



## wwPDB EM Validation Summary Report ⓘ

Mar 17, 2025 – 03:20 PM JST

PDB ID : 8YYM  
EMDB ID : EMD-39676  
Title : Cryo-EM structure of cylindrical fiber of MyD88 TIR  
Authors : Kasai, K.; Imamura, K.; Narita, A.; Makino, F.; Miyata, T.; Kato, T.; Namba, K.; Onishi, H.; Tochio, H.  
Deposited on : 2024-04-04  
Resolution : 3.30 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>.

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

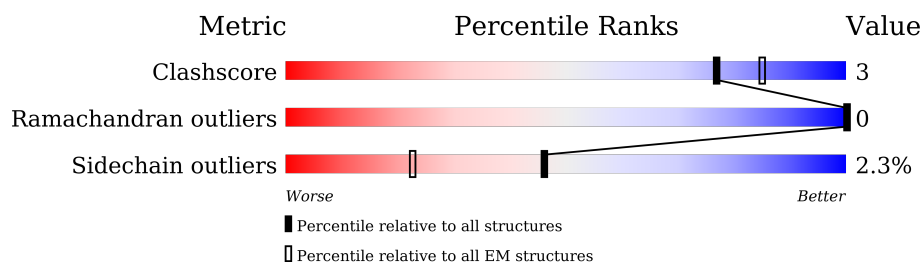
EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.4

# 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 3.30 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	A	144	
1	AA	144	
1	AB	144	
1	AC	144	
1	B	144	
1	BA	144	
1	BB	144	
1	BC	144	

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Mol	Chain	Length	Quality of chain
1	C	144	
1	CA	144	
1	CB	144	
1	CC	144	
1	D	144	
1	DA	144	
1	DB	144	
1	DC	144	
1	E	144	
1	EA	144	
1	EB	144	
1	EC	144	
1	F	144	
1	FA	144	
1	FB	144	
1	FC	144	
1	G	144	
1	GA	144	
1	GB	144	
1	GC	144	
1	H	144	
1	HA	144	
1	HB	144	
1	HC	144	
1	I	144	

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Mol	Chain	Length	Quality of chain
1	IA	144	
1	IB	144	
1	IC	144	
1	J	144	
1	JA	144	
1	JB	144	
1	JC	144	
1	K	144	
1	KA	144	
1	KB	144	
1	KC	144	
1	L	144	
1	LA	144	
1	LB	144	
1	LC	144	
1	M	144	
1	MA	144	
1	MB	144	
1	MC	144	
1	N	144	
1	NA	144	
1	NB	144	
1	NC	144	
1	O	144	
1	OA	144	





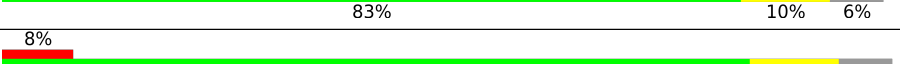
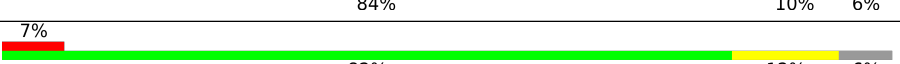
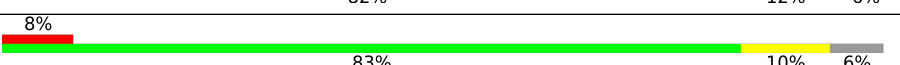
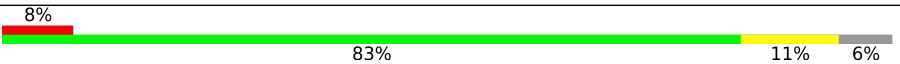

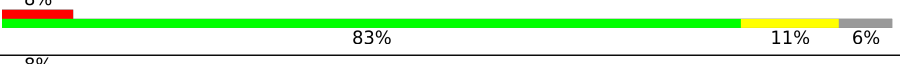
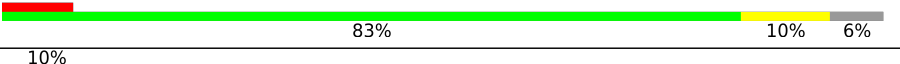
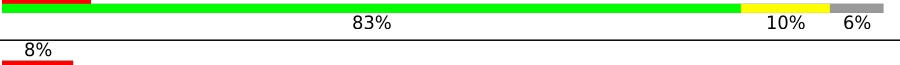

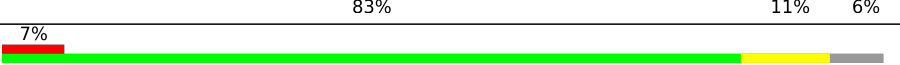

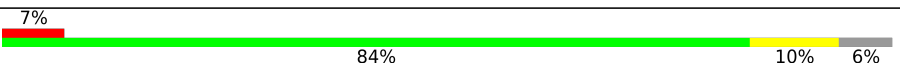





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Mol	Chain	Length	Quality of chain
1	OB	144	
1	OC	144	
1	P	144	
1	PA	144	
1	PB	144	
1	PC	144	
1	Q	144	
1	QA	144	
1	QB	144	
1	QC	144	
1	R	144	
1	RA	144	
1	RB	144	
1	RC	144	
1	S	144	
1	SA	144	
1	SB	144	
1	SC	144	
1	T	144	
1	TA	144	
1	TB	144	
1	TC	144	
1	U	144	
1	UA	144	
1	UB	144	

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Mol	Chain	Length	Quality of chain
1	UC	144	
1	V	144	
1	VA	144	
1	VB	144	
1	VC	144	
1	W	144	
1	WA	144	
1	WB	144	
1	WC	144	
1	X	144	
1	XA	144	
1	XB	144	
1	XC	144	
1	Y	144	
1	YA	144	
1	YB	144	
1	YC	144	
1	Z	144	
1	ZA	144	
1	ZB	144	
1	ZC	144	

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 115856 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 Myeloid differentiation primary response protein MyD88.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	AA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	AB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	AC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	B	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	BA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	BB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	BC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	C	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	CA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	CB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	CC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	D	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	DA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	DB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	DC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	E	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	EA	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	EB	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	EC	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	F	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	FA	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	FB	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	FC	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	G	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	GA	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	GB	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	GC	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	H	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	HA	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	HB	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	HC	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	I	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	IA	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	IB	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	IC	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	J	135	Total 1114	C 718	N 188	O 197	S 11	0	0
1	JA	135	Total 1114	C 718	N 188	O 197	S 11	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	JB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	JC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	K	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	KA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	KB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	KC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	L	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	LA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	LB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	LC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	M	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	MA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	MB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	MC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	N	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	NA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	NB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	NC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	O	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	OA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	OB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	OC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	P	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	PA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	PB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	PC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	Q	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	QA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	QB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	QC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	R	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	RA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	RB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	RC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	S	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	SA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	SB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	SC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	T	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	TA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	TB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	TC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	UA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	UB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	UC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	V	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	VA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	VB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	VC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	W	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	WA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	WB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	WC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	X	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	XA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	XB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	XC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	Y	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	YA	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	YB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	YC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	Z	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		

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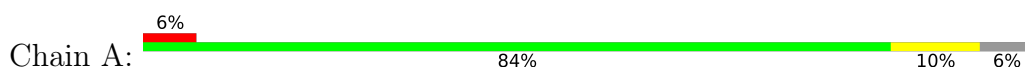
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Mol	Chain	Residues	Atoms					AltConf	Trace
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1	ZB	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		
1	ZC	135	Total	C	N	O	S	0	0
			1114	718	188	197	11		

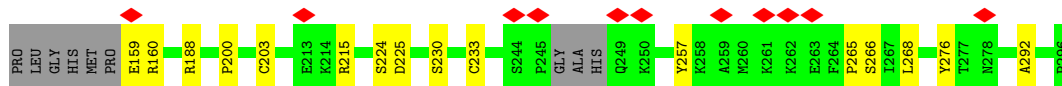
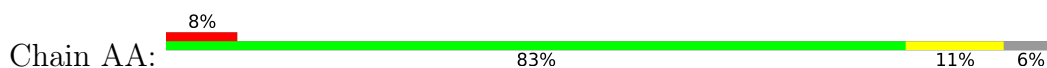
### 3 Residue-property plots [i](#)

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.

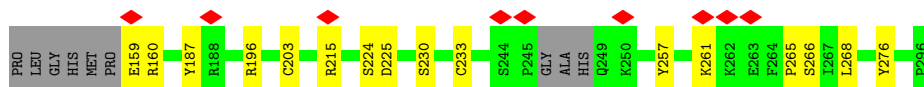
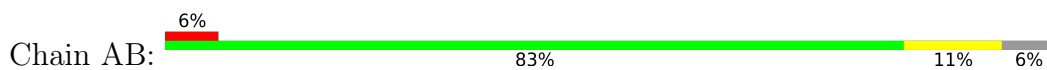
- Molecule 1: Myeloid differentiation primary response protein MyD88



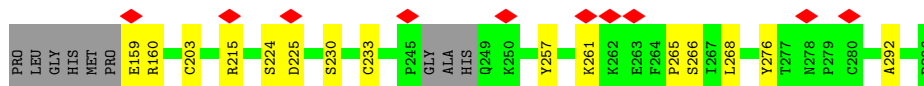
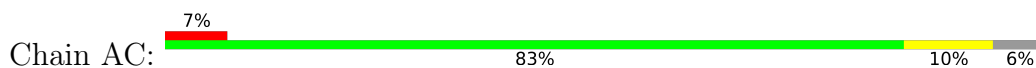
- Molecule 1: Myeloid differentiation primary response protein MyD88



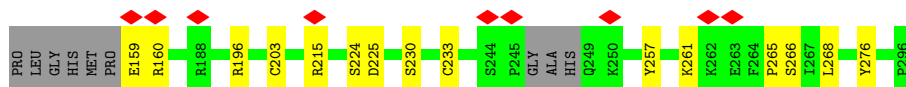
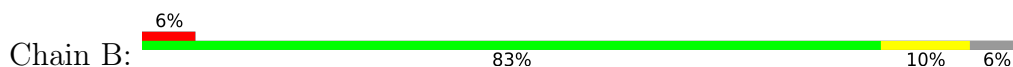
- Molecule 1: Myeloid differentiation primary response protein MyD88



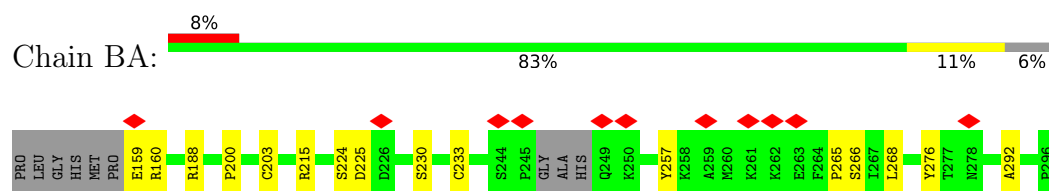
- Molecule 1: Myeloid differentiation primary response protein MyD88



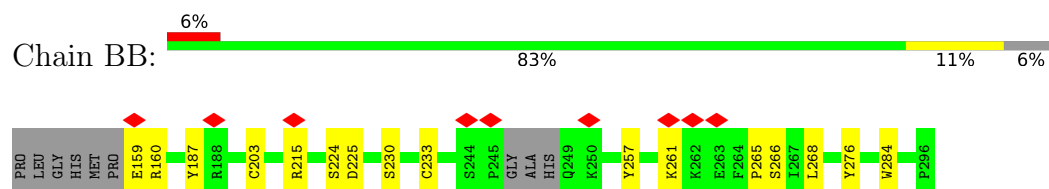
- Molecule 1: Myeloid differentiation primary response protein MyD88



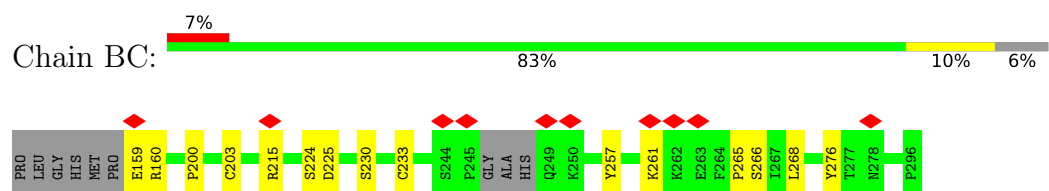
- Molecule 1: Myeloid differentiation primary response protein MyD88



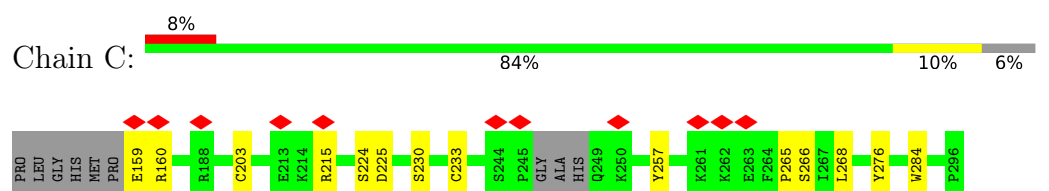
- Molecule 1: Myeloid differentiation primary response protein MyD88



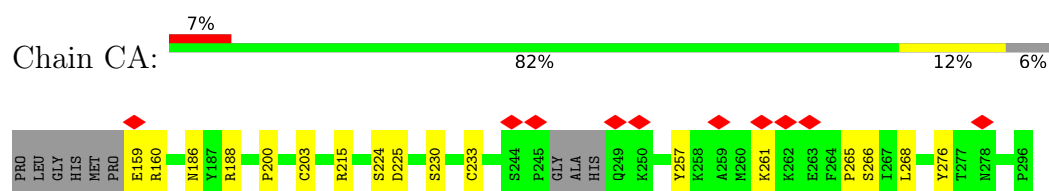
- Molecule 1: Myeloid differentiation primary response protein MyD88



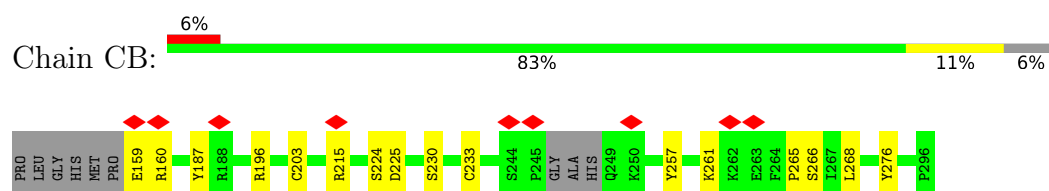
- Molecule 1: Myeloid differentiation primary response protein MyD88



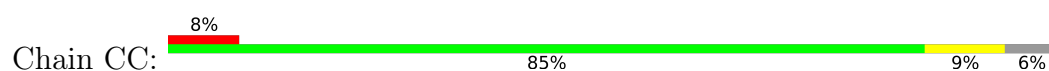
- Molecule 1: Myeloid differentiation primary response protein MyD88

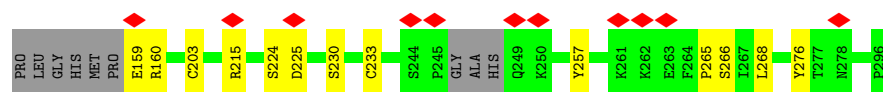


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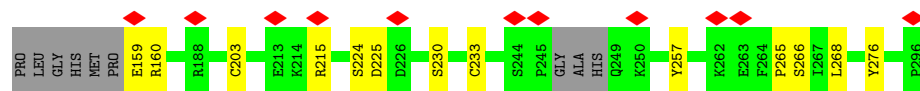
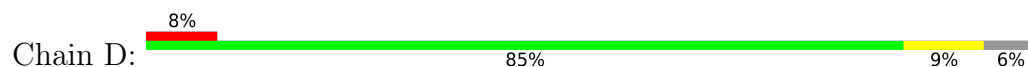


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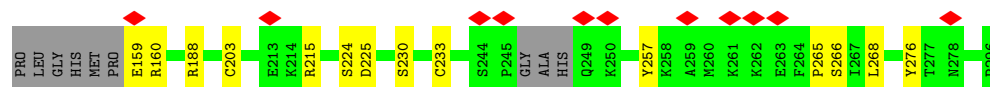
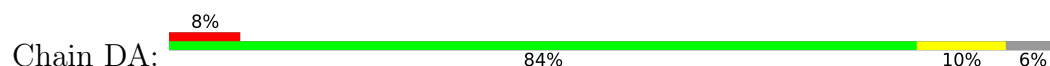




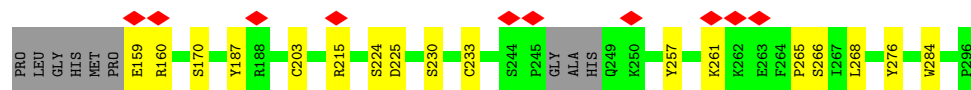
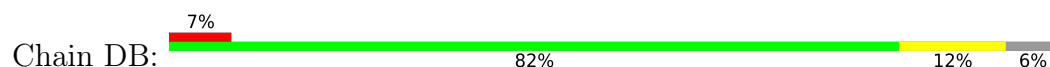
- Molecule 1: Myeloid differentiation primary response protein MyD88



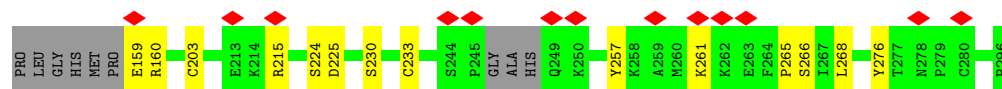
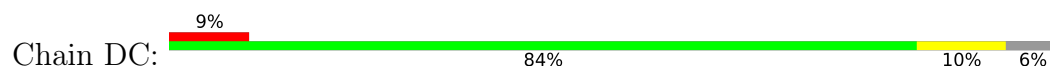
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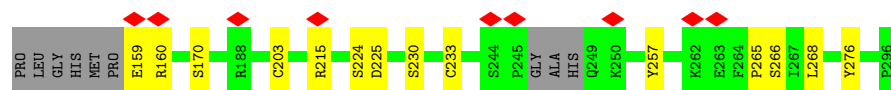
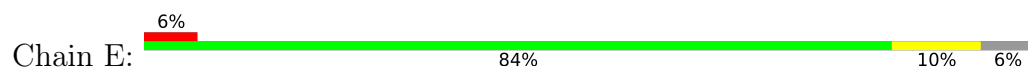
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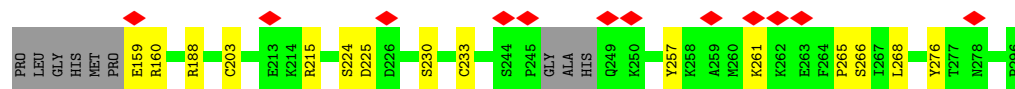
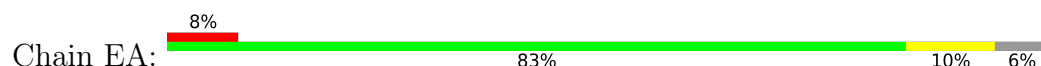
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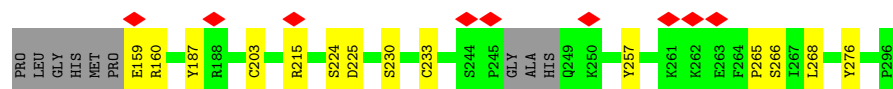
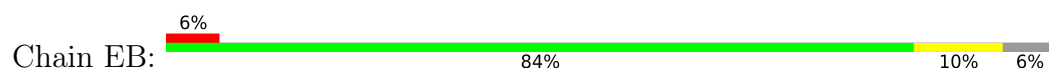
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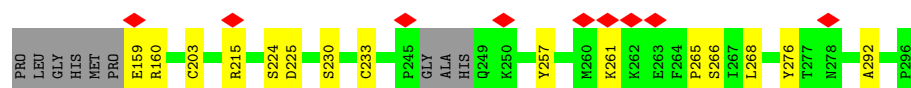
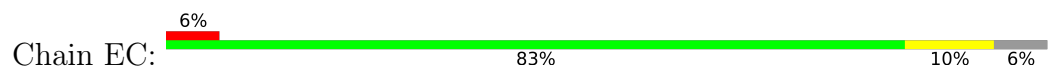
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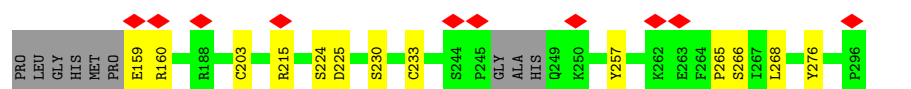
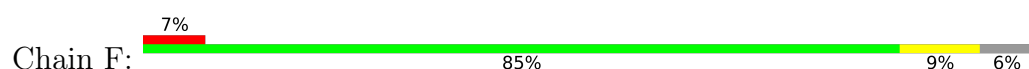
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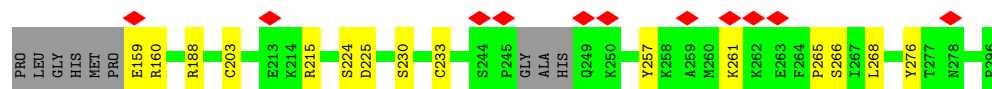
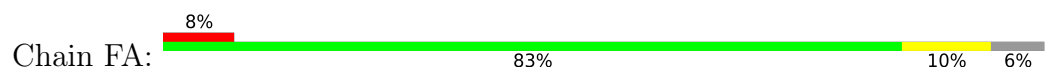
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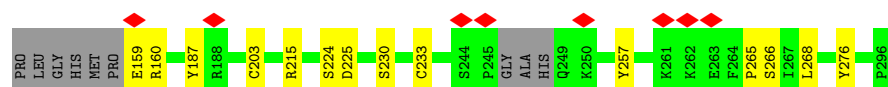
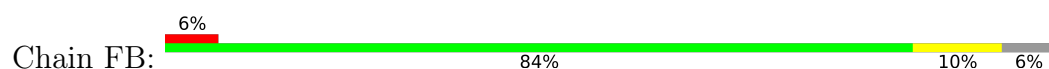
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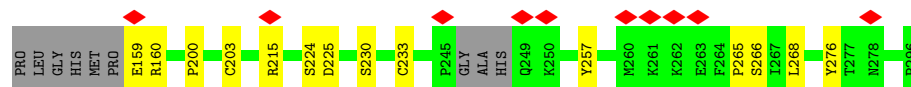
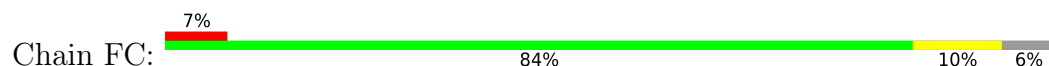
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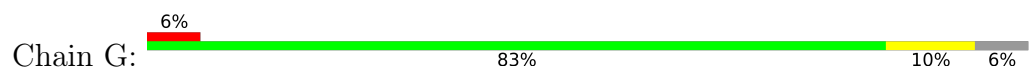
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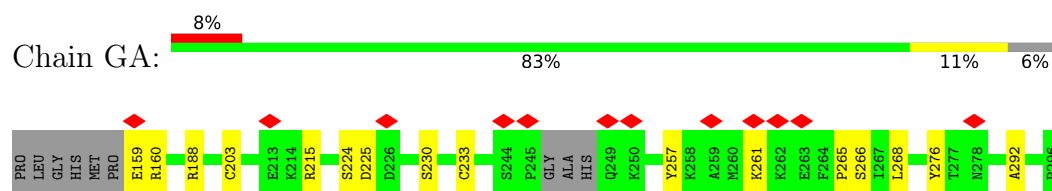


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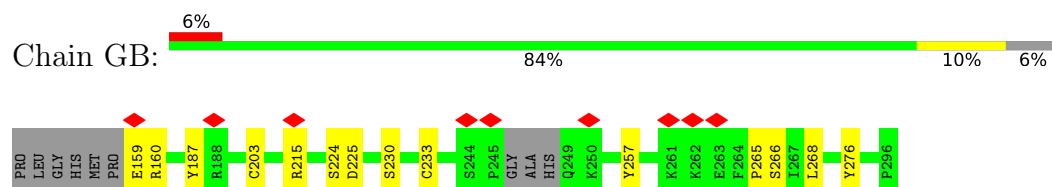




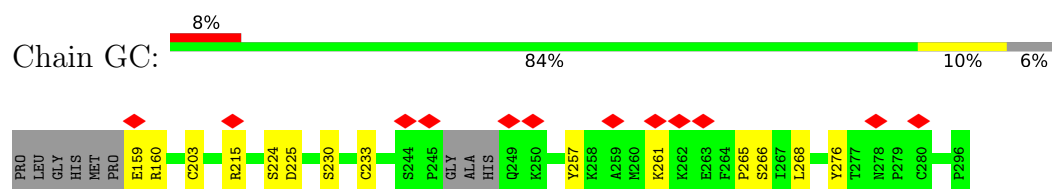
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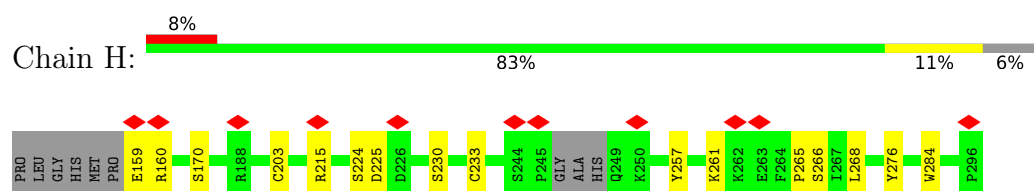
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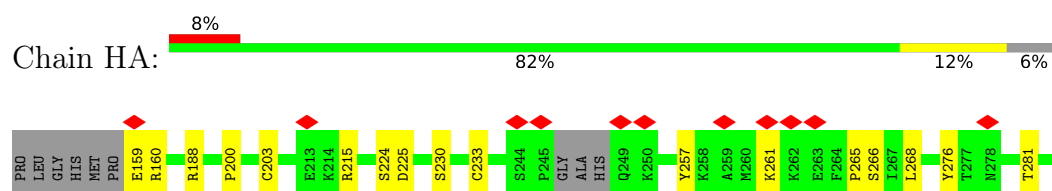
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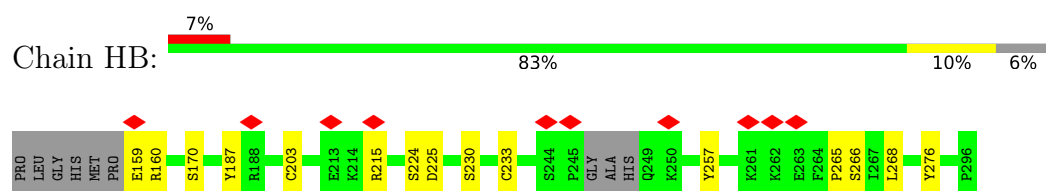
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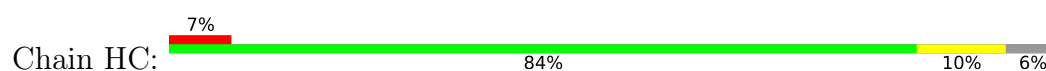
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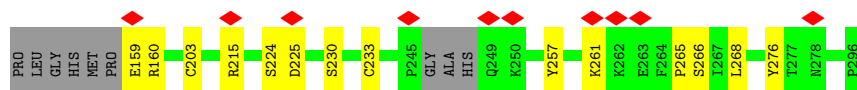


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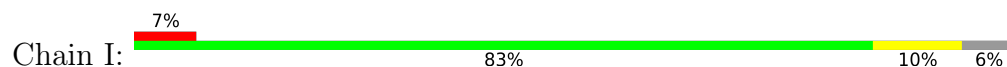


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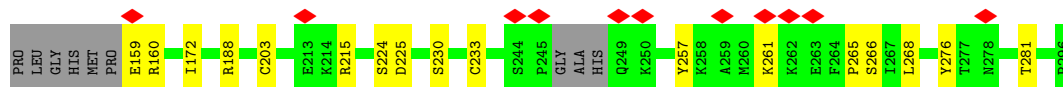
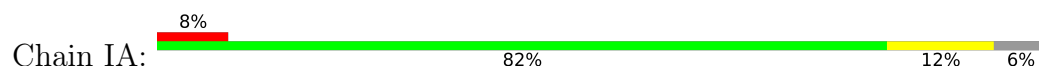




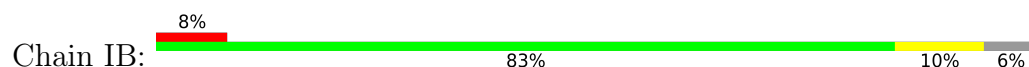
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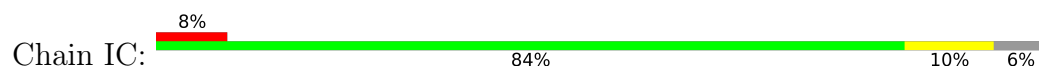
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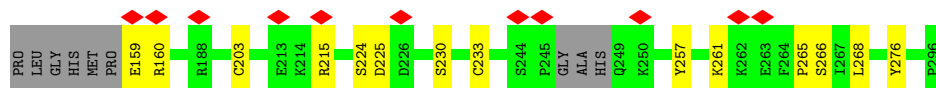
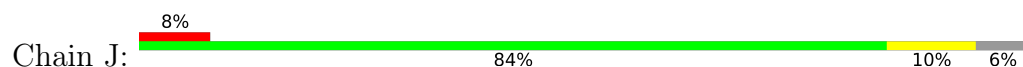
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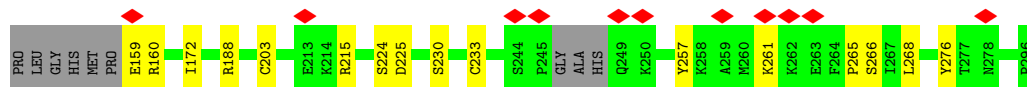
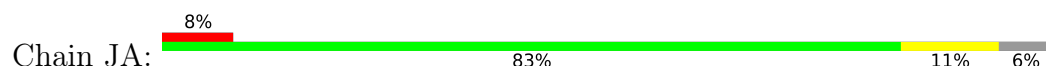
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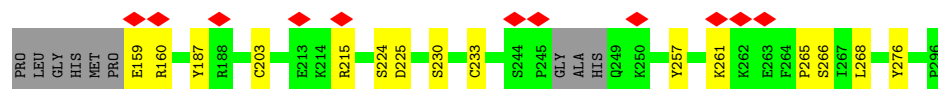
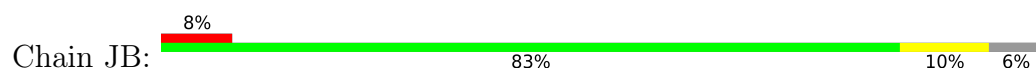
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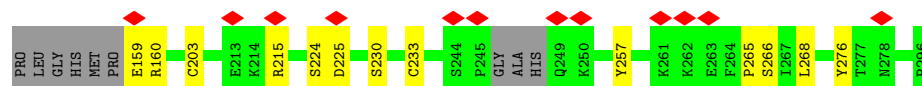
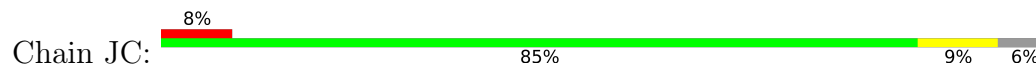
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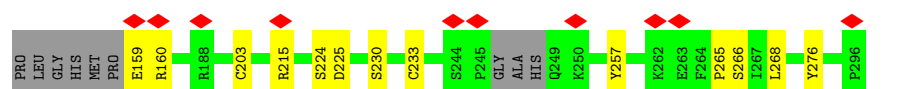
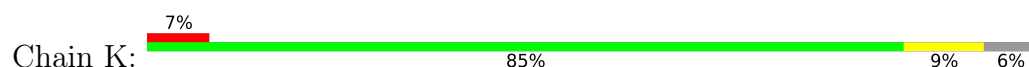
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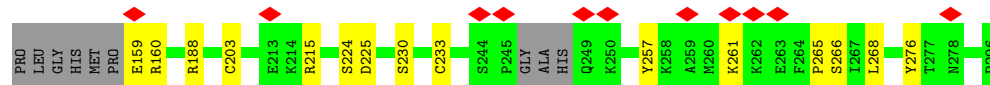
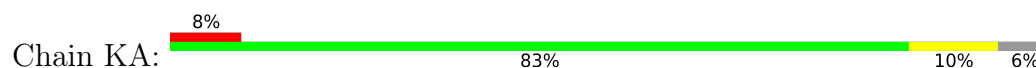
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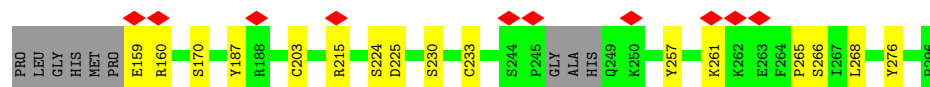
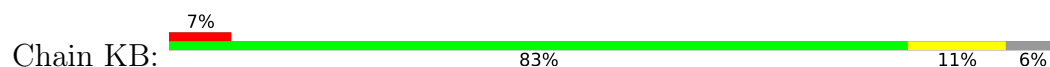
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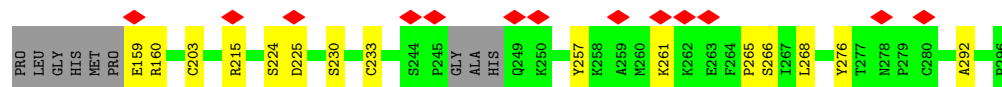
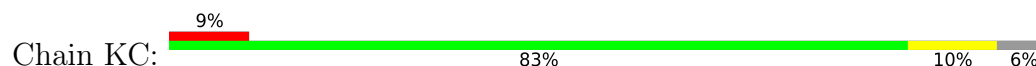
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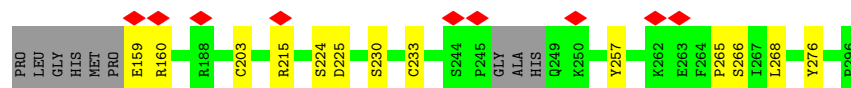
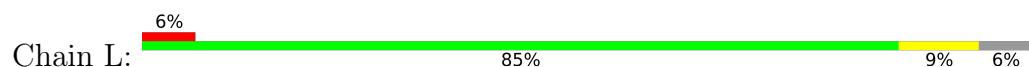
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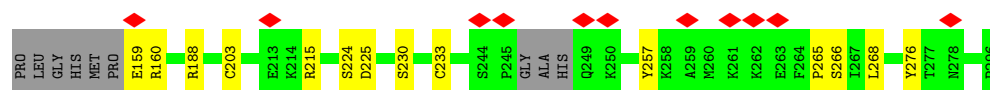


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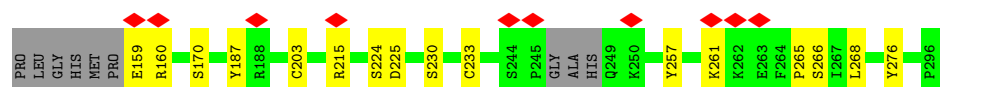
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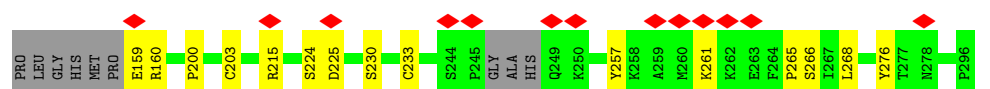
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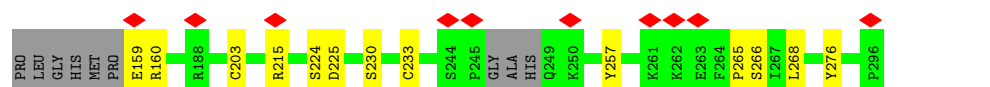
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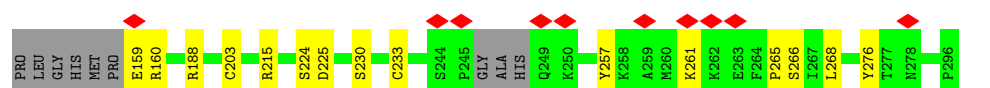
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Chain M: 




- Molecule 1: Myeloid differentiation primary response protein MyD88

Chain MA: 




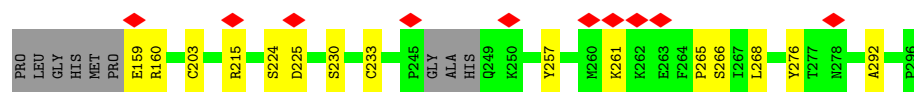
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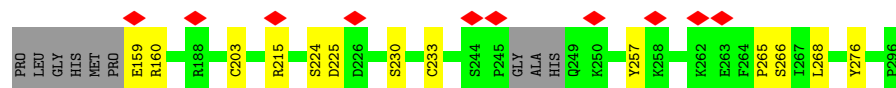
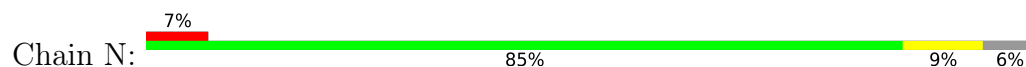


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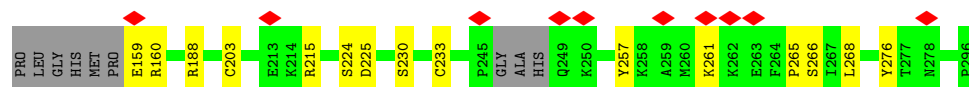
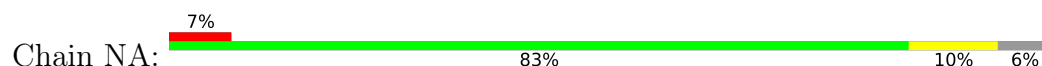
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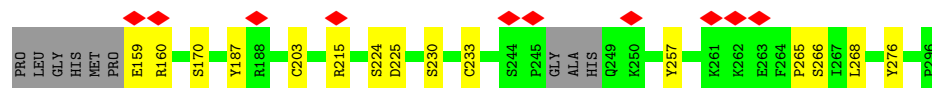
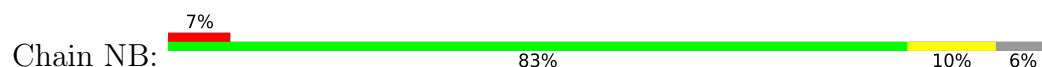
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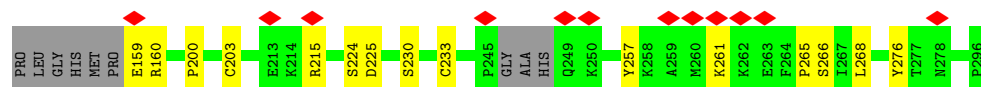
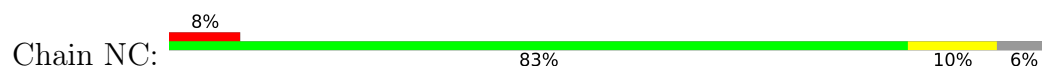
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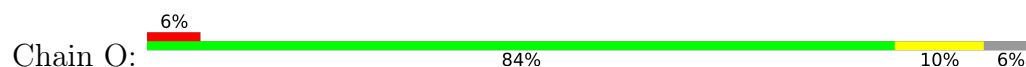
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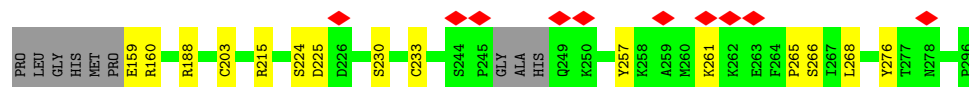
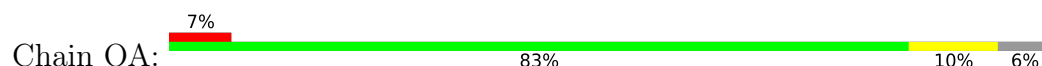
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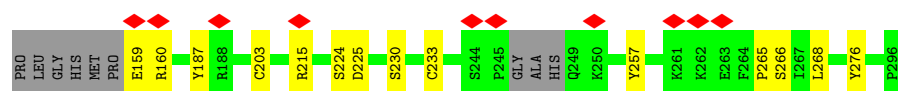
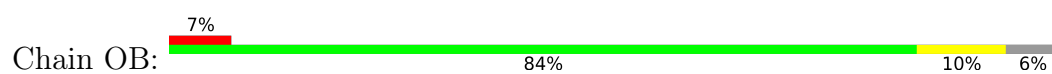
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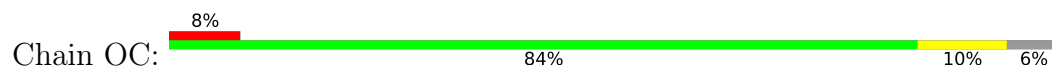
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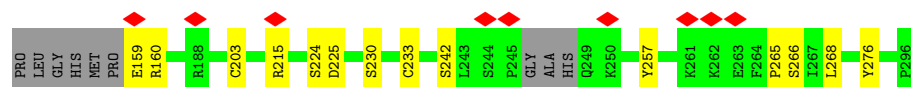
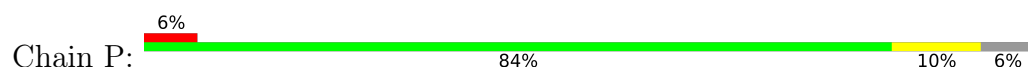
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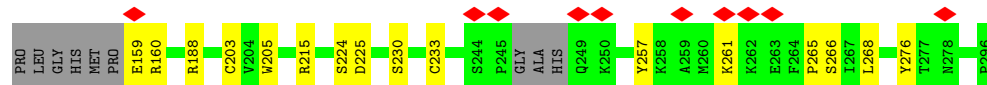
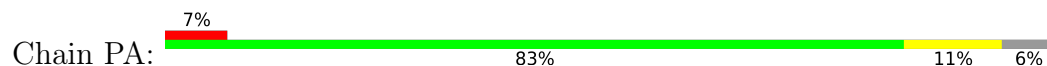
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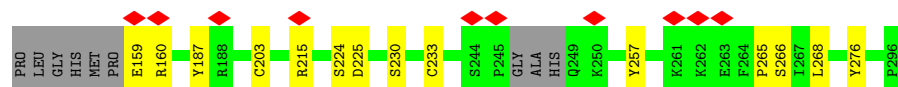
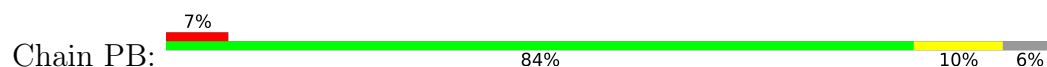
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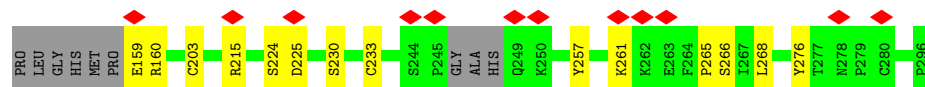
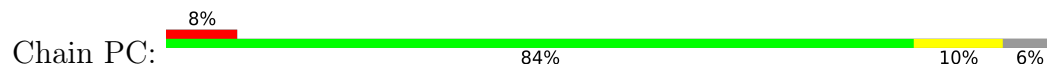
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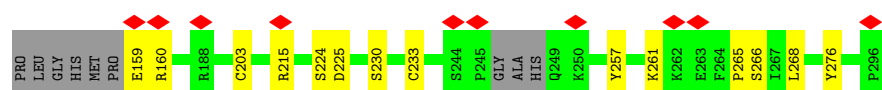
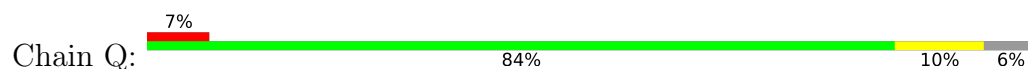
- Molecule 1: Myeloid differentiation primary response protein MyD88



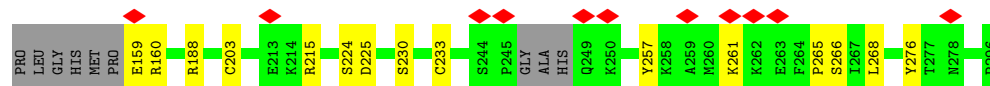
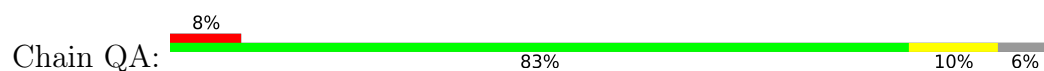
- Molecule 1: Myeloid differentiation primary response protein MyD88



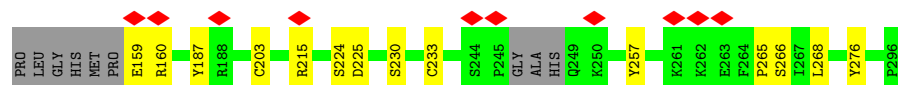
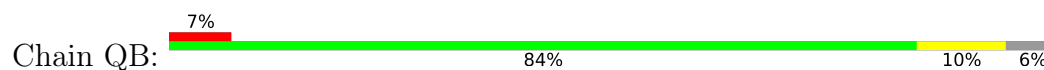
- Molecule 1: Myeloid differentiation primary response protein MyD88



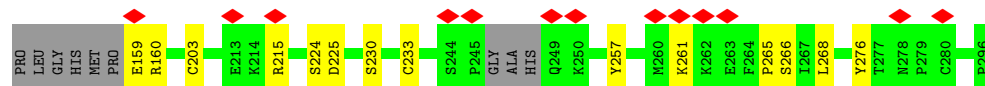
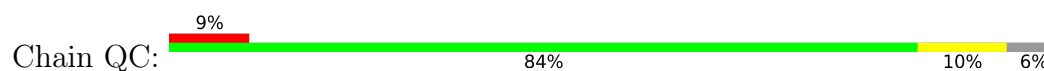
- Molecule 1: Myeloid differentiation primary response protein MyD88



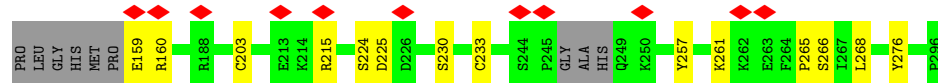
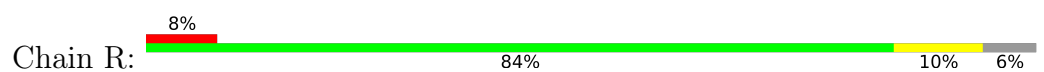
- Molecule 1: Myeloid differentiation primary response protein MyD88



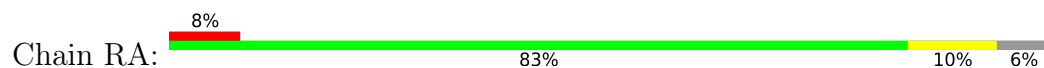
- Molecule 1: Myeloid differentiation primary response protein MyD88



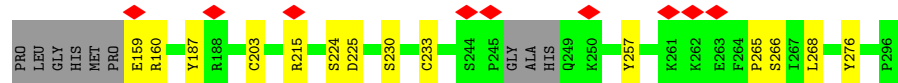
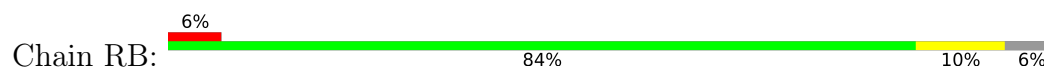
- Molecule 1: Myeloid differentiation primary response protein MyD88



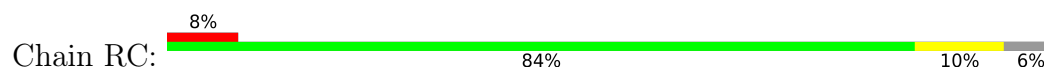
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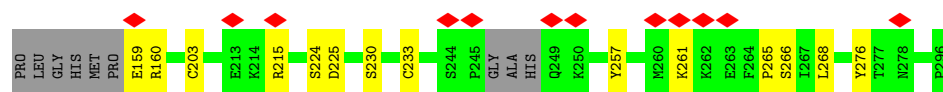


- Molecule 1: Myeloid differentiation primary response protein MyD88

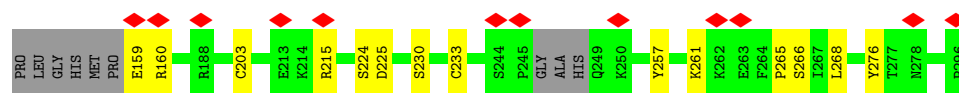
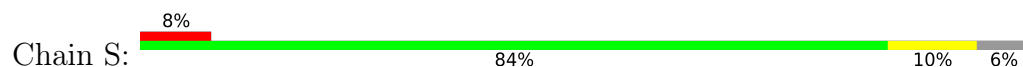


- Molecule 1: Myeloid differentiation primary response protein MyD88

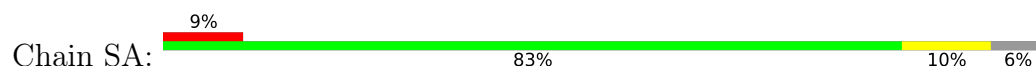




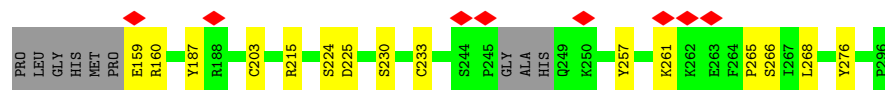
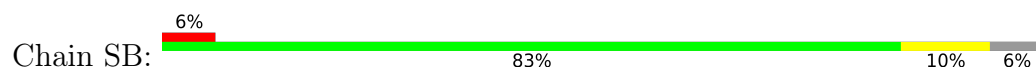
- Molecule 1: Myeloid differentiation primary response protein MyD88



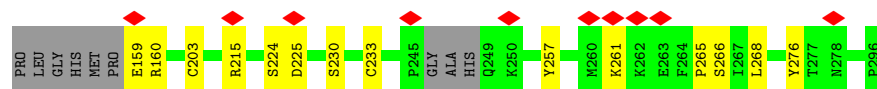
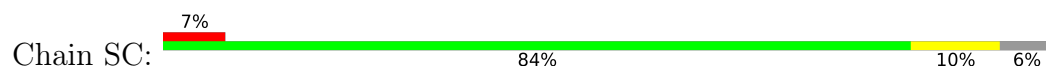
- Molecule 1: Myeloid differentiation primary response protein MyD88



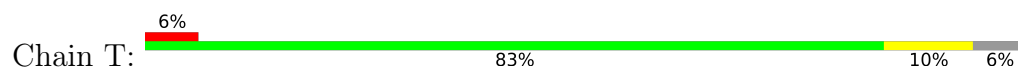
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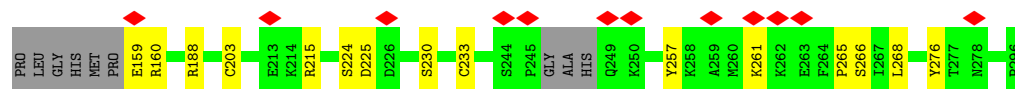
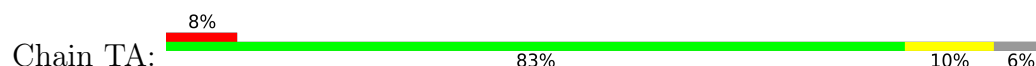
- Molecule 1: Myeloid differentiation primary response protein MyD88



- Molecule 1: Myeloid differentiation primary response protein MyD88

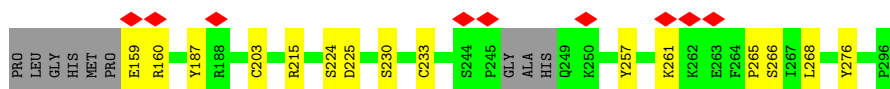
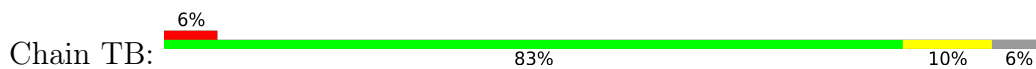


- Molecule 1: Myeloid differentiation primary response protein MyD88

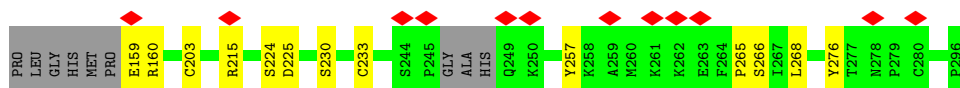
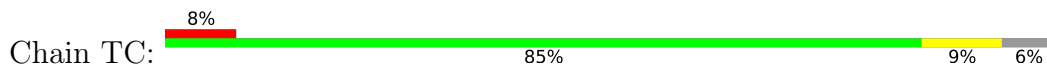


- Molecule 1: Myeloid differentiation primary response protein MyD88

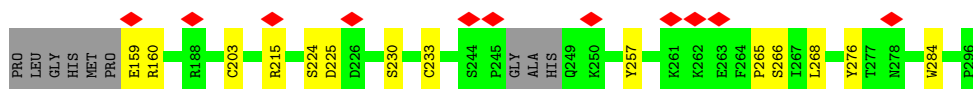
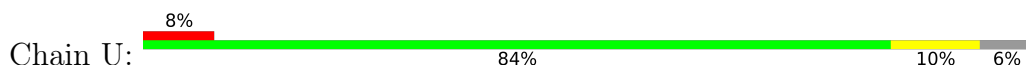




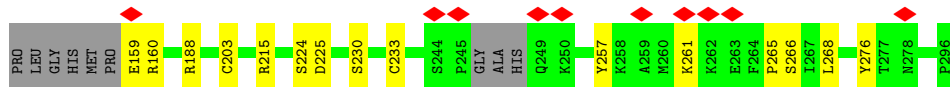
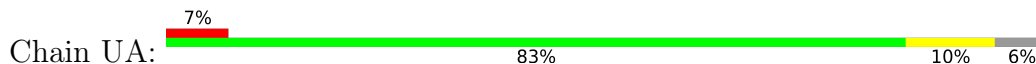
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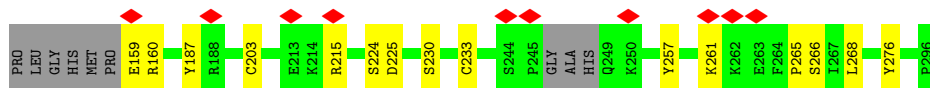
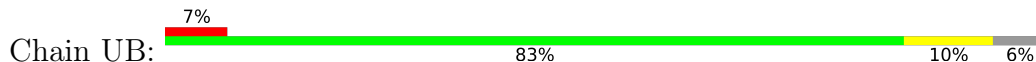
- Molecule 1: Myeloid differentiation primary response protein MyD88



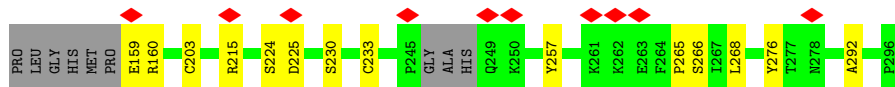
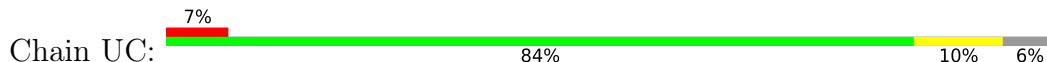
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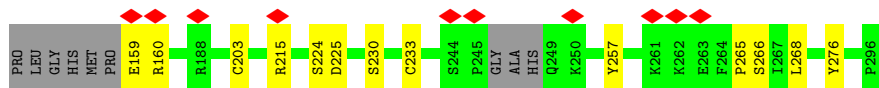
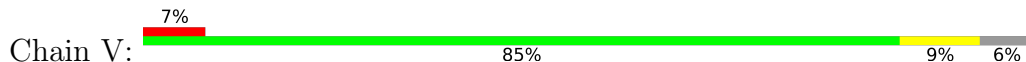
- Molecule 1: Myeloid differentiation primary response protein MyD88

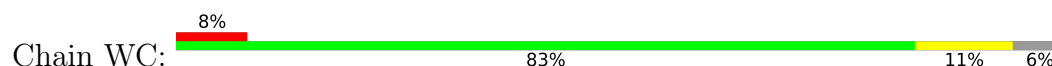
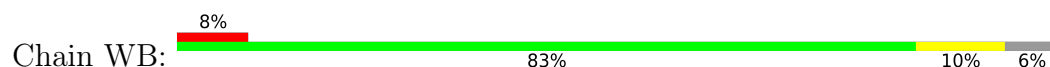
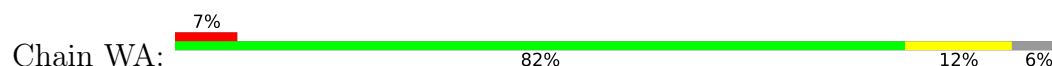
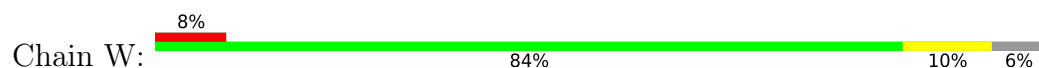
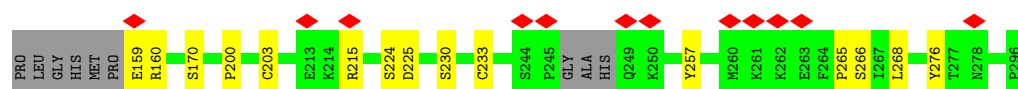
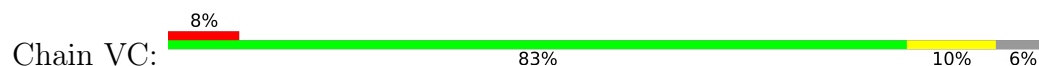
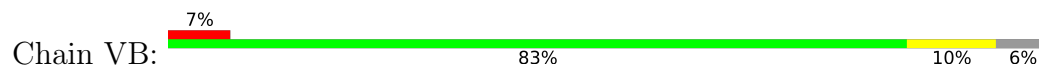
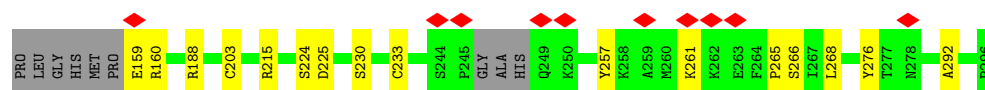
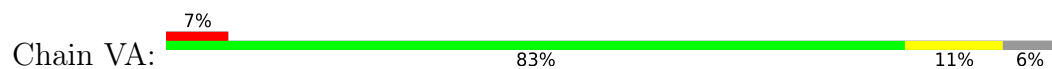


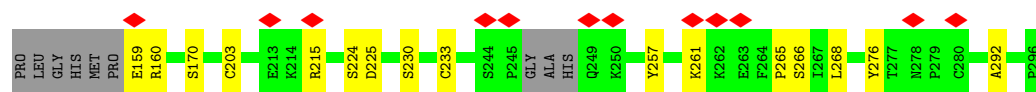
- Molecule 1: Myeloid differentiation primary response protein MyD88



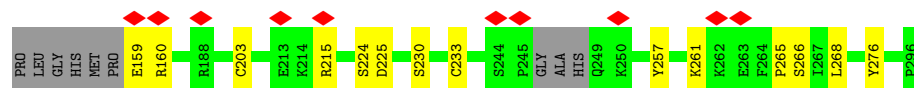
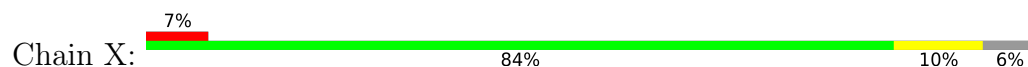
- Molecule 1: Myeloid differentiation primary response protein MyD88



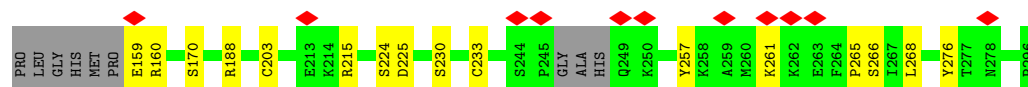
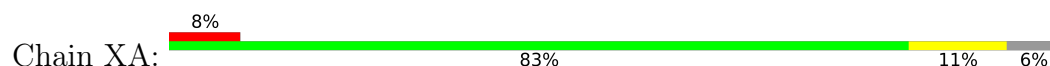




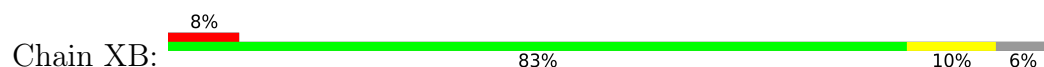
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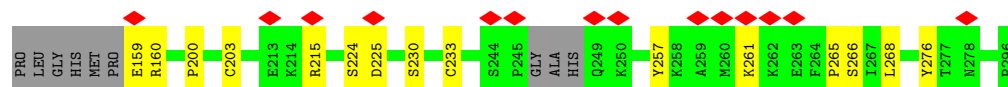
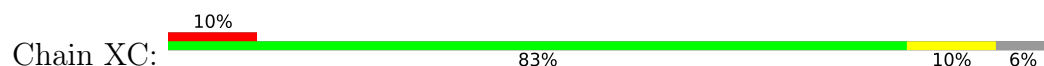
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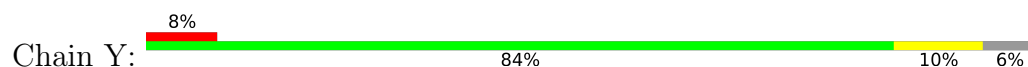
- Molecule 1: Myeloid differentiation primary response protein MyD88



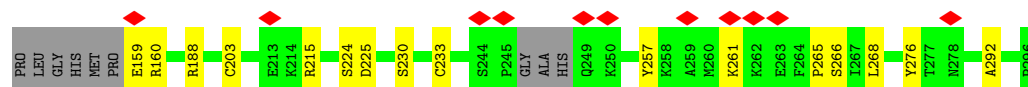
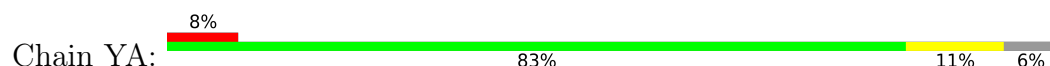
- Molecule 1: Myeloid differentiation primary response protein MyD88



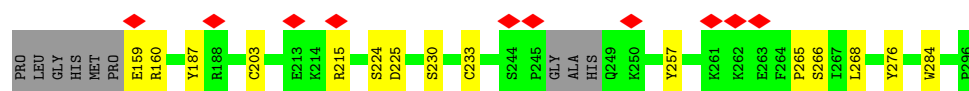
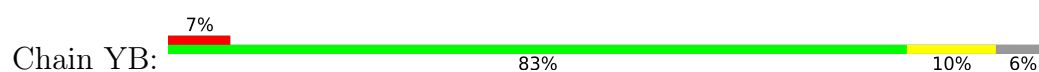
- Molecule 1: Myeloid differentiation primary response protein MyD88



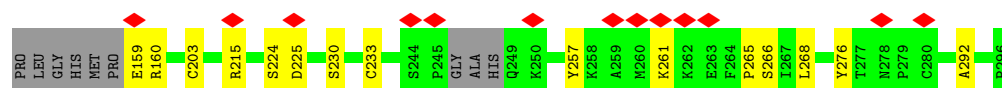
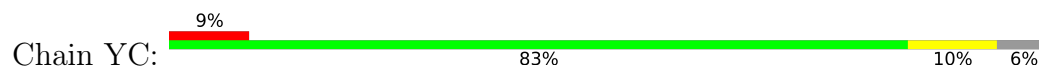
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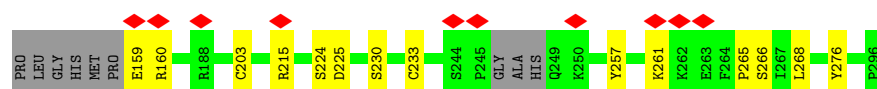
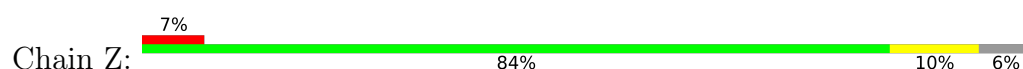
- Molecule 1: Myeloid differentiation primary response protein MyD88



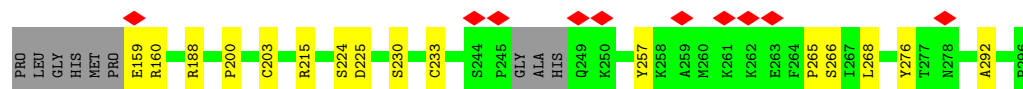
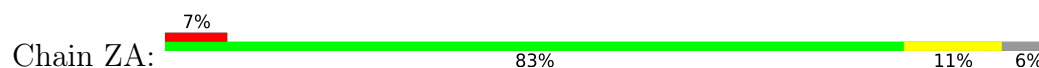
- Molecule 1: Myeloid differentiation primary response protein MyD88



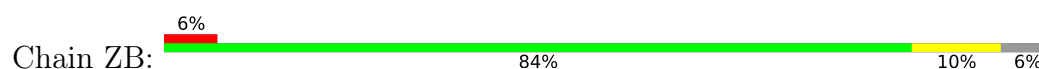
- Molecule 1: Myeloid differentiation primary response protein MyD88



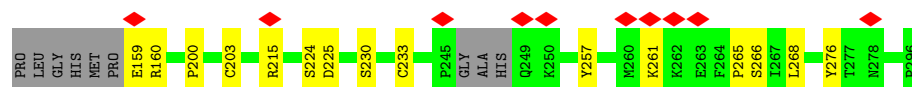
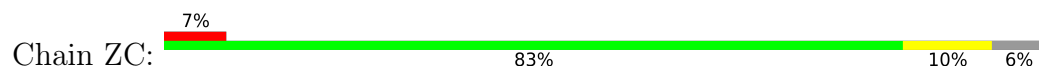
- Molecule 1: Myeloid differentiation primary response protein MyD88



- Molecule 1: Myeloid differentiation primary response protein MyD88



- Molecule 1: Myeloid differentiation primary response protein MyD88



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26680	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.257	Depositor
Minimum map value	-0.470	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.4	Depositor
Map size ( $\text{\AA}$ )	505.0, 505.0, 505.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.01, 1.01, 1.01	Depositor

## 5 Model quality [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.32	0/1138	0.48	0/1535
1	AA	0.32	0/1138	0.49	0/1535
1	AB	0.32	0/1138	0.48	0/1535
1	AC	0.32	0/1138	0.49	0/1535
1	B	0.32	0/1138	0.49	0/1535
1	BA	0.32	0/1138	0.49	0/1535
1	BB	0.32	0/1138	0.49	0/1535
1	BC	0.32	0/1138	0.49	0/1535
1	C	0.32	0/1138	0.48	0/1535
1	CA	0.32	0/1138	0.49	0/1535
1	CB	0.32	0/1138	0.49	0/1535
1	CC	0.32	0/1138	0.48	0/1535
1	D	0.32	0/1138	0.48	0/1535
1	DA	0.32	0/1138	0.49	0/1535
1	DB	0.32	0/1138	0.49	0/1535
1	DC	0.32	0/1138	0.48	0/1535
1	E	0.32	0/1138	0.49	0/1535
1	EA	0.32	0/1138	0.49	0/1535
1	EB	0.32	0/1138	0.49	0/1535
1	EC	0.32	0/1138	0.49	0/1535
1	F	0.32	0/1138	0.49	0/1535
1	FA	0.32	0/1138	0.48	0/1535
1	FB	0.32	0/1138	0.48	0/1535
1	FC	0.32	0/1138	0.49	0/1535
1	G	0.32	0/1138	0.48	0/1535
1	GA	0.32	0/1138	0.49	0/1535
1	GB	0.32	0/1138	0.49	0/1535
1	GC	0.32	0/1138	0.49	0/1535
1	H	0.32	0/1138	0.49	0/1535
1	HA	0.32	0/1138	0.48	0/1535
1	HB	0.32	0/1138	0.49	0/1535
1	HC	0.32	0/1138	0.49	0/1535
1	I	0.32	0/1138	0.49	0/1535
1	IA	0.32	0/1138	0.49	0/1535

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	IB	0.32	0/1138	0.49	0/1535
1	IC	0.32	0/1138	0.49	0/1535
1	J	0.32	0/1138	0.49	0/1535
1	JA	0.32	0/1138	0.48	0/1535
1	JB	0.32	0/1138	0.48	0/1535
1	JC	0.32	0/1138	0.48	0/1535
1	K	0.32	0/1138	0.48	0/1535
1	KA	0.32	0/1138	0.49	0/1535
1	KB	0.32	0/1138	0.49	0/1535
1	KC	0.32	0/1138	0.48	0/1535
1	L	0.32	0/1138	0.49	0/1535
1	LA	0.32	0/1138	0.49	0/1535
1	LB	0.32	0/1138	0.48	0/1535
1	LC	0.32	0/1138	0.48	0/1535
1	M	0.32	0/1138	0.49	0/1535
1	MA	0.32	0/1138	0.48	0/1535
1	MB	0.32	0/1138	0.49	0/1535
1	MC	0.32	0/1138	0.49	0/1535
1	N	0.32	0/1138	0.49	0/1535
1	NA	0.32	0/1138	0.49	0/1535
1	NB	0.32	0/1138	0.48	0/1535
1	NC	0.32	0/1138	0.49	0/1535
1	O	0.32	0/1138	0.48	0/1535
1	OA	0.32	0/1138	0.49	0/1535
1	OB	0.32	0/1138	0.48	0/1535
1	OC	0.32	0/1138	0.49	0/1535
1	P	0.32	0/1138	0.49	0/1535
1	PA	0.32	0/1138	0.49	0/1535
1	PB	0.32	0/1138	0.48	0/1535
1	PC	0.32	0/1138	0.49	0/1535
1	Q	0.32	0/1138	0.49	0/1535
1	QA	0.32	0/1138	0.49	0/1535
1	QB	0.32	0/1138	0.49	0/1535
1	QC	0.32	0/1138	0.49	0/1535
1	R	0.32	0/1138	0.49	0/1535
1	RA	0.32	0/1138	0.48	0/1535
1	RB	0.32	0/1138	0.49	0/1535
1	RC	0.32	0/1138	0.49	0/1535
1	S	0.32	0/1138	0.49	0/1535
1	SA	0.32	0/1138	0.48	0/1535
1	SB	0.32	0/1138	0.49	0/1535
1	SC	0.32	0/1138	0.48	0/1535
1	T	0.32	0/1138	0.48	0/1535

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	TA	0.32	0/1138	0.49	0/1535
1	TB	0.32	0/1138	0.49	0/1535
1	TC	0.32	0/1138	0.49	0/1535
1	U	0.32	0/1138	0.48	0/1535
1	UA	0.32	0/1138	0.49	0/1535
1	UB	0.32	0/1138	0.49	0/1535
1	UC	0.32	0/1138	0.49	0/1535
1	V	0.32	0/1138	0.48	0/1535
1	VA	0.32	0/1138	0.49	0/1535
1	VB	0.32	0/1138	0.49	0/1535
1	VC	0.32	0/1138	0.49	0/1535
1	W	0.32	0/1138	0.49	0/1535
1	WA	0.32	0/1138	0.49	0/1535
1	WB	0.32	0/1138	0.48	0/1535
1	WC	0.32	0/1138	0.48	0/1535
1	X	0.32	0/1138	0.49	0/1535
1	XA	0.32	0/1138	0.49	0/1535
1	XB	0.32	0/1138	0.49	0/1535
1	XC	0.32	0/1138	0.49	0/1535
1	Y	0.32	0/1138	0.49	0/1535
1	YA	0.32	0/1138	0.49	0/1535
1	YB	0.32	0/1138	0.48	0/1535
1	YC	0.32	0/1138	0.49	0/1535
1	Z	0.32	0/1138	0.49	0/1535
1	ZA	0.32	0/1138	0.48	0/1535
1	ZB	0.32	0/1138	0.49	0/1535
1	ZC	0.32	0/1138	0.49	0/1535
All	All	0.32	0/118352	0.49	0/159640

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1114	0	1136	6	0
1	AA	1114	0	1136	8	0
1	AB	1114	0	1136	8	0
1	AC	1114	0	1136	8	0
1	B	1114	0	1136	7	0
1	BA	1114	0	1136	8	0
1	BB	1114	0	1136	9	0
1	BC	1114	0	1136	7	0
1	C	1114	0	1136	6	0
1	CA	1114	0	1136	10	0
1	CB	1114	0	1136	9	0
1	CC	1114	0	1136	5	0
1	D	1114	0	1136	5	0
1	DA	1114	0	1136	6	0
1	DB	1114	0	1136	9	0
1	DC	1114	0	1136	6	0
1	E	1114	0	1136	6	0
1	EA	1114	0	1136	8	0
1	EB	1114	0	1136	6	0
1	EC	1114	0	1136	7	0
1	F	1114	0	1136	5	0
1	FA	1114	0	1136	7	0
1	FB	1114	0	1136	6	0
1	FC	1114	0	1136	7	0
1	G	1114	0	1136	7	0
1	GA	1114	0	1136	8	0
1	GB	1114	0	1136	6	0
1	GC	1114	0	1136	6	0
1	H	1114	0	1136	8	0
1	HA	1114	0	1136	9	0
1	HB	1114	0	1136	8	0
1	HC	1114	0	1136	6	0
1	I	1114	0	1136	7	0
1	IA	1114	0	1136	10	0
1	IB	1114	0	1136	7	0
1	IC	1114	0	1136	6	0
1	J	1114	0	1136	6	0
1	JA	1114	0	1136	8	0
1	JB	1114	0	1136	7	0
1	JC	1114	0	1136	5	0
1	K	1114	0	1136	5	0
1	KA	1114	0	1136	7	0
1	KB	1114	0	1136	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	KC	1114	0	1136	7	0
1	L	1114	0	1136	5	0
1	LA	1114	0	1136	6	0
1	LB	1114	0	1136	8	0
1	LC	1114	0	1136	7	0
1	M	1114	0	1136	5	0
1	MA	1114	0	1136	7	0
1	MB	1114	0	1136	8	0
1	MC	1114	0	1136	7	0
1	N	1114	0	1136	5	0
1	NA	1114	0	1136	7	0
1	NB	1114	0	1136	7	0
1	NC	1114	0	1136	7	0
1	O	1114	0	1136	6	0
1	OA	1114	0	1136	7	0
1	OB	1114	0	1136	6	0
1	OC	1114	0	1136	6	0
1	P	1114	0	1136	6	0
1	PA	1114	0	1136	8	0
1	PB	1114	0	1136	6	0
1	PC	1114	0	1136	6	0
1	Q	1114	0	1136	6	0
1	QA	1114	0	1136	7	0
1	QB	1114	0	1136	6	0
1	QC	1114	0	1136	6	0
1	R	1114	0	1136	6	0
1	RA	1114	0	1136	7	0
1	RB	1114	0	1136	6	0
1	RC	1114	0	1136	6	0
1	S	1114	0	1136	6	0
1	SA	1114	0	1136	7	0
1	SB	1114	0	1136	7	0
1	SC	1114	0	1136	6	0
1	T	1114	0	1136	8	0
1	TA	1114	0	1136	8	0
1	TB	1114	0	1136	8	0
1	TC	1114	0	1136	5	0
1	U	1114	0	1136	6	0
1	UA	1114	0	1136	7	0
1	UB	1114	0	1136	7	0
1	UC	1114	0	1136	6	0
1	V	1114	0	1136	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	VA	1114	0	1136	8	0
1	VB	1114	0	1136	7	0
1	VC	1114	0	1136	7	0
1	W	1114	0	1136	6	0
1	WA	1114	0	1136	10	0
1	WB	1114	0	1136	7	0
1	WC	1114	0	1136	8	0
1	X	1114	0	1136	6	0
1	XA	1114	0	1136	8	0
1	XB	1114	0	1136	7	0
1	XC	1114	0	1136	8	0
1	Y	1114	0	1136	6	0
1	YA	1114	0	1136	8	0
1	YB	1114	0	1136	7	0
1	YC	1114	0	1136	7	0
1	Z	1114	0	1136	6	0
1	ZA	1114	0	1136	8	0
1	ZB	1114	0	1136	6	0
1	ZC	1114	0	1136	7	0
All	All	115856	0	118144	664	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 3.

The worst 5 of 664 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:188:ARG:NH1	1:CB:187:TYR:OH	2.32	0.62
1:BA:188:ARG:NH1	1:BB:187:TYR:OH	2.33	0.61
1:HA:188:ARG:NH1	1:HB:187:TYR:OH	2.33	0.61
1:AA:188:ARG:NH1	1:AB:187:TYR:OH	2.34	0.60
1:EA:188:ARG:NH1	1:EB:187:TYR:OH	2.35	0.60

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	A	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	AA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	AB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	AC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	B	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	BA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	BB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	BC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	C	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	CA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	CB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	CC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	D	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	DA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	DB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	DC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	E	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	EA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	EB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	EC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	F	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	FA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	FB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	FC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	G	131/144 (91%)	124 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	GB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	GC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	H	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	HA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	HB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	HC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	I	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	IA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	IB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	IC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	J	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	JA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	JB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	JC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	K	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	KA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	KB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	KC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	L	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	LA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	LB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	LC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	M	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	MA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	MB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	MC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	N	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	NA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	NB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	NC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	OA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	OB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	OC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	P	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	PA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	PB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	PC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	Q	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	QA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	QB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	QC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	R	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	RA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	RB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	RC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	S	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	SA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	SB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	SC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	T	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	TA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	TB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	TC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	U	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	UA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	UB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	UC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	V	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	VA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	VB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	VC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	W	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	WA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	WB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	WC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	X	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	XA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	XB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	XC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	Y	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	YA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	YB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	YC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	Z	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	ZA	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	ZB	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
1	ZC	131/144 (91%)	124 (95%)	7 (5%)	0	100	100
All	All	13624/14976 (91%)	12896 (95%)	728 (5%)	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	A	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	AA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	AB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	AC	128/134 (96%)	125 (98%)	3 (2%)	45	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	BA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	BB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	BC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	C	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	CA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	CB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	CC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	D	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	DA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	DB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	DC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	E	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	EA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	EB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	EC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	F	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	FA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	FB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	FC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	G	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	GA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	GB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	GC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	H	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	HA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	HB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	HC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	I	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	IA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	IB	128/134 (96%)	125 (98%)	3 (2%)	45	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	IC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	J	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	JA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	JB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	JC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	K	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	KA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	KB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	KC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	L	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	LA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	LB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	LC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	M	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	MA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	MB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	MC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	N	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	NA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	NB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	NC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	O	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	OA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	OB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	OC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	P	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	PA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	PB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	PC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	Q	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	QA	128/134 (96%)	125 (98%)	3 (2%)	45	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	QB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	QC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	R	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	RA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	RB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	RC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	S	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	SA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	SB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	SC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	T	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	TA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	TB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	TC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	U	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	UA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	UB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	UC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	V	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	VA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	VB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	VC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	W	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	WA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	WB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	WC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	X	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	XA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	XB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	XC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	Y	128/134 (96%)	125 (98%)	3 (2%)	45	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	YA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	YB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	YC	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	Z	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	ZA	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	ZB	128/134 (96%)	125 (98%)	3 (2%)	45	68
1	ZC	128/134 (96%)	125 (98%)	3 (2%)	45	68
All	All	13312/13936 (96%)	13000 (98%)	312 (2%)	46	68

5 of 312 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	TA	160	ARG
1	XC	203	CYS
1	TC	203	CYS
1	VB	266	SER
1	Z	160	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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.

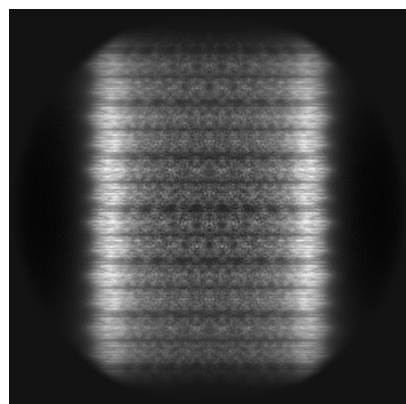
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39676. These allow visual inspection of the internal detail of the map and identification of artifacts.

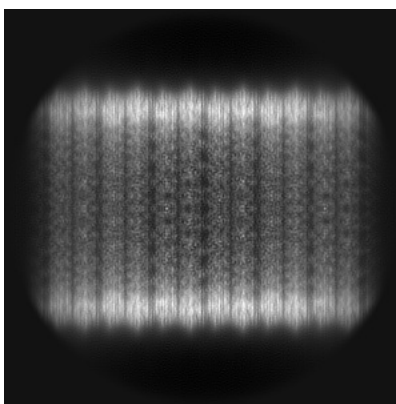
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

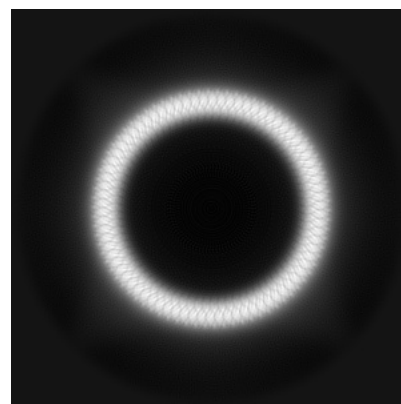
#### 6.1.1 Primary map



X

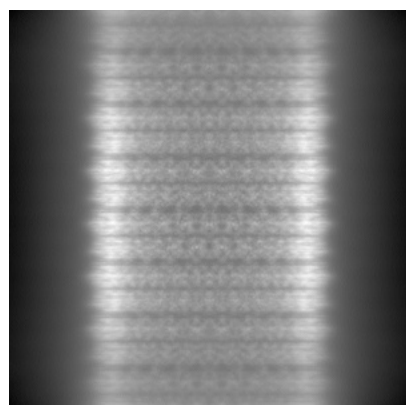


Y

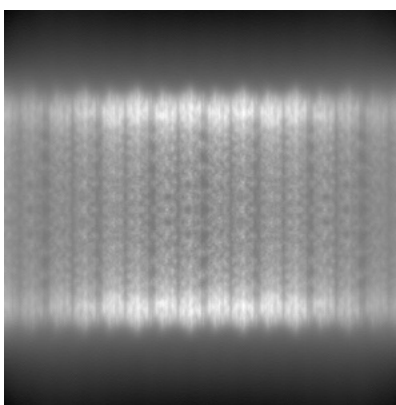


Z

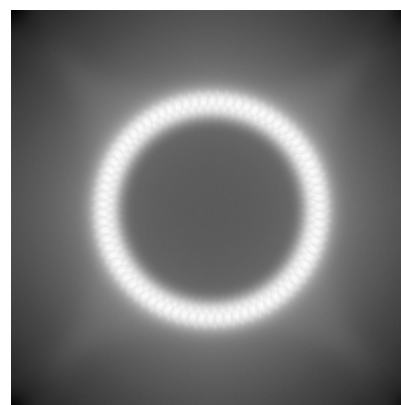
#### 6.1.2 Raw map



X



Y

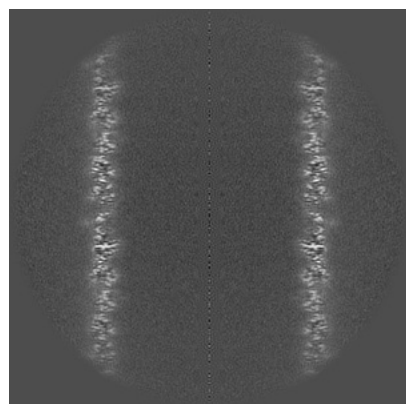


Z

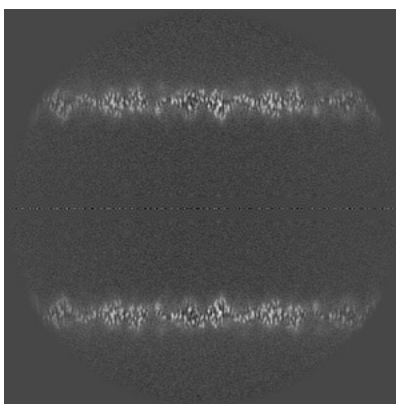
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

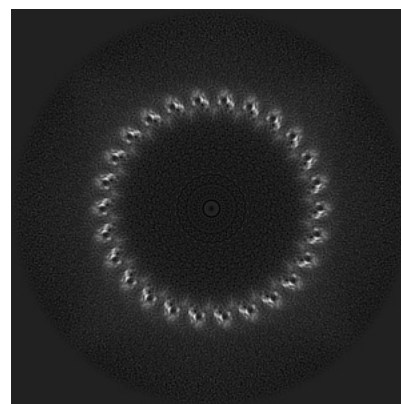
### 6.2.1 Primary map



X Index: 250

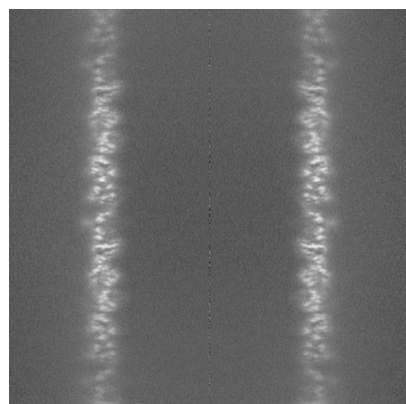


Y Index: 250

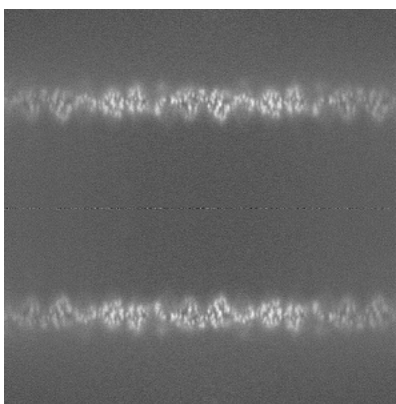


Z Index: 250

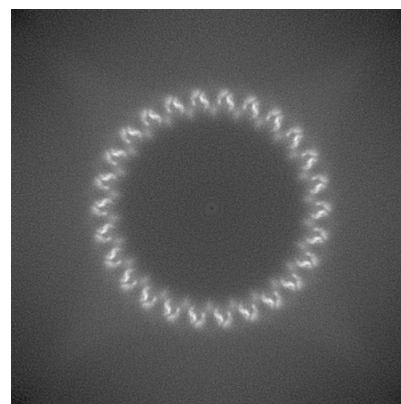
### 6.2.2 Raw map



X Index: 250



Y Index: 250



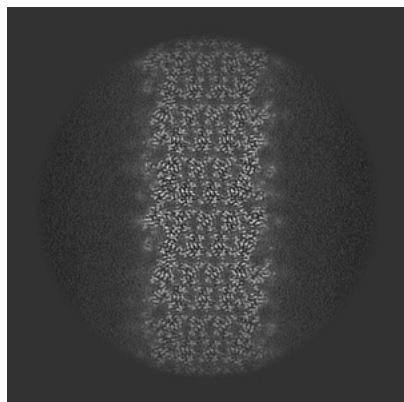
Z Index: 250

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

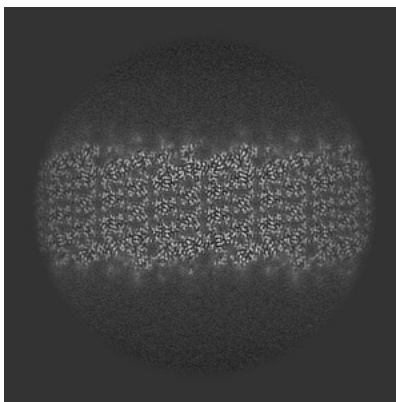


## 6.3 Largest variance slices [i](#)

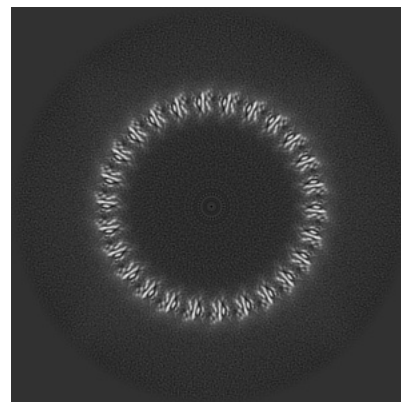
### 6.3.1 Primary map



X Index: 124

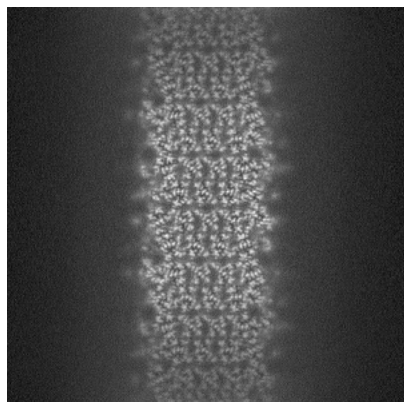


Y Index: 376

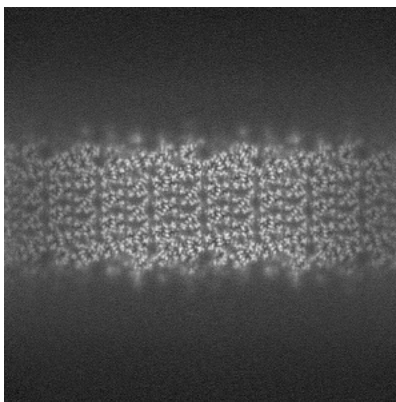


Z Index: 269

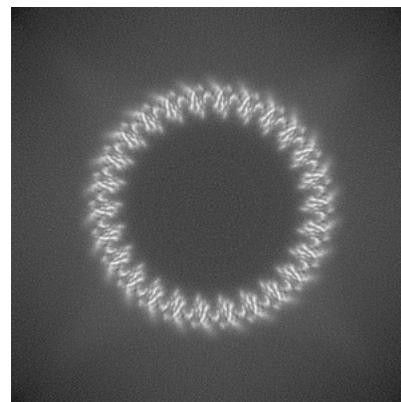
### 6.3.2 Raw map



X Index: 375



Y Index: 375

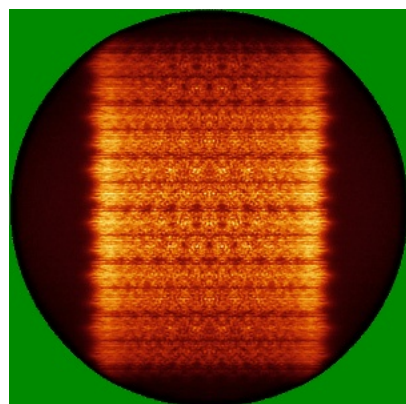


Z Index: 233

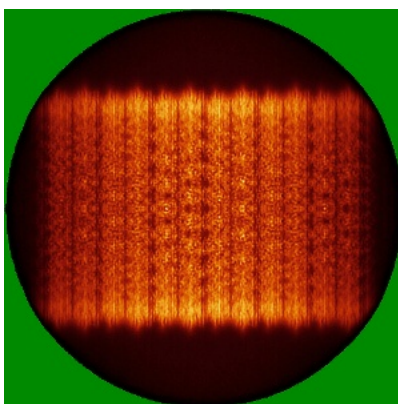
The images above show the largest variance slices of the map in three orthogonal directions.

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

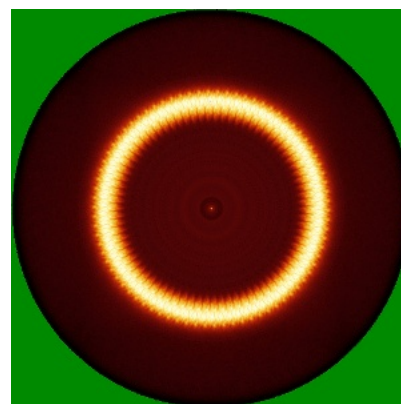
### 6.4.1 Primary map



X

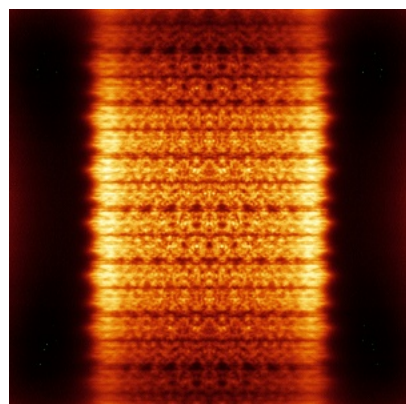


Y

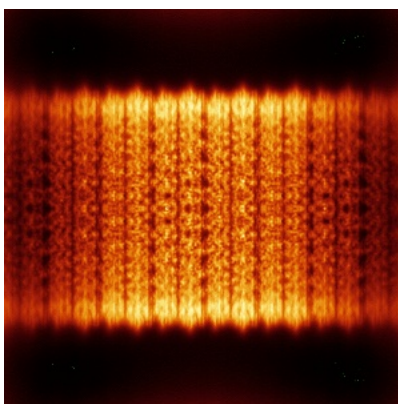


Z

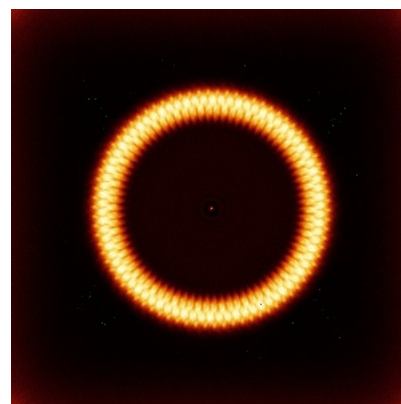
### 6.4.2 Raw map



X



Y



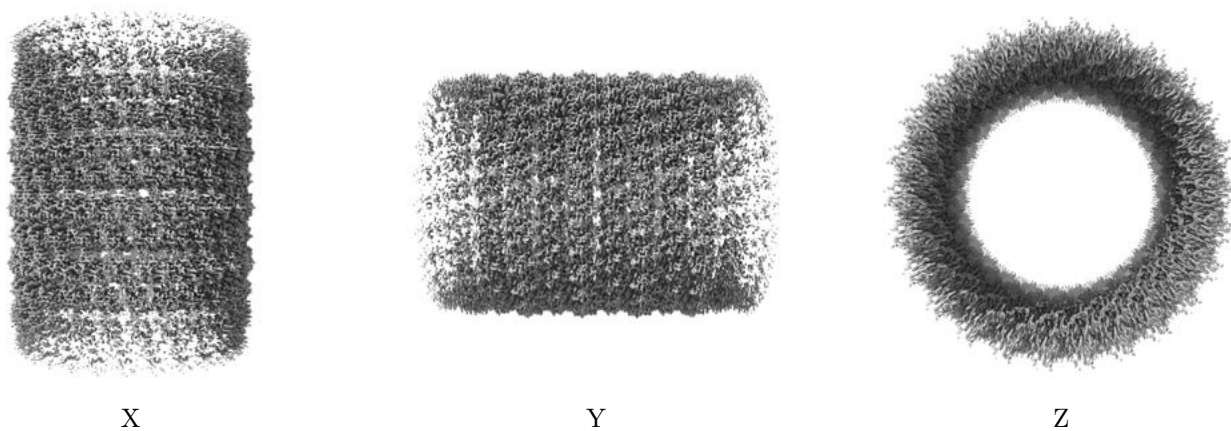
Z

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.



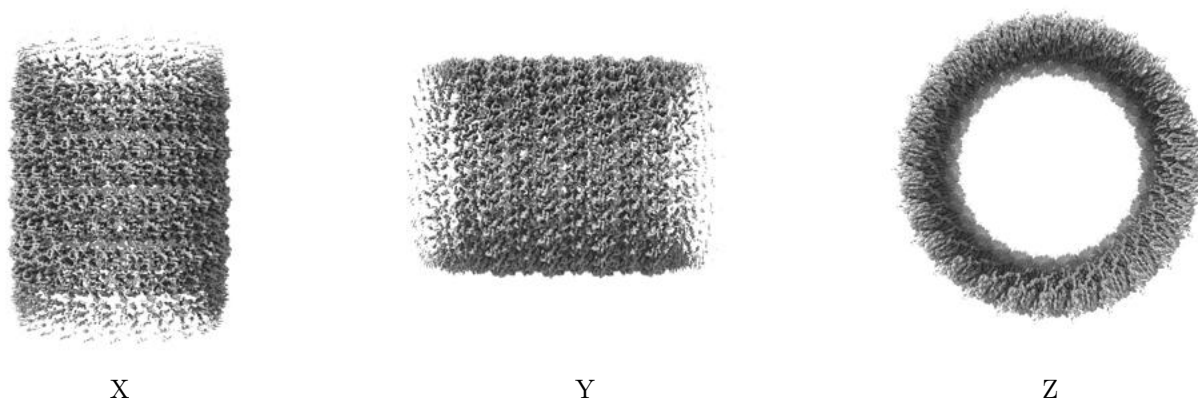
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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.

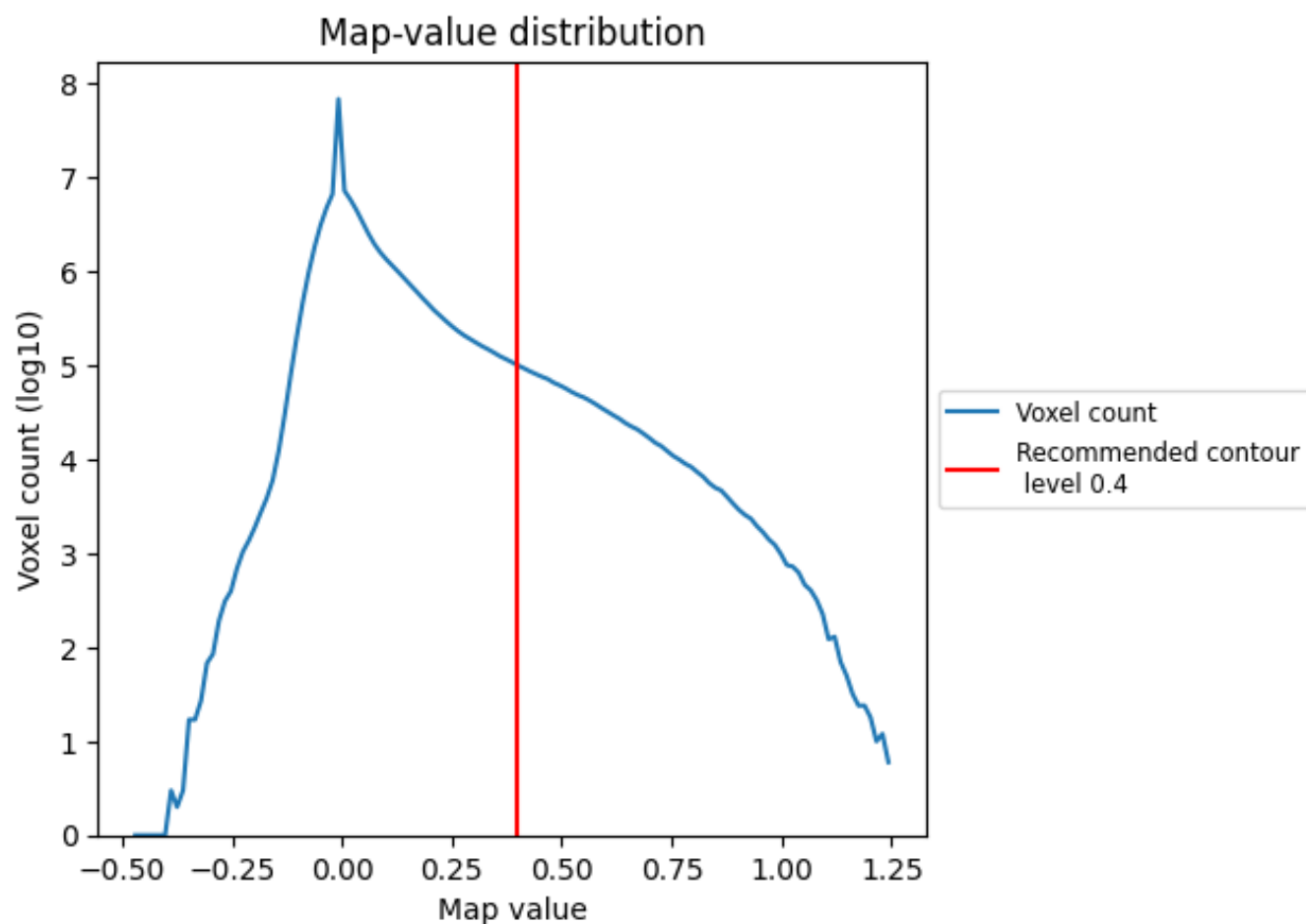
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

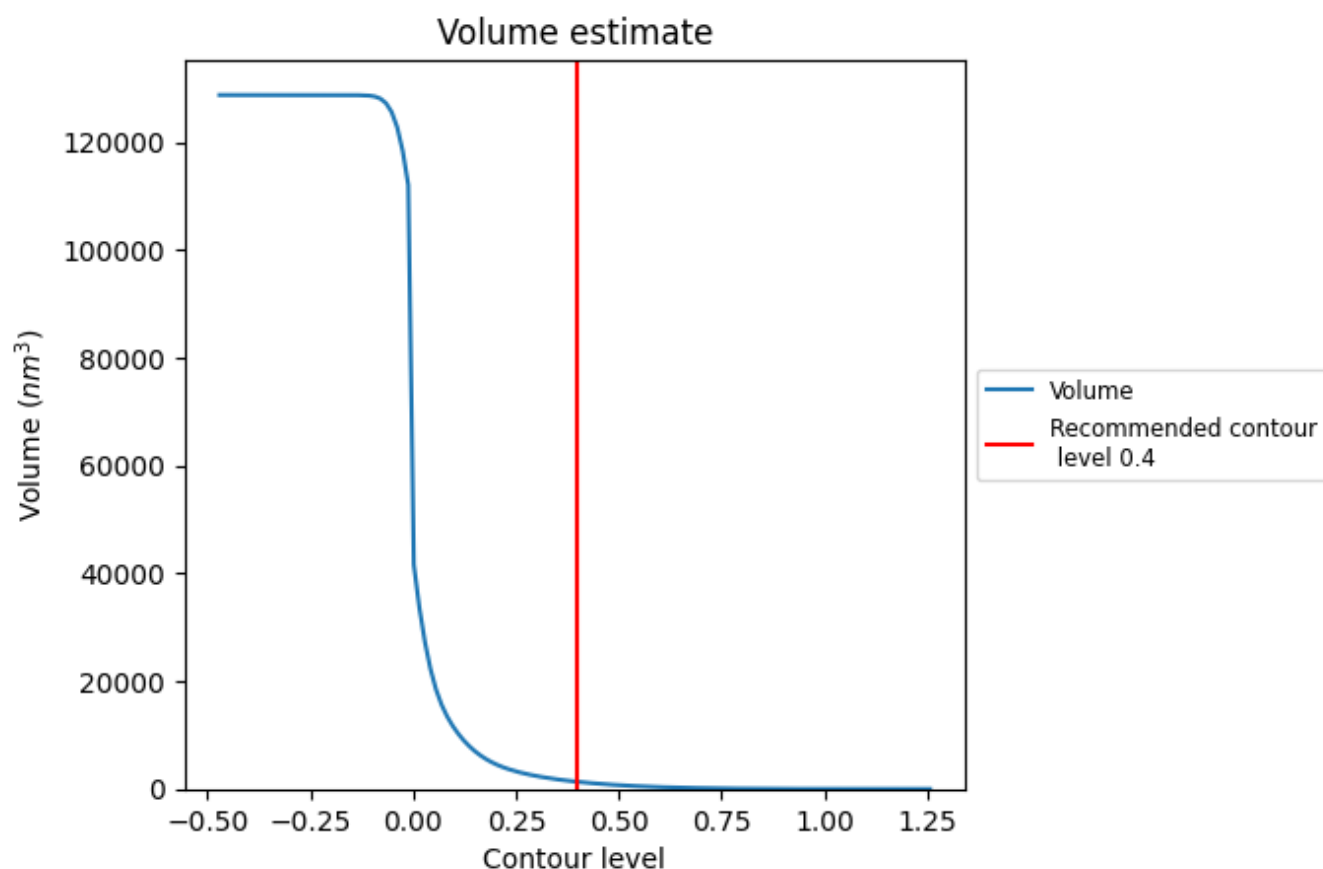
This section contains the results of statistical analysis of the map.

### 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.

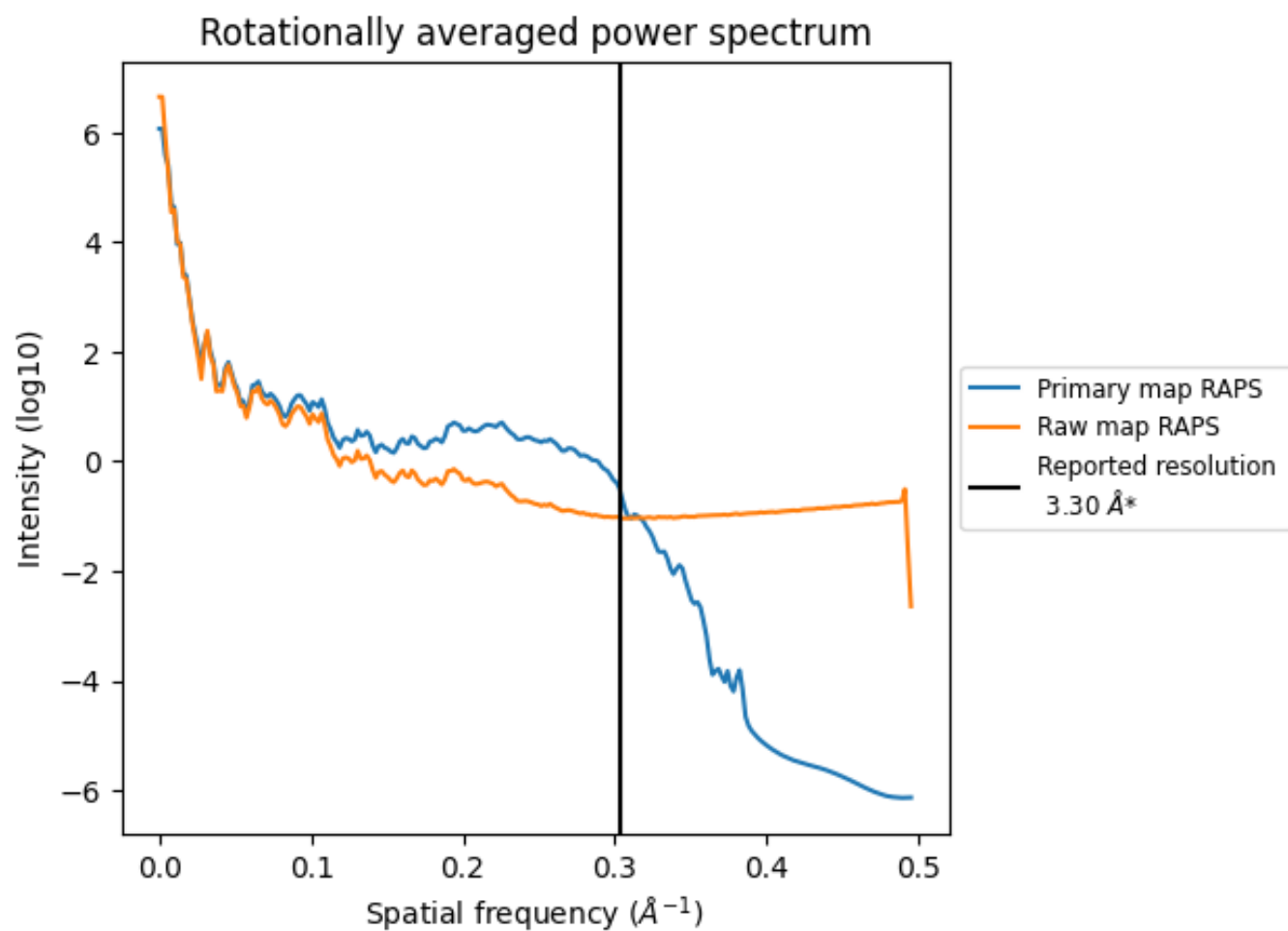
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1329 nm<sup>3</sup>; this corresponds to an approximate mass of 1201 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 ⓘ

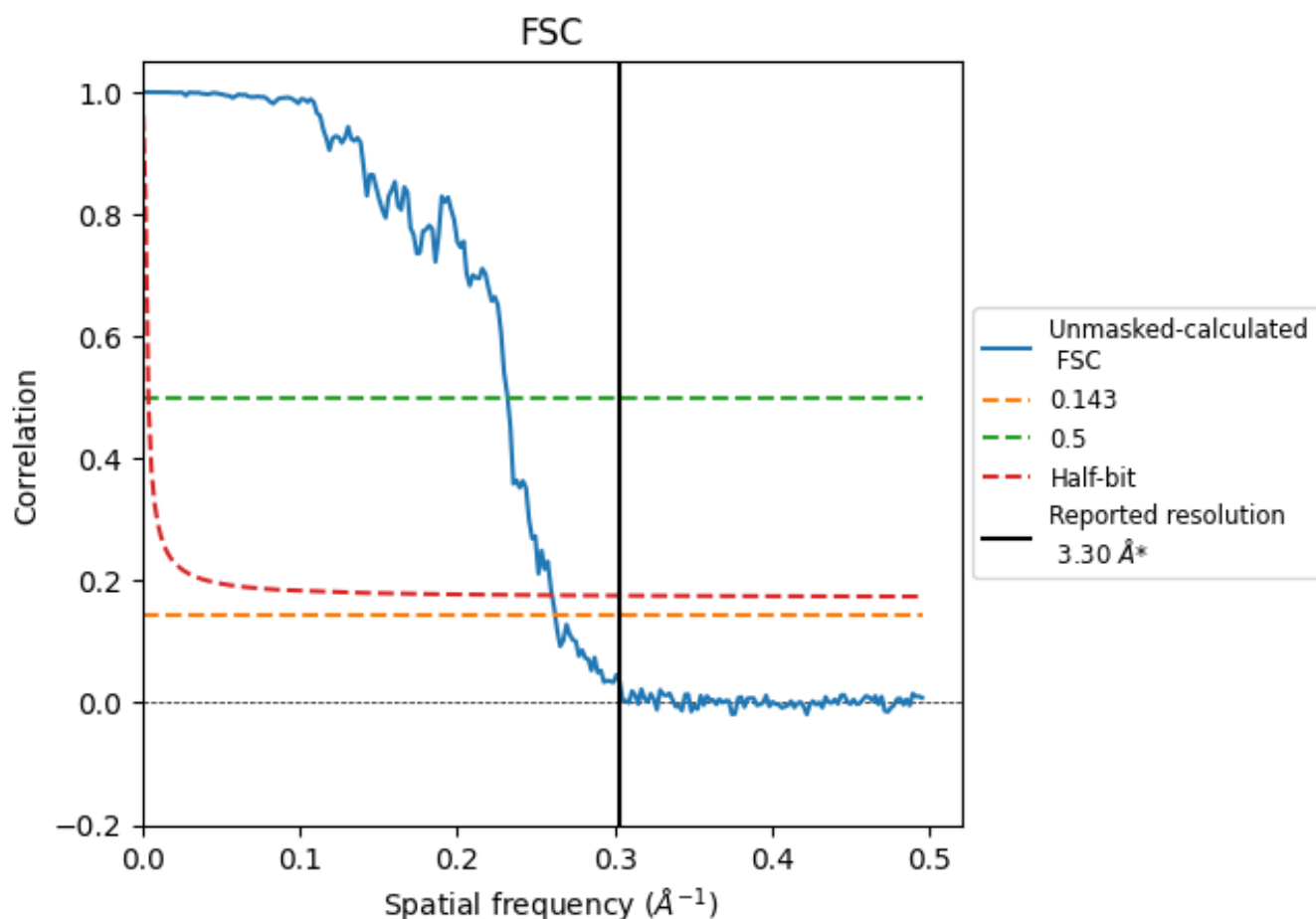


\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 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 0.303 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

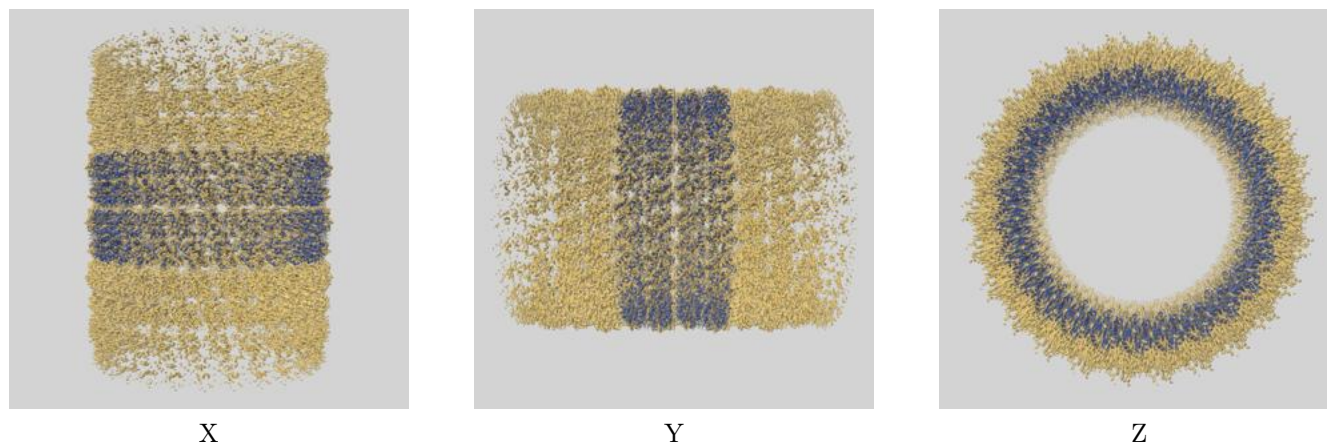
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	4.31	3.84

\*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 3.82 differs from the reported value 3.3 by more than 10 %

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

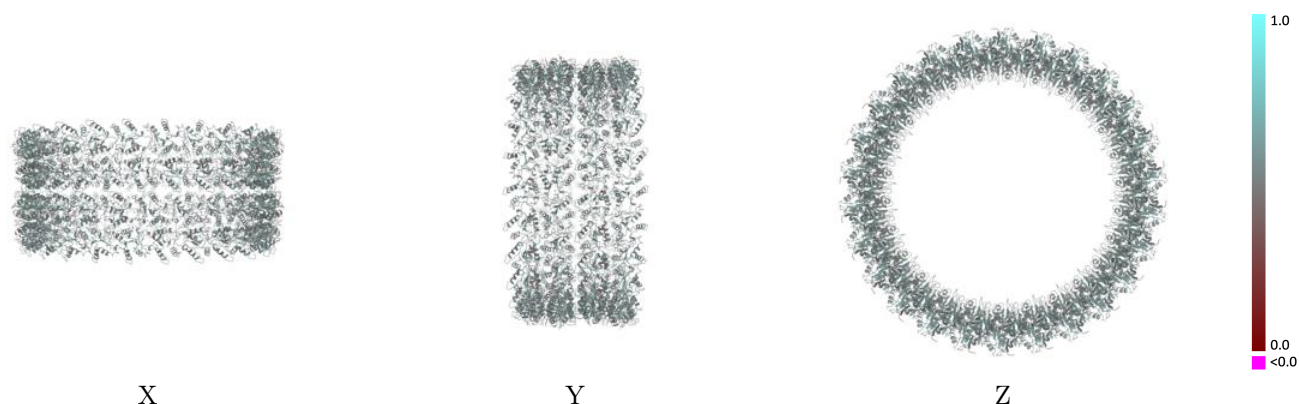
This section contains information regarding the fit between EMDB map EMD-39676 and PDB model 8YYM. Per-residue inclusion information can be found in section [3](#) on page [13](#).

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



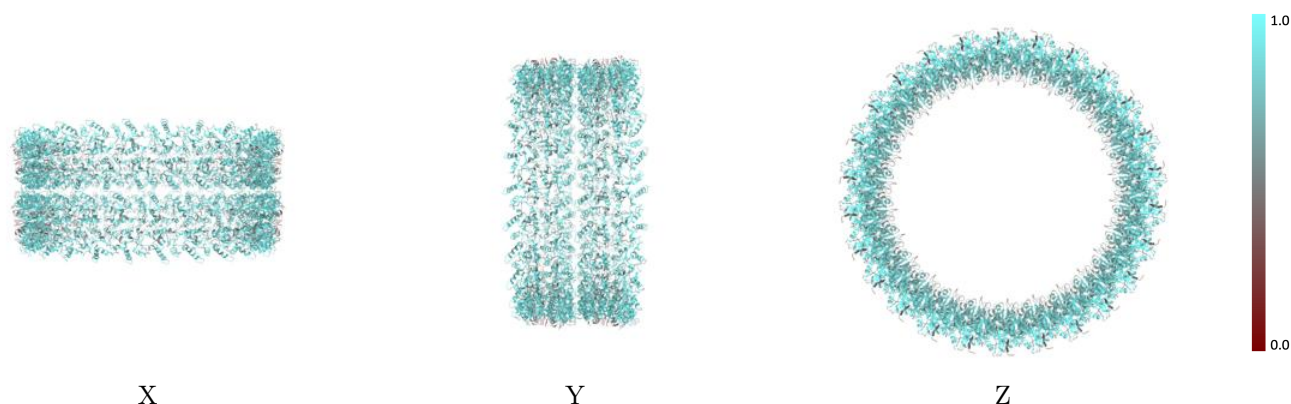
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



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

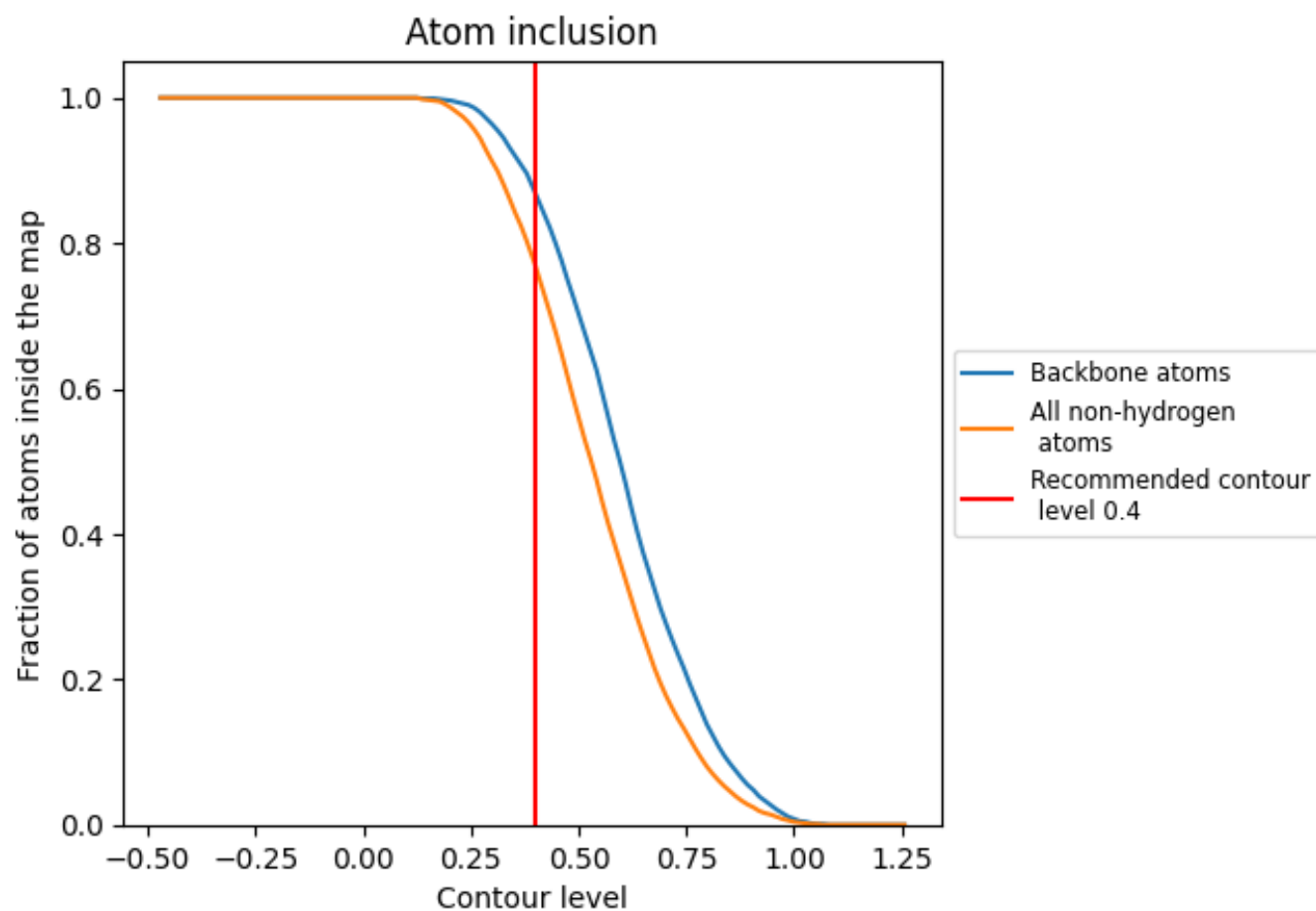
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.4).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 77% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7690	 0.5170
A	 0.7740	 0.5130
AA	 0.7690	 0.5190
AB	 0.7780	 0.5140
AC	 0.7620	 0.5190
B	 0.7740	 0.5140
BA	 0.7670	 0.5190
BB	 0.7810	 0.5130
BC	 0.7610	 0.5190
C	 0.7730	 0.5140
CA	 0.7680	 0.5210
CB	 0.7730	 0.5130
CC	 0.7520	 0.5200
D	 0.7680	 0.5130
DA	 0.7680	 0.5210
DB	 0.7760	 0.5140
DC	 0.7510	 0.5200
E	 0.7740	 0.5150
EA	 0.7670	 0.5210
EB	 0.7750	 0.5150
EC	 0.7610	 0.5190
F	 0.7760	 0.5160
FA	 0.7710	 0.5200
FB	 0.7800	 0.5160
FC	 0.7580	 0.5200
G	 0.7850	 0.5170
GA	 0.7670	 0.5210
GB	 0.7800	 0.5120
GC	 0.7520	 0.5200
H	 0.7800	 0.5130
HA	 0.7620	 0.5210
HB	 0.7810	 0.5140
HC	 0.7580	 0.5210
I	 0.7800	 0.5170
IA	 0.7700	 0.5220



























































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Chain	Atom inclusion	Q-score
IB	 0.7800	 0.5140
IC	 0.7520	 0.5210
J	 0.7730	 0.5160
JA	 0.7690	 0.5200
JB	 0.7740	 0.5140
JC	 0.7540	 0.5200
K	 0.7700	 0.5140
KA	 0.7680	 0.5190
KB	 0.7670	 0.5120
KC	 0.7570	 0.5200
L	 0.7660	 0.5150
LA	 0.7700	 0.5190
LB	 0.7790	 0.5140
LC	 0.7540	 0.5180
M	 0.7820	 0.5140
MA	 0.7690	 0.5200
MB	 0.7840	 0.5140
MC	 0.7590	 0.5200
N	 0.7710	 0.5130
NA	 0.7700	 0.5200
NB	 0.7760	 0.5130
NC	 0.7570	 0.5200
O	 0.7780	 0.5140
OA	 0.7670	 0.5210
OB	 0.7740	 0.5110
OC	 0.7560	 0.5200
P	 0.7720	 0.5130
PA	 0.7680	 0.5210
PB	 0.7750	 0.5120
PC	 0.7510	 0.5190
Q	 0.7740	 0.5120
QA	 0.7660	 0.5180
QB	 0.7750	 0.5120
QC	 0.7520	 0.5170
R	 0.7700	 0.5150
RA	 0.7620	 0.5170
RB	 0.7770	 0.5140
RC	 0.7570	 0.5170
S	 0.7750	 0.5150
SA	 0.7640	 0.5190
SB	 0.7840	 0.5140
SC	 0.7580	 0.5190

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Chain	Atom inclusion	Q-score
T	 0.7780	 0.5130
TA	 0.7640	 0.5180
TB	 0.7820	 0.5110
TC	 0.7540	 0.5200
U	 0.7810	 0.5110
UA	 0.7700	 0.5200
UB	 0.7810	 0.5130
UC	 0.7580	 0.5210
V	 0.7770	 0.5160
VA	 0.7720	 0.5210
VB	 0.7800	 0.5150
VC	 0.7570	 0.5190
W	 0.7740	 0.5170
WA	 0.7650	 0.5190
WB	 0.7760	 0.5170
WC	 0.7550	 0.5190
X	 0.7670	 0.5160
XA	 0.7660	 0.5210
XB	 0.7750	 0.5140
XC	 0.7490	 0.5190
Y	 0.7630	 0.5140
YA	 0.7710	 0.5190
YB	 0.7790	 0.5130
YC	 0.7500	 0.5200
Z	 0.7760	 0.5130
ZA	 0.7720	 0.5210
ZB	 0.7850	 0.5130
ZC	 0.7610	 0.5200