



## wwPDB EM Validation Summary Report ⓘ

Sep 8, 2025 – 12:30 PM EDT

PDB ID : 9NGV / pdb\_00009ngv  
EMDB ID : EMD-49394  
Title : In situ cryo-EM structure of periplasmic ring (PR) of the Legionella Dot/Icm T4SS machine.  
Authors : Yue, J.; Jun, L.  
Deposited on : 2025-02-22  
Resolution : 3.04 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](mailto: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.dev126  
MolProbity : 4-5-2 with Phenix2.0rc1  
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) : 2.45.1

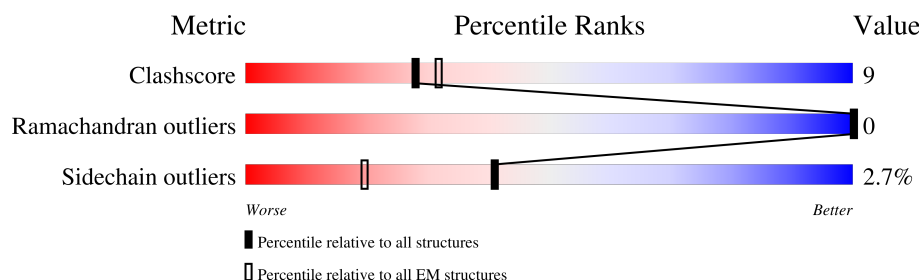
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.04 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  $\geq 3$ , 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	16	<div> <div>12%</div> <div>69%</div> <div>31%</div> </div>
1	Ah	16	<div> <div>19%</div> <div>81%</div> <div>19%</div> </div>
1	Ao	16	<div> <div>19%</div> <div>62%</div> <div>38%</div> </div>
1	Av	16	<div> <div>6%</div> <div>81%</div> <div>19%</div> </div>
1	Bc	16	<div> <div>12%</div> <div>75%</div> <div>25%</div> </div>
1	Bj	16	<div> <div>6%</div> <div>75%</div> <div>25%</div> </div>
1	Bq	16	<div> <div>6%</div> <div>81%</div> <div>19%</div> </div>
1	Bx	16	<div> <div>19%</div> <div>88%</div> <div>12%</div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	Ce	16	
1	Cl	16	
1	Cs	16	
1	Cz	16	
1	Dg	16	
1	Dn	16	
1	Du	16	
1	Eb	16	
1	Ei	16	
1	Ep	16	
2	Ab	9	
2	Ai	9	
2	Ap	9	
2	Aw	9	
2	Bd	9	
2	Bk	9	
2	Br	9	
2	By	9	
2	Cf	9	
2	Cm	9	
2	Ct	9	
2	Da	9	
2	Dh	9	
2	Do	9	
2	Dv	9	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	Ec	9	
2	Ej	9	
2	Eq	9	
3	Ac	16	
3	Aj	16	
3	Aq	16	
3	Ax	16	
3	Be	16	
3	Bl	16	
3	Bs	16	
3	Bz	16	
3	Cg	16	
3	Cn	16	
3	Cu	16	
3	Db	16	
3	Di	16	
3	Dp	16	
3	Dw	16	
3	Ed	16	
3	Ek	16	
3	Er	16	
4	Ad	5	
4	Ak	5	
4	Ar	5	
4	Ay	5	














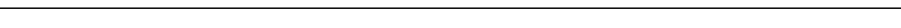

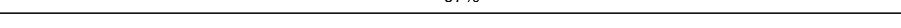
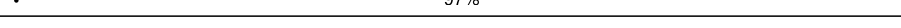
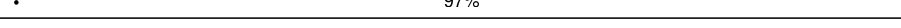
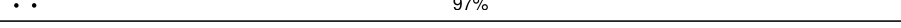
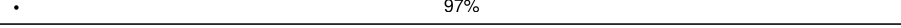
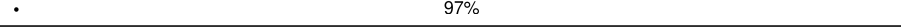
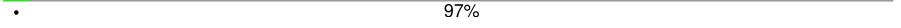
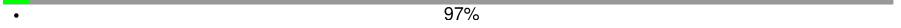
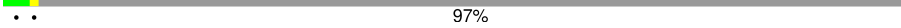
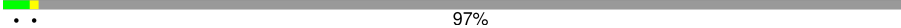
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	Bf	5	
4	Bm	5	
4	Bt	5	
4	Ca	5	
4	Ch	5	
4	Co	5	
4	Cv	5	
4	Dc	5	
4	Dj	5	
4	Dq	5	
4	Dx	5	
4	Ee	5	
4	El	5	
4	Es	5	
5	Ae	269	
5	Al	269	
5	As	269	
5	Az	269	
5	Bg	269	
5	Bn	269	
5	Bu	269	
5	Cb	269	
5	Ci	269	
5	Cp	269	
5	Cw	269	










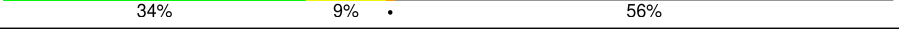
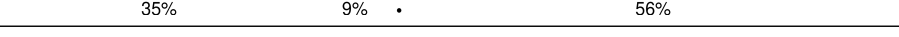


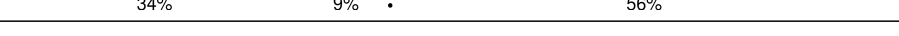




Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	Dd	269	 19% 5% 77%
5	Dk	269	 18% 5% 77%
5	Dr	269	 19% 5% 77%
5	Dy	269	 18% 5% 77%
5	Ef	269	 18% 5% 77%
5	Em	269	 18% 5% 77%
5	Et	269	 19% 5% 77%
6	Af	1048	 97%
6	Am	1048	 97%
6	At	1048	 97%
6	Ba	1048	 97%
6	Bh	1048	 97%
6	Bo	1048	 97%
6	Bv	1048	 97%
6	Cc	1048	 97%
6	Cj	1048	 97%
6	Cq	1048	 97%
6	Cx	1048	 97%
6	De	1048	 97%
6	Dl	1048	 97%
6	Ds	1048	 97%
6	Dz	1048	 97%
6	Eg	1048	 97%
6	En	1048	 97%
6	Eu	1048	 97%

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
7	Ag	361	 33% 10% 56%
7	An	361	 35% 9% 56%
7	Au	361	 34% 10% 56%
7	Bb	361	 36% 9% 56%
7	Bi	361	 35% 9% 56%
7	Bp	361	 32% 12% 56%
7	Bw	361	 37% 7% 56%
7	Cd	361	 34% 10% 56%
7	Ck	361	 37% 7% 56%
7	Cr	361	 34% 9% 56%
7	Cy	361	 35% 9% 56%
7	Df	361	 34% 9% 56%
7	Dm	361	 35% 9% 56%
7	Dt	361	 34% 9% 56%
7	Ea	361	 31% 13% 56%
7	Eh	361	 35% 9% 56%
7	Eo	361	 34% 10% 56%
7	Ev	361	 36% 8% 56%

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 42066 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 unknown peptide A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Ah	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Ao	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Av	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Bc	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Bj	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Bq	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Bx	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Ce	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Cl	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Cs	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Cz	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Dg	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Dn	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Du	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Eb	16	Total	C	N	O	S	0	0
			117	71	20	25	1		
1	Ei	16	Total	C	N	O	S	0	0
			117	71	20	25	1		

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ep	16	Total	C	N	O	S	0	0
			117	71	20	25	1		

- Molecule 2 is a protein called unknown peptide B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ab	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Ai	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Ap	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Aw	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Bd	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Bk	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Br	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	By	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Cf	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Cm	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Ct	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Da	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Dh	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Do	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Dv	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Ec	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Ej	9	Total	C	N	O	S	0	0
			61	35	12	12	2		
2	Eq	9	Total	C	N	O	S	0	0
			61	35	12	12	2		

- Molecule 3 is a protein called unknown peptide C.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	Ac	16	Total	C	N	O	0	0
			125	78	21	26		
3	Aj	16	Total	C	N	O	0	0
			125	78	21	26		
3	Aq	16	Total	C	N	O	0	0
			125	78	21	26		
3	Ax	16	Total	C	N	O	0	0
			125	78	21	26		
3	Be	16	Total	C	N	O	0	0
			125	78	21	26		
3	Bl	16	Total	C	N	O	0	0
			125	78	21	26		
3	Bs	16	Total	C	N	O	0	0
			125	78	21	26		
3	Bz	16	Total	C	N	O	0	0
			125	78	21	26		
3	Cg	16	Total	C	N	O	0	0
			125	78	21	26		
3	Cn	16	Total	C	N	O	0	0
			125	78	21	26		
3	Cu	16	Total	C	N	O	0	0
			125	78	21	26		
3	Db	16	Total	C	N	O	0	0
			125	78	21	26		
3	Di	16	Total	C	N	O	0	0
			125	78	21	26		
3	Dp	16	Total	C	N	O	0	0
			125	78	21	26		
3	Dw	16	Total	C	N	O	0	0
			125	78	21	26		
3	Ed	16	Total	C	N	O	0	0
			125	78	21	26		
3	Ek	16	Total	C	N	O	0	0
			125	78	21	26		
3	Er	16	Total	C	N	O	0	0
			125	78	21	26		

- Molecule 4 is a protein called unknown peptide D.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	Ad	5	Total	C	N	O	0	0
			36	23	5	8		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms				AltConf	Trace
4	Ak	5	Total	C	N	O	0	0
			36	23	5	8		
4	Ar	5	Total	C	N	O	0	0
			36	23	5	8		
4	Ay	5	Total	C	N	O	0	0
			36	23	5	8		
4	Bf	5	Total	C	N	O	0	0
			36	23	5	8		
4	Bm	5	Total	C	N	O	0	0
			36	23	5	8		
4	Bt	5	Total	C	N	O	0	0
			36	23	5	8		
4	Ca	5	Total	C	N	O	0	0
			36	23	5	8		
4	Ch	5	Total	C	N	O	0	0
			36	23	5	8		
4	Co	5	Total	C	N	O	0	0
			36	23	5	8		
4	Cv	5	Total	C	N	O	0	0
			36	23	5	8		
4	Dc	5	Total	C	N	O	0	0
			36	23	5	8		
4	Dj	5	Total	C	N	O	0	0
			36	23	5	8		
4	Dq	5	Total	C	N	O	0	0
			36	23	5	8		
4	Dx	5	Total	C	N	O	0	0
			36	23	5	8		
4	Ee	5	Total	C	N	O	0	0
			36	23	5	8		
4	El	5	Total	C	N	O	0	0
			36	23	5	8		
4	Es	5	Total	C	N	O	0	0
			36	23	5	8		

- Molecule 5 is a protein called IcmG (DotF).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ae	63	Total	C	N	O	S	0	0
			484	308	84	91	1		
5	Al	63	Total	C	N	O	S	0	0
			484	308	84	91	1		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
5	As	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Az	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Bg	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Bn	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Bu	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Cb	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Ci	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Cp	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Cw	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Dd	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Dk	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Dr	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Dy	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Ef	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Em	63	Total 484	C 308	N 84	O 91	S 1	0	0
5	Et	63	Total 484	C 308	N 84	O 91	S 1	0	0

- Molecule 6 is a protein called IcmE (DotG).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Af	34	Total 276	C 168	N 47	O 60	S 1	0	0
6	Am	34	Total 276	C 168	N 47	O 60	S 1	0	0
6	At	34	Total 276	C 168	N 47	O 60	S 1	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Ba	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Bh	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Bo	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Bv	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Cc	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Cj	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Cq	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Cx	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	De	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Dl	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Ds	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Dz	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Eg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	En	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
6	Eu	34	Total	C	N	O	S	0	0
			276	168	47	60	1		

- Molecule 7 is a protein called IcmK (DotH).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ag	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
7	An	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
7	Au	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		
7	Bb	160	Total	C	N	O	S	0	0
			1238	795	207	233	3		

*Continued on next page...*

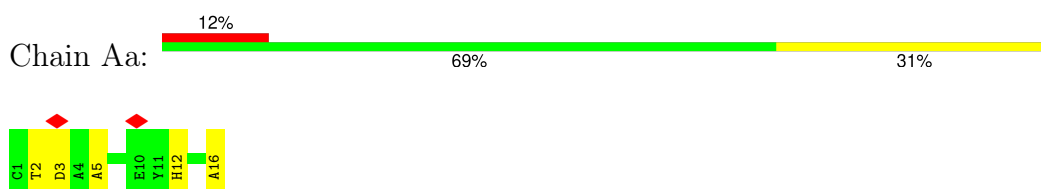
*Continued from previous page...*

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Bi	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Bp	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Bw	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Cd	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Ck	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Cr	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Cy	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Df	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Dm	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Dt	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Ea	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Eh	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Eo	160	Total 1238	C 795	N 207	O 233	S 3	0	0
7	Ev	160	Total 1238	C 795	N 207	O 233	S 3	0	0

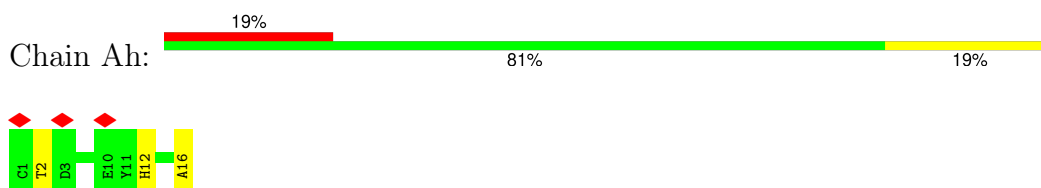
### 3 Residue-property plots [i](#)

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.

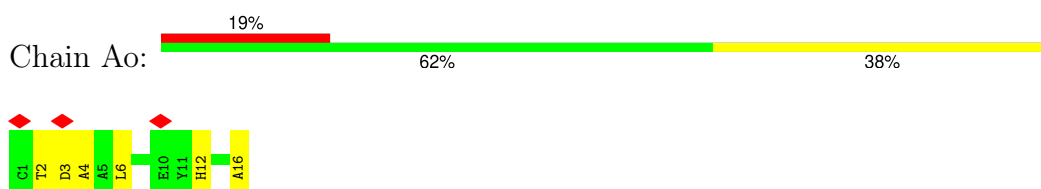
- Molecule 1: unknown peptide A



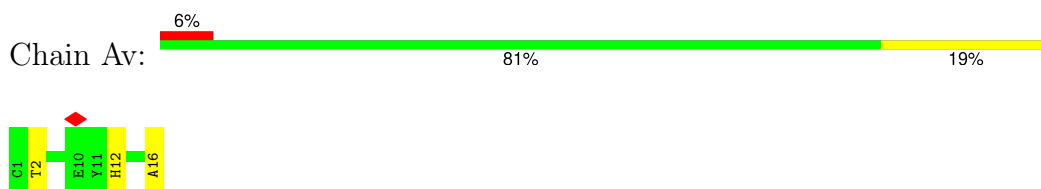
- Molecule 1: unknown peptide A



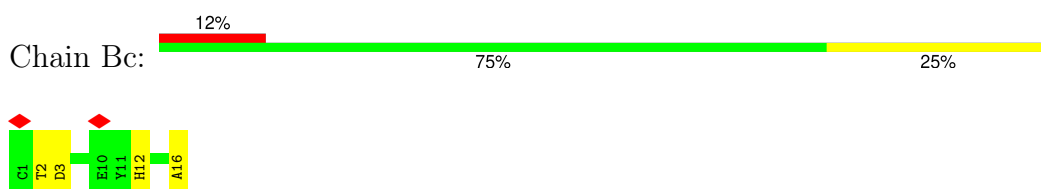
- Molecule 1: unknown peptide A



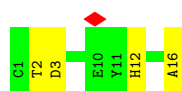
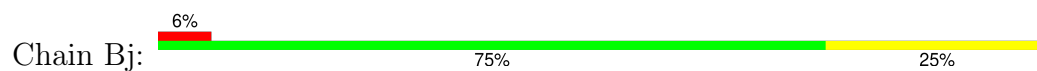
- Molecule 1: unknown peptide A



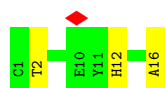
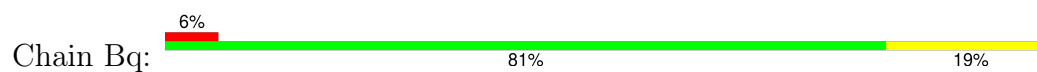
- Molecule 1: unknown peptide A



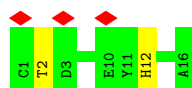
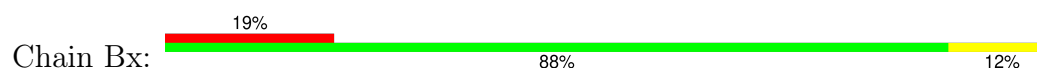
- Molecule 1: unknown peptide A



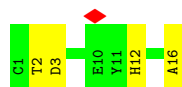
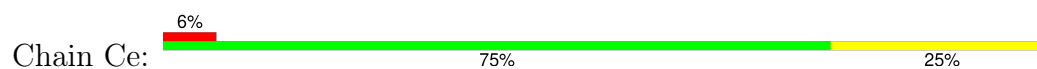
- Molecule 1: unknown peptide A



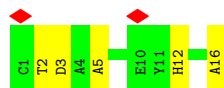
- Molecule 1: unknown peptide A



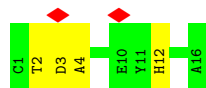
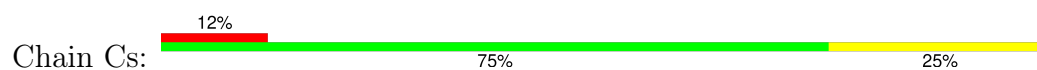
- Molecule 1: unknown peptide A



- Molecule 1: unknown peptide A



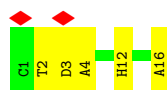
- Molecule 1: unknown peptide A



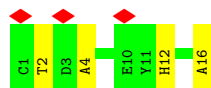
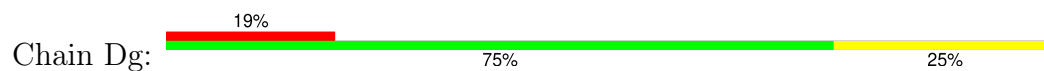
- Molecule 1: unknown peptide A



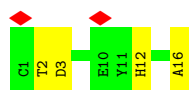
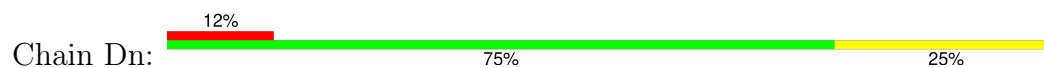




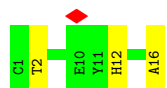
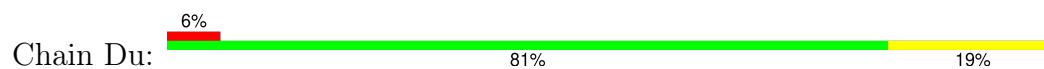
- Molecule 1: unknown peptide A



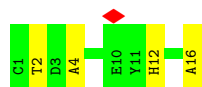
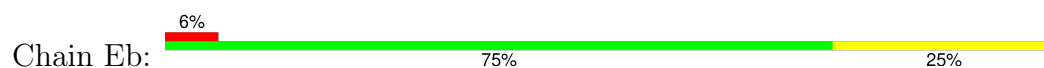
- Molecule 1: unknown peptide A



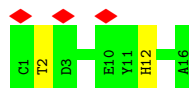
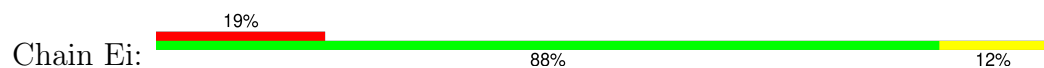
- Molecule 1: unknown peptide A



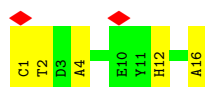
- Molecule 1: unknown peptide A



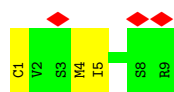
- Molecule 1: unknown peptide A



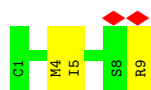
- Molecule 1: unknown peptide A



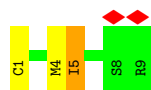
- Molecule 2: unknown peptide B



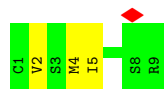
- Molecule 2: unknown peptide B



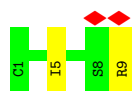
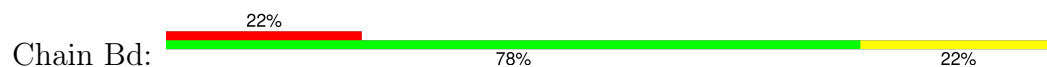
- Molecule 2: unknown peptide B



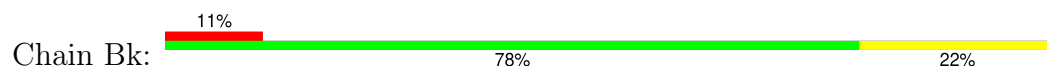
- Molecule 2: unknown peptide B



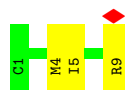
- Molecule 2: unknown peptide B



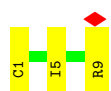
- Molecule 2: unknown peptide B



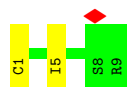
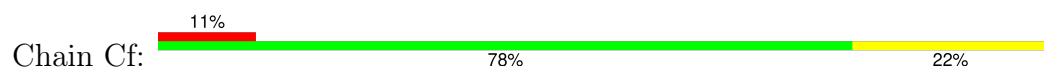
- Molecule 2: unknown peptide B



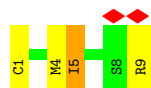
- Molecule 2: unknown peptide B



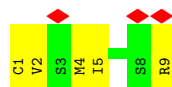
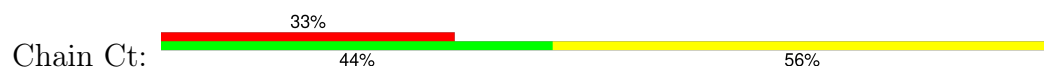
- Molecule 2: unknown peptide B



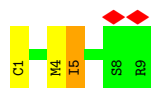
- Molecule 2: unknown peptide B



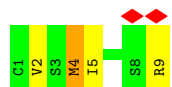
- Molecule 2: unknown peptide B



- Molecule 2: unknown peptide B

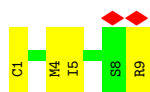


- Molecule 2: unknown peptide B

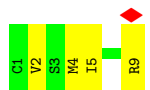


- Molecule 2: unknown peptide B

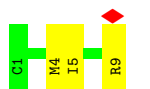




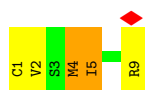
- Molecule 2: unknown peptide B



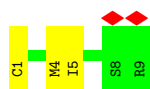
- Molecule 2: unknown peptide B



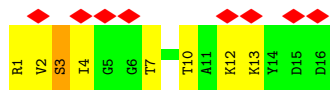
- Molecule 2: unknown peptide B



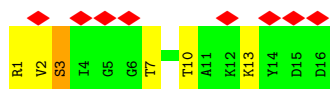
- Molecule 2: unknown peptide B



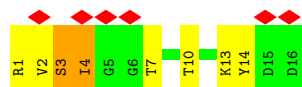
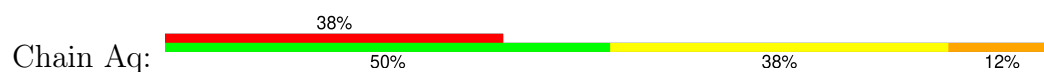
- Molecule 3: unknown peptide C



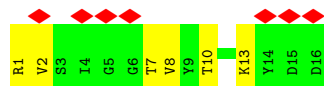
- Molecule 3: unknown peptide C



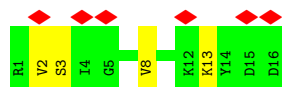
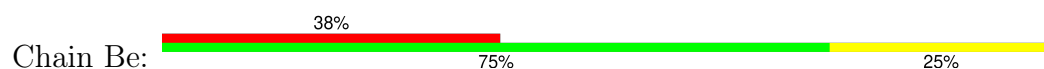
- Molecule 3: unknown peptide C



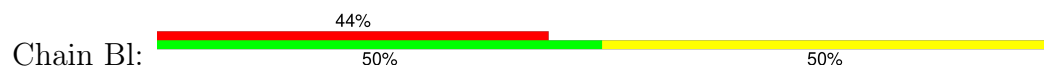
- Molecule 3: unknown peptide C



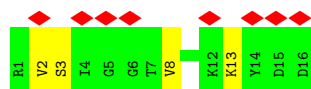
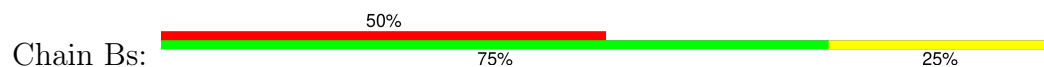
- Molecule 3: unknown peptide C



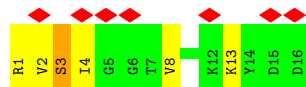
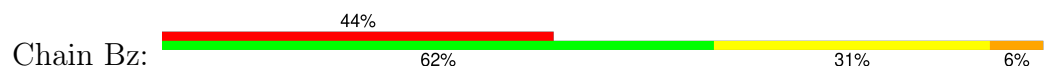
- Molecule 3: unknown peptide C



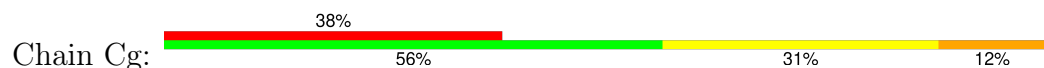
- Molecule 3: unknown peptide C



- Molecule 3: unknown peptide C

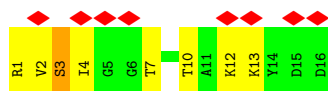


- Molecule 3: unknown peptide C

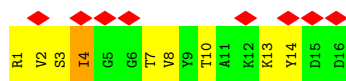




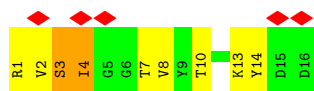
- Molecule 3: unknown peptide C



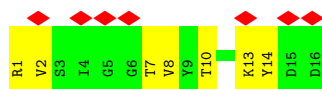
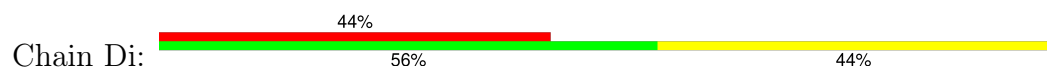
- Molecule 3: unknown peptide C



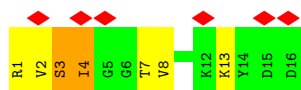
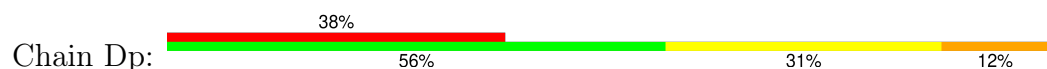
- Molecule 3: unknown peptide C



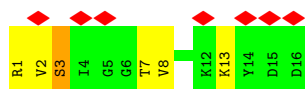
- Molecule 3: unknown peptide C



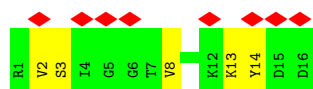
- Molecule 3: unknown peptide C



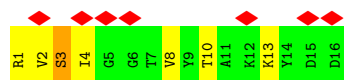
- Molecule 3: unknown peptide C



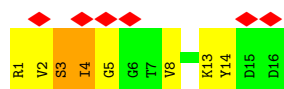
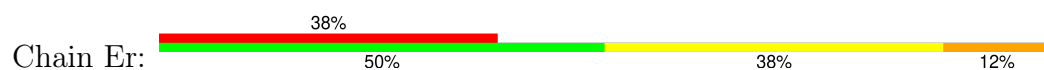
- Molecule 3: unknown peptide C



- Molecule 3: unknown peptide C



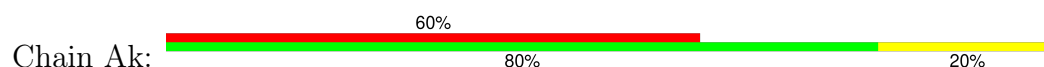
- Molecule 3: unknown peptide C



- Molecule 4: unknown peptide D



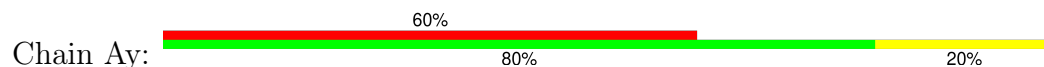
- Molecule 4: unknown peptide D



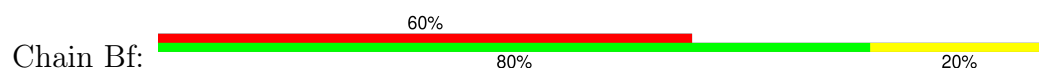
- Molecule 4: unknown peptide D



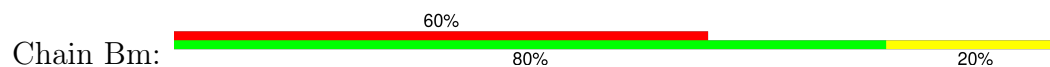
- Molecule 4: unknown peptide D



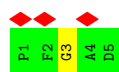
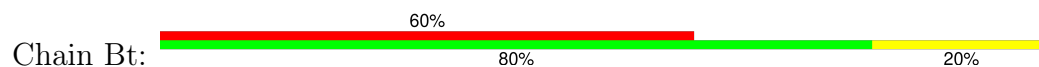
- Molecule 4: unknown peptide D



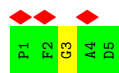
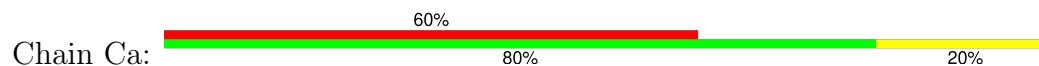
- Molecule 4: unknown peptide D



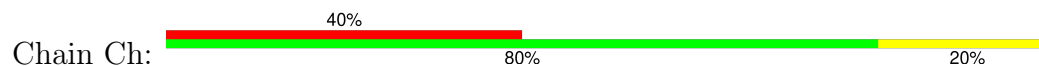
- Molecule 4: unknown peptide D



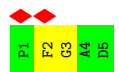
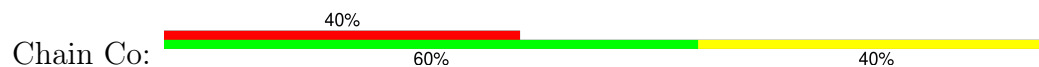
- Molecule 4: unknown peptide D



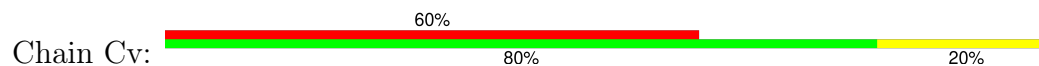
- Molecule 4: unknown peptide D



- Molecule 4: unknown peptide D



- Molecule 4: unknown peptide D



- Molecule 4: unknown peptide D

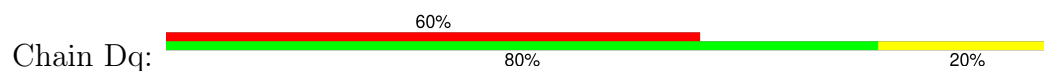




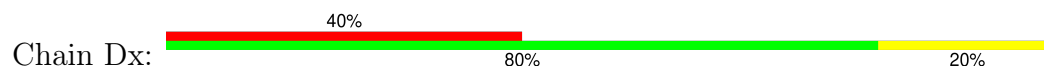
- Molecule 4: unknown peptide D



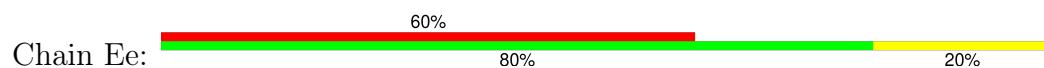
- Molecule 4: unknown peptide D



- Molecule 4: unknown peptide D



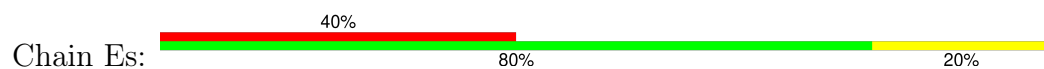
- Molecule 4: unknown peptide D



- Molecule 4: unknown peptide D



- Molecule 4: unknown peptide D



- Molecule 5: IcmG (DotF)

Chain Ae:  19% 5% 77%

MET	MET	ALA	GLU	HIS	ASP	GLN	ASN	SER	ASP	GLY	THR	LYS	PHE	ALA	GLU	SER	ASP	LEU	LEU	ASP	SER	TYR	ASP	GLN	GLY	ALA	GLY	GLN	VAL
VAL	PHE	ILE	GLU	MET	VAL	VAL	LYS	LYS	ILE	ILE	THR	TRP	MET	PHE	PHE	GLN	SER	ASP	LEU	VAL	SER	SER	GLN	VAL	THR	PRO	ALA	ILE	ASP
ASP	PRO	ASP	LEU	ASP	LYS	VAL	VAL	VAL	ALA	ASP	THR	GLU	THR	LYS	THR	GLN	SER	LEU	VAL	SER	ARG	SER	GLU	VAL	THR	LEU	SER	GLN	GLN
SER	GLU	VAL	ILE	ASN	VAL	VAL	MET	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
GLU	VAL	ILE	ASN	VAL	VAL	VAL	MET	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
R207	I212	Q213	I216	R219	A220	W221	R253	I254	L255	V261	I262	K263	F264	S269															

• Molecule 5: IcmG (DotF)

Chain Al:  19% 5% 77%

MET	MET	ALA	GLU	HIS	ASP	GLN	ASN	SER	ASP	GLY	THR	LYS	PHE	ALA	GLU	SER	ASP	LEU	LEU	ASP	SER	TYR	ASP	GLN	GLY	ALA	GLY	GLN	VAL
VAL	PHE	ILE	GLU	MET	VAL	VAL	LYS	LYS	ILE	ILE	THR	TRP	MET	PHE	PHE	GLN	SER	ASP	LEU	VAL	SER	SER	GLN	VAL	THR	PRO	ALA	ILE	ASP
ASP	PRO	ASP	LEU	ASP	LYS	VAL	VAL	VAL	ALA	ASP	THR	GLU	THR	LYS	THR	GLN	SER	LEU	VAL	SER	ARG	SER	GLU	VAL	THR	LEU	SER	GLN	GLN
SER	GLU	VAL	ILE	ASN	VAL	VAL	MET	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
GLU	VAL	ILE	ASN	VAL	VAL	VAL	MET	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
R207	I212	Q213	R219	I223	D248	R253	I254	L255	V261	I262	K263	F264	S269																

• Molecule 5: IcmG (DotF)

Chain As:  19% 5% 77%

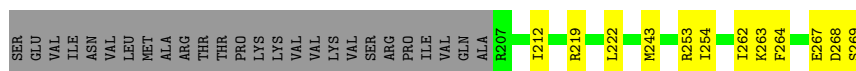
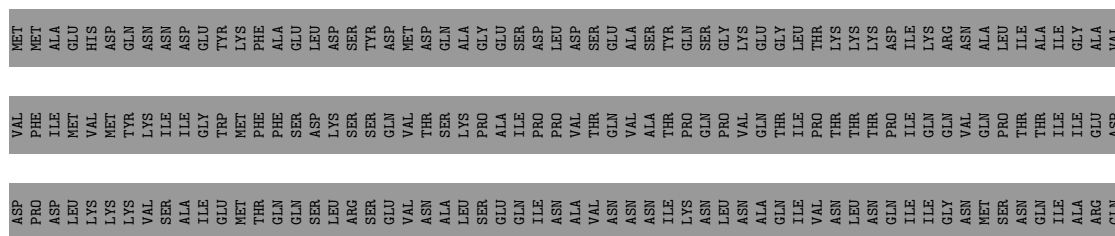
MET	MET	ALA	GLU	HIS	ASP	GLN	ASN	SER	ASP	GLY	THR	LYS	PHE	ALA	GLU	SER	ASP	LEU	LEU	ASP	SER	TYR	ASP	GLN	GLY	ALA	GLY	GLN	VAL
VAL	PHE	ILE	GLU	MET	VAL	VAL	LYS	LYS	ILE	ILE	THR	TRP	MET	PHE	PHE	GLN	SER	ASP	LEU	VAL	SER	SER	GLN	VAL	THR	PRO	ALA	ILE	ASP
ASP	PRO	ASP	LEU	ASP	LYS	VAL	VAL	VAL	ALA	ASP	THR	GLU	THR	LYS	THR	GLN	SER	LEU	VAL	SER	ARG	SER	GLU	VAL	THR	LEU	SER	GLN	GLN
SER	GLU	VAL	ILE	ASN	VAL	VAL	MET	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
GLU	VAL	ILE	ASN	VAL	VAL	VAL	MET	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
R207	I212	Q213	R219	R233	L250	R253	I254	L255	V261	I262	K263	F264	D268	S269															

• Molecule 5: IcmG (DotF)

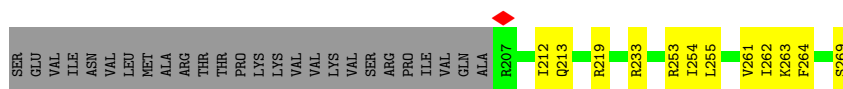
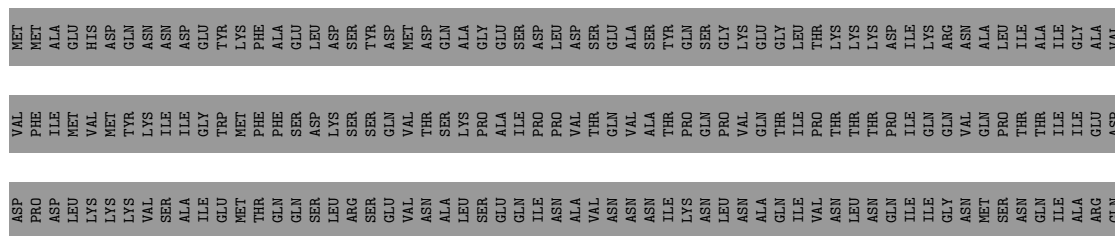
Chain Az:  18% 6% 77%

MET	MET	ALA	GLU	HIS	ASP	GLN	ASN	SER	ASP	GLY	THR	LYS	PHE	ALA	GLU	SER	ASP	LEU	LEU	ASP	SER	TYR	ASP	GLN	GLY	ALA	GLY	GLN	VAL
VAL	PHE	ILE	GLU	MET	VAL	VAL	LYS	LYS	ILE	ILE	THR	TRP	MET	PHE	PHE	GLN	SER	ASP	LEU	VAL	SER	SER	GLN	VAL	THR	PRO	ALA	ILE	ASP
ASP	PRO	ASP	LEU	ASP	LYS	VAL	VAL	VAL	ALA	ASP	THR	GLU	THR	LYS	THR	GLN	SER	LEU	VAL	SER	ARG	SER	GLU	VAL	THR	LEU	SER	GLN	GLN
SER	GLU	VAL	ILE	ASN	VAL	VAL	MET	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
GLU	VAL	ILE	ASN	VAL	VAL	VAL	MET	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
R207	I212	Q213	R219	R233	L250	R253	I254	L255	V261	I262	K263	F264	D268	S269															

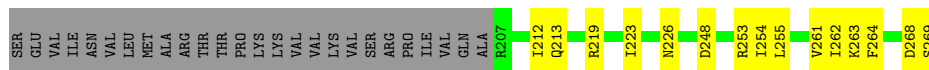
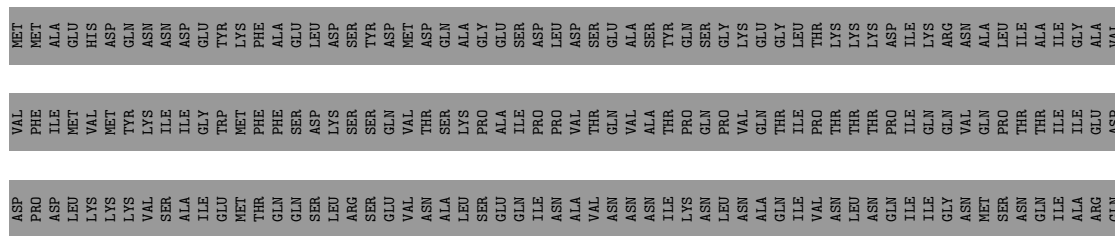
- Molecule 5: IcmG (DotF)



- Molecule 5: IcmG (DotF)



- Molecule 5: IcmG (DotF)



- Molecule 5: IcmG (DotF)

77%

- Molecule 5: IcmG (DotF)

77%

- Molecule 5: IcmG (DotF)

77%

- Molecule 5: IcmG (DotF)

77%

ASP	PRO	ASP	LEU	LYS	LYS	VAL	ALA	SER	THR	GLU	MET	THR	GLN	GLN	SER	LEU	ARG	SER	GLU	VAL	ASN	ALA	ASN	ASN	ASN	LYS	ASN	LEU	ALA	GLN	ILE	VAL	ASN	GLN	ILE	GLY	ASN	MET	SER	ASN	GLN	ILE	ALA	ARG
SER	GLU	VAL	ILE	ASN	VAL	LEU	MET	ALA	ARG	THR	PRO	LYS	LYS	VAL	VAL	LYS	VAL	SER	ARG	PRO	ILE	VAL	ALA	R267	I212	Q213	R219	I223	D248	S249	L250	R253	I254	L255	V261	I262	K263	F264	S269					

- Molecule 5: IcmG (DotF)

Chain Dd: 

[illegible]

SER	GLU	VAL	ILE	ASN	VAL	LEU	MET	ALA	ARG	THR	THR	PRO	LYS	LYS	VAL	LYS	VAL	SER	ARG	PRO	ILE	ILE	GLN	ALA	R207	I212	R219	R233	L250	R253	I254	L255	V261	I262	R263	F264	D268	S269
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------

- Molecule 5: IcmG (DotF)

Chain Dk: 

[illegible]

SER	GLU	VAL	ILE	ASN	VAL	LEU	MET	ALA	ARG	THR	THR	PRO	LYS	LYS	VAL	VAL	LYS	VAL	SER	ARG	ARG	PRO	ILE	VAL	GLN	ALA	R207	L212	R219	R233	M243	L250	G252	R253	L254	L255	V261	L262	G263	P264	D268	S269
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

- Molecule 5: IcmG (DotF)

Chain Dr:  19% 5% 77%

[illegible]

SER	GLU	VAL	ILE	ASN	VAL	LEU	MET	ARG	ALA	THR	THR	PRO	LYS	LYS	VAL	VAL	LYS	VAL	SER	ARG	PRO	PRO	ILE	ILE	VAL	GLN	ALA		R207	I212		R219		M243	D248	D249	L250		R253	I254		I262	K263	F264		E267	D268		S269
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	------	------	--	------	--	------	------	------	------	--	------	------	--	------	------	------	--	------	------	--	------

- Molecule 5: IcmG (DotF)









ASP	VAL	THR	THR	ILE	THR	GLY	GLY	ASN	ASN	ILE	THR	VAL	ALA	ASN	GLY	VAL	GLY	ARG	SER	THR	LEU	GLU	ASN	ALA	VAL	ILE	GLY	LEU	ALA	THR	THR	VAL	GLY	LYS	ALA	THR	TRP	SER	GLN	GLN	ALA	GLN	GLN	LEU	PHE	ASN	THR	PRO	THR	THR	VAL	GLU	VAL	THR	GLY	GLY	LEU	ILE	LEU	PHE	THR	GLN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 6: IcmE (DotG)

Chain At:  97%

[illegible]

- Molecule 6: IcmE (DotG)

- Molecule 6: IcmE (DotG)



- Molecule 6: IcmE (DotG)

Chain Bv:  97%

[illegible]

- Molecule 6: IcmE (DotG)

Chain Cc:  97%

[illegible]

[illegible]

- Molecule 6: IcmE (DotG)

Chain Cj:  97%

[illegible]

ASP	VAL	THR	THR	ILE	THR	GLY	ASN	ILE	THR	THR	VAL	ALA	ASN	GLY	VAL	ARG	GLY	SER	THR	LEU	GLU	ASN	ALA	VAL	ILE	GLY	LEU	ALA	THR	THR	VAL	GLY	LYS	ALA	SER	GLN	GLN	ALA	GLN	GLN	LEU	PHE	ASN	THR	PRO	THR	THR	VAL	GLY	THR	THR	GLY	LEU	ILE	GLY	PHE	THR	GLN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 6: IcmE (DotG)

Chain Cq:  97%

[illegible]



[illegible]

- Molecule 6: IcmE (DotG)

Chain Cx:  97%

[illegible]



VAL	THR	THR	ILE	GLY	GLY	GLY	ASN	ASN	ILE	THR	VAL	ALA	ASN	GLY	VAL	GLY	ARG	SER	THR	LEU	GLU	ASN	ALA	VAL	VAL	GLY	LYS	ALA	THR	SER	GLN	GLN	ALA	GLN	GLN	LEU	PHE	ASN	THR	PRO	THR	THR	VAL	GLU	VAL	THR	GLY	ILE	LEU	PHE	THR	GLN	ASN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 6: IcmE (DotG)

Chain D1:  97%

[illegible]

THR	GLN	ASP	VAL	THR	THR	ILE	GLY	GLY	THR	GLY	GLY	ASN	ASN	ILE	THR	VAL	ALA	ALA	ASN	GLY	VAL	GLY	ARG	SER	THR	LEU	GLU	ASN	ALA	VAL	ILE	GLY	LEU	ALA	THR	VAL	GLY	LYS	THR	TRP	SER	GLN	GLN	ALA	GLN	GLN	GLN	LEU	PHE	ASN	THR	PRO	THR	THR	THR	VAL	GLU	VAL	VAL	TYR	SER	GLY	THR	GLY	LEU	ILE	LEU	PHE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 6: IcmE (DotG)

Chain Ds:  97%

[illegible]

THR	GLN	ASP	VAL	THR	THR	ILE	GLY	GLY	THR	GLY	ASN	ASN	ILE	THR	VAL	ALA	ALA	ASN	GLY	VAL	GLY	ARG	SER	THR	LEU	GLU	ASN	ALA	VAL	ILE	GLY	LEU	ALA	THR	VAL	GLY	LYS	THR	TRP	SER	GLN	GLN	ALA	GLN	GLN	GLN	LEU	PHE	ASN	THR	PRO	THR	THR	THR	VAL	GLU	VAL	VAL	TYR	SER	GLY	THR	GLY	LEU	ILE	LEU	PHE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 6: IcmE (DotG)

Chain Dz:  97%

[illegible]

[illegible]

- Molecule 6: IcmE (DotG)

Chain Eg:  97%

[illegible]

ILE	GLY	THR	GLY	THR	GLY	GLY	ASN	ASN	ILE	THR	VAL	VAL	ALA	ASN	GLY	VAL	GLY	ARG	SER	THR	LEU	GLU	ASN	ALA	ALA	VAL	ILE	GLY	LEU	ALA	THR	THR	VAL	GLY	LYS	ALA	TRP	SER	SER	GLN	GLN	ALA	GLN	GLN	LEU	PHE	PHE	ASN	THR	THR	PRO	THR	THR	THR	VAL	VAL	VAL	TYR	SER	SER	GLY	THR	THR	THR	GLY	LEU	ILE	LEU																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
PHE	THR	GLN	ASP	VAL	THR	THR	THR	ILE																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				

● Molecule 6: IcmE (DotG)

Chain En: .. 97%

SER	ILE	ALA	GLN	GLY	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY</
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-------

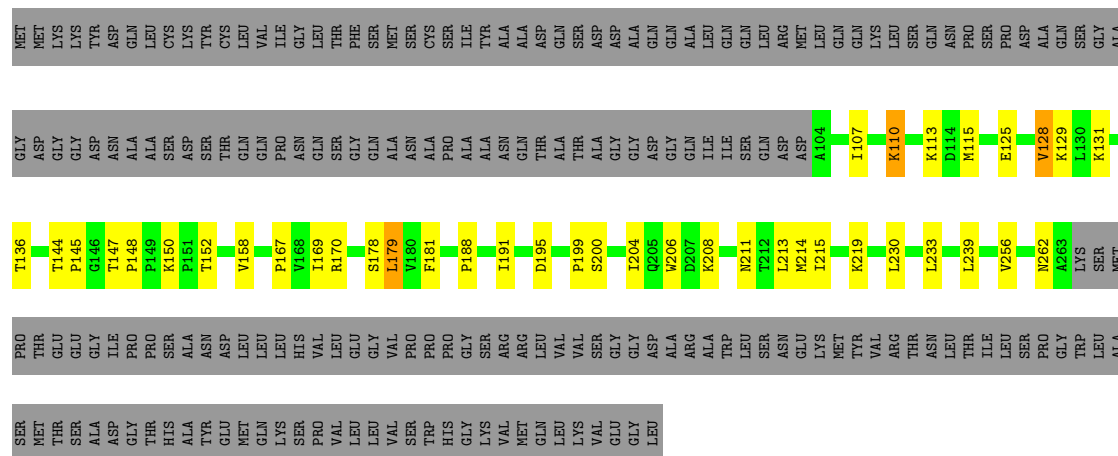
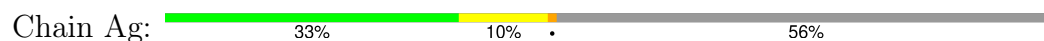
- Molecule 6: IcmE (DotG)

Chain Eu:  97%

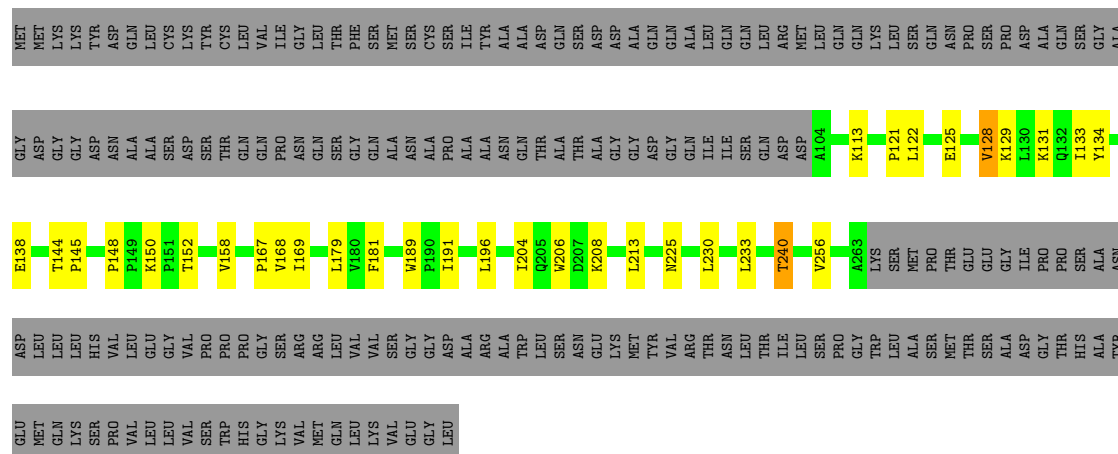
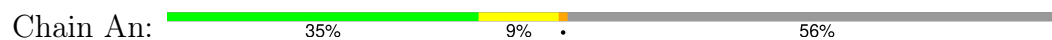
[illegible]



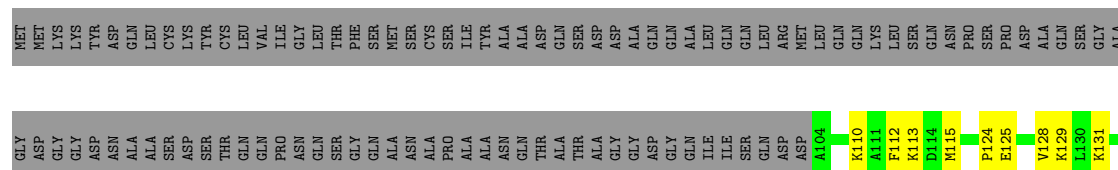
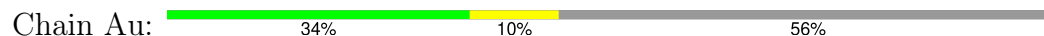
- Molecule 7: IcmK (DotH)

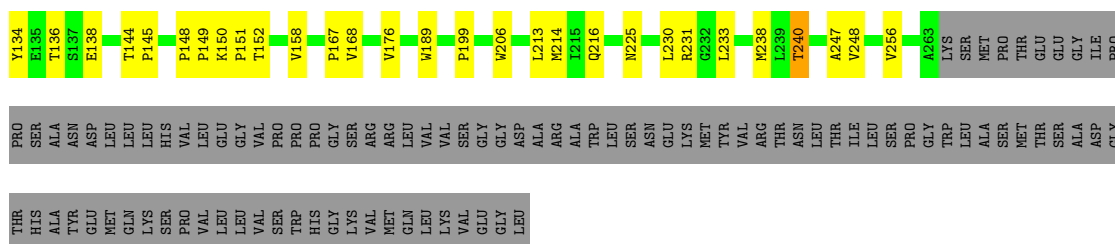


- Molecule 7: IcmK (DotH)

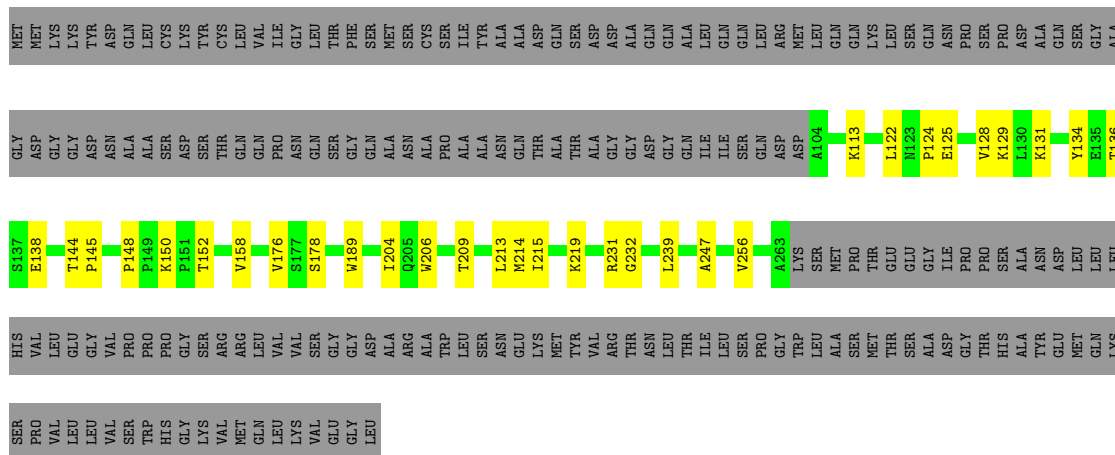
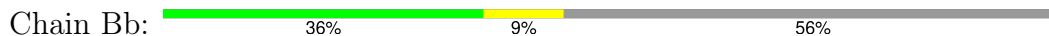


- Molecule 7: IcmK (DotH)

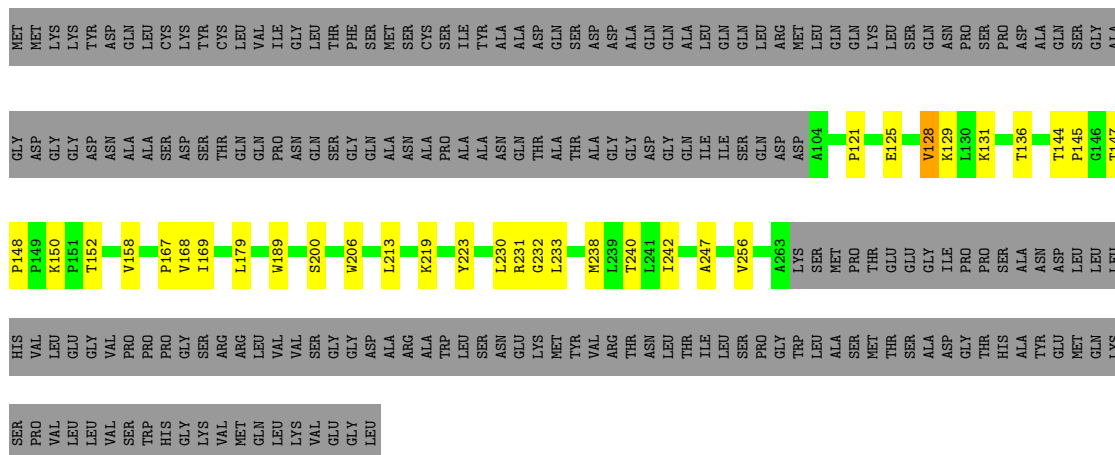
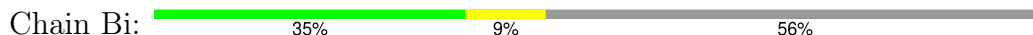




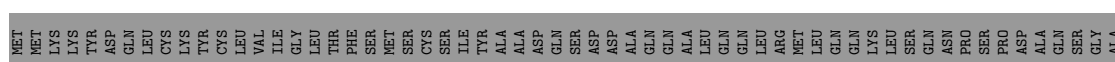
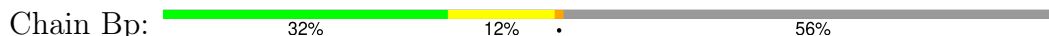
- Molecule 7: IcmK (DotH)

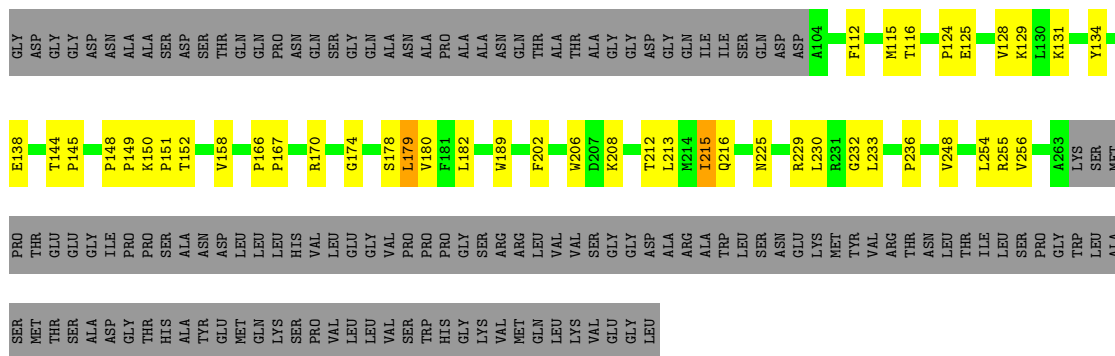


- Molecule 7: IcmK (DotH)

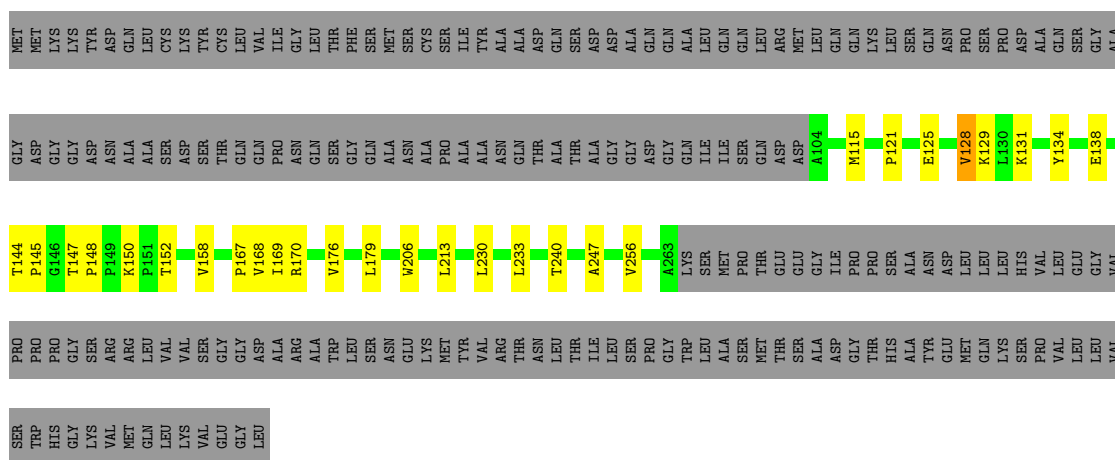
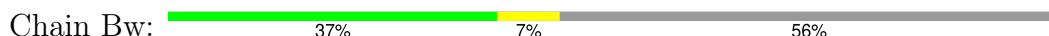


- Molecule 7: IcmK (DotH)

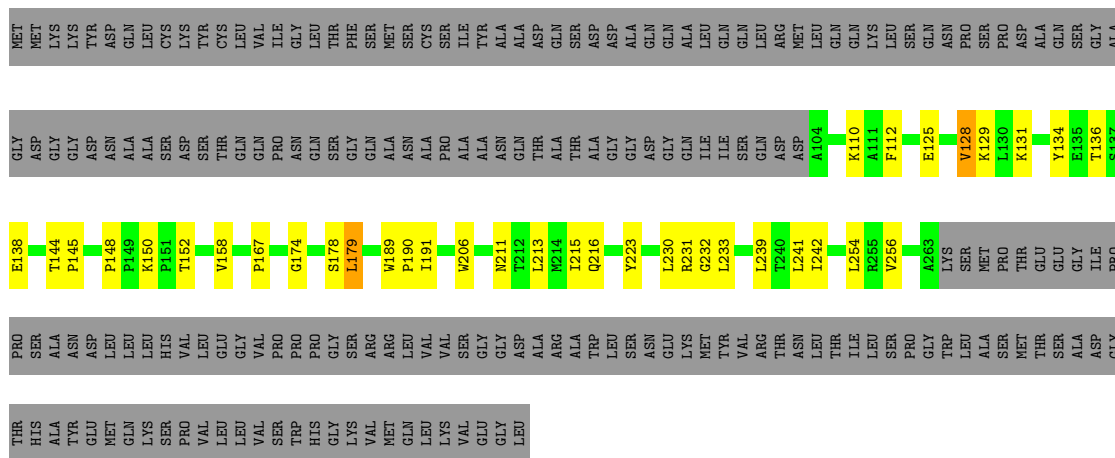
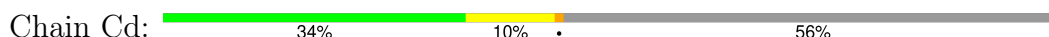




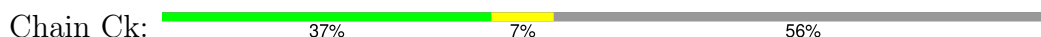
- Molecule 7: IcmK (DotH)



- Molecule 7: IcmK (DotH)

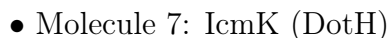


- Molecule 7: IcmK (DotH)

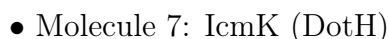




Response	Percentage
Yes, the U.S. is a democracy	34%
No, the U.S. is not a democracy	9%
Don't know	56%



Response	Percentage
Yes, the U.S. is a democracy	35%
No, the U.S. is not a democracy	9%
Don't know	56%



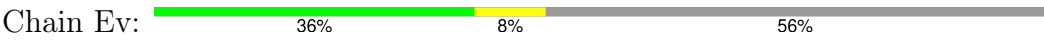
Response	Percentage
Yes	34%
No	9%
Don't know	56%





ALA  
TYR  
GLU  
MET  
GLN  
LYS  
SER  
PRO  
VAL  
LEU  
VAL  
SER  
TRP  
HIS  
GLY  
LYS  
VAL  
MET  
GLN  
LEU  
VAL  
GLY  
LEU

● Molecule 7: IcmK (DotH)



MET  
MET  
LYS  
LYS  
TYR  
ASP  
GLN  
LEU  
CYS  
LYS  
TYR  
CYS  
LEU  
VAL  
HIS  
GLY  
LEU  
THR  
PHE  
SER  
MET  
SER  
CYS  
VAL  
GLY  
LEU

GLY  
ASP  
GLY  
ASP  
ASN  
ALA  
SER  
ASP  
THR  
GLN  
PRO  
ASN  
GLN  
SER  
GLY  
GLN  
ALA  
ASN  
THR  
THR  
ALA  
GLY  
GLY  
GLN  
ILE  
ILE  
SER  
ASP  
ASP  
ASP  
A104  
K113  
P121  
E125  
V128  
K129  
L130  
K131  
T136  
T144  
P145

G146  
T147  
P149  
K150  
P151  
T152  
V158  
P167  
R170  
W189  
P190  
I191  
D195  
W206  
N211  
T212  
L213  
R231  
G232  
L233  
N234  
V237  
N238  
L239  
T240  
V248  
V256  
A263  
LYS  
SER  
MET  
PRO  
THR  
GLU  
GLY  
ILE  
PRO  
PRO  
HIS  
SER  
ALA  
LEU  
TRP  
GLY  
LEU  
ALA  
SER  
MET  
THR  
SER  
ALA  
ASP  
GLY  
THR  
HIS  
ALA  
TYR  
ASN  
GLY  
MET  
LEU  
LEU  
HIS

VAL  
LEU  
GLY  
VAL  
PRO  
PRO  
GLY  
SER  
ARG  
ARG  
LEU  
VAL  
VAL  
SER  
GLY  
GLY  
ASP  
ALA  
ARG  
ALA  
TRP  
LEU  
SER  
ASN  
GLY  
LYS  
MET  
TYR  
VAL  
ARG  
THR  
ASN  
LEU  
THR  
ILE  
LEU  
SER  
GLY  
TRP  
LEU  
ALA  
SER  
MET  
THR  
SER  
ALA  
ASP  
GLY  
THR  
HIS  
ALA  
TYR  
ASN  
GLY  
MET  
GLN  
LYS  
SER

PRO  
VAL  
LEU  
VAL  
SER  
TRP  
HIS  
LYS  
VAL  
MET  
GLN  
LEU  
VAL  
VAL  
GLY  
GLY  
LEU

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76406	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TECNAI 12	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	73	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.503	Depositor
Minimum map value	-1.764	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.2	Depositor
Map size ( $\text{\AA}$ )	598.08, 598.08, 598.08	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.335, 1.335, 1.335	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	Aa	0.10	0/118	0.26	0/158
1	Ah	0.09	0/118	0.23	0/158
1	Ao	0.09	0/118	0.26	0/158
1	Av	0.07	0/118	0.21	0/158
1	Bc	0.07	0/118	0.22	0/158
1	Bj	0.07	0/118	0.22	0/158
1	Bq	0.06	0/118	0.20	0/158
1	Bx	0.08	0/118	0.23	0/158
1	Ce	0.08	0/118	0.23	0/158
1	Cl	0.08	0/118	0.21	0/158
1	Cs	0.07	0/118	0.21	0/158
1	Cz	0.07	0/118	0.23	0/158
1	Dg	0.07	0/118	0.21	0/158
1	Dn	0.07	0/118	0.20	0/158
1	Du	0.13	0/118	0.32	0/158
1	Eb	0.06	0/118	0.22	0/158
1	Ei	0.08	0/118	0.24	0/158
1	Ep	0.10	0/118	0.24	0/158
2	Ab	0.10	0/60	0.26	0/76
2	Ai	0.07	0/60	0.23	0/76
2	Ap	0.09	0/60	0.30	0/76
2	Aw	0.09	0/60	0.29	0/76
2	Bd	0.10	0/60	0.32	0/76
2	Bk	0.12	0/60	0.45	0/76
2	Br	0.11	0/60	0.25	0/76
2	By	0.12	0/60	0.39	0/76
2	Cf	0.11	0/60	0.36	0/76
2	Cm	0.09	0/60	0.27	0/76
2	Ct	0.11	0/60	0.27	0/76
2	Da	0.08	0/60	0.30	0/76
2	Dh	0.08	0/60	0.30	0/76
2	Do	0.08	0/60	0.26	0/76
2	Dv	0.17	0/60	0.56	0/76
2	Ec	0.11	0/60	0.27	0/76

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	Ej	0.08	0/60	0.31	0/76
2	Eq	0.09	0/60	0.29	0/76
3	Ac	0.15	0/126	0.39	0/167
3	Aj	0.09	0/126	0.31	0/167
3	Aq	0.10	0/126	0.35	0/167
3	Ax	0.09	0/126	0.30	0/167
3	Be	0.10	0/126	0.31	0/167
3	Bl	0.12	0/126	0.35	0/167
3	Bs	0.12	0/126	0.31	0/167
3	Bz	0.14	0/126	0.37	0/167
3	Cg	0.12	0/126	0.36	0/167
3	Cn	0.12	0/126	0.40	0/167
3	Cu	0.10	0/126	0.36	0/167
3	Db	0.10	0/126	0.37	0/167
3	Di	0.08	0/126	0.29	0/167
3	Dp	0.14	0/126	0.34	0/167
3	Dw	0.13	0/126	0.32	0/167
3	Ed	0.12	0/126	0.31	0/167
3	Ek	0.13	0/126	0.37	0/167
3	Er	0.11	0/126	0.37	0/167
4	Ad	0.14	0/37	0.25	0/47
4	Ak	0.07	0/37	0.16	0/47
4	Ar	0.09	0/37	0.23	0/47
4	Ay	0.09	0/37	0.23	0/47
4	Bf	0.07	0/37	0.17	0/47
4	Bm	0.08	0/37	0.27	0/47
4	Bt	0.06	0/37	0.17	0/47
4	Ca	0.07	0/37	0.18	0/47
4	Ch	0.08	0/37	0.23	0/47
4	Co	0.08	0/37	0.27	0/47
4	Cv	0.06	0/37	0.17	0/47
4	Dc	0.07	0/37	0.22	0/47
4	Dj	0.09	0/37	0.23	0/47
4	Dq	0.07	0/37	0.18	0/47
4	Dx	0.09	0/37	0.22	0/47
4	Ee	0.06	0/37	0.17	0/47
4	El	0.07	0/37	0.19	0/47
4	Es	0.07	0/37	0.19	0/47
5	Ae	0.11	0/491	0.27	0/660
5	Al	0.19	0/491	0.35	0/660
5	As	0.11	0/491	0.27	0/660
5	Az	0.11	0/491	0.30	0/660
5	Bg	0.10	0/491	0.27	0/660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
5	Bn	0.11	0/491	0.32	0/660
5	Bu	0.11	0/491	0.27	0/660
5	Cb	0.12	0/491	0.30	0/660
5	Ci	0.13	0/491	0.31	0/660
5	Cp	0.11	0/491	0.29	0/660
5	Cw	0.11	0/491	0.29	0/660
5	Dd	0.11	0/491	0.29	0/660
5	Dk	0.12	0/491	0.31	0/660
5	Dr	0.11	0/491	0.27	0/660
5	Dy	0.11	0/491	0.31	0/660
5	Ef	0.11	0/491	0.27	0/660
5	Em	0.12	0/491	0.29	0/660
5	Et	0.12	0/491	0.30	0/660
6	Af	0.13	0/278	0.29	0/377
6	Am	0.10	0/278	0.24	0/377
6	At	0.13	0/278	0.33	0/377
6	Ba	0.10	0/278	0.23	0/377
6	Bh	0.10	0/278	0.20	0/377
6	Bo	0.11	0/278	0.25	0/377
6	Bv	0.11	0/278	0.23	0/377
6	Cc	0.10	0/278	0.23	0/377
6	Cj	0.12	0/278	0.24	0/377
6	Cq	0.12	0/278	0.26	0/377
6	Cx	0.11	0/278	0.26	0/377
6	De	0.11	0/278	0.29	0/377
6	Dl	0.10	0/278	0.26	0/377
6	Ds	0.11	0/278	0.23	0/377
6	Dz	0.11	0/278	0.21	0/377
6	Eg	0.10	0/278	0.24	0/377
6	En	0.09	0/278	0.23	0/377
6	Eu	0.11	0/278	0.25	0/377
7	Ag	0.15	0/1269	0.29	0/1734
7	An	0.13	0/1269	0.31	0/1734
7	Au	0.12	0/1269	0.27	0/1734
7	Bb	0.12	0/1269	0.29	0/1734
7	Bi	0.13	0/1269	0.28	0/1734
7	Bp	0.15	0/1269	0.31	0/1734
7	Bw	0.13	0/1269	0.33	0/1734
7	Cd	0.12	0/1269	0.28	0/1734
7	Ck	0.13	0/1269	0.30	0/1734
7	Cr	0.13	0/1269	0.29	0/1734
7	Cy	0.13	0/1269	0.30	0/1734
7	Df	0.13	0/1269	0.27	0/1734

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
7	Dm	0.14	0/1269	0.31	0/1734
7	Dt	0.13	0/1269	0.28	0/1734
7	Ea	0.14	0/1269	0.29	0/1734
7	Eh	0.13	0/1269	0.32	0/1734
7	Eo	0.12	0/1269	0.28	0/1734
7	Ev	0.14	0/1269	0.30	0/1734
All	All	0.12	0/42822	0.29	0/57942

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 [i](#)

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	117	0	111	4	0
1	Ah	117	0	111	3	0
1	Ao	117	0	111	4	0
1	Av	117	0	111	3	0
1	Bc	117	0	111	3	0
1	Bj	117	0	111	5	0
1	Bq	117	0	111	3	0
1	Bx	117	0	111	2	0
1	Ce	117	0	111	4	0
1	Cl	117	0	111	4	0
1	Cs	117	0	111	4	0
1	Cz	117	0	111	4	0
1	Dg	117	0	111	4	0
1	Dn	117	0	111	3	0
1	Du	117	0	111	3	0
1	Eb	117	0	111	4	0
1	Ei	117	0	111	2	0
1	Ep	117	0	111	6	0
2	Ab	61	0	65	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Ai	61	0	65	3	0
2	Ap	61	0	65	5	0
2	Aw	61	0	65	4	0
2	Bd	61	0	65	2	0
2	Bk	61	0	65	2	0
2	Br	61	0	65	3	0
2	By	61	0	65	3	0
2	Cf	61	0	65	2	0
2	Cm	61	0	65	5	0
2	Ct	61	0	65	6	0
2	Da	61	0	65	4	0
2	Dh	61	0	65	6	0
2	Do	61	0	65	5	0
2	Dv	61	0	65	7	0
2	Ec	61	0	65	3	0
2	Ej	61	0	65	7	0
2	Eq	61	0	65	4	0
3	Ac	125	0	126	4	0
3	Aj	125	0	126	3	0
3	Aq	125	0	126	5	0
3	Ax	125	0	126	4	0
3	Be	125	0	126	4	0
3	Bl	125	0	126	7	0
3	Bs	125	0	126	3	0
3	Bz	125	0	126	6	0
3	Cg	125	0	126	5	0
3	Cn	125	0	126	4	0
3	Cu	125	0	126	7	0
3	Db	125	0	126	6	0
3	Di	125	0	126	5	0
3	Dp	125	0	126	6	0
3	Dw	125	0	126	6	0
3	Ed	125	0	126	5	0
3	Ek	125	0	126	7	0
3	Er	125	0	126	7	0
4	Ad	36	0	30	3	0
4	Ak	36	0	30	1	0
4	Ar	36	0	30	3	0
4	Ay	36	0	30	2	0
4	Bf	36	0	30	1	0
4	Bm	36	0	30	1	0
4	Bt	36	0	30	1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Ca	36	0	30	1	0
4	Ch	36	0	30	1	0
4	Co	36	0	30	2	0
4	Cv	36	0	30	1	0
4	Dc	36	0	30	2	0
4	Dj	36	0	30	4	0
4	Dq	36	0	30	1	0
4	Dx	36	0	30	1	0
4	Ee	36	0	30	1	0
4	El	36	0	30	2	0
4	Es	36	0	30	1	0
5	Ae	484	0	502	11	0
5	Al	484	0	502	11	0
5	As	484	0	502	14	0
5	Az	484	0	502	13	0
5	Bg	484	0	502	10	0
5	Bn	484	0	502	12	0
5	Bu	484	0	502	11	0
5	Cb	484	0	502	13	0
5	Ci	484	0	502	13	0
5	Cp	484	0	502	12	0
5	Cw	484	0	502	13	0
5	Dd	484	0	502	13	0
5	Dk	484	0	502	13	0
5	Dr	484	0	502	11	0
5	Dy	484	0	502	14	0
5	Ef	484	0	502	12	0
5	Em	484	0	502	14	0
5	Et	484	0	502	14	0
6	Af	276	0	263	7	0
6	Am	276	0	263	6	0
6	At	276	0	263	3	0
6	Ba	276	0	263	4	0
6	Bh	276	0	263	4	0
6	Bo	276	0	263	6	0
6	Bv	276	0	263	4	0
6	Cc	276	0	263	4	0
6	Cj	276	0	263	3	0
6	Cq	276	0	263	4	0
6	Cx	276	0	263	6	0
6	De	276	0	263	4	0
6	Dl	276	0	263	5	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Ds	276	0	263	4	0
6	Dz	276	0	263	3	0
6	Eg	276	0	263	5	0
6	En	276	0	263	6	0
6	Eu	276	0	263	2	0
7	Ag	1238	0	1252	36	0
7	An	1238	0	1252	28	0
7	Au	1238	0	1252	35	0
7	Bb	1238	0	1252	24	0
7	Bi	1238	0	1252	26	0
7	Bp	1238	0	1252	38	0
7	Bw	1238	0	1252	24	0
7	Cd	1238	0	1252	29	0
7	Ck	1238	0	1252	22	0
7	Cr	1238	0	1252	30	0
7	Cy	1238	0	1252	30	0
7	Df	1238	0	1252	31	0
7	Dm	1238	0	1252	27	0
7	Dt	1238	0	1252	29	0
7	Ea	1238	0	1252	40	0
7	Eh	1238	0	1252	28	0
7	Eo	1238	0	1252	29	0
7	Ev	1238	0	1252	29	0
All	All	42066	0	42282	794	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 794 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)
2:Ec:5:ILE:HD11	7:Eo:136:THR:HG23	1.61	0.82
2:Br:5:ILE:HD11	7:Cd:136:THR:HG23	1.61	0.82
7:Ag:136:THR:HG23	2:Eq:5:ILE:HD11	1.62	0.81
2:Ai:5:ILE:HD11	7:Au:136:THR:HG23	1.66	0.77
2:Dv:5:ILE:HD11	7:Eh:136:THR:HG23	1.67	0.76

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	14/16 (88%)	14 (100%)	0	0	100	100
1	Ah	14/16 (88%)	14 (100%)	0	0	100	100
1	Ao	14/16 (88%)	14 (100%)	0	0	100	100
1	Av	14/16 (88%)	14 (100%)	0	0	100	100
1	Bc	14/16 (88%)	14 (100%)	0	0	100	100
1	Bj	14/16 (88%)	14 (100%)	0	0	100	100
1	Bq	14/16 (88%)	14 (100%)	0	0	100	100
1	Bx	14/16 (88%)	14 (100%)	0	0	100	100
1	Ce	14/16 (88%)	14 (100%)	0	0	100	100
1	Cl	14/16 (88%)	14 (100%)	0	0	100	100
1	Cs	14/16 (88%)	14 (100%)	0	0	100	100
1	Cz	14/16 (88%)	14 (100%)	0	0	100	100
1	Dg	14/16 (88%)	14 (100%)	0	0	100	100
1	Dn	14/16 (88%)	14 (100%)	0	0	100	100
1	Du	14/16 (88%)	14 (100%)	0	0	100	100
1	Eb	14/16 (88%)	14 (100%)	0	0	100	100
1	Ei	14/16 (88%)	14 (100%)	0	0	100	100
1	Ep	14/16 (88%)	14 (100%)	0	0	100	100
2	Ab	7/9 (78%)	7 (100%)	0	0	100	100
2	Ai	7/9 (78%)	7 (100%)	0	0	100	100
2	Ap	7/9 (78%)	7 (100%)	0	0	100	100
2	Aw	7/9 (78%)	7 (100%)	0	0	100	100
2	Bd	7/9 (78%)	7 (100%)	0	0	100	100
2	Bk	7/9 (78%)	7 (100%)	0	0	100	100
2	Br	7/9 (78%)	7 (100%)	0	0	100	100

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	By	7/9 (78%)	7 (100%)	0	0	100	100
2	Cf	7/9 (78%)	7 (100%)	0	0	100	100
2	Cm	7/9 (78%)	7 (100%)	0	0	100	100
2	Ct	7/9 (78%)	7 (100%)	0	0	100	100
2	Da	7/9 (78%)	7 (100%)	0	0	100	100
2	Dh	7/9 (78%)	7 (100%)	0	0	100	100
2	Do	7/9 (78%)	7 (100%)	0	0	100	100
2	Dv	7/9 (78%)	7 (100%)	0	0	100	100
2	Ec	7/9 (78%)	7 (100%)	0	0	100	100
2	Ej	7/9 (78%)	7 (100%)	0	0	100	100
2	Eq	7/9 (78%)	7 (100%)	0	0	100	100
3	Ac	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Aj	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Aq	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Ax	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Be	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Bl	14/16 (88%)	12 (86%)	2 (14%)	0	100	100
3	Bs	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Bz	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Cg	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Cn	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Cu	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Db	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Di	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Dp	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Dw	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Ed	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Ek	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
3	Er	14/16 (88%)	13 (93%)	1 (7%)	0	100	100
4	Ad	3/5 (60%)	3 (100%)	0	0	100	100
4	Ak	3/5 (60%)	3 (100%)	0	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Ar	3/5 (60%)	3 (100%)	0	0	100	100
4	Ay	3/5 (60%)	3 (100%)	0	0	100	100
4	Bf	3/5 (60%)	3 (100%)	0	0	100	100
4	Bm	3/5 (60%)	3 (100%)	0	0	100	100
4	Bt	3/5 (60%)	3 (100%)	0	0	100	100
4	Ca	3/5 (60%)	3 (100%)	0	0	100	100
4	Ch	3/5 (60%)	3 (100%)	0	0	100	100
4	Co	3/5 (60%)	3 (100%)	0	0	100	100
4	Cv	3/5 (60%)	3 (100%)	0	0	100	100
4	Dc	3/5 (60%)	3 (100%)	0	0	100	100
4	Dj	3/5 (60%)	3 (100%)	0	0	100	100
4	Dq	3/5 (60%)	3 (100%)	0	0	100	100
4	Dx	3/5 (60%)	3 (100%)	0	0	100	100
4	Ee	3/5 (60%)	3 (100%)	0	0	100	100
4	El	3/5 (60%)	3 (100%)	0	0	100	100
4	Es	3/5 (60%)	3 (100%)	0	0	100	100
5	Ae	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
5	Al	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
5	As	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
5	Az	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
5	Bg	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
5	Bn	61/269 (23%)	61 (100%)	0	0	100	100
5	Bu	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
5	Cb	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
5	Ci	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
5	Cp	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
5	Cw	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
5	Dd	61/269 (23%)	61 (100%)	0	0	100	100
5	Dk	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
5	Dr	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
5	Dy	61/269 (23%)	60 (98%)	1 (2%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	Ef	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
5	Em	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
5	Et	61/269 (23%)	61 (100%)	0	0	100	100
6	Af	32/1048 (3%)	32 (100%)	0	0	100	100
6	Am	32/1048 (3%)	32 (100%)	0	0	100	100
6	At	32/1048 (3%)	32 (100%)	0	0	100	100
6	Ba	32/1048 (3%)	32 (100%)	0	0	100	100
6	Bh	32/1048 (3%)	32 (100%)	0	0	100	100
6	Bo	32/1048 (3%)	32 (100%)	0	0	100	100
6	Bv	32/1048 (3%)	32 (100%)	0	0	100	100
6	Cc	32/1048 (3%)	32 (100%)	0	0	100	100
6	Cj	32/1048 (3%)	32 (100%)	0	0	100	100
6	Cq	32/1048 (3%)	32 (100%)	0	0	100	100
6	Cx	32/1048 (3%)	32 (100%)	0	0	100	100
6	De	32/1048 (3%)	32 (100%)	0	0	100	100
6	Dl	32/1048 (3%)	32 (100%)	0	0	100	100
6	Ds	32/1048 (3%)	32 (100%)	0	0	100	100
6	Dz	32/1048 (3%)	32 (100%)	0	0	100	100
6	Eg	32/1048 (3%)	32 (100%)	0	0	100	100
6	En	32/1048 (3%)	32 (100%)	0	0	100	100
6	Eu	32/1048 (3%)	32 (100%)	0	0	100	100
7	Ag	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	An	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Au	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Bb	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Bi	158/361 (44%)	154 (98%)	4 (2%)	0	100	100
7	Bp	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Bw	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Cd	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Ck	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Cr	158/361 (44%)	155 (98%)	3 (2%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	Cy	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Df	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Dm	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Dt	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Ea	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Eh	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Eo	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
7	Ev	158/361 (44%)	155 (98%)	3 (2%)	0	100	100
All	All	5202/31032 (17%)	5105 (98%)	97 (2%)	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	Aa	11/11 (100%)	10 (91%)	1 (9%)	7	27
1	Ah	11/11 (100%)	11 (100%)	0	100	100
1	Ao	11/11 (100%)	9 (82%)	2 (18%)	1	6
1	Av	11/11 (100%)	11 (100%)	0	100	100
1	Bc	11/11 (100%)	10 (91%)	1 (9%)	7	27
1	Bj	11/11 (100%)	11 (100%)	0	100	100
1	Bq	11/11 (100%)	11 (100%)	0	100	100
1	Bx	11/11 (100%)	11 (100%)	0	100	100
1	Ce	11/11 (100%)	10 (91%)	1 (9%)	7	27
1	Cl	11/11 (100%)	10 (91%)	1 (9%)	7	27
1	Cs	11/11 (100%)	10 (91%)	1 (9%)	7	27
1	Cz	11/11 (100%)	10 (91%)	1 (9%)	7	27
1	Dg	11/11 (100%)	11 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Dn	11/11 (100%)	10 (91%)	1 (9%)	7	27
1	Du	11/11 (100%)	11 (100%)	0	100	100
1	Eb	11/11 (100%)	11 (100%)	0	100	100
1	Ei	11/11 (100%)	11 (100%)	0	100	100
1	Ep	11/11 (100%)	11 (100%)	0	100	100
2	Ab	7/7 (100%)	6 (86%)	1 (14%)	2	12
2	Ai	7/7 (100%)	7 (100%)	0	100	100
2	Ap	7/7 (100%)	6 (86%)	1 (14%)	2	12
2	Aw	7/7 (100%)	7 (100%)	0	100	100
2	Bd	7/7 (100%)	7 (100%)	0	100	100
2	Bk	7/7 (100%)	7 (100%)	0	100	100
2	Br	7/7 (100%)	7 (100%)	0	100	100
2	By	7/7 (100%)	7 (100%)	0	100	100
2	Cf	7/7 (100%)	7 (100%)	0	100	100
2	Cm	7/7 (100%)	6 (86%)	1 (14%)	2	12
2	Ct	7/7 (100%)	7 (100%)	0	100	100
2	Da	7/7 (100%)	6 (86%)	1 (14%)	2	12
2	Dh	7/7 (100%)	6 (86%)	1 (14%)	2	12
2	Do	7/7 (100%)	7 (100%)	0	100	100
2	Dv	7/7 (100%)	7 (100%)	0	100	100
2	Ec	7/7 (100%)	7 (100%)	0	100	100
2	Ej	7/7 (100%)	5 (71%)	2 (29%)	0	1
2	Eq	7/7 (100%)	7 (100%)	0	100	100
3	Ac	13/13 (100%)	10 (77%)	3 (23%)	0	3
3	Aj	13/13 (100%)	10 (77%)	3 (23%)	0	3
3	Aq	13/13 (100%)	9 (69%)	4 (31%)	0	1
3	Ax	13/13 (100%)	11 (85%)	2 (15%)	2	10
3	Be	13/13 (100%)	12 (92%)	1 (8%)	10	34
3	Bl	13/13 (100%)	12 (92%)	1 (8%)	10	34
3	Bs	13/13 (100%)	12 (92%)	1 (8%)	10	34
3	Bz	13/13 (100%)	12 (92%)	1 (8%)	10	34

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Cg	13/13 (100%)	10 (77%)	3 (23%)	0	3
3	Cn	13/13 (100%)	10 (77%)	3 (23%)	0	3
3	Cu	13/13 (100%)	10 (77%)	3 (23%)	0	3
3	Db	13/13 (100%)	9 (69%)	4 (31%)	0	1
3	Di	13/13 (100%)	11 (85%)	2 (15%)	2	10
3	Dp	13/13 (100%)	10 (77%)	3 (23%)	0	3
3	Dw	13/13 (100%)	11 (85%)	2 (15%)	2	10
3	Ed	13/13 (100%)	12 (92%)	1 (8%)	10	34
3	Ek	13/13 (100%)	11 (85%)	2 (15%)	2	10
3	Er	13/13 (100%)	11 (85%)	2 (15%)	2	10
4	Ad	3/3 (100%)	3 (100%)	0	100	100
4	Ak	3/3 (100%)	3 (100%)	0	100	100
4	Ar	3/3 (100%)	3 (100%)	0	100	100
4	Ay	3/3 (100%)	3 (100%)	0	100	100
4	Bf	3/3 (100%)	3 (100%)	0	100	100
4	Bm	3/3 (100%)	3 (100%)	0	100	100
4	Bt	3/3 (100%)	3 (100%)	0	100	100
4	Ca	3/3 (100%)	3 (100%)	0	100	100
4	Ch	3/3 (100%)	3 (100%)	0	100	100
4	Co	3/3 (100%)	3 (100%)	0	100	100
4	Cv	3/3 (100%)	3 (100%)	0	100	100
4	Dc	3/3 (100%)	3 (100%)	0	100	100
4	Dj	3/3 (100%)	3 (100%)	0	100	100
4	Dq	3/3 (100%)	3 (100%)	0	100	100
4	Dx	3/3 (100%)	3 (100%)	0	100	100
4	Ee	3/3 (100%)	3 (100%)	0	100	100
4	El	3/3 (100%)	3 (100%)	0	100	100
4	Es	3/3 (100%)	3 (100%)	0	100	100
5	Ae	53/237 (22%)	53 (100%)	0	100	100
5	Al	53/237 (22%)	53 (100%)	0	100	100
5	As	53/237 (22%)	53 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	Az	53/237 (22%)	52 (98%)	1 (2%)	52	76
5	Bg	53/237 (22%)	52 (98%)	1 (2%)	52	76
5	Bn	53/237 (22%)	53 (100%)	0	100	100
5	Bu	53/237 (22%)	52 (98%)	1 (2%)	52	76
5	Cb	53/237 (22%)	53 (100%)	0	100	100
5	Ci	53/237 (22%)	51 (96%)	2 (4%)	28	59
5	Cp	53/237 (22%)	52 (98%)	1 (2%)	52	76
5	Cw	53/237 (22%)	53 (100%)	0	100	100
5	Dd	53/237 (22%)	53 (100%)	0	100	100
5	Dk	53/237 (22%)	53 (100%)	0	100	100
5	Dr	53/237 (22%)	52 (98%)	1 (2%)	52	76
5	Dy	53/237 (22%)	53 (100%)	0	100	100
5	Ef	53/237 (22%)	53 (100%)	0	100	100
5	Em	53/237 (22%)	53 (100%)	0	100	100
5	Et	53/237 (22%)	52 (98%)	1 (2%)	52	76
6	Af	31/765 (4%)	30 (97%)	1 (3%)	34	64
6	Am	31/765 (4%)	31 (100%)	0	100	100
6	At	31/765 (4%)	30 (97%)	1 (3%)	34	64
6	Ba	31/765 (4%)	30 (97%)	1 (3%)	34	64
6	Bh	31/765 (4%)	31 (100%)	0	100	100
6	Bo	31/765 (4%)	30 (97%)	1 (3%)	34	64
6	Bv	31/765 (4%)	31 (100%)	0	100	100
6	Cc	31/765 (4%)	31 (100%)	0	100	100
6	Cj	31/765 (4%)	31 (100%)	0	100	100
6	Cq	31/765 (4%)	30 (97%)	1 (3%)	34	64
6	Cx	31/765 (4%)	31 (100%)	0	100	100
6	De	31/765 (4%)	31 (100%)	0	100	100
6	Dl	31/765 (4%)	30 (97%)	1 (3%)	34	64
6	Ds	31/765 (4%)	31 (100%)	0	100	100
6	Dz	31/765 (4%)	31 (100%)	0	100	100
6	Eg	31/765 (4%)	31 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	En	31/765 (4%)	31 (100%)	0	100	100
6	Eu	31/765 (4%)	31 (100%)	0	100	100
7	Ag	137/300 (46%)	132 (96%)	5 (4%)	30	61
7	An	137/300 (46%)	135 (98%)	2 (2%)	60	80
7	Au	137/300 (46%)	135 (98%)	2 (2%)	60	80
7	Bb	137/300 (46%)	133 (97%)	4 (3%)	37	67
7	Bi	137/300 (46%)	135 (98%)	2 (2%)	60	80
7	Bp	137/300 (46%)	135 (98%)	2 (2%)	60	80
7	Bw	137/300 (46%)	134 (98%)	3 (2%)	47	73
7	Cd	137/300 (46%)	134 (98%)	3 (2%)	47	73
7	Ck	137/300 (46%)	134 (98%)	3 (2%)	47	73
7	Cr	137/300 (46%)	130 (95%)	7 (5%)	20	50
7	Cy	137/300 (46%)	135 (98%)	2 (2%)	60	80
7	Df	137/300 (46%)	134 (98%)	3 (2%)	47	73
7	Dm	137/300 (46%)	135 (98%)	2 (2%)	60	80
7	Dt	137/300 (46%)	133 (97%)	4 (3%)	37	67
7	Ea	137/300 (46%)	135 (98%)	2 (2%)	60	80
7	Eh	137/300 (46%)	133 (97%)	4 (3%)	37	67
7	Eo	137/300 (46%)	134 (98%)	3 (2%)	47	73
7	Ev	137/300 (46%)	135 (98%)	2 (2%)	60	80
All	All	4590/24048 (19%)	4464 (97%)	126 (3%)	41	68

5 of 126 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	Ci	249	SER
7	Eh	168	VAL
7	Cr	219	LYS
3	Ed	3	SER
7	Eo	128	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:



Mol	Chain	Res	Type
7	Dt	126	GLN
7	Eo	126	GLN
7	Dt	222	ASN
7	Eh	126	GLN
7	Ev	234	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 [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

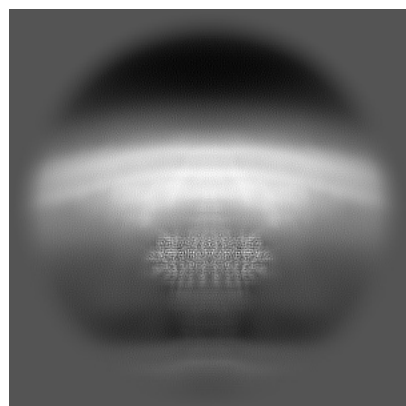
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49394. These allow visual inspection of the internal detail of the map and identification of artifacts.

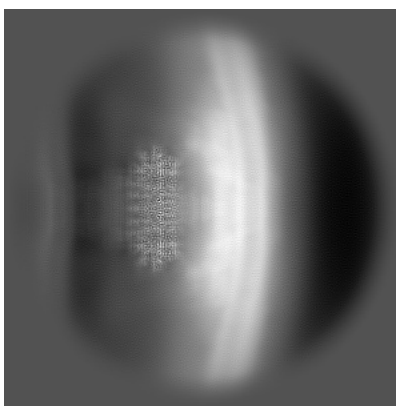
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

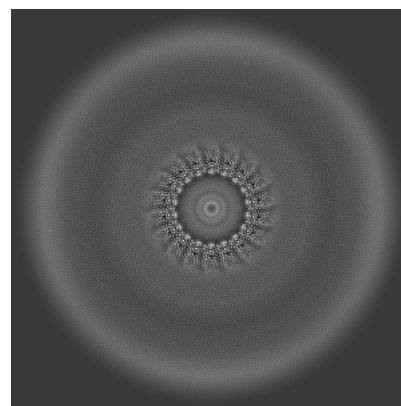
#### 6.1.1 Primary map



X

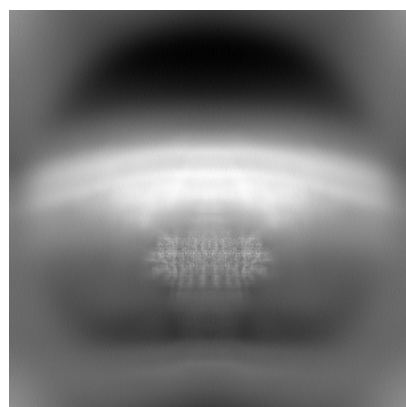


Y

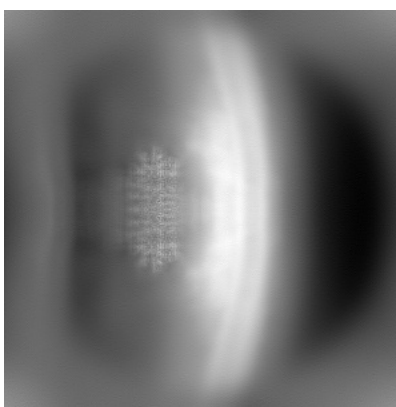


Z

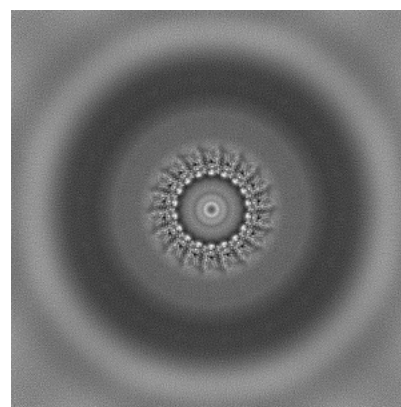
#### 6.1.2 Raw map



X



Y

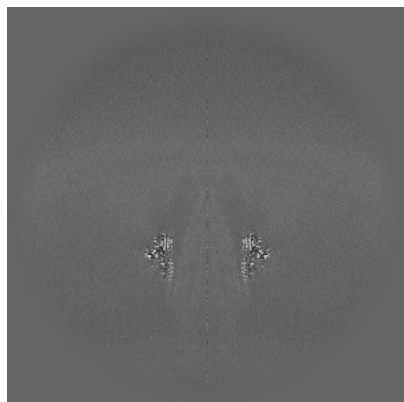


Z

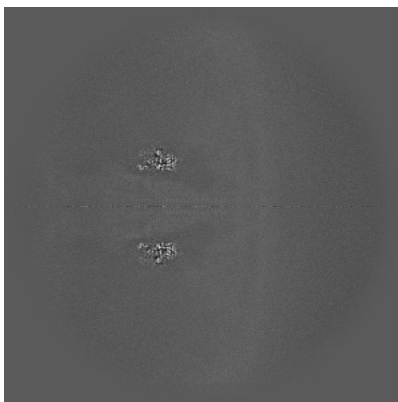
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

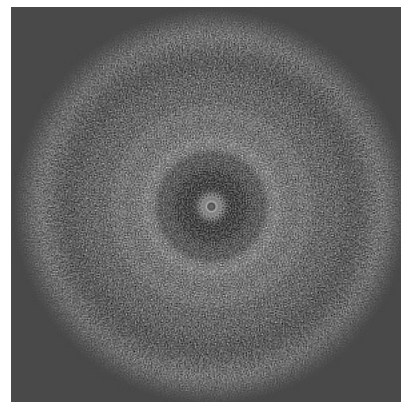
### 6.2.1 Primary map



X Index: 224

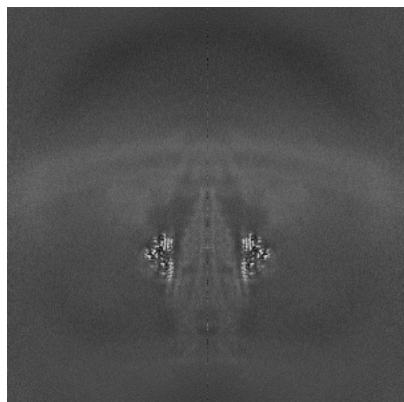


Y Index: 224

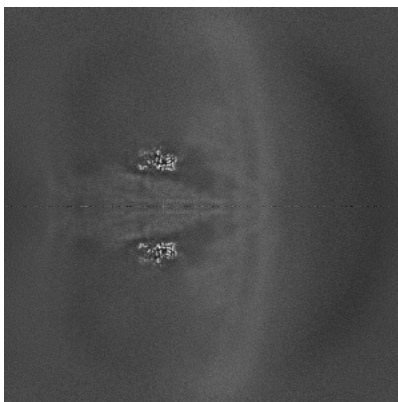


Z Index: 224

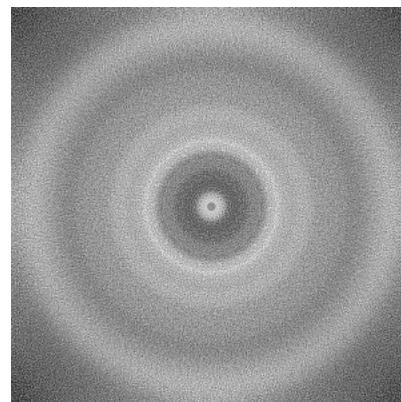
### 6.2.2 Raw map



X Index: 224



Y Index: 224

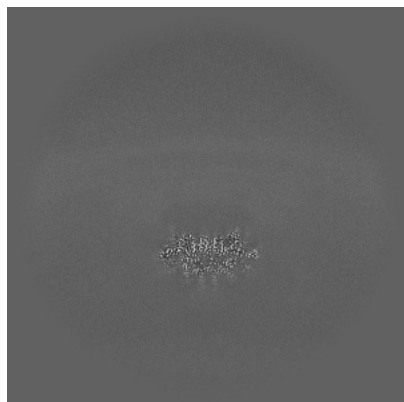


Z Index: 224

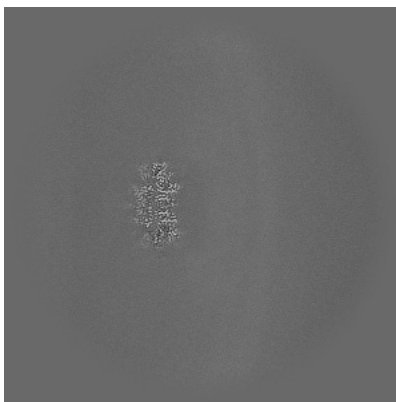
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

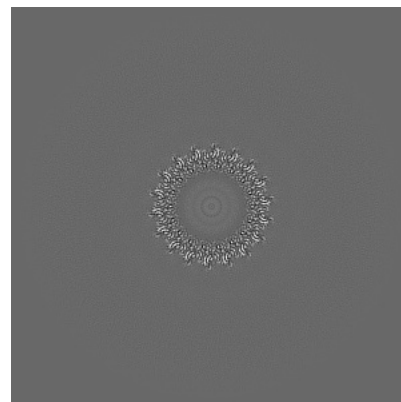
### 6.3.1 Primary map



X Index: 181

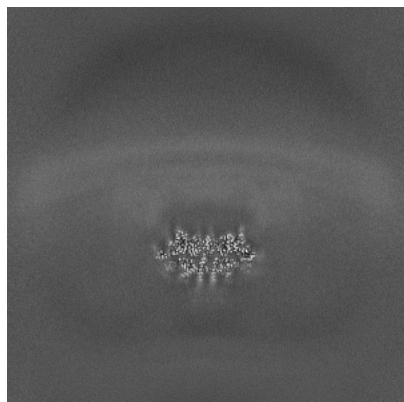


Y Index: 269

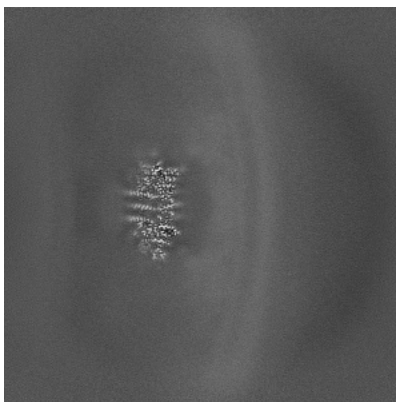


Z Index: 174

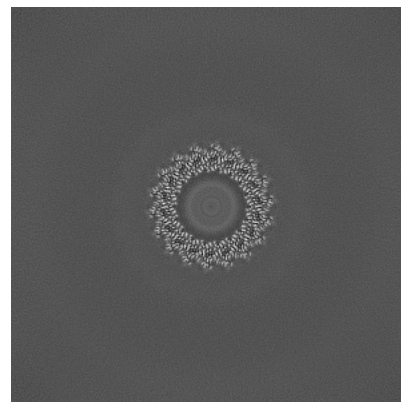
### 6.3.2 Raw map



X Index: 266



Y Index: 264

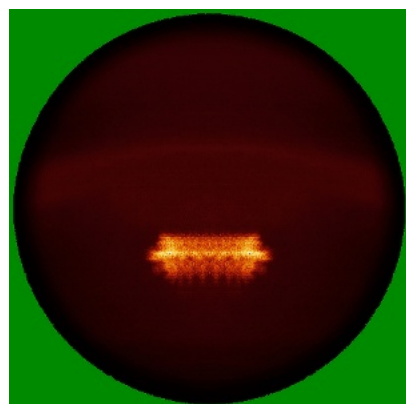


Z Index: 175

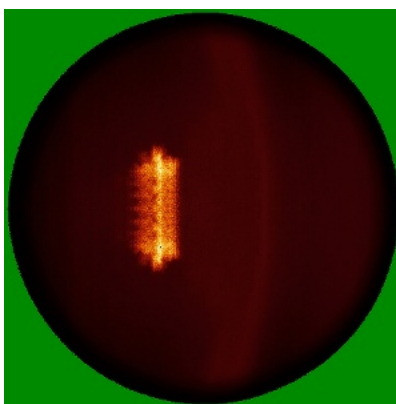
The images above show the largest variance slices of the map in three orthogonal directions.

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

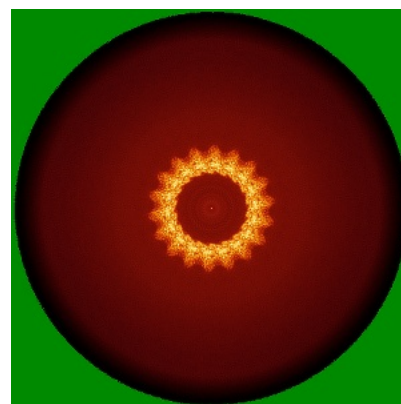
### 6.4.1 Primary map



X

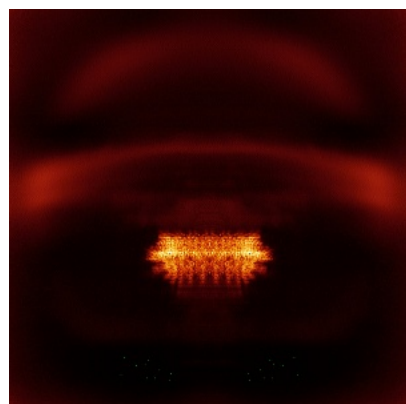


Y

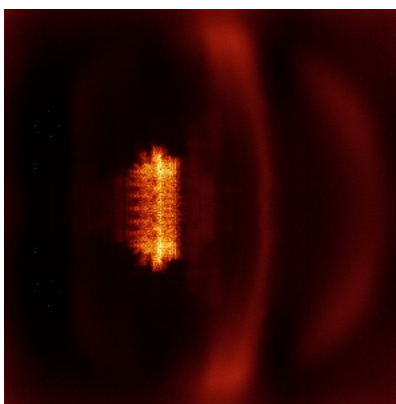


Z

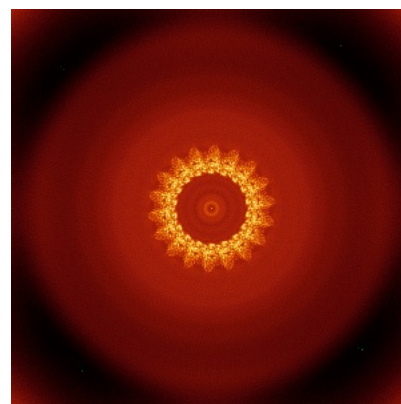
### 6.4.2 Raw map



X



Y



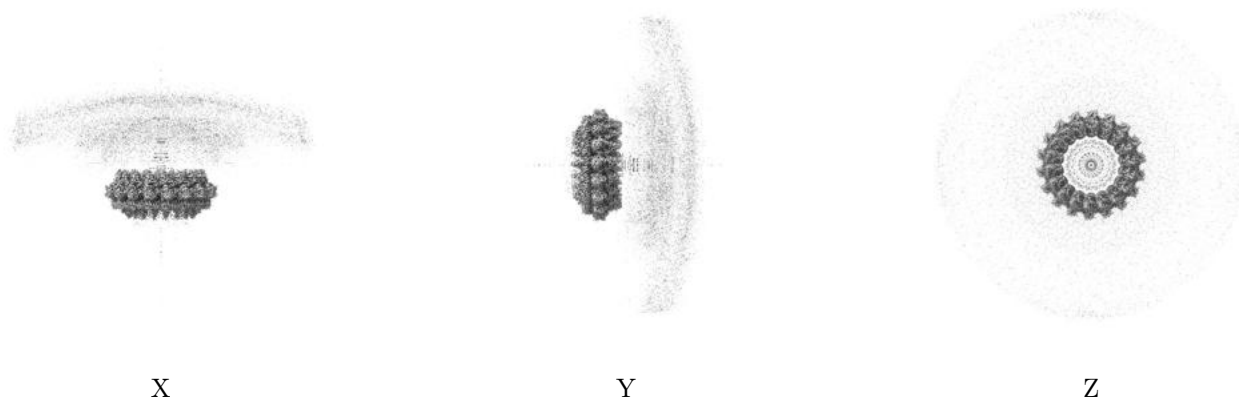
Z

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.



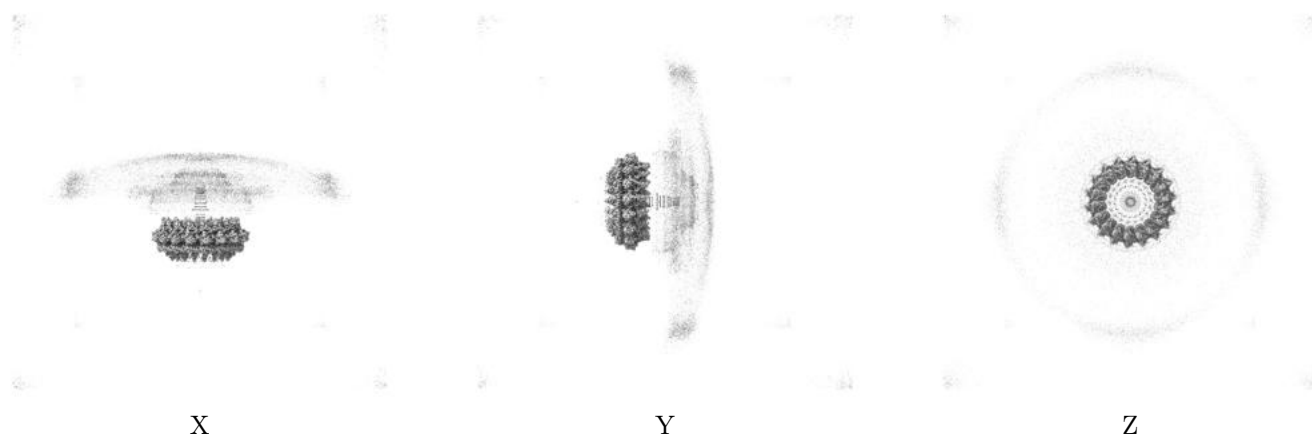
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

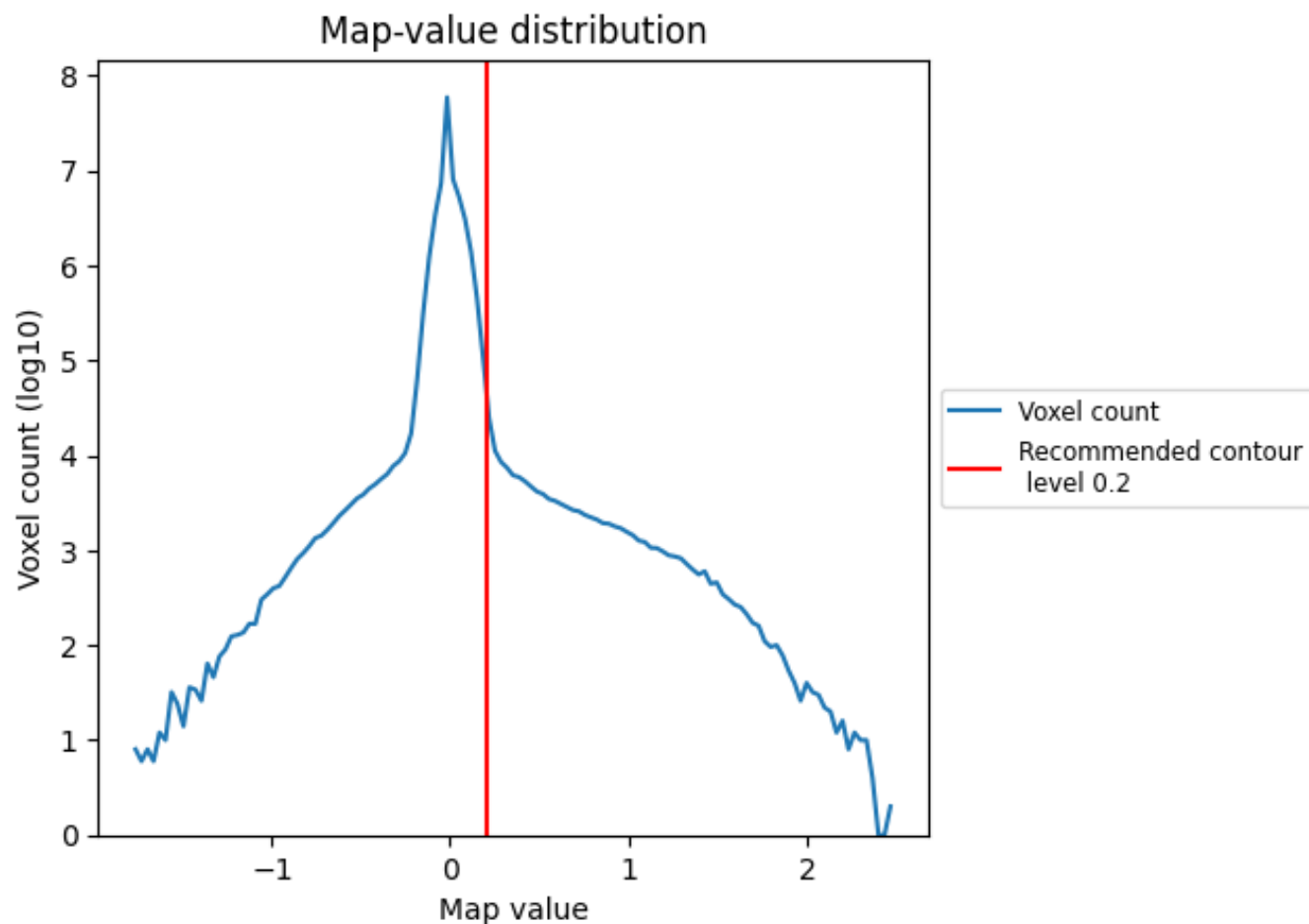
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

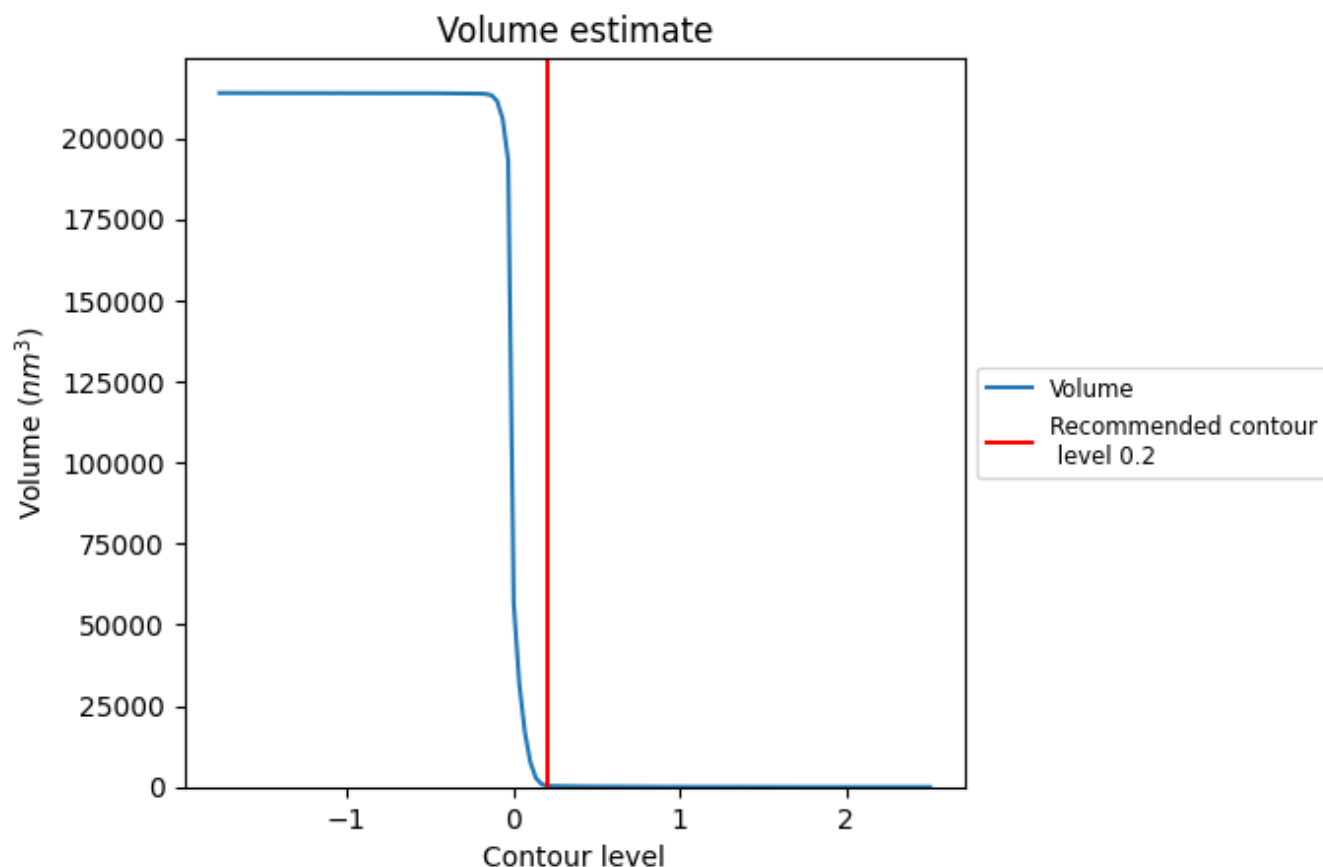
This section contains the results of statistical analysis of the map.

### 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](#)

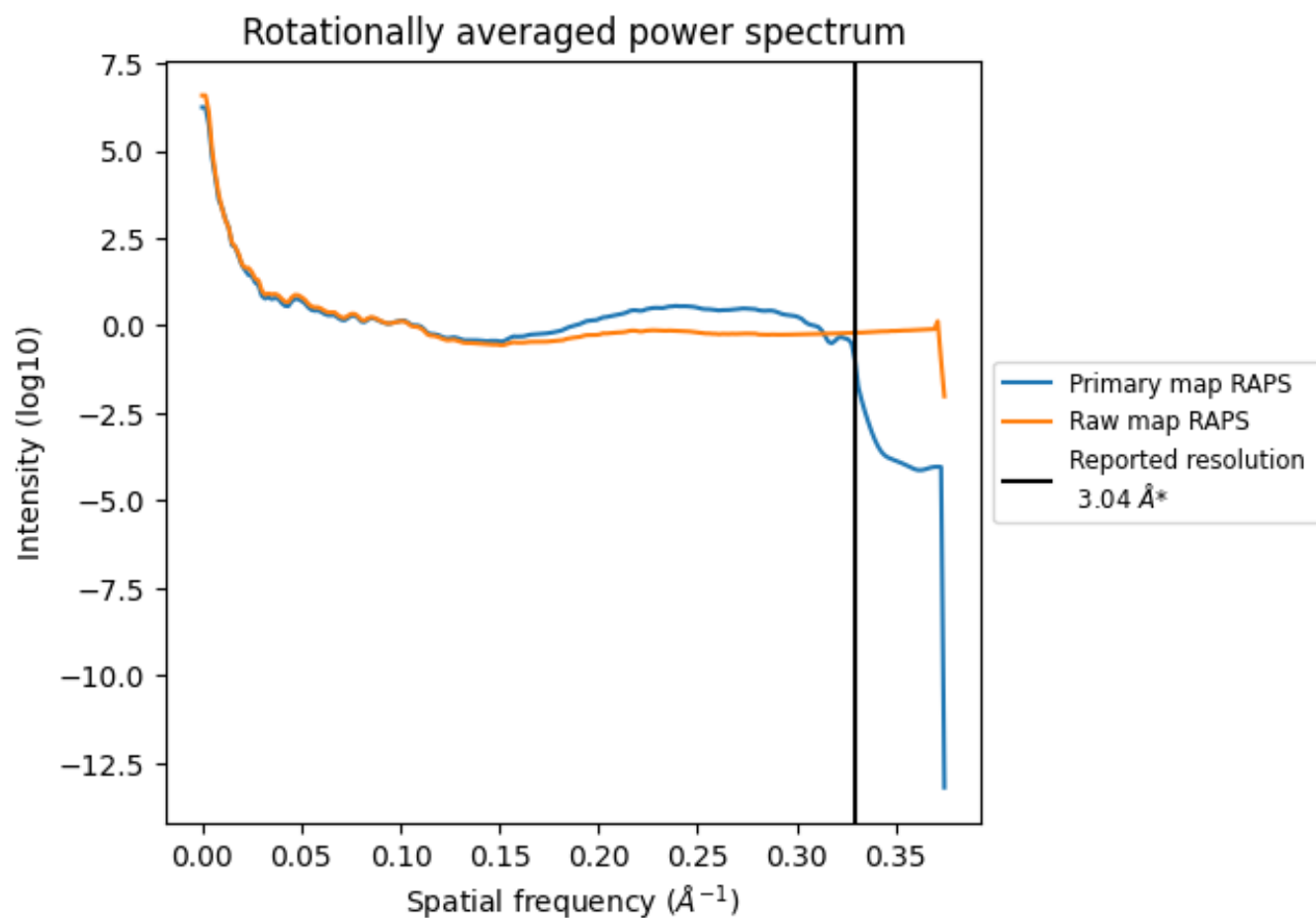


The volume at the recommended contour level is 428  $\text{nm}^3$ ; this corresponds to an approximate mass of 387 kDa.

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 ⓘ

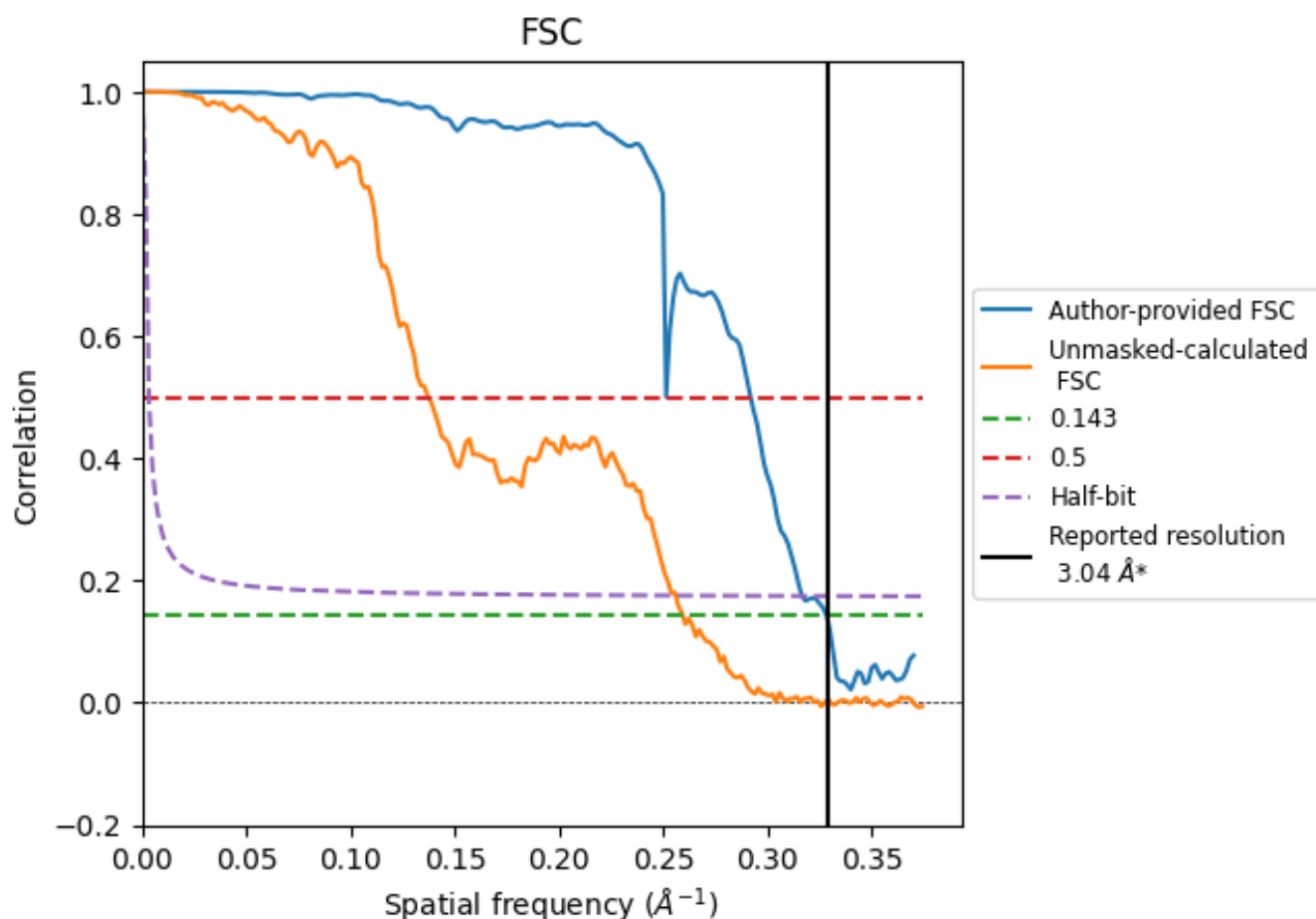


\*Reported resolution corresponds to spatial frequency of 0.329  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.329  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

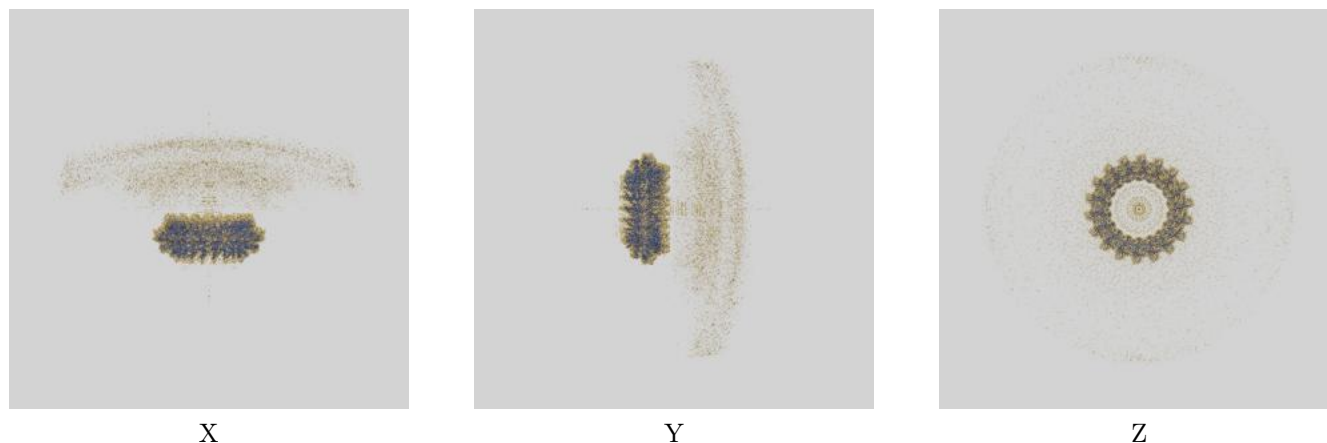
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.04	-	-
Author-provided FSC curve	3.04	3.42	3.16
Unmasked-calculated*	3.85	7.28	3.90

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.85 differs from the reported value 3.04 by more than 10 %

## 9 Map-model fit [i](#)

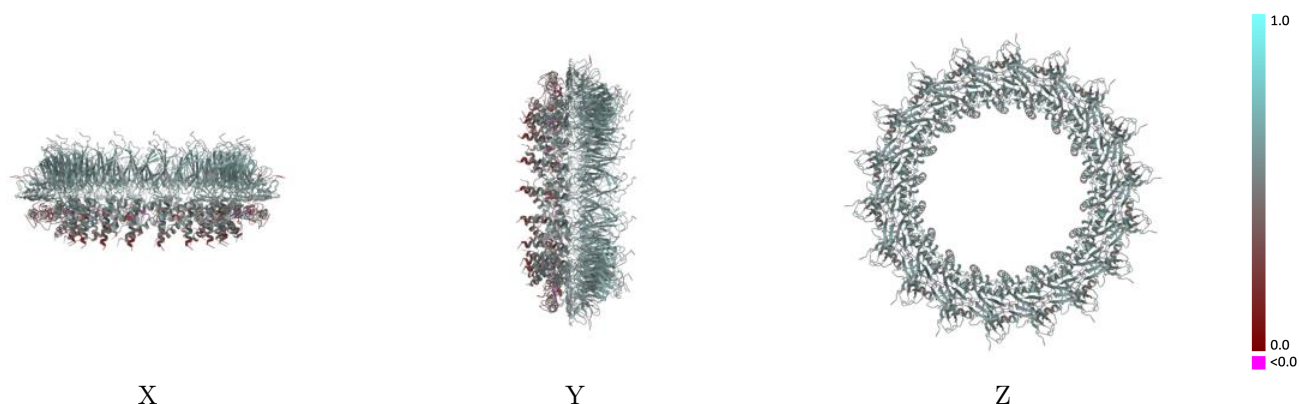
This section contains information regarding the fit between EMDB map EMD-49394 and PDB model 9NGV. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

### 9.1 Map-model overlay [i](#)



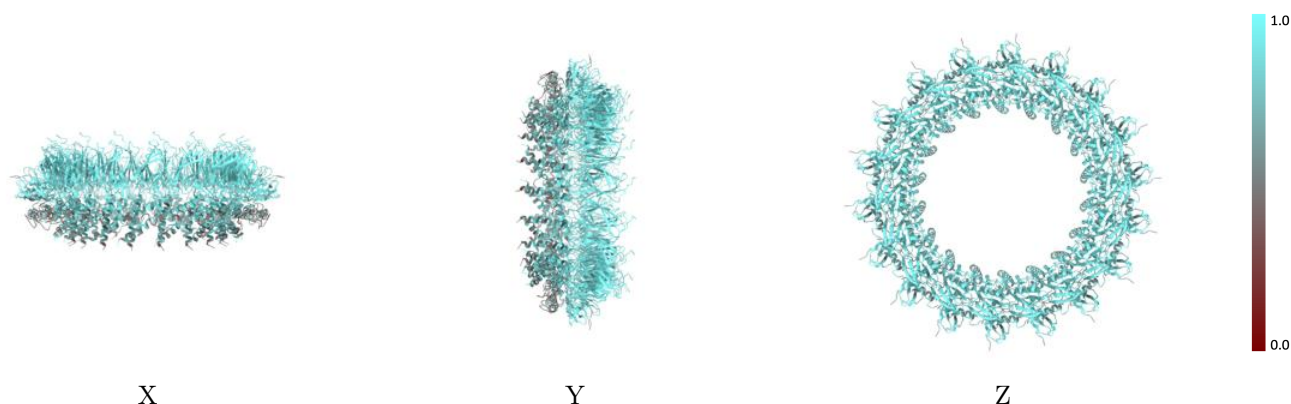
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



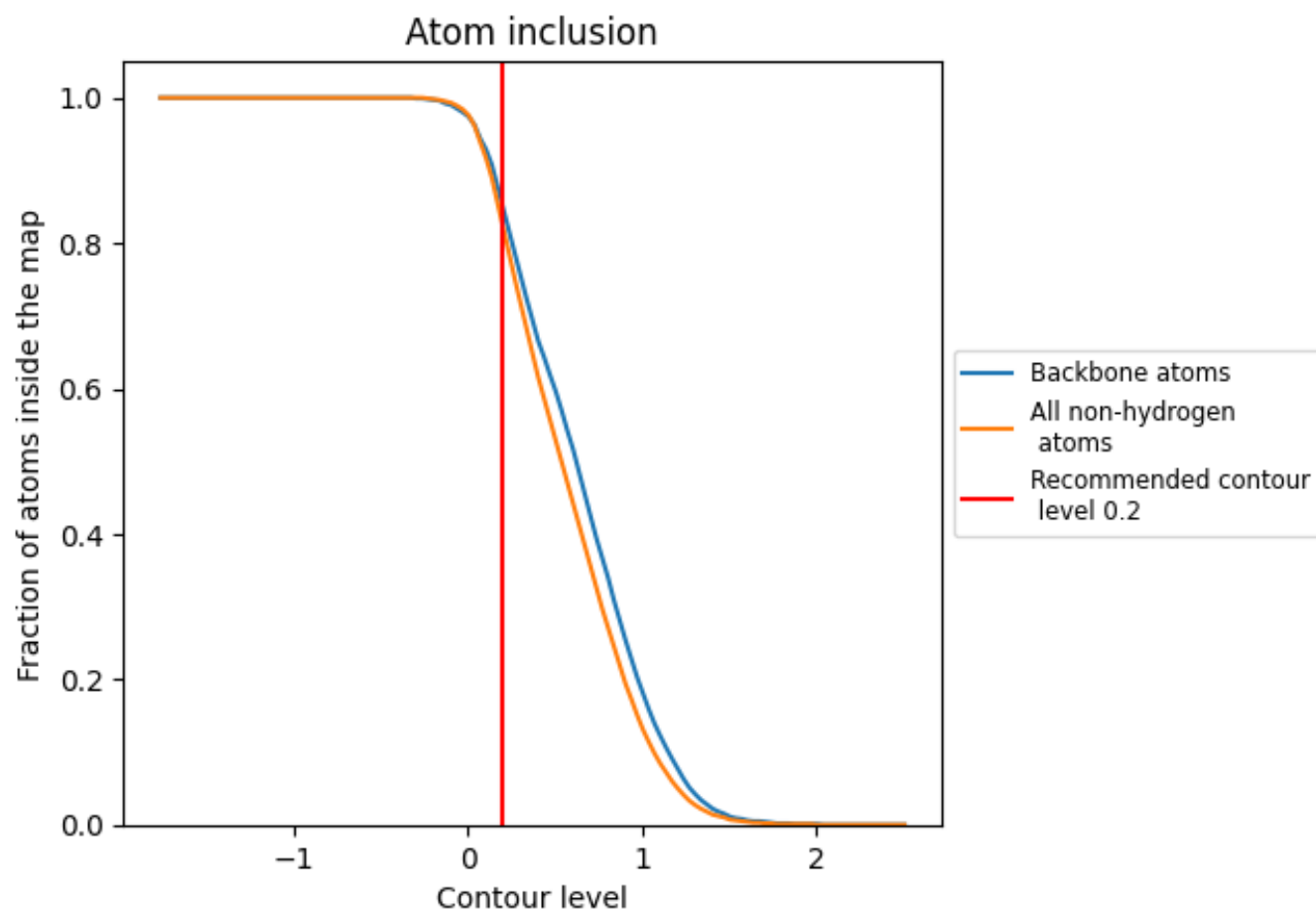
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 82% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8220	 0.5110
Aa	 0.5950	 0.4440
Ab	 0.6100	 0.3260
Ac	 0.4380	 0.2980
Ad	 0.2780	 0.1990
Ae	 0.8410	 0.5190
Af	 0.7900	 0.5080
Ag	 0.9090	 0.5550
Ah	 0.5950	 0.4260
Ai	 0.6610	 0.3410
Aj	 0.4380	 0.3090
Ak	 0.3330	 0.2090
Al	 0.8620	 0.5210
Am	 0.7900	 0.5070
An	 0.9060	 0.5560
Ao	 0.5520	 0.4530
Ap	 0.6270	 0.3520
Aq	 0.4460	 0.3000
Ar	 0.3060	 0.1960
As	 0.8560	 0.5210
At	 0.7980	 0.5060
Au	 0.9070	 0.5550
Av	 0.5690	 0.4400
Aw	 0.6780	 0.3570
Ax	 0.4300	 0.3060
Ay	 0.3330	 0.1840
Az	 0.8500	 0.5180
Ba	 0.7980	 0.4970
Bb	 0.9040	 0.5540
Bc	 0.5860	 0.4370
Bd	 0.6440	 0.3430
Be	 0.4460	 0.3240
Bf	 0.3330	 0.1970
Bg	 0.8430	 0.5170
Bh	 0.7760	 0.4920



*Continued on next page...*





















































































*Continued from previous page...*

Chain	Atom inclusion	Q-score
Bi	 0.8960	 0.5530
Bj	 0.5950	 0.4470
Bk	 0.6270	 0.3460
Bl	 0.4460	 0.3210
Bm	 0.2500	 0.1680
Bn	 0.8500	 0.5150
Bo	 0.8160	 0.5030
Bp	 0.8960	 0.5540
Bq	 0.5780	 0.4310
Br	 0.6780	 0.3610
Bs	 0.4130	 0.3090
Bt	 0.3060	 0.2320
Bu	 0.8410	 0.5190
Bv	 0.8200	 0.5050
Bw	 0.8990	 0.5540
Bx	 0.5600	 0.4370
By	 0.6440	 0.3440
Bz	 0.4550	 0.3000
Ca	 0.3330	 0.1850
Cb	 0.8430	 0.5160
Cc	 0.7870	 0.5030
Cd	 0.8960	 0.5510
Ce	 0.5950	 0.4420
Cf	 0.6100	 0.3350
Cg	 0.4460	 0.3070
Ch	 0.3060	 0.2080
Ci	 0.8540	 0.5190
Cj	 0.7830	 0.5040
Ck	 0.9000	 0.5550
Cl	 0.5860	 0.4370
Cm	 0.6100	 0.3360
Cn	 0.4380	 0.2910
Co	 0.3060	 0.1780
Cp	 0.8350	 0.5170
Cq	 0.7980	 0.5000
Cr	 0.9050	 0.5550
Cs	 0.6210	 0.4420
Ct	 0.6440	 0.3340
Cu	 0.4460	 0.3040
Cv	 0.3330	 0.2120
Cw	 0.8620	 0.5220
Cx	 0.7980	 0.5050

*Continued on next page...*



















*Continued from previous page...*

Chain	Atom inclusion	Q-score
Cy	 0.9090	 0.5560
Cz	 0.5690	 0.4530
Da	 0.6610	 0.3470
Db	 0.4550	 0.3060
Dc	 0.3060	 0.1860
Dd	 0.8560	 0.5190
De	 0.7940	 0.5060
Df	 0.9050	 0.5560
Dg	 0.5600	 0.4330
Dh	 0.6610	 0.3490
Di	 0.4300	 0.3110
Dj	 0.2780	 0.1890
Dk	 0.8500	 0.5240
Dl	 0.8010	 0.4980
Dm	 0.9050	 0.5540
Dn	 0.6030	 0.4280
Do	 0.6100	 0.3410
Dp	 0.4710	 0.3130
Dq	 0.3330	 0.1920
Dr	 0.8410	 0.5180
Ds	 0.7760	 0.4950
Dt	 0.9000	 0.5550
Du	 0.6120	 0.4330
Dv	 0.6100	 0.3440
Dw	 0.4550	 0.3160
Dx	 0.3060	 0.1690
Dy	 0.8450	 0.5180
Dz	 0.8120	 0.5120
Ea	 0.9000	 0.5550
Eb	 0.5690	 0.4170
Ec	 0.6440	 0.3610
Ed	 0.4130	 0.3100
Ee	 0.3060	 0.2330
Ef	 0.8390	 0.5190
Eg	 0.8160	 0.5120
Eh	 0.8960	 0.5550
Ei	 0.5780	 0.4320
Ej	 0.6950	 0.3560
Ek	 0.4630	 0.3050
El	 0.3060	 0.2070
Em	 0.8450	 0.5200
En	 0.7900	 0.5050

*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
Eo	 0.8960	 0.5530
Ep	 0.5950	 0.4380
Eq	 0.6440	 0.3420
Er	 0.4550	 0.3100
Es	 0.3060	 0.2300
Et	 0.8540	 0.5190
Eu	 0.7830	 0.5020
Ev	 0.9000	 0.5560