



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:50 AM UTC

PDB ID : 6OWG / pdb_00006owg
EMDB ID : EMD-20207
Title : Structure of a synthetic beta-carboxysome shell, T=4
Authors : Sutter, M.; Laughlin, T.G.; Davies, K.M.; Kerfeld, C.A.
Deposited on : 2019-05-09
Resolution : 2.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

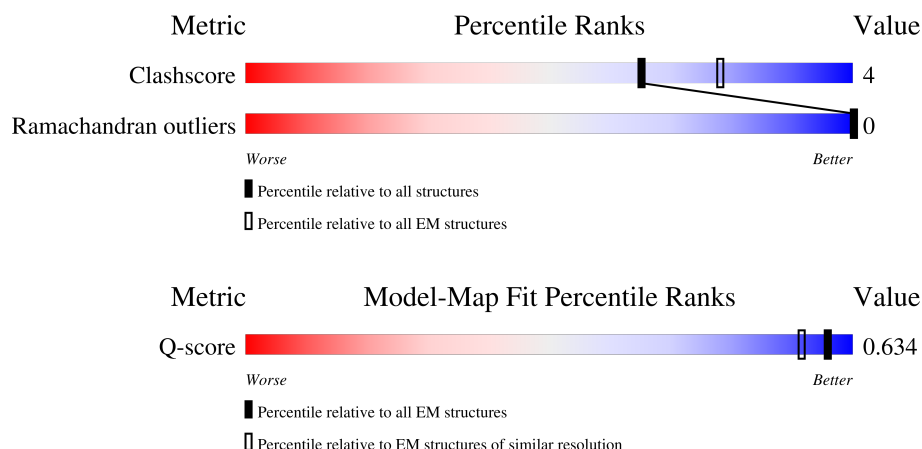
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.60 Å.

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



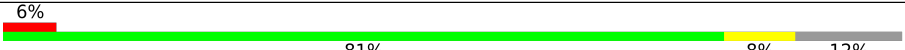
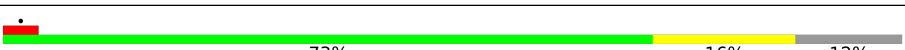
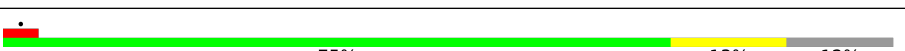
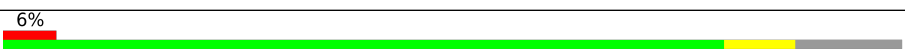
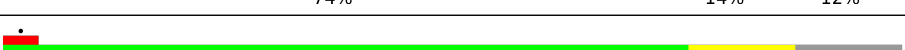
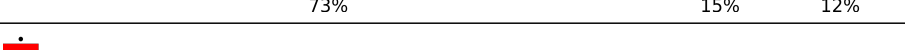
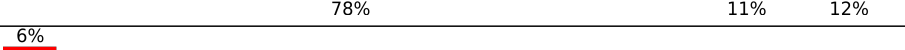
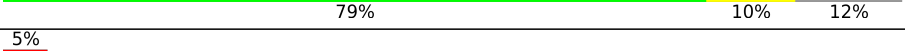
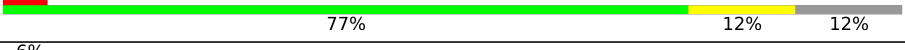
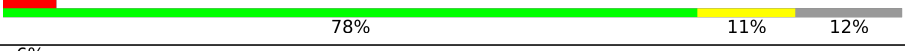
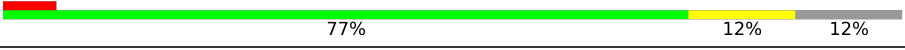
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	8728 (2.10 - 3.10)

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

Mol	Chain	Length	Quality of chain
1	0	113	
1	2	113	
1	3	113	
1	4	113	
1	6	113	

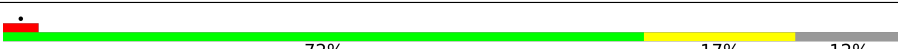
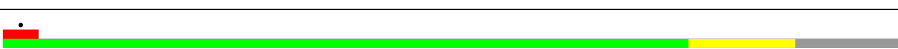
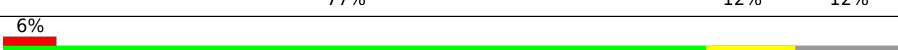
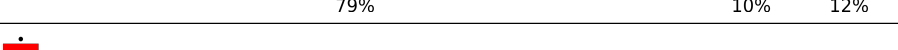
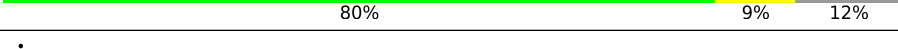
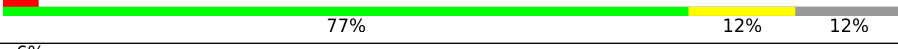
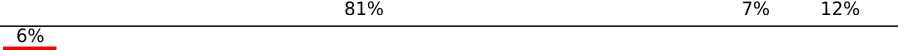
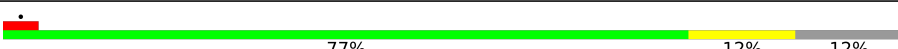
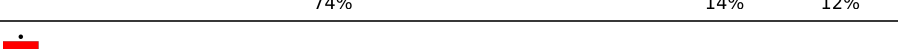
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Mol	Chain	Length	Quality of chain
1	7	113	
1	8	113	
1	A	113	
1	A0	113	
1	A1	113	
1	A2	113	
1	A4	113	
1	A5	113	
1	A6	113	
1	A8	113	
1	A9	113	
1	AA	113	
1	AC	113	
1	AD	113	
1	AE	113	
1	AG	113	
1	AH	113	
1	AI	113	
1	AK	113	
1	AL	113	
1	AM	113	
1	AO	113	
1	AP	113	
1	AQ	113	
1	AS	113	

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Mol	Chain	Length	Quality of chain
1	AT	113	
1	AU	113	
1	AW	113	
1	AX	113	
1	AY	113	
1	B	113	
1	B0	113	
1	B1	113	
1	B2	113	
1	B4	113	
1	B5	113	
1	B6	113	
1	B8	113	
1	B9	113	
1	BA	113	
1	BC	113	
1	BD	113	
1	BE	113	
1	BG	113	
1	BH	113	
1	BI	113	
1	BK	113	
1	BL	113	
1	BM	113	
1	BO	113	

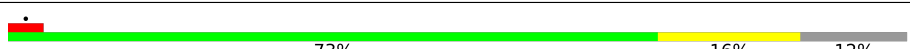
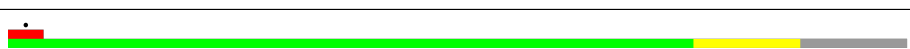
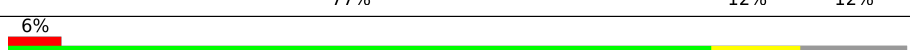
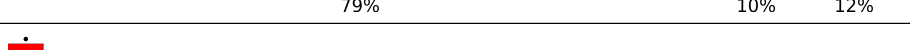
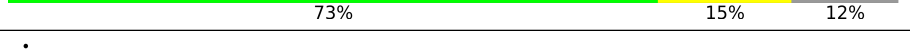
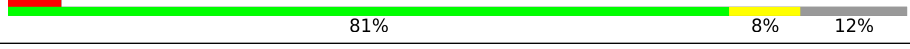
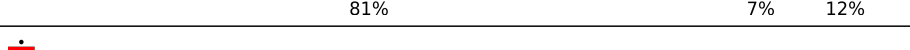
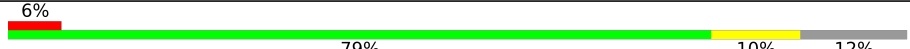
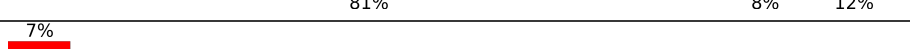
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Mol	Chain	Length	Quality of chain
1	BP	113	
1	BQ	113	
1	BS	113	
1	BT	113	
1	BU	113	
1	BW	113	
1	BX	113	
1	BY	113	
1	C	113	
1	C0	113	
1	C1	113	
1	C2	113	
1	C4	113	
1	C5	113	
1	C6	113	
1	C8	113	
1	C9	113	
1	CA	113	
1	CC	113	
1	CD	113	
1	CE	113	
1	CG	113	
1	CH	113	
1	CI	113	
1	CK	113	

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Mol	Chain	Length	Quality of chain
1	CL	113	
1	CM	113	
1	CO	113	
1	CP	113	
1	CQ	113	
1	CS	113	
1	CT	113	
1	CU	113	
1	CW	113	
1	CX	113	
1	CY	113	
1	D0	113	
1	D1	113	
1	D2	113	
1	D4	113	
1	D5	113	
1	D6	113	
1	D8	113	
1	D9	113	
1	DA	113	
1	DC	113	
1	DD	113	
1	DE	113	
1	DG	113	
1	DH	113	

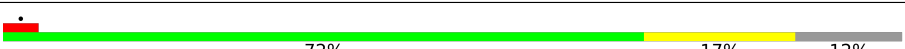
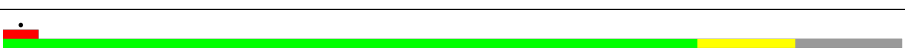
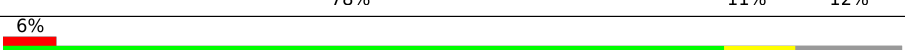
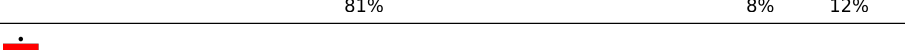
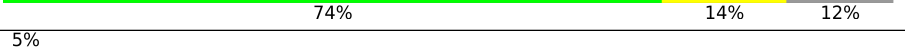
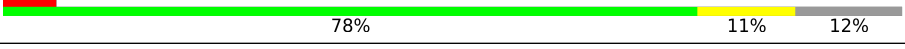
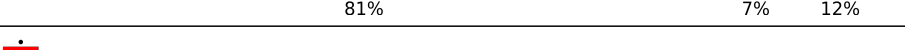
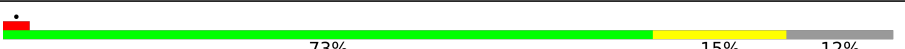
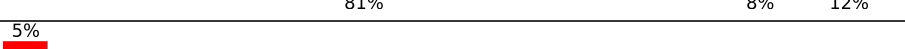
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Mol	Chain	Length	Quality of chain
1	DI	113	
1	DK	113	
1	DL	113	
1	DM	113	
1	DO	113	
1	DP	113	
1	DQ	113	
1	DS	113	
1	DT	113	
1	DU	113	
1	DW	113	
1	DX	113	
1	DY	113	
1	E	113	
1	E0	113	
1	E1	113	
1	E2	113	
1	E4	113	
1	E5	113	
1	E6	113	
1	EA	113	
1	EC	113	
1	ED	113	
1	EE	113	
1	EG	113	

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Mol	Chain	Length	Quality of chain
1	EH	113	
1	EI	113	
1	EK	113	
1	EL	113	
1	EM	113	
1	EO	113	
1	EP	113	
1	EQ	113	
1	ES	113	
1	ET	113	
1	EU	113	
1	EW	113	
1	EX	113	
1	EY	113	
1	F	113	
1	G	113	
1	I	113	
1	J	113	
1	K	113	
1	M	113	
1	N	113	
1	O	113	
1	Q	113	
1	R	113	
1	S	113	

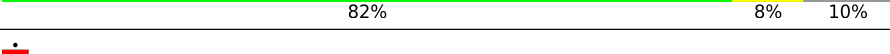
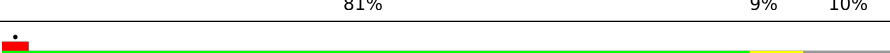
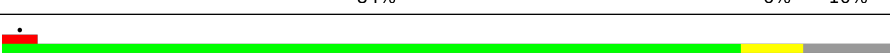
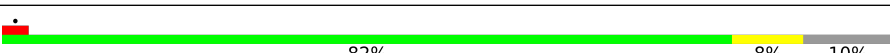
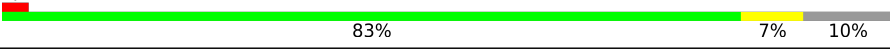
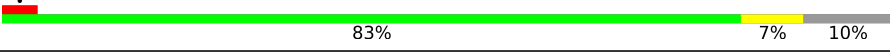
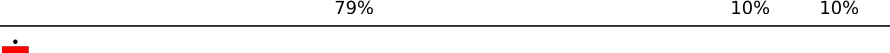
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Mol	Chain	Length	Quality of chain
1	U	113	
1	V	113	
1	W	113	
1	Y	113	
1	Z	113	
1	a	113	
1	b	113	
1	c	113	
1	e	113	
1	f	113	
1	g	113	
1	i	113	
1	j	113	
1	k	113	
1	m	113	
1	n	113	
1	o	113	
1	q	113	
1	r	113	
1	s	113	
1	u	113	
1	v	113	
1	w	113	
1	y	113	
1	z	113	

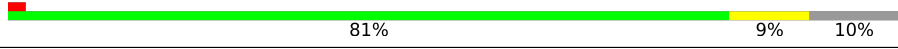
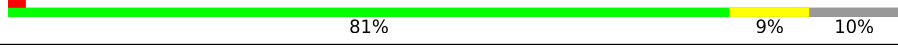
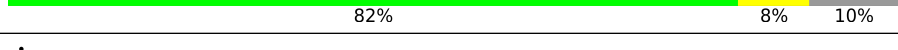
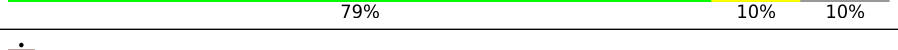
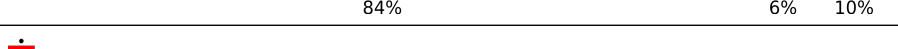
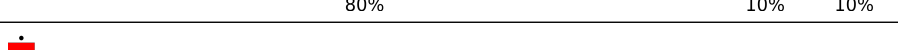
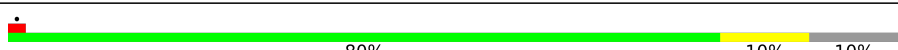
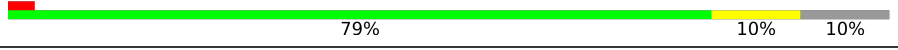
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Mol	Chain	Length	Quality of chain
2	1	105	 81%9%10%
2	5	105	 81%9%10%
2	9	105	 81%9%10%
2	A3	105	 81%9%10%
2	A7	105	 82%8%10%
2	AB	105	 81%9%10%
2	AF	105	 84%6%10%
2	AJ	105	 83%7%10%
2	AN	105	 82%8%10%
2	AR	105	 83%7%10%
2	AV	105	 80%10%10%
2	AZ	105	 83%7%10%
2	B3	105	 83%7%10%
2	B7	105	 83%7%10%
2	BB	105	 83%7%10%
2	BF	105	 80%10%10%
2	BJ	105	 82%8%10%
2	BN	105	 83%7%10%
2	BR	105	 81%9%10%
2	BV	105	 85%5%10%
2	BZ	105	 83%7%10%
2	C3	105	 83%7%10%
2	C7	105	 79%10%10%
2	CB	105	 79%10%10%
2	CF	105	 82%8%10%

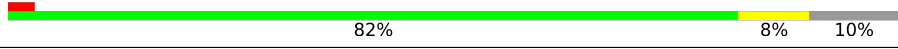
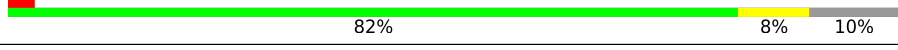
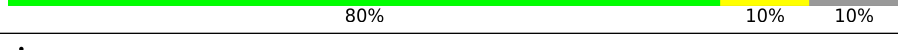
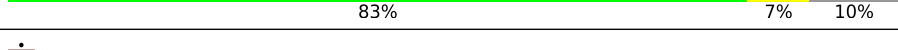
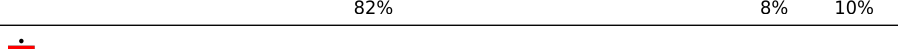
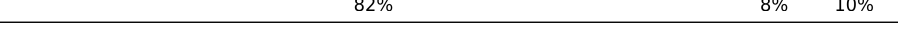
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Mol	Chain	Length	Quality of chain
2	CJ	105	 81%9%10%
2	CN	105	 81%9%10%
2	CR	105	 81%9%10%
2	CV	105	 81%9%10%
2	CZ	105	 83%7%10%
2	D	105	 83%7%10%
2	D3	105	 82%8%10%
2	D7	105	 79%10%10%
2	DB	105	 84%6%10%
2	DF	105	 80%10%10%
2	DJ	105	 81%9%10%
2	DN	105	 81%9%10%
2	DR	105	 83%7%10%
2	DV	105	 83%7%10%
2	DZ	105	 80%10%10%
2	E3	105	 80%10%10%
2	E7	105	 83%7%10%
2	EB	105	 84%6%10%
2	EF	105	 80%10%10%
2	EJ	105	 81%9%10%
2	EN	105	 81%9%10%
2	ER	105	 79%10%10%
2	EV	105	 83%7%10%
2	EZ	105	 83%7%10%
2	H	105	 84%6%10%

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Mol	Chain	Length	Quality of chain
2	L	105	 82%8%10%
2	P	105	 80%10%10%
2	T	105	 82%8%10%
2	X	105	 82%8%10%
2	d	105	 80%10%10%
2	h	105	 83%7%10%
2	l	105	 80%10%10%
2	p	105	 83%7%10%
2	t	105	 82%8%10%
2	x	105	 82%8%10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 178080 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 Microcompartments protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	B	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	C	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	E	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	F	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	G	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	I	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	J	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	K	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	M	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	N	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	O	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	Q	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	R	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	S	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	U	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	V	100	Total	C	N	O	S	0	0
			752	473	133	144	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	W	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	Y	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	Z	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	0	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	2	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	3	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	4	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	6	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	7	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	8	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	a	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	b	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	c	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	e	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	f	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	g	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	i	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	j	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	k	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	m	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	n	100	Total 752	C 473	N 133	O 144	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	o	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	q	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	r	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	s	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	u	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	v	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	w	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	y	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	z	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AA	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AC	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AD	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AE	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AG	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AH	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AI	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AK	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AL	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AM	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AO	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AP	100	Total 752	C 473	N 133	O 144	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AQ	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AS	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AT	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AU	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AW	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AX	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	AY	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	A0	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	A1	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	A2	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	A4	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	A5	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	A6	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	A8	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	A9	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BA	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BC	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BD	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BE	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BG	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BH	100	Total 752	C 473	N 133	O 144	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BI	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BK	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BL	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BM	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BO	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BP	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BQ	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BS	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BT	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BU	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BW	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BX	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	BY	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	B0	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	B1	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	B2	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	B4	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	B5	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	B6	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	B8	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	B9	100	Total 752	C 473	N 133	O 144	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CC	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CD	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CE	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CG	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CH	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CI	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CK	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CL	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CM	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CO	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CP	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CQ	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CS	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CT	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CU	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CW	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CX	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	CY	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	C0	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	C1	100	Total 752	C 473	N 133	O 144	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	C4	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	C5	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	C6	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	C8	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	C9	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DA	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DC	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DD	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DE	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DG	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DH	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DI	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DK	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DL	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DM	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DO	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DP	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DQ	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DS	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DT	100	Total 752	C 473	N 133	O 144	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DU	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DW	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DX	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	DY	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	D0	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	D1	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	D2	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	D4	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	D5	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	D6	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	D8	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	D9	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	EA	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	EC	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	ED	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	EE	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	EG	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	EH	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	EI	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	EK	100	Total 752	C 473	N 133	O 144	S 2	0	0
1	EL	100	Total 752	C 473	N 133	O 144	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	EM	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	EO	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	EP	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	EQ	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	ES	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	ET	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	EU	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	EW	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	EX	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	EY	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	E0	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	E1	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	E2	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	E4	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	E5	100	Total	C	N	O	S	0	0
			752	473	133	144	2		
1	E6	100	Total	C	N	O	S	0	0
			752	473	133	144	2		

- Molecule 2 is a protein called Ethanolamine utilization protein EutN/carboxysome structural protein Ccml.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	H	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	L	94	Total	C	N	O	S	0	0
			712	450	126	131	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	T	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	X	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	1	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	5	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	9	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	d	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	h	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	l	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	p	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	t	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	x	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	AB	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	AF	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	AJ	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	AN	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	AR	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	AV	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	AZ	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	A3	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	A7	94	Total 712	C 450	N 126	O 131	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	BB	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	BF	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	BJ	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	BN	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	BR	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	BV	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	BZ	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	B3	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	B7	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	CB	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	CF	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	CJ	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	CN	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	CR	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	CV	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	CZ	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	C3	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	C7	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	DB	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	DF	94	Total 712	C 450	N 126	O 131	S 5	0	0
2	DJ	94	Total 712	C 450	N 126	O 131	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	DN	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	DR	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	DV	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	DZ	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	D3	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	D7	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	EB	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	EF	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	EJ	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	EN	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	ER	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	EV	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	EZ	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	E3	94	Total	C	N	O	S	0	0
			712	450	126	131	5		
2	E7	94	Total	C	N	O	S	0	0
			712	450	126	131	5		

There are 600 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	96	GLY	-	expression tag	UNP K9YFK1
D	97	SER	-	expression tag	UNP K9YFK1
D	98	TRP	-	expression tag	UNP K9YFK1
D	99	SER	-	expression tag	UNP K9YFK1
D	100	HIS	-	expression tag	UNP K9YFK1
D	101	PRO	-	expression tag	UNP K9YFK1
D	102	GLN	-	expression tag	UNP K9YFK1
D	103	PHE	-	expression tag	UNP K9YFK1
D	104	GLU	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	105	LYS	-	expression tag	UNP K9YFK1
H	96	GLY	-	expression tag	UNP K9YFK1
H	97	SER	-	expression tag	UNP K9YFK1
H	98	TRP	-	expression tag	UNP K9YFK1
H	99	SER	-	expression tag	UNP K9YFK1
H	100	HIS	-	expression tag	UNP K9YFK1
H	101	PRO	-	expression tag	UNP K9YFK1
H	102	GLN	-	expression tag	UNP K9YFK1
H	103	PHE	-	expression tag	UNP K9YFK1
H	104	GLU	-	expression tag	UNP K9YFK1
H	105	LYS	-	expression tag	UNP K9YFK1
L	96	GLY	-	expression tag	UNP K9YFK1
L	97	SER	-	expression tag	UNP K9YFK1
L	98	TRP	-	expression tag	UNP K9YFK1
L	99	SER	-	expression tag	UNP K9YFK1
L	100	HIS	-	expression tag	UNP K9YFK1
L	101	PRO	-	expression tag	UNP K9YFK1
L	102	GLN	-	expression tag	UNP K9YFK1
L	103	PHE	-	expression tag	UNP K9YFK1
L	104	GLU	-	expression tag	UNP K9YFK1
L	105	LYS	-	expression tag	UNP K9YFK1
P	96	GLY	-	expression tag	UNP K9YFK1
P	97	SER	-	expression tag	UNP K9YFK1
P	98	TRP	-	expression tag	UNP K9YFK1
P	99	SER	-	expression tag	UNP K9YFK1
P	100	HIS	-	expression tag	UNP K9YFK1
P	101	PRO	-	expression tag	UNP K9YFK1
P	102	GLN	-	expression tag	UNP K9YFK1
P	103	PHE	-	expression tag	UNP K9YFK1
P	104	GLU	-	expression tag	UNP K9YFK1
P	105	LYS	-	expression tag	UNP K9YFK1
T	96	GLY	-	expression tag	UNP K9YFK1
T	97	SER	-	expression tag	UNP K9YFK1
T	98	TRP	-	expression tag	UNP K9YFK1
T	99	SER	-	expression tag	UNP K9YFK1
T	100	HIS	-	expression tag	UNP K9YFK1
T	101	PRO	-	expression tag	UNP K9YFK1
T	102	GLN	-	expression tag	UNP K9YFK1
T	103	PHE	-	expression tag	UNP K9YFK1
T	104	GLU	-	expression tag	UNP K9YFK1
T	105	LYS	-	expression tag	UNP K9YFK1
X	96	GLY	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
X	97	SER	-	expression tag	UNP K9YFK1
X	98	TRP	-	expression tag	UNP K9YFK1
X	99	SER	-	expression tag	UNP K9YFK1
X	100	HIS	-	expression tag	UNP K9YFK1
X	101	PRO	-	expression tag	UNP K9YFK1
X	102	GLN	-	expression tag	UNP K9YFK1
X	103	PHE	-	expression tag	UNP K9YFK1
X	104	GLU	-	expression tag	UNP K9YFK1
X	105	LYS	-	expression tag	UNP K9YFK1
1	96	GLY	-	expression tag	UNP K9YFK1
1	97	SER	-	expression tag	UNP K9YFK1
1	98	TRP	-	expression tag	UNP K9YFK1
1	99	SER	-	expression tag	UNP K9YFK1
1	100	HIS	-	expression tag	UNP K9YFK1
1	101	PRO	-	expression tag	UNP K9YFK1
1	102	GLN	-	expression tag	UNP K9YFK1
1	103	PHE	-	expression tag	UNP K9YFK1
1	104	GLU	-	expression tag	UNP K9YFK1
1	105	LYS	-	expression tag	UNP K9YFK1
5	96	GLY	-	expression tag	UNP K9YFK1
5	97	SER	-	expression tag	UNP K9YFK1
5	98	TRP	-	expression tag	UNP K9YFK1
5	99	SER	-	expression tag	UNP K9YFK1
5	100	HIS	-	expression tag	UNP K9YFK1
5	101	PRO	-	expression tag	UNP K9YFK1
5	102	GLN	-	expression tag	UNP K9YFK1
5	103	PHE	-	expression tag	UNP K9YFK1
5	104	GLU	-	expression tag	UNP K9YFK1
5	105	LYS	-	expression tag	UNP K9YFK1
9	96	GLY	-	expression tag	UNP K9YFK1
9	97	SER	-	expression tag	UNP K9YFK1
9	98	TRP	-	expression tag	UNP K9YFK1
9	99	SER	-	expression tag	UNP K9YFK1
9	100	HIS	-	expression tag	UNP K9YFK1
9	101	PRO	-	expression tag	UNP K9YFK1
9	102	GLN	-	expression tag	UNP K9YFK1
9	103	PHE	-	expression tag	UNP K9YFK1
9	104	GLU	-	expression tag	UNP K9YFK1
9	105	LYS	-	expression tag	UNP K9YFK1
d	96	GLY	-	expression tag	UNP K9YFK1
d	97	SER	-	expression tag	UNP K9YFK1
d	98	TRP	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
d	99	SER	-	expression tag	UNP K9YFK1
d	100	HIS	-	expression tag	UNP K9YFK1
d	101	PRO	-	expression tag	UNP K9YFK1
d	102	GLN	-	expression tag	UNP K9YFK1
d	103	PHE	-	expression tag	UNP K9YFK1
d	104	GLU	-	expression tag	UNP K9YFK1
d	105	LYS	-	expression tag	UNP K9YFK1
h	96	GLY	-	expression tag	UNP K9YFK1
h	97	SER	-	expression tag	UNP K9YFK1
h	98	TRP	-	expression tag	UNP K9YFK1
h	99	SER	-	expression tag	UNP K9YFK1
h	100	HIS	-	expression tag	UNP K9YFK1
h	101	PRO	-	expression tag	UNP K9YFK1
h	102	GLN	-	expression tag	UNP K9YFK1
h	103	PHE	-	expression tag	UNP K9YFK1
h	104	GLU	-	expression tag	UNP K9YFK1
h	105	LYS	-	expression tag	UNP K9YFK1
l	96	GLY	-	expression tag	UNP K9YFK1
l	97	SER	-	expression tag	UNP K9YFK1
l	98	TRP	-	expression tag	UNP K9YFK1
l	99	SER	-	expression tag	UNP K9YFK1
l	100	HIS	-	expression tag	UNP K9YFK1
l	101	PRO	-	expression tag	UNP K9YFK1
l	102	GLN	-	expression tag	UNP K9YFK1
l	103	PHE	-	expression tag	UNP K9YFK1
l	104	GLU	-	expression tag	UNP K9YFK1
l	105	LYS	-	expression tag	UNP K9YFK1
p	96	GLY	-	expression tag	UNP K9YFK1
p	97	SER	-	expression tag	UNP K9YFK1
p	98	TRP	-	expression tag	UNP K9YFK1
p	99	SER	-	expression tag	UNP K9YFK1
p	100	HIS	-	expression tag	UNP K9YFK1
p	101	PRO	-	expression tag	UNP K9YFK1
p	102	GLN	-	expression tag	UNP K9YFK1
p	103	PHE	-	expression tag	UNP K9YFK1
p	104	GLU	-	expression tag	UNP K9YFK1
p	105	LYS	-	expression tag	UNP K9YFK1
t	96	GLY	-	expression tag	UNP K9YFK1
t	97	SER	-	expression tag	UNP K9YFK1
t	98	TRP	-	expression tag	UNP K9YFK1
t	99	SER	-	expression tag	UNP K9YFK1
t	100	HIS	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
t	101	PRO	-	expression tag	UNP K9YFK1
t	102	GLN	-	expression tag	UNP K9YFK1
t	103	PHE	-	expression tag	UNP K9YFK1
t	104	GLU	-	expression tag	UNP K9YFK1
t	105	LYS	-	expression tag	UNP K9YFK1
x	96	GLY	-	expression tag	UNP K9YFK1
x	97	SER	-	expression tag	UNP K9YFK1
x	98	TRP	-	expression tag	UNP K9YFK1
x	99	SER	-	expression tag	UNP K9YFK1
x	100	HIS	-	expression tag	UNP K9YFK1
x	101	PRO	-	expression tag	UNP K9YFK1
x	102	GLN	-	expression tag	UNP K9YFK1
x	103	PHE	-	expression tag	UNP K9YFK1
x	104	GLU	-	expression tag	UNP K9YFK1
x	105	LYS	-	expression tag	UNP K9YFK1
AB	96	GLY	-	expression tag	UNP K9YFK1
AB	97	SER	-	expression tag	UNP K9YFK1
AB	98	TRP	-	expression tag	UNP K9YFK1
AB	99	SER	-	expression tag	UNP K9YFK1
AB	100	HIS	-	expression tag	UNP K9YFK1
AB	101	PRO	-	expression tag	UNP K9YFK1
AB	102	GLN	-	expression tag	UNP K9YFK1
AB	103	PHE	-	expression tag	UNP K9YFK1
AB	104	GLU	-	expression tag	UNP K9YFK1
AB	105	LYS	-	expression tag	UNP K9YFK1
AF	96	GLY	-	expression tag	UNP K9YFK1
AF	97	SER	-	expression tag	UNP K9YFK1
AF	98	TRP	-	expression tag	UNP K9YFK1
AF	99	SER	-	expression tag	UNP K9YFK1
AF	100	HIS	-	expression tag	UNP K9YFK1
AF	101	PRO	-	expression tag	UNP K9YFK1
AF	102	GLN	-	expression tag	UNP K9YFK1
AF	103	PHE	-	expression tag	UNP K9YFK1
AF	104	GLU	-	expression tag	UNP K9YFK1
AF	105	LYS	-	expression tag	UNP K9YFK1
AJ	96	GLY	-	expression tag	UNP K9YFK1
AJ	97	SER	-	expression tag	UNP K9YFK1
AJ	98	TRP	-	expression tag	UNP K9YFK1
AJ	99	SER	-	expression tag	UNP K9YFK1
AJ	100	HIS	-	expression tag	UNP K9YFK1
AJ	101	PRO	-	expression tag	UNP K9YFK1
AJ	102	GLN	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
AJ	103	PHE	-	expression tag	UNP K9YFK1
AJ	104	GLU	-	expression tag	UNP K9YFK1
AJ	105	LYS	-	expression tag	UNP K9YFK1
AN	96	GLY	-	expression tag	UNP K9YFK1
AN	97	SER	-	expression tag	UNP K9YFK1
AN	98	TRP	-	expression tag	UNP K9YFK1
AN	99	SER	-	expression tag	UNP K9YFK1
AN	100	HIS	-	expression tag	UNP K9YFK1
AN	101	PRO	-	expression tag	UNP K9YFK1
AN	102	GLN	-	expression tag	UNP K9YFK1
AN	103	PHE	-	expression tag	UNP K9YFK1
AN	104	GLU	-	expression tag	UNP K9YFK1
AN	105	LYS	-	expression tag	UNP K9YFK1
AR	96	GLY	-	expression tag	UNP K9YFK1
AR	97	SER	-	expression tag	UNP K9YFK1
AR	98	TRP	-	expression tag	UNP K9YFK1
AR	99	SER	-	expression tag	UNP K9YFK1
AR	100	HIS	-	expression tag	UNP K9YFK1
AR	101	PRO	-	expression tag	UNP K9YFK1
AR	102	GLN	-	expression tag	UNP K9YFK1
AR	103	PHE	-	expression tag	UNP K9YFK1
AR	104	GLU	-	expression tag	UNP K9YFK1
AR	105	LYS	-	expression tag	UNP K9YFK1
AV	96	GLY	-	expression tag	UNP K9YFK1
AV	97	SER	-	expression tag	UNP K9YFK1
AV	98	TRP	-	expression tag	UNP K9YFK1
AV	99	SER	-	expression tag	UNP K9YFK1
AV	100	HIS	-	expression tag	UNP K9YFK1
AV	101	PRO	-	expression tag	UNP K9YFK1
AV	102	GLN	-	expression tag	UNP K9YFK1
AV	103	PHE	-	expression tag	UNP K9YFK1
AV	104	GLU	-	expression tag	UNP K9YFK1
AV	105	LYS	-	expression tag	UNP K9YFK1
AZ	96	GLY	-	expression tag	UNP K9YFK1
AZ	97	SER	-	expression tag	UNP K9YFK1
AZ	98	TRP	-	expression tag	UNP K9YFK1
AZ	99	SER	-	expression tag	UNP K9YFK1
AZ	100	HIS	-	expression tag	UNP K9YFK1
AZ	101	PRO	-	expression tag	UNP K9YFK1
AZ	102	GLN	-	expression tag	UNP K9YFK1
AZ	103	PHE	-	expression tag	UNP K9YFK1
AZ	104	GLU	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
AZ	105	LYS	-	expression tag	UNP K9YFK1
A3	96	GLY	-	expression tag	UNP K9YFK1
A3	97	SER	-	expression tag	UNP K9YFK1
A3	98	TRP	-	expression tag	UNP K9YFK1
A3	99	SER	-	expression tag	UNP K9YFK1
A3	100	HIS	-	expression tag	UNP K9YFK1
A3	101	PRO	-	expression tag	UNP K9YFK1
A3	102	GLN	-	expression tag	UNP K9YFK1
A3	103	PHE	-	expression tag	UNP K9YFK1
A3	104	GLU	-	expression tag	UNP K9YFK1
A3	105	LYS	-	expression tag	UNP K9YFK1
A7	96	GLY	-	expression tag	UNP K9YFK1
A7	97	SER	-	expression tag	UNP K9YFK1
A7	98	TRP	-	expression tag	UNP K9YFK1
A7	99	SER	-	expression tag	UNP K9YFK1
A7	100	HIS	-	expression tag	UNP K9YFK1
A7	101	PRO	-	expression tag	UNP K9YFK1
A7	102	GLN	-	expression tag	UNP K9YFK1
A7	103	PHE	-	expression tag	UNP K9YFK1
A7	104	GLU	-	expression tag	UNP K9YFK1
A7	105	LYS	-	expression tag	UNP K9YFK1
BB	96	GLY	-	expression tag	UNP K9YFK1
BB	97	SER	-	expression tag	UNP K9YFK1
BB	98	TRP	-	expression tag	UNP K9YFK1
BB	99	SER	-	expression tag	UNP K9YFK1
BB	100	HIS	-	expression tag	UNP K9YFK1
BB	101	PRO	-	expression tag	UNP K9YFK1
BB	102	GLN	-	expression tag	UNP K9YFK1
BB	103	PHE	-	expression tag	UNP K9YFK1
BB	104	GLU	-	expression tag	UNP K9YFK1
BB	105	LYS	-	expression tag	UNP K9YFK1
BF	96	GLY	-	expression tag	UNP K9YFK1
BF	97	SER	-	expression tag	UNP K9YFK1
BF	98	TRP	-	expression tag	UNP K9YFK1
BF	99	SER	-	expression tag	UNP K9YFK1
BF	100	HIS	-	expression tag	UNP K9YFK1
BF	101	PRO	-	expression tag	UNP K9YFK1
BF	102	GLN	-	expression tag	UNP K9YFK1
BF	103	PHE	-	expression tag	UNP K9YFK1
BF	104	GLU	-	expression tag	UNP K9YFK1
BF	105	LYS	-	expression tag	UNP K9YFK1
BJ	96	GLY	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
BJ	97	SER	-	expression tag	UNP K9YFK1
BJ	98	TRP	-	expression tag	UNP K9YFK1
BJ	99	SER	-	expression tag	UNP K9YFK1
BJ	100	HIS	-	expression tag	UNP K9YFK1
BJ	101	PRO	-	expression tag	UNP K9YFK1
BJ	102	GLN	-	expression tag	UNP K9YFK1
BJ	103	PHE	-	expression tag	UNP K9YFK1
BJ	104	GLU	-	expression tag	UNP K9YFK1
BJ	105	LYS	-	expression tag	UNP K9YFK1
BN	96	GLY	-	expression tag	UNP K9YFK1
BN	97	SER	-	expression tag	UNP K9YFK1
BN	98	TRP	-	expression tag	UNP K9YFK1
BN	99	SER	-	expression tag	UNP K9YFK1
BN	100	HIS	-	expression tag	UNP K9YFK1
BN	101	PRO	-	expression tag	UNP K9YFK1
BN	102	GLN	-	expression tag	UNP K9YFK1
BN	103	PHE	-	expression tag	UNP K9YFK1
BN	104	GLU	-	expression tag	UNP K9YFK1
BN	105	LYS	-	expression tag	UNP K9YFK1
BR	96	GLY	-	expression tag	UNP K9YFK1
BR	97	SER	-	expression tag	UNP K9YFK1
BR	98	TRP	-	expression tag	UNP K9YFK1
BR	99	SER	-	expression tag	UNP K9YFK1
BR	100	HIS	-	expression tag	UNP K9YFK1
BR	101	PRO	-	expression tag	UNP K9YFK1
BR	102	GLN	-	expression tag	UNP K9YFK1
BR	103	PHE	-	expression tag	UNP K9YFK1
BR	104	GLU	-	expression tag	UNP K9YFK1
BR	105	LYS	-	expression tag	UNP K9YFK1
BV	96	GLY	-	expression tag	UNP K9YFK1
BV	97	SER	-	expression tag	UNP K9YFK1
BV	98	TRP	-	expression tag	UNP K9YFK1
BV	99	SER	-	expression tag	UNP K9YFK1
BV	100	HIS	-	expression tag	UNP K9YFK1
BV	101	PRO	-	expression tag	UNP K9YFK1
BV	102	GLN	-	expression tag	UNP K9YFK1
BV	103	PHE	-	expression tag	UNP K9YFK1
BV	104	GLU	-	expression tag	UNP K9YFK1
BV	105	LYS	-	expression tag	UNP K9YFK1
BZ	96	GLY	-	expression tag	UNP K9YFK1
BZ	97	SER	-	expression tag	UNP K9YFK1
BZ	98	TRP	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
BZ	99	SER	-	expression tag	UNP K9YFK1
BZ	100	HIS	-	expression tag	UNP K9YFK1
BZ	101	PRO	-	expression tag	UNP K9YFK1
BZ	102	GLN	-	expression tag	UNP K9YFK1
BZ	103	PHE	-	expression tag	UNP K9YFK1
BZ	104	GLU	-	expression tag	UNP K9YFK1
BZ	105	LYS	-	expression tag	UNP K9YFK1
B3	96	GLY	-	expression tag	UNP K9YFK1
B3	97	SER	-	expression tag	UNP K9YFK1
B3	98	TRP	-	expression tag	UNP K9YFK1
B3	99	SER	-	expression tag	UNP K9YFK1
B3	100	HIS	-	expression tag	UNP K9YFK1
B3	101	PRO	-	expression tag	UNP K9YFK1
B3	102	GLN	-	expression tag	UNP K9YFK1
B3	103	PHE	-	expression tag	UNP K9YFK1
B3	104	GLU	-	expression tag	UNP K9YFK1
B3	105	LYS	-	expression tag	UNP K9YFK1
B7	96	GLY	-	expression tag	UNP K9YFK1
B7	97	SER	-	expression tag	UNP K9YFK1
B7	98	TRP	-	expression tag	UNP K9YFK1
B7	99	SER	-	expression tag	UNP K9YFK1
B7	100	HIS	-	expression tag	UNP K9YFK1
B7	101	PRO	-	expression tag	UNP K9YFK1
B7	102	GLN	-	expression tag	UNP K9YFK1
B7	103	PHE	-	expression tag	UNP K9YFK1
B7	104	GLU	-	expression tag	UNP K9YFK1
B7	105	LYS	-	expression tag	UNP K9YFK1
CB	96	GLY	-	expression tag	UNP K9YFK1
CB	97	SER	-	expression tag	UNP K9YFK1
CB	98	TRP	-	expression tag	UNP K9YFK1
CB	99	SER	-	expression tag	UNP K9YFK1
CB	100	HIS	-	expression tag	UNP K9YFK1
CB	101	PRO	-	expression tag	UNP K9YFK1
CB	102	GLN	-	expression tag	UNP K9YFK1
CB	103	PHE	-	expression tag	UNP K9YFK1
CB	104	GLU	-	expression tag	UNP K9YFK1
CB	105	LYS	-	expression tag	UNP K9YFK1
CF	96	GLY	-	expression tag	UNP K9YFK1
CF	97	SER	-	expression tag	UNP K9YFK1
CF	98	TRP	-	expression tag	UNP K9YFK1
CF	99	SER	-	expression tag	UNP K9YFK1
CF	100	HIS	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
CF	101	PRO	-	expression tag	UNP K9YFK1
CF	102	GLN	-	expression tag	UNP K9YFK1
CF	103	PHE	-	expression tag	UNP K9YFK1
CF	104	GLU	-	expression tag	UNP K9YFK1
CF	105	LYS	-	expression tag	UNP K9YFK1
CJ	96	GLY	-	expression tag	UNP K9YFK1
CJ	97	SER	-	expression tag	UNP K9YFK1
CJ	98	TRP	-	expression tag	UNP K9YFK1
CJ	99	SER	-	expression tag	UNP K9YFK1
CJ	100	HIS	-	expression tag	UNP K9YFK1
CJ	101	PRO	-	expression tag	UNP K9YFK1
CJ	102	GLN	-	expression tag	UNP K9YFK1
CJ	103	PHE	-	expression tag	UNP K9YFK1
CJ	104	GLU	-	expression tag	UNP K9YFK1
CJ	105	LYS	-	expression tag	UNP K9YFK1
CN	96	GLY	-	expression tag	UNP K9YFK1
CN	97	SER	-	expression tag	UNP K9YFK1
CN	98	TRP	-	expression tag	UNP K9YFK1
CN	99	SER	-	expression tag	UNP K9YFK1
CN	100	HIS	-	expression tag	UNP K9YFK1
CN	101	PRO	-	expression tag	UNP K9YFK1
CN	102	GLN	-	expression tag	UNP K9YFK1
CN	103	PHE	-	expression tag	UNP K9YFK1
CN	104	GLU	-	expression tag	UNP K9YFK1
CN	105	LYS	-	expression tag	UNP K9YFK1
CR	96	GLY	-	expression tag	UNP K9YFK1
CR	97	SER	-	expression tag	UNP K9YFK1
CR	98	TRP	-	expression tag	UNP K9YFK1
CR	99	SER	-	expression tag	UNP K9YFK1
CR	100	HIS	-	expression tag	UNP K9YFK1
CR	101	PRO	-	expression tag	UNP K9YFK1
CR	102	GLN	-	expression tag	UNP K9YFK1
CR	103	PHE	-	expression tag	UNP K9YFK1
CR	104	GLU	-	expression tag	UNP K9YFK1
CR	105	LYS	-	expression tag	UNP K9YFK1
CV	96	GLY	-	expression tag	UNP K9YFK1
CV	97	SER	-	expression tag	UNP K9YFK1
CV	98	TRP	-	expression tag	UNP K9YFK1
CV	99	SER	-	expression tag	UNP K9YFK1
CV	100	HIS	-	expression tag	UNP K9YFK1
CV	101	PRO	-	expression tag	UNP K9YFK1
CV	102	GLN	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
CV	103	PHE	-	expression tag	UNP K9YFK1
CV	104	GLU	-	expression tag	UNP K9YFK1
CV	105	LYS	-	expression tag	UNP K9YFK1
CZ	96	GLY	-	expression tag	UNP K9YFK1
CZ	97	SER	-	expression tag	UNP K9YFK1
CZ	98	TRP	-	expression tag	UNP K9YFK1
CZ	99	SER	-	expression tag	UNP K9YFK1
CZ	100	HIS	-	expression tag	UNP K9YFK1
CZ	101	PRO	-	expression tag	UNP K9YFK1
CZ	102	GLN	-	expression tag	UNP K9YFK1
CZ	103	PHE	-	expression tag	UNP K9YFK1
CZ	104	GLU	-	expression tag	UNP K9YFK1
CZ	105	LYS	-	expression tag	UNP K9YFK1
C3	96	GLY	-	expression tag	UNP K9YFK1
C3	97	SER	-	expression tag	UNP K9YFK1
C3	98	TRP	-	expression tag	UNP K9YFK1
C3	99	SER	-	expression tag	UNP K9YFK1
C3	100	HIS	-	expression tag	UNP K9YFK1
C3	101	PRO	-	expression tag	UNP K9YFK1
C3	102	GLN	-	expression tag	UNP K9YFK1
C3	103	PHE	-	expression tag	UNP K9YFK1
C3	104	GLU	-	expression tag	UNP K9YFK1
C3	105	LYS	-	expression tag	UNP K9YFK1
C7	96	GLY	-	expression tag	UNP K9YFK1
C7	97	SER	-	expression tag	UNP K9YFK1
C7	98	TRP	-	expression tag	UNP K9YFK1
C7	99	SER	-	expression tag	UNP K9YFK1
C7	100	HIS	-	expression tag	UNP K9YFK1
C7	101	PRO	-	expression tag	UNP K9YFK1
C7	102	GLN	-	expression tag	UNP K9YFK1
C7	103	PHE	-	expression tag	UNP K9YFK1
C7	104	GLU	-	expression tag	UNP K9YFK1
C7	105	LYS	-	expression tag	UNP K9YFK1
DB	96	GLY	-	expression tag	UNP K9YFK1
DB	97	SER	-	expression tag	UNP K9YFK1
DB	98	TRP	-	expression tag	UNP K9YFK1
DB	99	SER	-	expression tag	UNP K9YFK1
DB	100	HIS	-	expression tag	UNP K9YFK1
DB	101	PRO	-	expression tag	UNP K9YFK1
DB	102	GLN	-	expression tag	UNP K9YFK1
DB	103	PHE	-	expression tag	UNP K9YFK1
DB	104	GLU	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
DB	105	LYS	-	expression tag	UNP K9YFK1
DF	96	GLY	-	expression tag	UNP K9YFK1
DF	97	SER	-	expression tag	UNP K9YFK1
DF	98	TRP	-	expression tag	UNP K9YFK1
DF	99	SER	-	expression tag	UNP K9YFK1
DF	100	HIS	-	expression tag	UNP K9YFK1
DF	101	PRO	-	expression tag	UNP K9YFK1
DF	102	GLN	-	expression tag	UNP K9YFK1
DF	103	PHE	-	expression tag	UNP K9YFK1
DF	104	GLU	-	expression tag	UNP K9YFK1
DF	105	LYS	-	expression tag	UNP K9YFK1
DJ	96	GLY	-	expression tag	UNP K9YFK1
DJ	97	SER	-	expression tag	UNP K9YFK1
DJ	98	TRP	-	expression tag	UNP K9YFK1
DJ	99	SER	-	expression tag	UNP K9YFK1
DJ	100	HIS	-	expression tag	UNP K9YFK1
DJ	101	PRO	-	expression tag	UNP K9YFK1
DJ	102	GLN	-	expression tag	UNP K9YFK1
DJ	103	PHE	-	expression tag	UNP K9YFK1
DJ	104	GLU	-	expression tag	UNP K9YFK1
DJ	105	LYS	-	expression tag	UNP K9YFK1
DN	96	GLY	-	expression tag	UNP K9YFK1
DN	97	SER	-	expression tag	UNP K9YFK1
DN	98	TRP	-	expression tag	UNP K9YFK1
DN	99	SER	-	expression tag	UNP K9YFK1
DN	100	HIS	-	expression tag	UNP K9YFK1
DN	101	PRO	-	expression tag	UNP K9YFK1
DN	102	GLN	-	expression tag	UNP K9YFK1
DN	103	PHE	-	expression tag	UNP K9YFK1
DN	104	GLU	-	expression tag	UNP K9YFK1
DN	105	LYS	-	expression tag	UNP K9YFK1
DR	96	GLY	-	expression tag	UNP K9YFK1
DR	97	SER	-	expression tag	UNP K9YFK1
DR	98	TRP	-	expression tag	UNP K9YFK1
DR	99	SER	-	expression tag	UNP K9YFK1
DR	100	HIS	-	expression tag	UNP K9YFK1
DR	101	PRO	-	expression tag	UNP K9YFK1
DR	102	GLN	-	expression tag	UNP K9YFK1
DR	103	PHE	-	expression tag	UNP K9YFK1
DR	104	GLU	-	expression tag	UNP K9YFK1
DR	105	LYS	-	expression tag	UNP K9YFK1
DV	96	GLY	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
DV	97	SER	-	expression tag	UNP K9YFK1
DV	98	TRP	-	expression tag	UNP K9YFK1
DV	99	SER	-	expression tag	UNP K9YFK1
DV	100	HIS	-	expression tag	UNP K9YFK1
DV	101	PRO	-	expression tag	UNP K9YFK1
DV	102	GLN	-	expression tag	UNP K9YFK1
DV	103	PHE	-	expression tag	UNP K9YFK1
DV	104	GLU	-	expression tag	UNP K9YFK1
DV	105	LYS	-	expression tag	UNP K9YFK1
DZ	96	GLY	-	expression tag	UNP K9YFK1
DZ	97	SER	-	expression tag	UNP K9YFK1
DZ	98	TRP	-	expression tag	UNP K9YFK1
DZ	99	SER	-	expression tag	UNP K9YFK1
DZ	100	HIS	-	expression tag	UNP K9YFK1
DZ	101	PRO	-	expression tag	UNP K9YFK1
DZ	102	GLN	-	expression tag	UNP K9YFK1
DZ	103	PHE	-	expression tag	UNP K9YFK1
DZ	104	GLU	-	expression tag	UNP K9YFK1
DZ	105	LYS	-	expression tag	UNP K9YFK1
D3	96	GLY	-	expression tag	UNP K9YFK1
D3	97	SER	-	expression tag	UNP K9YFK1
D3	98	TRP	-	expression tag	UNP K9YFK1
D3	99	SER	-	expression tag	UNP K9YFK1
D3	100	HIS	-	expression tag	UNP K9YFK1
D3	101	PRO	-	expression tag	UNP K9YFK1
D3	102	GLN	-	expression tag	UNP K9YFK1
D3	103	PHE	-	expression tag	UNP K9YFK1
D3	104	GLU	-	expression tag	UNP K9YFK1
D3	105	LYS	-	expression tag	UNP K9YFK1
D7	96	GLY	-	expression tag	UNP K9YFK1
D7	97	SER	-	expression tag	UNP K9YFK1
D7	98	TRP	-	expression tag	UNP K9YFK1
D7	99	SER	-	expression tag	UNP K9YFK1
D7	100	HIS	-	expression tag	UNP K9YFK1
D7	101	PRO	-	expression tag	UNP K9YFK1
D7	102	GLN	-	expression tag	UNP K9YFK1
D7	103	PHE	-	expression tag	UNP K9YFK1
D7	104	GLU	-	expression tag	UNP K9YFK1
D7	105	LYS	-	expression tag	UNP K9YFK1
EB	96	GLY	-	expression tag	UNP K9YFK1
EB	97	SER	-	expression tag	UNP K9YFK1
EB	98	TRP	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
EB	99	SER	-	expression tag	UNP K9YFK1
EB	100	HIS	-	expression tag	UNP K9YFK1
EB	101	PRO	-	expression tag	UNP K9YFK1
EB	102	GLN	-	expression tag	UNP K9YFK1
EB	103	PHE	-	expression tag	UNP K9YFK1
EB	104	GLU	-	expression tag	UNP K9YFK1
EB	105	LYS	-	expression tag	UNP K9YFK1
EF	96	GLY	-	expression tag	UNP K9YFK1
EF	97	SER	-	expression tag	UNP K9YFK1
EF	98	TRP	-	expression tag	UNP K9YFK1
EF	99	SER	-	expression tag	UNP K9YFK1
EF	100	HIS	-	expression tag	UNP K9YFK1
EF	101	PRO	-	expression tag	UNP K9YFK1
EF	102	GLN	-	expression tag	UNP K9YFK1
EF	103	PHE	-	expression tag	UNP K9YFK1
EF	104	GLU	-	expression tag	UNP K9YFK1
EF	105	LYS	-	expression tag	UNP K9YFK1
EJ	96	GLY	-	expression tag	UNP K9YFK1
EJ	97	SER	-	expression tag	UNP K9YFK1
EJ	98	TRP	-	expression tag	UNP K9YFK1
EJ	99	SER	-	expression tag	UNP K9YFK1
EJ	100	HIS	-	expression tag	UNP K9YFK1
EJ	101	PRO	-	expression tag	UNP K9YFK1
EJ	102	GLN	-	expression tag	UNP K9YFK1
EJ	103	PHE	-	expression tag	UNP K9YFK1
EJ	104	GLU	-	expression tag	UNP K9YFK1
EJ	105	LYS	-	expression tag	UNP K9YFK1
EN	96	GLY	-	expression tag	UNP K9YFK1
EN	97	SER	-	expression tag	UNP K9YFK1
EN	98	TRP	-	expression tag	UNP K9YFK1
EN	99	SER	-	expression tag	UNP K9YFK1
EN	100	HIS	-	expression tag	UNP K9YFK1
EN	101	PRO	-	expression tag	UNP K9YFK1
EN	102	GLN	-	expression tag	UNP K9YFK1
EN	103	PHE	-	expression tag	UNP K9YFK1
EN	104	GLU	-	expression tag	UNP K9YFK1
EN	105	LYS	-	expression tag	UNP K9YFK1
ER	96	GLY	-	expression tag	UNP K9YFK1
ER	97	SER	-	expression tag	UNP K9YFK1
ER	98	TRP	-	expression tag	UNP K9YFK1
ER	99	SER	-	expression tag	UNP K9YFK1
ER	100	HIS	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
ER	101	PRO	-	expression tag	UNP K9YFK1
ER	102	GLN	-	expression tag	UNP K9YFK1
ER	103	PHE	-	expression tag	UNP K9YFK1
ER	104	GLU	-	expression tag	UNP K9YFK1
ER	105	LYS	-	expression tag	UNP K9YFK1
EV	96	GLY	-	expression tag	UNP K9YFK1
EV	97	SER	-	expression tag	UNP K9YFK1
EV	98	TRP	-	expression tag	UNP K9YFK1
EV	99	SER	-	expression tag	UNP K9YFK1
EV	100	HIS	-	expression tag	UNP K9YFK1
EV	101	PRO	-	expression tag	UNP K9YFK1
EV	102	GLN	-	expression tag	UNP K9YFK1
EV	103	PHE	-	expression tag	UNP K9YFK1
EV	104	GLU	-	expression tag	UNP K9YFK1
EV	105	LYS	-	expression tag	UNP K9YFK1
EZ	96	GLY	-	expression tag	UNP K9YFK1
EZ	97	SER	-	expression tag	UNP K9YFK1
EZ	98	TRP	-	expression tag	UNP K9YFK1
EZ	99	SER	-	expression tag	UNP K9YFK1
EZ	100	HIS	-	expression tag	UNP K9YFK1
EZ	101	PRO	-	expression tag	UNP K9YFK1
EZ	102	GLN	-	expression tag	UNP K9YFK1
EZ	103	PHE	-	expression tag	UNP K9YFK1
EZ	104	GLU	-	expression tag	UNP K9YFK1
EZ	105	LYS	-	expression tag	UNP K9YFK1
E3	96	GLY	-	expression tag	UNP K9YFK1
E3	97	SER	-	expression tag	UNP K9YFK1
E3	98	TRP	-	expression tag	UNP K9YFK1
E3	99	SER	-	expression tag	UNP K9YFK1
E3	100	HIS	-	expression tag	UNP K9YFK1
E3	101	PRO	-	expression tag	UNP K9YFK1
E3	102	GLN	-	expression tag	UNP K9YFK1
E3	103	PHE	-	expression tag	UNP K9YFK1
E3	104	GLU	-	expression tag	UNP K9YFK1
E3	105	LYS	-	expression tag	UNP K9YFK1
E7	96	GLY	-	expression tag	UNP K9YFK1
E7	97	SER	-	expression tag	UNP K9YFK1
E7	98	TRP	-	expression tag	UNP K9YFK1
E7	99	SER	-	expression tag	UNP K9YFK1
E7	100	HIS	-	expression tag	UNP K9YFK1
E7	101	PRO	-	expression tag	UNP K9YFK1
E7	102	GLN	-	expression tag	UNP K9YFK1

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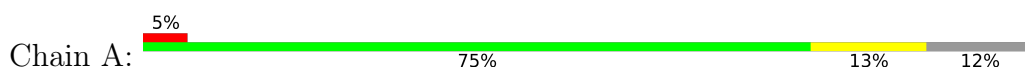
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Chain	Residue	Modelled	Actual	Comment	Reference
E7	103	PHE	-	expression tag	UNP K9YFK1
E7	104	GLU	-	expression tag	UNP K9YFK1
E7	105	LYS	-	expression tag	UNP K9YFK1

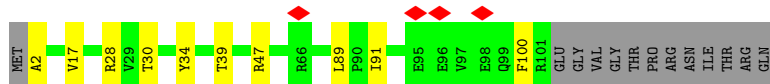
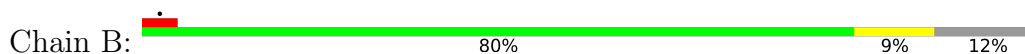
3 Residue-property plots [i](#)

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.

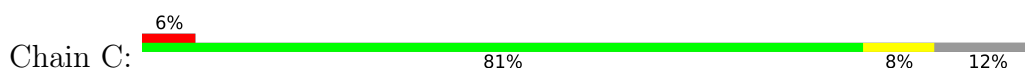
- Molecule 1: Microcompartments protein



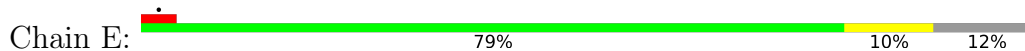
- Molecule 1: Microcompartments protein



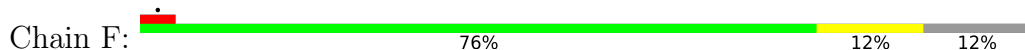
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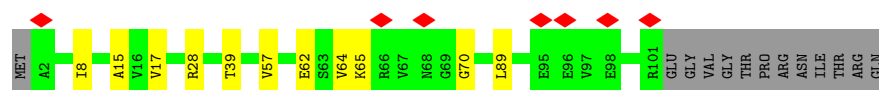
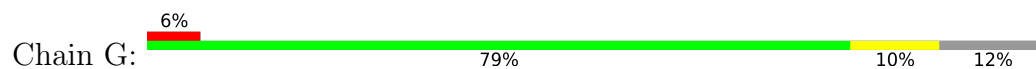
- Molecule 1: Microcompartments protein



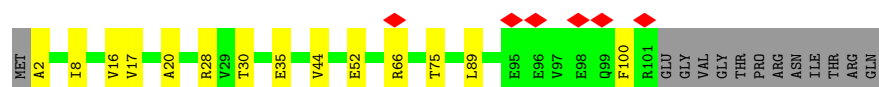
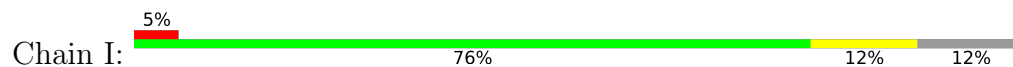
- Molecule 1: Microcompartments protein



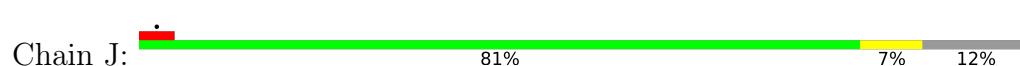
● Molecule 1: Microcompartments protein



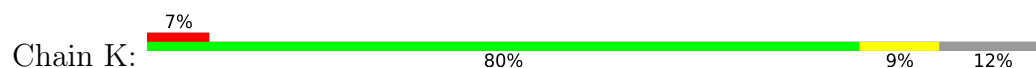
● Molecule 1: Microcompartments protein



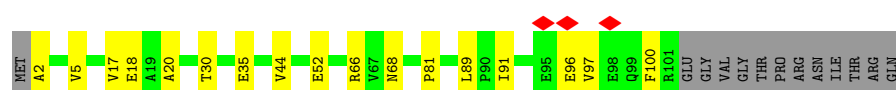
● Molecule 1: Microcompartments protein



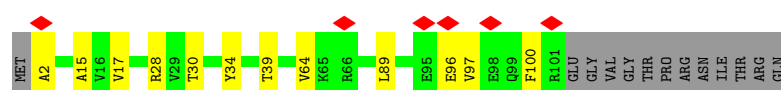
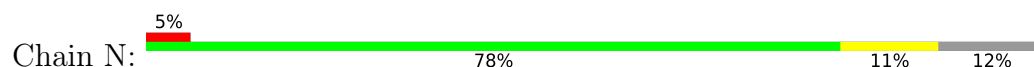
● Molecule 1: Microcompartments protein



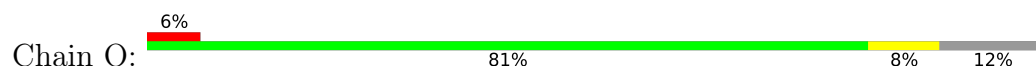
● Molecule 1: Microcompartments protein

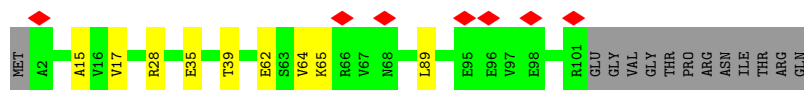


● Molecule 1: Microcompartments protein

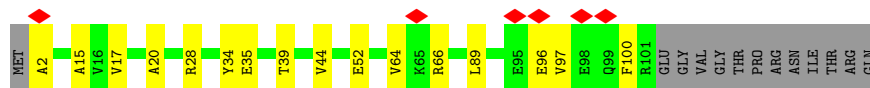
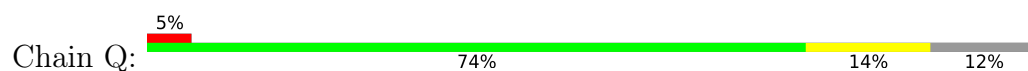


● Molecule 1: Microcompartments protein

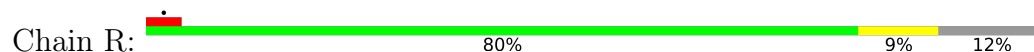




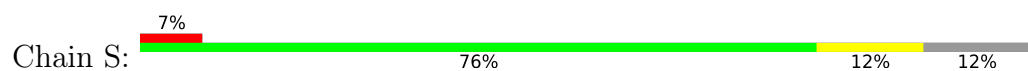
- Molecule 1: Microcompartments protein



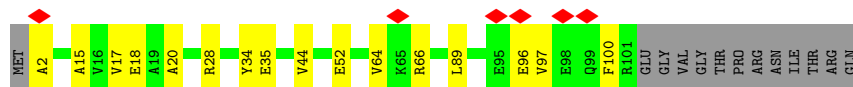
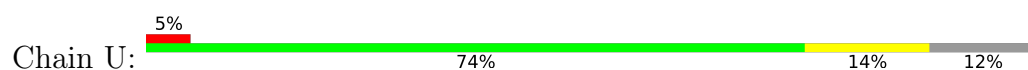
- Molecule 1: Microcompartments protein



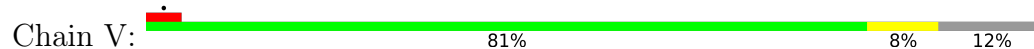
- Molecule 1: Microcompartments protein



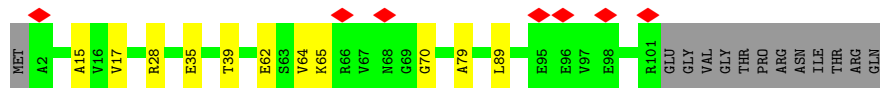
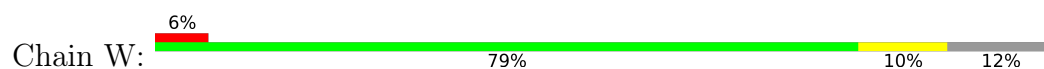
- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein

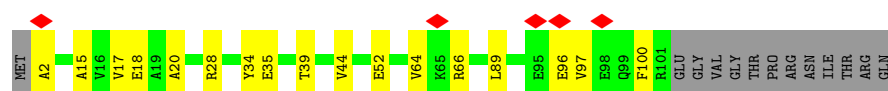


- Molecule 1: Microcompartments protein



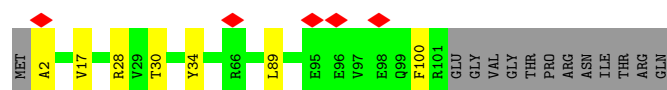
- Molecule 1: Microcompartments protein

Chain Y:  73% 15% 12%



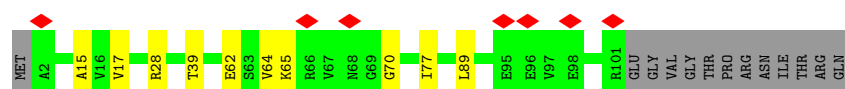
• Molecule 1: Microcompartments protein

Chain Z:  82% 6% 12%



• Molecule 1: Microcompartments protein

Chain 0:  6% 80% 9% 12%



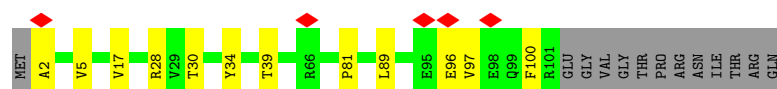
• Molecule 1: Microcompartments protein

Chain 2:  76% 12% 12%



• Molecule 1: Microcompartments protein

Chain 3:  78% 11% 12%



• Molecule 1: Microcompartments protein

Chain 4:  6% 80% 9% 12%



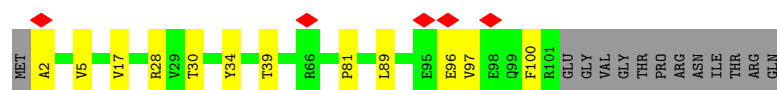
• Molecule 1: Microcompartments protein

Chain 6:  73% 15% 12%



• Molecule 1: Microcompartments protein

Chain 7:  78% 11% 12%



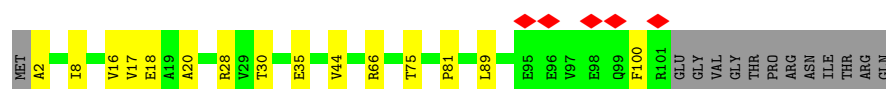
• Molecule 1: Microcompartments protein

Chain 8:  6% 81% 8% 12%



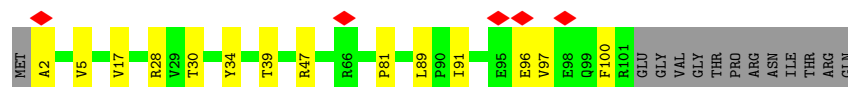
• Molecule 1: Microcompartments protein

Chain a:  75% 13% 12%



• Molecule 1: Microcompartments protein

Chain b:  76% 12% 12%



• Molecule 1: Microcompartments protein

Chain c:  6% 81% 8% 12%



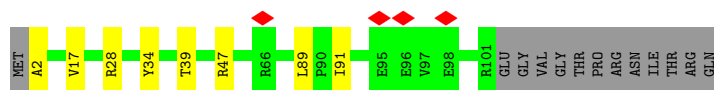
• Molecule 1: Microcompartments protein

Chain e:  5% 77% 12% 12%

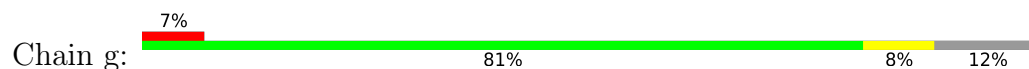


• Molecule 1: Microcompartments protein

Chain f:  81% 7% 12%



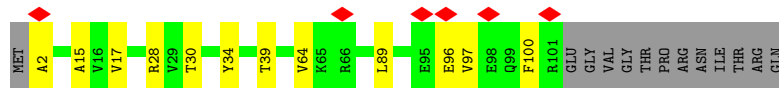
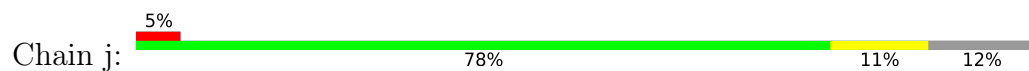
- Molecule 1: Microcompartments protein



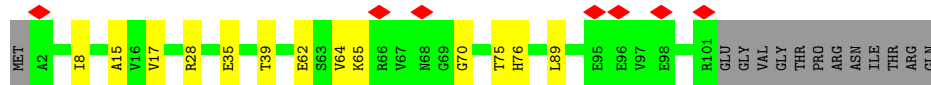
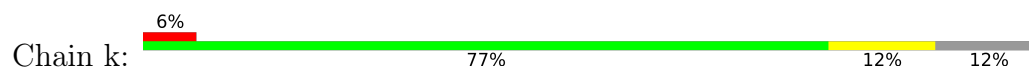
- Molecule 1: Microcompartments protein



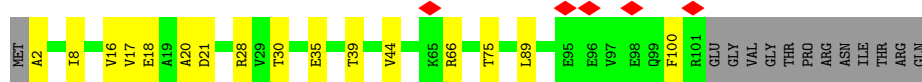
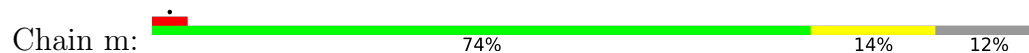
- Molecule 1: Microcompartments protein



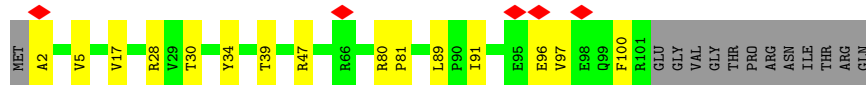
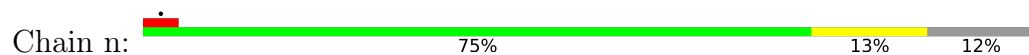
- Molecule 1: Microcompartments protein



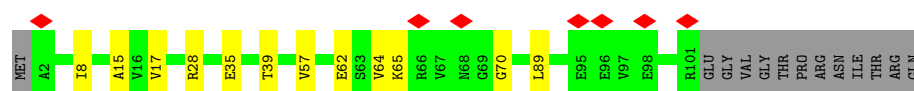
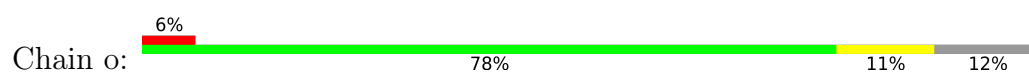
- Molecule 1: Microcompartments protein



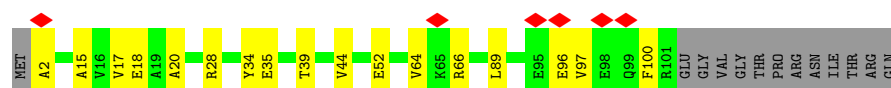
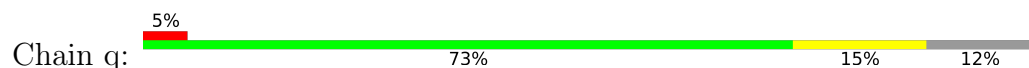
- Molecule 1: Microcompartments protein



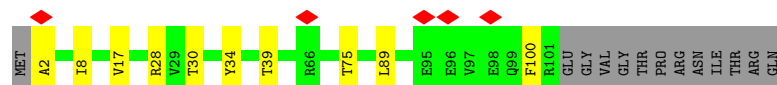
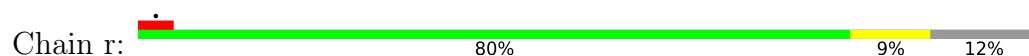
- Molecule 1: Microcompartments protein



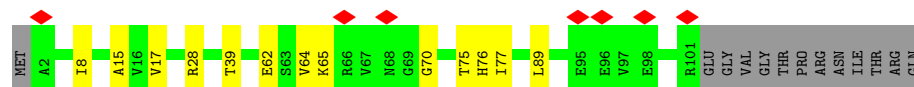
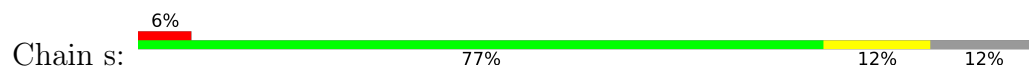
- Molecule 1: Microcompartments protein



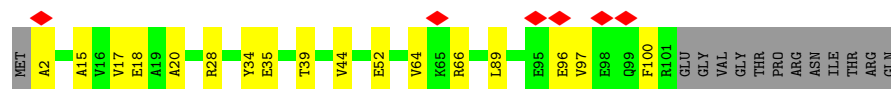
- Molecule 1: Microcompartments protein



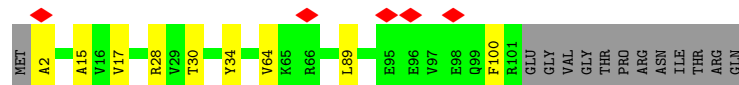
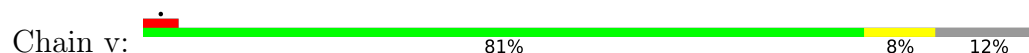
- Molecule 1: Microcompartments protein



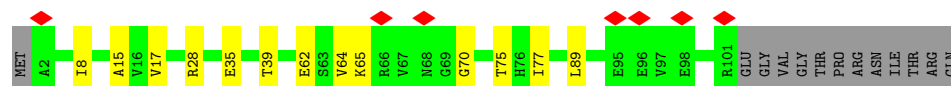
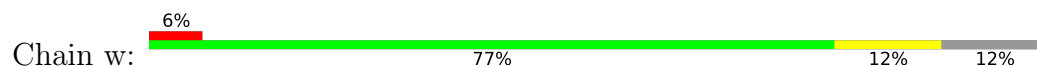
- Molecule 1: Microcompartments protein



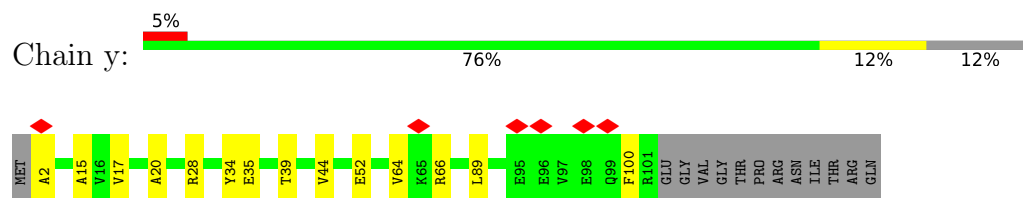
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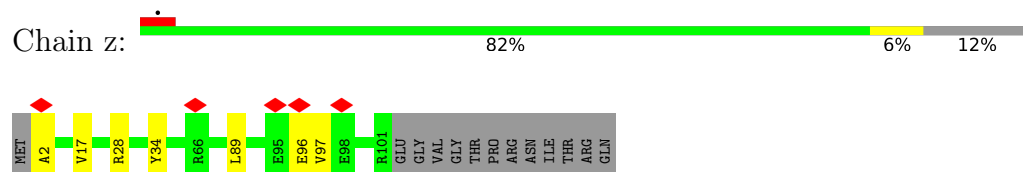
- Molecule 1: Microcompartments protein



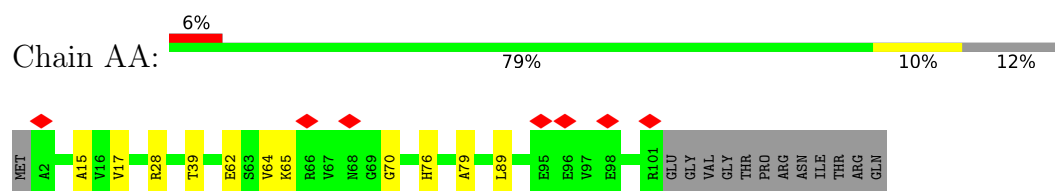
• Molecule 1: Microcompartments protein



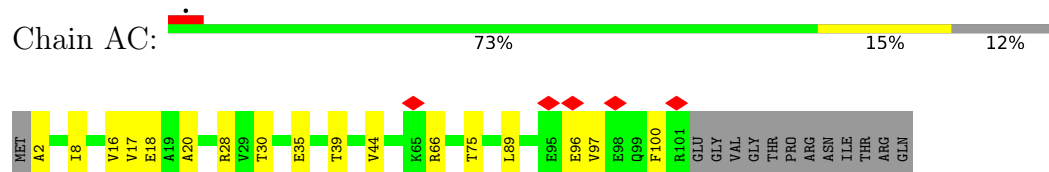
• Molecule 1: Microcompartments protein



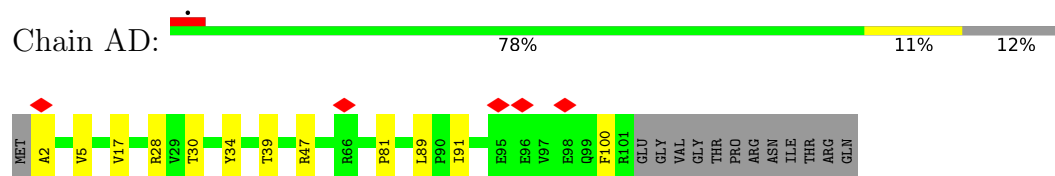
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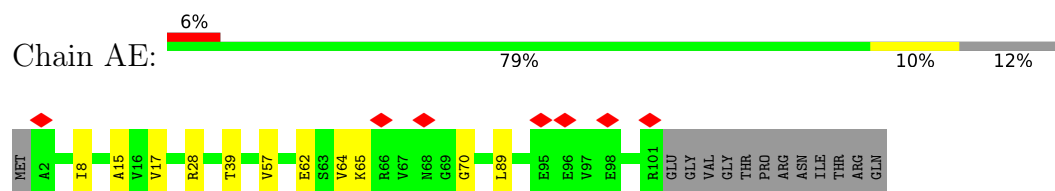
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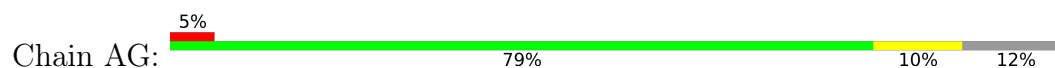
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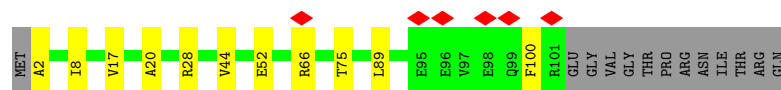


• Molecule 1: Microcompartments protein

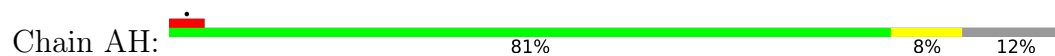


• Molecule 1: Microcompartments protein

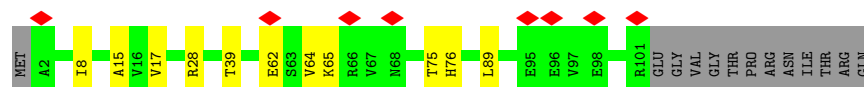
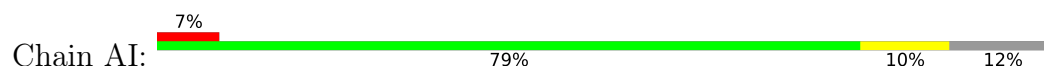




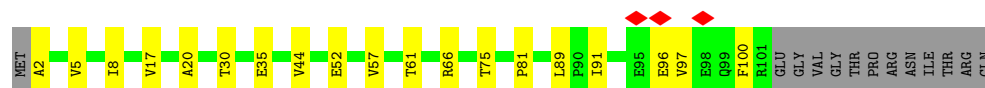
- Molecule 1: Microcompartments protein



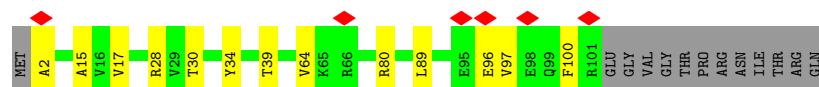
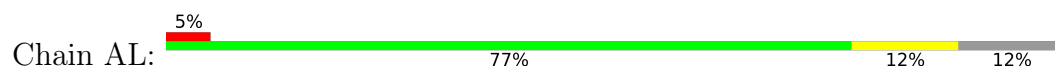
- Molecule 1: Microcompartments protein



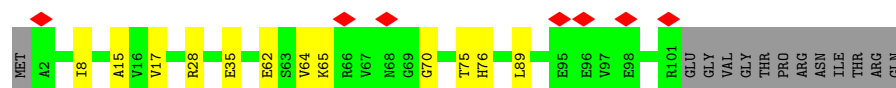
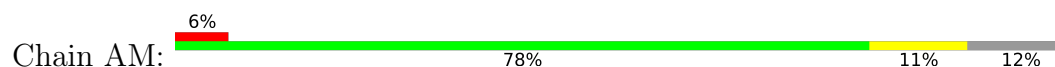
- Molecule 1: Microcompartments protein



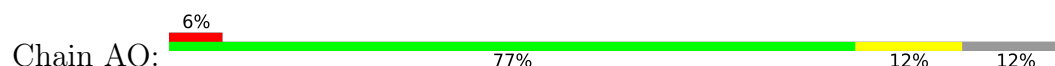
- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein

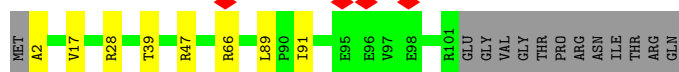


- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein

Chain AP:  81% 7% 12%



- Molecule 1: Microcompartments protein

Chain AQ:  6% 81% 8% 12%



- Molecule 1: Microcompartments protein

Chain AS:  73% 16% 12%



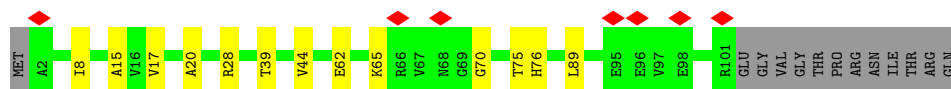
- Molecule 1: Microcompartments protein

Chain AT:  81% 7% 12%



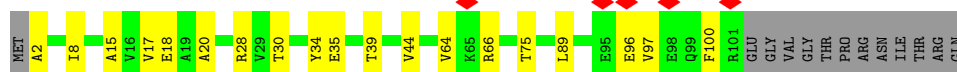
- Molecule 1: Microcompartments protein

Chain AU:  6% 77% 12% 12%



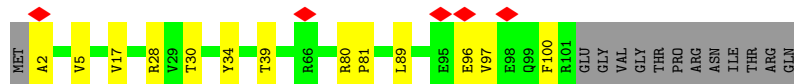
- Molecule 1: Microcompartments protein

Chain AW:  72% 17% 12%

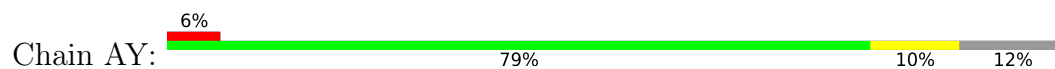


- Molecule 1: Microcompartments protein

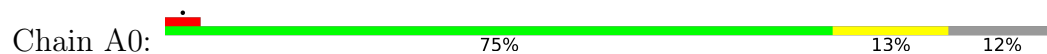
Chain AX:  77% 12% 12%



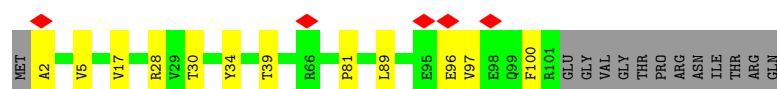
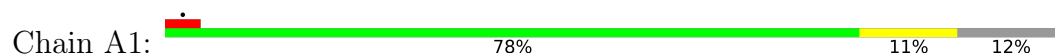
• Molecule 1: Microcompartments protein



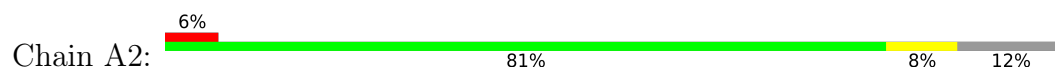
• Molecule 1: Microcompartments protein



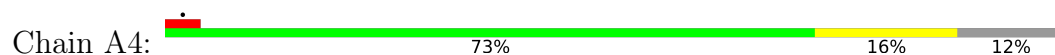
• Molecule 1: Microcompartments protein



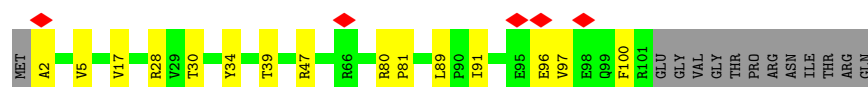
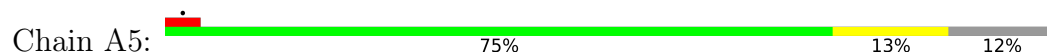
• Molecule 1: Microcompartments protein



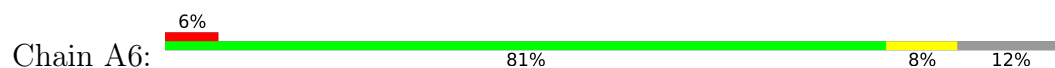
• Molecule 1: Microcompartments protein



• Molecule 1: Microcompartments protein

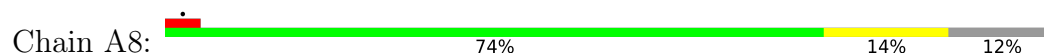


• Molecule 1: Microcompartments protein

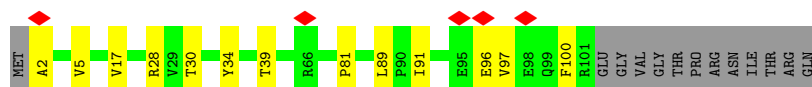
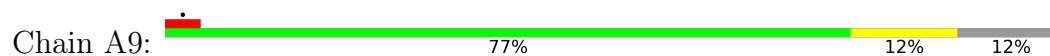




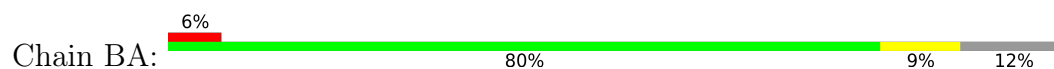
- Molecule 1: Microcompartments protein



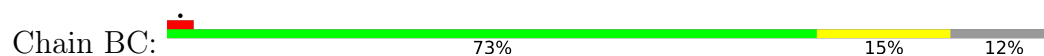
- Molecule 1: Microcompartments protein



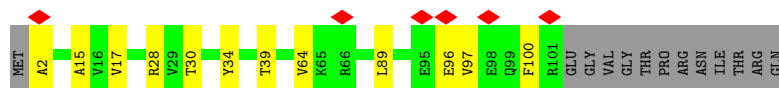
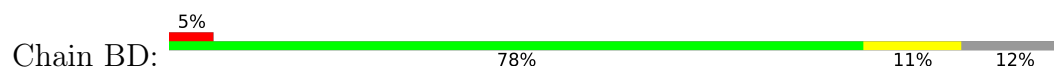
- Molecule 1: Microcompartments protein



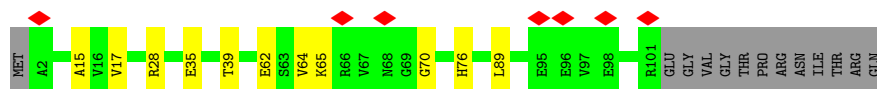
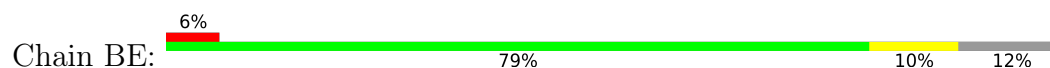
- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein

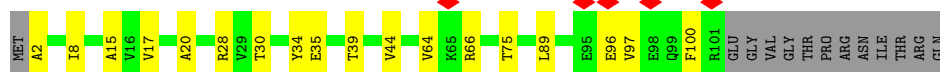


- Molecule 1: Microcompartments protein



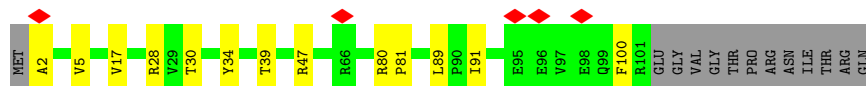
- Molecule 1: Microcompartments protein

Chain BG:  73% 16% 12%



- Molecule 1: Microcompartments protein

Chain BH:  77% 12% 12%



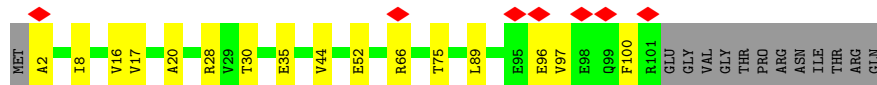
- Molecule 1: Microcompartments protein

Chain BI:  6% 79% 10% 12%



- Molecule 1: Microcompartments protein

Chain BK:  6% 74% 14% 12%



- Molecule 1: Microcompartments protein

Chain BL:  81% 7% 12%



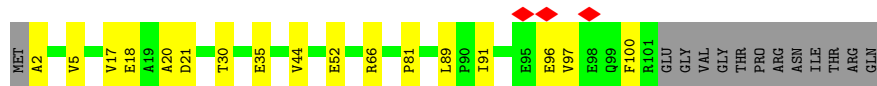
- Molecule 1: Microcompartments protein

Chain BM:  6% 81% 8% 12%

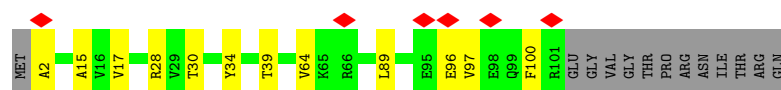
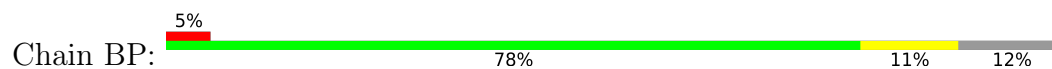


- Molecule 1: Microcompartments protein

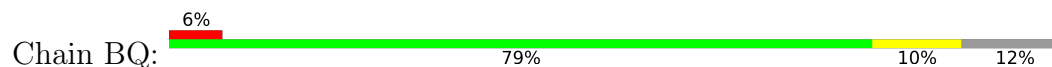
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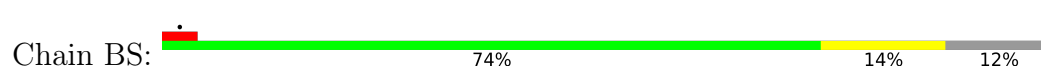
• Molecule 1: Microcompartments protein



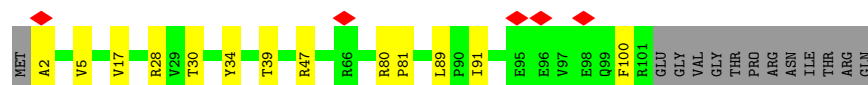
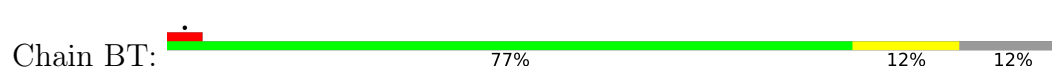
• Molecule 1: Microcompartments protein



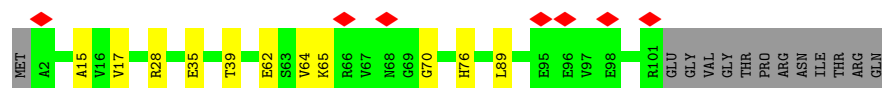
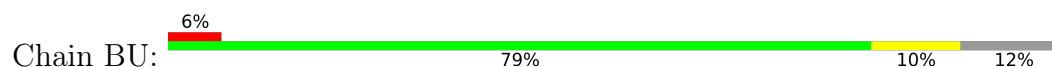
• Molecule 1: Microcompartments protein



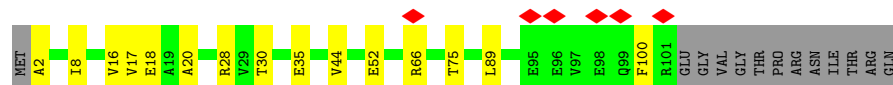
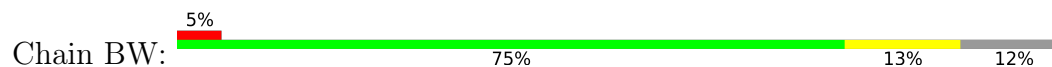
• Molecule 1: Microcompartments protein



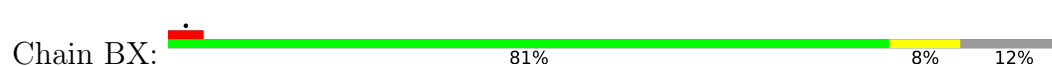
• Molecule 1: Microcompartments protein

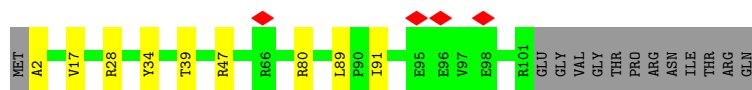


• Molecule 1: Microcompartments protein

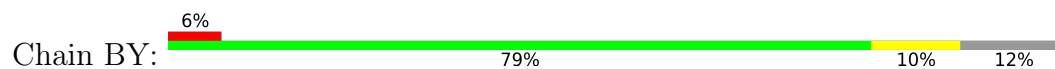


• Molecule 1: Microcompartments protein

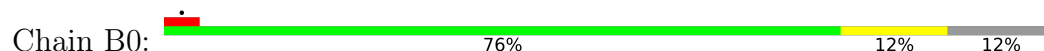




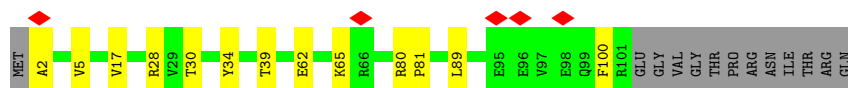
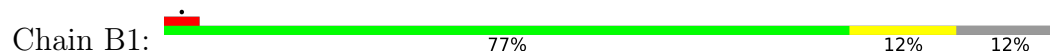
- Molecule 1: Microcompartments protein



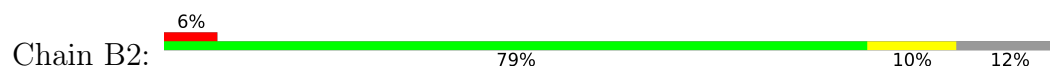
- Molecule 1: Microcompartments protein



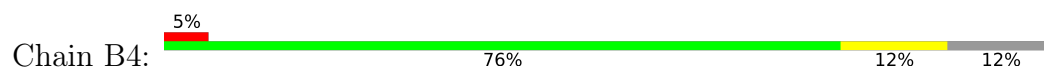
- Molecule 1: Microcompartments protein



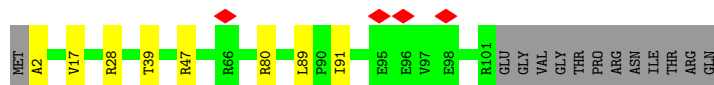
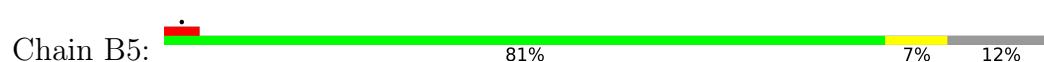
- Molecule 1: Microcompartments protein



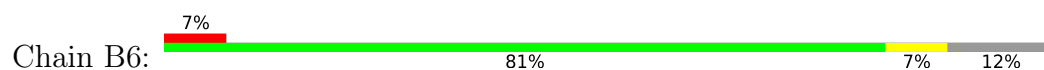
- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein



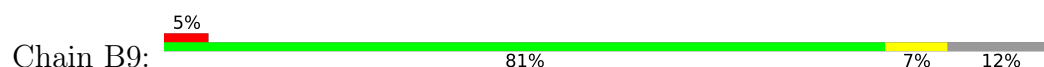
- Molecule 1: Microcompartments protein



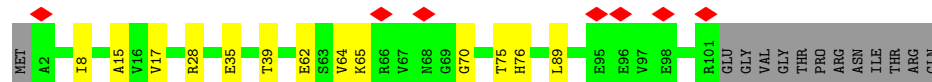
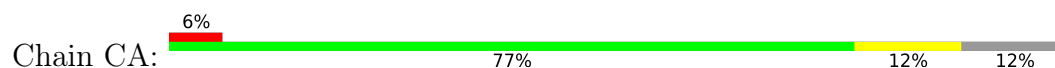
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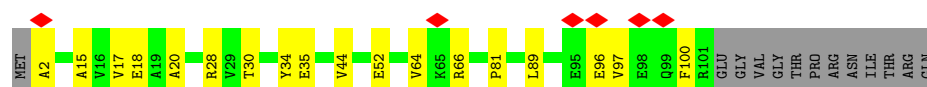
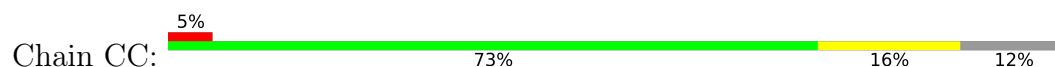
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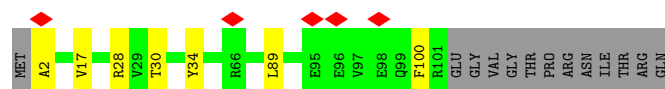
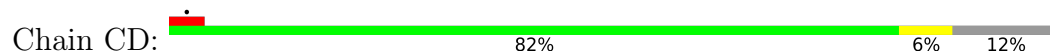
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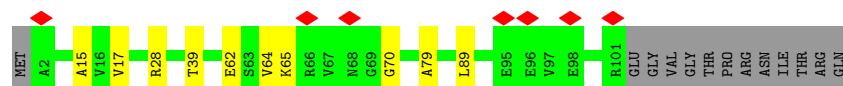
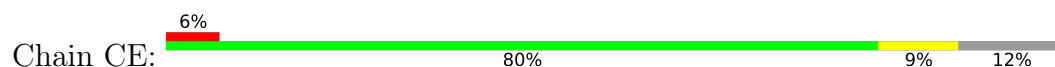
- Molecule 1: Microcompartments protein



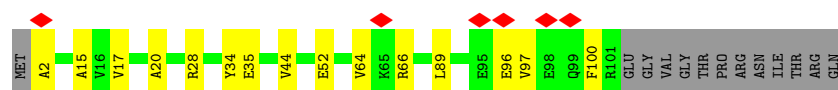
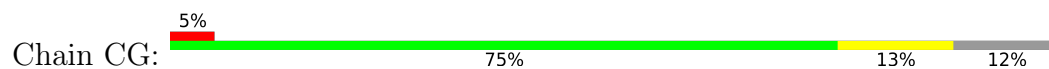
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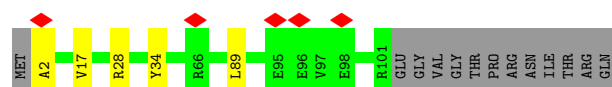
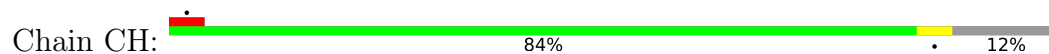
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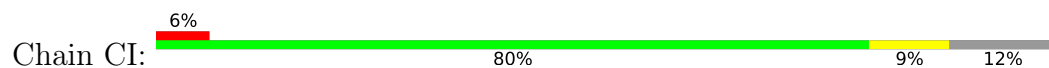
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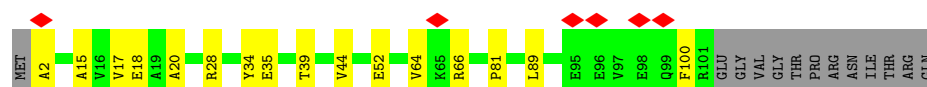
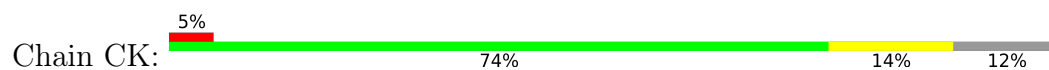
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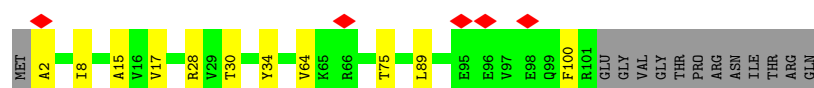
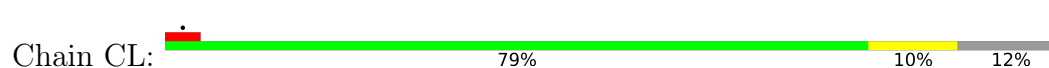
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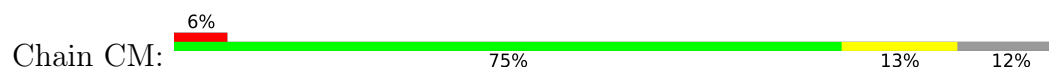
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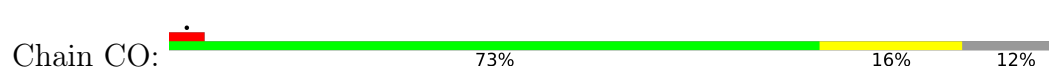
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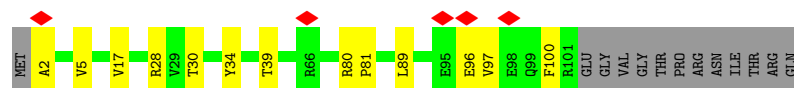
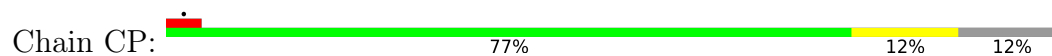


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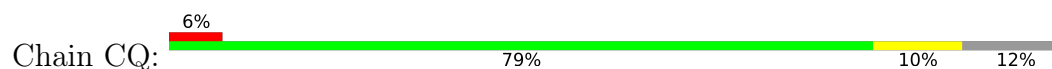




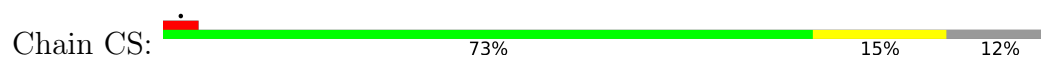
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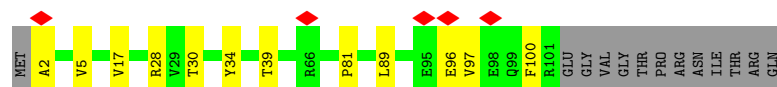
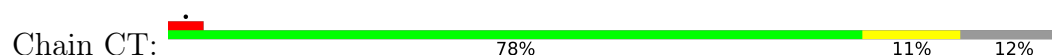
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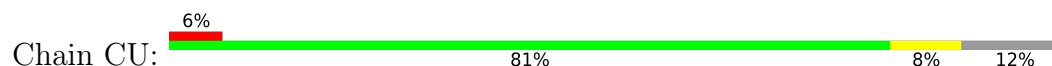
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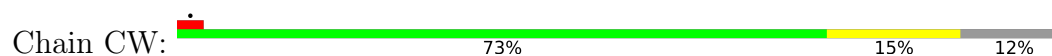
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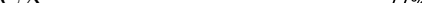
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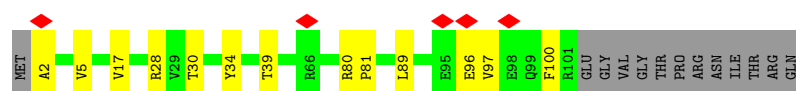


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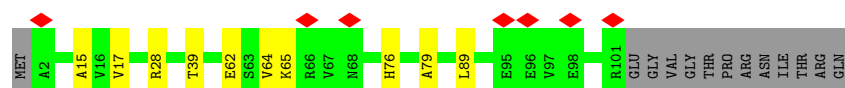
- Molecule 1: Microcompartments protein

Chain CX:  77% 12% 12%

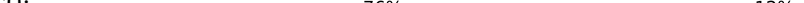


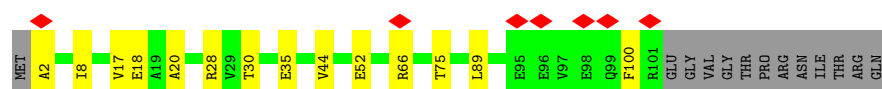
- Molecule 1: Microcompartments protein

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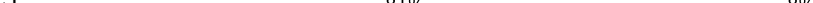


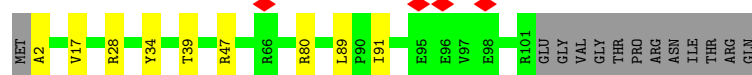
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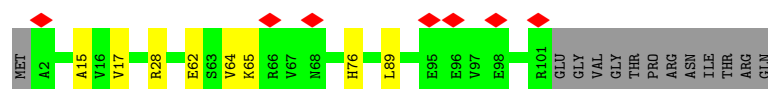
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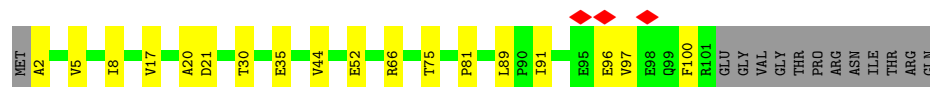
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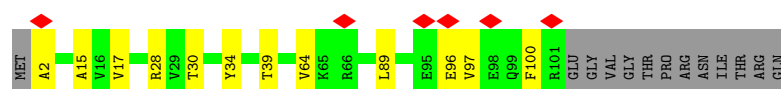
- Molecule 1: Microcompartments protein

Chain C4: 73% 16% 12%

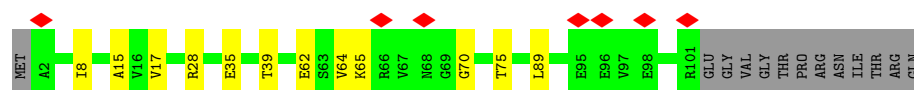
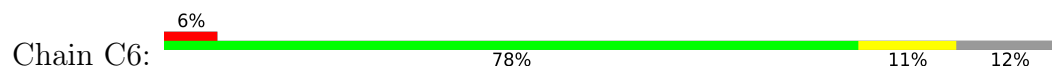


- Molecule 1: Microcompartments protein

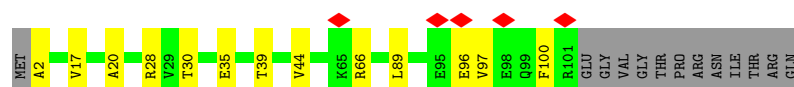
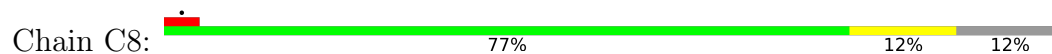
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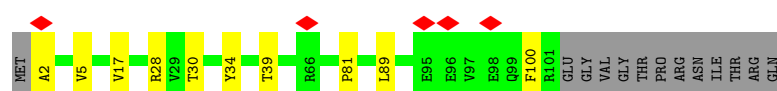
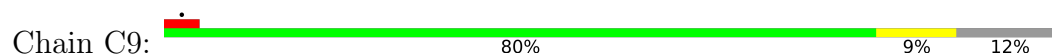
● Molecule 1: Microcompartments protein



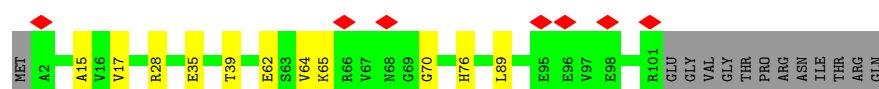
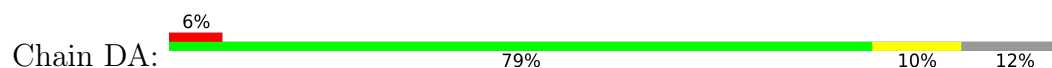
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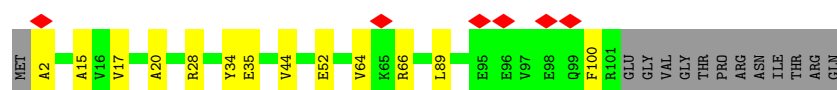
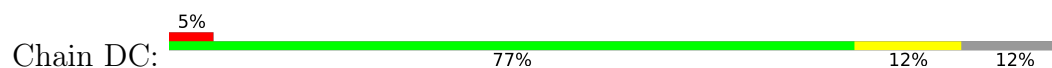
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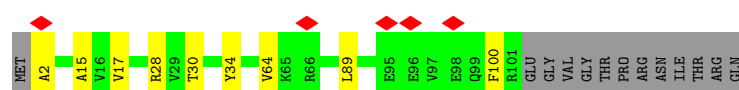
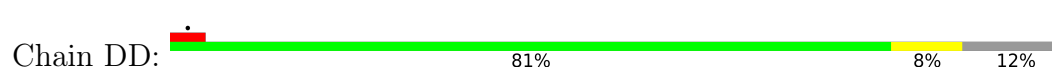
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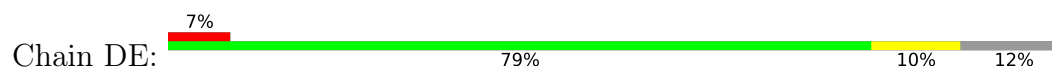
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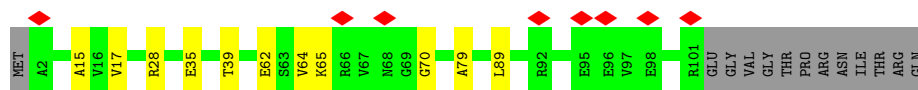


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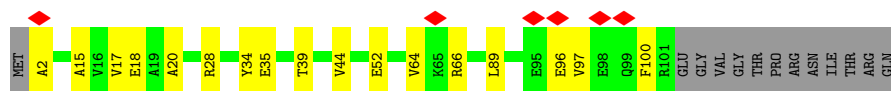
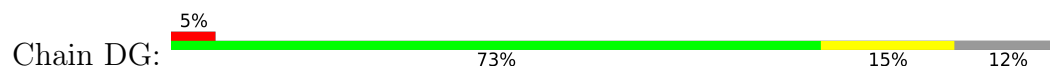


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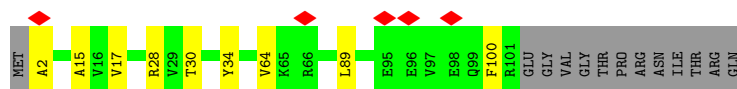
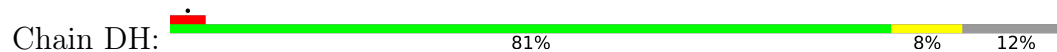




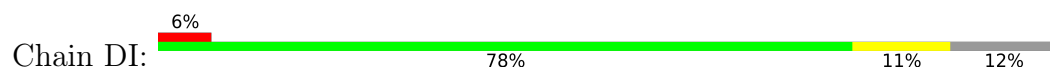
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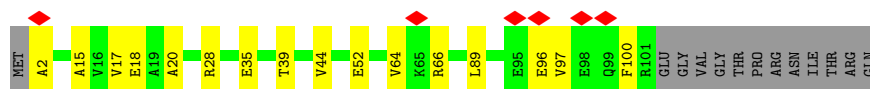
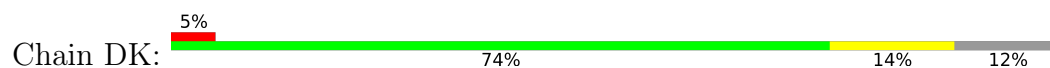
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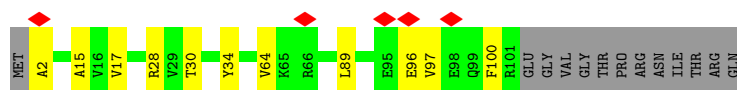
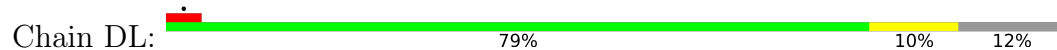
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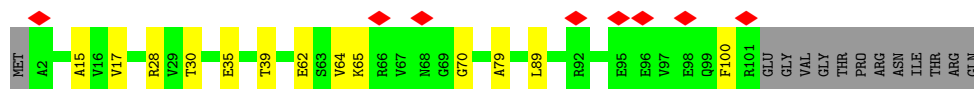
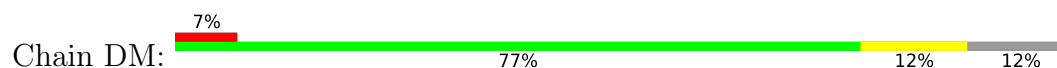
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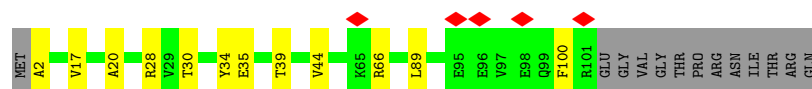
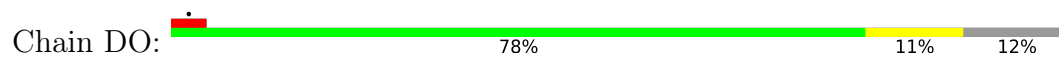
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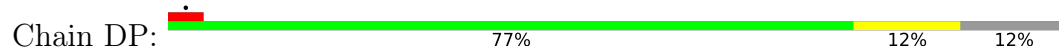
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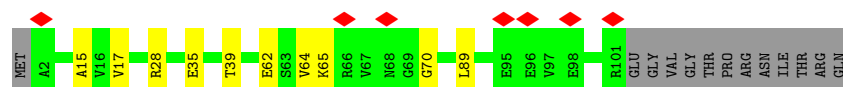
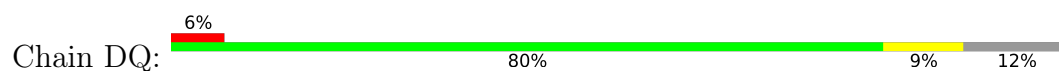
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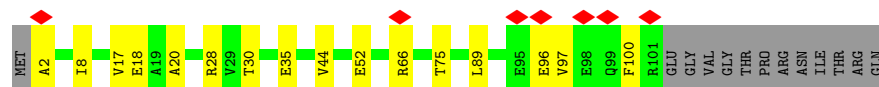
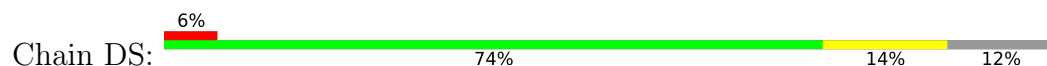
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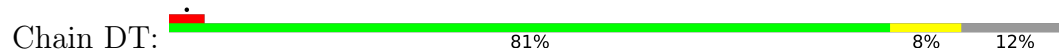
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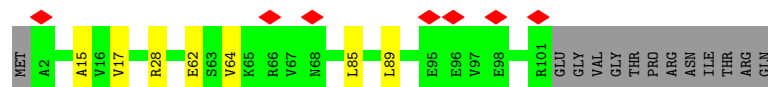
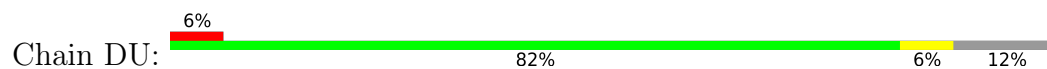
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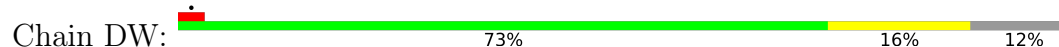
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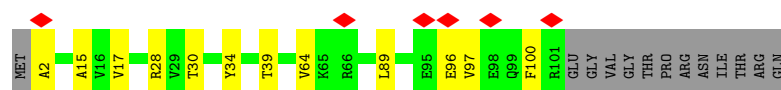
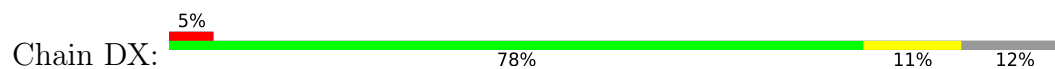
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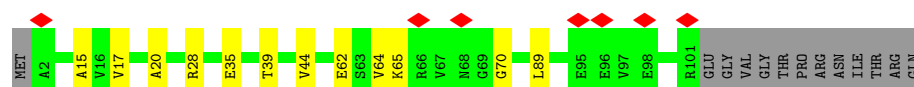
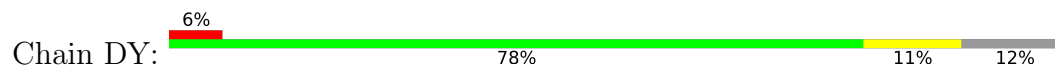
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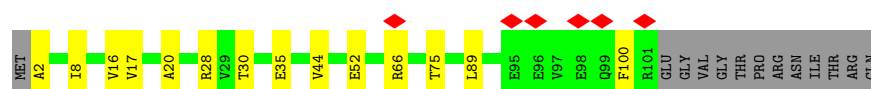
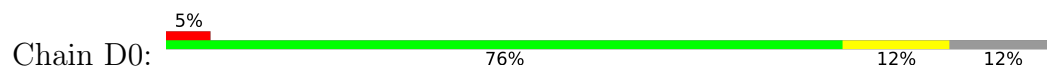
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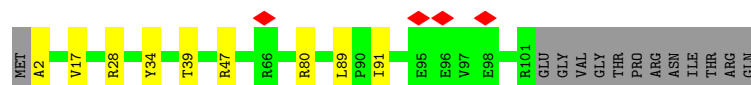
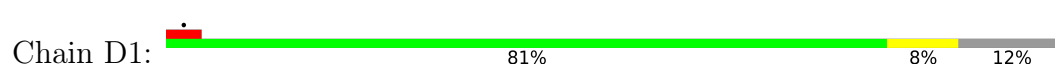
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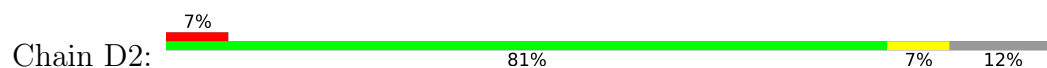
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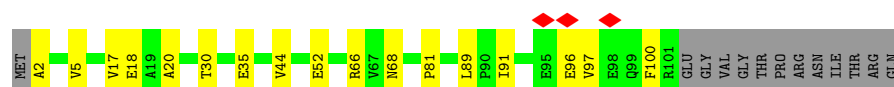
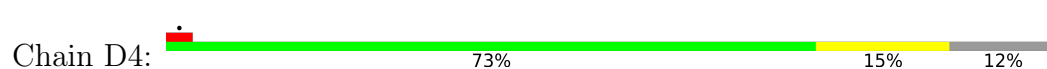
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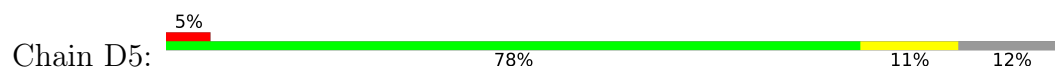
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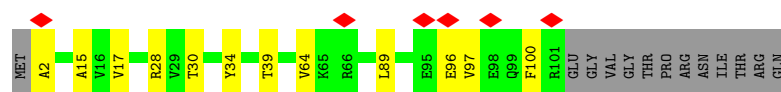


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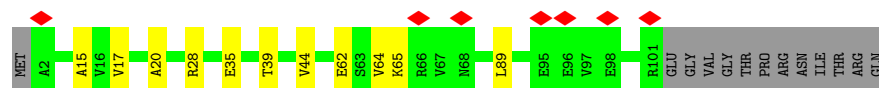
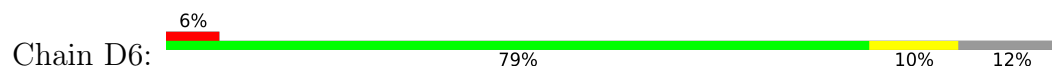


• Molecule 1: Microcompartments protein

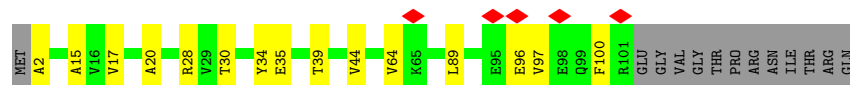
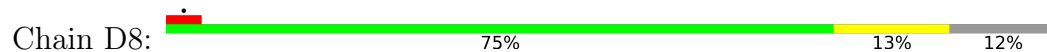




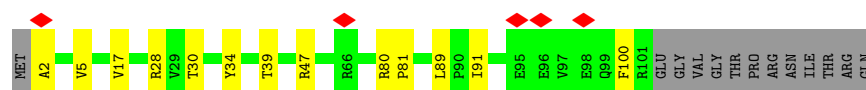
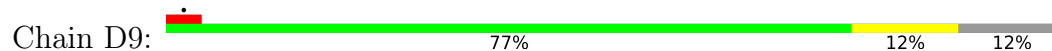
- Molecule 1: Microcompartments protein



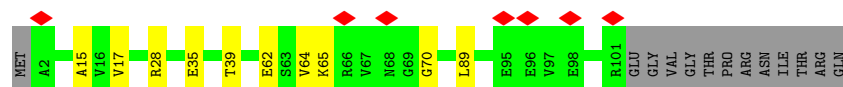
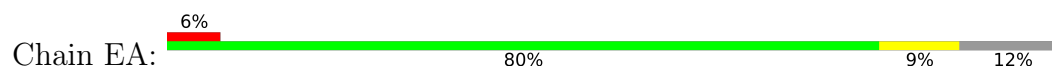
- Molecule 1: Microcompartments protein



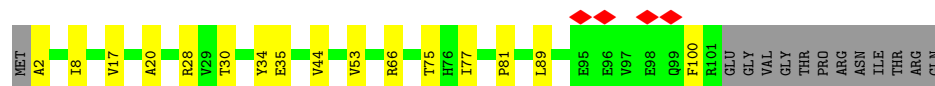
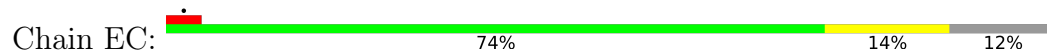
- Molecule 1: Microcompartments protein



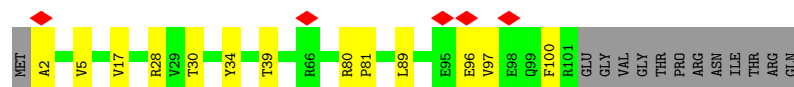
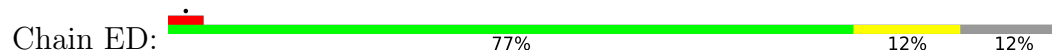
- Molecule 1: Microcompartments protein



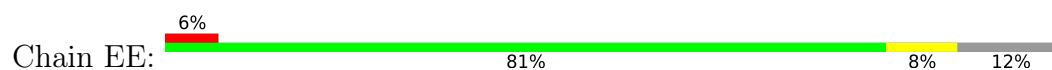
- Molecule 1: Microcompartments protein



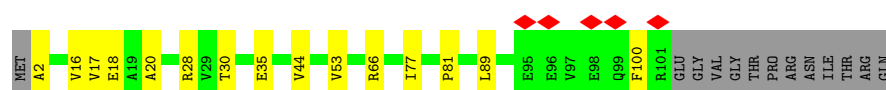
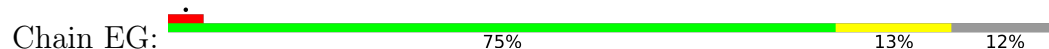
- Molecule 1: Microcompartments protein



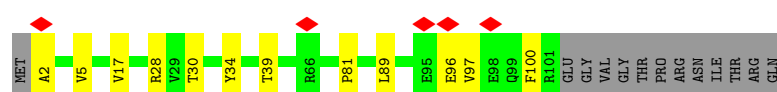
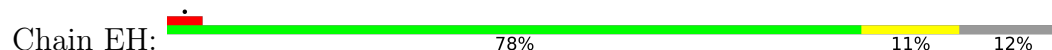
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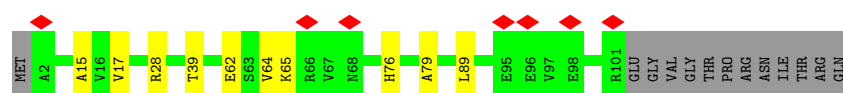
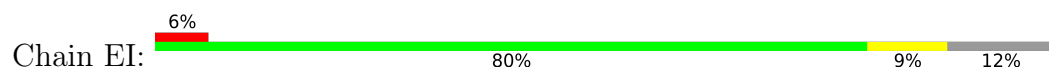
- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein



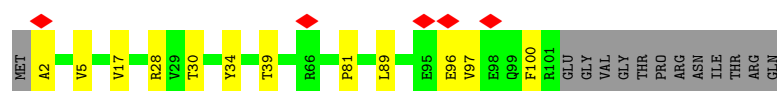
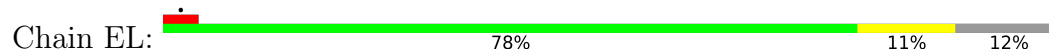
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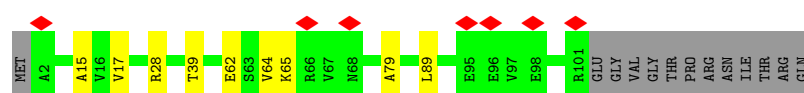
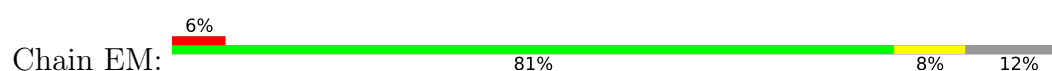
- Molecule 1: Microcompartments protein



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- Molecule 1: Microcompartments protein



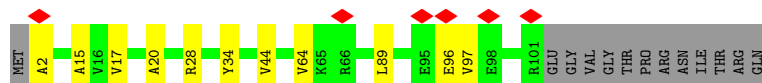
• Molecule 1: Microcompartments protein

Chain EO:  74% 14% 12%



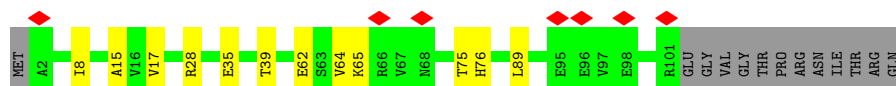
• Molecule 1: Microcompartments protein

Chain EP:  79% 10% 12%



• Molecule 1: Microcompartments protein

Chain EQ:  78% 11% 12%



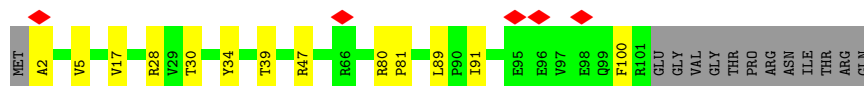
• Molecule 1: Microcompartments protein

Chain ES:  75% 13% 12%



• Molecule 1: Microcompartments protein

Chain ET:  77% 12% 12%



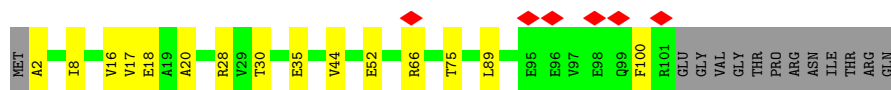
• Molecule 1: Microcompartments protein

Chain EU:  81% 8% 12%

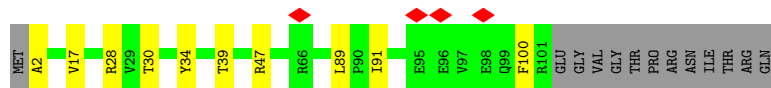
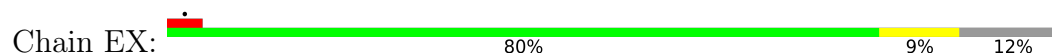


• Molecule 1: Microcompartments protein

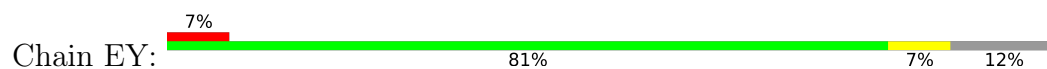
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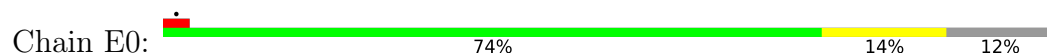
- Molecule 1: Microcompartments protein



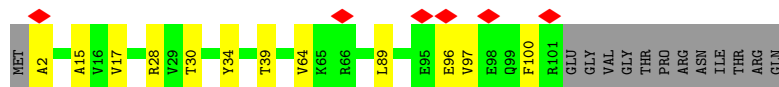
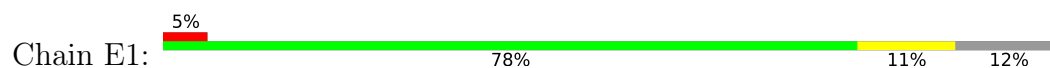
- Molecule 1: Microcompartments protein



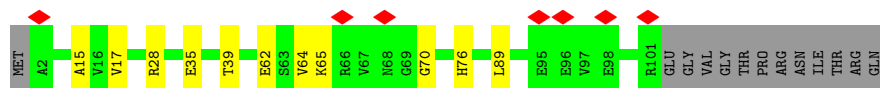
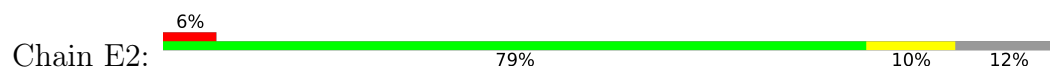
- Molecule 1: Microcompartments protein



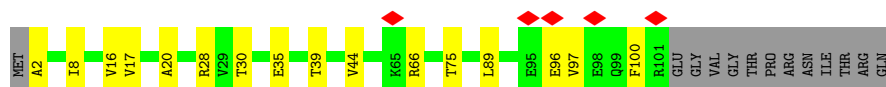
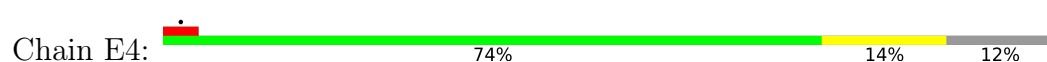
- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein

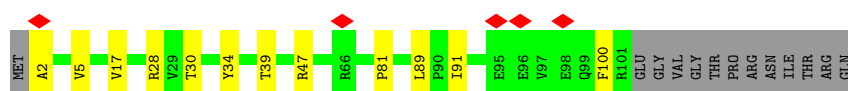


- Molecule 1: Microcompartments protein



- Molecule 1: Microcompartments protein

Chain E5:  78% 11% 12%



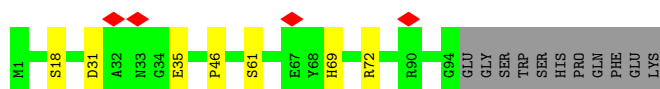
- Molecule 1: Microcompartments protein

Chain E6:  6% 80% 9% 12%



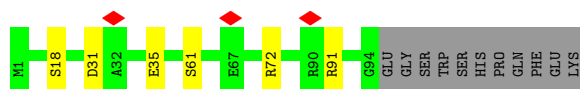
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

Chain D:  83% 7% 10%



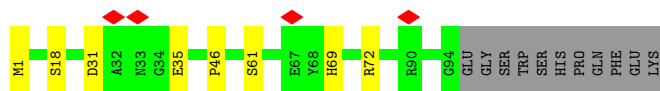
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

Chain H:  84% 6% 10%



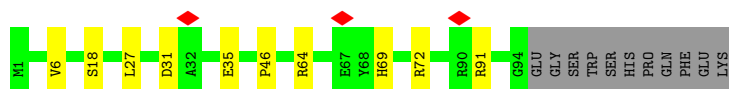
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

Chain L:  82% 8% 10%



- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

Chain P:  80% 10% 10%

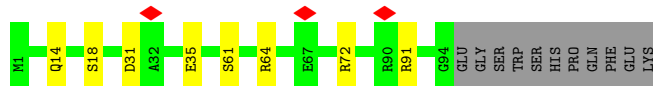
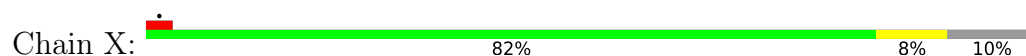


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

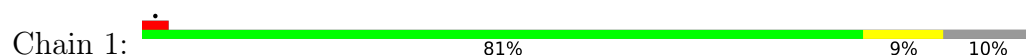
Chain T:  82% 8% 10%



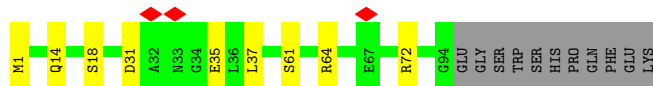
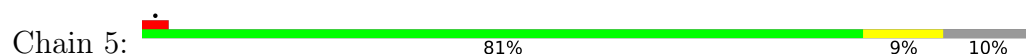
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



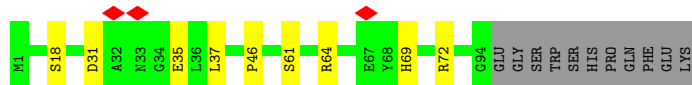
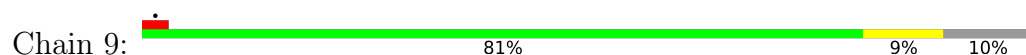
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



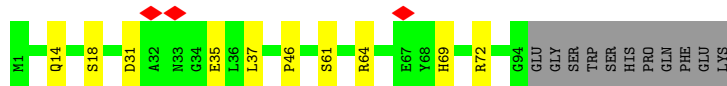
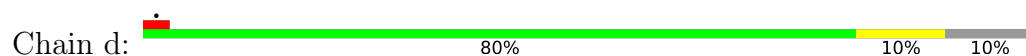
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



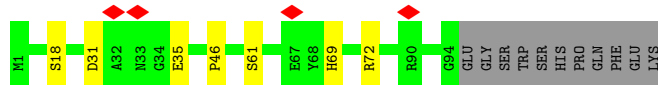
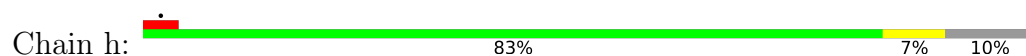
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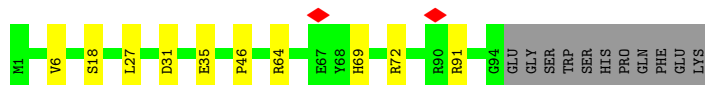
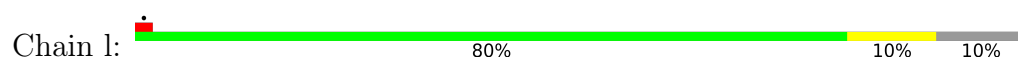
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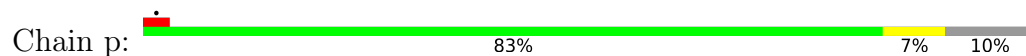
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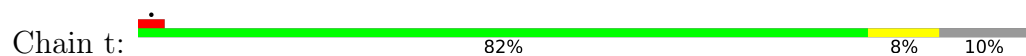
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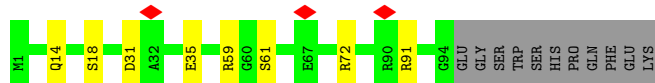
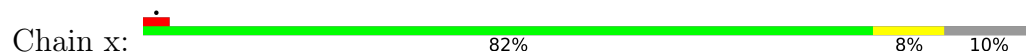
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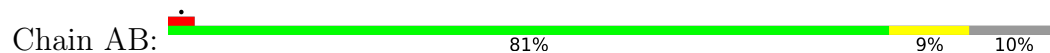
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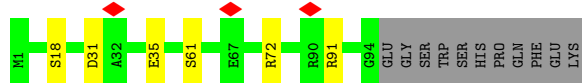
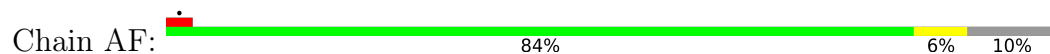
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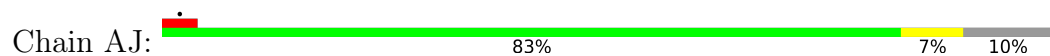
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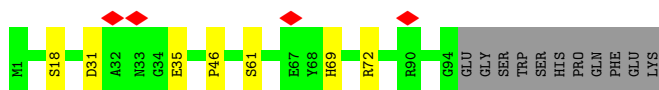


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

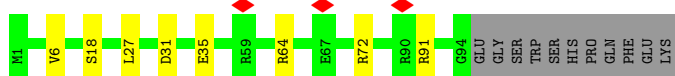
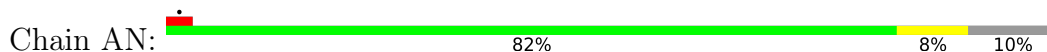


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

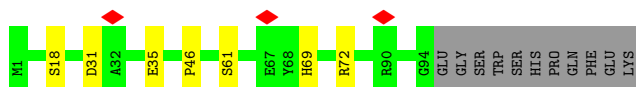
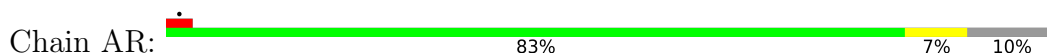




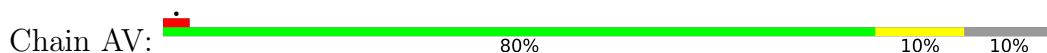
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



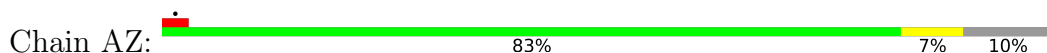
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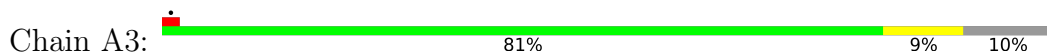
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



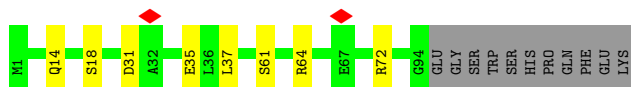
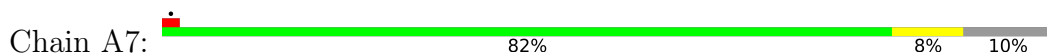
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



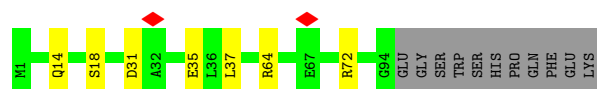
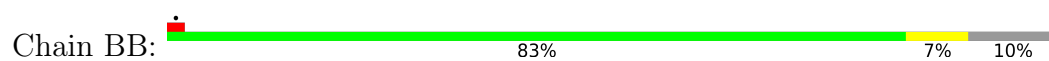
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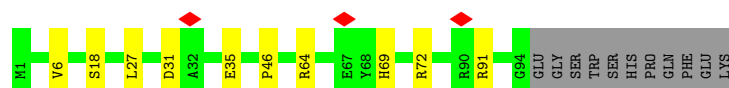
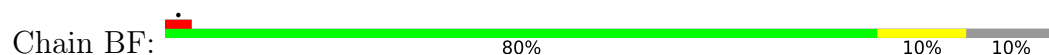
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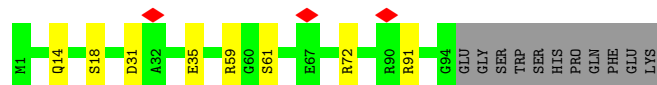
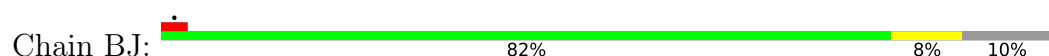
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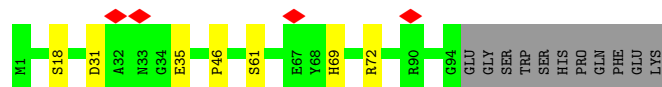
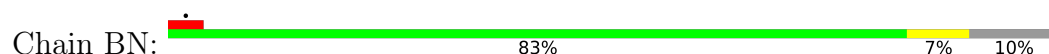
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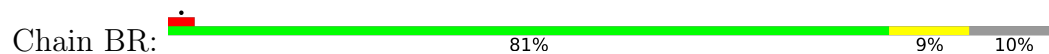
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



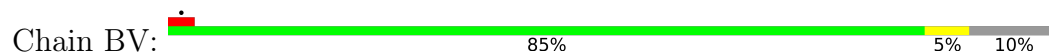
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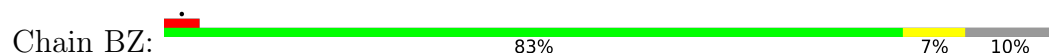
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml

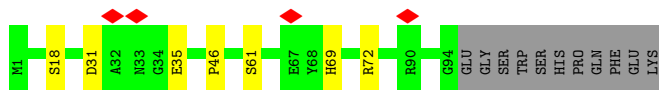


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml

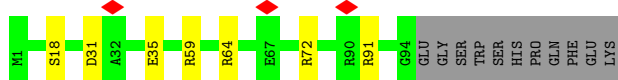
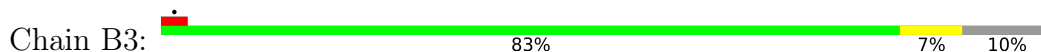


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml

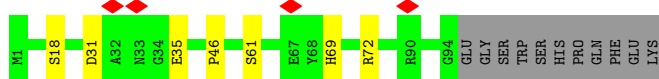
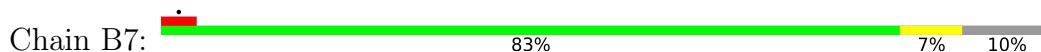




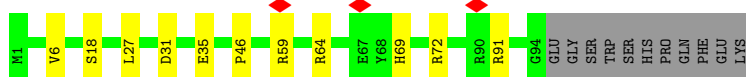
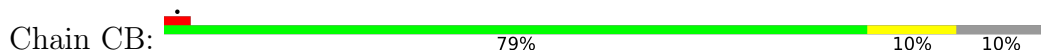
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



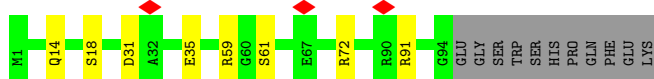
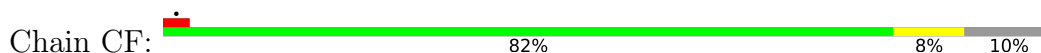
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



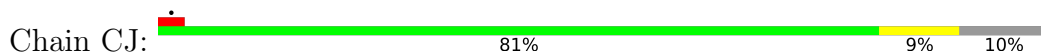
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



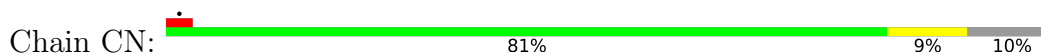
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



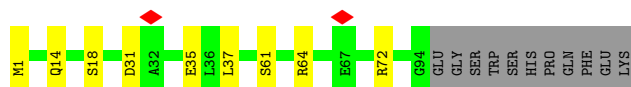
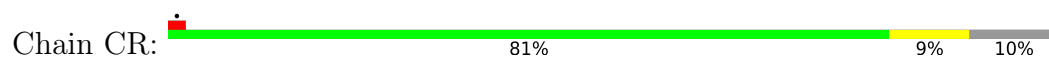
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



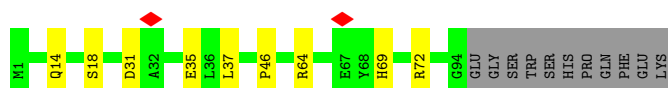
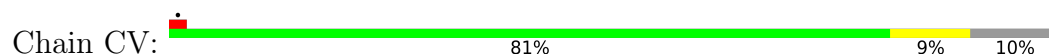
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



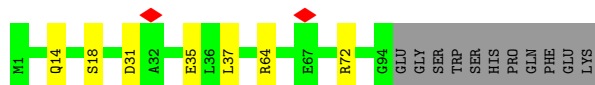
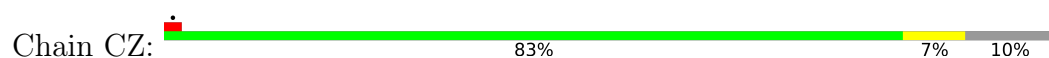
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



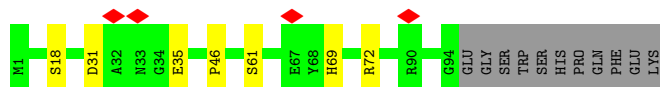
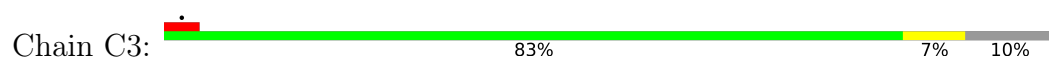
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



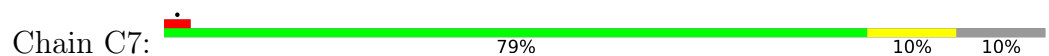
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



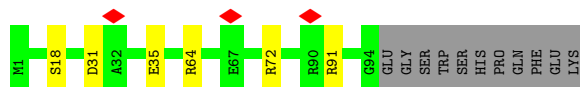
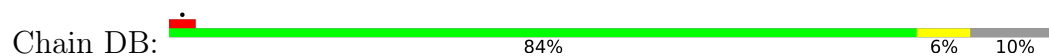
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



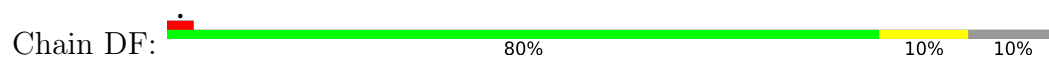
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

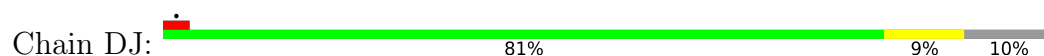


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

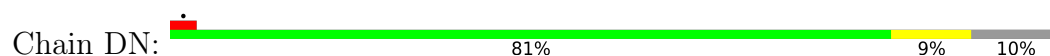




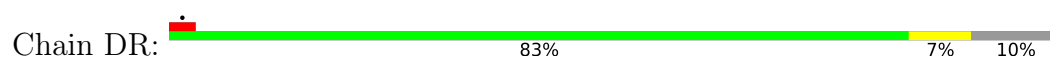
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



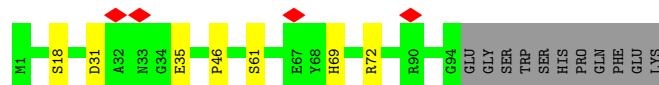
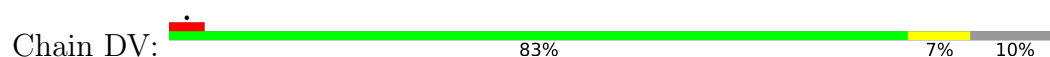
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



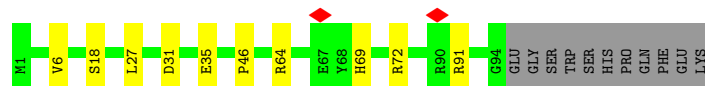
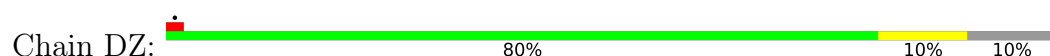
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



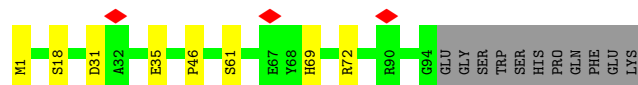
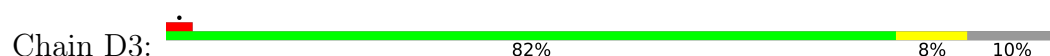
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



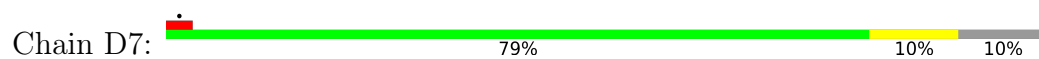
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



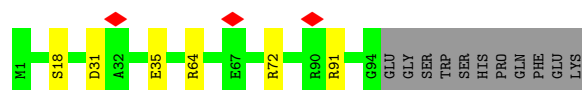
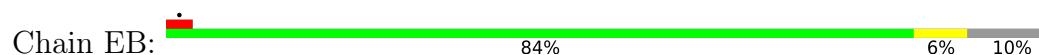
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



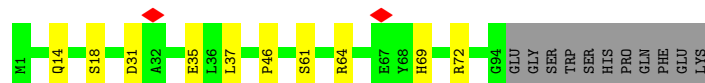
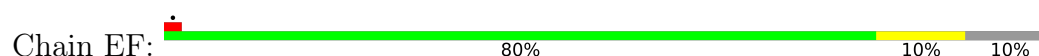
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



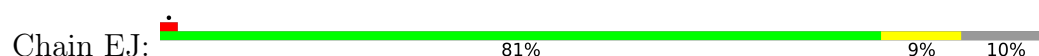
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



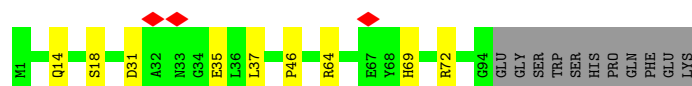
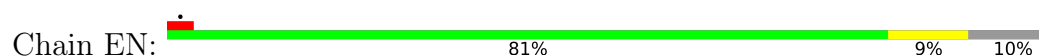
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



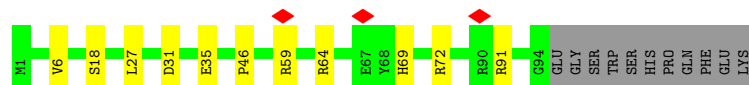
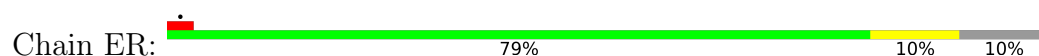
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



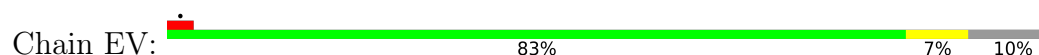
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

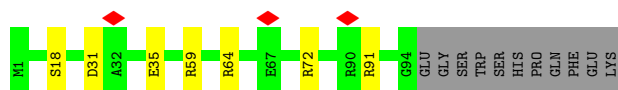


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

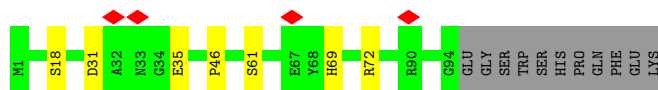
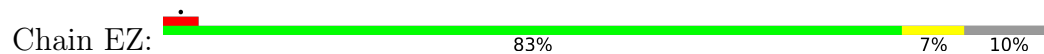


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

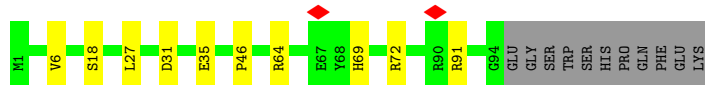
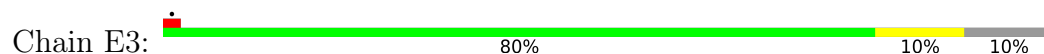




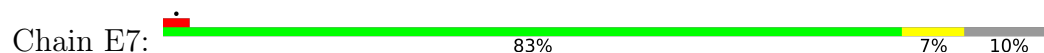
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein Ccml



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	35384	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	56000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	9.441	Depositor
Minimum map value	-5.735	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.8	Depositor
Map size (Å)	245.8608, 245.8608, 245.8608	wwPDB
Map dimensions	276, 276, 276	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8908, 0.8908, 0.8908	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	0	0.24	0/761	0.49	0/1033
1	2	0.24	0/761	0.54	1/1033 (0.1%)
1	3	0.25	0/761	0.50	0/1033
1	4	0.24	0/761	0.49	0/1033
1	6	0.24	0/761	0.54	1/1033 (0.1%)
1	7	0.25	0/761	0.50	0/1033
1	8	0.24	0/761	0.49	0/1033
1	A	0.24	0/761	0.55	1/1033 (0.1%)
1	A0	0.24	0/761	0.55	1/1033 (0.1%)
1	A1	0.25	0/761	0.50	0/1033
1	A2	0.24	0/761	0.49	0/1033
1	A4	0.24	0/761	0.54	1/1033 (0.1%)
1	A5	0.25	0/761	0.50	0/1033
1	A6	0.24	0/761	0.50	0/1033
1	A8	0.24	0/761	0.54	1/1033 (0.1%)
1	A9	0.25	0/761	0.51	0/1033
1	AA	0.24	0/761	0.49	0/1033
1	AC	0.24	0/761	0.55	1/1033 (0.1%)
1	AD	0.25	0/761	0.51	0/1033
1	AE	0.25	0/761	0.50	0/1033
1	AG	0.24	0/761	0.55	1/1033 (0.1%)
1	AH	0.25	0/761	0.51	0/1033
1	AI	0.26	0/761	0.51	0/1033
1	AK	0.25	0/761	0.55	1/1033 (0.1%)
1	AL	0.25	0/761	0.51	0/1033
1	AM	0.24	0/761	0.49	0/1033
1	AO	0.24	0/761	0.55	1/1033 (0.1%)
1	AP	0.24	0/761	0.51	0/1033
1	AQ	0.26	0/761	0.51	0/1033
1	AS	0.25	0/761	0.56	1/1033 (0.1%)
1	AT	0.25	0/761	0.51	0/1033
1	AU	0.24	0/761	0.49	0/1033
1	AW	0.24	0/761	0.54	1/1033 (0.1%)
1	AX	0.25	0/761	0.51	0/1033

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AY	0.25	0/761	0.50	0/1033
1	B	0.24	0/761	0.51	0/1033
1	B0	0.24	0/761	0.54	1/1033 (0.1%)
1	B1	0.25	0/761	0.51	0/1033
1	B2	0.25	0/761	0.51	0/1033
1	B4	0.24	0/761	0.56	1/1033 (0.1%)
1	B5	0.25	0/761	0.51	0/1033
1	B6	0.25	0/761	0.50	0/1033
1	B8	0.25	0/761	0.55	1/1033 (0.1%)
1	B9	0.25	0/761	0.51	0/1033
1	BA	0.24	0/761	0.49	0/1033
1	BC	0.25	0/761	0.56	1/1033 (0.1%)
1	BD	0.25	0/761	0.51	0/1033
1	BE	0.24	0/761	0.49	0/1033
1	BG	0.24	0/761	0.54	1/1033 (0.1%)
1	BH	0.24	0/761	0.51	0/1033
1	BI	0.25	0/761	0.52	0/1033
1	BK	0.24	0/761	0.55	1/1033 (0.1%)
1	BL	0.25	0/761	0.52	0/1033
1	BM	0.25	0/761	0.51	0/1033
1	BO	0.25	0/761	0.55	1/1033 (0.1%)
1	BP	0.25	0/761	0.52	0/1033
1	BQ	0.24	0/761	0.49	0/1033
1	BS	0.23	0/761	0.54	1/1033 (0.1%)
1	BT	0.25	0/761	0.51	0/1033
1	BU	0.25	0/761	0.51	0/1033
1	BW	0.24	0/761	0.55	1/1033 (0.1%)
1	BX	0.25	0/761	0.51	0/1033
1	BY	0.25	0/761	0.50	0/1033
1	C	0.25	0/761	0.51	0/1033
1	C0	0.24	0/761	0.55	1/1033 (0.1%)
1	C1	0.25	0/761	0.52	0/1033
1	C2	0.25	0/761	0.50	0/1033
1	C4	0.25	0/761	0.56	1/1033 (0.1%)
1	C5	0.25	0/761	0.52	0/1033
1	C6	0.24	0/761	0.49	0/1033
1	C8	0.24	0/761	0.54	1/1033 (0.1%)
1	C9	0.24	0/761	0.51	0/1033
1	CA	0.24	0/761	0.49	0/1033
1	CC	0.24	0/761	0.55	1/1033 (0.1%)
1	CD	0.25	0/761	0.49	0/1033
1	CE	0.24	0/761	0.49	0/1033
1	CG	0.24	0/761	0.55	1/1033 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CH	0.24	0/761	0.50	0/1033
1	CI	0.24	0/761	0.49	0/1033
1	CK	0.24	0/761	0.54	1/1033 (0.1%)
1	CL	0.25	0/761	0.50	0/1033
1	CM	0.24	0/761	0.49	0/1033
1	CO	0.24	0/761	0.54	0/1033
1	CP	0.25	0/761	0.50	0/1033
1	CQ	0.25	0/761	0.50	0/1033
1	CS	0.24	0/761	0.54	1/1033 (0.1%)
1	CT	0.25	0/761	0.50	0/1033
1	CU	0.24	0/761	0.49	0/1033
1	CW	0.24	0/761	0.55	1/1033 (0.1%)
1	CX	0.25	0/761	0.50	0/1033
1	CY	0.24	0/761	0.49	0/1033
1	D0	0.24	0/761	0.55	1/1033 (0.1%)
1	D1	0.24	0/761	0.51	0/1033
1	D2	0.25	0/761	0.51	0/1033
1	D4	0.25	0/761	0.55	1/1033 (0.1%)
1	D5	0.25	0/761	0.51	0/1033
1	D6	0.24	0/761	0.49	0/1033
1	D8	0.24	0/761	0.54	0/1033
1	D9	0.25	0/761	0.51	0/1033
1	DA	0.25	0/761	0.51	0/1033
1	DC	0.23	0/761	0.54	1/1033 (0.1%)
1	DD	0.25	0/761	0.50	0/1033
1	DE	0.25	0/761	0.49	0/1033
1	DG	0.24	0/761	0.55	1/1033 (0.1%)
1	DH	0.25	0/761	0.50	0/1033
1	DI	0.24	0/761	0.49	0/1033
1	DK	0.24	0/761	0.55	1/1033 (0.1%)
1	DL	0.25	0/761	0.50	0/1033
1	DM	0.24	0/761	0.49	0/1033
1	DO	0.24	0/761	0.54	1/1033 (0.1%)
1	DP	0.25	0/761	0.51	0/1033
1	DQ	0.25	0/761	0.51	0/1033
1	DS	0.24	0/761	0.55	1/1033 (0.1%)
1	DT	0.25	0/761	0.51	0/1033
1	DU	0.26	0/761	0.51	0/1033
1	DW	0.25	0/761	0.55	1/1033 (0.1%)
1	DX	0.25	0/761	0.51	0/1033
1	DY	0.24	0/761	0.49	0/1033
1	E	0.24	0/761	0.55	1/1033 (0.1%)
1	E0	0.24	0/761	0.55	1/1033 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	E1	0.25	0/761	0.52	0/1033
1	E2	0.24	0/761	0.49	0/1033
1	E4	0.24	0/761	0.54	1/1033 (0.1%)
1	E5	0.25	0/761	0.51	0/1033
1	E6	0.25	0/761	0.50	0/1033
1	EA	0.25	0/761	0.51	0/1033
1	EC	0.24	0/761	0.55	1/1033 (0.1%)
1	ED	0.25	0/761	0.50	0/1033
1	EE	0.24	0/761	0.49	0/1033
1	EG	0.24	0/761	0.55	1/1033 (0.1%)
1	EH	0.25	0/761	0.50	0/1033
1	EI	0.25	0/761	0.50	0/1033
1	EK	0.24	0/761	0.54	1/1033 (0.1%)
1	EL	0.25	0/761	0.50	0/1033
1	EM	0.24	0/761	0.49	0/1033
1	EO	0.25	0/761	0.56	1/1033 (0.1%)
1	EP	0.25	0/761	0.51	0/1033
1	EQ	0.24	0/761	0.49	0/1033
1	ES	0.24	0/761	0.54	1/1033 (0.1%)
1	ET	0.25	0/761	0.51	0/1033
1	EU	0.25	0/761	0.51	0/1033
1	EW	0.24	0/761	0.56	1/1033 (0.1%)
1	EX	0.25	0/761	0.51	0/1033
1	EY	0.25	0/761	0.50	0/1033
1	F	0.25	0/761	0.51	0/1033
1	G	0.24	0/761	0.50	0/1033
1	I	0.24	0/761	0.55	1/1033 (0.1%)
1	J	0.25	0/761	0.51	0/1033
1	K	0.25	0/761	0.51	0/1033
1	M	0.24	0/761	0.54	1/1033 (0.1%)
1	N	0.25	0/761	0.51	0/1033
1	O	0.24	0/761	0.49	0/1033
1	Q	0.24	0/761	0.54	1/1033 (0.1%)
1	R	0.25	0/761	0.50	0/1033
1	S	0.24	0/761	0.49	0/1033
1	U	0.24	0/761	0.55	1/1033 (0.1%)
1	V	0.25	0/761	0.50	0/1033
1	W	0.24	0/761	0.49	0/1033
1	Y	0.24	0/761	0.55	1/1033 (0.1%)
1	Z	0.25	0/761	0.50	0/1033
1	a	0.24	0/761	0.55	1/1033 (0.1%)
1	b	0.25	0/761	0.50	0/1033
1	c	0.25	0/761	0.50	0/1033

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	e	0.24	0/761	0.56	1/1033 (0.1%)
1	f	0.25	0/761	0.51	0/1033
1	g	0.25	0/761	0.50	0/1033
1	i	0.25	0/761	0.55	1/1033 (0.1%)
1	j	0.25	0/761	0.51	0/1033
1	k	0.24	0/761	0.49	0/1033
1	m	0.24	0/761	0.54	1/1033 (0.1%)
1	n	0.25	0/761	0.51	0/1033
1	o	0.25	0/761	0.51	0/1033
1	q	0.24	0/761	0.55	1/1033 (0.1%)
1	r	0.25	0/761	0.50	0/1033
1	s	0.24	0/761	0.49	0/1033
1	u	0.24	0/761	0.54	1/1033 (0.1%)
1	v	0.25	0/761	0.50	0/1033
1	w	0.24	0/761	0.49	0/1033
1	y	0.24	0/761	0.55	1/1033 (0.1%)
1	z	0.25	0/761	0.50	0/1033
2	1	0.27	0/722	0.52	0/980
2	5	0.26	0/722	0.49	0/980
2	9	0.26	0/722	0.50	0/980
2	A3	0.27	0/722	0.50	0/980
2	A7	0.26	0/722	0.49	0/980
2	AB	0.26	0/722	0.51	0/980
2	AF	0.26	0/722	0.49	0/980
2	AJ	0.26	0/722	0.48	0/980
2	AN	0.26	0/722	0.48	0/980
2	AR	0.26	0/722	0.49	0/980
2	AV	0.27	0/722	0.48	0/980
2	AZ	0.25	0/722	0.49	0/980
2	B3	0.26	0/722	0.49	0/980
2	B7	0.26	0/722	0.49	0/980
2	BB	0.26	0/722	0.50	0/980
2	BF	0.27	0/722	0.50	0/980
2	BJ	0.26	0/722	0.50	0/980
2	BN	0.26	0/722	0.48	0/980
2	BR	0.26	0/722	0.48	0/980
2	BV	0.25	0/722	0.49	0/980
2	BZ	0.26	0/722	0.49	0/980
2	C3	0.26	0/722	0.49	0/980
2	C7	0.26	0/722	0.48	0/980
2	CB	0.26	0/722	0.49	0/980
2	CF	0.26	0/722	0.51	0/980
2	CJ	0.26	0/722	0.52	0/980

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	CN	0.26	0/722	0.52	0/980
2	CR	0.26	0/722	0.49	0/980
2	CV	0.26	0/722	0.50	0/980
2	CZ	0.26	0/722	0.50	0/980
2	D	0.26	0/722	0.48	0/980
2	D3	0.26	0/722	0.49	0/980
2	D7	0.26	0/722	0.48	0/980
2	DB	0.25	0/722	0.50	0/980
2	DF	0.27	0/722	0.51	0/980
2	DJ	0.27	0/722	0.51	0/980
2	DN	0.27	0/722	0.51	0/980
2	DR	0.25	0/722	0.49	0/980
2	DV	0.26	0/722	0.49	0/980
2	DZ	0.27	0/722	0.49	0/980
2	E3	0.27	0/722	0.50	0/980
2	E7	0.25	0/722	0.49	0/980
2	EB	0.26	0/722	0.49	0/980
2	EF	0.26	0/722	0.50	0/980
2	EJ	0.26	0/722	0.50	0/980
2	EN	0.26	0/722	0.50	0/980
2	ER	0.26	0/722	0.48	0/980
2	EV	0.26	0/722	0.49	0/980
2	EZ	0.26	0/722	0.49	0/980
2	H	0.25	0/722	0.49	0/980
2	L	0.26	0/722	0.49	0/980
2	P	0.27	0/722	0.49	0/980
2	T	0.26	0/722	0.52	0/980
2	X	0.26	0/722	0.51	0/980
2	d	0.26	0/722	0.49	0/980
2	h	0.26	0/722	0.49	0/980
2	l	0.27	0/722	0.50	0/980
2	p	0.26	0/722	0.49	0/980
2	t	0.26	0/722	0.52	0/980
2	x	0.26	0/722	0.51	0/980
All	All	0.25	0/180300	0.51	58/244740 (0.0%)

There are no bond length outliers.

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AG	66	ARG	N-CA-C	-5.26	105.94	114.09
1	A	66	ARG	N-CA-C	-5.25	105.96	114.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DS	66	ARG	N-CA-C	-5.24	105.97	114.09
1	I	66	ARG	N-CA-C	-5.24	105.97	114.09
1	AO	66	ARG	N-CA-C	-5.23	105.98	114.09

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	0	752	0	770	9	0
1	2	752	0	770	10	0
1	3	752	0	770	9	0
1	4	752	0	770	8	0
1	6	752	0	770	12	0
1	7	752	0	770	9	0
1	8	752	0	770	7	0
1	A	752	0	770	10	0
1	A0	752	0	770	11	0
1	A1	752	0	770	9	0
1	A2	752	0	770	7	0
1	A4	752	0	770	13	0
1	A5	752	0	770	11	0
1	A6	752	0	770	7	0
1	A8	752	0	770	11	0
1	A9	752	0	770	11	0
1	AA	752	0	770	10	0
1	AC	752	0	770	13	0
1	AD	752	0	770	11	0
1	AE	752	0	770	8	0
1	AG	752	0	770	7	0
1	AH	752	0	770	7	0
1	AI	752	0	770	8	0
1	AK	752	0	770	12	0
1	AL	752	0	770	10	0
1	AM	752	0	770	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AO	752	0	770	9	0
1	AP	752	0	770	7	0
1	AQ	752	0	770	8	0
1	AS	752	0	770	12	0
1	AT	752	0	770	7	0
1	AU	752	0	770	10	0
1	AW	752	0	770	14	0
1	AX	752	0	770	12	0
1	AY	752	0	770	9	0
1	B	752	0	770	8	0
1	B0	752	0	770	11	0
1	B1	752	0	770	12	0
1	B2	752	0	770	9	0
1	B4	752	0	770	9	0
1	B5	752	0	770	7	0
1	B6	752	0	770	7	0
1	B8	752	0	770	12	0
1	B9	752	0	770	7	0
1	BA	752	0	770	8	0
1	BC	752	0	770	12	0
1	BD	752	0	770	9	0
1	BE	752	0	770	10	0
1	BG	752	0	770	13	0
1	BH	752	0	770	11	0
1	BI	752	0	770	10	0
1	BK	752	0	770	11	0
1	BL	752	0	770	7	0
1	BM	752	0	770	7	0
1	BO	752	0	770	12	0
1	BP	752	0	770	9	0
1	BQ	752	0	770	10	0
1	BS	752	0	770	12	0
1	BT	752	0	770	11	0
1	BU	752	0	770	9	0
1	BW	752	0	770	11	0
1	BX	752	0	770	8	0
1	BY	752	0	770	8	0
1	C	752	0	770	7	0
1	C0	752	0	770	10	0
1	C1	752	0	770	8	0
1	C2	752	0	770	6	0
1	C4	752	0	770	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C5	752	0	770	9	0
1	C6	752	0	770	9	0
1	C8	752	0	770	10	0
1	C9	752	0	770	9	0
1	CA	752	0	770	10	0
1	CC	752	0	770	13	0
1	CD	752	0	770	7	0
1	CE	752	0	770	9	0
1	CG	752	0	770	10	0
1	CH	752	0	770	6	0
1	CI	752	0	770	9	0
1	CK	752	0	770	12	0
1	CL	752	0	770	8	0
1	CM	752	0	770	12	0
1	CO	752	0	770	13	0
1	CP	752	0	770	11	0
1	CQ	752	0	770	8	0
1	CS	752	0	770	11	0
1	CT	752	0	770	10	0
1	CU	752	0	770	7	0
1	CW	752	0	770	12	0
1	CX	752	0	770	10	0
1	CY	752	0	770	8	0
1	D0	752	0	770	10	0
1	D1	752	0	770	8	0
1	D2	752	0	770	6	0
1	D4	752	0	770	12	0
1	D5	752	0	770	10	0
1	D6	752	0	770	9	0
1	D8	752	0	770	12	0
1	D9	752	0	770	11	0
1	DA	752	0	770	9	0
1	DC	752	0	770	9	0
1	DD	752	0	770	7	0
1	DE	752	0	770	10	0
1	DG	752	0	770	12	0
1	DH	752	0	770	7	0
1	DI	752	0	770	11	0
1	DK	752	0	770	11	0
1	DL	752	0	770	8	0
1	DM	752	0	770	11	0
1	DO	752	0	770	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DP	752	0	770	12	0
1	DQ	752	0	770	8	0
1	DS	752	0	770	11	0
1	DT	752	0	770	8	0
1	DU	752	0	770	6	0
1	DW	752	0	770	12	0
1	DX	752	0	770	9	0
1	DY	752	0	770	9	0
1	E	752	0	770	9	0
1	E0	752	0	770	11	0
1	E1	752	0	770	9	0
1	E2	752	0	770	10	0
1	E4	752	0	770	12	0
1	E5	752	0	770	11	0
1	E6	752	0	770	8	0
1	EA	752	0	770	8	0
1	EC	752	0	770	11	0
1	ED	752	0	770	10	0
1	EE	752	0	770	7	0
1	EG	752	0	770	11	0
1	EH	752	0	770	10	0
1	EI	752	0	770	8	0
1	EK	752	0	770	13	0
1	EL	752	0	770	9	0
1	EM	752	0	770	7	0
1	EO	752	0	770	11	0
1	EP	752	0	770	8	0
1	EQ	752	0	770	10	0
1	ES	752	0	770	12	0
1	ET	752	0	770	12	0
1	EU	752	0	770	7	0
1	EW	752	0	770	11	0
1	EX	752	0	770	8	0
1	EY	752	0	770	6	0
1	F	752	0	770	12	0
1	G	752	0	770	8	0
1	I	752	0	770	10	0
1	J	752	0	770	7	0
1	K	752	0	770	7	0
1	M	752	0	770	12	0
1	N	752	0	770	9	0
1	O	752	0	770	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	752	0	770	12	0
1	R	752	0	770	9	0
1	S	752	0	770	12	0
1	U	752	0	770	11	0
1	V	752	0	770	7	0
1	W	752	0	770	10	0
1	Y	752	0	770	12	0
1	Z	752	0	770	7	0
1	a	752	0	770	11	0
1	b	752	0	770	10	0
1	c	752	0	770	7	0
1	e	752	0	770	9	0
1	f	752	0	770	7	0
1	g	752	0	770	6	0
1	i	752	0	770	11	0
1	j	752	0	770	9	0
1	k	752	0	770	10	0
1	m	752	0	770	12	0
1	n	752	0	770	12	0
1	o	752	0	770	9	0
1	q	752	0	770	12	0
1	r	752	0	770	9	0
1	s	752	0	770	11	0
1	u	752	0	770	12	0
1	v	752	0	770	7	0
1	w	752	0	770	11	0
1	y	752	0	770	10	0
1	z	752	0	770	7	0
2	1	712	0	737	7	0
2	5	712	0	737	7	0
2	9	712	0	737	6	0
2	A3	712	0	737	6	0
2	A7	712	0	737	6	0
2	AB	712	0	737	7	0
2	AF	712	0	737	4	0
2	AJ	712	0	737	4	0
2	AN	712	0	737	5	0
2	AR	712	0	737	4	0
2	AV	712	0	737	6	0
2	AZ	712	0	737	5	0
2	B3	712	0	737	5	0
2	B7	712	0	737	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	BB	712	0	737	5	0
2	BF	712	0	737	6	0
2	BJ	712	0	737	6	0
2	BN	712	0	737	4	0
2	BR	712	0	737	6	0
2	BV	712	0	737	4	0
2	BZ	712	0	737	4	0
2	C3	712	0	737	4	0
2	C7	712	0	737	7	0
2	CB	712	0	737	7	0
2	CF	712	0	737	6	0
2	CJ	712	0	737	7	0
2	CN	712	0	737	7	0
2	CR	712	0	737	7	0
2	CV	712	0	737	6	0
2	CZ	712	0	737	5	0
2	D	712	0	737	4	0
2	D3	712	0	737	5	0
2	D7	712	0	737	7	0
2	DB	712	0	737	4	0
2	DF	712	0	737	8	0
2	DJ	712	0	737	7	0
2	DN	712	0	737	7	0
2	DR	712	0	737	5	0
2	DV	712	0	737	4	0
2	DZ	712	0	737	6	0
2	E3	712	0	737	6	0
2	E7	712	0	737	5	0
2	EB	712	0	737	4	0
2	EF	712	0	737	7	0
2	EJ	712	0	737	6	0
2	EN	712	0	737	6	0
2	ER	712	0	737	7	0
2	EV	712	0	737	5	0
2	EZ	712	0	737	4	0
2	H	712	0	737	4	0
2	L	712	0	737	5	0
2	P	712	0	737	6	0
2	T	712	0	737	6	0
2	X	712	0	737	6	0
2	d	712	0	737	7	0
2	h	712	0	737	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	l	712	0	737	6	0
2	p	712	0	737	5	0
2	t	712	0	737	6	0
2	x	712	0	737	6	0
All	All	178080	0	182820	1430	0

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

The worst 5 of 1430 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:CQ:79:ALA:HB2	2:CR:14:GLN:HG3	1.75	0.69
1:EM:79:ALA:HB2	2:EN:14:GLN:HG3	1.76	0.68
1:BI:79:ALA:HB2	2:BJ:14:GLN:HG3	1.75	0.68
1:EI:79:ALA:HB2	2:EJ:14:GLN:HG3	1.76	0.67
1:4:79:ALA:HB2	2:5:14:GLN:HG3	1.76	0.67

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	2	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	3	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	4	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	6	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	7	98/113 (87%)	97 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	8	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	A	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	A0	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	A1	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	A2	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	A4	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	A5	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	A6	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	A8	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	A9	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	AA	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AC	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AD	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	AE	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AG	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AH	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	AI	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AK	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AL	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AM	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AO	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AP	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	AQ	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AS	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AT	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AU	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AW	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AX	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	AY	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	B	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	B0	98/113 (87%)	95 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B1	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	B2	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	B4	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	B5	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	B6	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	B8	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	B9	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BA	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BC	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BD	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BE	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BG	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BH	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	BI	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BK	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BL	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	BM	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BO	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BP	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BQ	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BS	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BT	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	BU	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BW	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BX	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	BY	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	C	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	C0	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	C1	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	C2	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	C4	98/113 (87%)	95 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C5	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	C6	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	C8	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	C9	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	CA	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	CC	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CD	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	CE	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	CG	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CH	85/113 (75%)	84 (99%)	1 (1%)	0	100	100
1	CI	12/113 (11%)	11 (92%)	1 (8%)	0	100	100
1	CK	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CL	39/113 (34%)	38 (97%)	1 (3%)	0	100	100
1	CO	27/113 (24%)	27 (100%)	0	0	100	100
1	CP	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	CQ	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	CS	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CT	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	CU	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	CW	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CX	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	CY	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	D0	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	D1	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	D2	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	D4	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	D5	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	D6	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	D8	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	D9	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	DA	98/113 (87%)	96 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DC	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	DD	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	DE	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	DG	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	DH	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	DI	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	DK	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	DL	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	DM	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	DO	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	DP	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	DQ	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	DS	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	DT	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	DU	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	DW	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	DX	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	DY	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	E	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	E0	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	E1	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	E2	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	E4	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	E5	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	E6	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	EA	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	EC	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	ED	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	EE	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	EG	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	EH	98/113 (87%)	97 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EI	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	EK	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	EL	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	EM	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	EO	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	EP	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	EQ	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	ES	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	ET	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	EU	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	EW	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	EX	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	EY	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	F	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	G	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	I	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	J	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	K	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	M	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	N	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	O	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	Q	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	R	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	S	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	U	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	V	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	W	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	Y	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	Z	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	a	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	b	98/113 (87%)	97 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	c	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	e	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	f	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	g	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	i	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	j	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	k	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	m	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	n	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	o	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	q	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	r	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	s	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	u	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	v	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
1	w	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	y	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	z	98/113 (87%)	97 (99%)	1 (1%)	0	100	100
2	1	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	5	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	9	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	A3	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	A7	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	AB	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	AF	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	AJ	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	AN	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	AR	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	AV	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	AZ	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	B3	92/105 (88%)	90 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B7	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	BB	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	BF	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	BJ	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	BN	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	BR	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	BV	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	BZ	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	C3	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	C7	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	CB	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	CF	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	CJ	46/105 (44%)	44 (96%)	2 (4%)	0	100	100
2	CR	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	CV	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	CZ	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	D	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	D3	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	D7	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	DB	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	DF	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	DJ	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	DN	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	DR	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	DV	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	DZ	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	E3	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	E7	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	EB	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	EF	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	EJ	92/105 (88%)	89 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	EN	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	ER	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	EV	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	EZ	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	H	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	L	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	P	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	T	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	X	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	d	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	h	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	l	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	p	92/105 (88%)	90 (98%)	2 (2%)	0	100	100
2	t	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
2	x	92/105 (88%)	89 (97%)	3 (3%)	0	100	100
All	All	22695/26422 (86%)	22168 (98%)	527 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no 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.

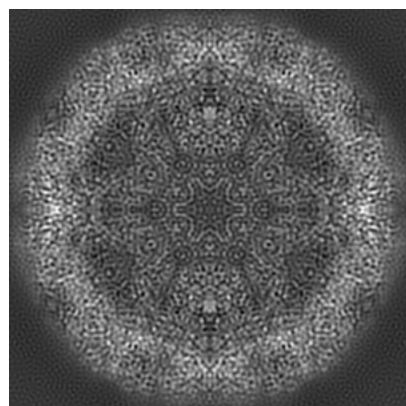
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20207. These allow visual inspection of the internal detail of the map and identification of artifacts.

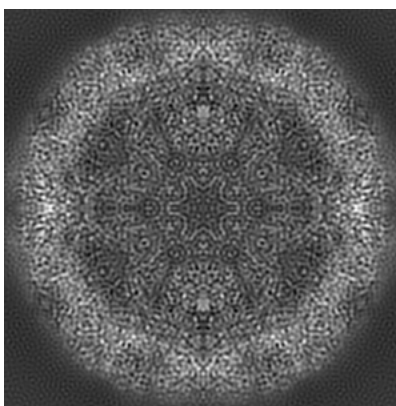
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

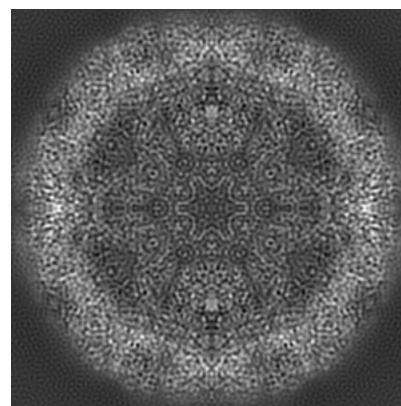
6.1.1 Primary map



X

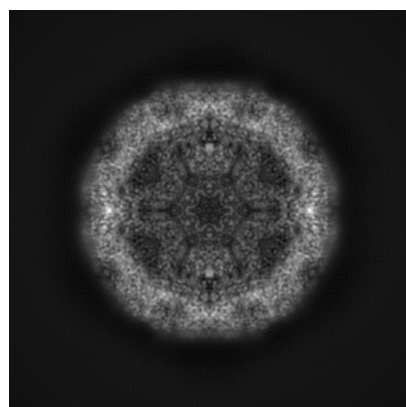


Y

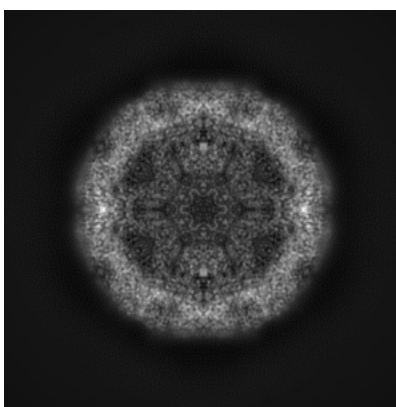


Z

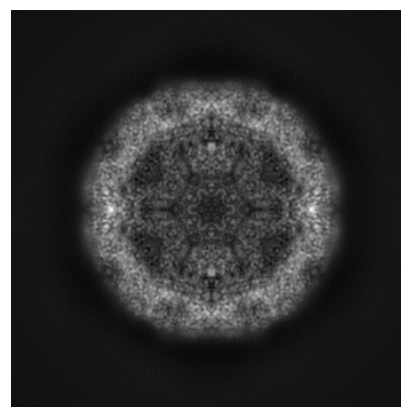
6.1.2 Raw map



X



Y

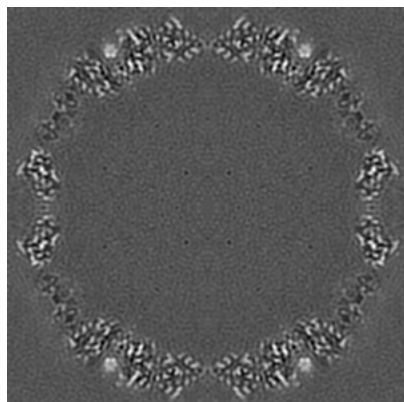


Z

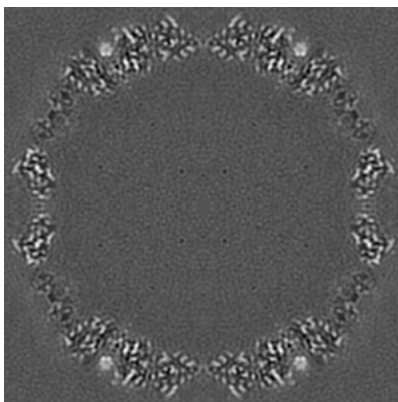
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

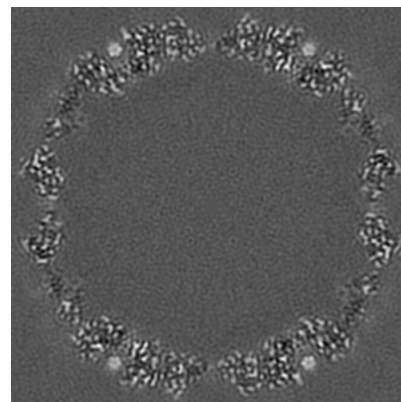
6.2.1 Primary map



X Index: 138

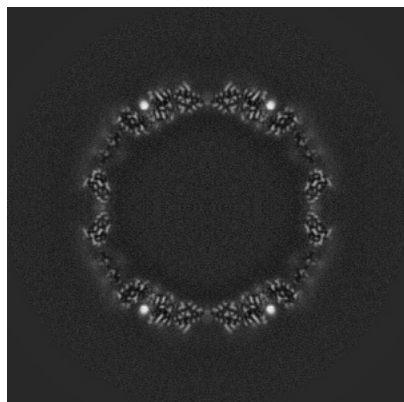


Y Index: 138

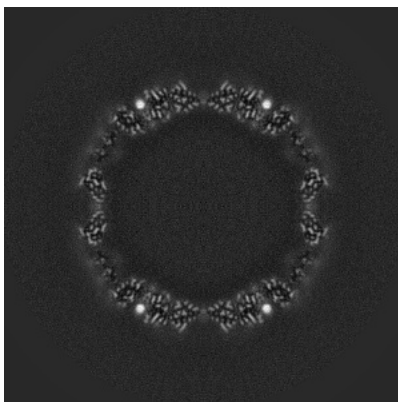


Z Index: 138

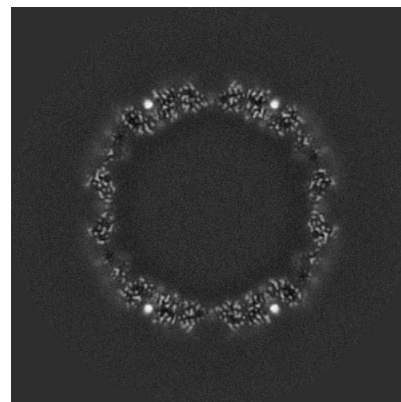
6.2.2 Raw map



X Index: 212



Y Index: 212

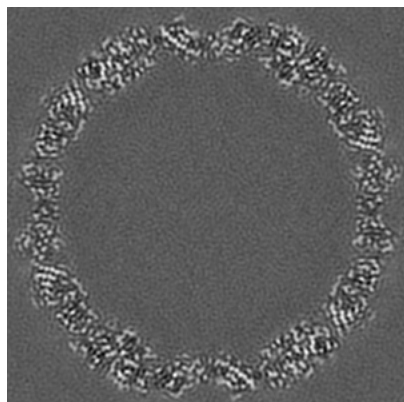


Z Index: 212

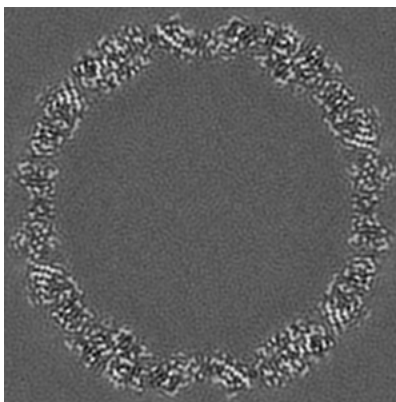
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

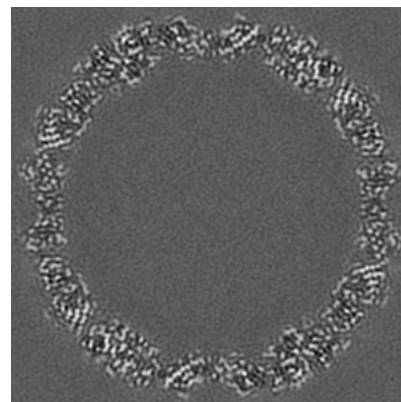
6.3.1 Primary map



X Index: 125

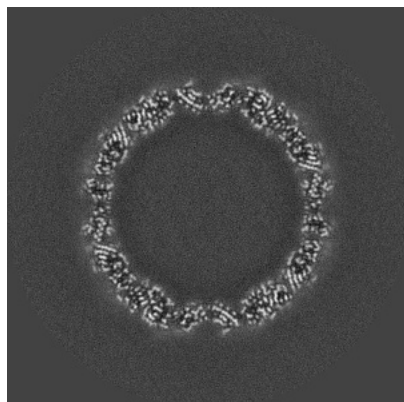


Y Index: 125

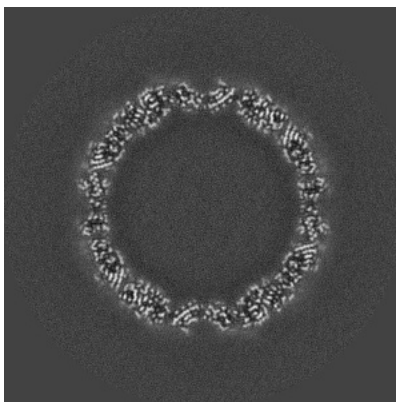


Z Index: 150

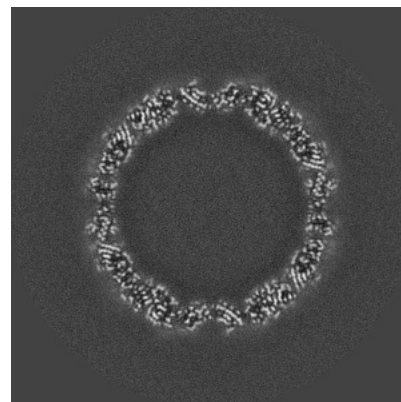
6.3.2 Raw map



X Index: 199



Y Index: 225

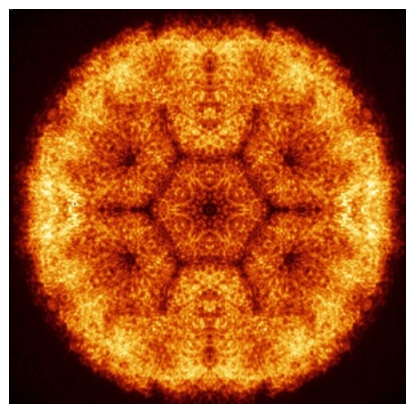


Z Index: 198

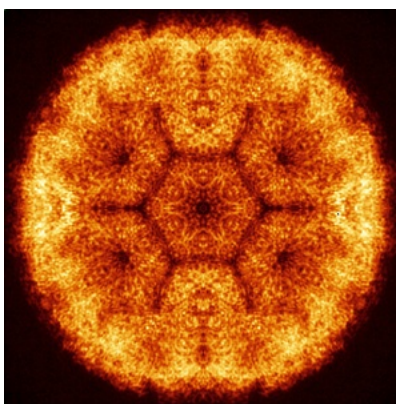
The images above show the largest variance slices of the map in three orthogonal directions.

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

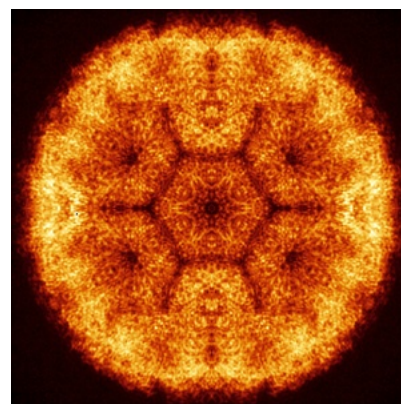
6.4.1 Primary map



X

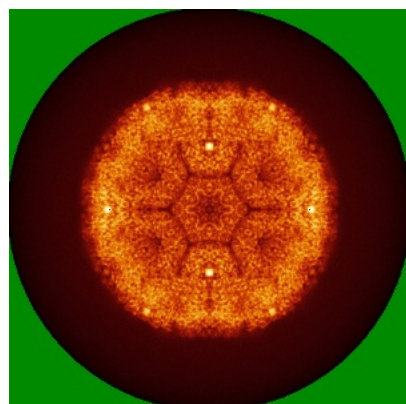


Y

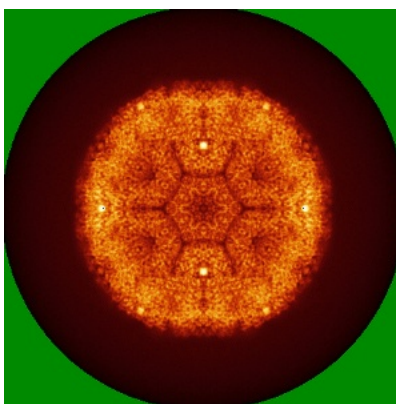


Z

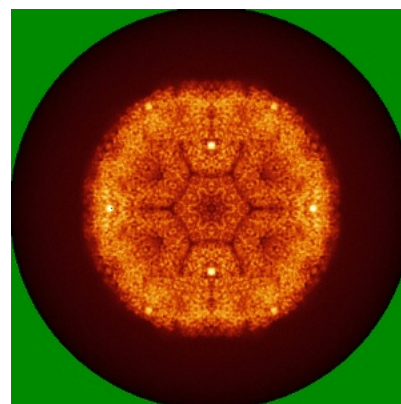
6.4.2 Raw map



X



Y

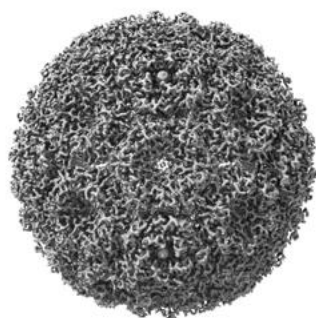


Z

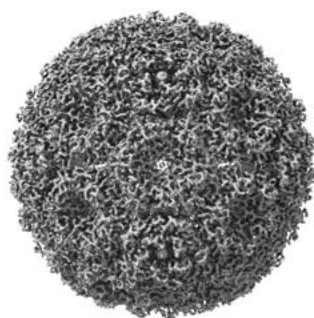
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

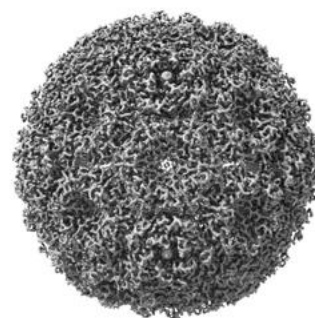
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

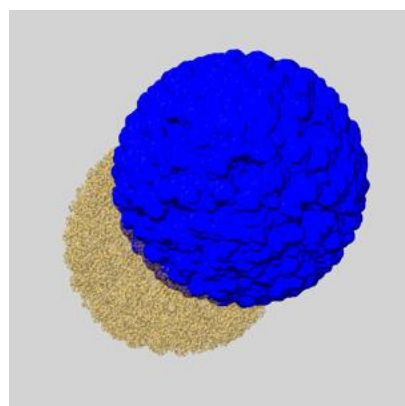
6.6 Mask visualisation [i](#)

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

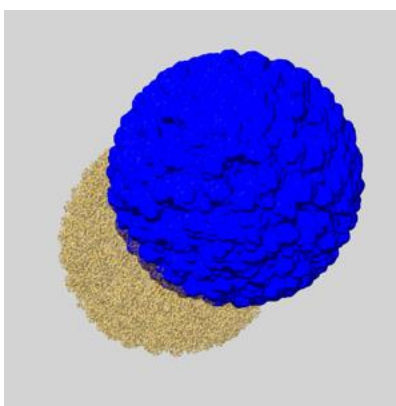
A mask typically either:

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

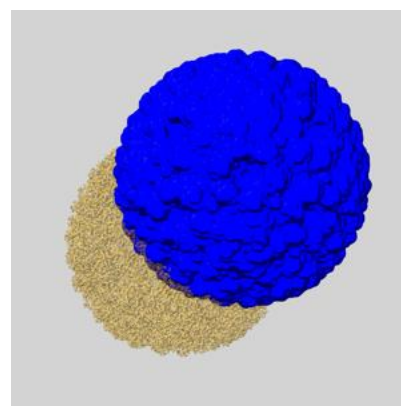
6.6.1 emd_20207_msk_1.map [i](#)



X



Y

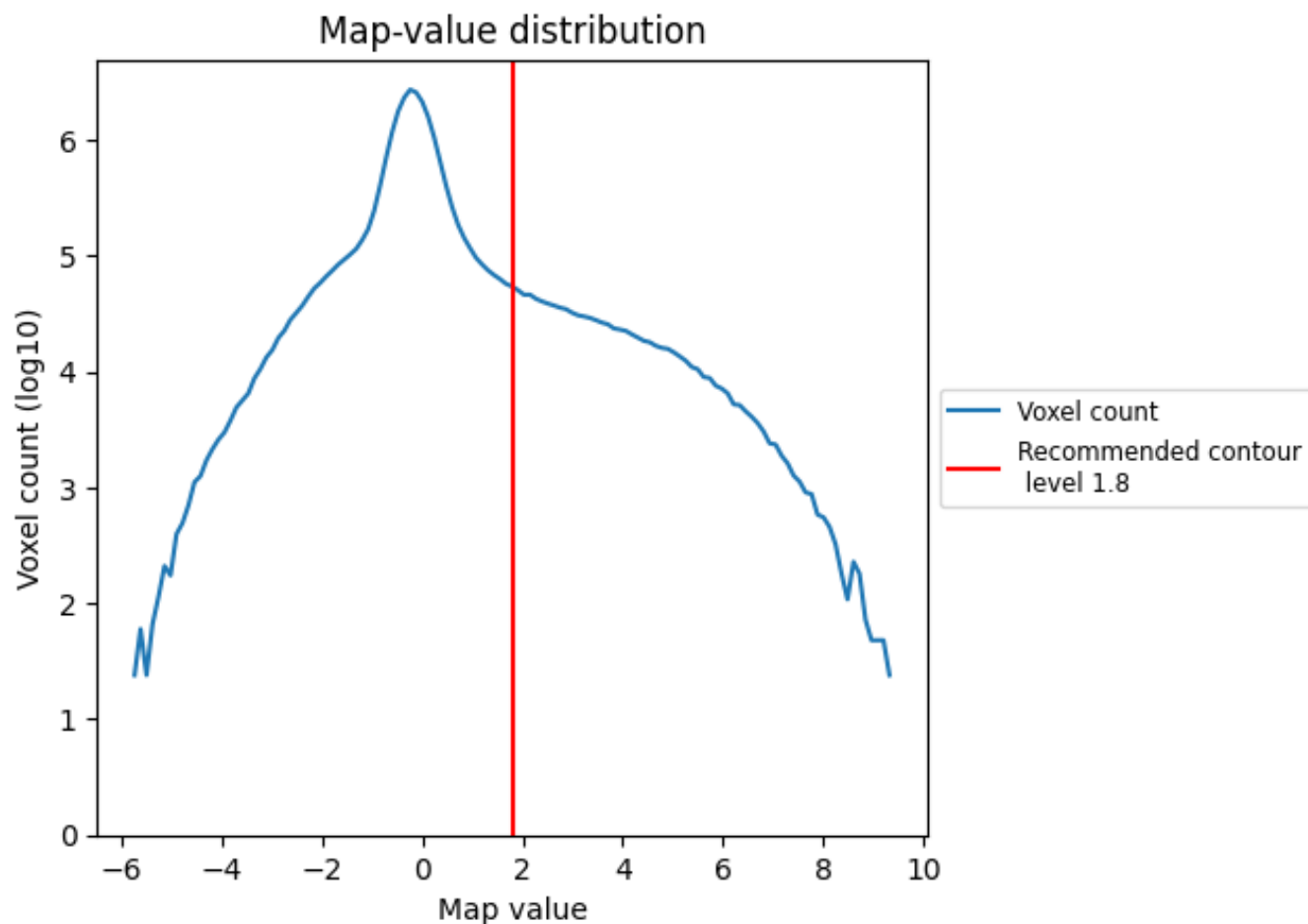


Z

7 Map analysis [i](#)

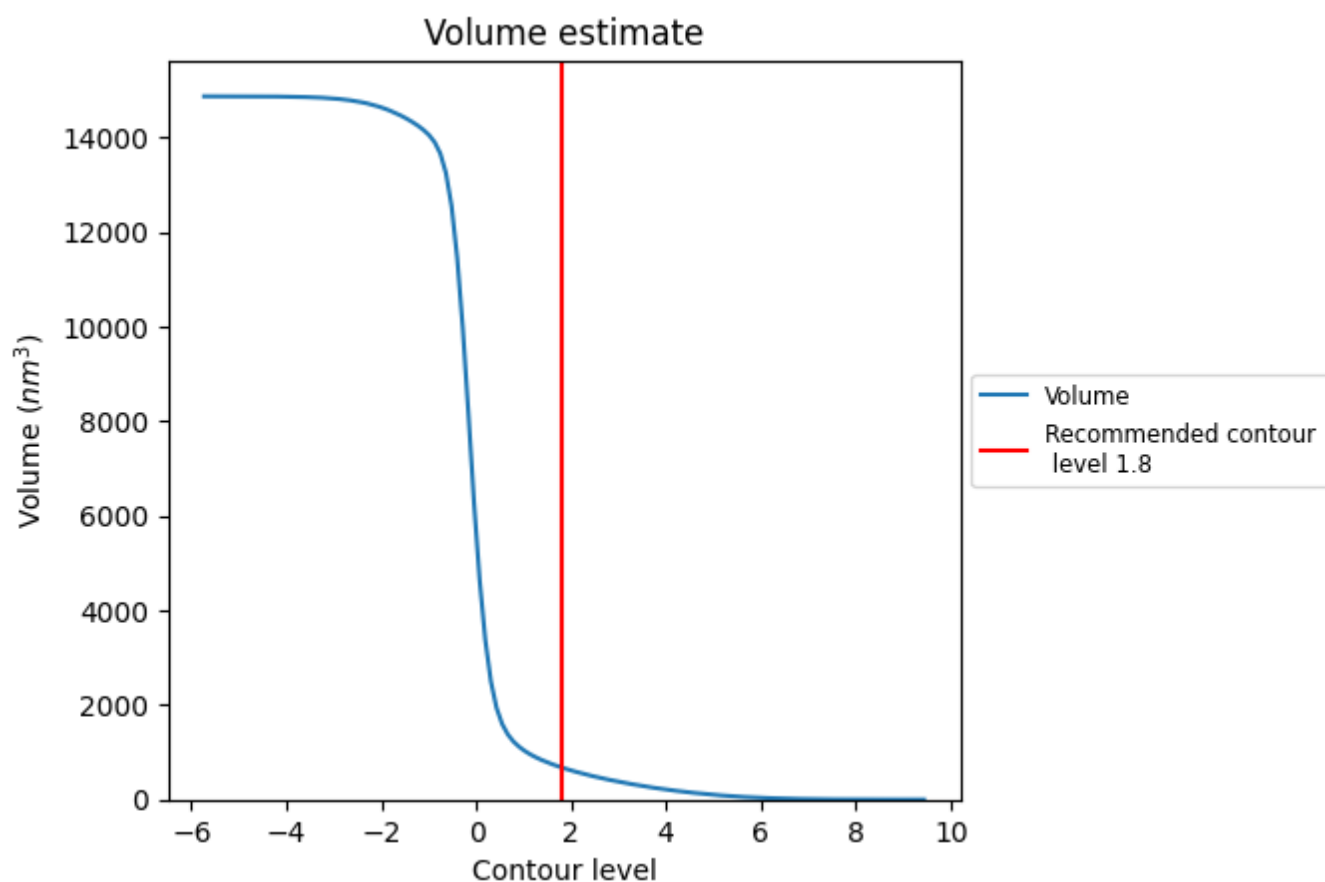
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

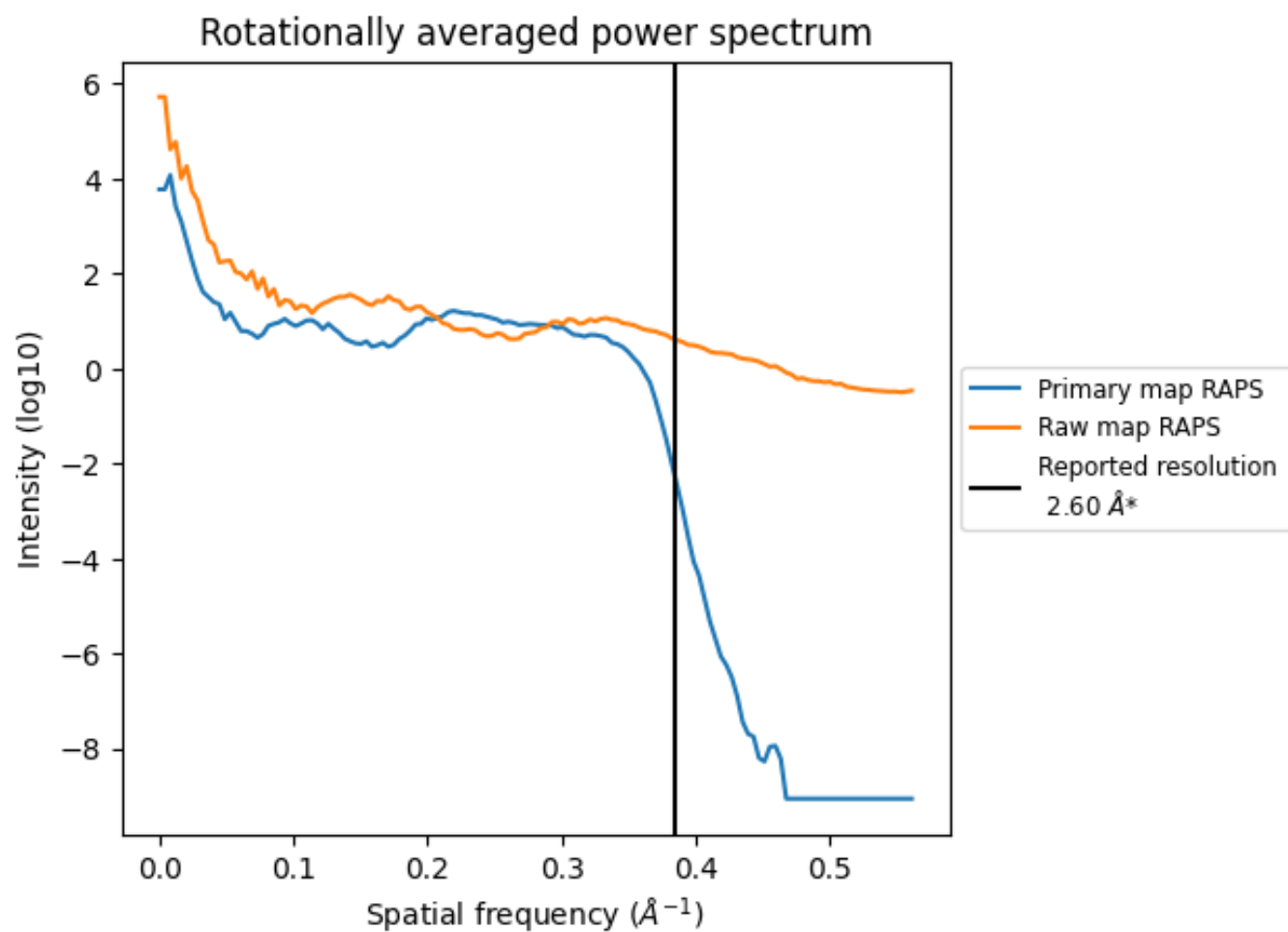
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 678 nm³; this corresponds to an approximate mass of 613 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 ⓘ

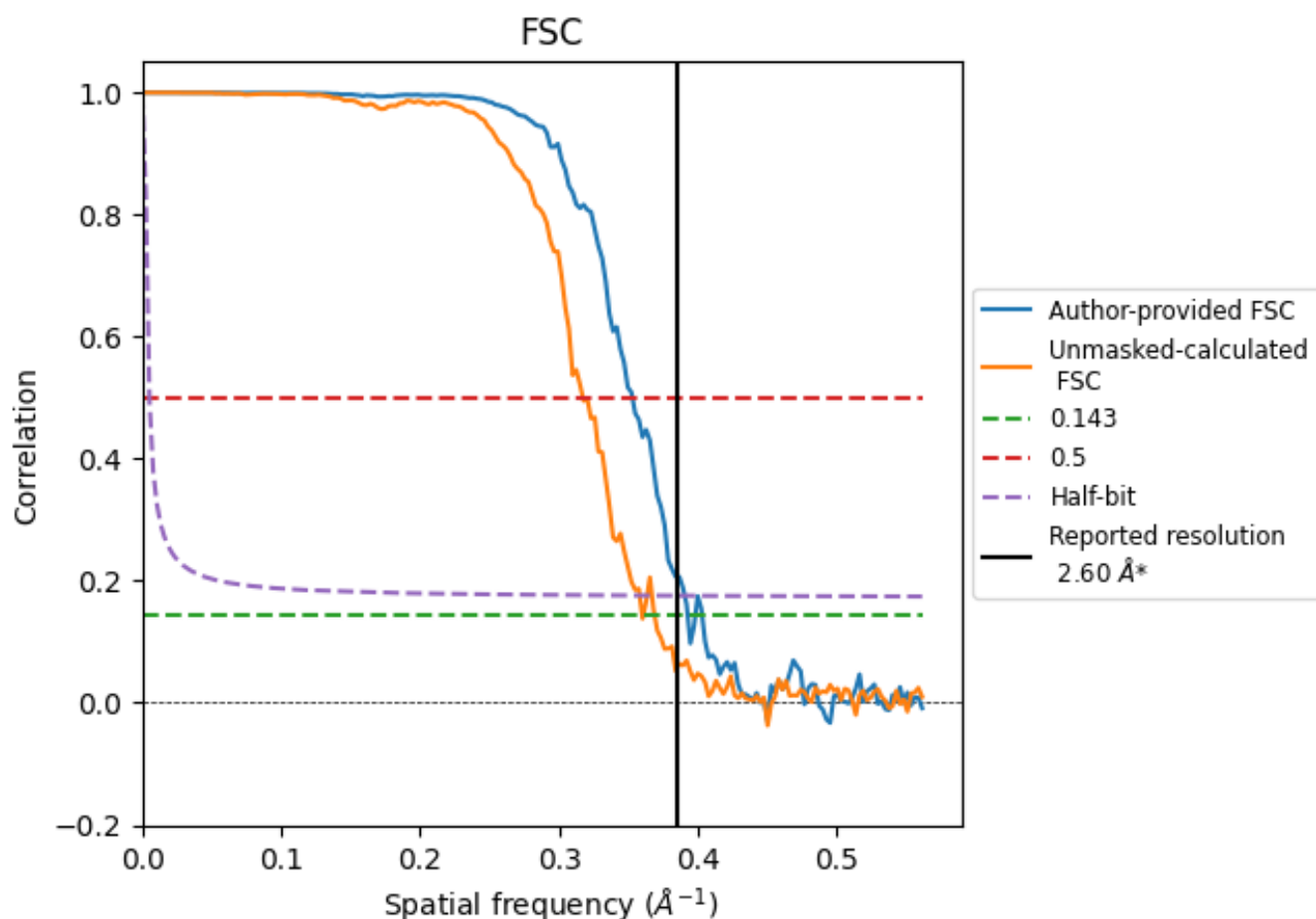


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

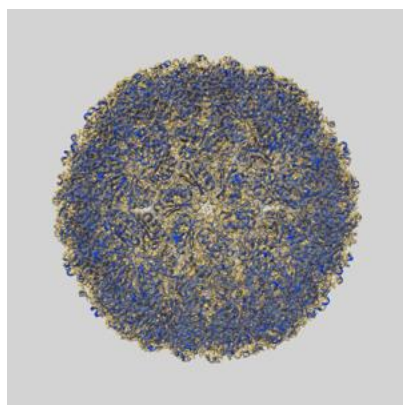
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.55	2.83	2.56
Unmasked-calculated*	2.78	3.15	2.79

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

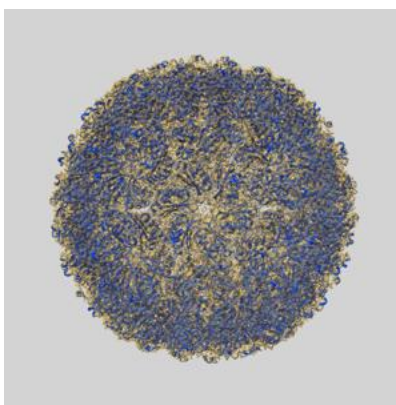
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20207 and PDB model 6OWG. Per-residue inclusion information can be found in [section 3](#) on [page 40](#).

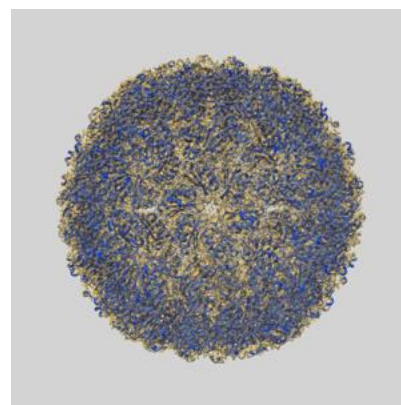
9.1 Map-model overlay [i](#)



X



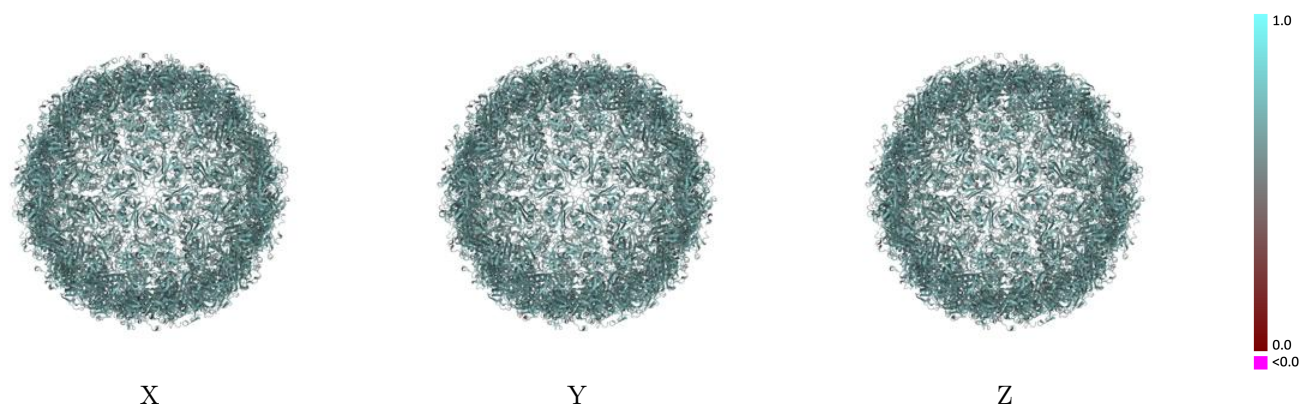
Y



Z

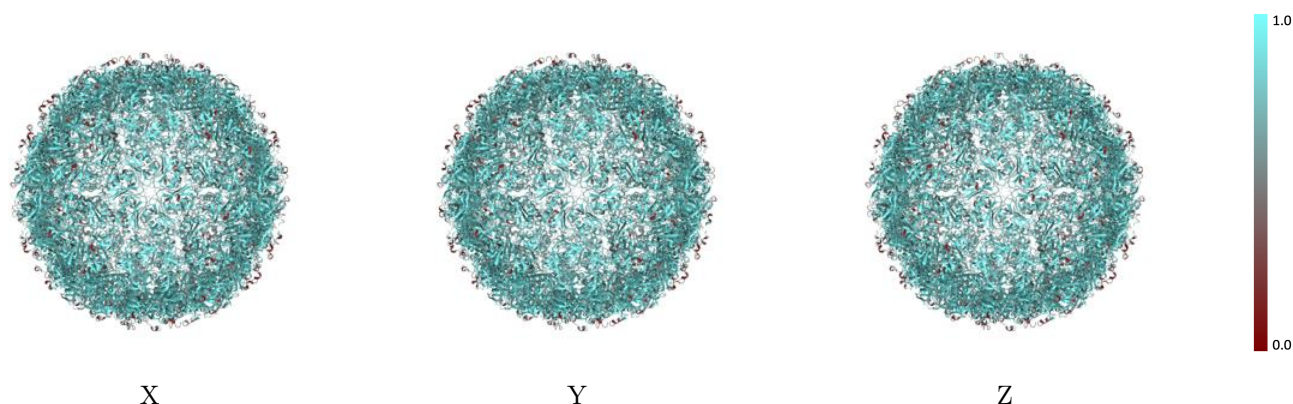
The images above show the 3D surface view of the map at the recommended contour level 1.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



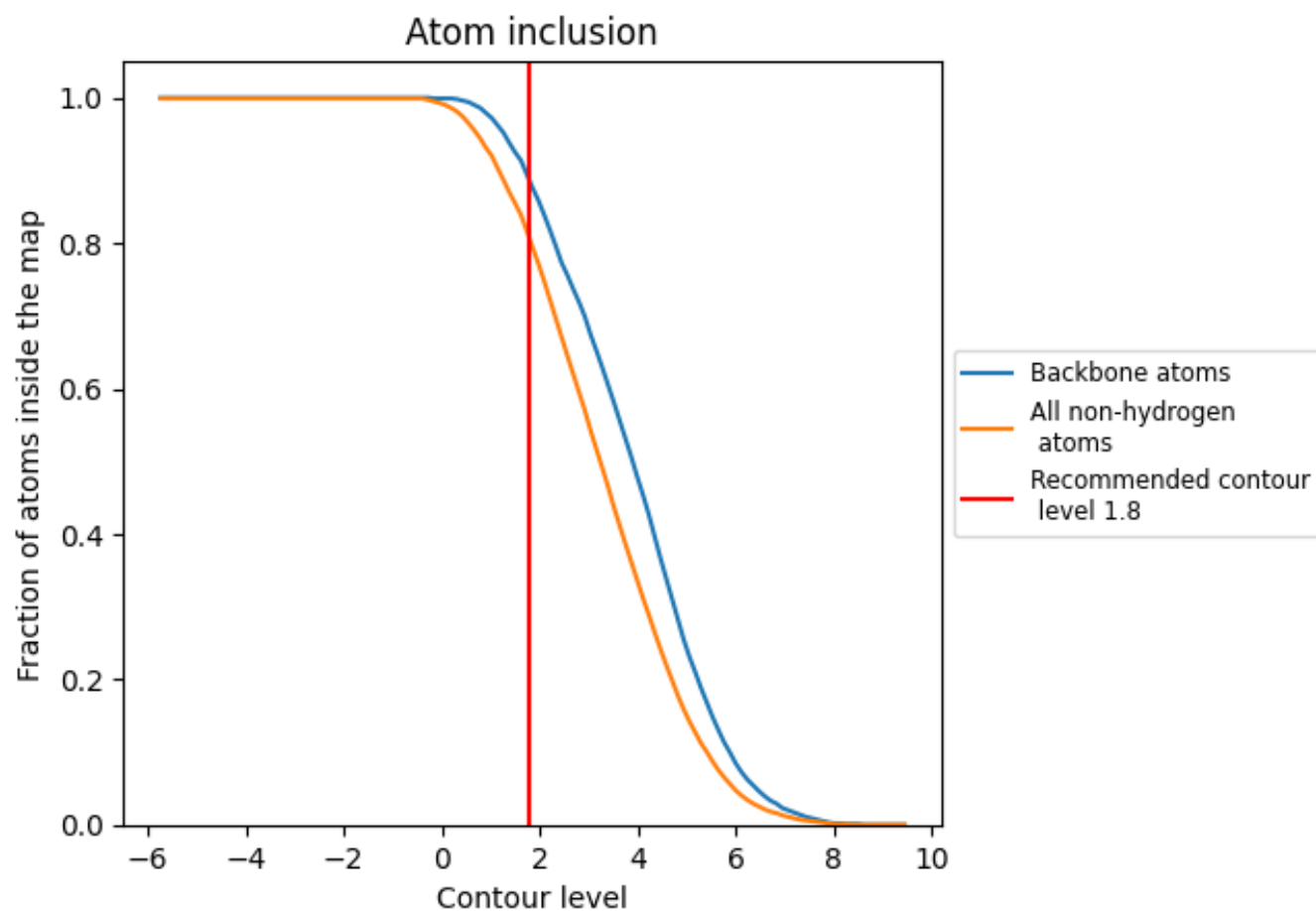
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8050	 0.6340
0	 0.7810	 0.6340
1	 0.8380	 0.6350
2	 0.8050	 0.6290
3	 0.8080	 0.6370
4	 0.7840	 0.6320
5	 0.8340	 0.6320
6	 0.8080	 0.6290
7	 0.8090	 0.6350
8	 0.7860	 0.6340
9	 0.8320	 0.6330
A	 0.7990	 0.6360
A0	 0.8050	 0.6310
A1	 0.8080	 0.6340
A2	 0.7840	 0.6330
A3	 0.8370	 0.6320
A4	 0.8070	 0.6320
A5	 0.8090	 0.6370
A6	 0.7850	 0.6340
A7	 0.8380	 0.6330
A8	 0.8070	 0.6300
A9	 0.8080	 0.6380
AA	 0.7780	 0.6310
AB	 0.8350	 0.6360
AC	 0.8010	 0.6350
AD	 0.8140	 0.6370
AE	 0.7730	 0.6340
AF	 0.8340	 0.6330
AG	 0.7990	 0.6350
AH	 0.8110	 0.6340
AI	 0.7810	 0.6320
AJ	 0.8340	 0.6330
AK	 0.7960	 0.6310
AL	 0.8040	 0.6360
AM	 0.7780	 0.6340



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Chain	Atom inclusion	Q-score
AN	 0.8320	 0.6370
AO	 0.7970	 0.6320
AP	 0.8090	 0.6310
AQ	 0.7800	 0.6310
AR	 0.8350	 0.6380
AS	 0.8010	 0.6350
AT	 0.8070	 0.6340
AU	 0.7770	 0.6340
AV	 0.8340	 0.6330
AW	 0.8010	 0.6310
AX	 0.8110	 0.6400
AY	 0.7710	 0.6290
AZ	 0.8370	 0.6330
B	 0.8090	 0.6300
B0	 0.7970	 0.6340
B1	 0.8090	 0.6390
B2	 0.7740	 0.6330
B3	 0.8350	 0.6340
B4	 0.8000	 0.6390
B5	 0.8120	 0.6300
B6	 0.7780	 0.6300
B7	 0.8340	 0.6370
B8	 0.7990	 0.6350
B9	 0.8050	 0.6340
BA	 0.7840	 0.6350
BB	 0.8410	 0.6320
BC	 0.8010	 0.6330
BD	 0.8080	 0.6340
BE	 0.7780	 0.6330
BF	 0.8350	 0.6380
BG	 0.8040	 0.6330
BH	 0.8090	 0.6390
BI	 0.7740	 0.6350
BJ	 0.8300	 0.6390
BK	 0.7970	 0.6340
BL	 0.8110	 0.6360
BM	 0.7770	 0.6310
BN	 0.8340	 0.6340
BO	 0.8030	 0.6320
BP	 0.8080	 0.6380
BQ	 0.7800	 0.6340
BR	 0.8310	 0.6330

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Chain	Atom inclusion	Q-score
BS	 0.8010	 0.6340
BT	 0.8120	 0.6400
BU	 0.7750	 0.6340
BV	 0.8320	 0.6340
BW	 0.7990	 0.6310
BX	 0.8120	 0.6300
BY	 0.7780	 0.6320
BZ	 0.8320	 0.6360
C	 0.7810	 0.6320
C0	 0.8010	 0.6310
C1	 0.8080	 0.6290
C2	 0.7780	 0.6280
C3	 0.8320	 0.6370
C4	 0.7990	 0.6330
C5	 0.8080	 0.6380
C6	 0.7800	 0.6370
C7	 0.8320	 0.6330
C8	 0.8000	 0.6330
C9	 0.8120	 0.6390
CA	 0.7800	 0.6330
CB	 0.8310	 0.6340
CC	 0.7970	 0.6290
CD	 0.8050	 0.6360
CE	 0.7810	 0.6340
CF	 0.8370	 0.6370
CG	 0.7960	 0.6300
CH	 0.8030	 0.6360
CI	 0.7810	 0.6370
CJ	 0.8380	 0.6360
CK	 0.7970	 0.6310
CL	 0.8030	 0.6360
CM	 0.7840	 0.6350
CN	 0.8380	 0.6360
CO	 0.8070	 0.6310
CP	 0.8090	 0.6350
CQ	 0.7840	 0.6350
CR	 0.8370	 0.6330
CS	 0.8040	 0.6290
CT	 0.8080	 0.6370
CU	 0.7860	 0.6320
CV	 0.8400	 0.6330
CW	 0.8080	 0.6260

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Chain	Atom inclusion	Q-score
CX	 0.8080	 0.6340
CY	 0.7850	 0.6340
CZ	 0.8350	 0.6330
D	 0.8320	 0.6310
D0	 0.8000	 0.6320
D1	 0.8140	 0.6280
D2	 0.7770	 0.6280
D3	 0.8370	 0.6370
D4	 0.8000	 0.6340
D5	 0.8050	 0.6360
D6	 0.7800	 0.6330
D7	 0.8320	 0.6350
D8	 0.7990	 0.6340
D9	 0.8120	 0.6380
DA	 0.7750	 0.6340
DB	 0.8340	 0.6350
DC	 0.8000	 0.6320
DD	 0.8010	 0.6370
DE	 0.7780	 0.6350
DF	 0.8350	 0.6320
DG	 0.7990	 0.6310
DH	 0.8040	 0.6360
DI	 0.7820	 0.6330
DJ	 0.8380	 0.6310
DK	 0.8000	 0.6320
DL	 0.8010	 0.6370
DM	 0.7810	 0.6340
DN	 0.8350	 0.6340
DO	 0.8040	 0.6290
DP	 0.8110	 0.6390
DQ	 0.7730	 0.6370
DR	 0.8340	 0.6360
DS	 0.7990	 0.6320
DT	 0.8110	 0.6330
DU	 0.7810	 0.6280
DV	 0.8340	 0.6360
DW	 0.8000	 0.6320
DX	 0.8070	 0.6360
DY	 0.7800	 0.6320
DZ	 0.8350	 0.6370
E	 0.8010	 0.6310
E0	 0.7950	 0.6330

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Chain	Atom inclusion	Q-score
E1	 0.8050	 0.6350
E2	 0.7800	 0.6330
E3	 0.8370	 0.6340
E4	 0.8000	 0.6320
E5	 0.8140	 0.6390
E6	 0.7770	 0.6360
E7	 0.8370	 0.6340
EA	 0.7770	 0.6330
EB	 0.8340	 0.6310
EC	 0.8050	 0.6270
ED	 0.8090	 0.6370
EE	 0.7850	 0.6310
EF	 0.8410	 0.6340
EG	 0.8050	 0.6270
EH	 0.8070	 0.6390
EI	 0.7820	 0.6340
EJ	 0.8350	 0.6320
EK	 0.8070	 0.6330
EL	 0.8080	 0.6390
EM	 0.7860	 0.6310
EN	 0.8340	 0.6340
EO	 0.7960	 0.6330
EP	 0.8050	 0.6360
EQ	 0.7810	 0.6310
ER	 0.8310	 0.6350
ES	 0.7970	 0.6350
ET	 0.8110	 0.6390
EU	 0.7730	 0.6370
EV	 0.8370	 0.6360
EW	 0.7990	 0.6360
EX	 0.8110	 0.6320
EY	 0.7780	 0.6310
EZ	 0.8320	 0.6350
F	 0.8110	 0.6400
G	 0.7730	 0.6320
H	 0.8350	 0.6320
I	 0.7970	 0.6350
J	 0.8120	 0.6330
K	 0.7800	 0.6290
L	 0.8340	 0.6350
M	 0.7960	 0.6300
N	 0.8040	 0.6370

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Chain	Atom inclusion	Q-score
O	 0.7780	 0.6340
P	 0.8340	 0.6380
Q	 0.7970	 0.6350
R	 0.8030	 0.6330
S	 0.7810	 0.6350
T	 0.8380	 0.6350
U	 0.7990	 0.6340
V	 0.8030	 0.6330
W	 0.7820	 0.6350
X	 0.8380	 0.6370
Y	 0.7990	 0.6320
Z	 0.8040	 0.6330
a	 0.8070	 0.6310
b	 0.8070	 0.6370
c	 0.7820	 0.6330
d	 0.8340	 0.6330
e	 0.7990	 0.6360
f	 0.8120	 0.6320
g	 0.7780	 0.6320
h	 0.8320	 0.6350
i	 0.7990	 0.6320
j	 0.8070	 0.6350
k	 0.7800	 0.6330
l	 0.8370	 0.6370
m	 0.8030	 0.6300
n	 0.8090	 0.6390
o	 0.7710	 0.6360
p	 0.8340	 0.6350
q	 0.7960	 0.6330
r	 0.8010	 0.6330
s	 0.7820	 0.6350
t	 0.8380	 0.6370
u	 0.7990	 0.6340
v	 0.8040	 0.6330
w	 0.7810	 0.6370
x	 0.8370	 0.6350
y	 0.7970	 0.6300
z	 0.8040	 0.6340