



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:19 AM UTC

PDB ID : 8PHQ / pdb\_00008phq  
EMDB ID : EMD-17671  
Title : Top cap of the Borrelia bacteriophage BB1 procapsid, fivefold-symmetrized outer shell  
Authors : Rumnieks, J.; Fuzik, T.; Tars, K.  
Deposited on : 2023-06-20  
Resolution : 2.69 Å(reported)  
Based on initial model : .

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>.

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

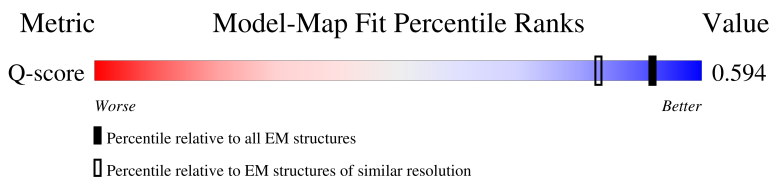
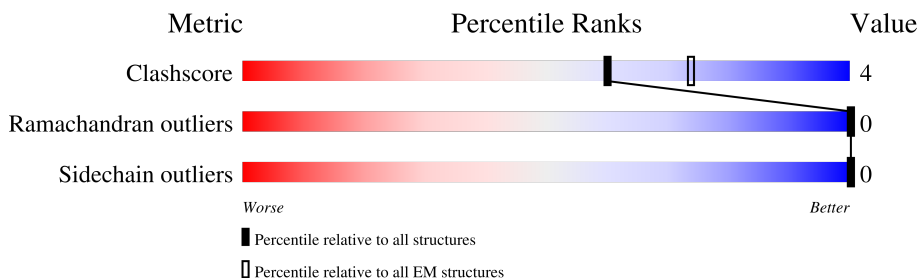
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.69 Å.

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






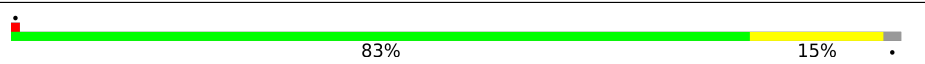
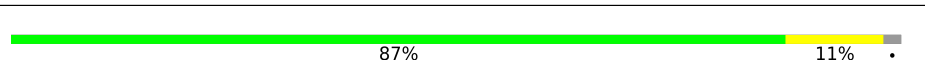

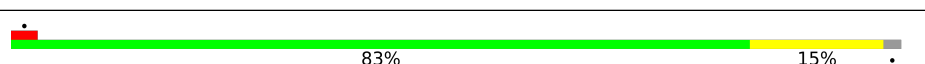
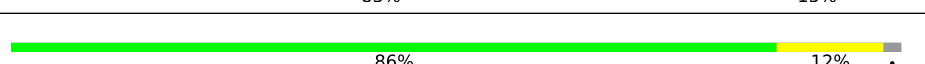
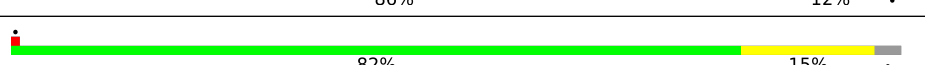
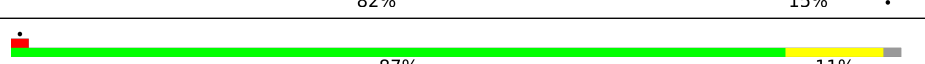
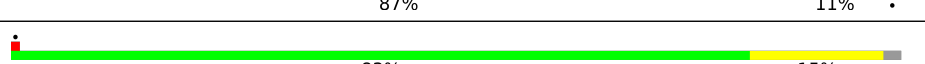
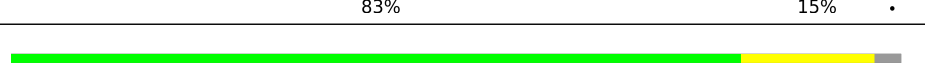

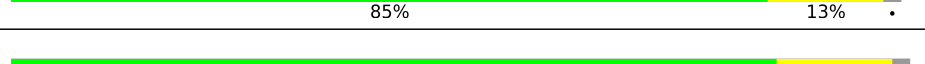





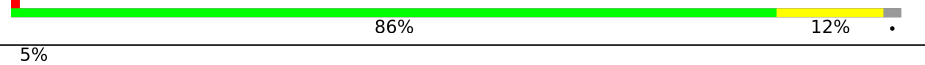
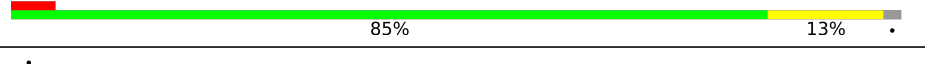


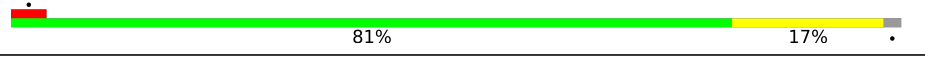

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	9309 ( 2.19 - 3.19 )

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	319	<p>85% 12% .</p>
1	AB	319	<p>86% 13% .</p>
1	AC	319	<p>88% 10% .</p>
1	AJ	319	<p>86% 11% .</p>




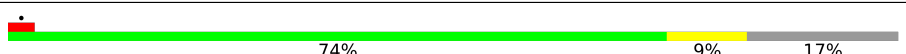
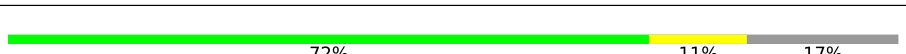
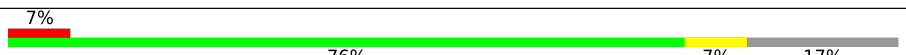
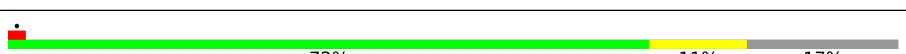
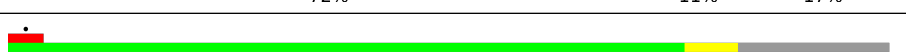

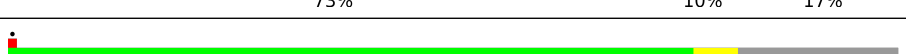
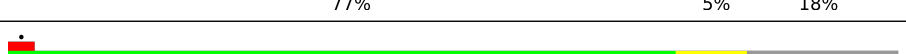
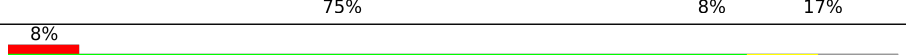
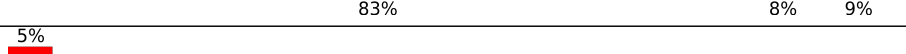
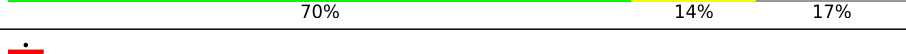











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Mol	Chain	Length	Quality of chain
1	AK	319	 84% 14%
1	AL	319	 83% 15%
1	AS	319	 83% 13%
1	AT	319	 83% 15%
1	AU	319	 87% 11%
1	BB	319	 84% 13%
1	BC	319	 83% 15%
1	BD	319	 86% 12%
1	BK	319	 82% 15%
1	BL	319	 87% 11%
1	BM	319	 83% 15%
1	BT	319	 82% 15%
1	BU	319	 85% 13%
1	BV	319	 86% 13%
1	CC	319	 82% 16%
1	CD	319	 81% 17%
1	CE	319	 81% 17%
1	CL	319	 80% 18%
1	CM	319	 86% 12%
1	CN	319	 5% 85% 13%
1	CU	319	 82% 16%
1	CV	319	 84% 14%
1	CW	319	 81% 17%
2	AD	185	 76% 8% 16%
2	AE	185	 76% 6% 18%











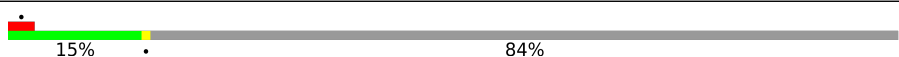

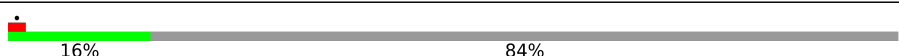
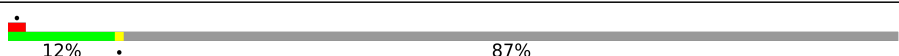
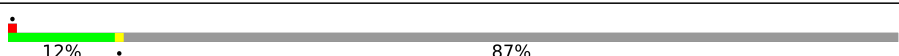
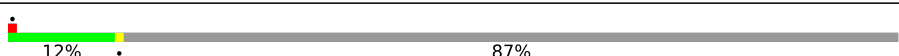

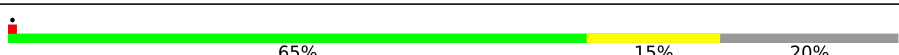
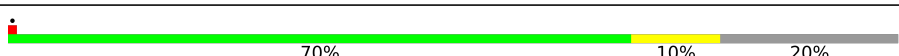
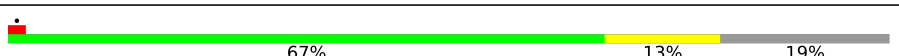



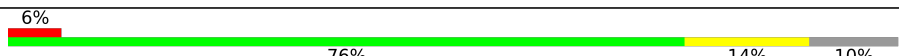
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Mol	Chain	Length	Quality of chain
2	AF	185	 76% 8% 17%
2	AM	185	 75% 8% 17%
2	AN	185	 72% 11% 17%
2	AV	185	 74% 9% 17%
2	AW	185	 72% 11% 17%
2	BE	185	 76% 7% 17%
2	BG	185	 72% 11% 17%
2	BO	185	 76% 6% 17%
2	BP	185	 73% 10% 17%
2	BX	185	 77% 5% 18%
2	BY	185	 75% 8% 17%
2	CF	185	 83% 8% 9%
2	CH	185	 70% 14% 17%
2	CO	185	 74% 9% 17%
2	CP	185	 72% 10% 17%
3	AG	230	 12% 87%
3	AH	230	 13% 84%
3	AI	230	 15% 84%
3	AP	230	 15% 84%
3	AQ	230	 16% 84%
3	AR	230	 16% 84%
3	AY	230	 14% 84%
3	AZ	230	 16% 84%
3	BA	230	 15% 84%
3	BH	230	 16% 84%

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Mol	Chain	Length	Quality of chain
3	BI	230	 15% 84%
3	BJ	230	 15% 84%
3	BQ	230	 10% 87%
3	BR	230	 13% 84%
3	BS	230	 15% 84%
3	BZ	230	 14% 84%
3	CA	230	 15% 84%
3	CB	230	 13% 84%
3	CI	230	 14% 84%
3	CJ	230	 12% 87%
3	CK	230	 15% 84%
3	CR	230	 13% 84%
3	CS	230	 16% 84%
3	CT	230	 12% 87%
3	CX	230	 12% 87%
3	CY	230	 12% 87%
3	CZ	230	 10% 87%
4	AO	190	 65% 15% 20%
4	AX	190	 70% 10% 20%
4	BF	190	 67% 13% 19%
4	BN	190	 69% 11% 20%
4	BW	190	 73% 9% 18%
4	CG	190	 67% 13% 20%
4	CQ	190	 6% 76% 14% 10%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 104341 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	AA	309	2488	1604	400	475	9	0	0
1	AB	313	2510	1616	404	481	9	0	0
1	AC	313	2510	1616	404	481	9	0	0
1	AJ	309	2488	1604	400	475	9	0	0
1	AK	313	2510	1616	404	481	9	0	0
1	AL	313	2510	1616	404	481	9	0	0
1	AS	309	2488	1604	400	475	9	0	0
1	AT	313	2510	1616	404	481	9	0	0
1	AU	313	2510	1616	404	481	9	0	0
1	BB	309	2488	1604	400	475	9	0	0
1	BC	313	2510	1616	404	481	9	0	0
1	BD	313	2510	1616	404	481	9	0	0
1	BK	309	2488	1604	400	475	9	0	0
1	BL	313	2510	1616	404	481	9	0	0
1	BM	313	2510	1616	404	481	9	0	0
1	BT	309	2488	1604	400	475	9	0	0
1	BU	313	2510	1616	404	481	9	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BV	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CC	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CD	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CE	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CL	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CM	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CN	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CU	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CV	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CW	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		

- Molecule 2 is a protein called Decorator protein P03.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AD	155	Total	C	N	O	S	0	0
			1178	742	197	235	4		
2	AE	152	Total	C	N	O	S	0	0
			1160	730	194	232	4		
2	AF	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	AM	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	AN	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	AV	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	AW	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	BE	154	Total	C	N	O	S	0	0
			1170	736	196	234	4		
2	BG	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	BO	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	BP	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	BX	152	Total	C	N	O	S	0	0
			1160	730	194	232	4		
2	BY	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	CF	168	Total	C	N	O	S	0	0
			1288	813	215	256	4		
2	CH	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	CO	153	Total	C	N	O	S	0	0
			1161	730	194	233	4		
2	CP	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		

- Molecule 3 is a protein called Scaffold protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	AG	30	Total	C	N	O	0	0
			266	174	47	45		
3	AH	37	Total	C	N	O	0	0
			315	203	55	57		
3	AI	37	Total	C	N	O	0	0
			315	203	55	57		
3	AP	37	Total	C	N	O	0	0
			315	203	55	57		
3	AQ	37	Total	C	N	O	0	0
			315	203	55	57		
3	AR	37	Total	C	N	O	0	0
			315	203	55	57		
3	AY	37	Total	C	N	O	0	0
			315	203	55	57		
3	AZ	37	Total	C	N	O	0	0
			315	203	55	57		
3	BA	37	Total	C	N	O	0	0
			315	203	55	57		
3	BH	37	Total	C	N	O	0	0
			315	203	55	57		
3	BI	37	Total	C	N	O	0	0
			315	203	55	57		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	BJ	37	Total	C	N	O	0	0
			315	203	55	57		
3	BQ	30	Total	C	N	O	0	0
			266	174	47	45		
3	BR	37	Total	C	N	O	0	0
			315	203	55	57		
3	BS	37	Total	C	N	O	0	0
			315	203	55	57		
3	BZ	37	Total	C	N	O	0	0
			315	203	55	57		
3	CA	37	Total	C	N	O	0	0
			315	203	55	57		
3	CB	37	Total	C	N	O	0	0
			315	203	55	57		
3	CI	37	Total	C	N	O	0	0
			315	203	55	57		
3	CJ	30	Total	C	N	O	0	0
			266	174	47	45		
3	CK	37	Total	C	N	O	0	0
			315	203	55	57		
3	CR	37	Total	C	N	O	0	0
			315	203	55	57		
3	CS	37	Total	C	N	O	0	0
			315	203	55	57		
3	CT	30	Total	C	N	O	0	0
			266	174	47	45		
3	CX	30	Total	C	N	O	0	0
			266	174	47	45		
3	CY	30	Total	C	N	O	0	0
			266	174	47	45		
3	CZ	30	Total	C	N	O	0	0
			266	174	47	45		

- Molecule 4 is a protein called Decorator protein P05.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AO	152	Total	C	N	O	S	0	0
			1195	761	203	229	2		
4	AX	152	Total	C	N	O	S	0	0
			1195	761	203	229	2		
4	BF	153	Total	C	N	O	S	0	0
			1203	767	203	231	2		

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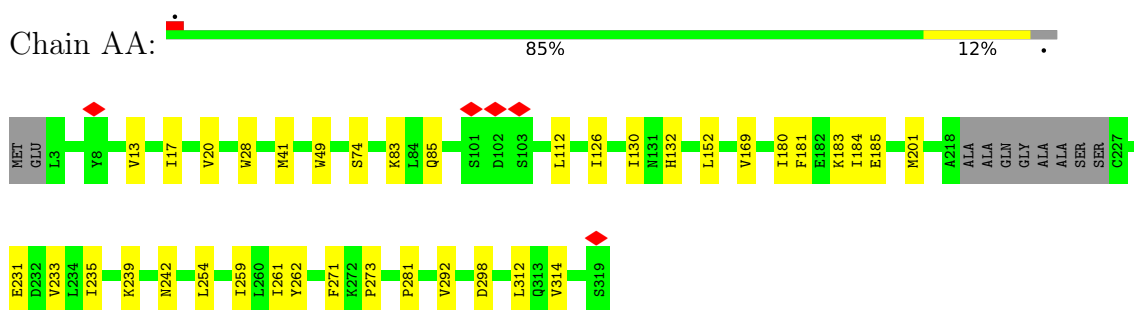
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>					<b>AltConf</b>	<b>Trace</b>
4	BN	152	Total	C	N	O	S	0	0
			1197	764	202	229	2		
4	BW	156	Total	C	N	O	S	0	0
			1222	776	208	235	3		
4	CG	152	Total	C	N	O	S	0	0
			1191	758	202	229	2		
4	CQ	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		

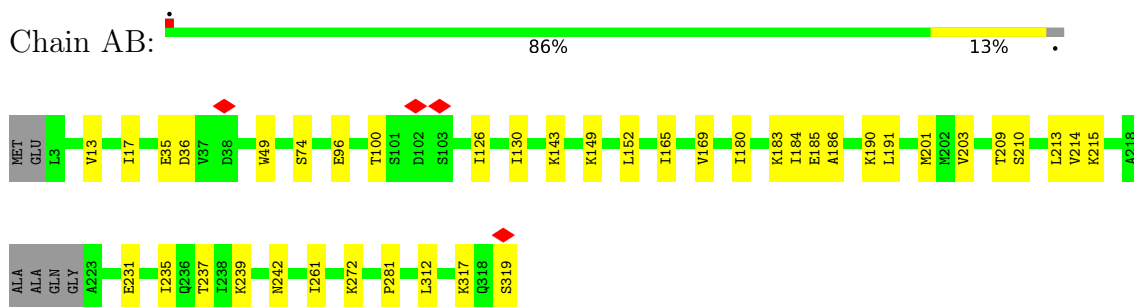
### 3 Residue-property plots [i](#)

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.

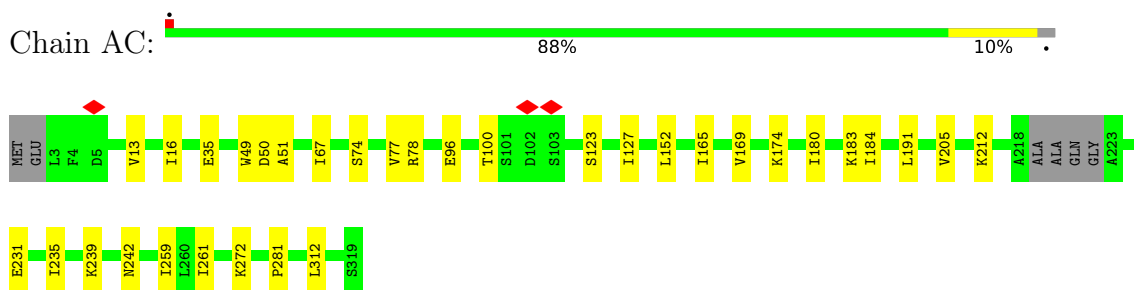
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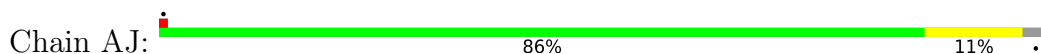
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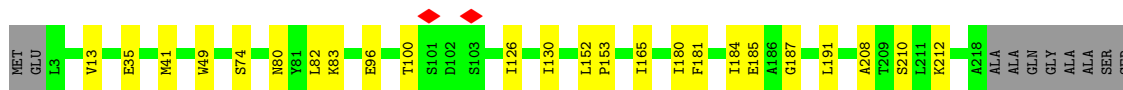


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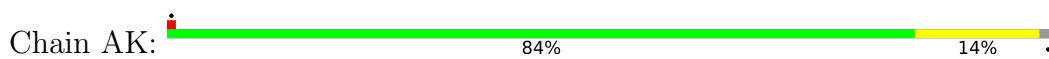


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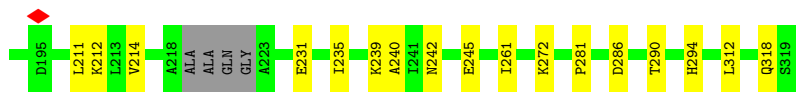
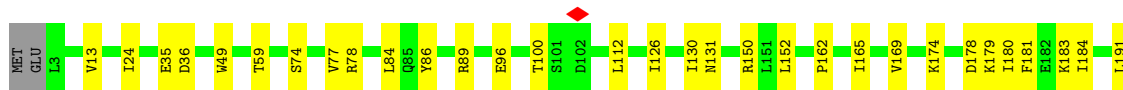
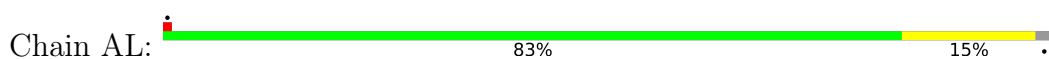




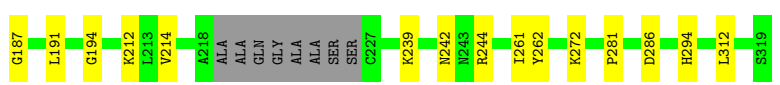
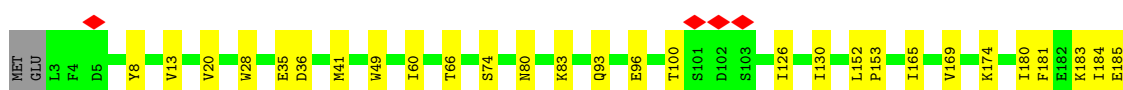
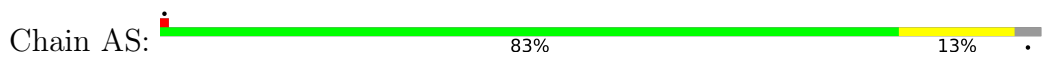
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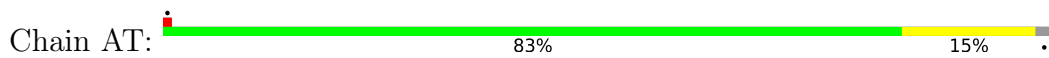
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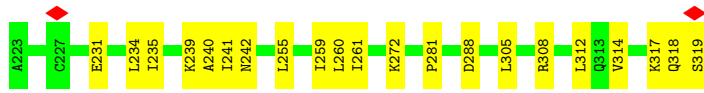


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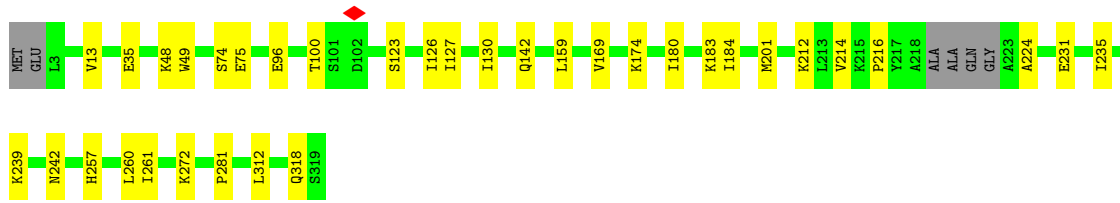
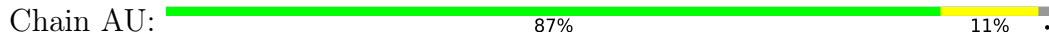


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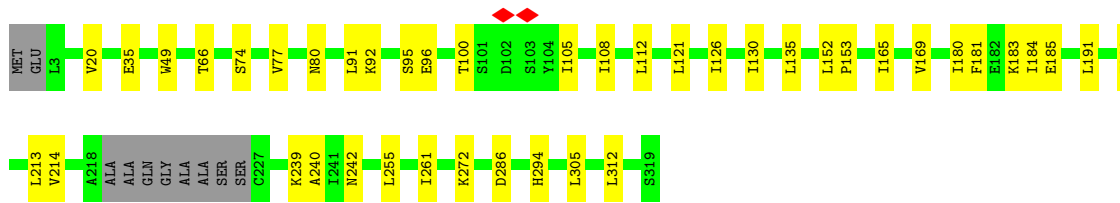
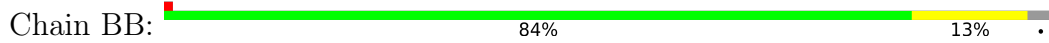




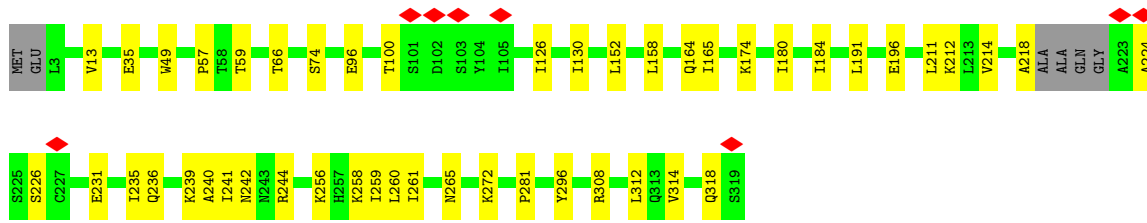
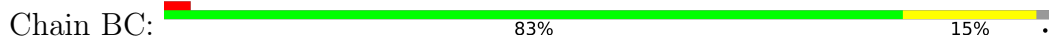
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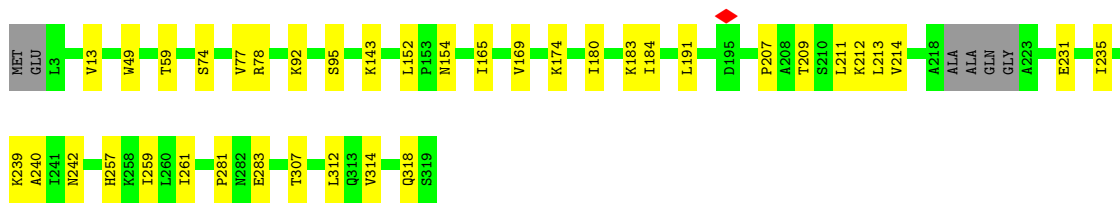
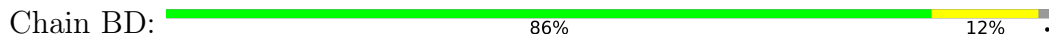
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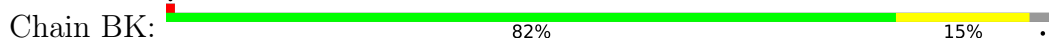
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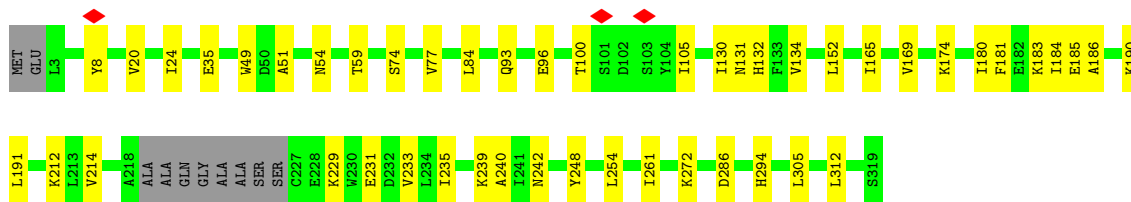


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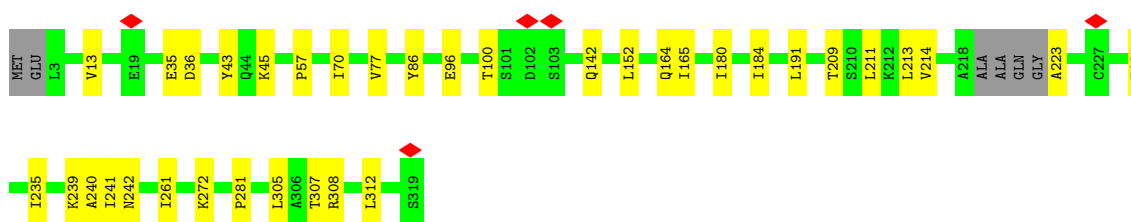


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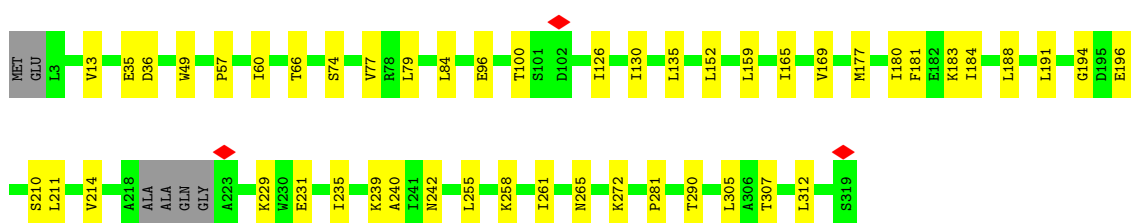
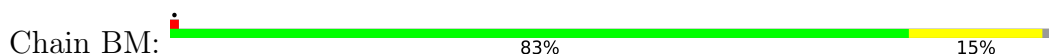




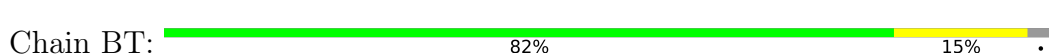
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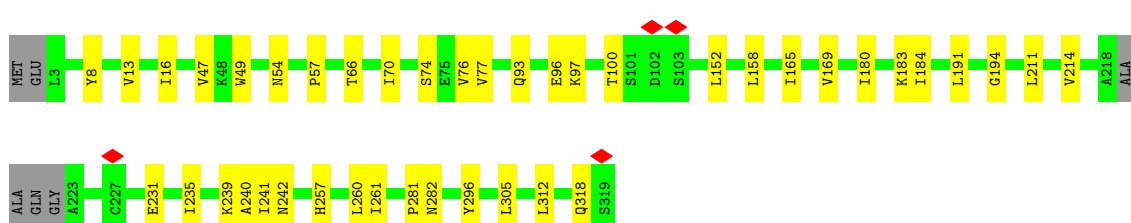
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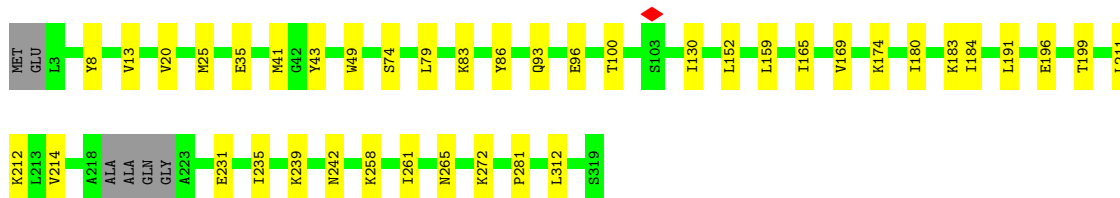
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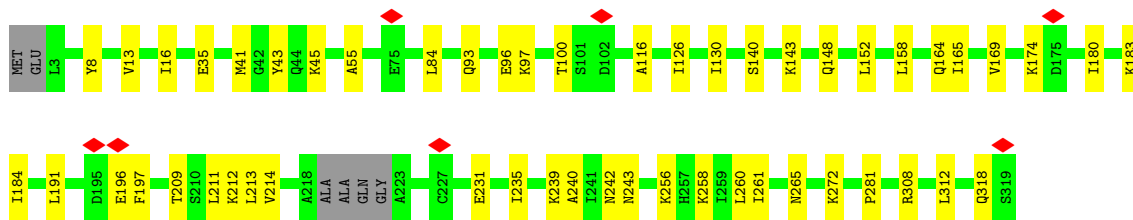
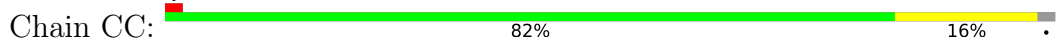
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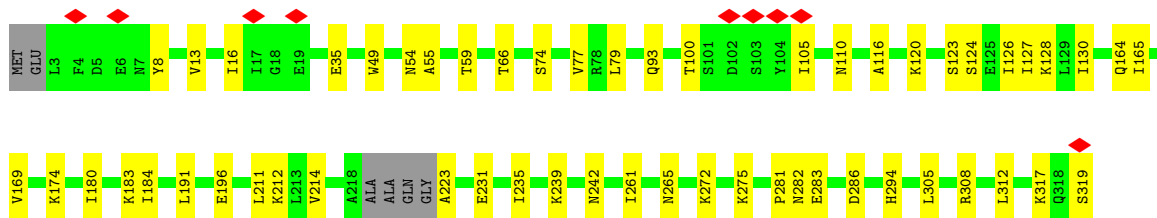
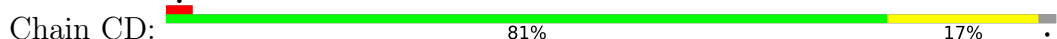
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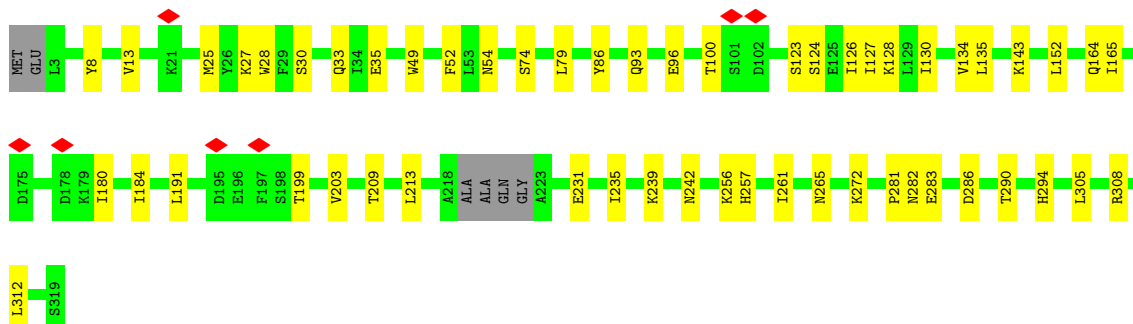
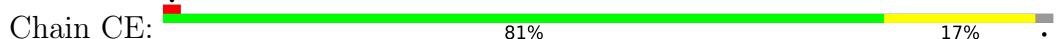
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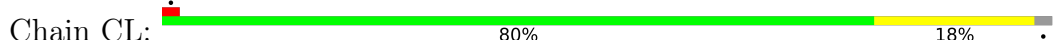
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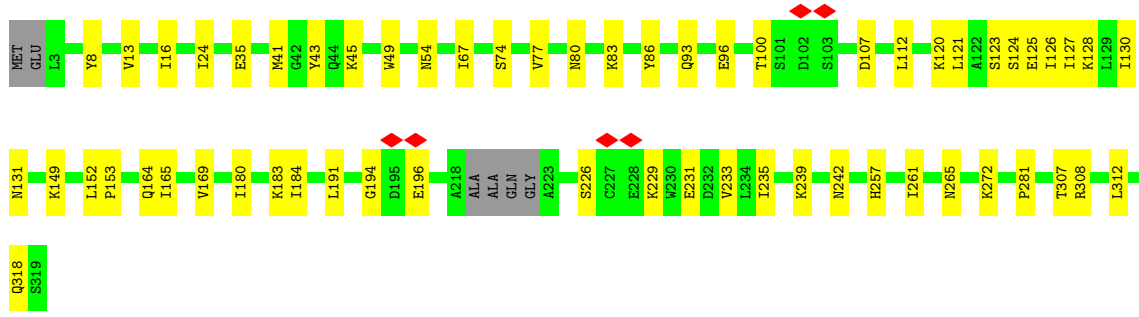


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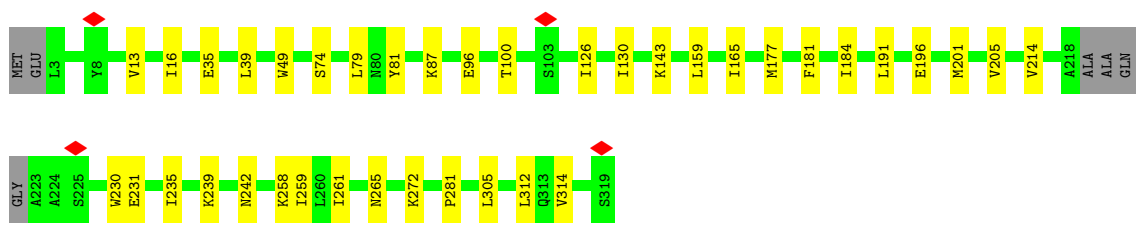
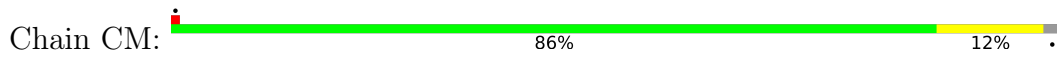


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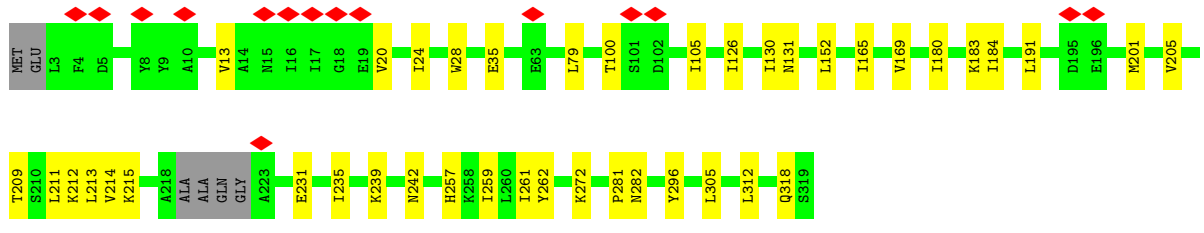
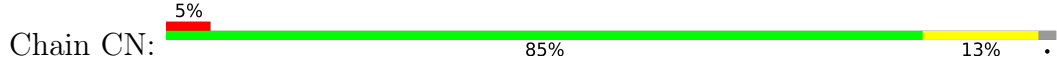




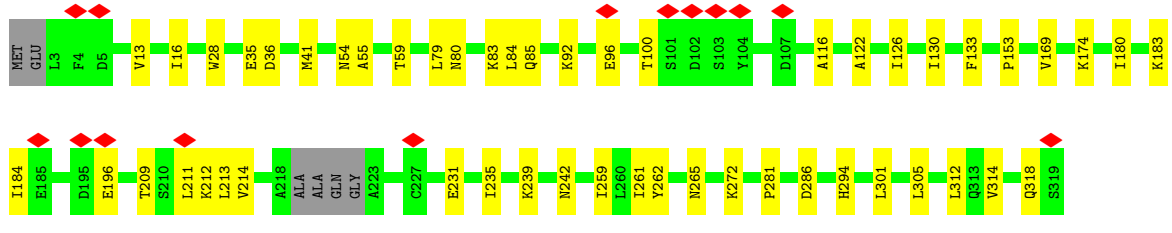
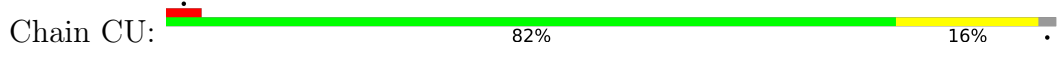
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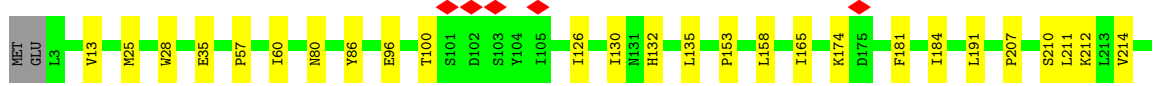
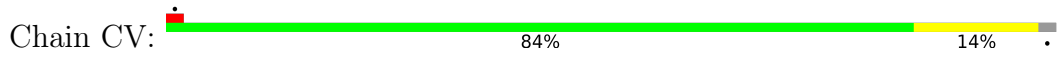
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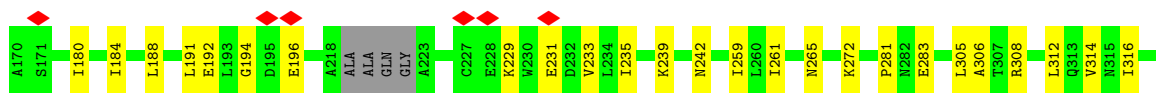
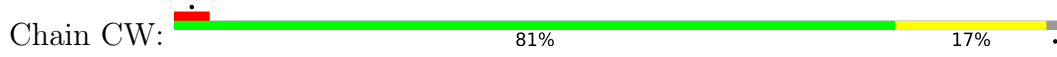


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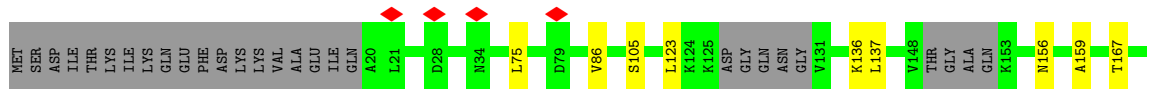
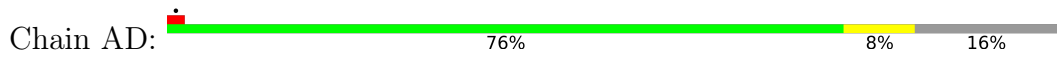




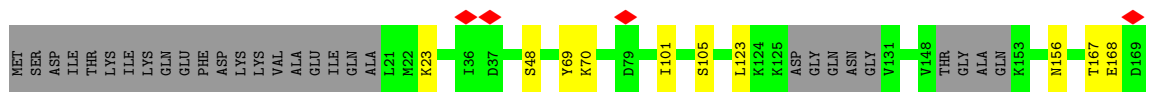
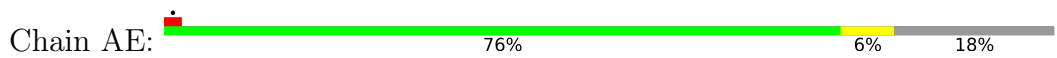
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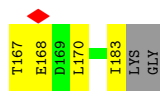
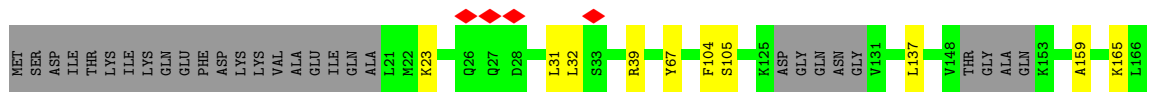
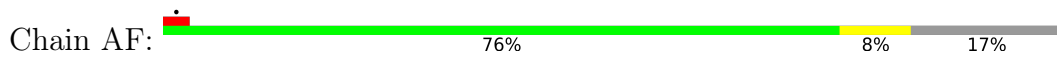
• Molecule 2: Decorator protein P03



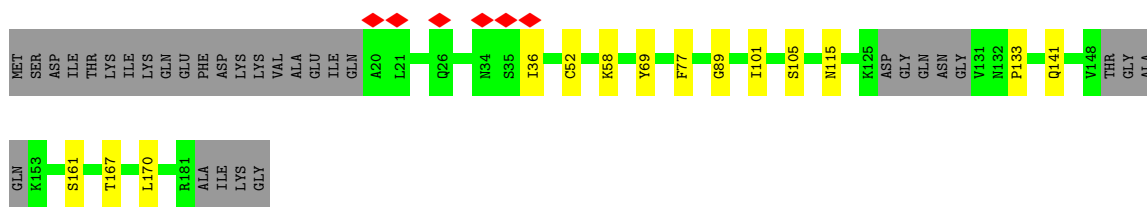
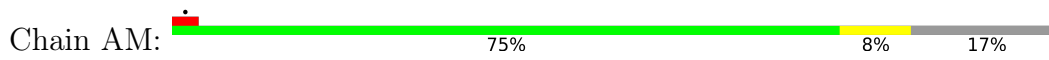
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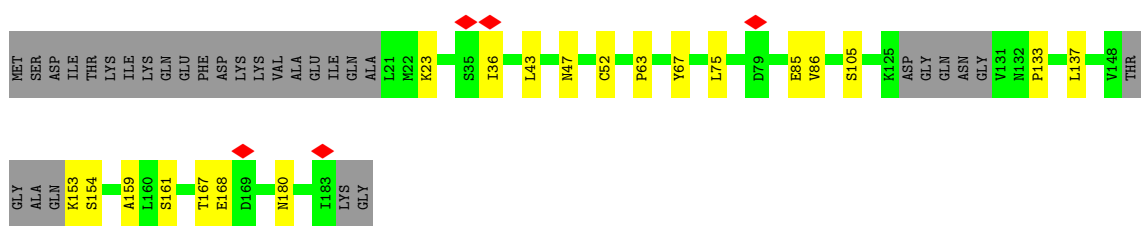
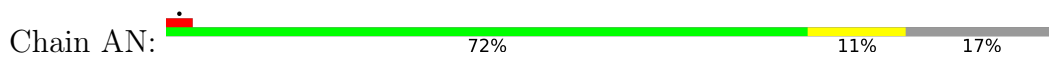
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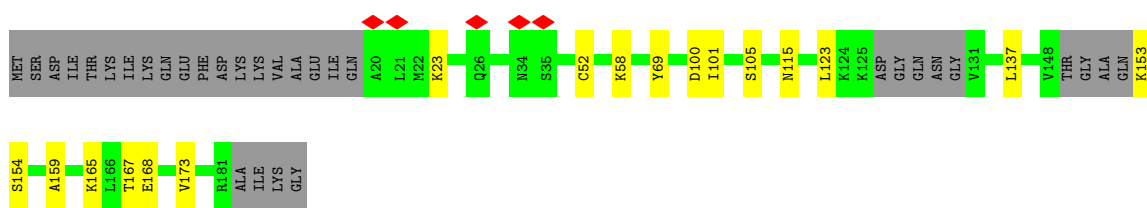
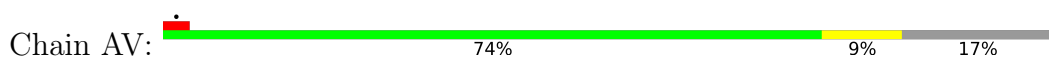
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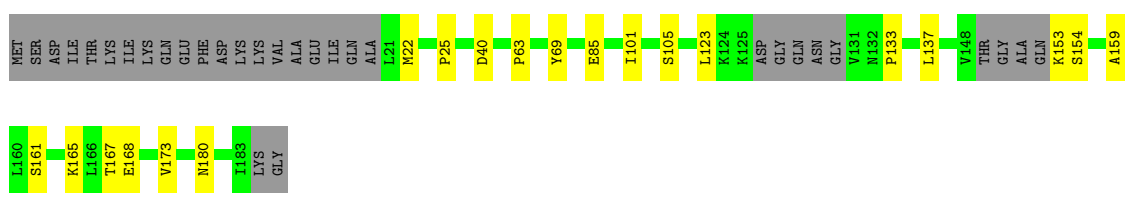
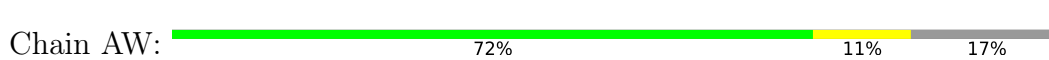
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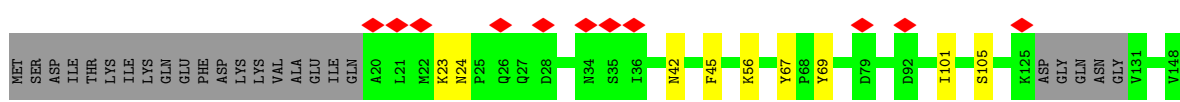
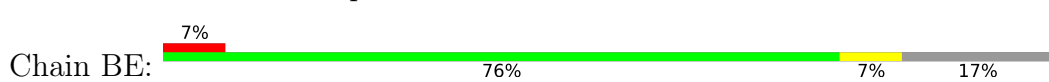
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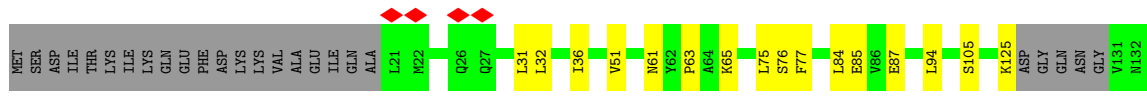
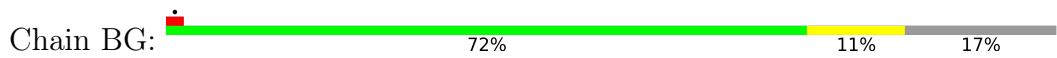


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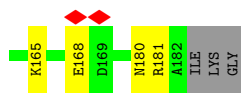
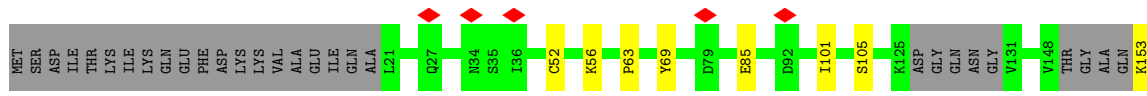
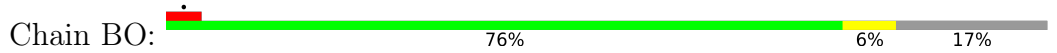




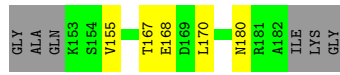
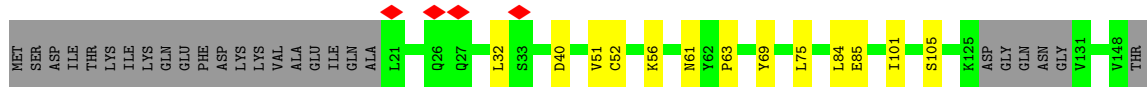
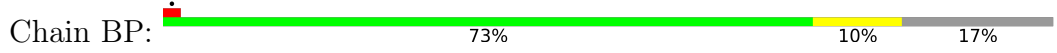
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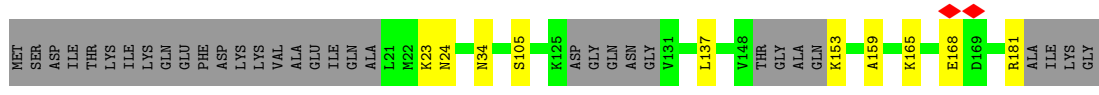
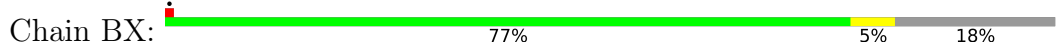
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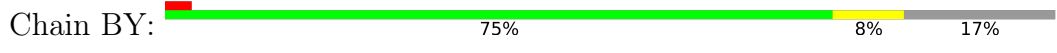
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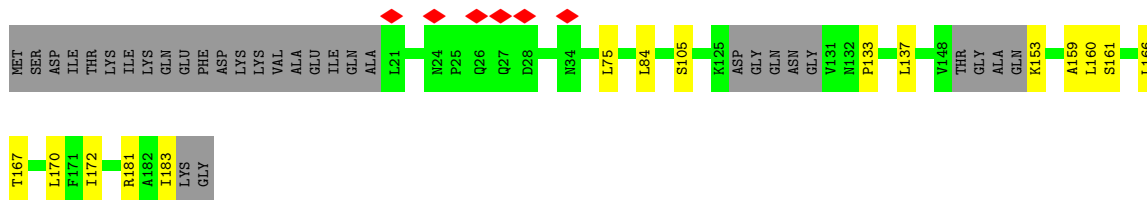


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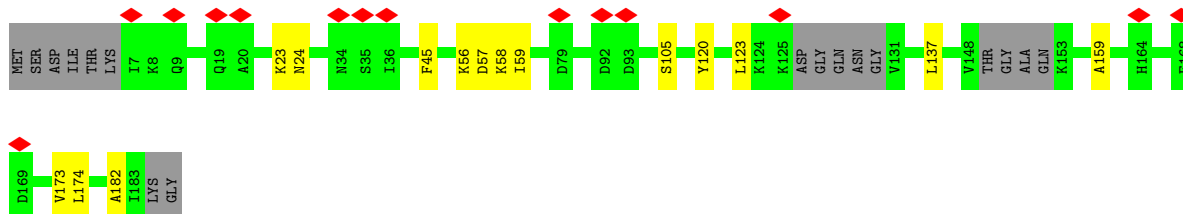
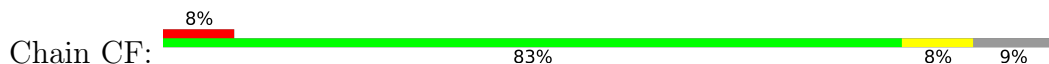


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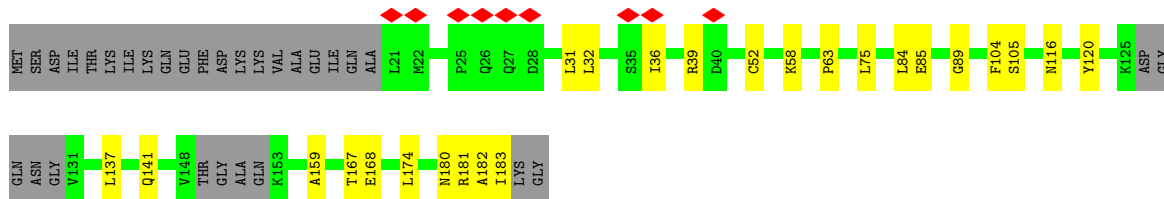




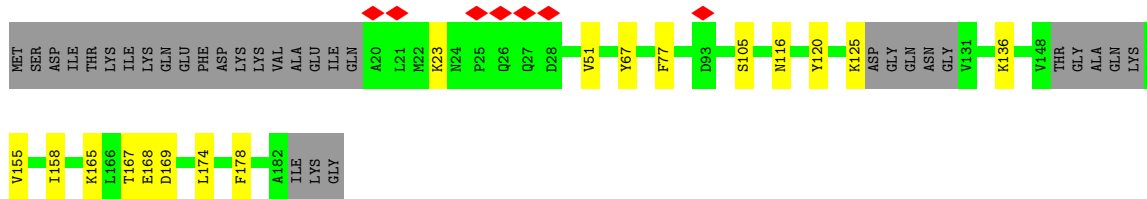
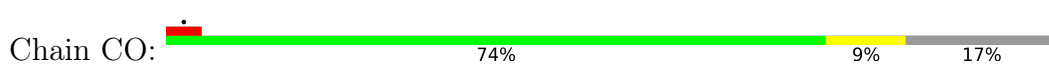
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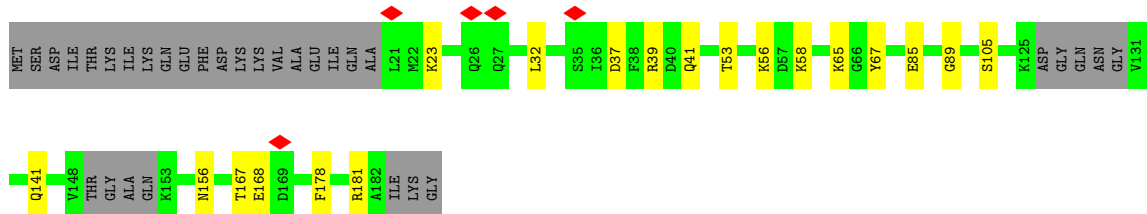
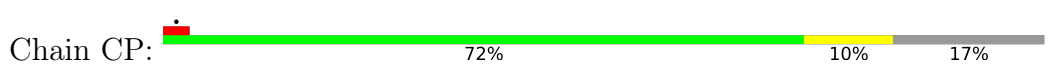
• Molecule 2: Decorator protein P03



• Molecule 2: Decorator protein P03



• Molecule 2: Decorator protein P03



• Molecule 3: Scaffold protein



MET	THR	LYS	GLU	LEU	ASP	GLN	ALA	GLN	ASP	LYS	GLU	GLU	GLN	GLN	ILE	LYS	ALA	ALA	ASP	THR	LYS	VAL	ILE	SER	SER	LEU	VAL	GLN	GLN	PHE	GLU	GLU	TYR	MET	LYS	ASN	ARG	PHE	LYS	GLU	GLN	ALA	ALA	ASN	SER	LYS	SER	LYS	GLY	TYR	THR	THR	SER	ARG	ASP	LEU	SER	ILE	GLN	ILE	ASN	GLU	ARG	ILE	THR		
LYS	GLU	ALA	VAL	VAL	GLU	ARG	GLN	ARG	ILE	LYS	GLN	LEU	LEU	GLU	ALA	GLU	GLU	ILE	ILE	ASN	THR	GLY	ILE	ILE	THR	THR	ALA	ALA	LYS	ALA	GLU	ASN	PHE	ASN	LYS	GLN	VAL	VAL	ASN	ILE	ASN	LYS	LEU	VAL	ALA	LYS	GLY	TYR	THR	THR	LYS	ASP	ILE	GLN	ILE	ALA	GLN	ARG	ARG	ILE	ALA	GLN	ASN	GLU	ARG	ILE	THR
LEU	VAL	ARG	PHE	PRO	ILE	GLU	GLN	ILE	ALA	ILE	ALA	VAL	SER	ASP	ILE	SER	HIS	ARG	THR	ASN	THR	GLY	GLU	ILE	ILE	THR	LEU	GLN	GLN	VAL	GLU	VAL	ASN	ILE	LYS	ALA	ALA	LYS	VAL	SER	SER	GLY	TYR	THR	THR	SER	SER	VAL	ASP	ASP	ASP	ILE	GLN	ILE	LYS	GLY	ASN	ASN	GLU	ARG	ILE	ALA	ALA				
ILE	LYS	SER	GLU	ALA	SER	LEU	ASP	GLN	ASP	ASN	F194	K211	Q212	R213	R214	K222	R223	HIS	LYS	THR	ASN	GLY	GLU	ILE	ILE	SER	SER	LEU	VAL	GLN	ALA	GLN	LYS	VAL	ASN	ILE	LYS	GLN	VAL	ALA	ASN	LYS	VAL	SER	GLY	TYR	THR	THR	SER	SER	VAL	ASP	ASP	ILE	GLN	ILE	ASN	GLU	ARG	ILE	ALA						

• Molecule 3: Scaffold protein



MET	THR	LYS	GLU	LEU	ASP	GLN	ALA	GLN	ASP	LYS	GLU	GLU	GLN	GLN	ILE	LYS	ALA	ALA	ASP	THR	LYS	VAL	ILE	ILE	SER	SER	LEU	VAL	GLN	GLN	PHE	GLU	GLU	TYR	MET	LYS	ASN	ARG	PHE	LYS	GLU	GLN	ALA	ALA	ASN	SER	LYS	SER	LYS	GLY	TYR	THR	THR	SER	ARG	ASP	LEU	SER	ILE	GLN	ILE	ASN	GLU	ARG	ILE	THR		
LYS	GLU	ALA	VAL	VAL	GLU	GLU	GLN	ILE	ALA	LYS	GLN	LEU	LEU	GLU	ALA	GLU	GLU	ARG	ALA	ASN	THR	GLY	GLU	ILE	ASP	LEU	LEU	GLN	GLN	VAL	ALA	GLU	ASN	PHE	LYS	LYS	VAL	VAL	ASN	ILE	ASN	LYS	VAL	ALA	LYS	SER	GLY	TYR	THR	THR	SER	SER	VAL	ASP	ASP	ASP	ILE	GLN	ILE	LYS	GLY	ASN	ASN	GLU	ARG	ILE	ALA	ALA
LEU	VAL	ARG	PHE	PRO	ILE	GLU	GLN	ILE	ALA	ILE	ALA	VAL	SER	ASP	ILE	SER	HIS	ARG	THR	ASN	THR	GLY	GLU	ILE	ILE	LEU	GLN	GLN	VAL	VAL	ALA	GLU	ASN	ASN	ILE	LYS	VAL	ALA	LYS	VAL	SER	SER	SER	GLY	TYR	THR	THR	SER	SER	VAL	ASP	ASP	ASP	ILE	GLN	ILE	LYS	GLY	ASN	ASN	GLU	ARG	ILE	ALA	ALA			
ILE	LYS	SER	GLU	ARG	A187	S188	L189	D190	S191	S192	N193	T200	E201	V202	Q204	A205	I206	K211	R214	I215	R223	HIS	LYS	THR	THR	SER	ILE	ALA	LYS	GLY	VAL	ASN	ILE	LYS	GLN	VAL	ALA	ASN	LYS	VAL	SER	LYS	GLY	TYR	THR	THR	SER	SER	VAL	ASP	ASP	ASP	ILE	GLN	ILE	ASN	GLU	ARG	ILE	ALA	ALA							

• Molecule 3: Scaffold protein



MET	THR	LYS	GLU	LEU	ASP	GLN	ALA	GLN	ASP	LYS	GLU	GLU	GLN	GLN	ILE	LYS	ALA	ALA	ASP	THR	LYS	VAL	ILE	ILE	SER	SER	LEU	VAL	GLN	GLN	PHE	GLU	GLU	TYR	MET	LYS	ASN	ARG	PHE	LYS	GLU	GLN	ALA	ALA	ASN	SER	LYS	SER	LYS	GLY	TYR	THR	THR	SER	ARG	ASP	LEU	SER	ILE	GLN	ILE	ASN	GLU	ARG	ILE	THR		
LYS	GLU	ALA	VAL	VAL	GLU	ARG	GLN	ARG	ILE	LYS	GLN	LEU	LEU	GLU	ALA	GLU	GLU	ARG	ALA	ASN	THR	GLY	GLU	ILE	ASP	LEU	LEU	GLN	GLN	VAL	ALA	GLU	ASN	PHE	LYS	LYS	VAL	VAL	ASN	ILE	ASN	LYS	VAL	ALA	LYS	SER	GLY	TYR	THR	THR	SER	SER	VAL	ASP	ASP	ASP	ILE	GLN	ILE	LYS	GLY	ASN	ASN	GLU	ARG	ILE	ALA	ALA
LEU	VAL	ARG	PHE	PRO	ILE	GLU	GLN	ILE	ALA	ILE	ALA	VAL	SER	ASP	ILE	SER	HIS	ARG	THR	ASN	THR	GLY	GLU	ILE	ILE	LEU	GLN	GLN	VAL	VAL	ALA	GLU	ASN	ASN	ILE	LYS	VAL	ALA	LYS	VAL	SER	SER	SER	GLY	TYR	THR	THR	SER	SER	VAL	ASP	ASP	ASP	ILE	GLN	ILE	LYS	GLY	ASN	ASN	GLU	ARG	ILE	ALA	ALA			
ILE	LYS	SER	GLU	ARG	A187	L190	D191	S192	N193	T200	Q204	R223	HIS	LYS	THR	THR	ASN	THR	ASN	THR	GLY	GLU	ILE	ILE	SER	SER	LEU	VAL	GLN	GLN	VAL	ALA	GLU	ASN	ASN	ILE	LYS	VAL	ALA	LYS	VAL	SER	LYS	GLY	TYR	THR	THR	SER	SER	VAL	ASP	ASP	ASP	ILE	GLN	ILE	ASN	GLU	ARG	ILE	ALA	ALA						

• Molecule 3: Scaffold protein



MET	THR	LYS	GLU	LEU	ASP	GLN	ALA	GLN	ASP	LYS	GLU	GLU	GLN	GLN	ILE	LYS	ALA	ALA	ASP	THR	LYS	VAL	ILE	ILE	SER	SER	LEU	VAL	GLN	GLN	PHE	GLU	GLU	TYR	MET	LYS	ASN	ARG	PHE	LYS	GLU	GLN	ALA	ALA	ASN	SER	LYS	SER	LYS	GLY	TYR	THR	THR	SER	ARG	ASP	LEU	SER	ILE	GLN	ILE	ASN	GLU	ARG	ILE	THR
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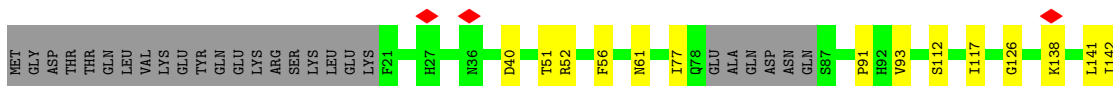
• Molecule 4: Decorator protein P05



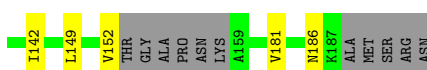
• Molecule 4: Decorator protein P05



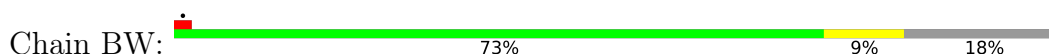
• Molecule 4: Decorator protein P05

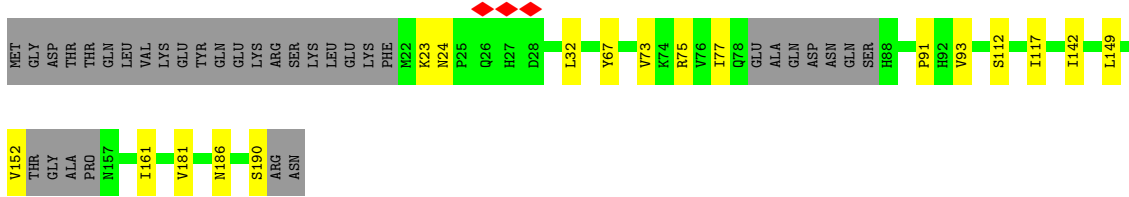


• Molecule 4: Decorator protein P05

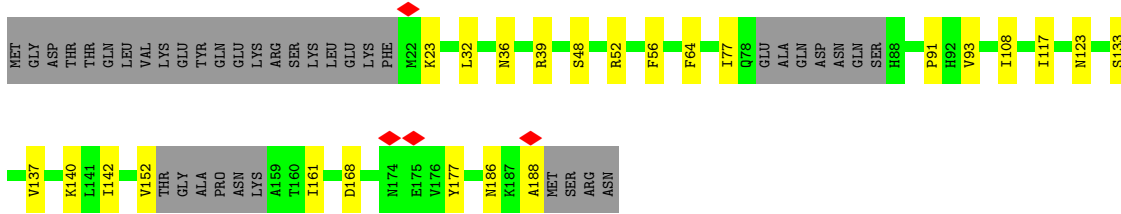


• Molecule 4: Decorator protein P05

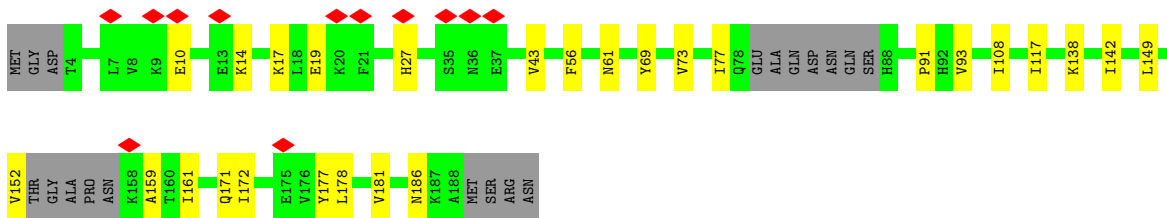
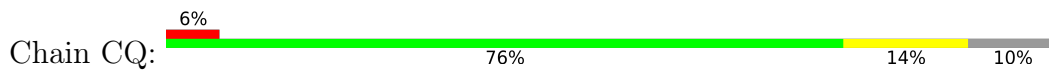




• Molecule 4: Decorator protein P05



• Molecule 4: Decorator protein P05



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	32029	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	44	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	165000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	533.50397, 533.50397, 533.50397	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8335999, 0.8335999, 0.8335999	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	AA	0.11	0/2536	0.28	0/3428
1	AB	0.12	0/2558	0.28	0/3458
1	AC	0.12	0/2558	0.28	0/3458
1	AJ	0.12	0/2536	0.28	0/3428
1	AK	0.11	0/2558	0.27	0/3458
1	AL	0.12	0/2558	0.28	0/3458
1	AS	0.12	0/2536	0.28	0/3428
1	AT	0.11	0/2558	0.27	0/3458
1	AU	0.12	0/2558	0.28	0/3458
1	BB	0.12	0/2536	0.29	0/3428
1	BC	0.12	0/2558	0.29	0/3458
1	BD	0.12	0/2558	0.29	0/3458
1	BK	0.12	0/2536	0.28	0/3428
1	BL	0.11	0/2558	0.28	0/3458
1	BM	0.11	0/2558	0.27	0/3458
1	BT	0.12	0/2536	0.28	0/3428
1	BU	0.12	0/2558	0.28	0/3458
1	BV	0.12	0/2558	0.29	0/3458
1	CC	0.11	0/2558	0.28	0/3458
1	CD	0.11	0/2558	0.28	0/3458
1	CE	0.10	0/2558	0.27	0/3458
1	CL	0.11	0/2558	0.28	0/3458
1	CM	0.11	0/2558	0.28	0/3458
1	CN	0.11	0/2558	0.27	0/3458
1	CU	0.11	0/2558	0.28	0/3458
1	CV	0.11	0/2558	0.27	0/3458
1	CW	0.10	0/2558	0.27	0/3458
2	AD	0.10	0/1195	0.28	0/1608
2	AE	0.09	0/1177	0.25	0/1583
2	AF	0.10	0/1190	0.26	0/1601
2	AM	0.11	0/1182	0.29	0/1590
2	AN	0.10	0/1190	0.28	0/1601
2	AV	0.10	0/1182	0.26	0/1590
2	AW	0.10	0/1190	0.26	0/1601

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	BE	0.09	0/1187	0.25	0/1597
2	BG	0.10	0/1190	0.28	0/1601
2	BO	0.10	0/1182	0.26	0/1590
2	BP	0.10	0/1182	0.26	0/1590
2	BX	0.11	0/1177	0.27	0/1583
2	BY	0.10	0/1190	0.27	0/1601
2	CF	0.11	0/1306	0.28	0/1755
2	CH	0.10	0/1190	0.27	0/1601
2	CO	0.09	0/1178	0.25	0/1586
2	CP	0.10	0/1182	0.25	0/1590
3	AG	0.12	0/272	0.25	0/365
3	AH	0.12	0/321	0.24	0/432
3	AI	0.11	0/321	0.23	0/432
3	AP	0.11	0/321	0.24	0/432
3	AQ	0.11	0/321	0.24	0/432
3	AR	0.12	0/321	0.21	0/432
3	AY	0.11	0/321	0.23	0/432
3	AZ	0.12	0/321	0.23	0/432
3	BA	0.12	0/321	0.23	0/432
3	BH	0.12	0/321	0.24	0/432
3	BI	0.10	0/321	0.24	0/432
3	BJ	0.11	0/321	0.23	0/432
3	BQ	0.11	0/272	0.25	0/365
3	BR	0.13	0/321	0.28	0/432
3	BS	0.13	0/321	0.29	0/432
3	BZ	0.12	0/321	0.24	0/432
3	CA	0.11	0/321	0.25	0/432
3	CB	0.12	0/321	0.22	0/432
3	CI	0.11	0/321	0.26	0/432
3	CJ	0.12	0/272	0.26	0/365
3	CK	0.10	0/321	0.22	0/432
3	CR	0.13	0/321	0.29	0/432
3	CS	0.11	0/321	0.25	0/432
3	CT	0.11	0/272	0.24	0/365
3	CX	0.11	0/272	0.25	0/365
3	CY	0.13	0/272	0.32	0/365
3	CZ	0.13	0/272	0.26	0/365
4	AO	0.11	0/1216	0.28	0/1636
4	AX	0.11	0/1216	0.27	0/1636
4	BF	0.11	0/1225	0.28	0/1649
4	BN	0.11	0/1219	0.27	0/1641
4	BW	0.11	0/1243	0.28	0/1672
4	CG	0.10	0/1212	0.27	0/1632

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
4	CQ	0.10	0/1381	0.26	0/1855
All	All	0.11	0/106240	0.27	0/143370

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	2488	0	2527	22	0
1	AB	2510	0	2547	25	0
1	AC	2510	0	2547	19	0
1	AJ	2488	0	2527	21	0
1	AK	2510	0	2547	27	0
1	AL	2510	0	2547	33	0
1	AS	2488	0	2527	26	0
1	AT	2510	0	2547	27	0
1	AU	2510	0	2547	19	0
1	BB	2488	0	2527	25	0
1	BC	2510	0	2547	29	0
1	BD	2510	0	2547	25	0
1	BK	2488	0	2527	29	0
1	BL	2510	0	2547	24	0
1	BM	2510	0	2547	35	0
1	BT	2488	0	2527	30	0
1	BU	2510	0	2547	27	0
1	BV	2510	0	2547	27	0
1	CC	2510	0	2547	32	0
1	CD	2510	0	2547	34	0
1	CE	2510	0	2547	33	0
1	CL	2510	0	2547	35	0
1	CM	2510	0	2547	24	0
1	CN	2510	0	2547	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CU	2510	0	2547	32	0
1	CV	2510	0	2547	29	0
1	CW	2510	0	2547	35	0
2	AD	1178	0	1163	8	0
2	AE	1160	0	1142	7	0
2	AF	1173	0	1158	10	0
2	AM	1165	0	1147	10	0
2	AN	1173	0	1158	14	0
2	AV	1165	0	1147	10	0
2	AW	1173	0	1158	12	0
2	BE	1170	0	1152	9	0
2	BG	1173	0	1158	18	0
2	BO	1165	0	1147	8	0
2	BP	1165	0	1147	16	0
2	BX	1160	0	1142	7	0
2	BY	1173	0	1158	9	0
2	CF	1288	0	1279	12	0
2	CH	1173	0	1158	23	0
2	CO	1161	0	1139	11	0
2	CP	1165	0	1147	15	0
3	AG	266	0	265	2	0
3	AH	315	0	312	5	0
3	AI	315	0	312	1	0
3	AP	315	0	312	1	0
3	AQ	315	0	312	1	0
3	AR	315	0	312	1	0
3	AY	315	0	312	3	0
3	AZ	315	0	312	0	0
3	BA	315	0	312	1	0
3	BH	315	0	312	1	0
3	BI	315	0	312	2	0
3	BJ	315	0	312	2	0
3	BQ	266	0	265	4	0
3	BR	315	0	312	4	0
3	BS	315	0	312	2	0
3	BZ	315	0	312	2	0
3	CA	315	0	312	1	0
3	CB	315	0	312	5	0
3	CI	315	0	312	2	0
3	CJ	266	0	265	1	0
3	CK	315	0	312	2	0
3	CR	315	0	312	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	CS	315	0	312	0	0
3	CT	266	0	265	2	0
3	CX	266	0	265	2	0
3	CY	266	0	265	2	0
3	CZ	266	0	265	4	0
4	AO	1195	0	1189	19	0
4	AX	1195	0	1189	12	0
4	BF	1203	0	1190	17	0
4	BN	1197	0	1185	14	0
4	BW	1222	0	1214	12	0
4	CG	1191	0	1181	20	0
4	CQ	1358	0	1361	18	0
All	All	104341	0	104953	934	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 934 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)
4:CQ:77:ILE:HG13	4:CQ:91:PRO:HB3	1.68	0.76
1:CV:165:ILE:HD13	1:CV:191:LEU:HD23	1.68	0.75
1:CM:39:LEU:HD11	1:CM:81:TYR:HD2	1.49	0.75
1:AJ:165:ILE:HD13	1:AJ:191:LEU:HD23	1.69	0.73
1:AT:165:ILE:HD13	1:AT:191:LEU:HD23	1.69	0.73

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	305/319 (96%)	301 (99%)	4 (1%)	0	100	100
1	AB	309/319 (97%)	301 (97%)	8 (3%)	0	100	100
1	AC	309/319 (97%)	301 (97%)	8 (3%)	0	100	100
1	AJ	305/319 (96%)	299 (98%)	6 (2%)	0	100	100
1	AK	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	AL	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	AS	305/319 (96%)	300 (98%)	5 (2%)	0	100	100
1	AT	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	AU	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	BB	305/319 (96%)	301 (99%)	4 (1%)	0	100	100
1	BC	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	BD	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	BK	305/319 (96%)	301 (99%)	4 (1%)	0	100	100
1	BL	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	BM	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	BT	305/319 (96%)	301 (99%)	4 (1%)	0	100	100
1	BU	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	BV	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	CC	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CD	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CE	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CL	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CM	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	CN	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CU	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CV	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CW	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
2	AD	149/185 (80%)	148 (99%)	1 (1%)	0	100	100
2	AE	146/185 (79%)	145 (99%)	1 (1%)	0	100	100
2	AF	148/185 (80%)	146 (99%)	2 (1%)	0	100	100
2	AM	147/185 (80%)	142 (97%)	5 (3%)	0	100	100
2	AN	148/185 (80%)	145 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AV	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	AW	148/185 (80%)	147 (99%)	1 (1%)	0	100	100
2	BE	148/185 (80%)	146 (99%)	2 (1%)	0	100	100
2	BG	148/185 (80%)	144 (97%)	4 (3%)	0	100	100
2	BO	147/185 (80%)	144 (98%)	3 (2%)	0	100	100
2	BP	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	BX	146/185 (79%)	145 (99%)	1 (1%)	0	100	100
2	BY	148/185 (80%)	147 (99%)	1 (1%)	0	100	100
2	CF	162/185 (88%)	159 (98%)	3 (2%)	0	100	100
2	CH	148/185 (80%)	145 (98%)	3 (2%)	0	100	100
2	CO	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	CP	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
3	AG	28/230 (12%)	28 (100%)	0	0	100	100
3	AH	35/230 (15%)	35 (100%)	0	0	100	100
3	AI	35/230 (15%)	35 (100%)	0	0	100	100
3	AP	35/230 (15%)	35 (100%)	0	0	100	100
3	AQ	35/230 (15%)	35 (100%)	0	0	100	100
3	AR	35/230 (15%)	35 (100%)	0	0	100	100
3	AY	35/230 (15%)	35 (100%)	0	0	100	100
3	AZ	35/230 (15%)	35 (100%)	0	0	100	100
3	BA	35/230 (15%)	35 (100%)	0	0	100	100
3	BH	35/230 (15%)	35 (100%)	0	0	100	100
3	BI	35/230 (15%)	35 (100%)	0	0	100	100
3	BJ	35/230 (15%)	35 (100%)	0	0	100	100
3	BQ	28/230 (12%)	28 (100%)	0	0	100	100
3	BR	35/230 (15%)	35 (100%)	0	0	100	100
3	BS	35/230 (15%)	35 (100%)	0	0	100	100
3	BZ	35/230 (15%)	35 (100%)	0	0	100	100
3	CA	35/230 (15%)	35 (100%)	0	0	100	100
3	CB	35/230 (15%)	35 (100%)	0	0	100	100
3	CI	35/230 (15%)	35 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CJ	28/230 (12%)	28 (100%)	0	0	100	100
3	CK	35/230 (15%)	35 (100%)	0	0	100	100
3	CR	35/230 (15%)	35 (100%)	0	0	100	100
3	CS	35/230 (15%)	35 (100%)	0	0	100	100
3	CT	28/230 (12%)	28 (100%)	0	0	100	100
3	CX	28/230 (12%)	28 (100%)	0	0	100	100
3	CY	28/230 (12%)	28 (100%)	0	0	100	100
3	CZ	28/230 (12%)	28 (100%)	0	0	100	100
4	AO	146/190 (77%)	143 (98%)	3 (2%)	0	100	100
4	AX	146/190 (77%)	144 (99%)	2 (1%)	0	100	100
4	BF	147/190 (77%)	146 (99%)	1 (1%)	0	100	100
4	BN	146/190 (77%)	145 (99%)	1 (1%)	0	100	100
4	BW	150/190 (79%)	147 (98%)	3 (2%)	0	100	100
4	CG	146/190 (77%)	144 (99%)	2 (1%)	0	100	100
4	CQ	165/190 (87%)	159 (96%)	6 (4%)	0	100	100
All	All	12782/19298 (66%)	12613 (99%)	169 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	281/286 (98%)	281 (100%)	0	100	100
1	AB	283/286 (99%)	283 (100%)	0	100	100
1	AC	283/286 (99%)	283 (100%)	0	100	100
1	AJ	281/286 (98%)	281 (100%)	0	100	100
1	AK	283/286 (99%)	283 (100%)	0	100	100
1	AL	283/286 (99%)	283 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AS	281/286 (98%)	281 (100%)	0	100	100
1	AT	283/286 (99%)	283 (100%)	0	100	100
1	AU	283/286 (99%)	283 (100%)	0	100	100
1	BB	281/286 (98%)	281 (100%)	0	100	100
1	BC	283/286 (99%)	283 (100%)	0	100	100
1	BD	283/286 (99%)	283 (100%)	0	100	100
1	BK	281/286 (98%)	281 (100%)	0	100	100
1	BL	283/286 (99%)	283 (100%)	0	100	100
1	BM	283/286 (99%)	283 (100%)	0	100	100
1	BT	281/286 (98%)	281 (100%)	0	100	100
1	BU	283/286 (99%)	283 (100%)	0	100	100
1	BV	283/286 (99%)	283 (100%)	0	100	100
1	CC	283/286 (99%)	283 (100%)	0	100	100
1	CD	283/286 (99%)	283 (100%)	0	100	100
1	CE	283/286 (99%)	283 (100%)	0	100	100
1	CL	283/286 (99%)	283 (100%)	0	100	100
1	CM	283/286 (99%)	283 (100%)	0	100	100
1	CN	283/286 (99%)	283 (100%)	0	100	100
1	CU	283/286 (99%)	283 (100%)	0	100	100
1	CV	283/286 (99%)	283 (100%)	0	100	100
1	CW	283/286 (99%)	283 (100%)	0	100	100
2	AD	130/154 (84%)	130 (100%)	0	100	100
2	AE	129/154 (84%)	129 (100%)	0	100	100
2	AF	130/154 (84%)	130 (100%)	0	100	100
2	AM	129/154 (84%)	129 (100%)	0	100	100
2	AN	130/154 (84%)	130 (100%)	0	100	100
2	AV	129/154 (84%)	129 (100%)	0	100	100
2	AW	130/154 (84%)	130 (100%)	0	100	100
2	BE	129/154 (84%)	129 (100%)	0	100	100
2	BG	130/154 (84%)	130 (100%)	0	100	100
2	BO	129/154 (84%)	129 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	BP	129/154 (84%)	129 (100%)	0	100	100
2	BX	129/154 (84%)	129 (100%)	0	100	100
2	BY	130/154 (84%)	130 (100%)	0	100	100
2	CF	142/154 (92%)	142 (100%)	0	100	100
2	CH	130/154 (84%)	130 (100%)	0	100	100
2	CO	128/154 (83%)	128 (100%)	0	100	100
2	CP	129/154 (84%)	129 (100%)	0	100	100
3	AG	29/210 (14%)	29 (100%)	0	100	100
3	AH	35/210 (17%)	35 (100%)	0	100	100
3	AI	35/210 (17%)	35 (100%)	0	100	100
3	AP	35/210 (17%)	35 (100%)	0	100	100
3	AQ	35/210 (17%)	35 (100%)	0	100	100
3	AR	35/210 (17%)	35 (100%)	0	100	100
3	AY	35/210 (17%)	35 (100%)	0	100	100
3	AZ	35/210 (17%)	35 (100%)	0	100	100
3	BA	35/210 (17%)	35 (100%)	0	100	100
3	BH	35/210 (17%)	35 (100%)	0	100	100
3	BI	35/210 (17%)	35 (100%)	0	100	100
3	BJ	35/210 (17%)	35 (100%)	0	100	100
3	BQ	29/210 (14%)	29 (100%)	0	100	100
3	BR	35/210 (17%)	35 (100%)	0	100	100
3	BS	35/210 (17%)	35 (100%)	0	100	100
3	BZ	35/210 (17%)	35 (100%)	0	100	100
3	CA	35/210 (17%)	35 (100%)	0	100	100
3	CB	35/210 (17%)	35 (100%)	0	100	100
3	CI	35/210 (17%)	35 (100%)	0	100	100
3	CJ	29/210 (14%)	29 (100%)	0	100	100
3	CK	35/210 (17%)	35 (100%)	0	100	100
3	CR	35/210 (17%)	35 (100%)	0	100	100
3	CS	35/210 (17%)	35 (100%)	0	100	100
3	CT	29/210 (14%)	29 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CX	29/210 (14%)	29 (100%)	0	100	100
3	CY	29/210 (14%)	29 (100%)	0	100	100
3	CZ	29/210 (14%)	29 (100%)	0	100	100
4	AO	130/163 (80%)	130 (100%)	0	100	100
4	AX	130/163 (80%)	130 (100%)	0	100	100
4	BF	131/163 (80%)	131 (100%)	0	100	100
4	BN	130/163 (80%)	130 (100%)	0	100	100
4	BW	133/163 (82%)	133 (100%)	0	100	100
4	CG	129/163 (79%)	129 (100%)	0	100	100
4	CQ	148/163 (91%)	148 (100%)	0	100	100
All	All	11675/17151 (68%)	11675 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
1	BL	315	ASN
4	BW	186	ASN
1	CU	236	GLN
2	BO	164	HIS
1	BU	56	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.

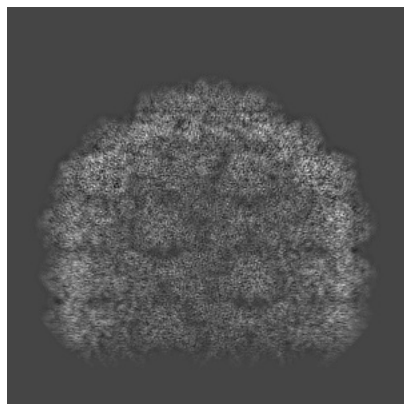
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17671. These allow visual inspection of the internal detail of the map and identification of artifacts.

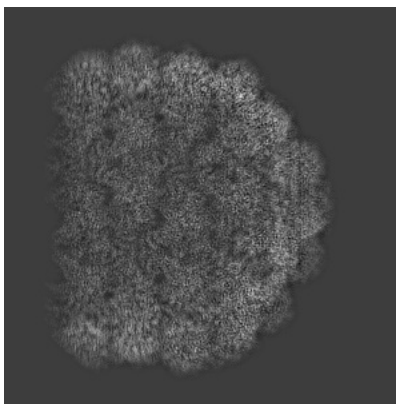
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

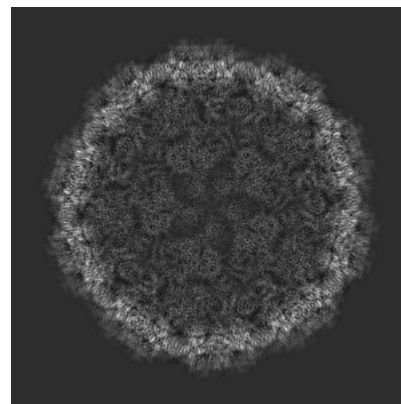
#### 6.1.1 Primary map



X

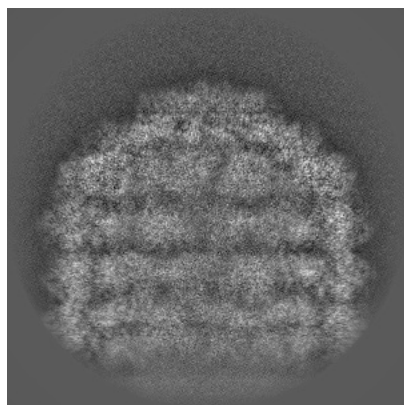


Y

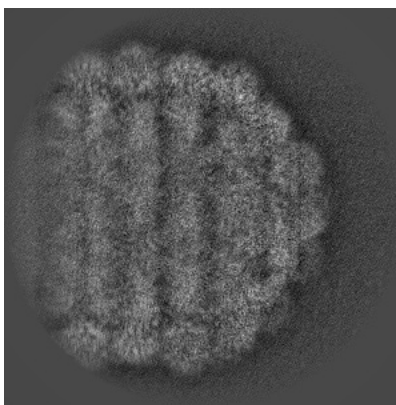


Z

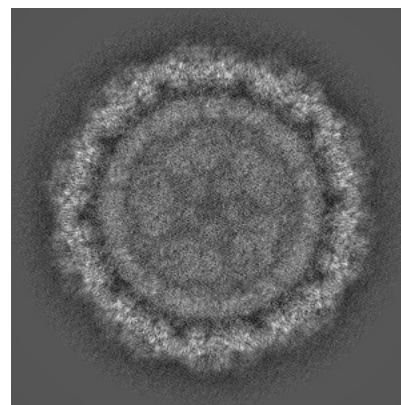
#### 6.1.2 Raw map



X



Y

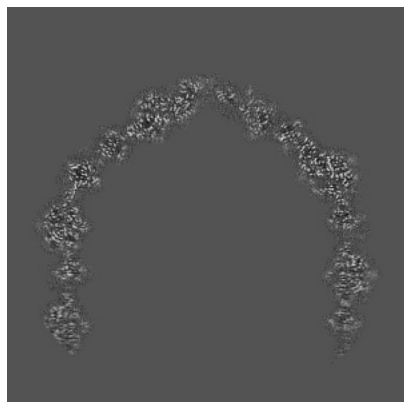


Z

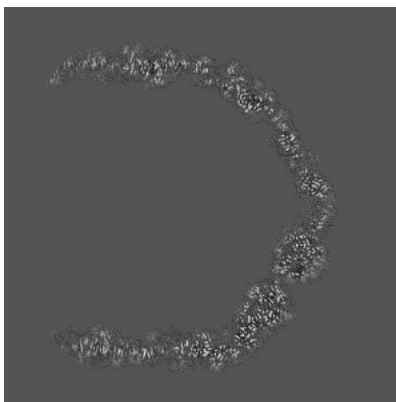
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

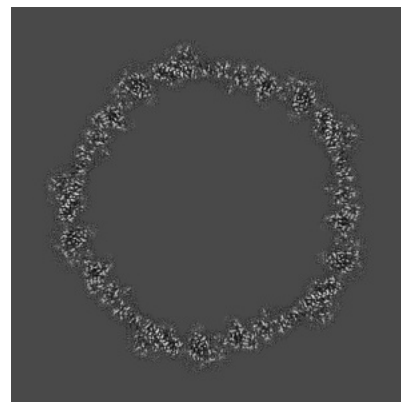
### 6.2.1 Primary map



X Index: 320

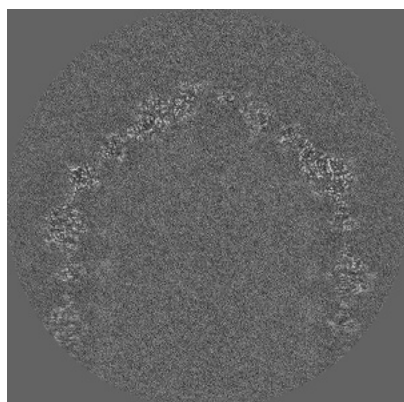


Y Index: 320

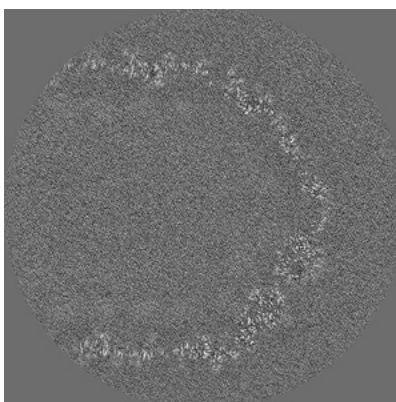


Z Index: 320

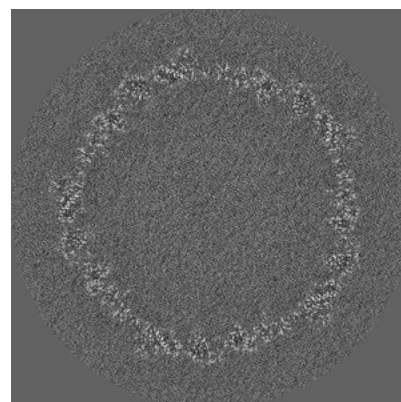
### 6.2.2 Raw map



X Index: 320



Y Index: 320

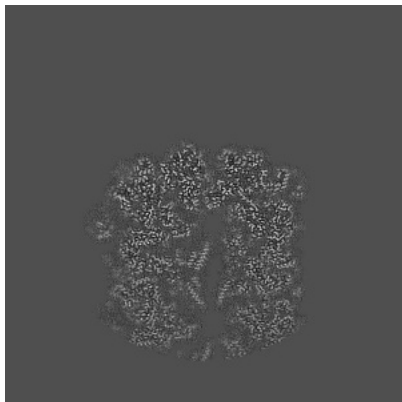


Z Index: 320

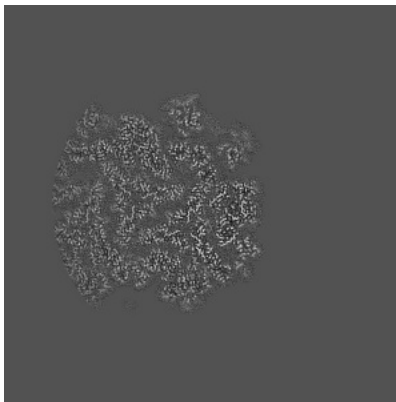
The images above show central slices of the map in three orthogonal directions.

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

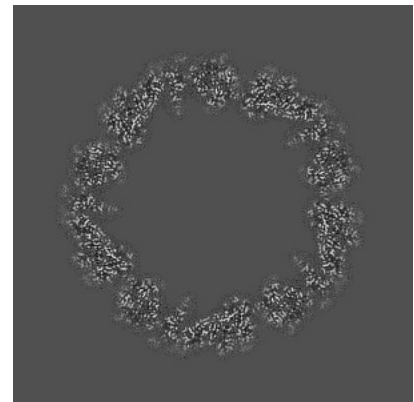
### 6.3.1 Primary map



X Index: 522

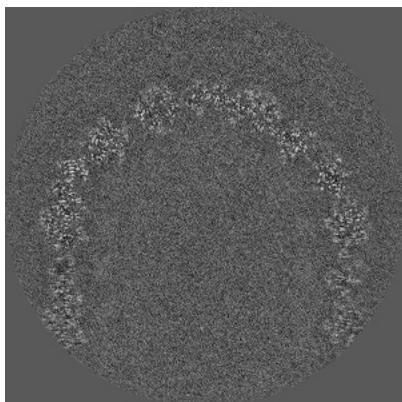


Y Index: 530

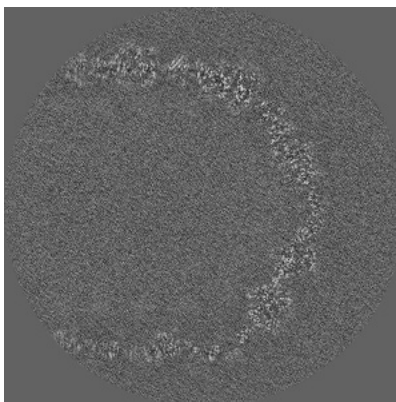


Z Index: 378

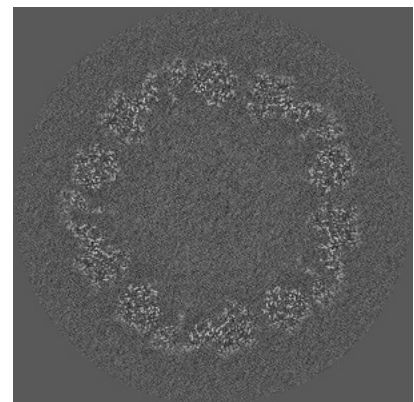
### 6.3.2 Raw map



X Index: 293



Y Index: 297

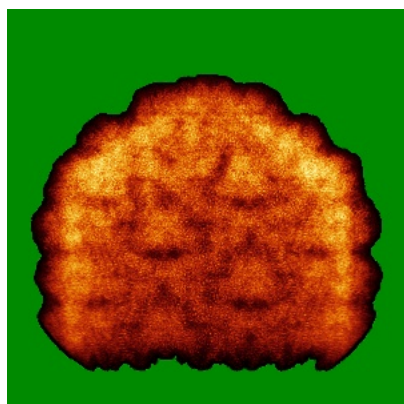


Z Index: 372

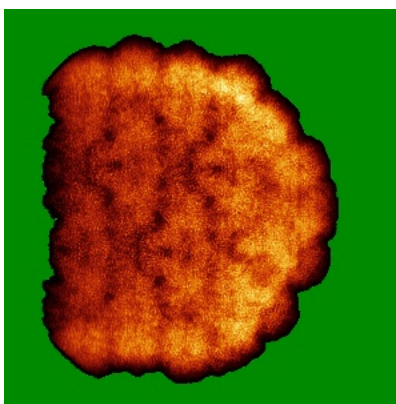
The images above show the largest variance slices of the map in three orthogonal directions.

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

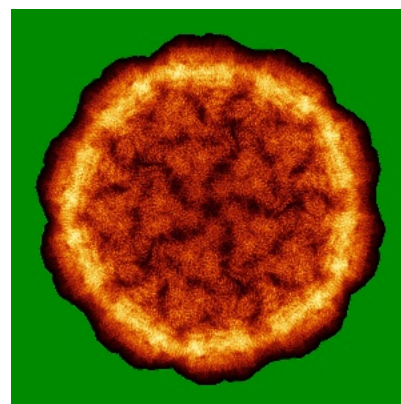
### 6.4.1 Primary map



X

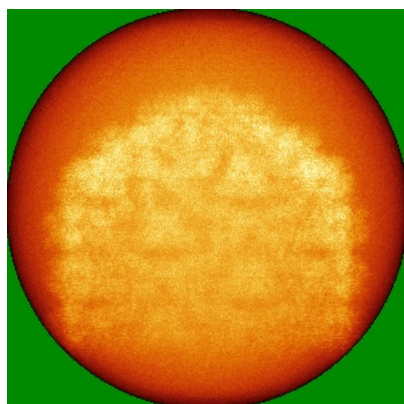


Y

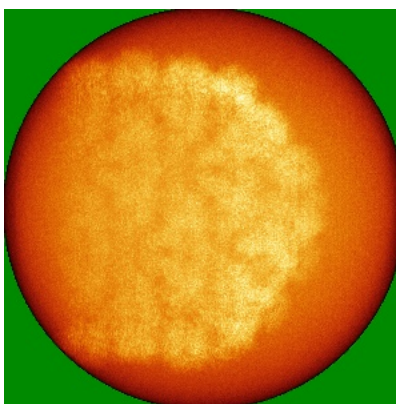


Z

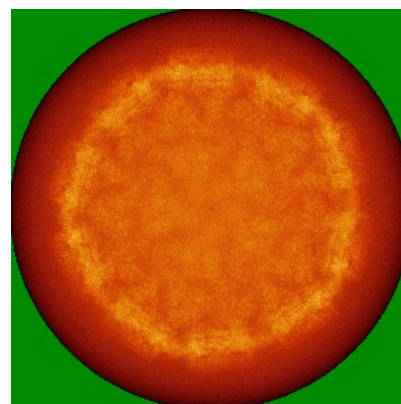
### 6.4.2 Raw map



X



Y

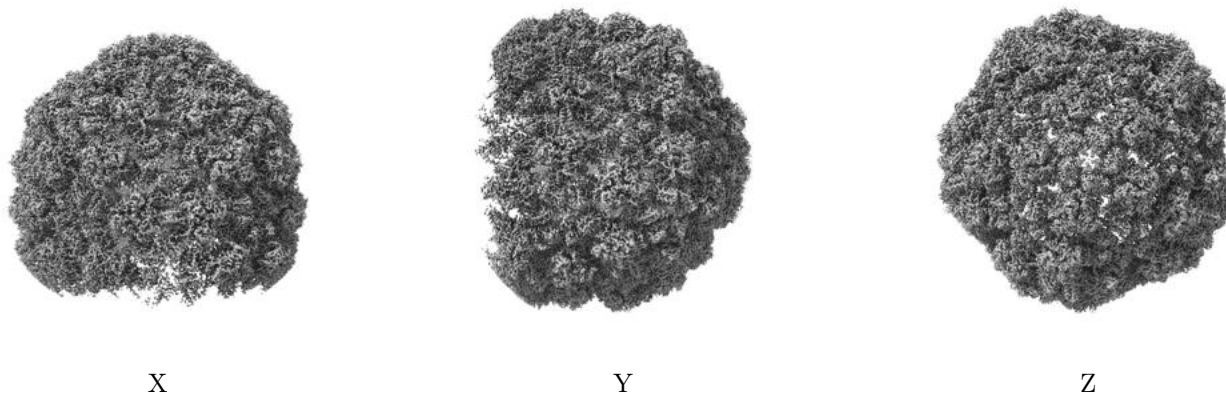


Z

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.

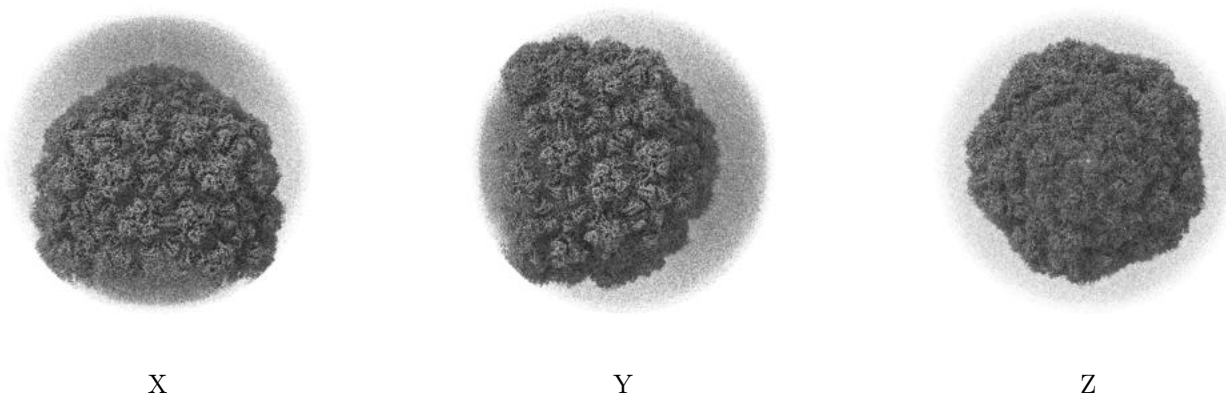
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.008. 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.

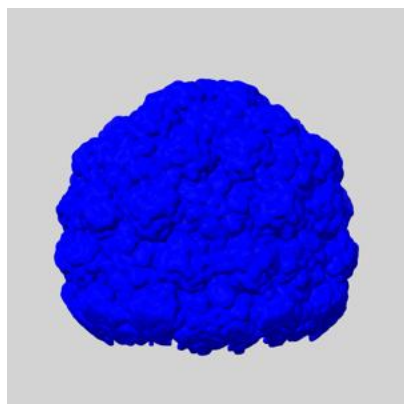
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

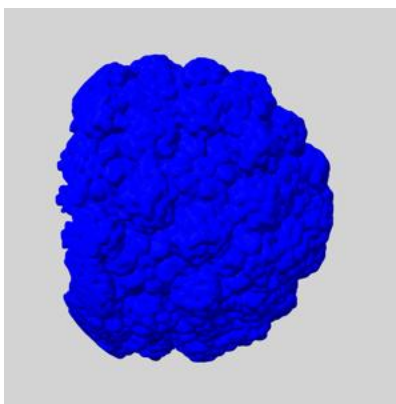
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

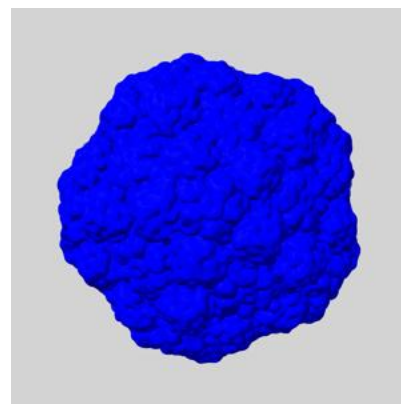
### 6.6.1 emd\_17671\_msk\_1.map [i](#)



X



Y

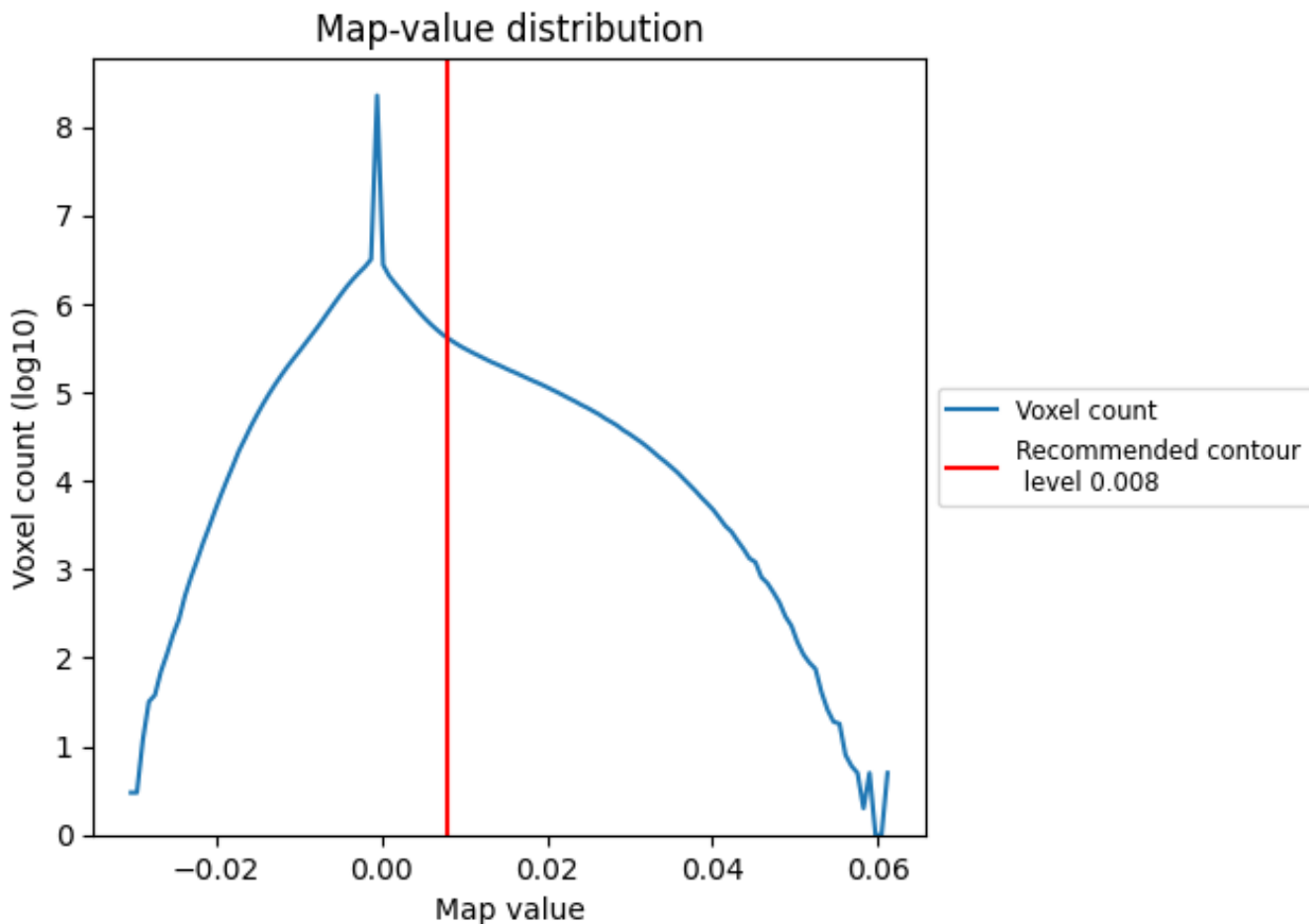


Z

## 7 Map analysis [i](#)

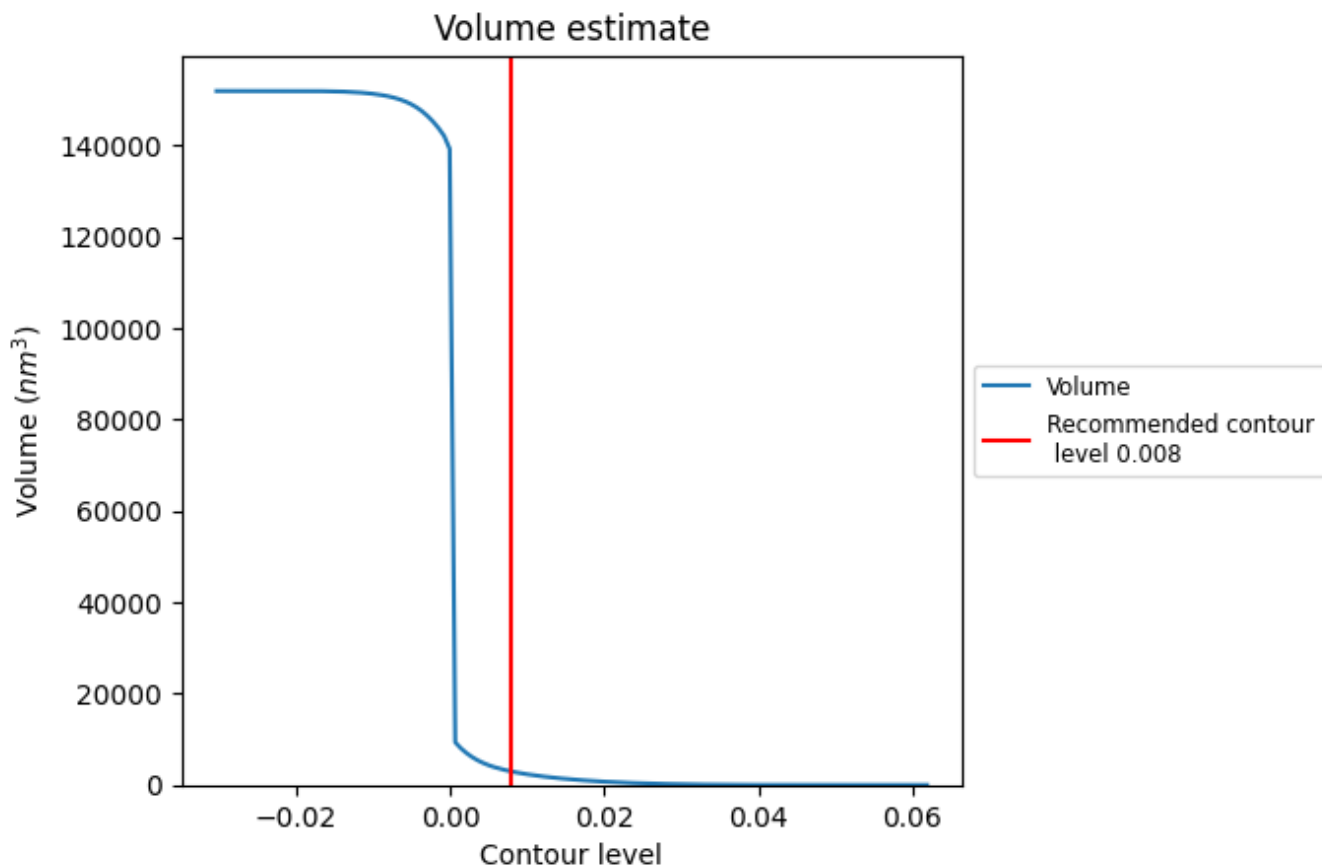
This section contains the results of statistical analysis of the map.

### 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.

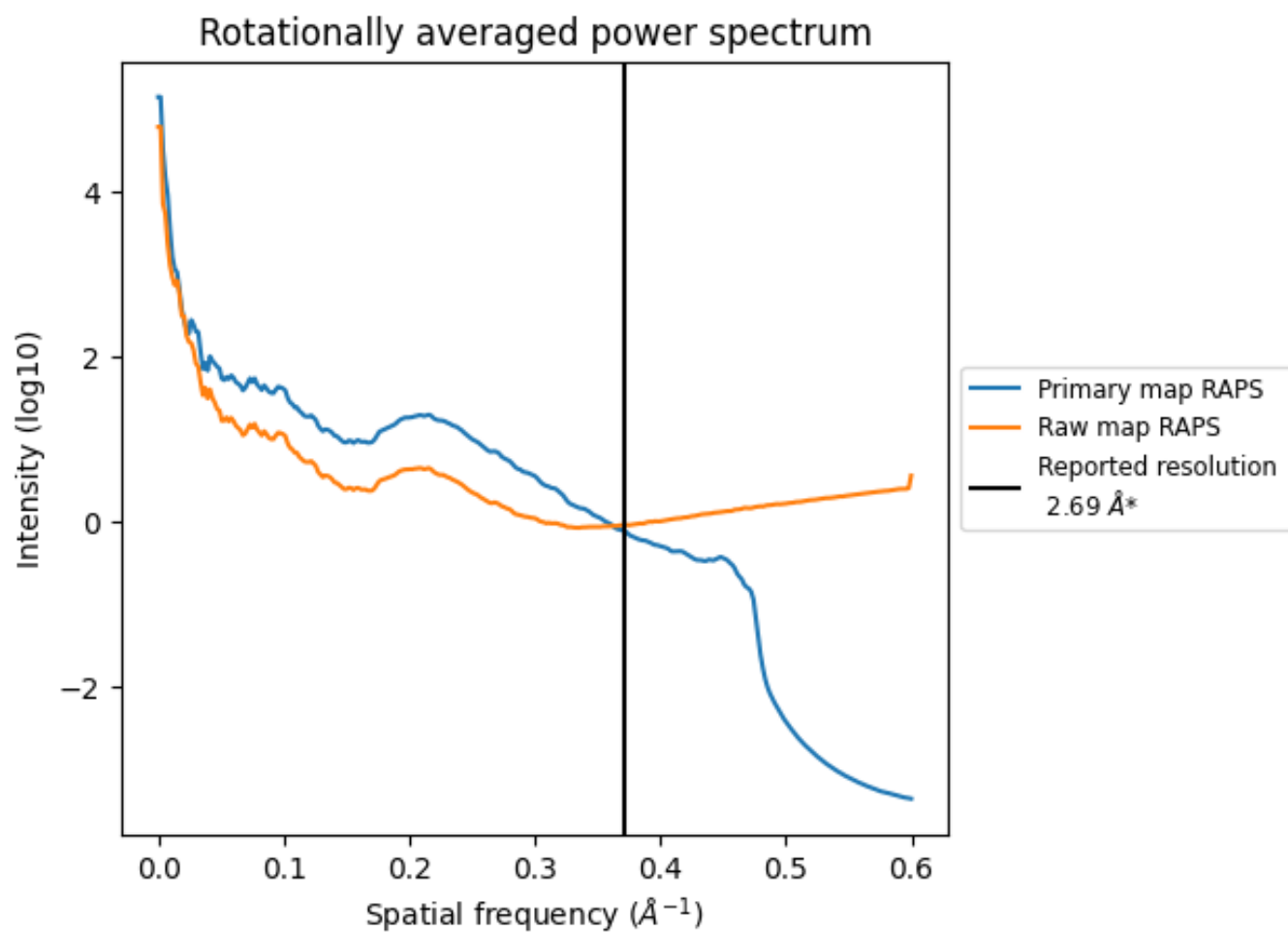
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2947 nm<sup>3</sup>; this corresponds to an approximate mass of 2662 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)

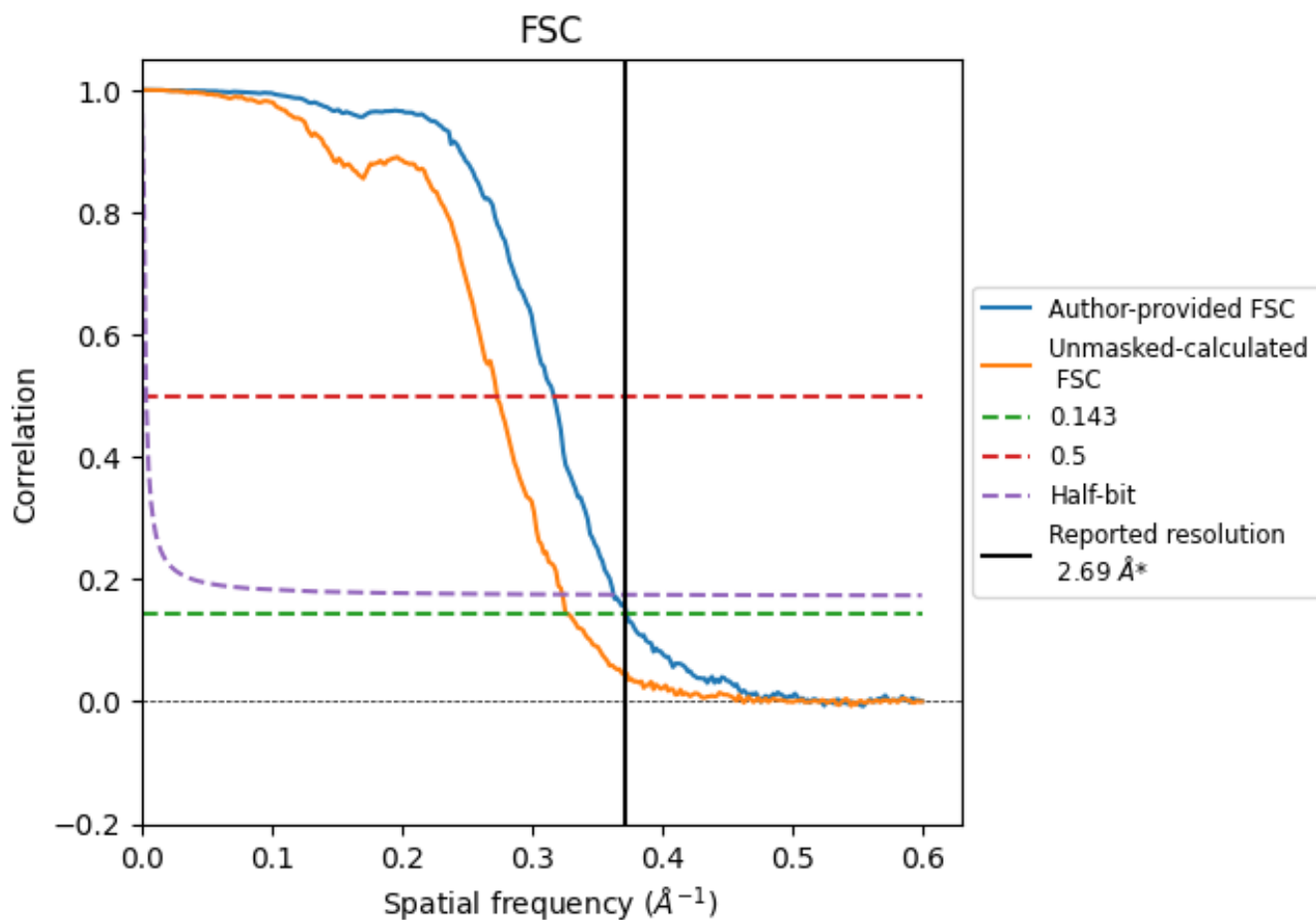


\*Reported resolution corresponds to spatial frequency of 0.372 Å<sup>-1</sup>

## 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 0.372 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.69	-	-
Author-provided FSC curve	2.68	3.16	2.75
Unmasked-calculated*	3.07	3.66	3.09

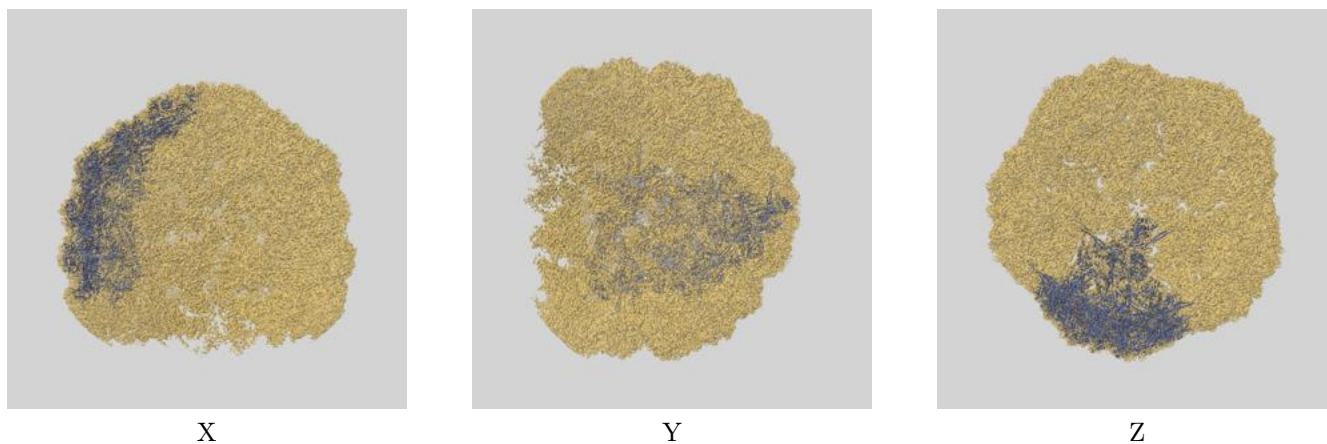
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.07 differs from the reported value 2.69 by more than 10 %

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

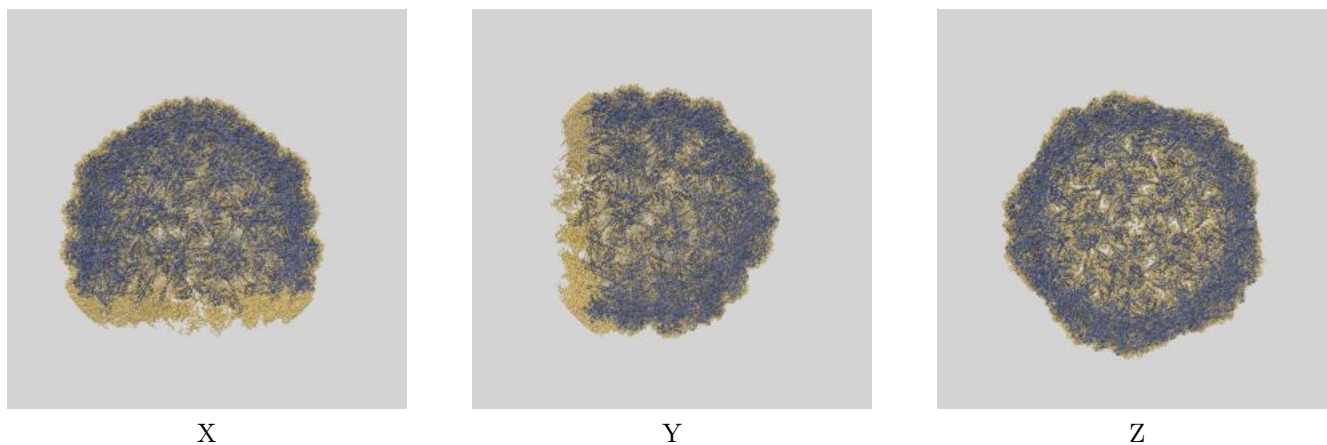
This section contains information regarding the fit between EMDB map EMD-17671 and PDB model 8PHQ. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlays

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

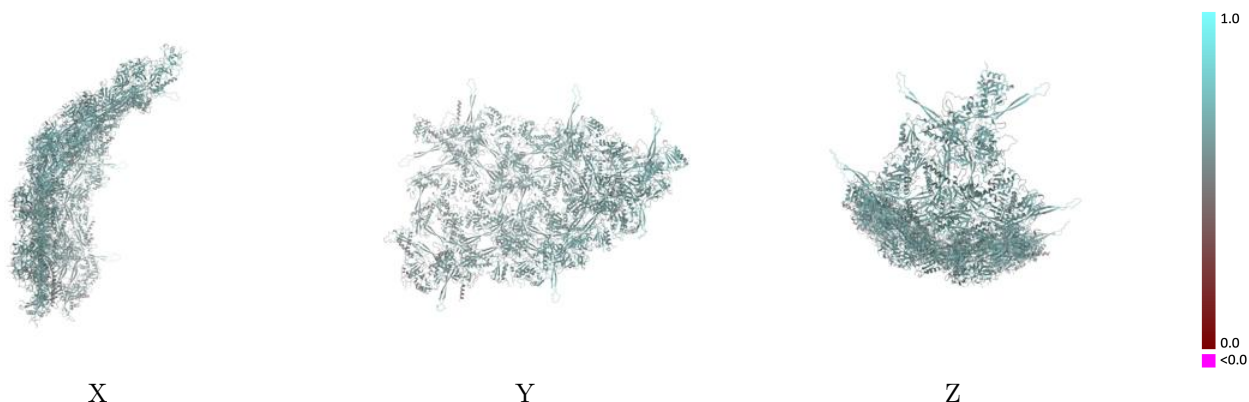


#### 9.1.2 Map-model assembly overlay [i](#)



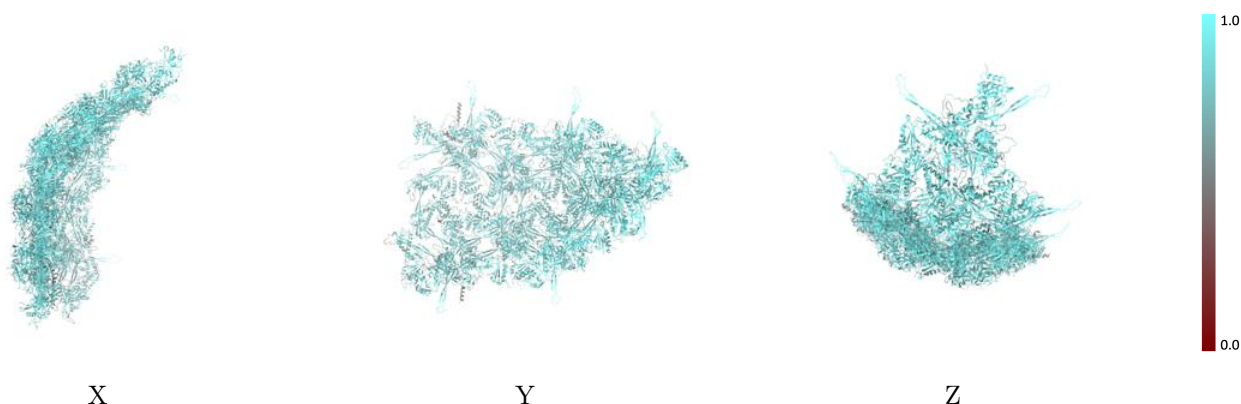
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



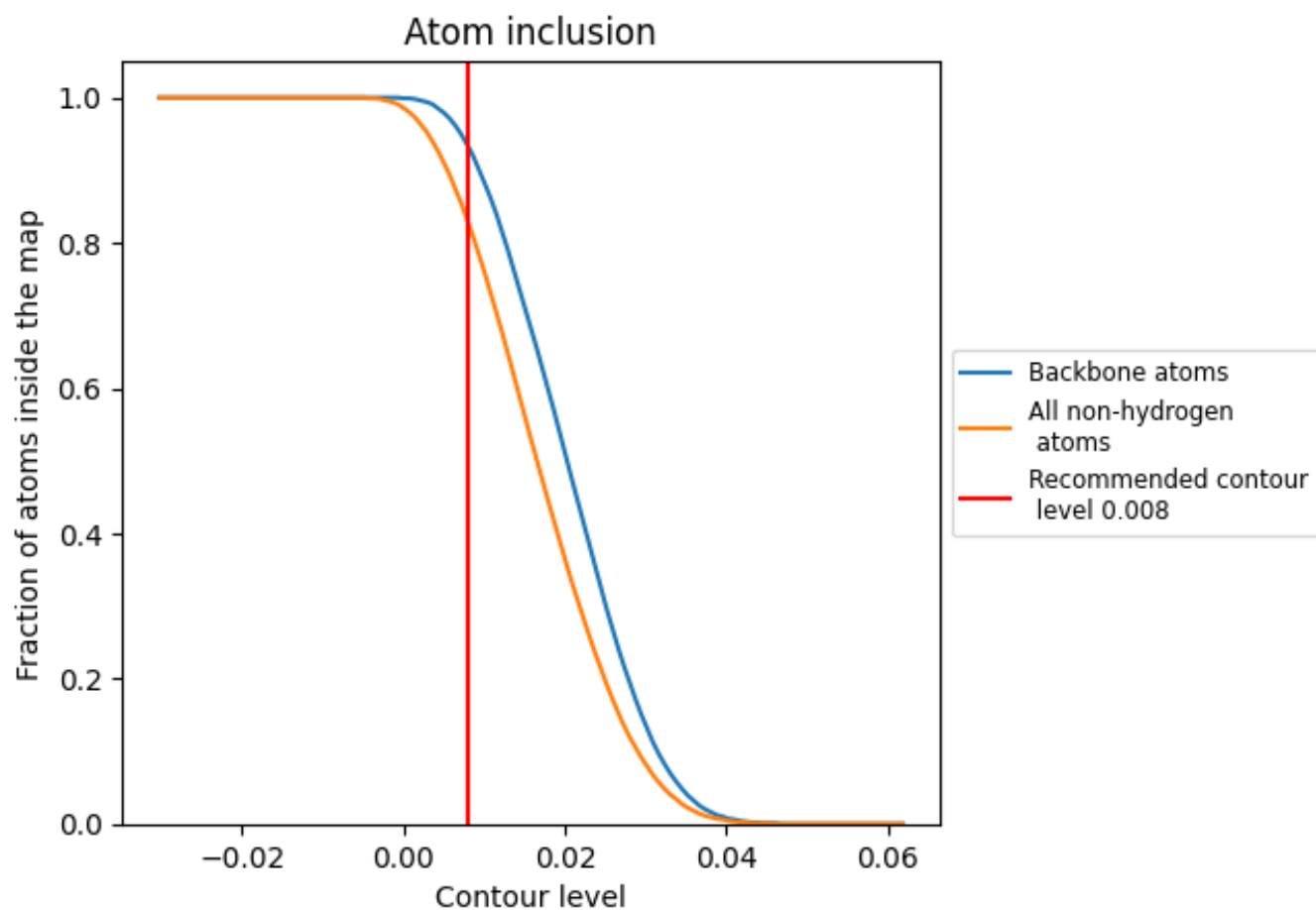
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 83% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8280	 0.5940
AA	 0.8630	 0.6280
AB	 0.8670	 0.6090
AC	 0.8790	 0.6160
AD	 0.8320	 0.6010
AE	 0.8160	 0.6060
AF	 0.8100	 0.5940
AG	 0.7170	 0.5830
AH	 0.7650	 0.5500
AI	 0.7100	 0.5520
AJ	 0.8910	 0.6310
AK	 0.8880	 0.6200
AL	 0.8900	 0.6220
AM	 0.8460	 0.6100
AN	 0.8330	 0.5950
AO	 0.8500	 0.6040
AP	 0.7560	 0.5740
AQ	 0.8080	 0.5650
AR	 0.8010	 0.5520
AS	 0.8910	 0.6330
AT	 0.8760	 0.6180
AU	 0.8880	 0.6230
AV	 0.8450	 0.6150
AW	 0.8610	 0.6170
AX	 0.8400	 0.6030
AY	 0.7000	 0.5660
AZ	 0.7950	 0.5810
BA	 0.7590	 0.5610
BB	 0.8800	 0.6280
BC	 0.8380	 0.5920
BD	 0.8540	 0.6040
BE	 0.7640	 0.5710
BF	 0.8220	 0.5940
BG	 0.8190	 0.5910
BH	 0.8050	 0.5520







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Chain	Atom inclusion	Q-score
BI	 0.7100	 0.5490
BJ	 0.7780	 0.5660
BK	 0.8710	 0.6250
BL	 0.8660	 0.6100
BM	 0.8610	 0.6010
BN	 0.8290	 0.5990
BO	 0.8190	 0.5930
BP	 0.8280	 0.5900
BQ	 0.7600	 0.5850
BR	 0.7520	 0.5470
BS	 0.7620	 0.5450
BT	 0.9000	 0.6350
BU	 0.8850	 0.6240
BV	 0.8790	 0.6230
BW	 0.8550	 0.6150
BX	 0.8630	 0.6150
BY	 0.8370	 0.6060
BZ	 0.8180	 0.5720
CA	 0.7650	 0.5680
CB	 0.7070	 0.5600
CC	 0.8010	 0.5680
CD	 0.8180	 0.5870
CE	 0.7780	 0.5550
CF	 0.7110	 0.5330
CG	 0.7930	 0.5710
CH	 0.7470	 0.5530
CI	 0.7300	 0.5060
CJ	 0.6820	 0.5210
CK	 0.6060	 0.4860
CL	 0.8080	 0.5790
CM	 0.8250	 0.5900
CN	 0.7590	 0.5640
CO	 0.7720	 0.5650
CP	 0.7800	 0.5800
CQ	 0.7440	 0.5370
CR	 0.7100	 0.5300
CS	 0.7260	 0.5280
CT	 0.6320	 0.5060
CU	 0.7760	 0.5620
CV	 0.7630	 0.5500
CW	 0.7430	 0.5430
CX	 0.7130	 0.4790

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Chain	Atom inclusion	Q-score
CY	 0.6780	 0.4980
CZ	 0.6900	 0.4780