



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 08:38 PM UTC

PDB ID : 7EYB / pdb_00007eyb
EMDB ID : EMD-31317
Title : core proteins
Authors : Liu, H.R.; Chen, W.Y.
Deposited on : 2021-05-30
Resolution : 3.70 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

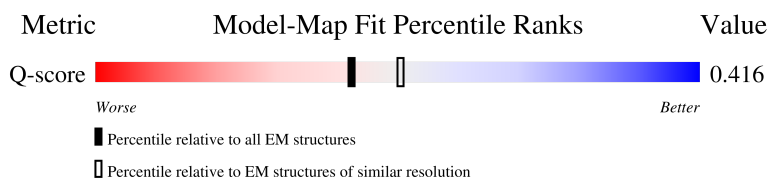
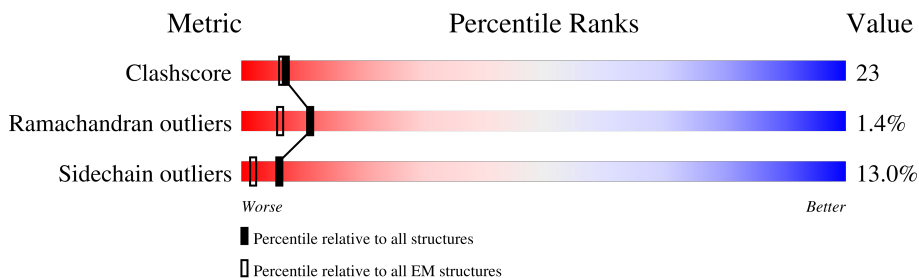
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	a	196	
1	b	196	
1	c	196	
1	d	196	

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Mol	Chain	Length	Quality of chain
1	e	196	
1	f	196	
1	g	196	
1	h	196	
2	A	747	
2	B	747	
2	C	747	
2	D	747	
2	E	747	
2	F	747	
2	G	747	
2	H	747	
3	I	1318	
3	J	1318	
3	K	1318	
3	L	1318	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 78184 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 Internal virion protein gp14.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	a	78	Total	C	N	O	0	0
			387	231	78	78		
1	b	78	Total	C	N	O	0	0
			387	231	78	78		
1	c	78	Total	C	N	O	0	0
			387	231	78	78		
1	d	78	Total	C	N	O	0	0
			387	231	78	78		
1	e	78	Total	C	N	O	0	0
			387	231	78	78		
1	f	78	Total	C	N	O	0	0
			387	231	78	78		
1	g	78	Total	C	N	O	0	0
			387	231	78	78		
1	h	78	Total	C	N	O	0	0
			387	231	78	78		

- Molecule 2 is a protein called Internal virion protein gp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	647	Total	C	N	O	S	0	0
			5148	3184	904	1031	29		
2	B	647	Total	C	N	O	S	0	0
			5148	3184	904	1031	29		
2	C	647	Total	C	N	O	S	0	0
			5148	3184	904	1031	29		
2	D	647	Total	C	N	O	S	0	0
			5148	3184	904	1031	29		
2	E	647	Total	C	N	O	S	0	0
			5148	3184	904	1031	29		
2	F	647	Total	C	N	O	S	0	0
			5148	3184	904	1031	29		
2	G	647	Total	C	N	O	S	0	0
			5148	3184	904	1031	29		

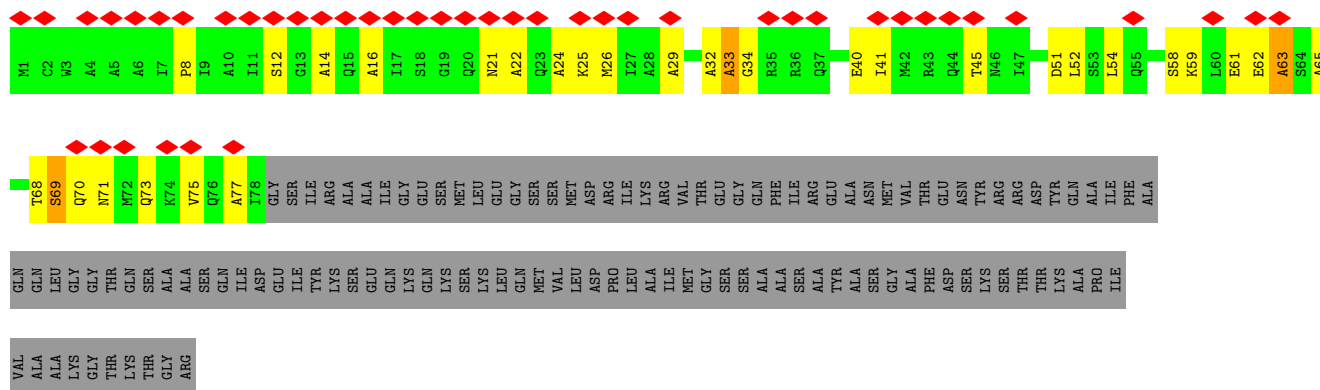
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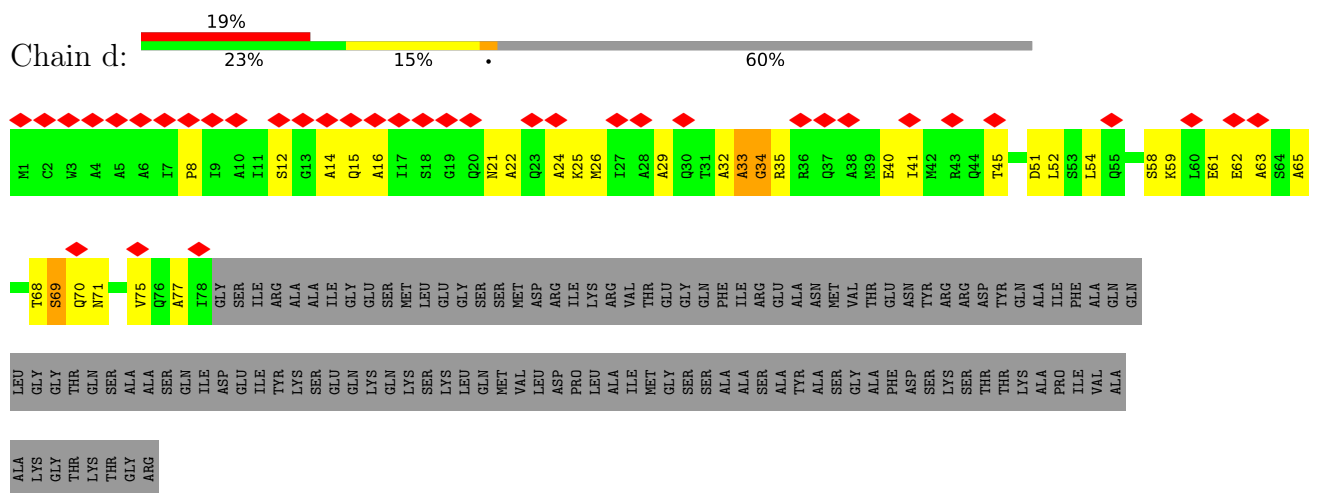
Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	647	Total	C	N	O	S	0	0
			5148	3184	904	1031	29		

- Molecule 3 is a protein called Peptidoglycan transglycosylase gp16.

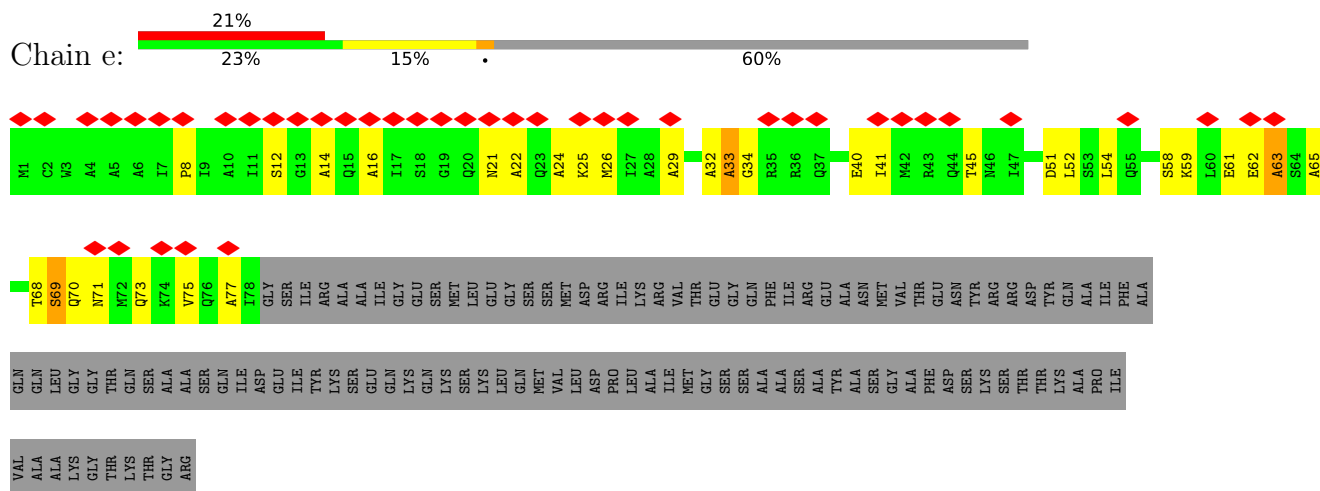
Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	1101	Total	C	N	O	S	0	0
			8476	5312	1492	1628	44		
3	J	1101	Total	C	N	O	S	0	0
			8476	5312	1492	1628	44		
3	K	1101	Total	C	N	O	S	0	0
			8476	5312	1492	1628	44		
3	L	1101	Total	C	N	O	S	0	0
			8476	5312	1492	1628	44		



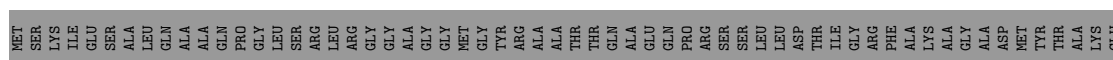
• Molecule 1: Internal virion protein gp14

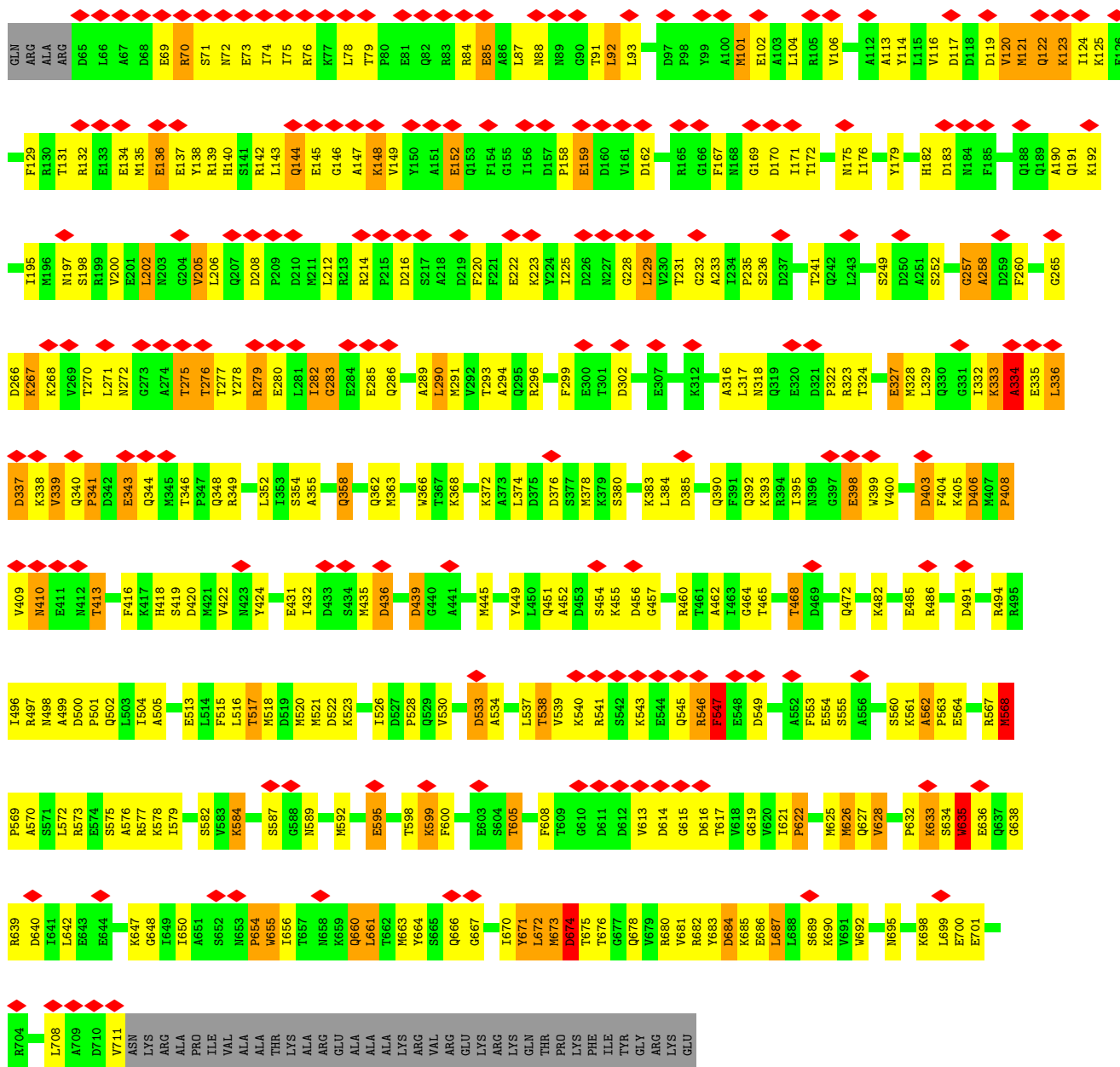


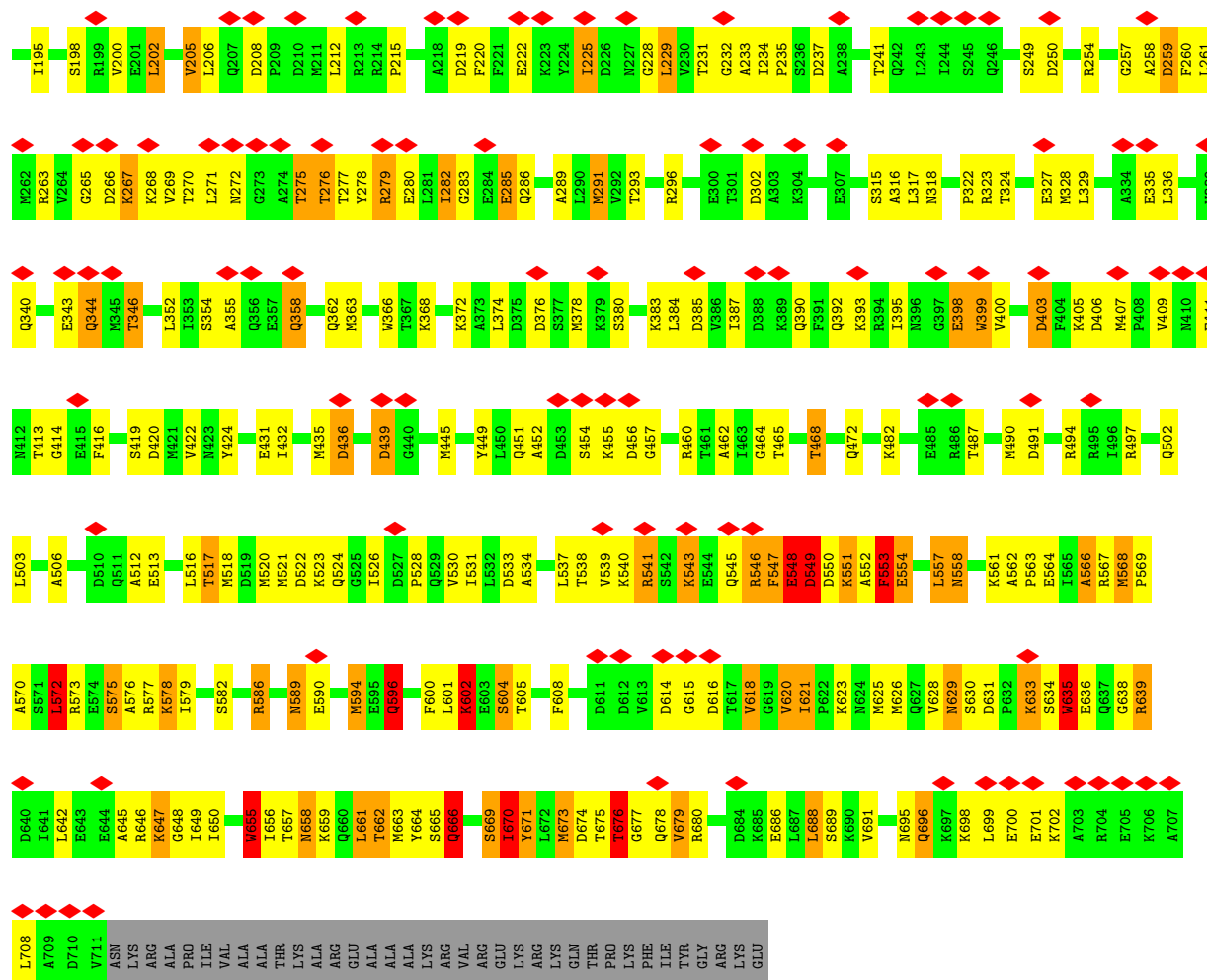
• Molecule 1: Internal virion protein gp14



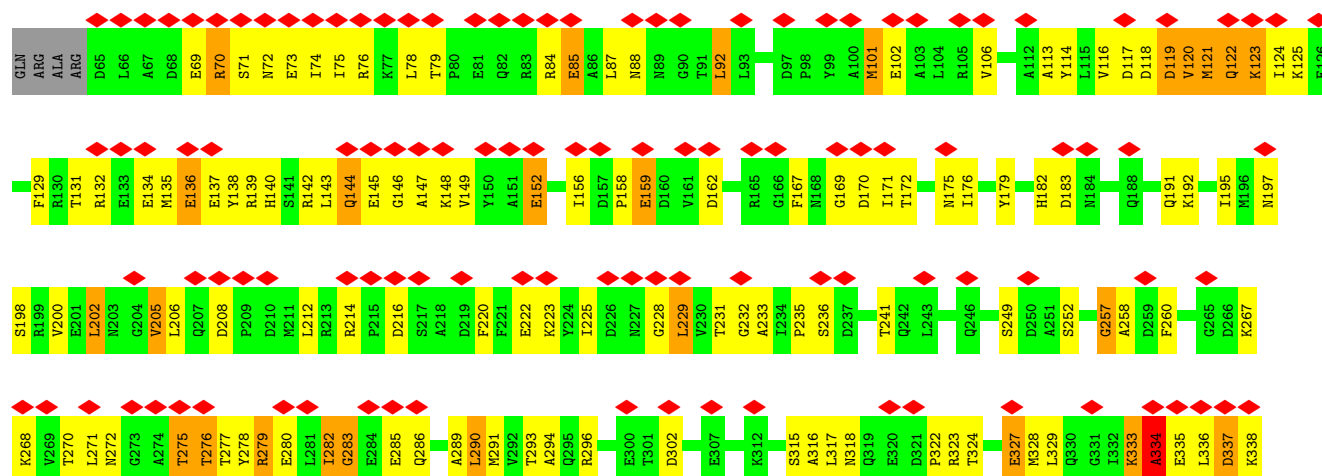
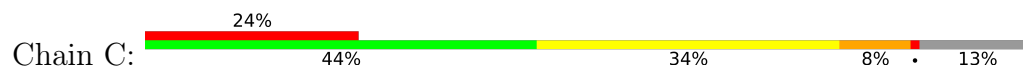
• Molecule 1: Internal virion protein gp14

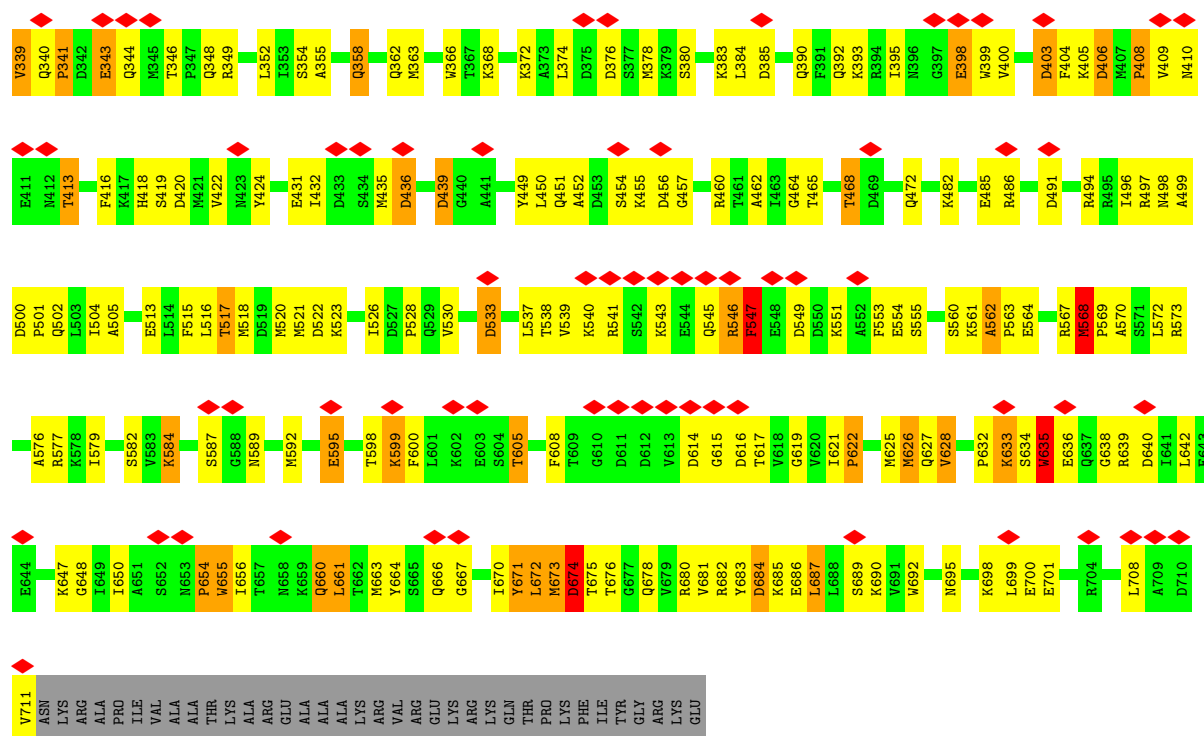




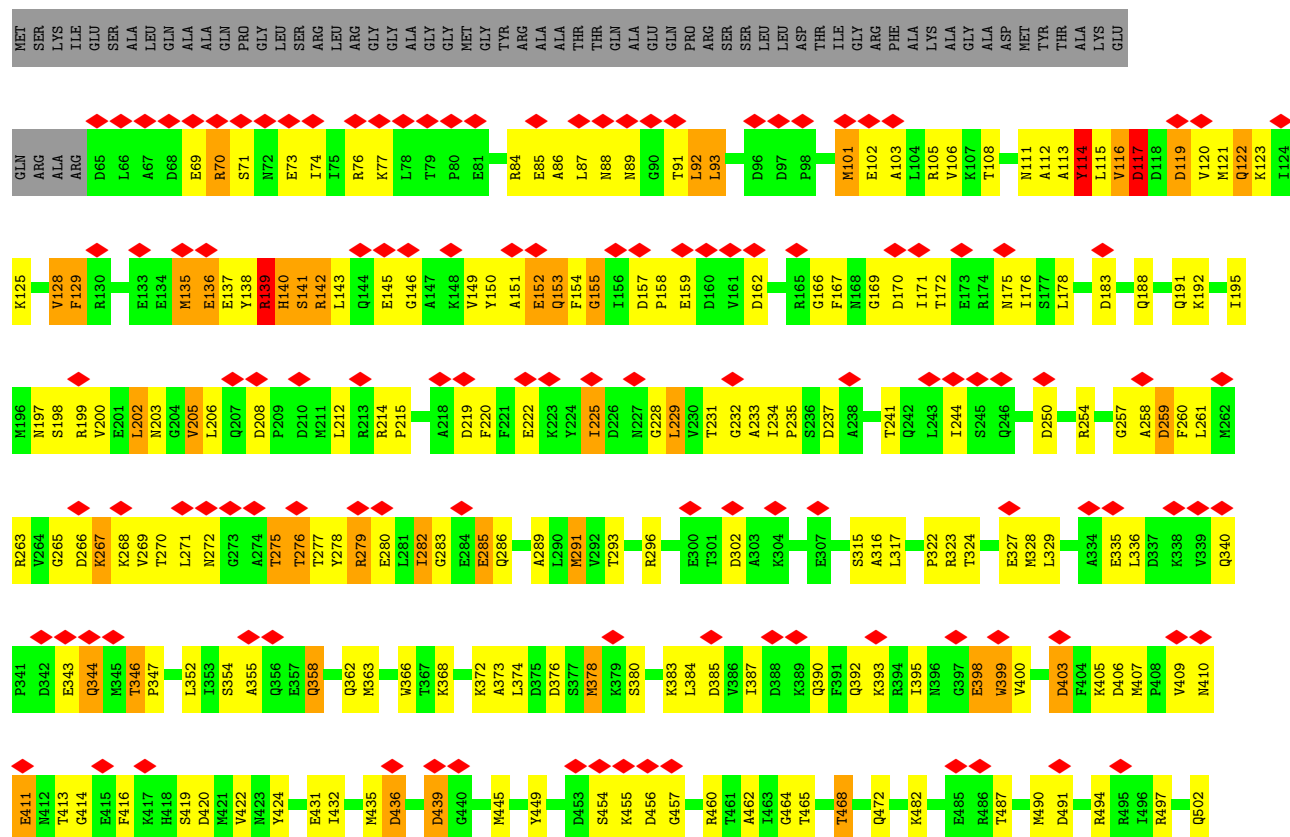


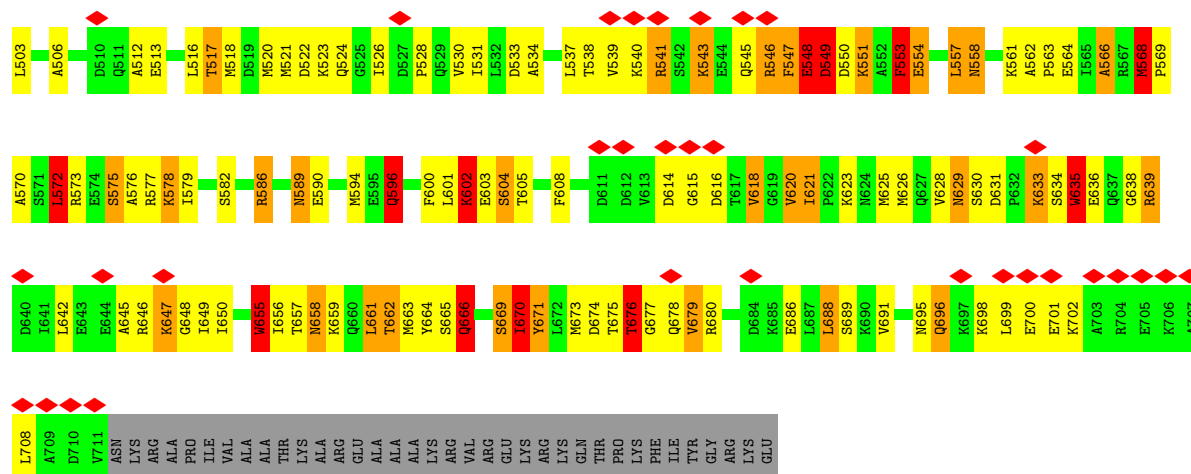
• Molecule 2: Internal virion protein gp15



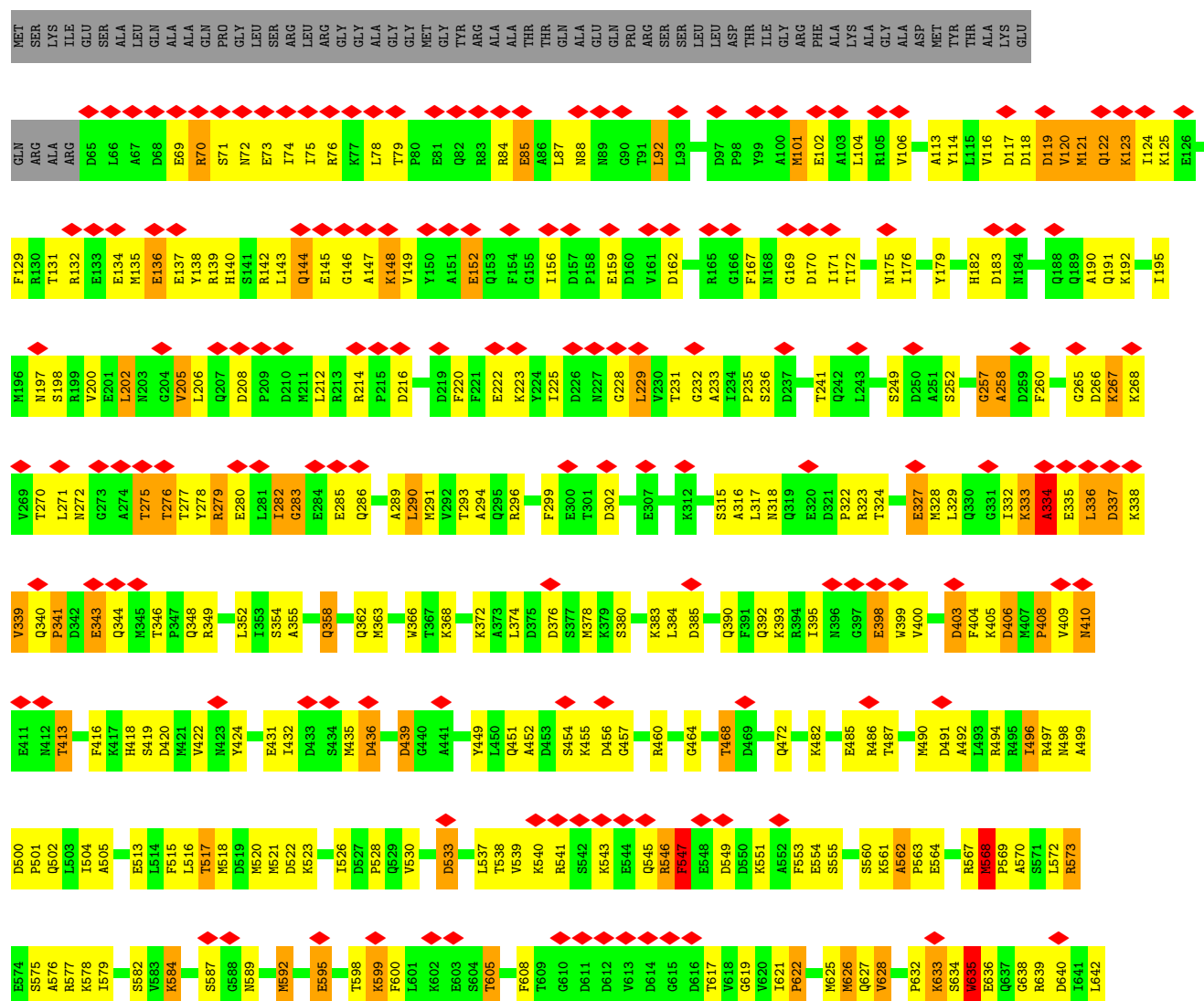
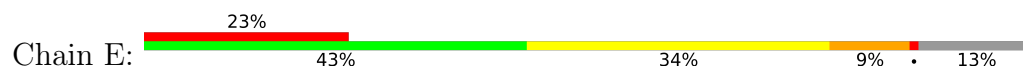


• Molecule 2: Internal virion protein gp15





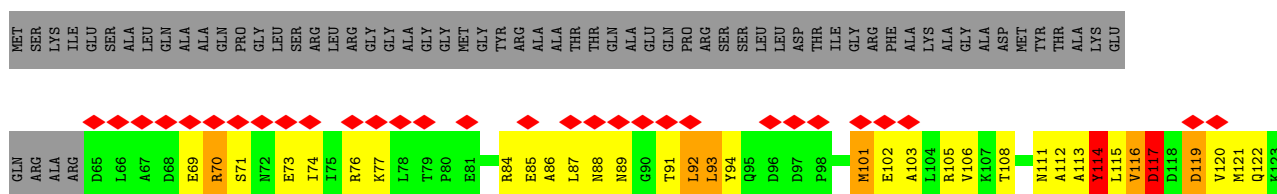
• Molecule 2: Internal virion protein gp15

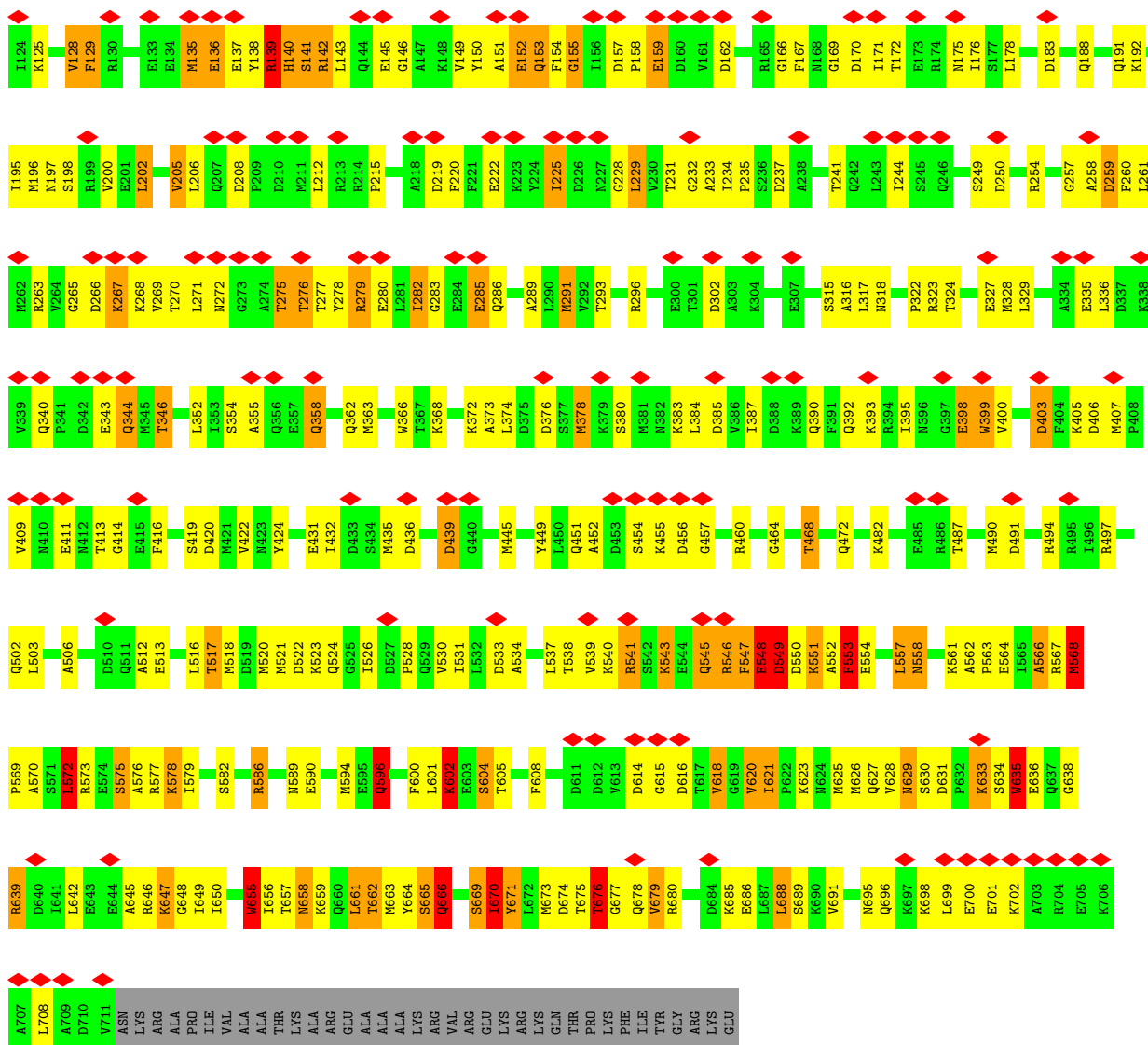


Chain G:

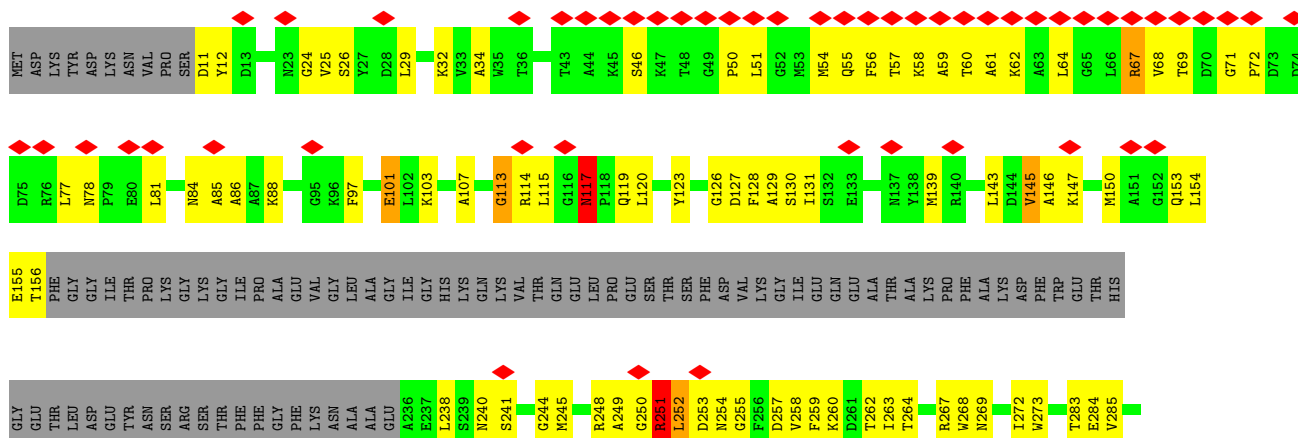


Chain H:

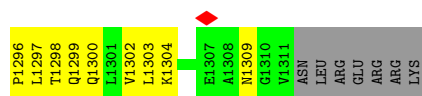




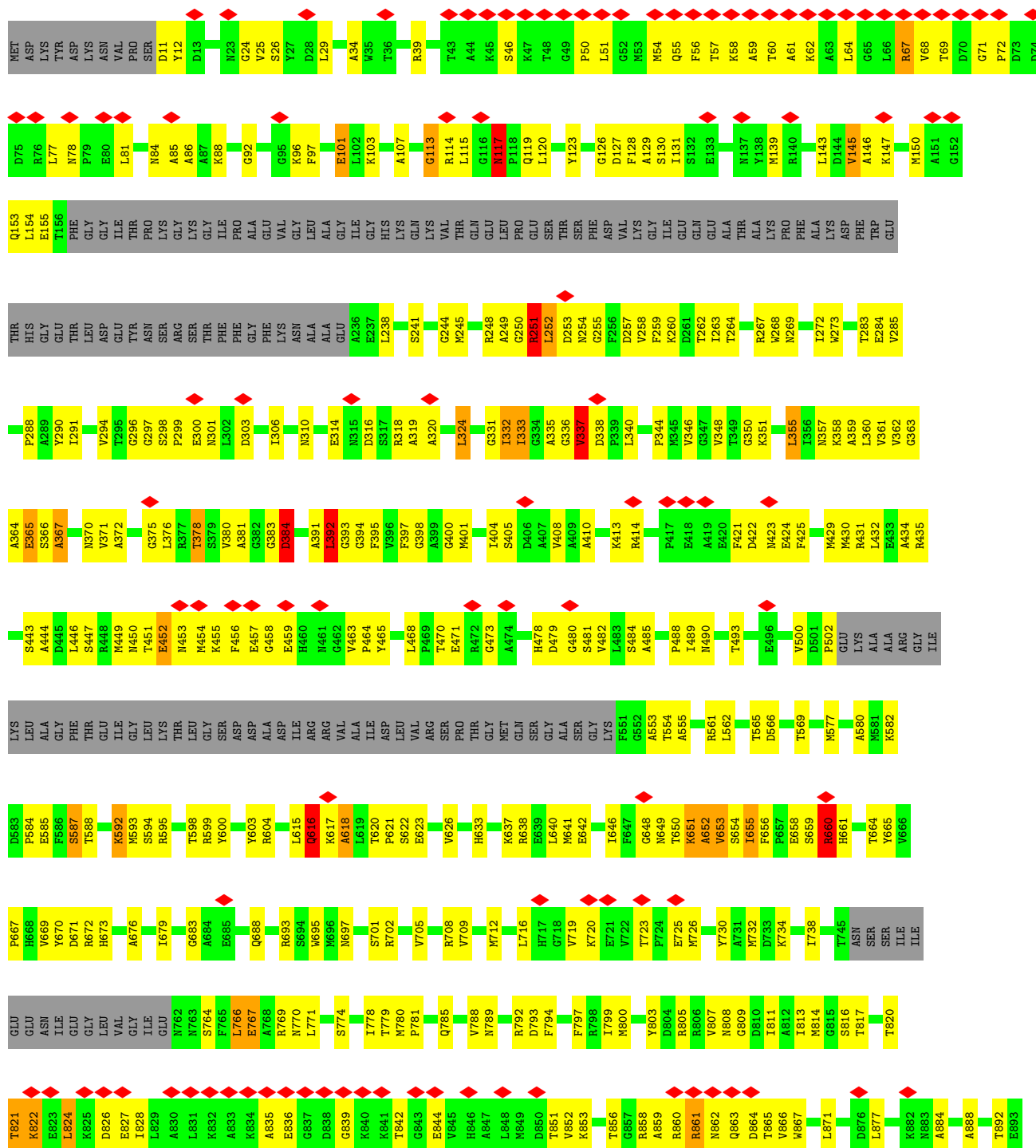
• Molecule 3: Peptidoglycan transglycosylase gp16

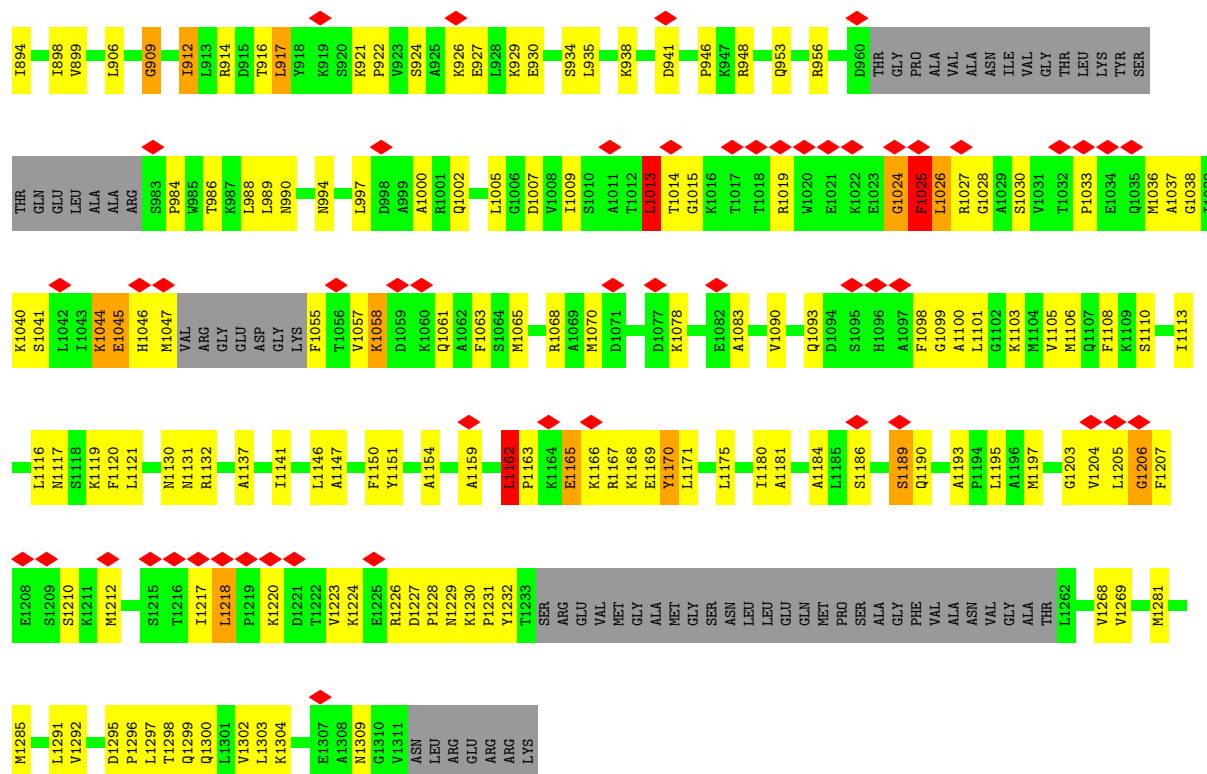




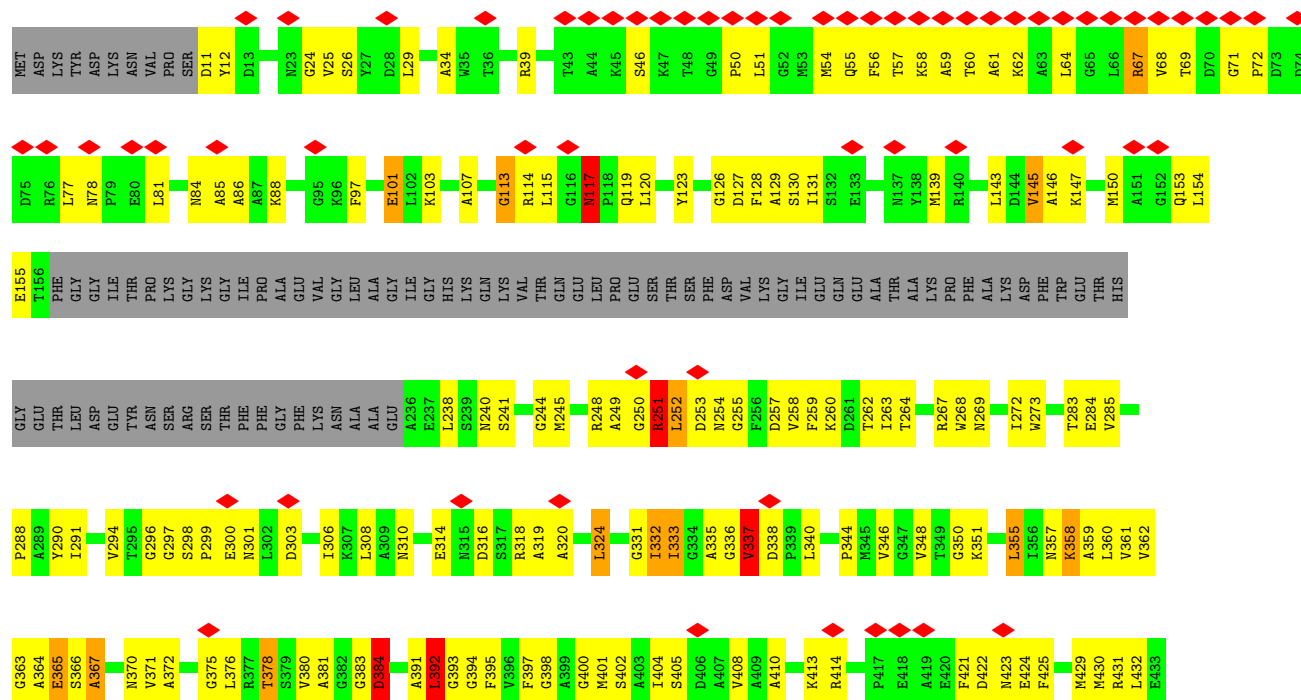


● Molecule 3: Peptidoglycan transglycosylase gp16





• Molecule 3: Peptidoglycan transglycosylase gp16







V1269	M1281	M1285	L1291	V1292	D1295	P1296	L1297	T1298	Q1299	Q1300	L1301	V1302	L1303	K1304	E1307	A1308	N1309	G1310	V1311	ASN	LEU	ARG	GLU	ARG	ARG	LYS	SER	ARG	GLU	VAL	MET	GLY	ALA	MET	GLY	SER	ASN	LEU	LEU	GLU	GLN	MET	PRO	SER	ALA	GLY	PHE	VAL	ALA	ASN	VAL	GLY	ALA	THR	L1262	
V1204	L1205	G1206	F1207	E1208	S1209	S1210	K1211	M1212	S1215	T1216	I1217	L1218	P1219	K1220	D1221	T1222	V1223	K1224	E1225	R1226	D1227	P1228	N1229	K1230	P1231	Y1232	T1233	SER	ARG	GLU	VAL	MET	GLY	ALA	MET	GLY	SER	ASN	LEU	LEU	GLU	GLN	MET	PRO	SER	ALA	GLY	PHE	VAL	ALA	ASN	VAL	GLY	ALA	THR	L1262
S1110	I1113	L1116	N1117	S1118	K1119	F1120	L1121	N1130	N1131	R1132	A1137	I1141	L1146	A1147	F1150	Y1151	A1154	A1159	L1162	P1163	K1164	E1165	K1166	R1167	K1168	E1169	Y1170	L1171	L1175	I1180	A1181	A1184	L1185	S1186	R1187	S1188	S1189	Q1190	A1193	P1194	L1195	A1196	M1197	G1203												
I1039	K1040	S1041	L1042	T1043	K1044	E1045	H1046	M1047	VAL	ARG	GLY	GLU	ASP	GLY	LYS	F1055	T1056	V1057	K1058	D1059	K1060	Q1061	A1062	F1063	S1064	M1065	R1068	A1069	M1070	D1071	L1072	M1073	D1077	K1078	E1082	A1083	V1090	Q1093	D1094	S1095	H1096	A1097	F1098	G1099	A1100	L1101	G1102	K1103	M1104	V1105	M1106	Q1107	F1108	K1109		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	74984	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	72.374	Depositor
Minimum map value	-46.971	Depositor
Average map value	0.038	Depositor
Map value standard deviation	2.961	Depositor
Recommended contour level	11	Depositor
Map size ($\text{\AA}$)	406.4, 406.4, 406.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.27, 1.27, 1.27	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	a	1.45	4/386 (1.0%)	1.89	18/537 (3.4%)
1	b	1.45	4/386 (1.0%)	1.88	20/537 (3.7%)
1	c	1.45	4/386 (1.0%)	1.88	19/537 (3.5%)
1	d	1.45	4/386 (1.0%)	1.88	20/537 (3.7%)
1	e	1.45	4/386 (1.0%)	1.89	19/537 (3.5%)
1	f	1.45	4/386 (1.0%)	1.88	20/537 (3.7%)
1	g	1.46	4/386 (1.0%)	1.90	19/537 (3.5%)
1	h	1.45	4/386 (1.0%)	1.88	19/537 (3.5%)
2	A	0.73	3/5226 (0.1%)	1.09	53/7039 (0.8%)
2	B	0.87	9/5226 (0.2%)	1.11	49/7039 (0.7%)
2	C	0.73	3/5226 (0.1%)	1.09	52/7039 (0.7%)
2	D	0.87	9/5226 (0.2%)	1.11	49/7039 (0.7%)
2	E	0.73	4/5226 (0.1%)	1.09	53/7039 (0.8%)
2	F	0.88	9/5226 (0.2%)	1.11	49/7039 (0.7%)
2	G	0.73	3/5226 (0.1%)	1.09	51/7039 (0.7%)
2	H	0.88	10/5226 (0.2%)	1.11	49/7039 (0.7%)
3	I	0.65	4/8620 (0.0%)	1.01	82/11617 (0.7%)
3	J	0.65	5/8620 (0.1%)	1.01	84/11617 (0.7%)
3	K	0.65	4/8620 (0.0%)	1.01	85/11617 (0.7%)
3	L	0.65	5/8620 (0.1%)	1.01	82/11617 (0.7%)
All	All	0.78	100/79376 (0.1%)	1.10	892/107076 (0.8%)

The worst 5 of 100 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	355	LEU	CA-C	-9.05	1.43	1.53
3	L	355	LEU	CA-C	-9.03	1.43	1.53
3	I	355	LEU	CA-C	-9.02	1.43	1.53
3	K	355	LEU	CA-C	-9.02	1.43	1.53
2	G	114	TYR	C-O	-7.05	1.15	1.24

The worst 5 of 892 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	1025	PHE	N-CA-C	-12.30	98.67	112.57
3	K	1025	PHE	N-CA-C	-12.30	98.67	112.57
3	I	1025	PHE	N-CA-C	-12.24	98.73	112.57
3	L	1025	PHE	N-CA-C	-12.24	98.73	112.57
3	J	1165	GLU	N-CA-C	-12.11	92.06	110.10

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	387	0	214	11	0
1	b	387	0	214	13	0
1	c	387	0	214	11	0
1	d	387	0	214	12	0
1	e	387	0	214	11	0
1	f	387	0	214	11	0
1	g	387	0	214	11	0
1	h	387	0	214	10	0
2	A	5148	0	5040	228	0
2	B	5148	0	5040	339	0
2	C	5148	0	5040	205	0
2	D	5148	0	5040	332	0
2	E	5148	0	5040	223	0
2	F	5148	0	5040	338	0
2	G	5148	0	5040	228	0
2	H	5148	0	5040	333	0
3	I	8476	0	8466	401	0
3	J	8476	0	8466	389	0
3	K	8476	0	8466	404	0
3	L	8476	0	8466	394	0
All	All	78184	0	75896	3602	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 23.

The worst 5 of 3602 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)
3:L:146:ALA:HB1	3:L:147:LYS:CG	1.42	1.49
3:J:146:ALA:HB1	3:J:147:LYS:CG	1.42	1.47
3:I:146:ALA:HB1	3:I:147:LYS:CG	1.42	1.47
3:K:146:ALA:HB1	3:K:147:LYS:CG	1.42	1.43
2:F:541:ARG:CG	2:F:546:ARG:HB3	1.61	1.31

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	a	76/196 (39%)	65 (86%)	10 (13%)	1 (1%)	9	38
1	b	76/196 (39%)	66 (87%)	8 (10%)	2 (3%)	4	28
1	c	76/196 (39%)	66 (87%)	9 (12%)	1 (1%)	9	38
1	d	76/196 (39%)	66 (87%)	9 (12%)	1 (1%)	9	38
1	e	76/196 (39%)	65 (86%)	10 (13%)	1 (1%)	9	38
1	f	76/196 (39%)	66 (87%)	9 (12%)	1 (1%)	9	38
1	g	76/196 (39%)	66 (87%)	8 (10%)	2 (3%)	4	28
1	h	76/196 (39%)	66 (87%)	9 (12%)	1 (1%)	9	38
2	A	645/747 (86%)	582 (90%)	56 (9%)	7 (1%)	11	42
2	B	645/747 (86%)	576 (89%)	56 (9%)	13 (2%)	6	32
2	C	645/747 (86%)	583 (90%)	55 (8%)	7 (1%)	11	42
2	D	645/747 (86%)	577 (90%)	55 (8%)	13 (2%)	6	32
2	E	645/747 (86%)	583 (90%)	55 (8%)	7 (1%)	11	42
2	F	645/747 (86%)	577 (90%)	55 (8%)	13 (2%)	6	32
2	G	645/747 (86%)	583 (90%)	55 (8%)	7 (1%)	11	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	645/747 (86%)	576 (89%)	56 (9%)	13 (2%)	6	32
3	I	1087/1318 (82%)	940 (86%)	133 (12%)	14 (1%)	9	38
3	J	1087/1318 (82%)	940 (86%)	133 (12%)	14 (1%)	9	38
3	K	1087/1318 (82%)	938 (86%)	135 (12%)	14 (1%)	9	38
3	L	1087/1318 (82%)	938 (86%)	135 (12%)	14 (1%)	9	38
All	All	10116/12816 (79%)	8919 (88%)	1051 (10%)	146 (1%)	11	37

5 of 146 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	334	ALA
2	A	339	VAL
2	B	570	ALA
2	B	676	THR
2	C	334	ALA

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	
2	A	552/624 (88%)	444 (80%)	108 (20%)	1	9
2	B	552/624 (88%)	434 (79%)	118 (21%)	1	7
2	C	552/624 (88%)	444 (80%)	108 (20%)	1	9
2	D	552/624 (88%)	434 (79%)	118 (21%)	1	7
2	E	552/624 (88%)	444 (80%)	108 (20%)	1	9
2	F	552/624 (88%)	434 (79%)	118 (21%)	1	7
2	G	552/624 (88%)	444 (80%)	108 (20%)	1	9
2	H	552/624 (88%)	434 (79%)	118 (21%)	1	7
3	I	890/1059 (84%)	857 (96%)	33 (4%)	30	54
3	J	890/1059 (84%)	857 (96%)	33 (4%)	30	54
3	K	890/1059 (84%)	857 (96%)	33 (4%)	30	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	L	890/1059 (84%)	857 (96%)	33 (4%)	30 54
All	All	7976/9228 (86%)	6940 (87%)	1036 (13%)	6 20

5 of 1036 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	766	LEU
3	J	620	THR
3	I	660	ARG
2	D	405	LYS
2	D	346	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 164 such sidechains are listed below:

Mol	Chain	Res	Type
3	J	697	ASN
3	K	1229	ASN
3	J	994	ASN
3	K	440	ASN
3	L	370	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

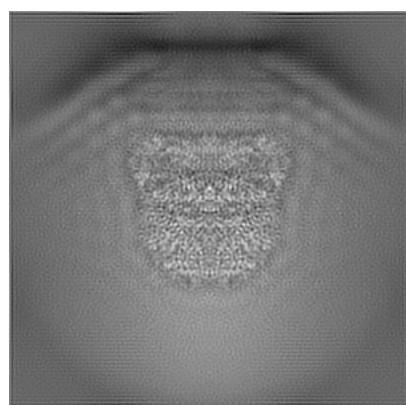
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31317. These allow visual inspection of the internal detail of the map and identification of artifacts.

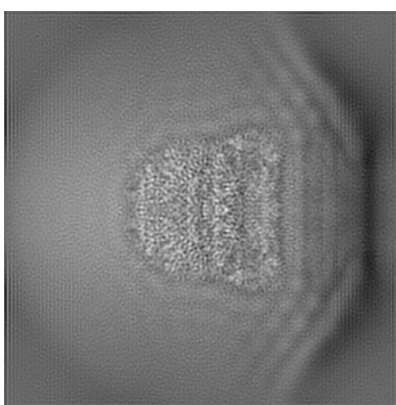
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

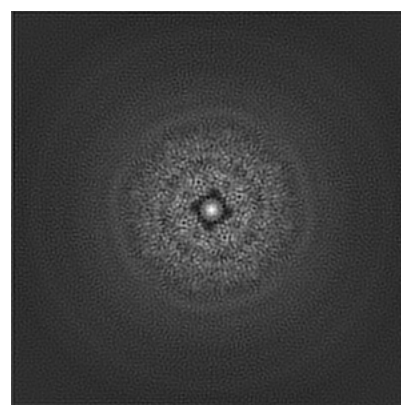
6.1.1 Primary map



X



Y

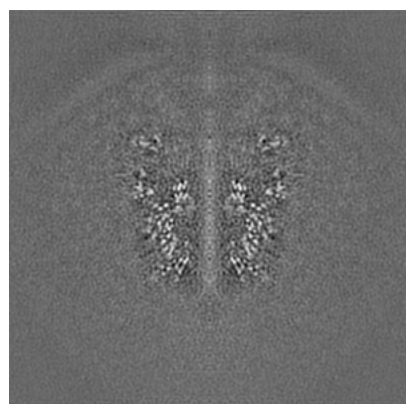


Z

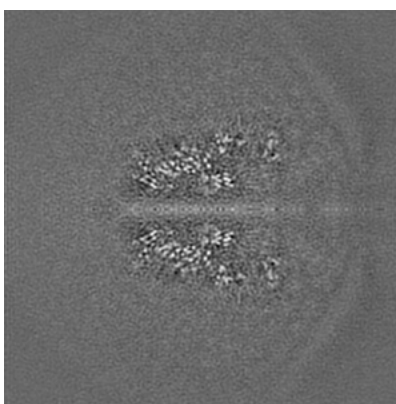
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

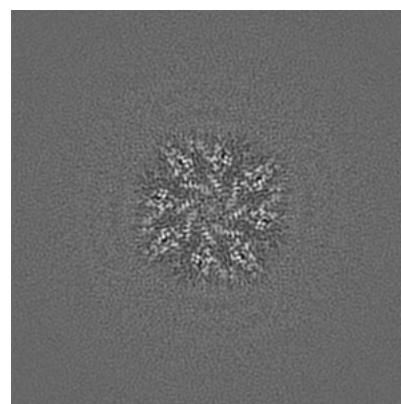
6.2.1 Primary map



X Index: 160



Y Index: 160

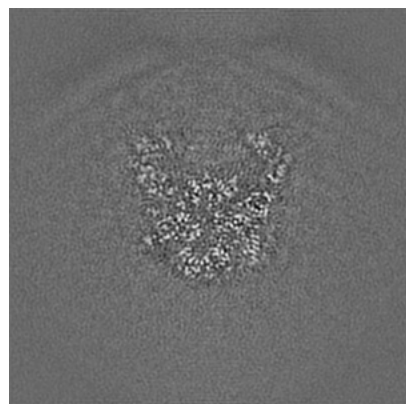


Z Index: 160

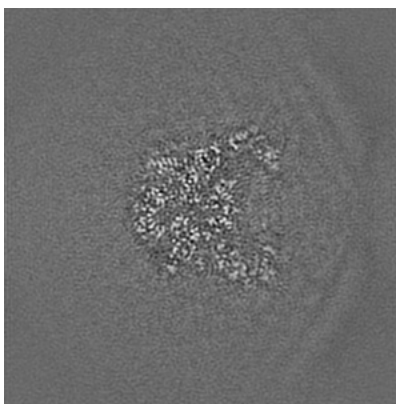
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

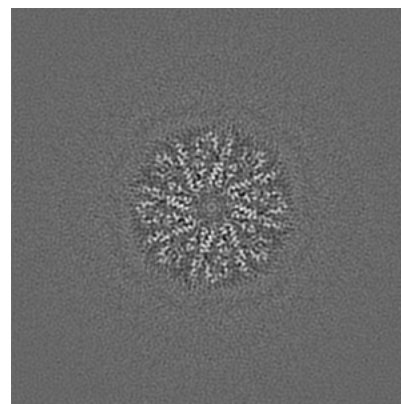
6.3.1 Primary map



X Index: 135



Y Index: 185

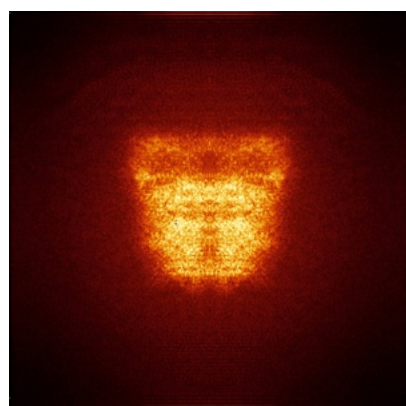


Z Index: 170

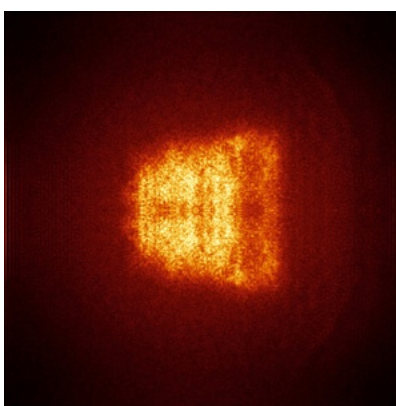
The images above show the largest variance slices of the map in three orthogonal directions.

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

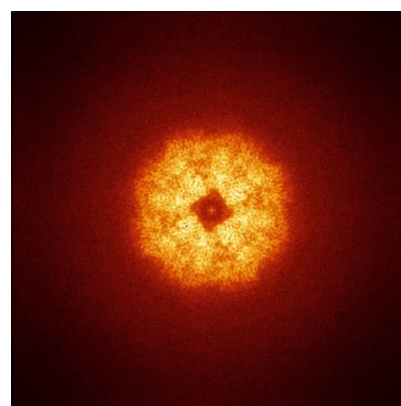
6.4.1 Primary map



X



Y

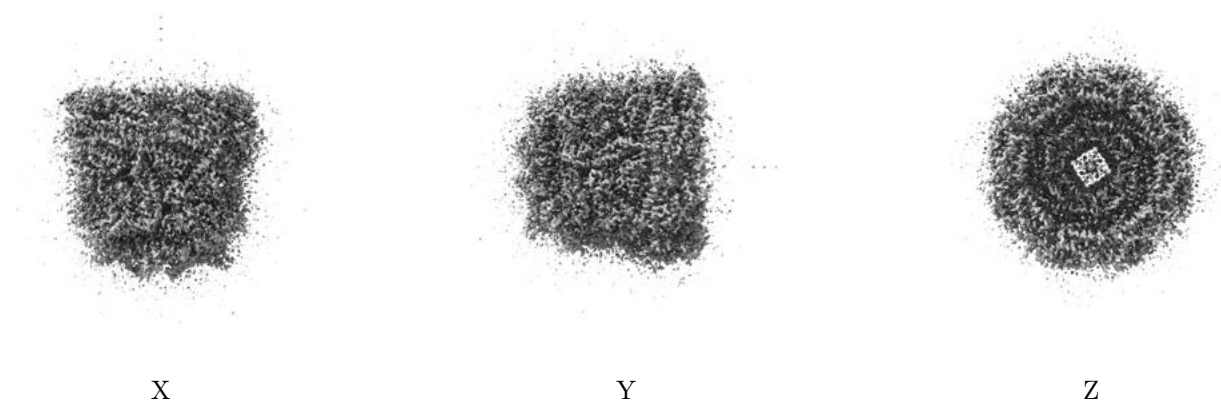


Z

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

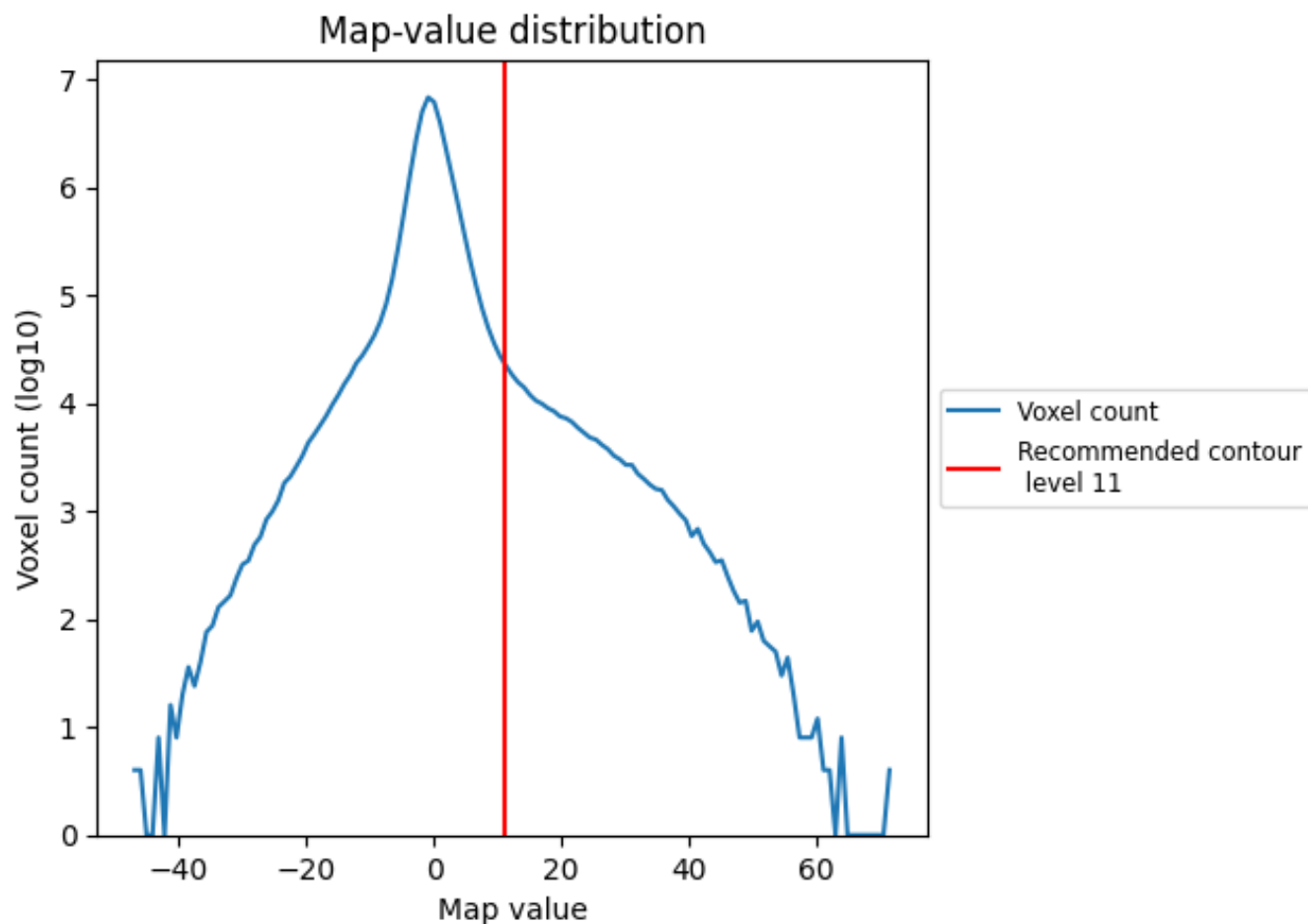
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

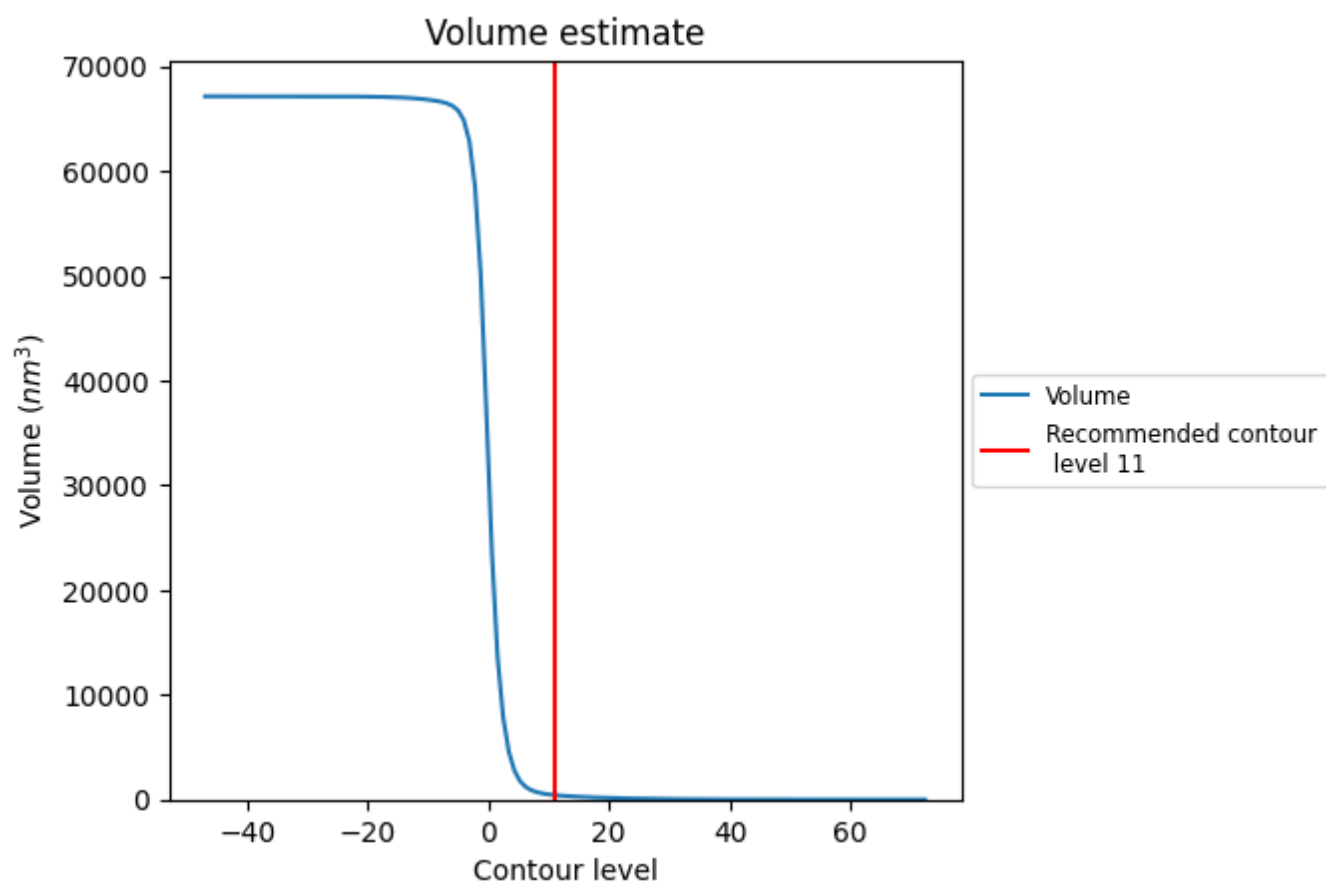
This section contains the results of statistical analysis of the map.

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.

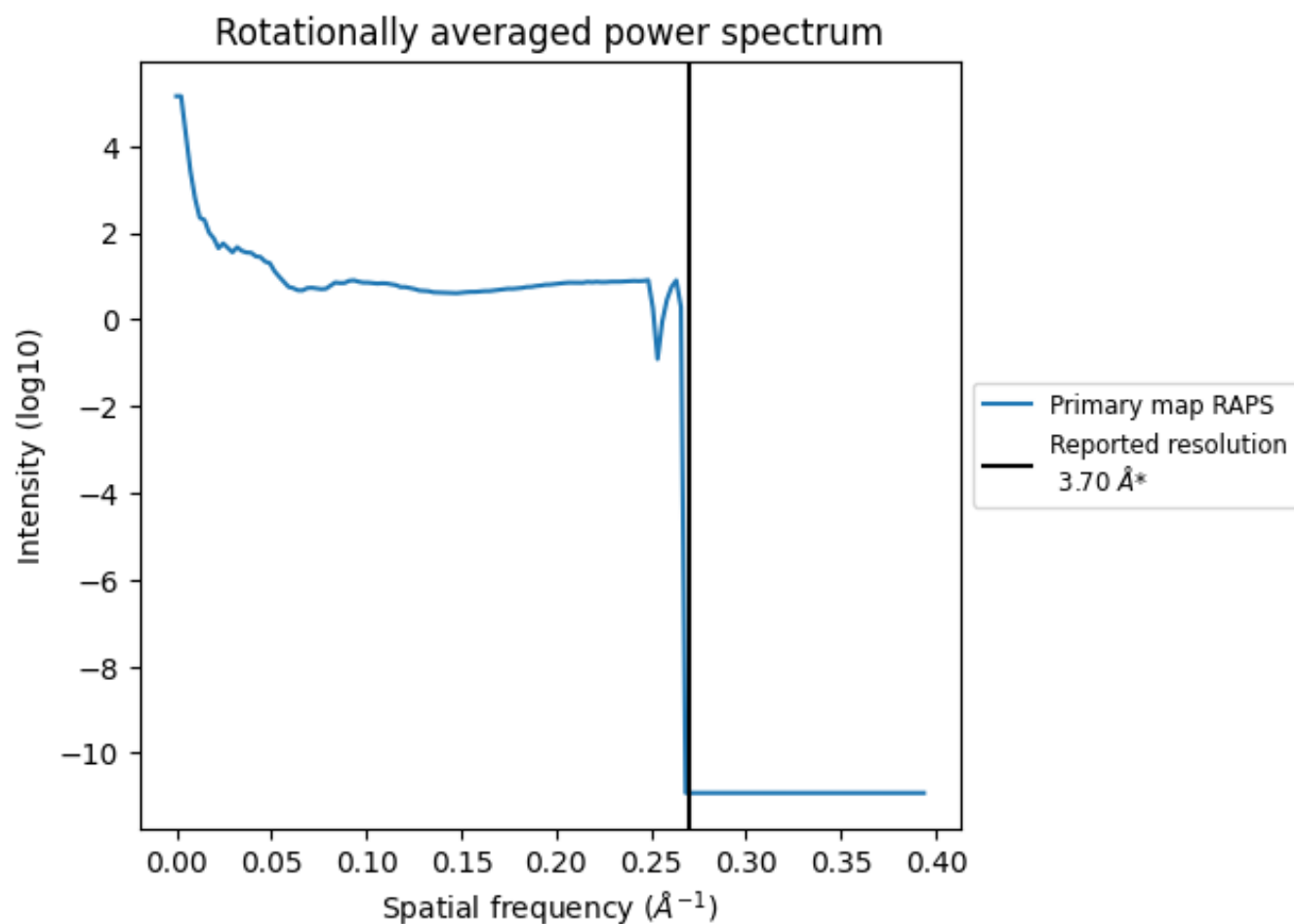
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 425 nm³; this corresponds to an approximate mass of 384 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 0.270 $\text{\AA}^{-1}$

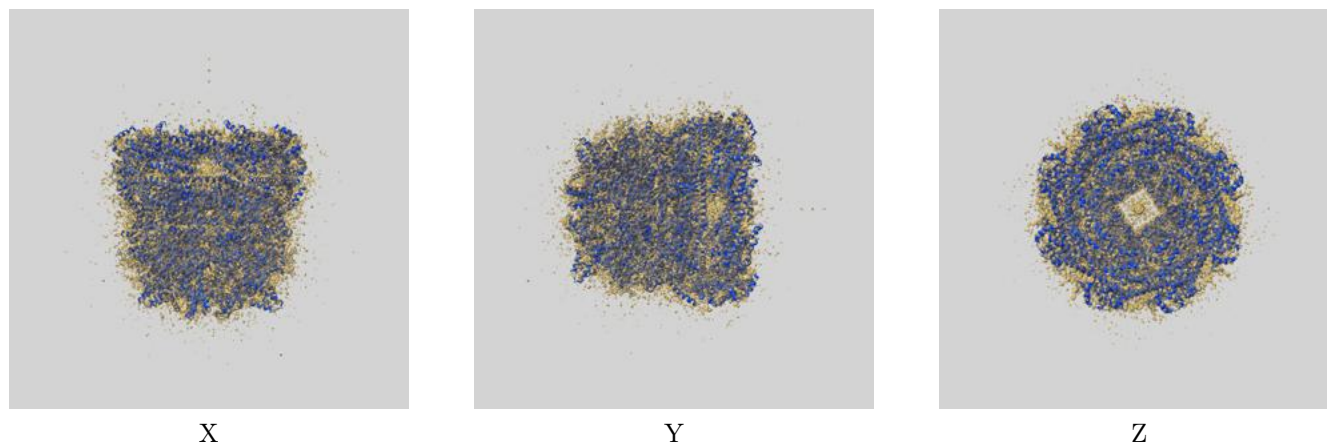
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

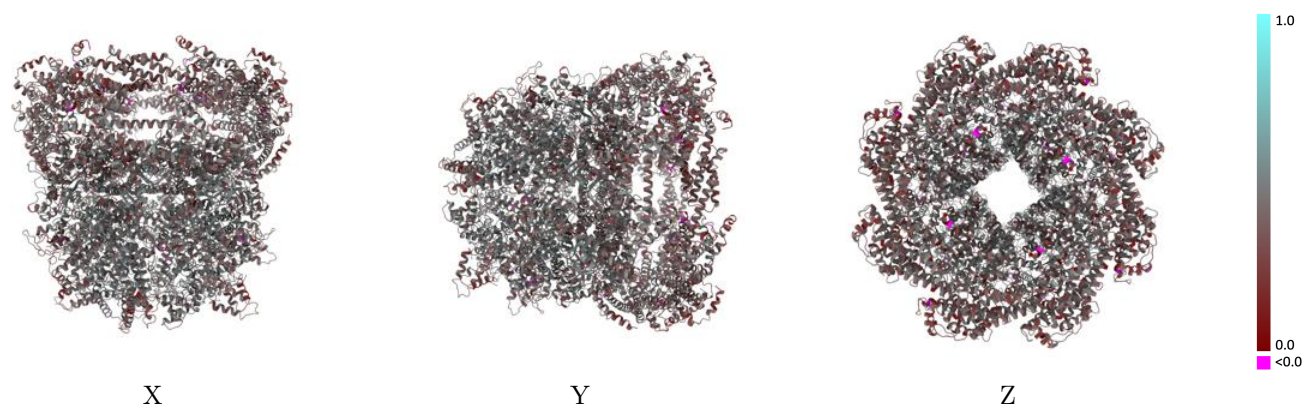
This section contains information regarding the fit between EMDB map EMD-31317 and PDB model 7EYB. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



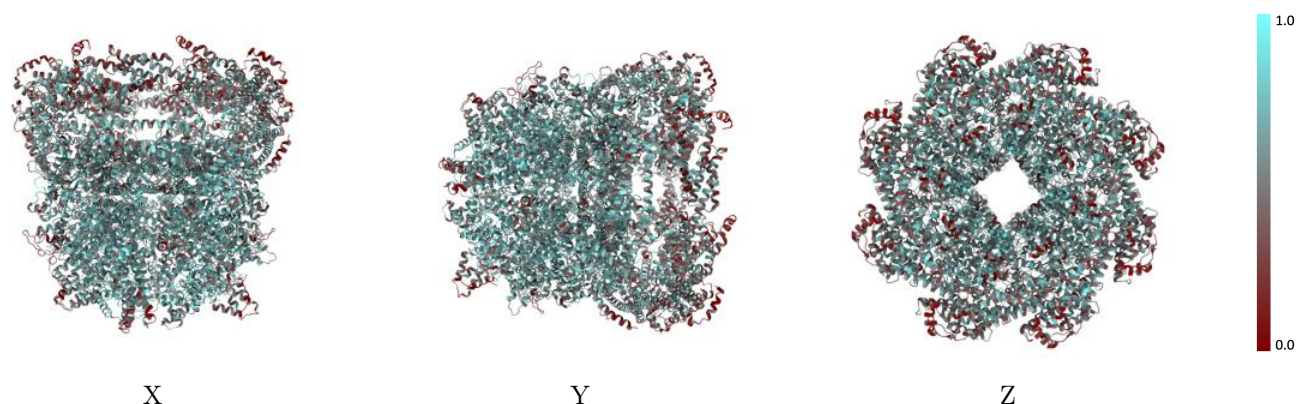
The images above show the 3D surface view of the map at the recommended contour level 11.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



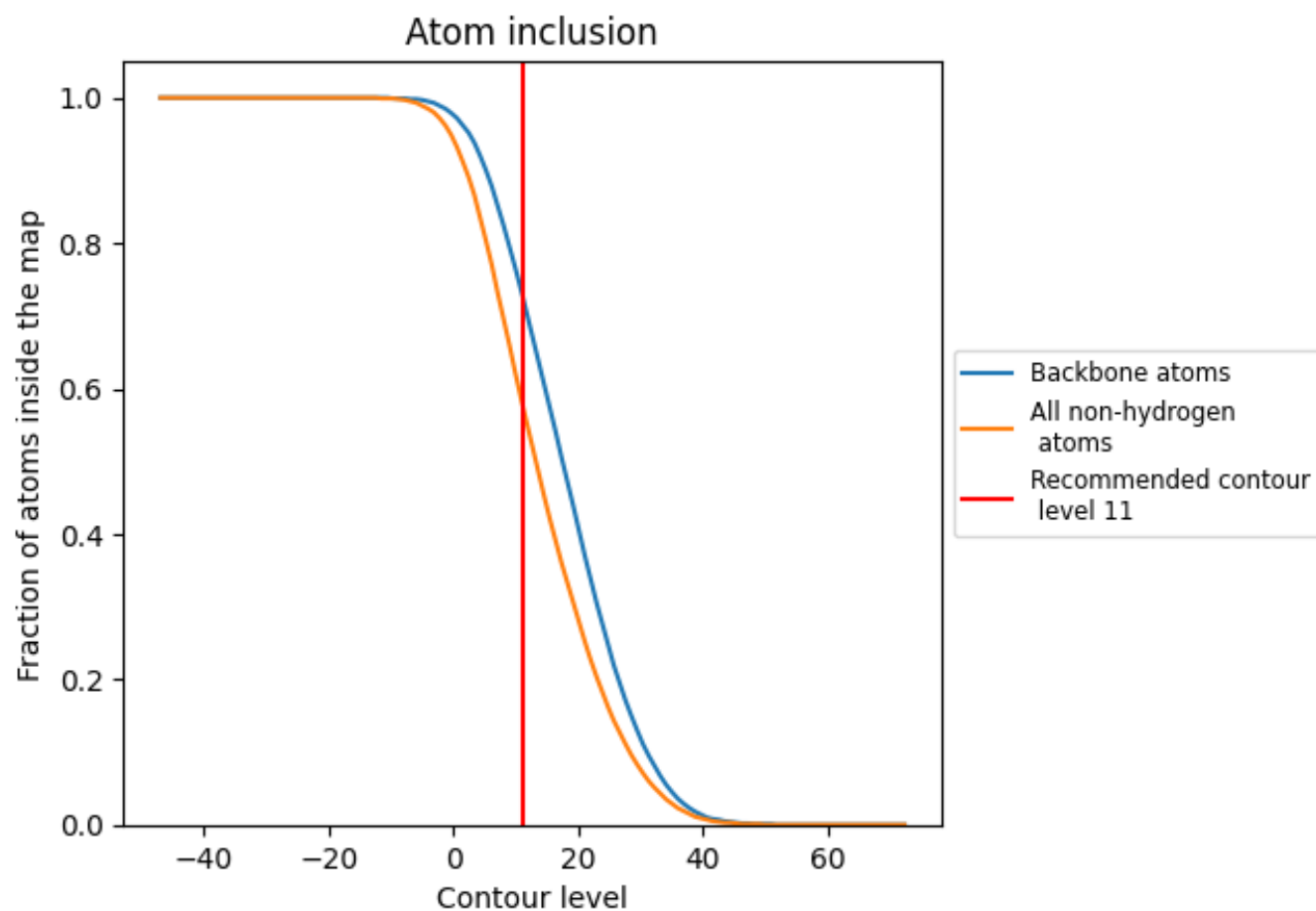
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 58% 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 (11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5810	 0.4160
A	 0.5480	 0.3970
B	 0.5560	 0.4040
C	 0.5500	 0.3990
D	 0.5540	 0.4050
E	 0.5480	 0.3990
F	 0.5540	 0.4050
G	 0.5490	 0.3980
H	 0.5510	 0.4050
I	 0.6270	 0.4420
J	 0.6290	 0.4410
K	 0.6290	 0.4400
L	 0.6300	 0.4410
a	 0.4440	 0.3700
b	 0.4830	 0.3200
c	 0.4470	 0.3680
d	 0.4780	 0.3170
e	 0.4500	 0.3660
f	 0.4730	 0.3210
g	 0.4470	 0.3650
h	 0.4780	 0.3210

