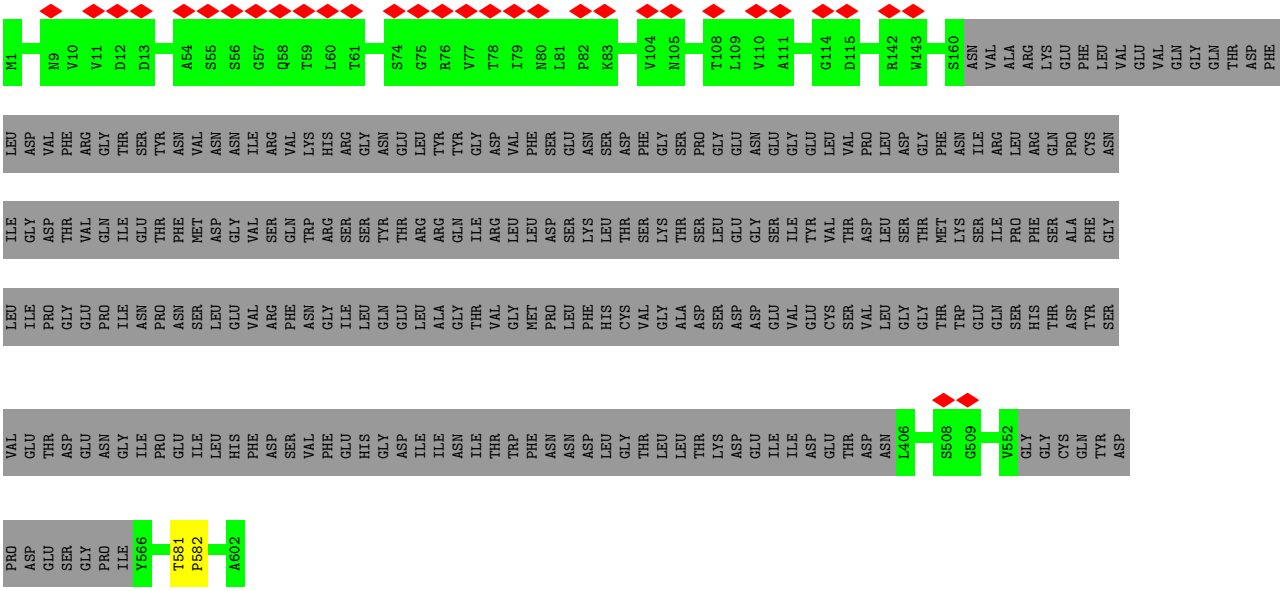
Chain	Residue	Modelled	Actual	Comment	Reference
A	442	GLU	ALA	engineered mutation	UNP P10928
A	530	THR	ALA	engineered mutation	UNP P10928
B	442	GLU	ALA	engineered mutation	UNP P10928
B	530	THR	ALA	engineered mutation	UNP P10928
C	442	GLU	ALA	engineered mutation	UNP P10928
C	530	THR	ALA	engineered mutation	UNP P10928
D	442	GLU	ALA	engineered mutation	UNP P10928
D	530	THR	ALA	engineered mutation	UNP P10928
E	442	GLU	ALA	engineered mutation	UNP P10928
E	530	THR	ALA	engineered mutation	UNP P10928
F	442	GLU	ALA	engineered mutation	UNP P10928
F	530	THR	ALA	engineered mutation	UNP P10928
G	442	GLU	ALA	engineered mutation	UNP P10928
G	530	THR	ALA	engineered mutation	UNP P10928
H	442	GLU	ALA	engineered mutation	UNP P10928
H	530	THR	ALA	engineered mutation	UNP P10928
I	442	GLU	ALA	engineered mutation	UNP P10928
I	530	THR	ALA	engineered mutation	UNP P10928
J	442	GLU	ALA	engineered mutation	UNP P10928
J	530	THR	ALA	engineered mutation	UNP P10928
K	442	GLU	ALA	engineered mutation	UNP P10928
K	530	THR	ALA	engineered mutation	UNP P10928
L	442	GLU	ALA	engineered mutation	UNP P10928
L	530	THR	ALA	engineered mutation	UNP P10928
M	442	GLU	ALA	engineered mutation	UNP P10928
M	530	THR	ALA	engineered mutation	UNP P10928
N	442	GLU	ALA	engineered mutation	UNP P10928
N	530	THR	ALA	engineered mutation	UNP P10928
O	442	GLU	ALA	engineered mutation	UNP P10928
O	530	THR	ALA	engineered mutation	UNP P10928
P	442	GLU	ALA	engineered mutation	UNP P10928
P	530	THR	ALA	engineered mutation	UNP P10928
Q	442	GLU	ALA	engineered mutation	UNP P10928
Q	530	THR	ALA	engineered mutation	UNP P10928
R	442	GLU	ALA	engineered mutation	UNP P10928
R	530	THR	ALA	engineered mutation	UNP P10928

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.

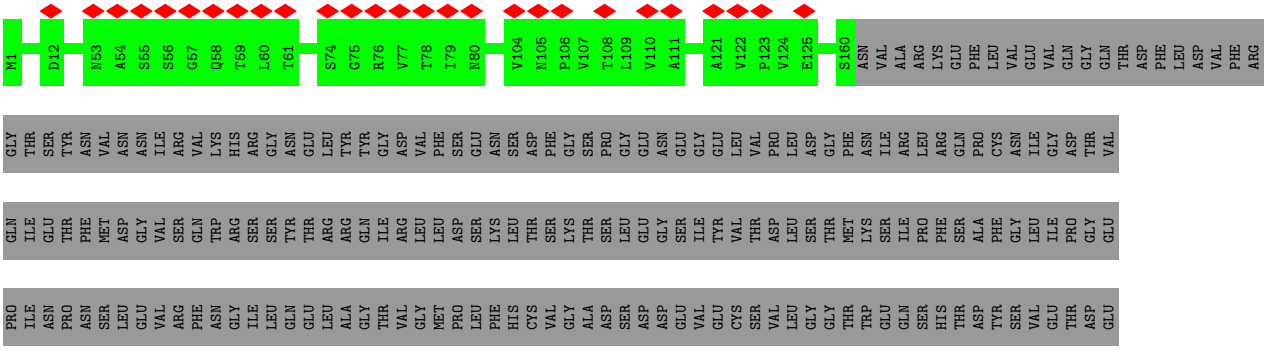
• Molecule 1: Baseplate structural protein Gp10

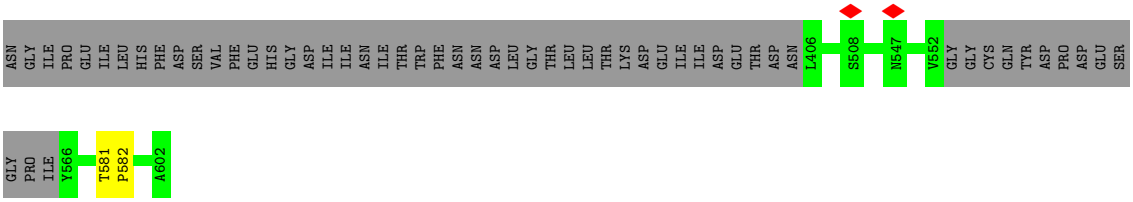
Chain A:



• Molecule 1: Baseplate structural protein Gp10

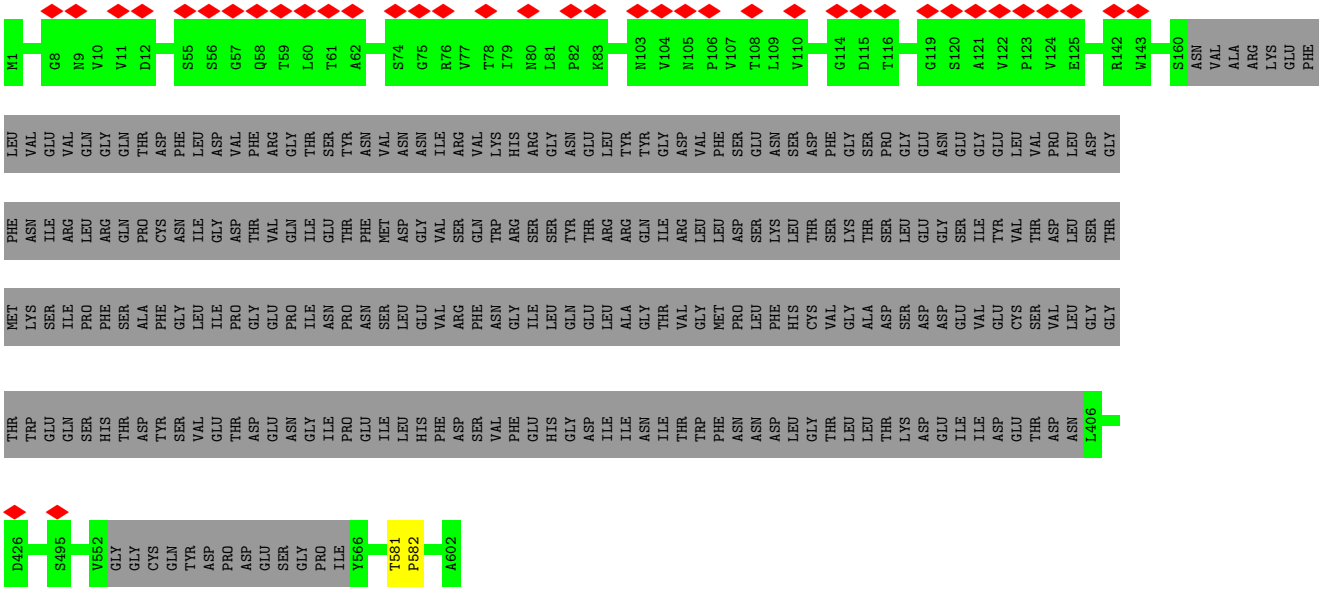
Chain B:





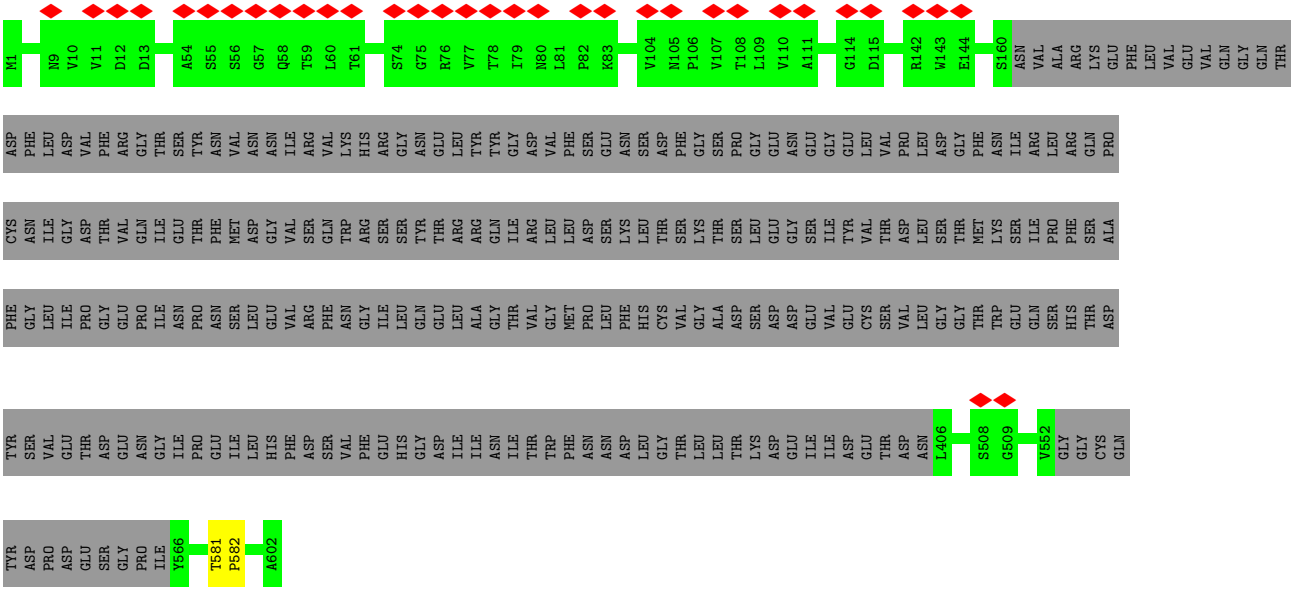
• Molecule 1: Baseplate structural protein Gp10

Chain C:



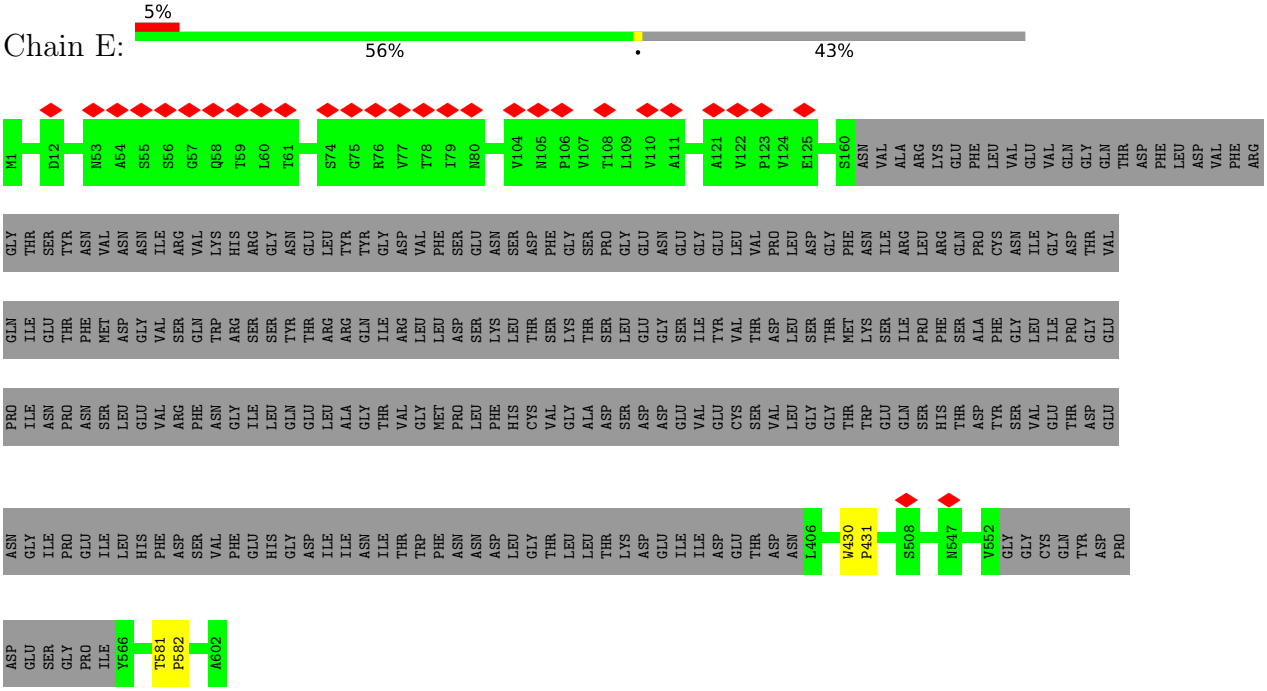
• Molecule 1: Baseplate structural protein Gp10

Chain D:



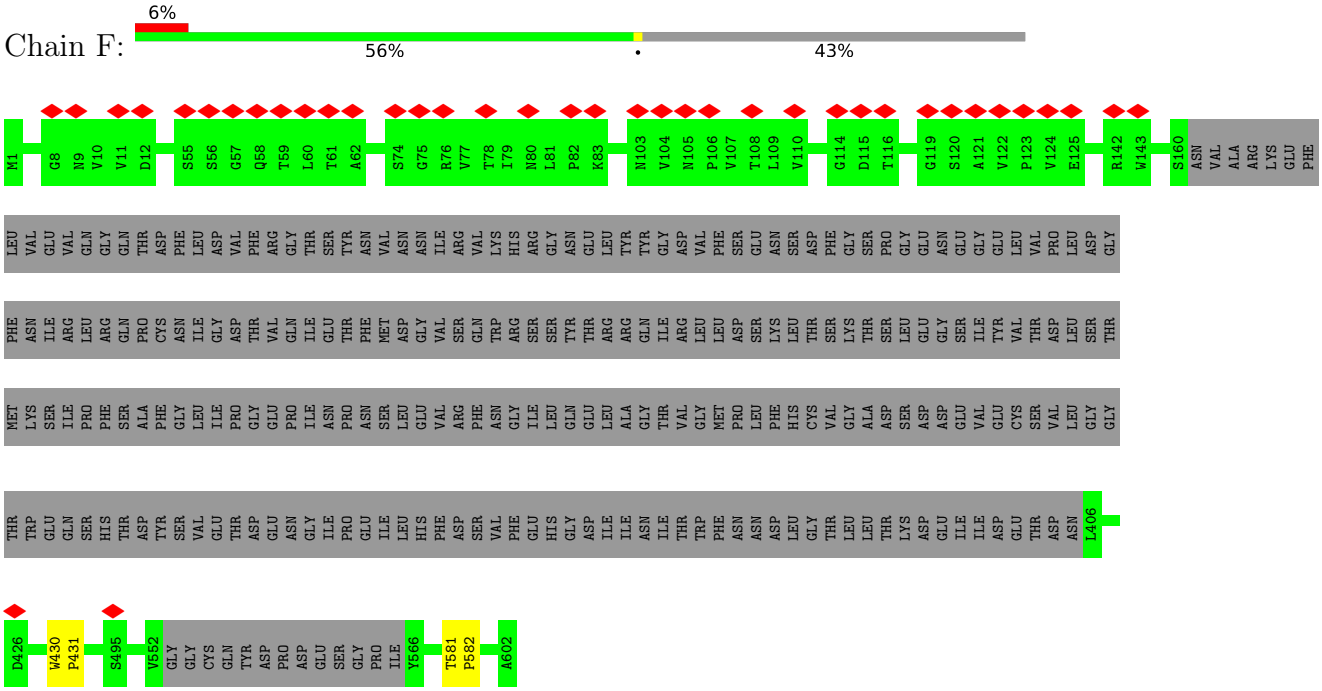
• Molecule 1: Baseplate structural protein Gp10

Chain E:



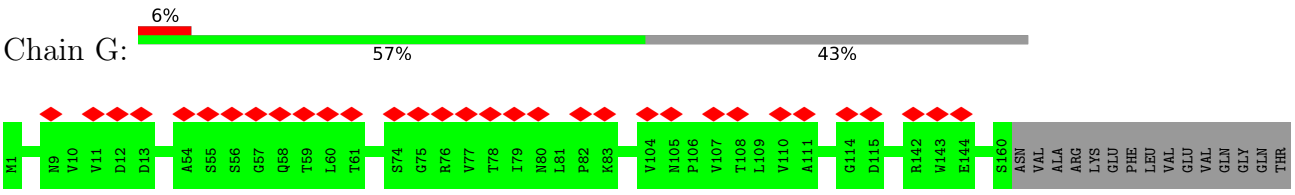
• Molecule 1: Baseplate structural protein Gp10

Chain F:



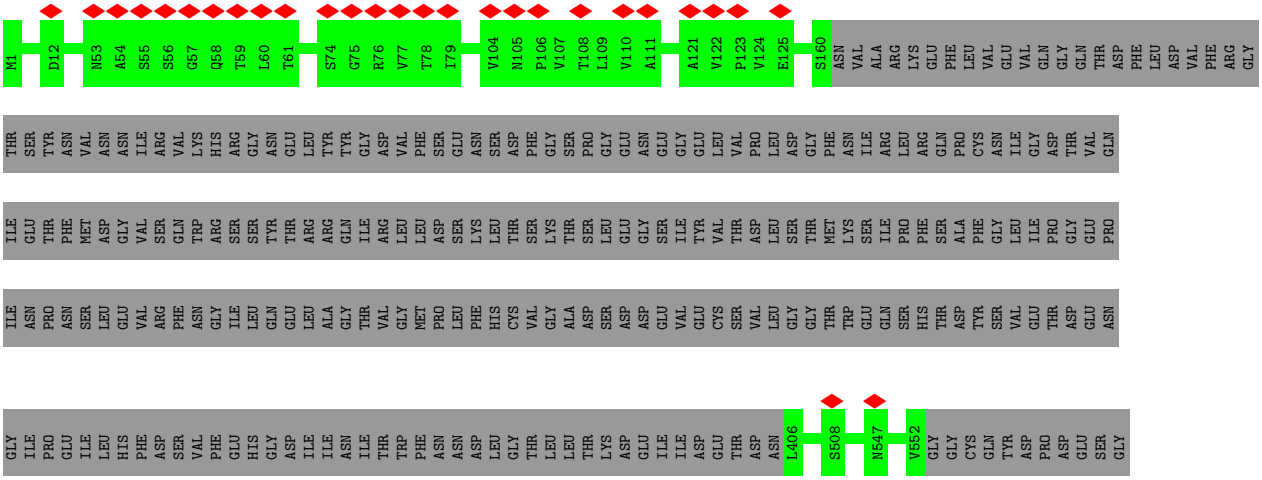
• Molecule 1: Baseplate structural protein Gp10

Chain G:



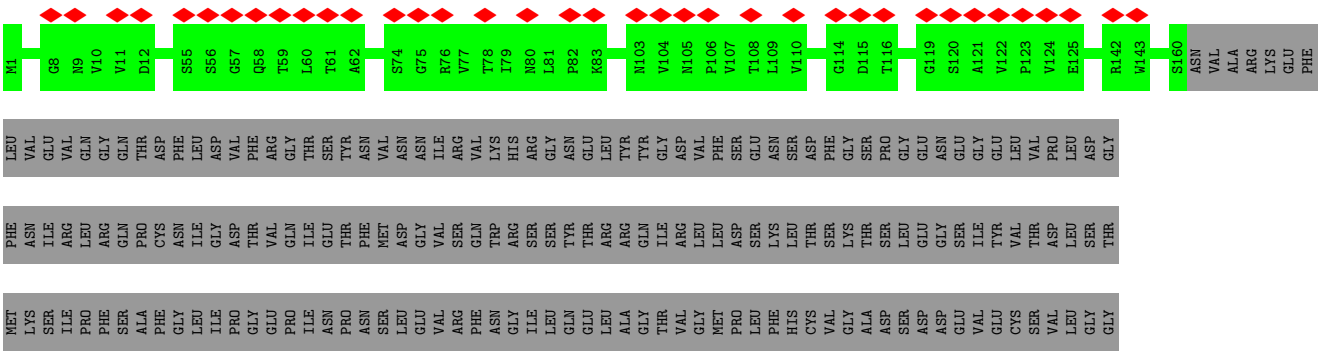
• Molecule 1: Baseplate structural protein Gp10

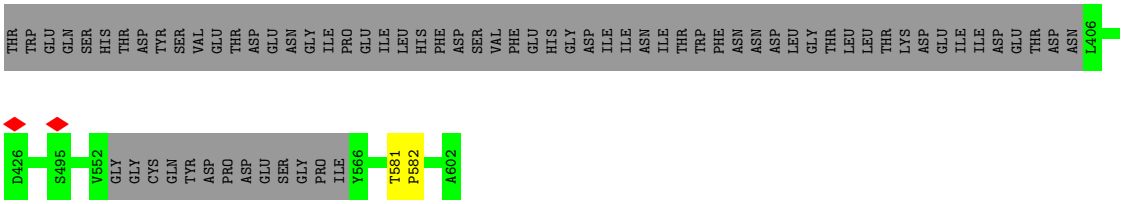
Chain H:



• Molecule 1: Baseplate structural protein Gp10

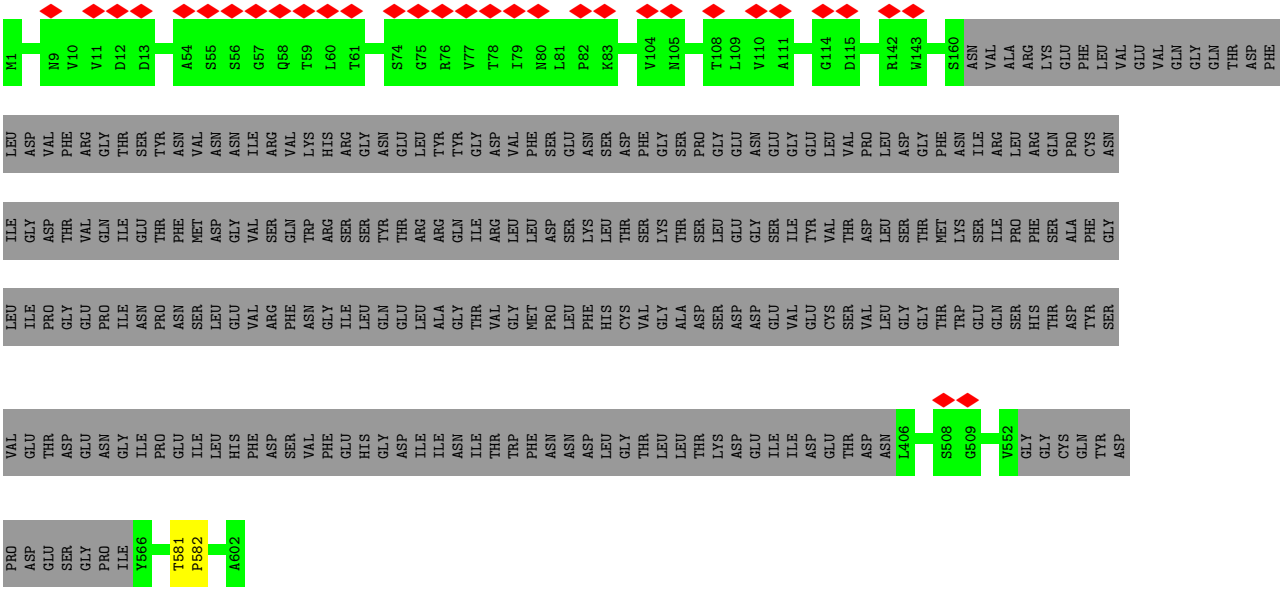
Chain I:





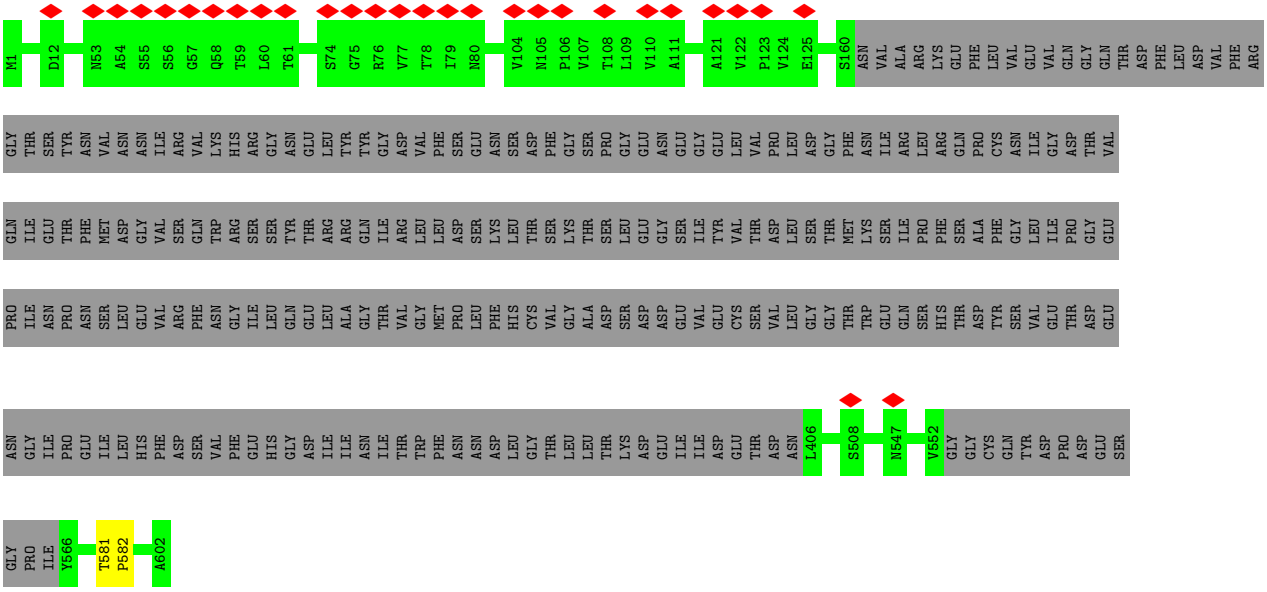
• Molecule 1: Baseplate structural protein Gp10

Chain J:



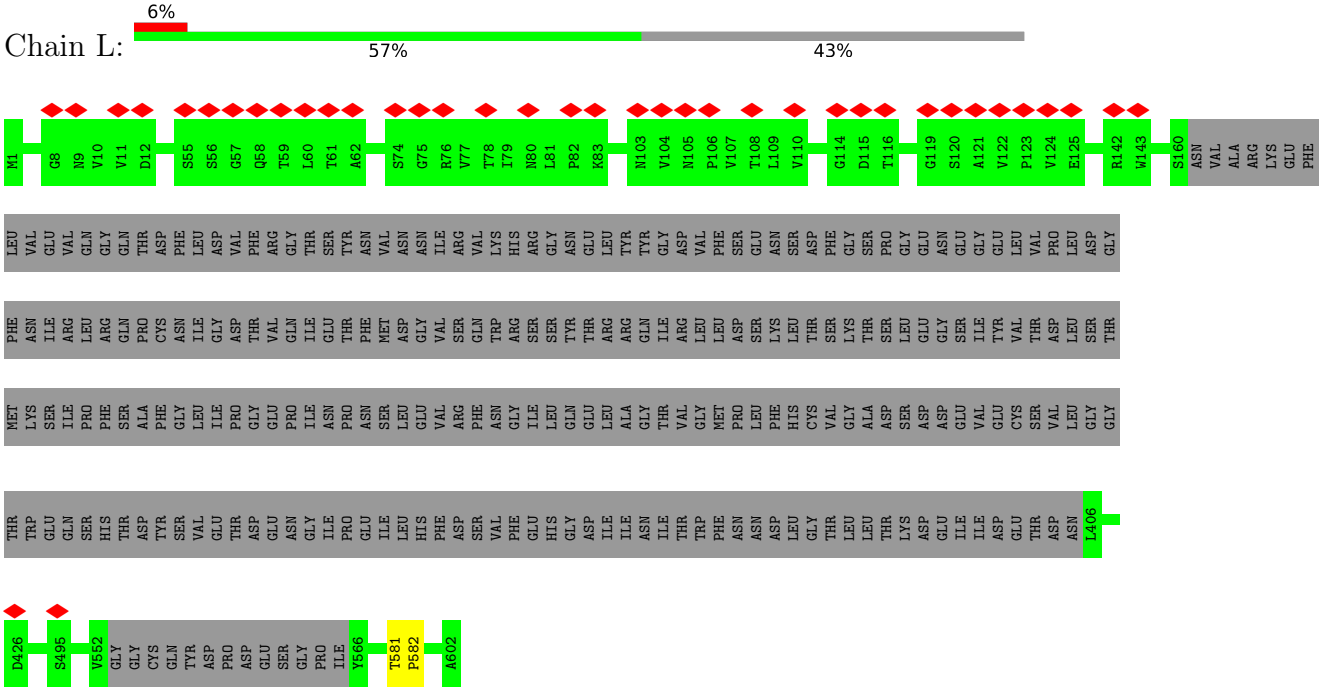
• Molecule 1: Baseplate structural protein Gp10

Chain K:



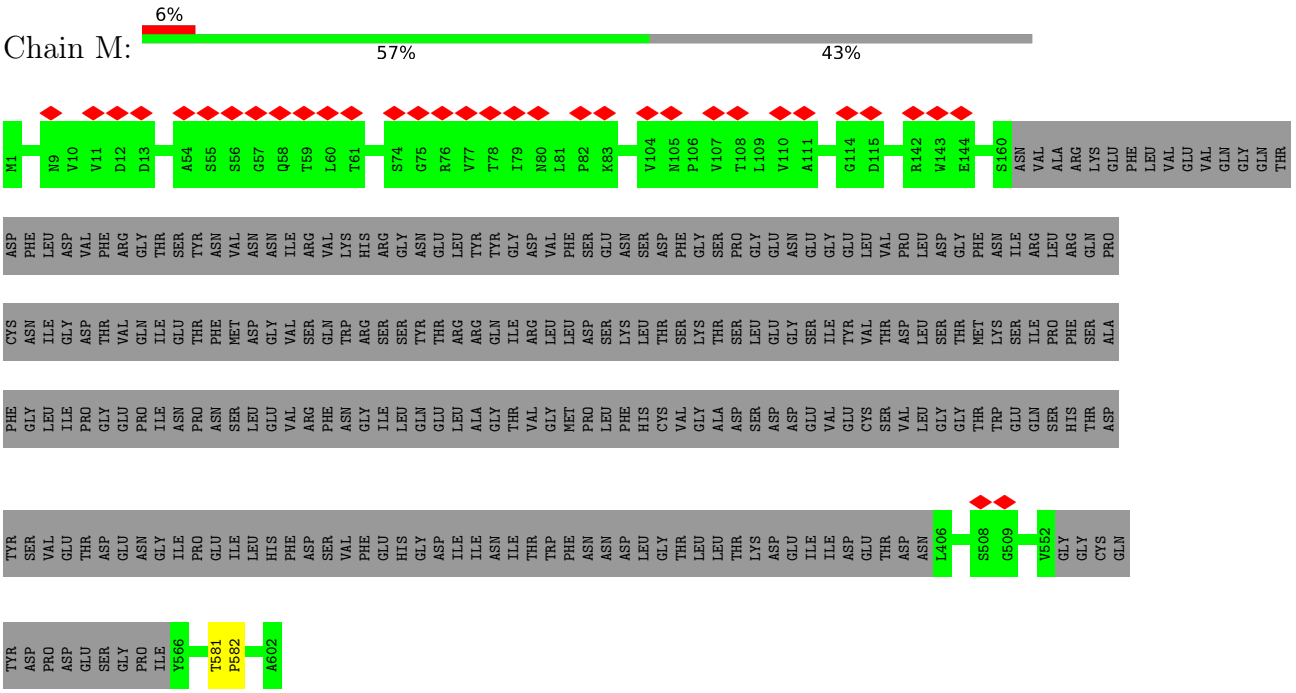
• Molecule 1: Baseplate structural protein Gp10

Chain L:



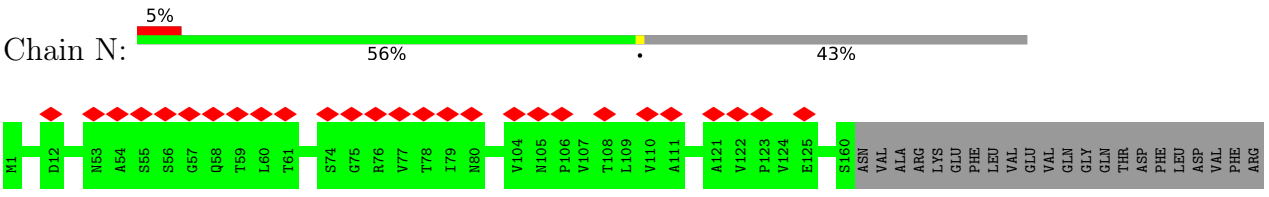
• Molecule 1: Baseplate structural protein Gp10

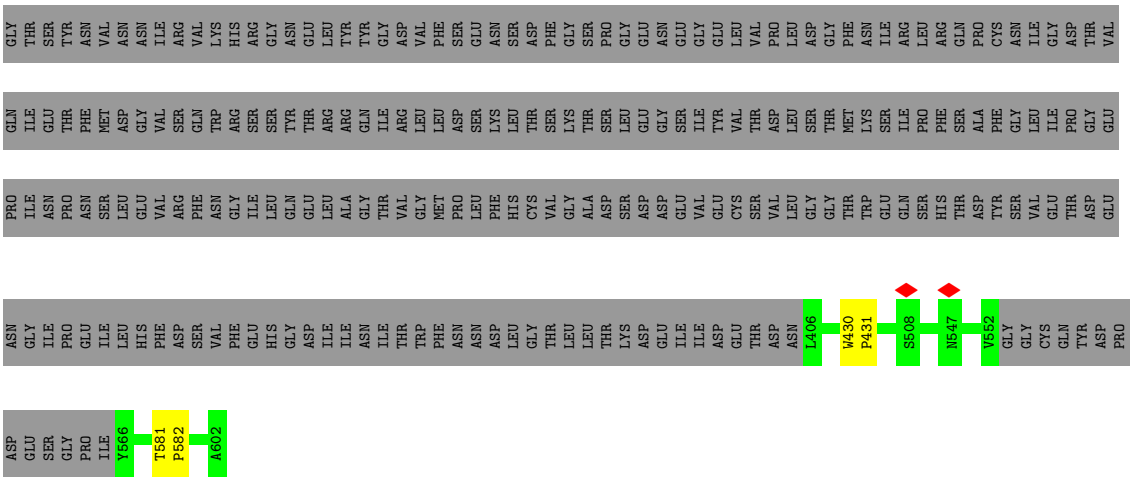
Chain M:



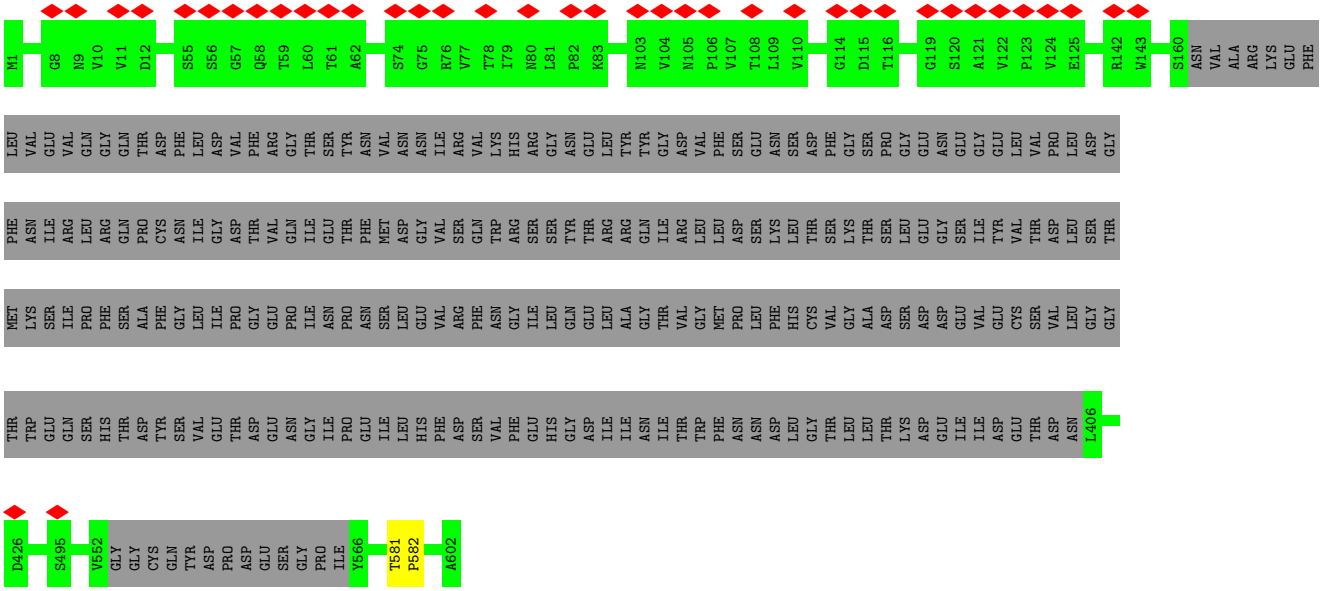
• Molecule 1: Baseplate structural protein Gp10

Chain N:

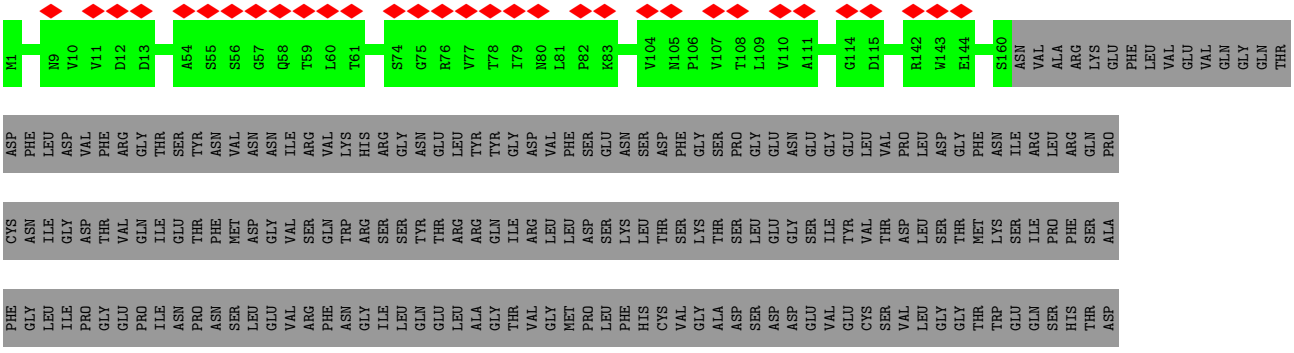


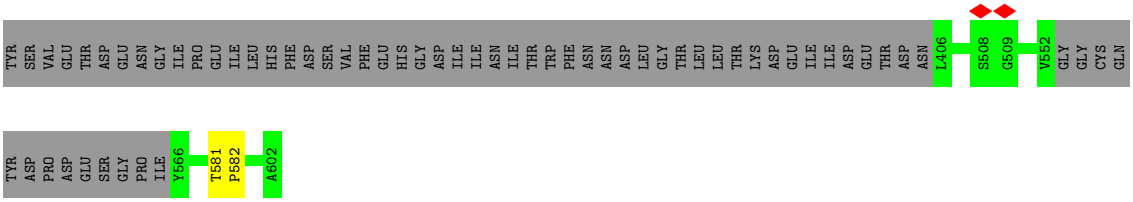


• Molecule 1: Baseplate structural protein Gp10



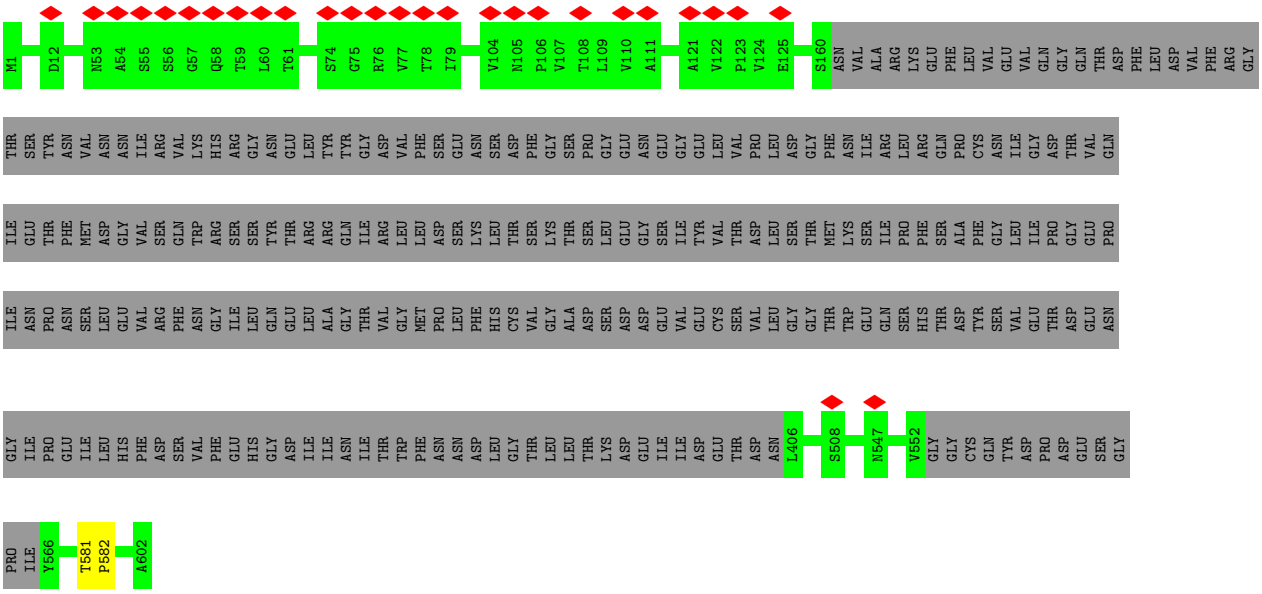
• Molecule 1: Baseplate structural protein Gp10





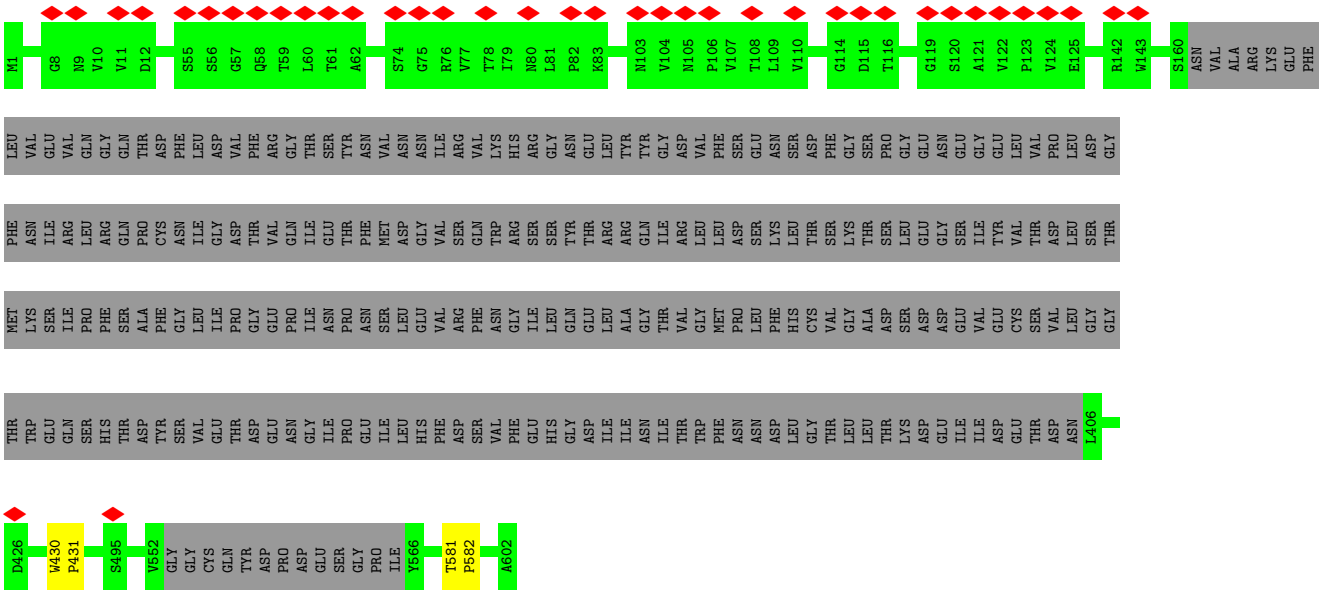
• Molecule 1: Baseplate structural protein Gp10

Chain Q:



• Molecule 1: Baseplate structural protein Gp10

Chain R:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	945	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	45000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	10.345	Depositor
Minimum map value	-7.648	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.45	Depositor
Map size (Å)	583.8291, 583.8291, 583.8291	wwPDB
Map dimensions	196, 196, 196	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.97872, 2.97872, 2.97872	Depositor

5 Model quality

5.1 Standard geometry

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	A	344	0	0	1	0
1	B	344	0	0	1	0
1	C	344	0	0	1	0
1	D	344	0	0	1	0
1	E	344	0	0	2	0
1	F	344	0	0	2	0
1	G	344	0	0	1	0
1	H	344	0	0	1	0
1	I	344	0	0	1	0
1	J	344	0	0	1	0
1	K	344	0	0	1	0
1	L	344	0	0	1	0
1	M	344	0	0	1	0
1	N	344	0	0	2	0
1	O	344	0	0	1	0
1	P	344	0	0	1	0
1	Q	344	0	0	1	0
1	R	344	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6192	0	0	22	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 4.

The worst 5 of 22 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)
1:D:581:THR:CA	1:D:582:PRO:CA	2.91	0.49
1:C:581:THR:CA	1:C:582:PRO:CA	2.91	0.48
1:E:581:THR:CA	1:E:582:PRO:CA	2.91	0.48
1:B:581:THR:CA	1:B:582:PRO:CA	2.91	0.48
1:R:581:THR:CA	1:R:582:PRO:CA	2.91	0.48

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains

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

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

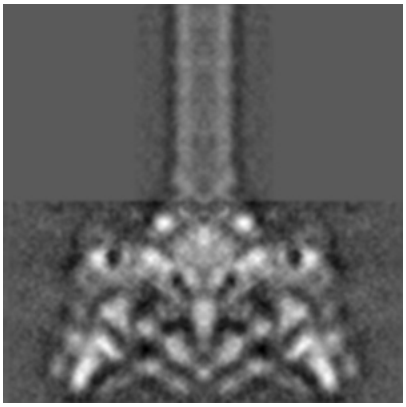
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-1048. These allow visual inspection of the internal detail of the map and identification of artifacts.

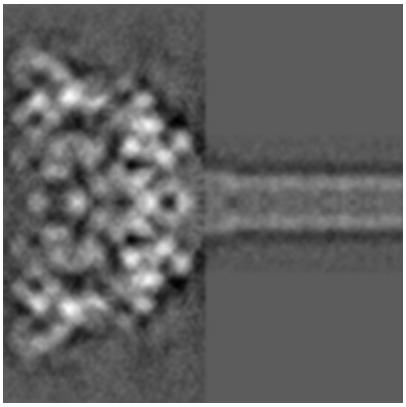
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

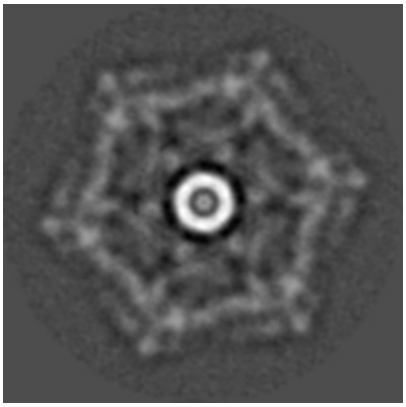
6.1.1 Primary map



X



Y

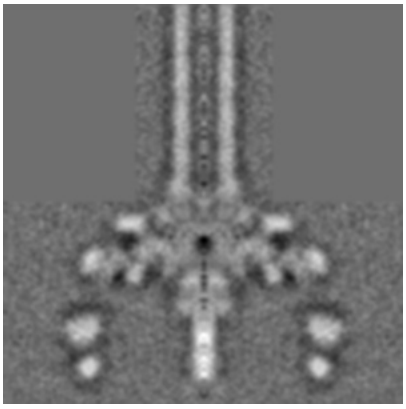


Z

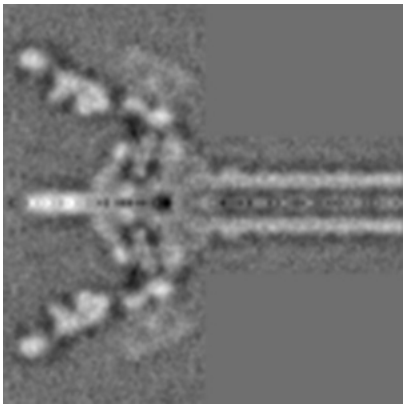
The images above show the map projected in three orthogonal directions.

6.2 Central slices

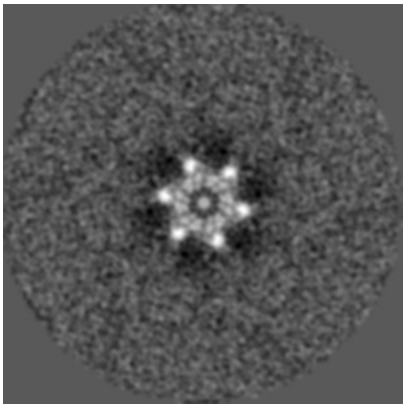
6.2.1 Primary map



X Index: 98



Y Index: 98

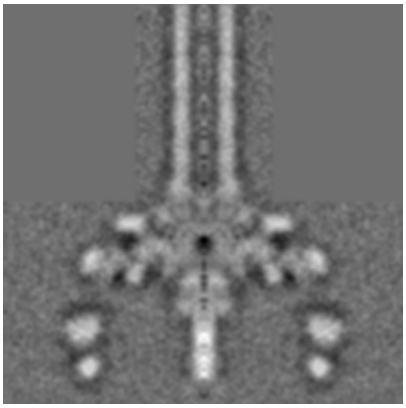


Z Index: 98

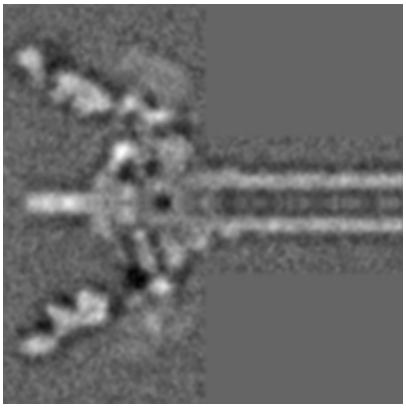
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

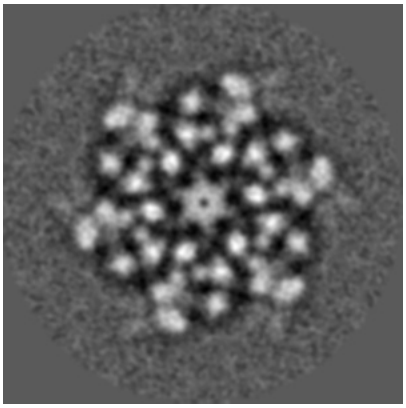
6.3.1 Primary map



X Index: 98



Y Index: 100



Z Index: 60

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 1.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

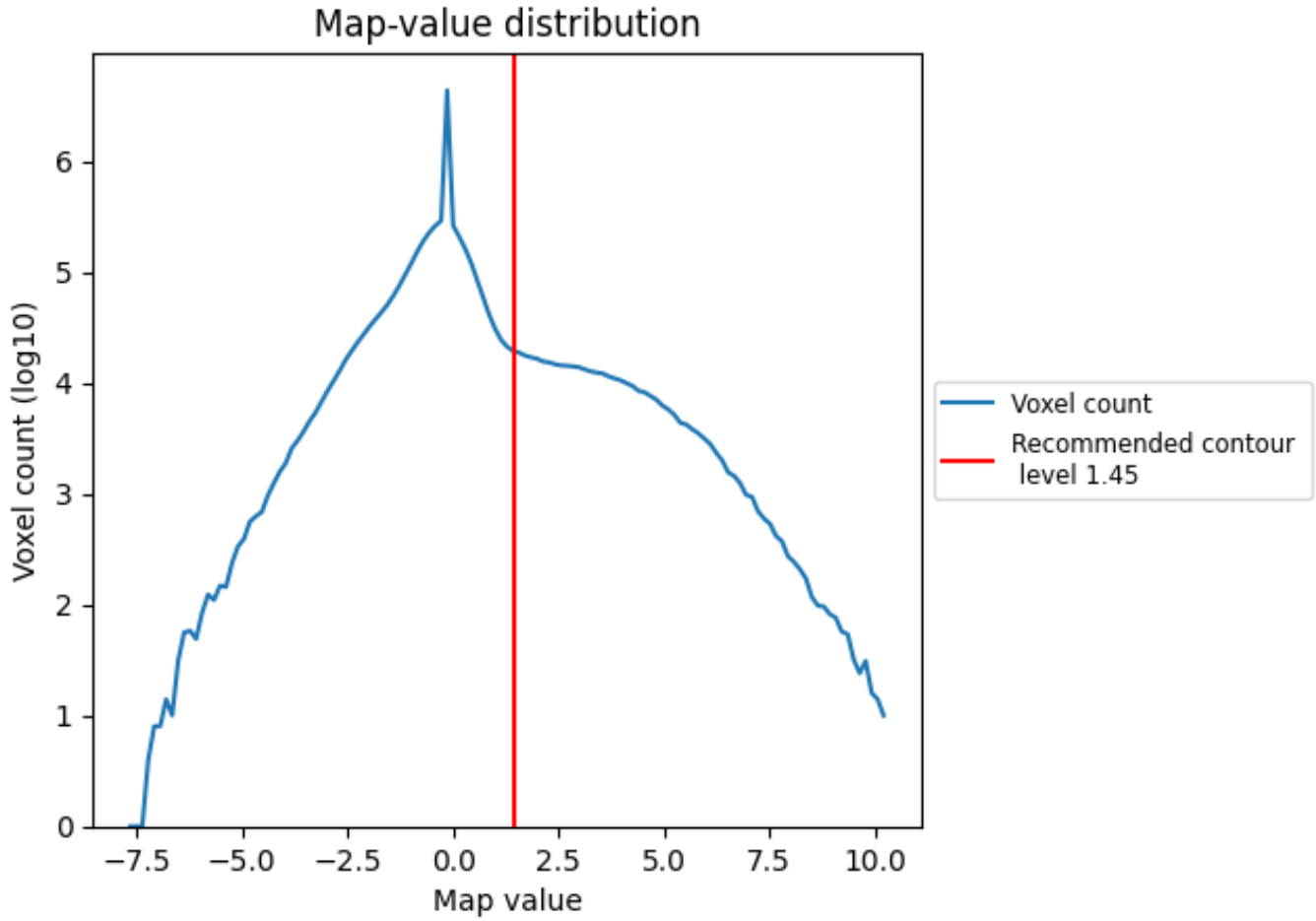
6.5 Mask visualisation (i)

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

7 Map analysis

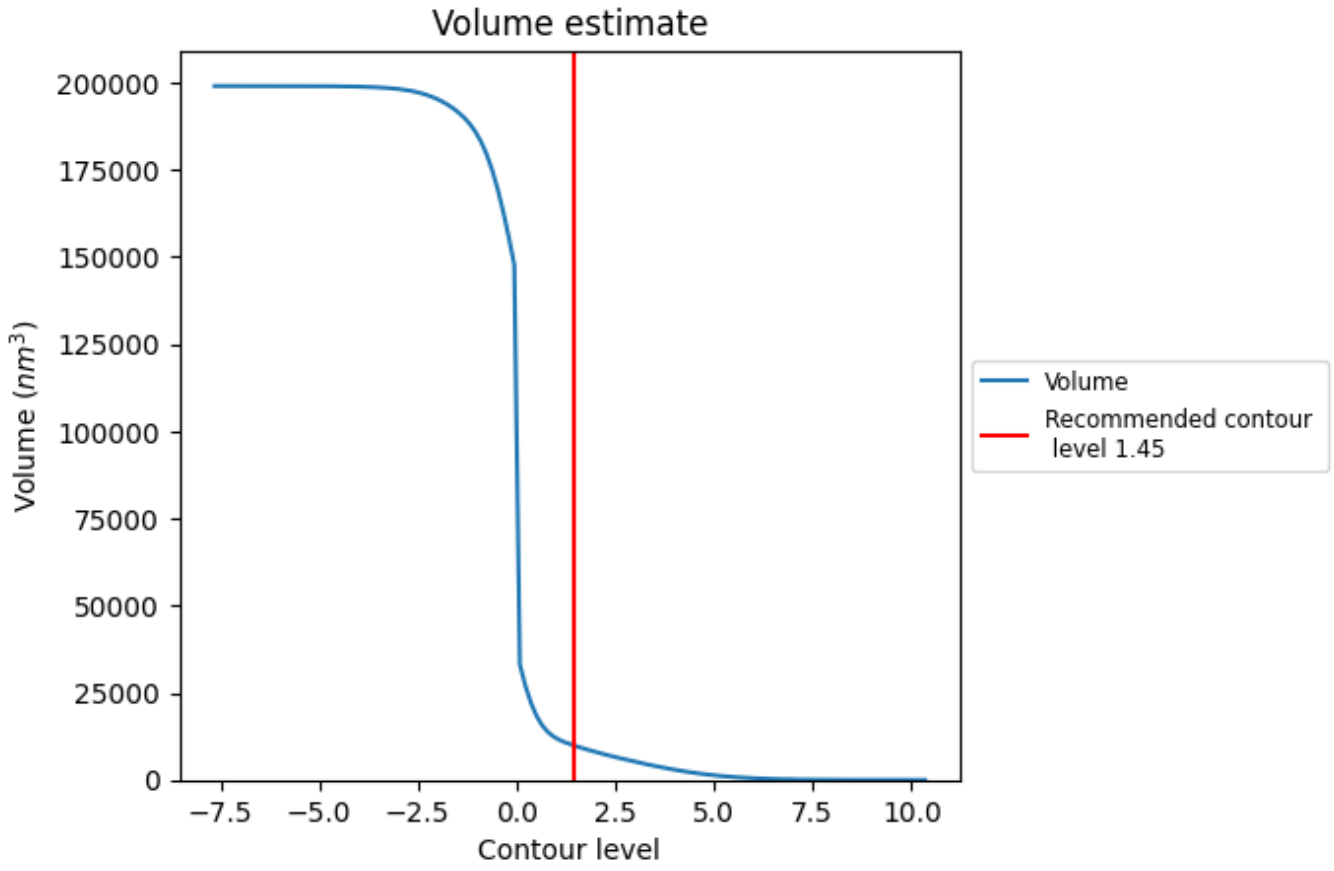
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

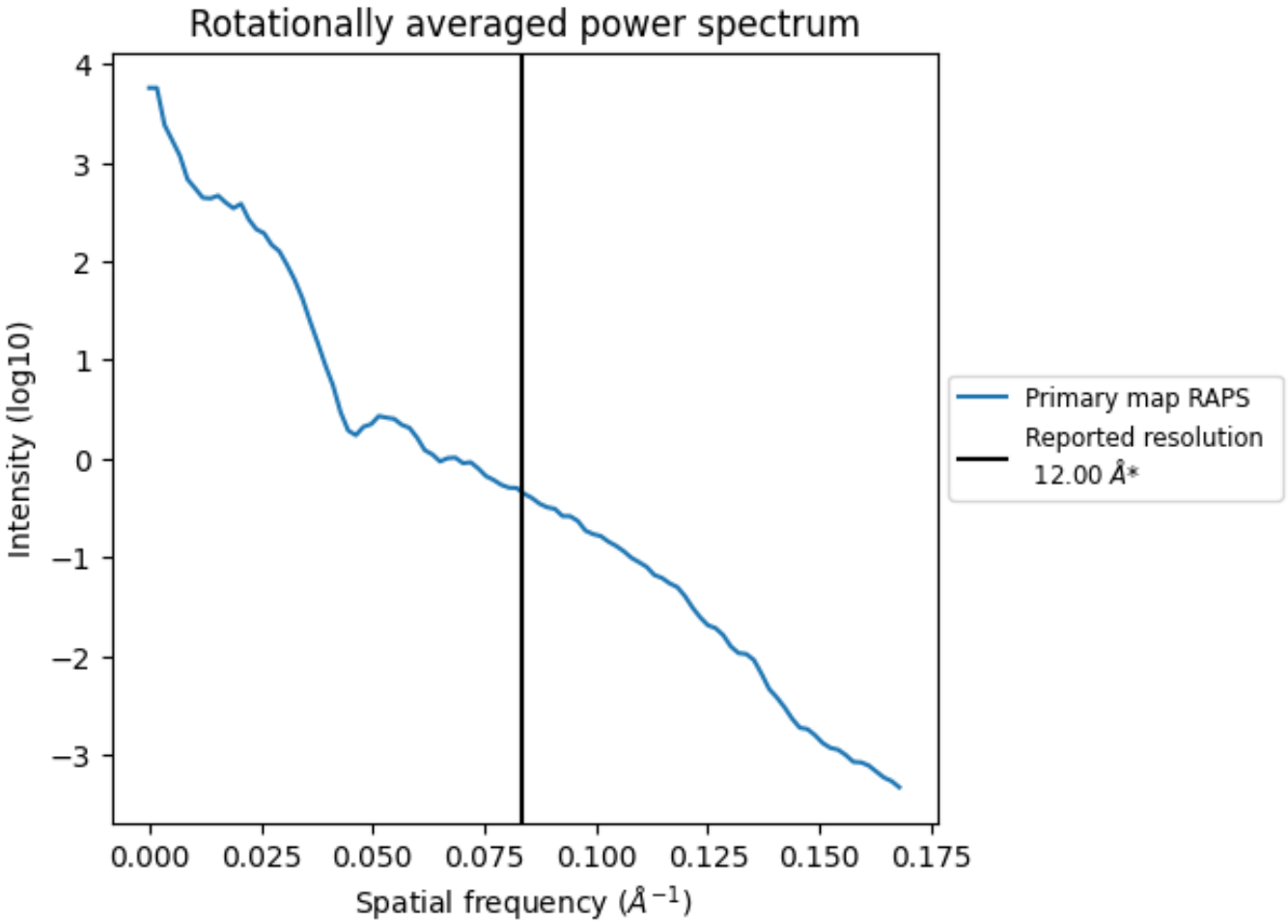
7.2 Volume estimate (i)



The volume at the recommended contour level is 9896 nm^3; this corresponds to an approximate mass of 8939 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 0.083 Å^{-1}

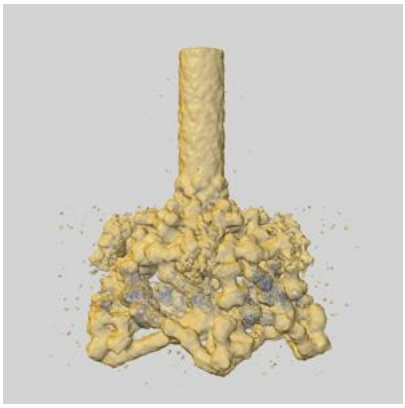
8 Fourier-Shell correlation (i)

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

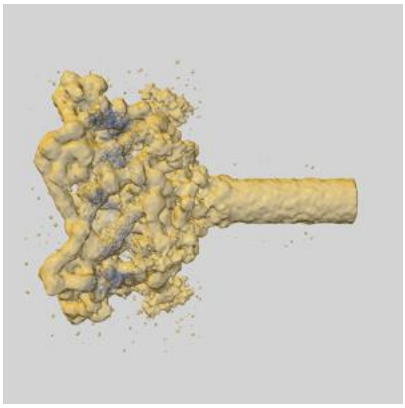
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-1048 and PDB model 2FL8. Per-residue inclusion information can be found in section 3 on page 6.

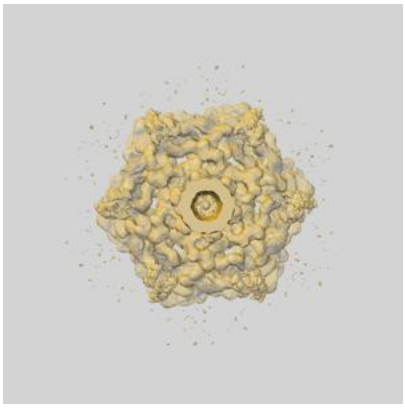
9.1 Map-model overlay



X



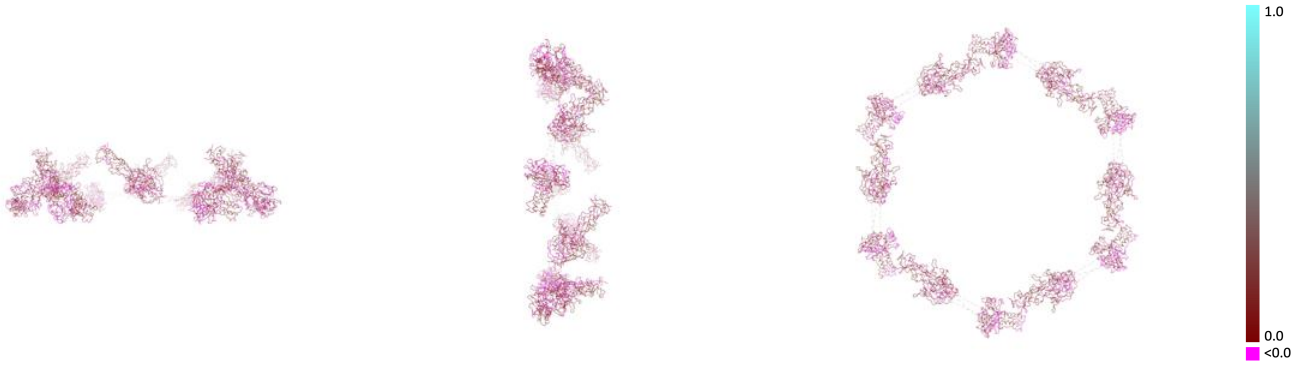
Y



Z

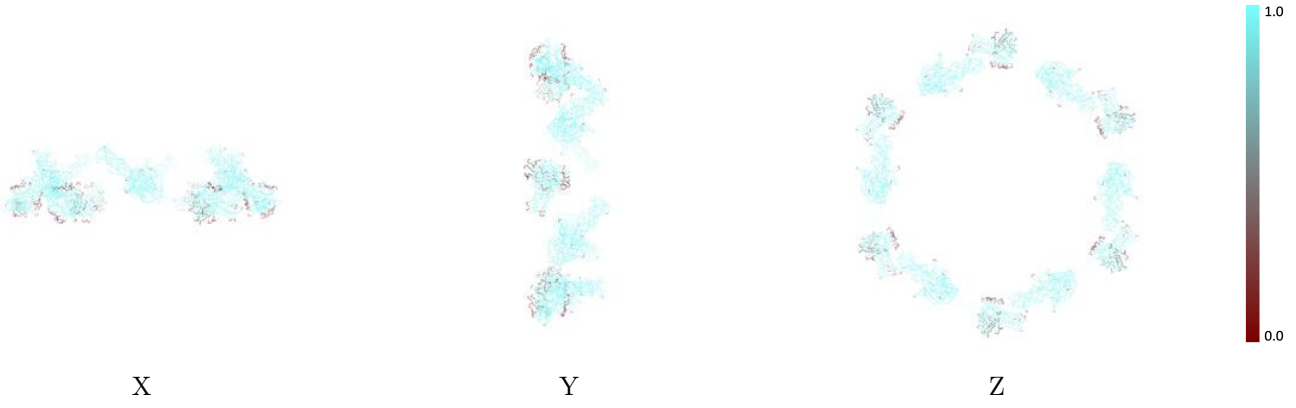
The images above show the 3D surface view of the map at the recommended contour level 1.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



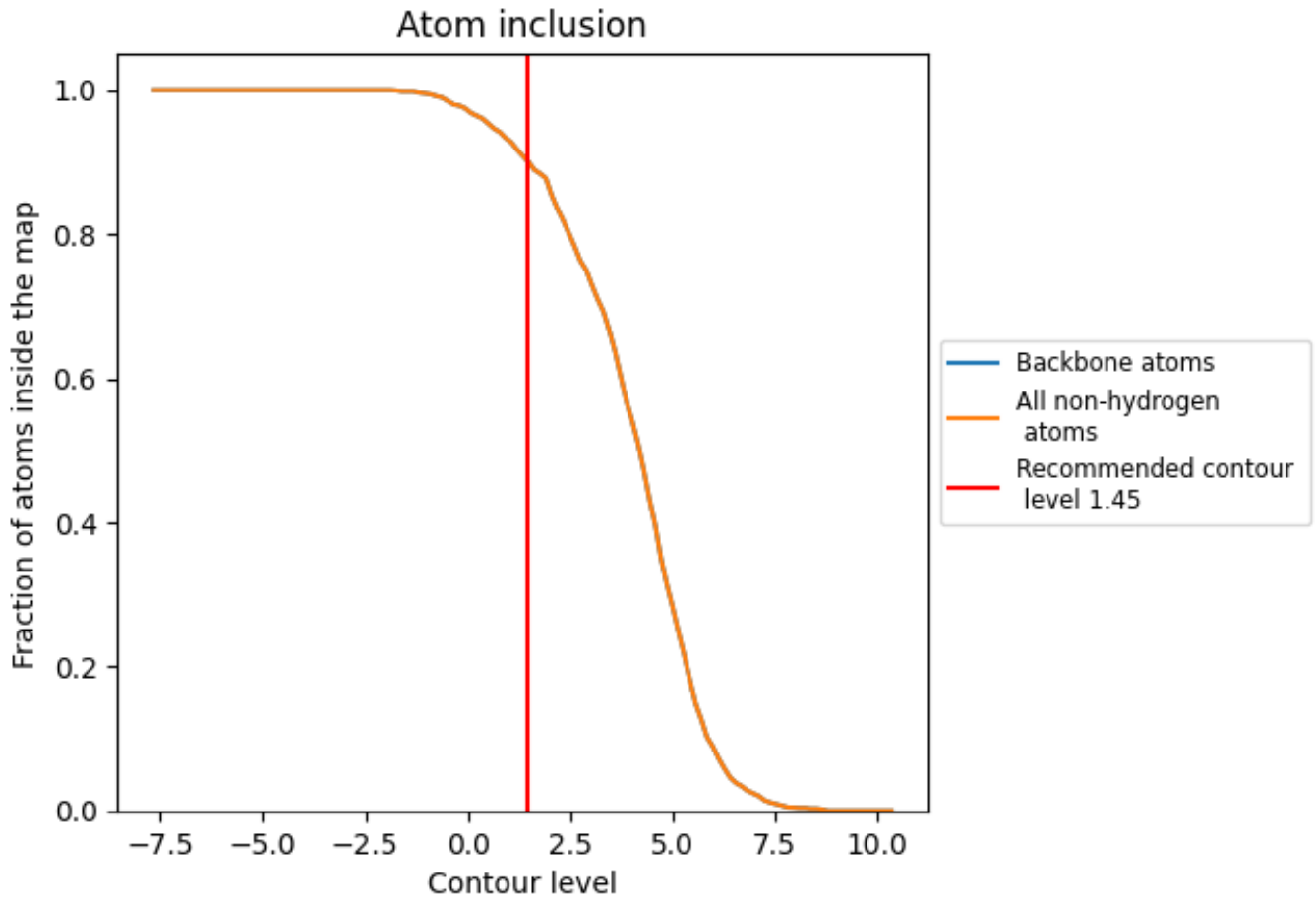
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.45).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (1.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9021	0.0490
A	0.9070	0.0590
B	0.9157	0.0260
C	0.8866	0.0670
D	0.9012	0.0550
E	0.9157	0.0350
F	0.8866	0.0610
G	0.9012	0.0470
H	0.9186	0.0540
I	0.8866	0.0450
J	0.9070	0.0420
K	0.9157	0.0570
L	0.8866	0.0410
M	0.9012	0.0460
N	0.9157	0.0490
O	0.8866	0.0530
P	0.9012	0.0550
Q	0.9186	0.0360
R	0.8866	0.0630