



Full wwPDB EM Validation Report ⓘ

Nov 27, 2022 – 11:33 AM EST

PDB ID : 6OWF
EMDB ID : EMD-20208
Title : Structure of a synthetic beta-carboxysome shell, T=3
Authors : Sutter, M.; Laughlin, T.G.; Davies, K.M.; Kerfeld, C.A.
Deposited on : 2019-05-09
Resolution : 3.00 Å (reported)

This is a Full wwPDB EM Validation 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.

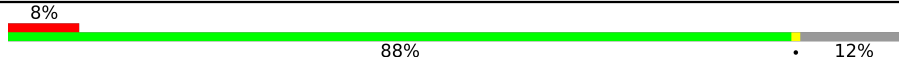

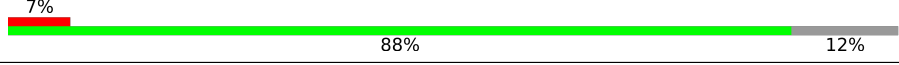
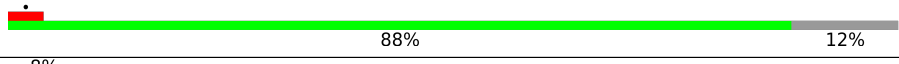
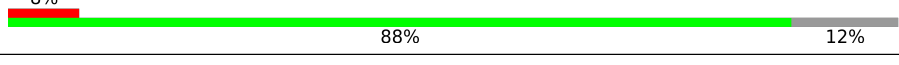
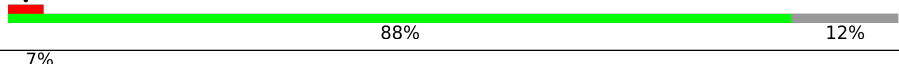
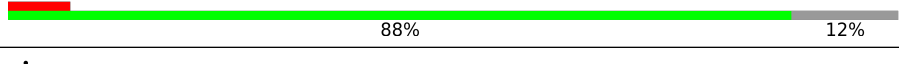
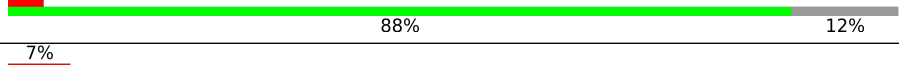
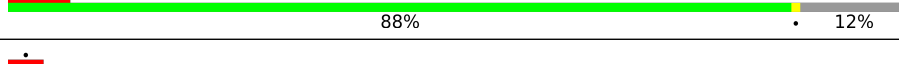
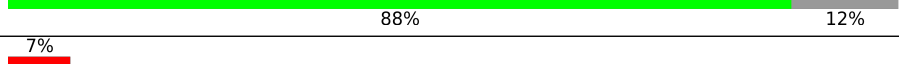
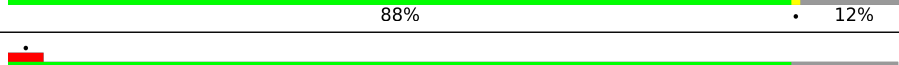
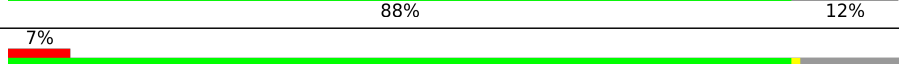
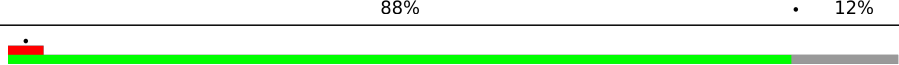
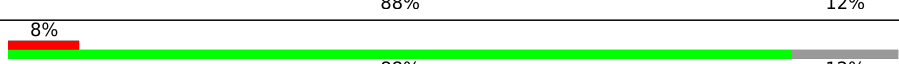
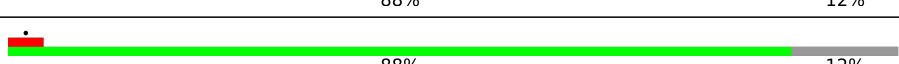
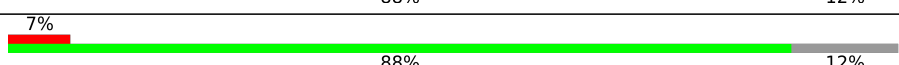
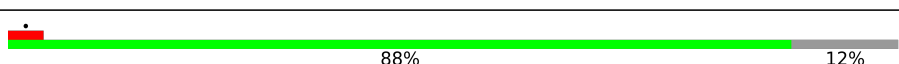

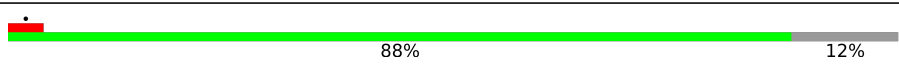
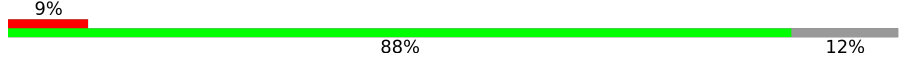

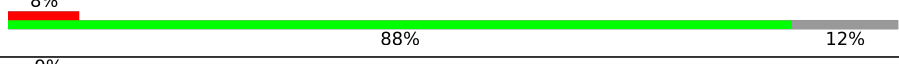
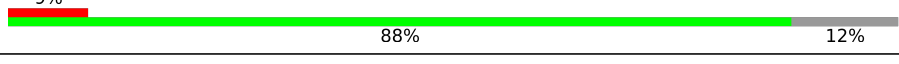


The types of validation reports are described at

<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:

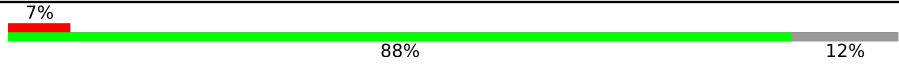
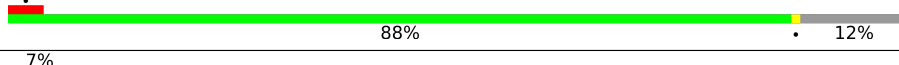
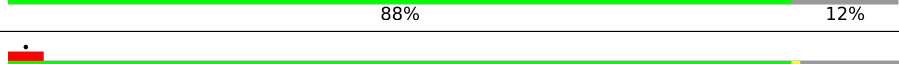
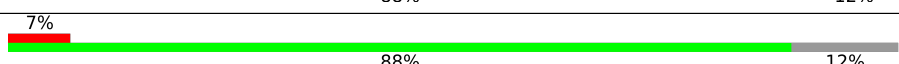

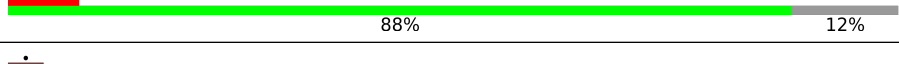
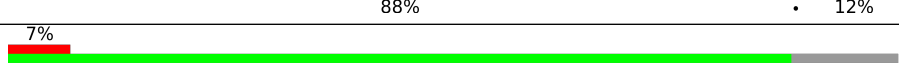

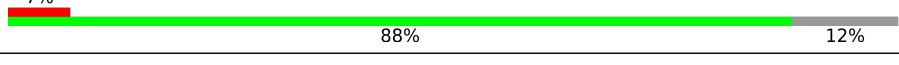

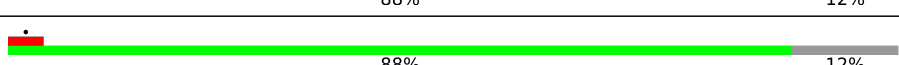

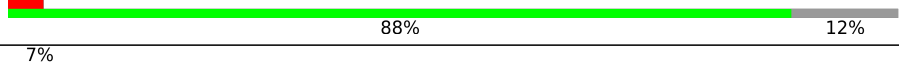


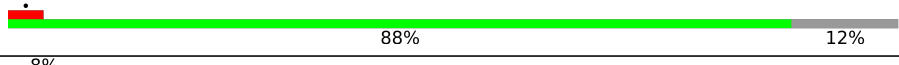







EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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Mol	Chain	Length	Quality of chain
1	A3	113	 8% 88% 12%
1	A5	113	 5% 88% 12%
1	A6	113	 7% 88% 12%
1	A8	113	 1% 88% 12%
1	A9	113	 8% 88% 12%
1	AB	113	 1% 88% 12%
1	AC	113	 7% 88% 12%
1	AE	113	 1% 88% 12%
1	AF	113	 7% 88% 12%
1	AH	113	 1% 88% 12%
1	AI	113	 7% 88% 12%
1	AK	113	 1% 88% 12%
1	AL	113	 7% 88% 12%
1	AN	113	 1% 88% 12%
1	AO	113	 8% 88% 12%
1	AQ	113	 1% 88% 12%
1	AR	113	 7% 88% 12%
1	AT	113	 1% 88% 12%
1	AU	113	 8% 88% 12%
1	AW	113	 1% 88% 12%
1	AX	113	 9% 88% 12%
1	AZ	113	 5% 88% 12%
1	B	113	 8% 88% 12%
1	B0	113	 9% 88% 12%
1	B2	113	 1% 88% 12%







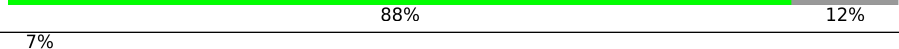
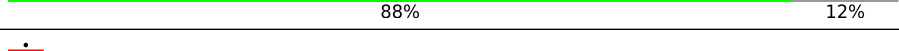
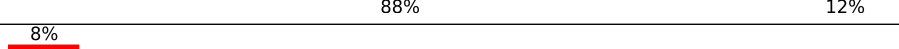
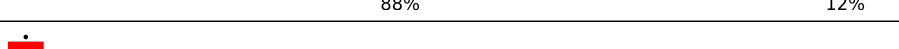
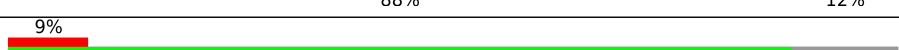

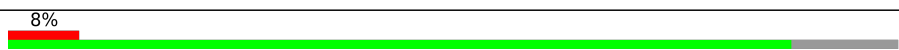

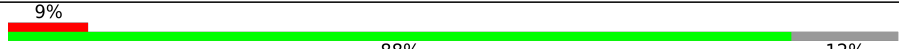





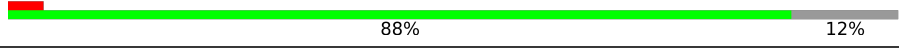
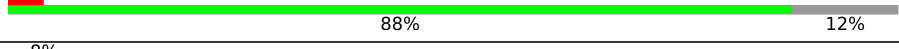



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Mol	Chain	Length	Quality of chain
1	B3	113	 7% 88% 12%
1	B5	113	 7% 88% 12%
1	B6	113	 7% 88% 12%
1	B8	113	 7% 88% 12%
1	B9	113	 7% 88% 12%
1	BB	113	 7% 88% 12%
1	BC	113	 8% 88% 12%
1	BE	113	 7% 88% 12%
1	BF	113	 7% 88% 12%
1	BH	113	 7% 88% 12%
1	BI	113	 7% 88% 12%
1	BK	113	 7% 88% 12%
1	BL	113	 7% 88% 12%
1	BN	113	 7% 88% 12%
1	BO	113	 7% 88% 12%
1	BQ	113	 7% 88% 12%
1	BR	113	 7% 88% 12%
1	BT	113	 7% 88% 12%
1	BU	113	 7% 88% 12%
1	BW	113	 7% 88% 12%
1	BX	113	 8% 88% 12%
1	BZ	113	 7% 88% 12%
1	C0	113	 7% 88% 12%
1	C2	113	7% 88% 12%
1	C3	113	7% 88% 12%

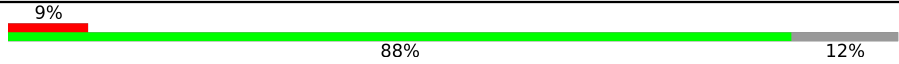
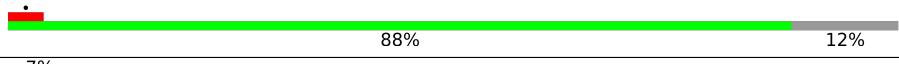
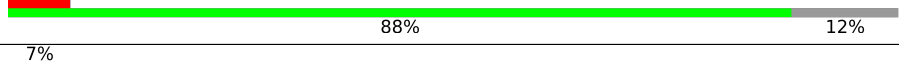
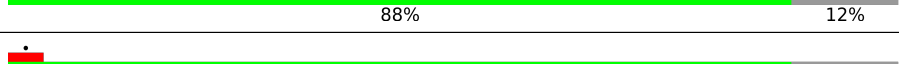
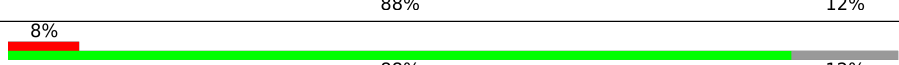

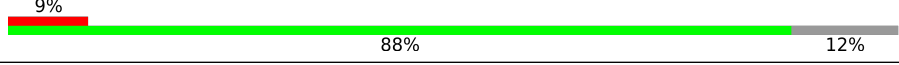
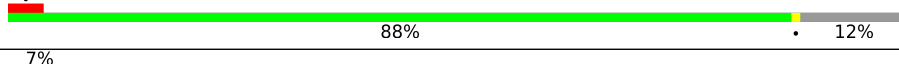
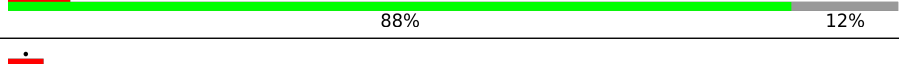

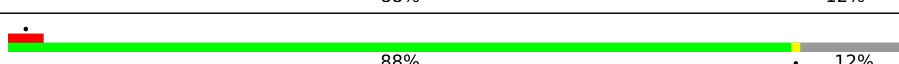
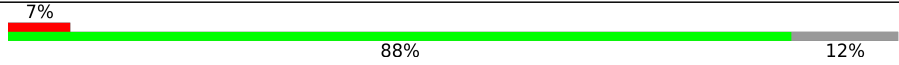
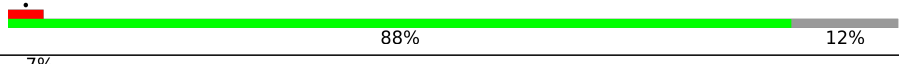
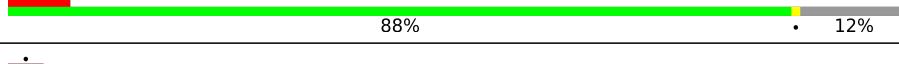
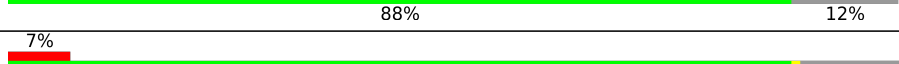


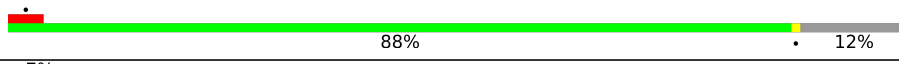
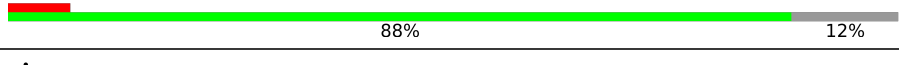
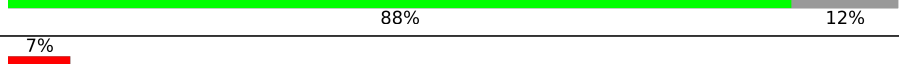
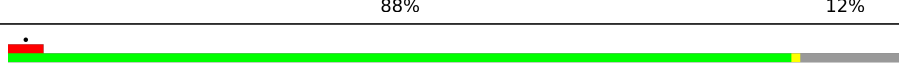
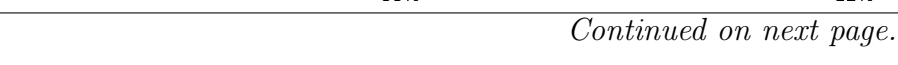


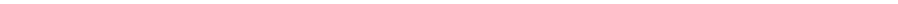
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Mol	Chain	Length	Quality of chain
1	C5	113	 88% 12%
1	C6	113	 88% 12%
1	C8	113	 88% 12%
1	C9	113	 88% 12%
1	CB	113	 88% 12%
1	CC	113	 88% 12%
1	CE	113	 88% 12%
1	CF	113	 88% 12%
1	CH	113	 88% 12%
1	CI	113	 88% 12%
1	CK	113	 88% 12%
1	CL	113	 88% 12%
1	CN	113	 88% 12%
1	CO	113	 88% 12%
1	CQ	113	 88% 12%
1	CR	113	 88% 12%
1	CT	113	 88% 12%
1	CU	113	 88% 12%
1	CW	113	 88% 12%
1	CX	113	 88% 12%
1	CZ	113	 88% 12%
1	D	113	 88% 12%
1	DB	113	 88% 12%
1	DC	113	 88% 12%
1	DE	113	 88% 12%

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Mol	Chain	Length	Quality of chain
1	DF	113	 9% 88% 12%
1	DH	113	 7% 88% 12%
1	DI	113	 7% 88% 12%
1	E	113	 7% 88% 12%
1	G	113	 7% 88% 12%
1	H	113	 8% 88% 12%
1	J	113	 7% 88% 12%
1	K	113	 9% 88% 12%
1	M	113	 7% 88% 12%
1	N	113	 7% 88% 12%
1	P	113	 7% 88% 12%
1	Q	113	 7% 88% 12%
1	S	113	 7% 88% 12%
1	T	113	 7% 88% 12%
1	V	113	 7% 88% 12%
1	W	113	 7% 88% 12%
1	Y	113	 7% 88% 12%
1	Z	113	 7% 88% 12%
1	a	113	 7% 88% 12%
1	b	113	 7% 88% 12%
1	d	113	 7% 88% 12%
1	e	113	 7% 88% 12%
1	g	113	 7% 88% 12%
1	h	113	 7% 88% 12%
1	j	113	 7% 88% 12%

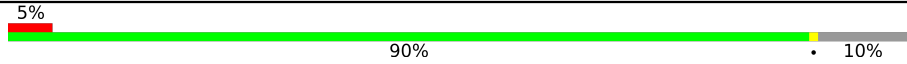
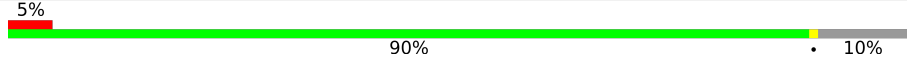
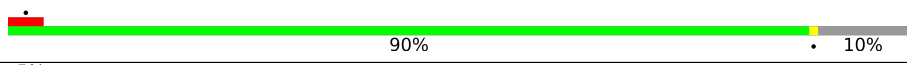
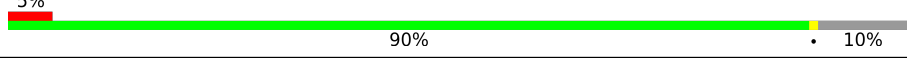
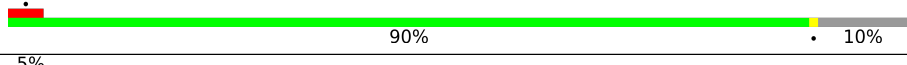
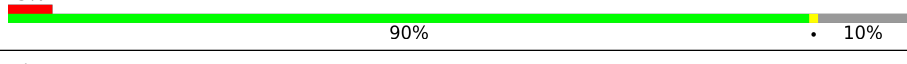
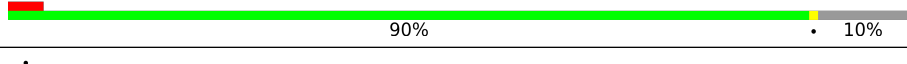
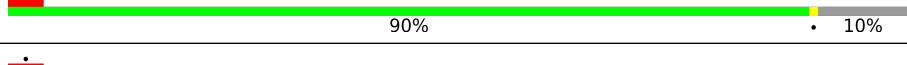
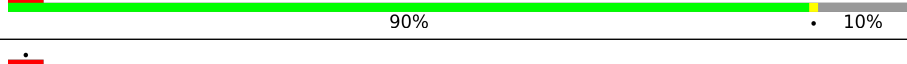
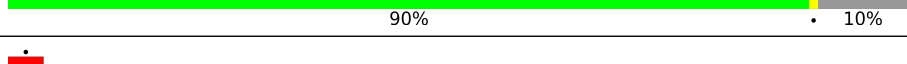
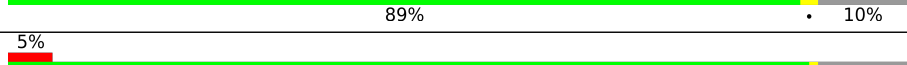
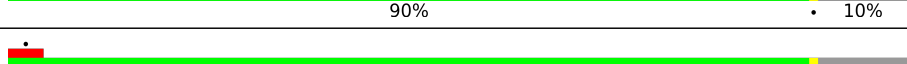

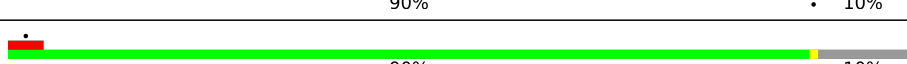
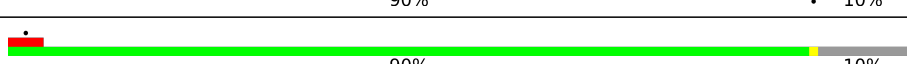
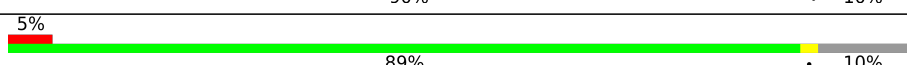
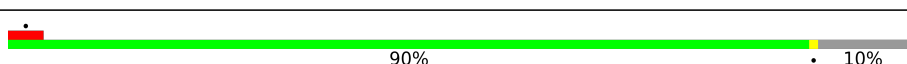
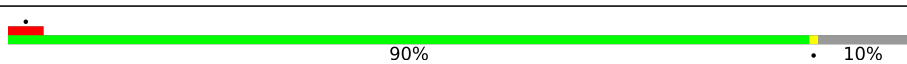
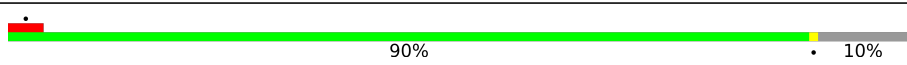
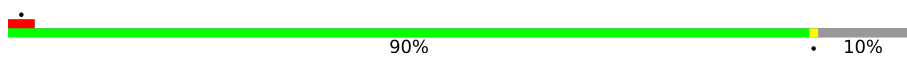
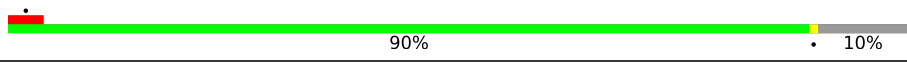
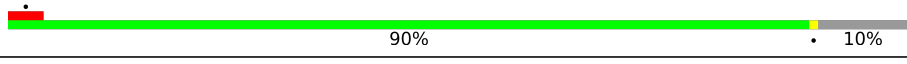
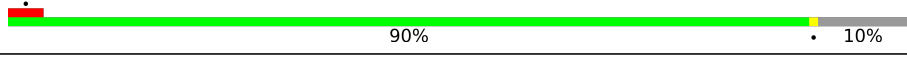


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Mol	Chain	Length	Quality of chain
1	k	113	7% 88% 12%
1	m	113	8% 88% 12%
1	n	113	7% 88% 12%
1	p	113	8% 88% 12%
1	q	113	8% 88% 12%
1	s	113	8% 88% 12%
1	t	113	8% 88% 12%
1	v	113	8% 88% 12%
1	w	113	8% 88% 12%
1	y	113	8% 88% 12%
1	z	113	9% 88% 12%
2	0	105	5% 90% 10%
2	3	105	5% 89% 10%
2	6	105	5% 90% 10%
2	9	105	5% 90% 10%
2	A1	105	5% 90% 10%
2	A4	105	5% 90% 10%
2	A7	105	5% 90% 10%
2	AA	105	5% 90% 10%
2	AD	105	5% 90% 10%
2	AG	105	5% 89% 10%
2	AJ	105	5% 90% 10%
2	AM	105	5% 90% 10%
2	AP	105	5% 90% 10%
2	AS	105	5% 90% 10%



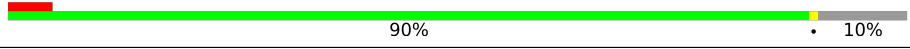




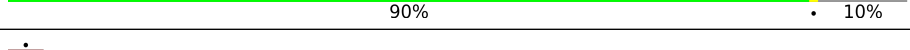
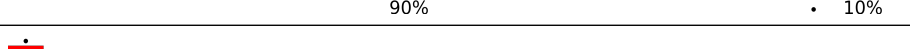
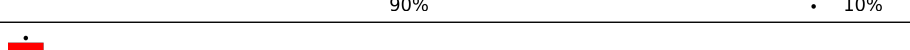

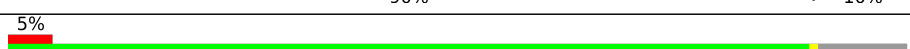


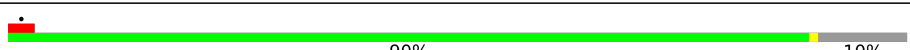






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Mol	Chain	Length	Quality of chain
2	AV	105	 5% 90% 10%
2	AY	105	 5% 90% 10%
2	B1	105	 5% 90% 10%
2	B4	105	 5% 90% 10%
2	B7	105	 5% 90% 10%
2	BA	105	 5% 90% 10%
2	BD	105	 5% 90% 10%
2	BG	105	 5% 90% 10%
2	BJ	105	 5% 90% 10%
2	BM	105	 5% 90% 10%
2	BP	105	 5% 89% 10%
2	BS	105	 5% 90% 10%
2	BV	105	 5% 90% 10%
2	BY	105	 5% 90% 10%
2	C	105	 5% 90% 10%
2	C1	105	 5% 90% 10%
2	C4	105	 5% 89% 10%
2	C7	105	 5% 90% 10%
2	CA	105	 5% 90% 10%
2	CD	105	 5% 90% 10%
2	CG	105	 5% 90% 10%
2	CJ	105	 5% 90% 10%
2	CM	105	 5% 90% 10%
2	CP	105	 5% 90% 10%
2	CS	105	 5% 90% 10%

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Mol	Chain	Length	Quality of chain
2	CV	105	 90% 10%
2	CY	105	 90% 10%
2	DA	105	 90% 10%
2	DD	105	 90% 10%
2	DG	105	 90% 10%
2	DJ	105	 90% 10%
2	F	105	 90% 10%
2	I	105	 90% 10%
2	L	105	 90% 10%
2	O	105	 90% 10%
2	R	105	 90% 10%
2	U	105	 90% 10%
2	X	105	 90% 10%
2	c	105	 90% 10%
2	f	105	 90% 10%
2	i	105	 90% 10%
2	l	105	 90% 10%
2	o	105	 90% 10%
2	r	105	 90% 10%
2	u	105	 90% 10%
2	x	105	 90% 10%

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 133500 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
			Total	C	N	O	S		
1	A	100	752	473	133	144	2	0	0
1	B	100	752	473	133	144	2	0	0
1	D	100	752	473	133	144	2	0	0
1	E	100	752	473	133	144	2	0	0
1	G	100	752	473	133	144	2	0	0
1	H	100	752	473	133	144	2	0	0
1	J	100	752	473	133	144	2	0	0
1	K	100	752	473	133	144	2	0	0
1	M	100	752	473	133	144	2	0	0
1	N	100	752	473	133	144	2	0	0
1	P	100	752	473	133	144	2	0	0
1	Q	100	752	473	133	144	2	0	0
1	S	100	752	473	133	144	2	0	0
1	T	100	752	473	133	144	2	0	0
1	V	100	752	473	133	144	2	0	0
1	W	100	752	473	133	144	2	0	0
1	Y	100	752	473	133	144	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	Z	100	752	473	133	144	2	0	0
1	1	100	752	473	133	144	2	0	0
1	2	100	752	473	133	144	2	0	0
1	4	100	752	473	133	144	2	0	0
1	5	100	752	473	133	144	2	0	0
1	7	100	752	473	133	144	2	0	0
1	8	100	752	473	133	144	2	0	0
1	a	100	752	473	133	144	2	0	0
1	b	100	752	473	133	144	2	0	0
1	d	100	752	473	133	144	2	0	0
1	e	100	752	473	133	144	2	0	0
1	g	100	752	473	133	144	2	0	0
1	h	100	752	473	133	144	2	0	0
1	j	100	752	473	133	144	2	0	0
1	k	100	752	473	133	144	2	0	0
1	m	100	752	473	133	144	2	0	0
1	n	100	752	473	133	144	2	0	0
1	p	100	752	473	133	144	2	0	0
1	q	100	752	473	133	144	2	0	0
1	s	100	752	473	133	144	2	0	0
1	t	100	752	473	133	144	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	v	100	752	473	133	144	2	0	0
1	w	100	752	473	133	144	2	0	0
1	y	100	752	473	133	144	2	0	0
1	z	100	752	473	133	144	2	0	0
1	AB	100	752	473	133	144	2	0	0
1	AC	100	752	473	133	144	2	0	0
1	AE	100	752	473	133	144	2	0	0
1	AF	100	752	473	133	144	2	0	0
1	AH	100	752	473	133	144	2	0	0
1	AI	100	752	473	133	144	2	0	0
1	AK	100	752	473	133	144	2	0	0
1	AL	100	752	473	133	144	2	0	0
1	AN	100	752	473	133	144	2	0	0
1	AO	100	752	473	133	144	2	0	0
1	AQ	100	752	473	133	144	2	0	0
1	AR	100	752	473	133	144	2	0	0
1	AT	100	752	473	133	144	2	0	0
1	AU	100	752	473	133	144	2	0	0
1	AW	100	752	473	133	144	2	0	0
1	AX	100	752	473	133	144	2	0	0
1	AZ	100	752	473	133	144	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A0	100	752	473	133	144	2	0	0
1	A2	100	752	473	133	144	2	0	0
1	A3	100	752	473	133	144	2	0	0
1	A5	100	752	473	133	144	2	0	0
1	A6	100	752	473	133	144	2	0	0
1	A8	100	752	473	133	144	2	0	0
1	A9	100	752	473	133	144	2	0	0
1	BB	100	752	473	133	144	2	0	0
1	BC	100	752	473	133	144	2	0	0
1	BE	100	752	473	133	144	2	0	0
1	BF	100	752	473	133	144	2	0	0
1	BH	100	752	473	133	144	2	0	0
1	BI	100	752	473	133	144	2	0	0
1	BK	100	752	473	133	144	2	0	0
1	BL	100	752	473	133	144	2	0	0
1	BN	100	752	473	133	144	2	0	0
1	BO	100	752	473	133	144	2	0	0
1	BQ	100	752	473	133	144	2	0	0
1	BR	100	752	473	133	144	2	0	0
1	BT	100	752	473	133	144	2	0	0
1	BU	100	752	473	133	144	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	BW	100	752	473	133	144	2	0	0
1	BX	100	752	473	133	144	2	0	0
1	BZ	100	752	473	133	144	2	0	0
1	B0	100	752	473	133	144	2	0	0
1	B2	100	752	473	133	144	2	0	0
1	B3	100	752	473	133	144	2	0	0
1	B5	100	752	473	133	144	2	0	0
1	B6	100	752	473	133	144	2	0	0
1	B8	100	752	473	133	144	2	0	0
1	B9	100	752	473	133	144	2	0	0
1	CB	100	752	473	133	144	2	0	0
1	CC	100	752	473	133	144	2	0	0
1	CE	100	752	473	133	144	2	0	0
1	CF	100	752	473	133	144	2	0	0
1	CH	100	752	473	133	144	2	0	0
1	CI	100	752	473	133	144	2	0	0
1	CK	100	752	473	133	144	2	0	0
1	CL	100	752	473	133	144	2	0	0
1	CN	100	752	473	133	144	2	0	0
1	CO	100	752	473	133	144	2	0	0
1	CQ	100	752	473	133	144	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	CR	100	752	473	133	144	2	0	0
1	CT	100	752	473	133	144	2	0	0
1	CU	100	752	473	133	144	2	0	0
1	CW	100	752	473	133	144	2	0	0
1	CX	100	752	473	133	144	2	0	0
1	CZ	100	752	473	133	144	2	0	0
1	C0	100	752	473	133	144	2	0	0
1	C2	100	752	473	133	144	2	0	0
1	C3	100	752	473	133	144	2	0	0
1	C5	100	752	473	133	144	2	0	0
1	C6	100	752	473	133	144	2	0	0
1	C8	100	752	473	133	144	2	0	0
1	C9	100	752	473	133	144	2	0	0
1	DB	100	752	473	133	144	2	0	0
1	DC	100	752	473	133	144	2	0	0
1	DE	100	752	473	133	144	2	0	0
1	DF	100	752	473	133	144	2	0	0
1	DH	100	752	473	133	144	2	0	0
1	DI	100	752	473	133	144	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	F	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	I	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	L	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	O	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	R	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	U	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	X	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	0	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	3	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	6	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	9	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	c	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	f	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	i	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	l	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	o	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	r	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	u	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	x	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	AA	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	AD	95	Total 721	C 455	N 127	O 134	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AG	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	AJ	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	AM	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	AP	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	AS	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	AV	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	AY	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	A1	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	A4	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	A7	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BA	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BD	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BG	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BJ	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BM	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BP	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BS	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BV	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	BY	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	B1	95	Total 721	C 455	N 127	O 134	S 5	0	0
2	B4	95	Total 721	C 455	N 127	O 134	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B7	95	721	455	127	134	5	0	0
2	CA	95	721	455	127	134	5	0	0
2	CD	95	721	455	127	134	5	0	0
2	CG	95	721	455	127	134	5	0	0
2	CJ	95	721	455	127	134	5	0	0
2	CM	95	721	455	127	134	5	0	0
2	CP	95	721	455	127	134	5	0	0
2	CS	95	721	455	127	134	5	0	0
2	CV	95	721	455	127	134	5	0	0
2	CY	95	721	455	127	134	5	0	0
2	C1	95	721	455	127	134	5	0	0
2	C4	95	721	455	127	134	5	0	0
2	C7	95	721	455	127	134	5	0	0
2	DA	95	721	455	127	134	5	0	0
2	DD	95	721	455	127	134	5	0	0
2	DG	95	721	455	127	134	5	0	0
2	DJ	95	721	455	127	134	5	0	0

There are 600 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	96	GLY	-	expression tag	UNP K9YFK1
C	97	SER	-	expression tag	UNP K9YFK1
C	98	TRP	-	expression tag	UNP K9YFK1
C	99	SER	-	expression tag	UNP K9YFK1
C	100	HIS	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	101	PRO	-	expression tag	UNP K9YFK1
C	102	GLN	-	expression tag	UNP K9YFK1
C	103	PHE	-	expression tag	UNP K9YFK1
C	104	GLU	-	expression tag	UNP K9YFK1
C	105	LYS	-	expression tag	UNP K9YFK1
F	96	GLY	-	expression tag	UNP K9YFK1
F	97	SER	-	expression tag	UNP K9YFK1
F	98	TRP	-	expression tag	UNP K9YFK1
F	99	SER	-	expression tag	UNP K9YFK1
F	100	HIS	-	expression tag	UNP K9YFK1
F	101	PRO	-	expression tag	UNP K9YFK1
F	102	GLN	-	expression tag	UNP K9YFK1
F	103	PHE	-	expression tag	UNP K9YFK1
F	104	GLU	-	expression tag	UNP K9YFK1
F	105	LYS	-	expression tag	UNP K9YFK1
I	96	GLY	-	expression tag	UNP K9YFK1
I	97	SER	-	expression tag	UNP K9YFK1
I	98	TRP	-	expression tag	UNP K9YFK1
I	99	SER	-	expression tag	UNP K9YFK1
I	100	HIS	-	expression tag	UNP K9YFK1
I	101	PRO	-	expression tag	UNP K9YFK1
I	102	GLN	-	expression tag	UNP K9YFK1
I	103	PHE	-	expression tag	UNP K9YFK1
I	104	GLU	-	expression tag	UNP K9YFK1
I	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
O	96	GLY	-	expression tag	UNP K9YFK1
O	97	SER	-	expression tag	UNP K9YFK1
O	98	TRP	-	expression tag	UNP K9YFK1
O	99	SER	-	expression tag	UNP K9YFK1
O	100	HIS	-	expression tag	UNP K9YFK1
O	101	PRO	-	expression tag	UNP K9YFK1
O	102	GLN	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
O	103	PHE	-	expression tag	UNP K9YFK1
O	104	GLU	-	expression tag	UNP K9YFK1
O	105	LYS	-	expression tag	UNP K9YFK1
R	96	GLY	-	expression tag	UNP K9YFK1
R	97	SER	-	expression tag	UNP K9YFK1
R	98	TRP	-	expression tag	UNP K9YFK1
R	99	SER	-	expression tag	UNP K9YFK1
R	100	HIS	-	expression tag	UNP K9YFK1
R	101	PRO	-	expression tag	UNP K9YFK1
R	102	GLN	-	expression tag	UNP K9YFK1
R	103	PHE	-	expression tag	UNP K9YFK1
R	104	GLU	-	expression tag	UNP K9YFK1
R	105	LYS	-	expression tag	UNP K9YFK1
U	96	GLY	-	expression tag	UNP K9YFK1
U	97	SER	-	expression tag	UNP K9YFK1
U	98	TRP	-	expression tag	UNP K9YFK1
U	99	SER	-	expression tag	UNP K9YFK1
U	100	HIS	-	expression tag	UNP K9YFK1
U	101	PRO	-	expression tag	UNP K9YFK1
U	102	GLN	-	expression tag	UNP K9YFK1
U	103	PHE	-	expression tag	UNP K9YFK1
U	104	GLU	-	expression tag	UNP K9YFK1
U	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
0	96	GLY	-	expression tag	UNP K9YFK1
0	97	SER	-	expression tag	UNP K9YFK1
0	98	TRP	-	expression tag	UNP K9YFK1
0	99	SER	-	expression tag	UNP K9YFK1
0	100	HIS	-	expression tag	UNP K9YFK1
0	101	PRO	-	expression tag	UNP K9YFK1
0	102	GLN	-	expression tag	UNP K9YFK1
0	103	PHE	-	expression tag	UNP K9YFK1
0	104	GLU	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
0	105	LYS	-	expression tag	UNP K9YFK1
3	96	GLY	-	expression tag	UNP K9YFK1
3	97	SER	-	expression tag	UNP K9YFK1
3	98	TRP	-	expression tag	UNP K9YFK1
3	99	SER	-	expression tag	UNP K9YFK1
3	100	HIS	-	expression tag	UNP K9YFK1
3	101	PRO	-	expression tag	UNP K9YFK1
3	102	GLN	-	expression tag	UNP K9YFK1
3	103	PHE	-	expression tag	UNP K9YFK1
3	104	GLU	-	expression tag	UNP K9YFK1
3	105	LYS	-	expression tag	UNP K9YFK1
6	96	GLY	-	expression tag	UNP K9YFK1
6	97	SER	-	expression tag	UNP K9YFK1
6	98	TRP	-	expression tag	UNP K9YFK1
6	99	SER	-	expression tag	UNP K9YFK1
6	100	HIS	-	expression tag	UNP K9YFK1
6	101	PRO	-	expression tag	UNP K9YFK1
6	102	GLN	-	expression tag	UNP K9YFK1
6	103	PHE	-	expression tag	UNP K9YFK1
6	104	GLU	-	expression tag	UNP K9YFK1
6	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
c	96	GLY	-	expression tag	UNP K9YFK1
c	97	SER	-	expression tag	UNP K9YFK1
c	98	TRP	-	expression tag	UNP K9YFK1
c	99	SER	-	expression tag	UNP K9YFK1
c	100	HIS	-	expression tag	UNP K9YFK1
c	101	PRO	-	expression tag	UNP K9YFK1
c	102	GLN	-	expression tag	UNP K9YFK1
c	103	PHE	-	expression tag	UNP K9YFK1
c	104	GLU	-	expression tag	UNP K9YFK1
c	105	LYS	-	expression tag	UNP K9YFK1
f	96	GLY	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
f	97	SER	-	expression tag	UNP K9YFK1
f	98	TRP	-	expression tag	UNP K9YFK1
f	99	SER	-	expression tag	UNP K9YFK1
f	100	HIS	-	expression tag	UNP K9YFK1
f	101	PRO	-	expression tag	UNP K9YFK1
f	102	GLN	-	expression tag	UNP K9YFK1
f	103	PHE	-	expression tag	UNP K9YFK1
f	104	GLU	-	expression tag	UNP K9YFK1
f	105	LYS	-	expression tag	UNP K9YFK1
i	96	GLY	-	expression tag	UNP K9YFK1
i	97	SER	-	expression tag	UNP K9YFK1
i	98	TRP	-	expression tag	UNP K9YFK1
i	99	SER	-	expression tag	UNP K9YFK1
i	100	HIS	-	expression tag	UNP K9YFK1
i	101	PRO	-	expression tag	UNP K9YFK1
i	102	GLN	-	expression tag	UNP K9YFK1
i	103	PHE	-	expression tag	UNP K9YFK1
i	104	GLU	-	expression tag	UNP K9YFK1
i	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
o	96	GLY	-	expression tag	UNP K9YFK1
o	97	SER	-	expression tag	UNP K9YFK1
o	98	TRP	-	expression tag	UNP K9YFK1
o	99	SER	-	expression tag	UNP K9YFK1
o	100	HIS	-	expression tag	UNP K9YFK1
o	101	PRO	-	expression tag	UNP K9YFK1
o	102	GLN	-	expression tag	UNP K9YFK1
o	103	PHE	-	expression tag	UNP K9YFK1
o	104	GLU	-	expression tag	UNP K9YFK1
o	105	LYS	-	expression tag	UNP K9YFK1
r	96	GLY	-	expression tag	UNP K9YFK1
r	97	SER	-	expression tag	UNP K9YFK1
r	98	TRP	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
r	99	SER	-	expression tag	UNP K9YFK1
r	100	HIS	-	expression tag	UNP K9YFK1
r	101	PRO	-	expression tag	UNP K9YFK1
r	102	GLN	-	expression tag	UNP K9YFK1
r	103	PHE	-	expression tag	UNP K9YFK1
r	104	GLU	-	expression tag	UNP K9YFK1
r	105	LYS	-	expression tag	UNP K9YFK1
u	96	GLY	-	expression tag	UNP K9YFK1
u	97	SER	-	expression tag	UNP K9YFK1
u	98	TRP	-	expression tag	UNP K9YFK1
u	99	SER	-	expression tag	UNP K9YFK1
u	100	HIS	-	expression tag	UNP K9YFK1
u	101	PRO	-	expression tag	UNP K9YFK1
u	102	GLN	-	expression tag	UNP K9YFK1
u	103	PHE	-	expression tag	UNP K9YFK1
u	104	GLU	-	expression tag	UNP K9YFK1
u	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
AA	96	GLY	-	expression tag	UNP K9YFK1
AA	97	SER	-	expression tag	UNP K9YFK1
AA	98	TRP	-	expression tag	UNP K9YFK1
AA	99	SER	-	expression tag	UNP K9YFK1
AA	100	HIS	-	expression tag	UNP K9YFK1
AA	101	PRO	-	expression tag	UNP K9YFK1
AA	102	GLN	-	expression tag	UNP K9YFK1
AA	103	PHE	-	expression tag	UNP K9YFK1
AA	104	GLU	-	expression tag	UNP K9YFK1
AA	105	LYS	-	expression tag	UNP K9YFK1
AD	96	GLY	-	expression tag	UNP K9YFK1
AD	97	SER	-	expression tag	UNP K9YFK1
AD	98	TRP	-	expression tag	UNP K9YFK1
AD	99	SER	-	expression tag	UNP K9YFK1
AD	100	HIS	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
AD	101	PRO	-	expression tag	UNP K9YFK1
AD	102	GLN	-	expression tag	UNP K9YFK1
AD	103	PHE	-	expression tag	UNP K9YFK1
AD	104	GLU	-	expression tag	UNP K9YFK1
AD	105	LYS	-	expression tag	UNP K9YFK1
AG	96	GLY	-	expression tag	UNP K9YFK1
AG	97	SER	-	expression tag	UNP K9YFK1
AG	98	TRP	-	expression tag	UNP K9YFK1
AG	99	SER	-	expression tag	UNP K9YFK1
AG	100	HIS	-	expression tag	UNP K9YFK1
AG	101	PRO	-	expression tag	UNP K9YFK1
AG	102	GLN	-	expression tag	UNP K9YFK1
AG	103	PHE	-	expression tag	UNP K9YFK1
AG	104	GLU	-	expression tag	UNP K9YFK1
AG	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
AJ	103	PHE	-	expression tag	UNP K9YFK1
AJ	104	GLU	-	expression tag	UNP K9YFK1
AJ	105	LYS	-	expression tag	UNP K9YFK1
AM	96	GLY	-	expression tag	UNP K9YFK1
AM	97	SER	-	expression tag	UNP K9YFK1
AM	98	TRP	-	expression tag	UNP K9YFK1
AM	99	SER	-	expression tag	UNP K9YFK1
AM	100	HIS	-	expression tag	UNP K9YFK1
AM	101	PRO	-	expression tag	UNP K9YFK1
AM	102	GLN	-	expression tag	UNP K9YFK1
AM	103	PHE	-	expression tag	UNP K9YFK1
AM	104	GLU	-	expression tag	UNP K9YFK1
AM	105	LYS	-	expression tag	UNP K9YFK1
AP	96	GLY	-	expression tag	UNP K9YFK1
AP	97	SER	-	expression tag	UNP K9YFK1
AP	98	TRP	-	expression tag	UNP K9YFK1
AP	99	SER	-	expression tag	UNP K9YFK1
AP	100	HIS	-	expression tag	UNP K9YFK1
AP	101	PRO	-	expression tag	UNP K9YFK1
AP	102	GLN	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
AP	103	PHE	-	expression tag	UNP K9YFK1
AP	104	GLU	-	expression tag	UNP K9YFK1
AP	105	LYS	-	expression tag	UNP K9YFK1
AS	96	GLY	-	expression tag	UNP K9YFK1
AS	97	SER	-	expression tag	UNP K9YFK1
AS	98	TRP	-	expression tag	UNP K9YFK1
AS	99	SER	-	expression tag	UNP K9YFK1
AS	100	HIS	-	expression tag	UNP K9YFK1
AS	101	PRO	-	expression tag	UNP K9YFK1
AS	102	GLN	-	expression tag	UNP K9YFK1
AS	103	PHE	-	expression tag	UNP K9YFK1
AS	104	GLU	-	expression tag	UNP K9YFK1
AS	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
AY	96	GLY	-	expression tag	UNP K9YFK1
AY	97	SER	-	expression tag	UNP K9YFK1
AY	98	TRP	-	expression tag	UNP K9YFK1
AY	99	SER	-	expression tag	UNP K9YFK1
AY	100	HIS	-	expression tag	UNP K9YFK1
AY	101	PRO	-	expression tag	UNP K9YFK1
AY	102	GLN	-	expression tag	UNP K9YFK1
AY	103	PHE	-	expression tag	UNP K9YFK1
AY	104	GLU	-	expression tag	UNP K9YFK1
AY	105	LYS	-	expression tag	UNP K9YFK1
A1	96	GLY	-	expression tag	UNP K9YFK1
A1	97	SER	-	expression tag	UNP K9YFK1
A1	98	TRP	-	expression tag	UNP K9YFK1
A1	99	SER	-	expression tag	UNP K9YFK1
A1	100	HIS	-	expression tag	UNP K9YFK1
A1	101	PRO	-	expression tag	UNP K9YFK1
A1	102	GLN	-	expression tag	UNP K9YFK1
A1	103	PHE	-	expression tag	UNP K9YFK1
A1	104	GLU	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
A1	105	LYS	-	expression tag	UNP K9YFK1
A4	96	GLY	-	expression tag	UNP K9YFK1
A4	97	SER	-	expression tag	UNP K9YFK1
A4	98	TRP	-	expression tag	UNP K9YFK1
A4	99	SER	-	expression tag	UNP K9YFK1
A4	100	HIS	-	expression tag	UNP K9YFK1
A4	101	PRO	-	expression tag	UNP K9YFK1
A4	102	GLN	-	expression tag	UNP K9YFK1
A4	103	PHE	-	expression tag	UNP K9YFK1
A4	104	GLU	-	expression tag	UNP K9YFK1
A4	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
BA	96	GLY	-	expression tag	UNP K9YFK1
BA	97	SER	-	expression tag	UNP K9YFK1
BA	98	TRP	-	expression tag	UNP K9YFK1
BA	99	SER	-	expression tag	UNP K9YFK1
BA	100	HIS	-	expression tag	UNP K9YFK1
BA	101	PRO	-	expression tag	UNP K9YFK1
BA	102	GLN	-	expression tag	UNP K9YFK1
BA	103	PHE	-	expression tag	UNP K9YFK1
BA	104	GLU	-	expression tag	UNP K9YFK1
BA	105	LYS	-	expression tag	UNP K9YFK1
BD	96	GLY	-	expression tag	UNP K9YFK1
BD	97	SER	-	expression tag	UNP K9YFK1
BD	98	TRP	-	expression tag	UNP K9YFK1
BD	99	SER	-	expression tag	UNP K9YFK1
BD	100	HIS	-	expression tag	UNP K9YFK1
BD	101	PRO	-	expression tag	UNP K9YFK1
BD	102	GLN	-	expression tag	UNP K9YFK1
BD	103	PHE	-	expression tag	UNP K9YFK1
BD	104	GLU	-	expression tag	UNP K9YFK1
BD	105	LYS	-	expression tag	UNP K9YFK1
BG	96	GLY	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
BG	97	SER	-	expression tag	UNP K9YFK1
BG	98	TRP	-	expression tag	UNP K9YFK1
BG	99	SER	-	expression tag	UNP K9YFK1
BG	100	HIS	-	expression tag	UNP K9YFK1
BG	101	PRO	-	expression tag	UNP K9YFK1
BG	102	GLN	-	expression tag	UNP K9YFK1
BG	103	PHE	-	expression tag	UNP K9YFK1
BG	104	GLU	-	expression tag	UNP K9YFK1
BG	105	LYS	-	expression tag	UNP K9YFK1
BJ	96	GLY	-	expression tag	UNP K9YFK1
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
BM	96	GLY	-	expression tag	UNP K9YFK1
BM	97	SER	-	expression tag	UNP K9YFK1
BM	98	TRP	-	expression tag	UNP K9YFK1
BM	99	SER	-	expression tag	UNP K9YFK1
BM	100	HIS	-	expression tag	UNP K9YFK1
BM	101	PRO	-	expression tag	UNP K9YFK1
BM	102	GLN	-	expression tag	UNP K9YFK1
BM	103	PHE	-	expression tag	UNP K9YFK1
BM	104	GLU	-	expression tag	UNP K9YFK1
BM	105	LYS	-	expression tag	UNP K9YFK1
BP	96	GLY	-	expression tag	UNP K9YFK1
BP	97	SER	-	expression tag	UNP K9YFK1
BP	98	TRP	-	expression tag	UNP K9YFK1
BP	99	SER	-	expression tag	UNP K9YFK1
BP	100	HIS	-	expression tag	UNP K9YFK1
BP	101	PRO	-	expression tag	UNP K9YFK1
BP	102	GLN	-	expression tag	UNP K9YFK1
BP	103	PHE	-	expression tag	UNP K9YFK1
BP	104	GLU	-	expression tag	UNP K9YFK1
BP	105	LYS	-	expression tag	UNP K9YFK1
BS	96	GLY	-	expression tag	UNP K9YFK1
BS	97	SER	-	expression tag	UNP K9YFK1
BS	98	TRP	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
BS	99	SER	-	expression tag	UNP K9YFK1
BS	100	HIS	-	expression tag	UNP K9YFK1
BS	101	PRO	-	expression tag	UNP K9YFK1
BS	102	GLN	-	expression tag	UNP K9YFK1
BS	103	PHE	-	expression tag	UNP K9YFK1
BS	104	GLU	-	expression tag	UNP K9YFK1
BS	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
BY	96	GLY	-	expression tag	UNP K9YFK1
BY	97	SER	-	expression tag	UNP K9YFK1
BY	98	TRP	-	expression tag	UNP K9YFK1
BY	99	SER	-	expression tag	UNP K9YFK1
BY	100	HIS	-	expression tag	UNP K9YFK1
BY	101	PRO	-	expression tag	UNP K9YFK1
BY	102	GLN	-	expression tag	UNP K9YFK1
BY	103	PHE	-	expression tag	UNP K9YFK1
BY	104	GLU	-	expression tag	UNP K9YFK1
BY	105	LYS	-	expression tag	UNP K9YFK1
B1	96	GLY	-	expression tag	UNP K9YFK1
B1	97	SER	-	expression tag	UNP K9YFK1
B1	98	TRP	-	expression tag	UNP K9YFK1
B1	99	SER	-	expression tag	UNP K9YFK1
B1	100	HIS	-	expression tag	UNP K9YFK1
B1	101	PRO	-	expression tag	UNP K9YFK1
B1	102	GLN	-	expression tag	UNP K9YFK1
B1	103	PHE	-	expression tag	UNP K9YFK1
B1	104	GLU	-	expression tag	UNP K9YFK1
B1	105	LYS	-	expression tag	UNP K9YFK1
B4	96	GLY	-	expression tag	UNP K9YFK1
B4	97	SER	-	expression tag	UNP K9YFK1
B4	98	TRP	-	expression tag	UNP K9YFK1
B4	99	SER	-	expression tag	UNP K9YFK1
B4	100	HIS	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
B4	101	PRO	-	expression tag	UNP K9YFK1
B4	102	GLN	-	expression tag	UNP K9YFK1
B4	103	PHE	-	expression tag	UNP K9YFK1
B4	104	GLU	-	expression tag	UNP K9YFK1
B4	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
CA	96	GLY	-	expression tag	UNP K9YFK1
CA	97	SER	-	expression tag	UNP K9YFK1
CA	98	TRP	-	expression tag	UNP K9YFK1
CA	99	SER	-	expression tag	UNP K9YFK1
CA	100	HIS	-	expression tag	UNP K9YFK1
CA	101	PRO	-	expression tag	UNP K9YFK1
CA	102	GLN	-	expression tag	UNP K9YFK1
CA	103	PHE	-	expression tag	UNP K9YFK1
CA	104	GLU	-	expression tag	UNP K9YFK1
CA	105	LYS	-	expression tag	UNP K9YFK1
CD	96	GLY	-	expression tag	UNP K9YFK1
CD	97	SER	-	expression tag	UNP K9YFK1
CD	98	TRP	-	expression tag	UNP K9YFK1
CD	99	SER	-	expression tag	UNP K9YFK1
CD	100	HIS	-	expression tag	UNP K9YFK1
CD	101	PRO	-	expression tag	UNP K9YFK1
CD	102	GLN	-	expression tag	UNP K9YFK1
CD	103	PHE	-	expression tag	UNP K9YFK1
CD	104	GLU	-	expression tag	UNP K9YFK1
CD	105	LYS	-	expression tag	UNP K9YFK1
CG	96	GLY	-	expression tag	UNP K9YFK1
CG	97	SER	-	expression tag	UNP K9YFK1
CG	98	TRP	-	expression tag	UNP K9YFK1
CG	99	SER	-	expression tag	UNP K9YFK1
CG	100	HIS	-	expression tag	UNP K9YFK1
CG	101	PRO	-	expression tag	UNP K9YFK1
CG	102	GLN	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
CG	103	PHE	-	expression tag	UNP K9YFK1
CG	104	GLU	-	expression tag	UNP K9YFK1
CG	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
CM	96	GLY	-	expression tag	UNP K9YFK1
CM	97	SER	-	expression tag	UNP K9YFK1
CM	98	TRP	-	expression tag	UNP K9YFK1
CM	99	SER	-	expression tag	UNP K9YFK1
CM	100	HIS	-	expression tag	UNP K9YFK1
CM	101	PRO	-	expression tag	UNP K9YFK1
CM	102	GLN	-	expression tag	UNP K9YFK1
CM	103	PHE	-	expression tag	UNP K9YFK1
CM	104	GLU	-	expression tag	UNP K9YFK1
CM	105	LYS	-	expression tag	UNP K9YFK1
CP	96	GLY	-	expression tag	UNP K9YFK1
CP	97	SER	-	expression tag	UNP K9YFK1
CP	98	TRP	-	expression tag	UNP K9YFK1
CP	99	SER	-	expression tag	UNP K9YFK1
CP	100	HIS	-	expression tag	UNP K9YFK1
CP	101	PRO	-	expression tag	UNP K9YFK1
CP	102	GLN	-	expression tag	UNP K9YFK1
CP	103	PHE	-	expression tag	UNP K9YFK1
CP	104	GLU	-	expression tag	UNP K9YFK1
CP	105	LYS	-	expression tag	UNP K9YFK1
CS	96	GLY	-	expression tag	UNP K9YFK1
CS	97	SER	-	expression tag	UNP K9YFK1
CS	98	TRP	-	expression tag	UNP K9YFK1
CS	99	SER	-	expression tag	UNP K9YFK1
CS	100	HIS	-	expression tag	UNP K9YFK1
CS	101	PRO	-	expression tag	UNP K9YFK1
CS	102	GLN	-	expression tag	UNP K9YFK1
CS	103	PHE	-	expression tag	UNP K9YFK1
CS	104	GLU	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
CS	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
CV	103	PHE	-	expression tag	UNP K9YFK1
CV	104	GLU	-	expression tag	UNP K9YFK1
CV	105	LYS	-	expression tag	UNP K9YFK1
CY	96	GLY	-	expression tag	UNP K9YFK1
CY	97	SER	-	expression tag	UNP K9YFK1
CY	98	TRP	-	expression tag	UNP K9YFK1
CY	99	SER	-	expression tag	UNP K9YFK1
CY	100	HIS	-	expression tag	UNP K9YFK1
CY	101	PRO	-	expression tag	UNP K9YFK1
CY	102	GLN	-	expression tag	UNP K9YFK1
CY	103	PHE	-	expression tag	UNP K9YFK1
CY	104	GLU	-	expression tag	UNP K9YFK1
CY	105	LYS	-	expression tag	UNP K9YFK1
C1	96	GLY	-	expression tag	UNP K9YFK1
C1	97	SER	-	expression tag	UNP K9YFK1
C1	98	TRP	-	expression tag	UNP K9YFK1
C1	99	SER	-	expression tag	UNP K9YFK1
C1	100	HIS	-	expression tag	UNP K9YFK1
C1	101	PRO	-	expression tag	UNP K9YFK1
C1	102	GLN	-	expression tag	UNP K9YFK1
C1	103	PHE	-	expression tag	UNP K9YFK1
C1	104	GLU	-	expression tag	UNP K9YFK1
C1	105	LYS	-	expression tag	UNP K9YFK1
C4	96	GLY	-	expression tag	UNP K9YFK1
C4	97	SER	-	expression tag	UNP K9YFK1
C4	98	TRP	-	expression tag	UNP K9YFK1
C4	99	SER	-	expression tag	UNP K9YFK1
C4	100	HIS	-	expression tag	UNP K9YFK1
C4	101	PRO	-	expression tag	UNP K9YFK1
C4	102	GLN	-	expression tag	UNP K9YFK1
C4	103	PHE	-	expression tag	UNP K9YFK1
C4	104	GLU	-	expression tag	UNP K9YFK1
C4	105	LYS	-	expression tag	UNP K9YFK1
C7	96	GLY	-	expression tag	UNP K9YFK1

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Chain	Residue	Modelled	Actual	Comment	Reference
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
DA	96	GLY	-	expression tag	UNP K9YFK1
DA	97	SER	-	expression tag	UNP K9YFK1
DA	98	TRP	-	expression tag	UNP K9YFK1
DA	99	SER	-	expression tag	UNP K9YFK1
DA	100	HIS	-	expression tag	UNP K9YFK1
DA	101	PRO	-	expression tag	UNP K9YFK1
DA	102	GLN	-	expression tag	UNP K9YFK1
DA	103	PHE	-	expression tag	UNP K9YFK1
DA	104	GLU	-	expression tag	UNP K9YFK1
DA	105	LYS	-	expression tag	UNP K9YFK1
DD	96	GLY	-	expression tag	UNP K9YFK1
DD	97	SER	-	expression tag	UNP K9YFK1
DD	98	TRP	-	expression tag	UNP K9YFK1
DD	99	SER	-	expression tag	UNP K9YFK1
DD	100	HIS	-	expression tag	UNP K9YFK1
DD	101	PRO	-	expression tag	UNP K9YFK1
DD	102	GLN	-	expression tag	UNP K9YFK1
DD	103	PHE	-	expression tag	UNP K9YFK1
DD	104	GLU	-	expression tag	UNP K9YFK1
DD	105	LYS	-	expression tag	UNP K9YFK1
DG	96	GLY	-	expression tag	UNP K9YFK1
DG	97	SER	-	expression tag	UNP K9YFK1
DG	98	TRP	-	expression tag	UNP K9YFK1
DG	99	SER	-	expression tag	UNP K9YFK1
DG	100	HIS	-	expression tag	UNP K9YFK1
DG	101	PRO	-	expression tag	UNP K9YFK1
DG	102	GLN	-	expression tag	UNP K9YFK1
DG	103	PHE	-	expression tag	UNP K9YFK1
DG	104	GLU	-	expression tag	UNP K9YFK1
DG	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

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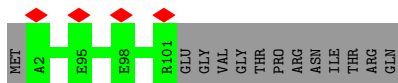
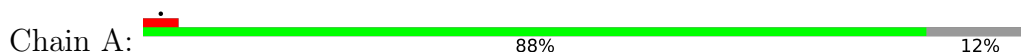
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Chain	Residue	Modelled	Actual	Comment	Reference
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DJ	100	HIS	-	expression tag	UNP K9YFK1
DJ	101	PRO	-	expression tag	UNP K9YFK1
DJ	102	GLN	-	expression tag	UNP K9YFK1
DJ	103	PHE	-	expression tag	UNP K9YFK1
DJ	104	GLU	-	expression tag	UNP K9YFK1
DJ	105	LYS	-	expression tag	UNP K9YFK1

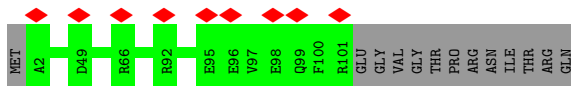
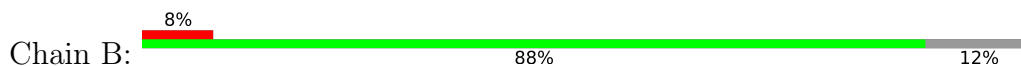
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

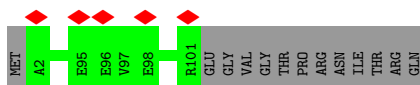
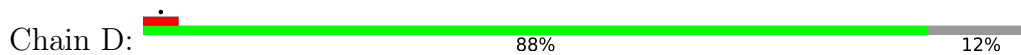
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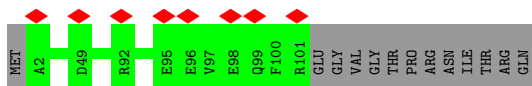
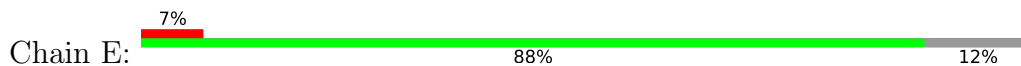
- Molecule 1: Microcompartments protein



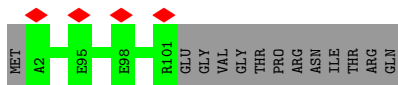
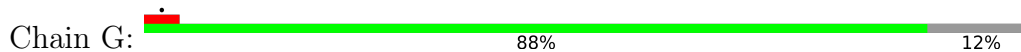
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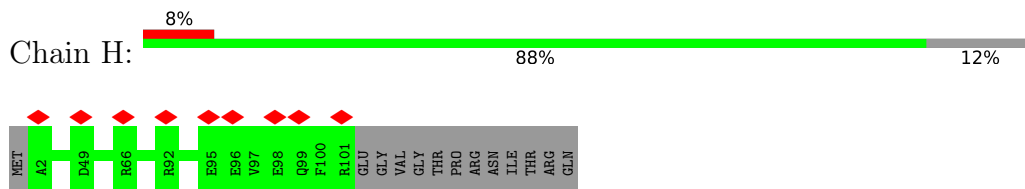
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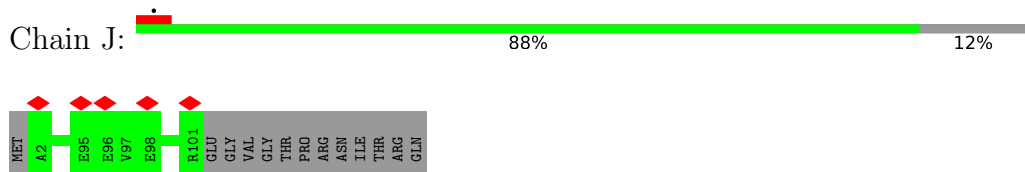
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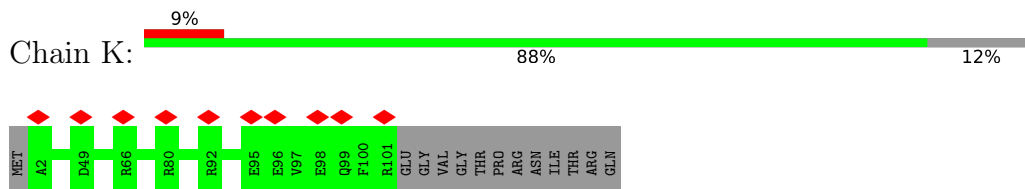
• Molecule 1: Microcompartments protein



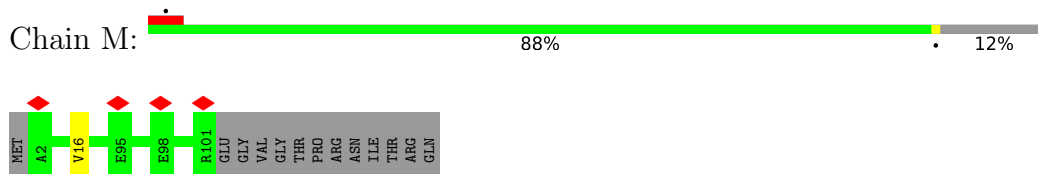
• Molecule 1: Microcompartments protein



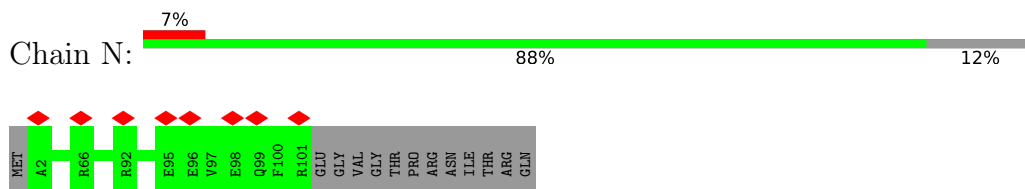
• Molecule 1: Microcompartments protein



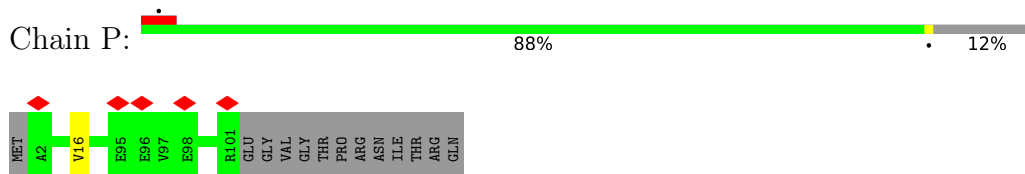
• Molecule 1: Microcompartments protein



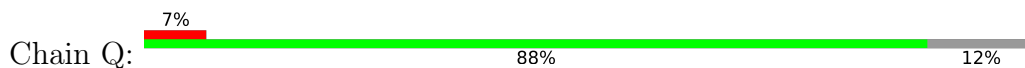
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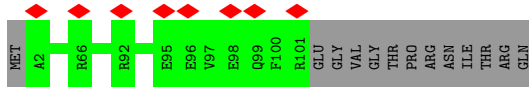


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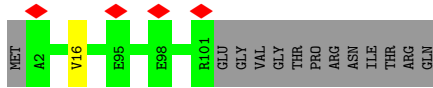
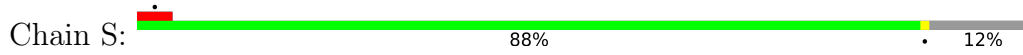


• Molecule 1: Microcompartments protein

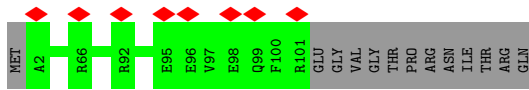
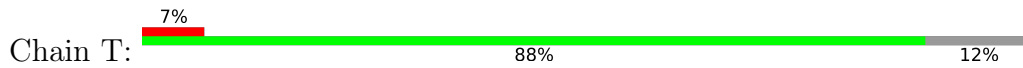




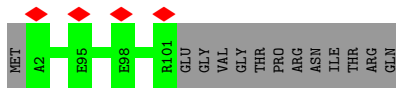
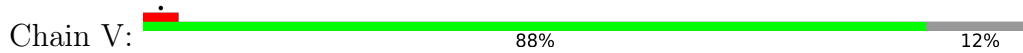
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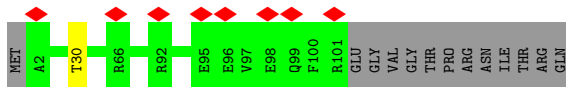
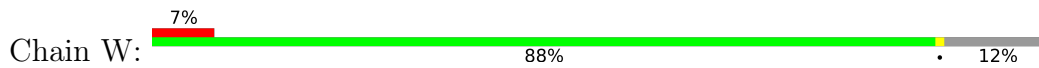
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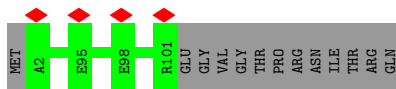
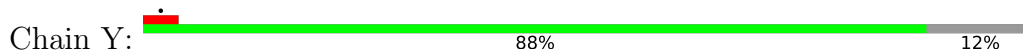
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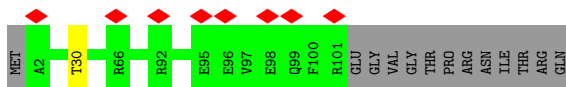
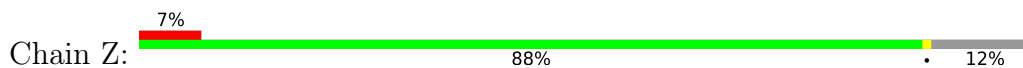
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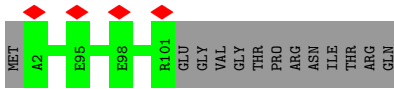
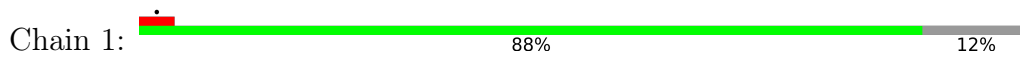
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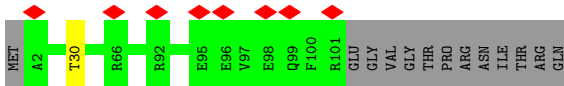
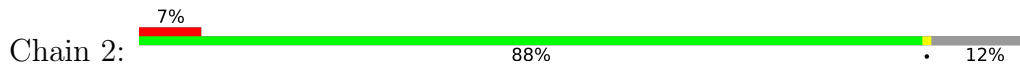
- Molecule 1: Microcompartments protein



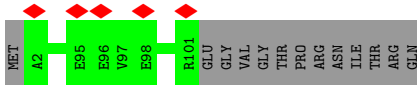
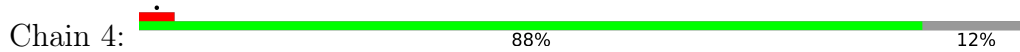
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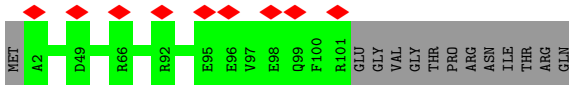
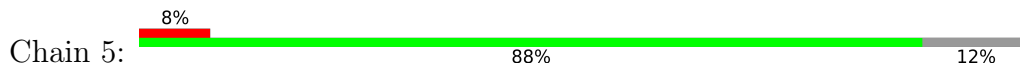
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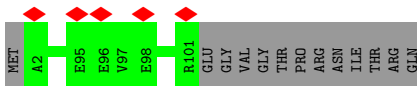
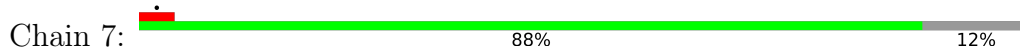
- Molecule 1: Microcompartments protein



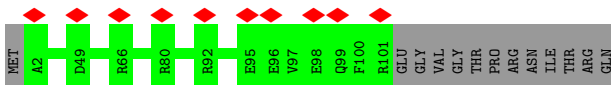
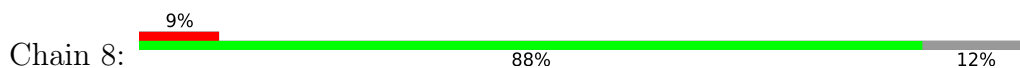
- Molecule 1: Microcompartments protein



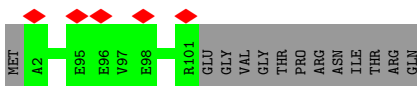
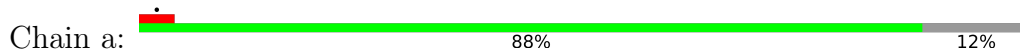
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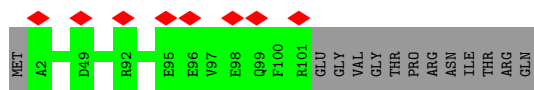
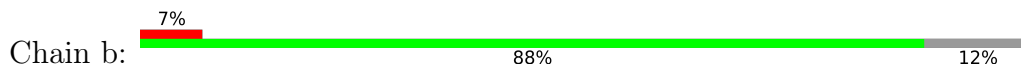
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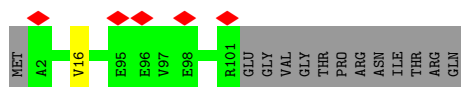
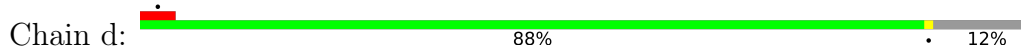
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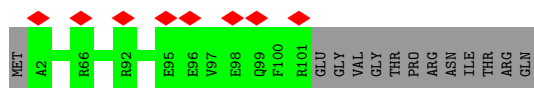
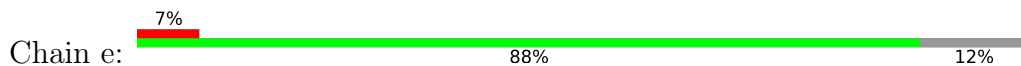
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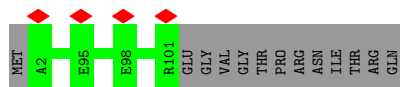
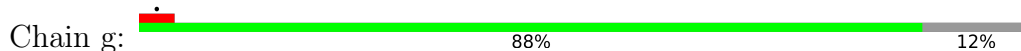
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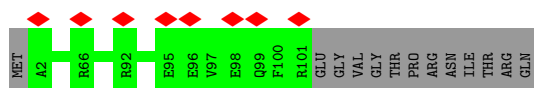
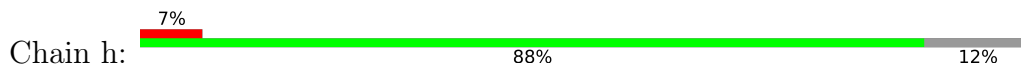
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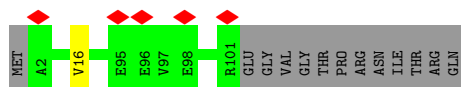
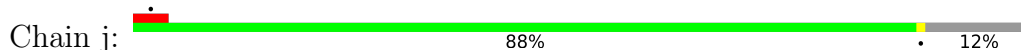
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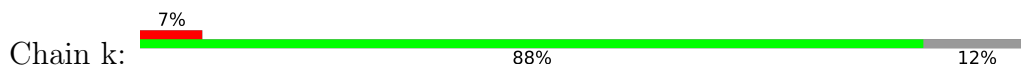
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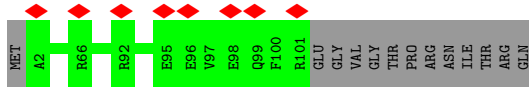


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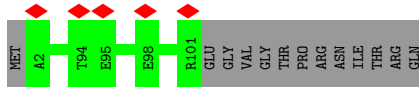
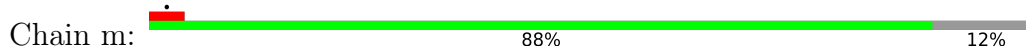


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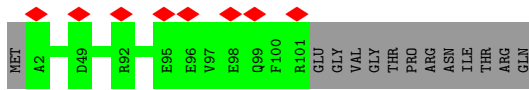
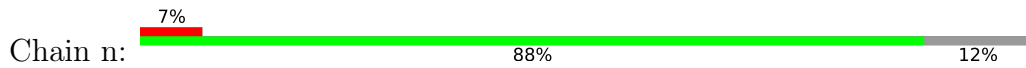




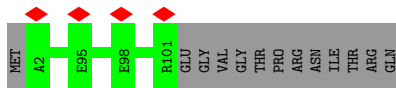
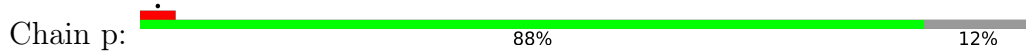
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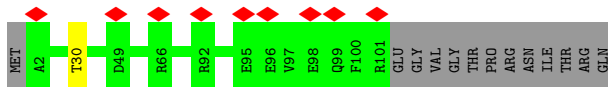
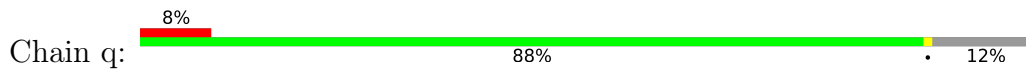
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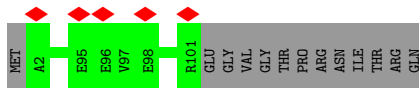
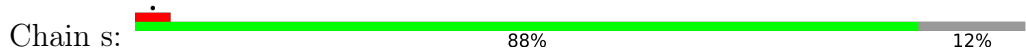
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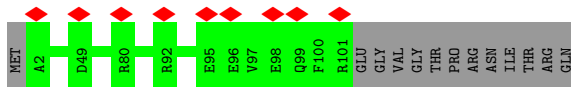
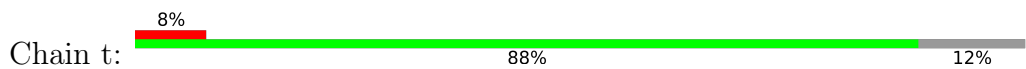
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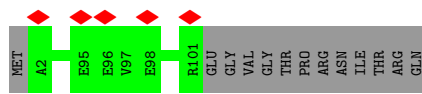
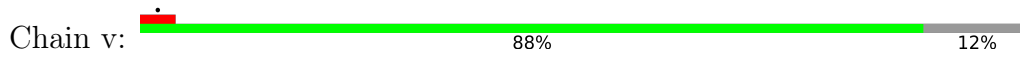
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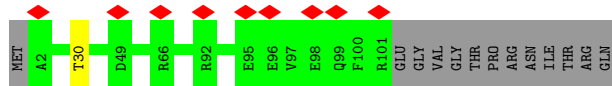
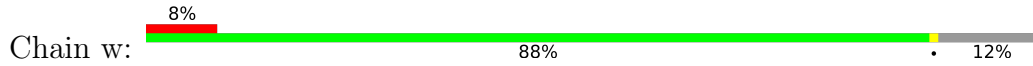
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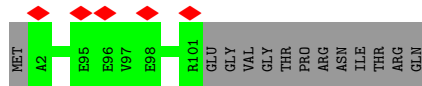
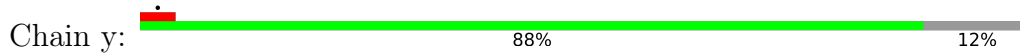
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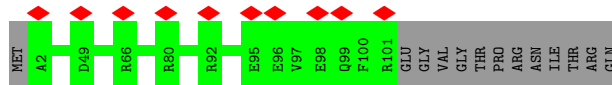
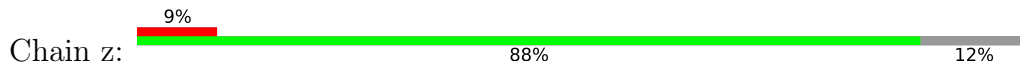
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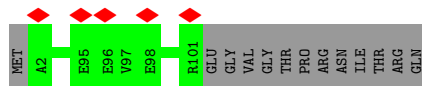
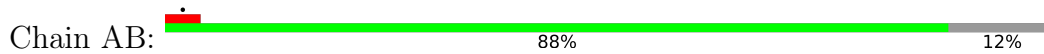
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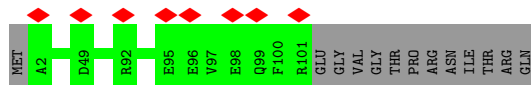
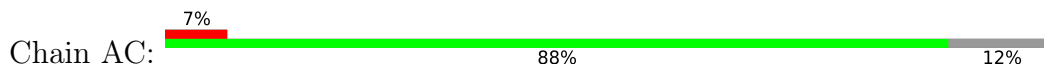
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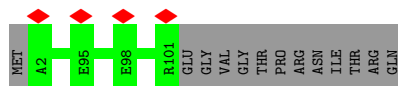
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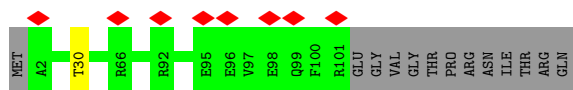
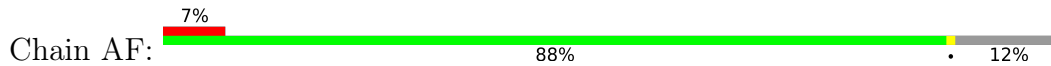
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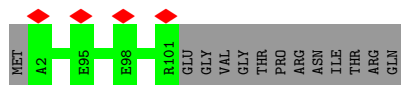
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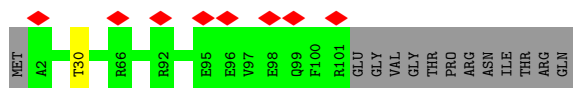
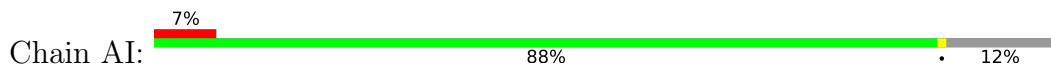
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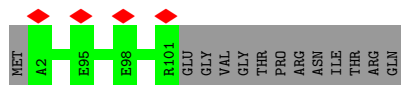
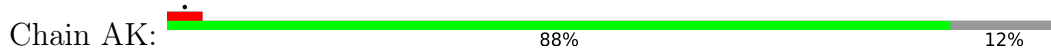
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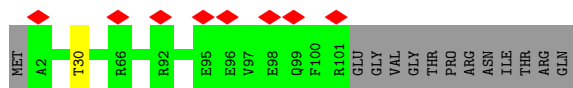
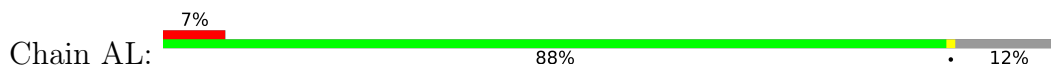
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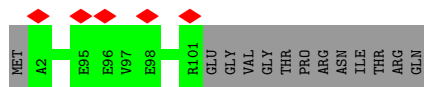
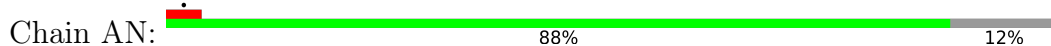
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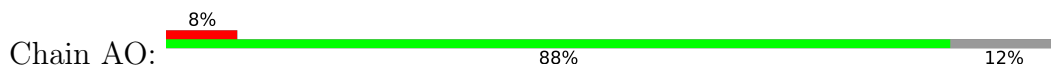
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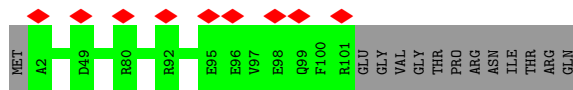


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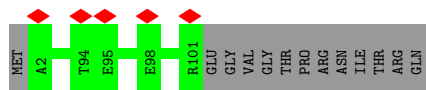
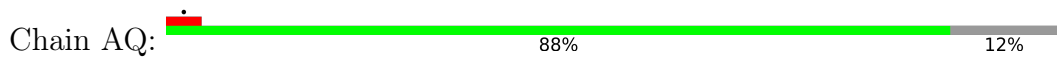


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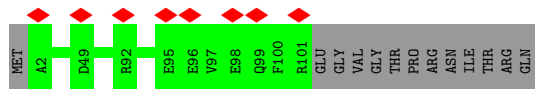




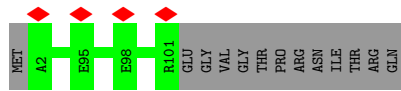
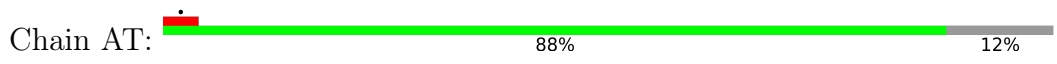
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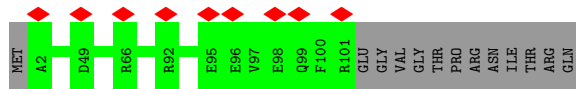
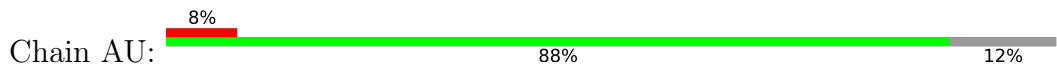
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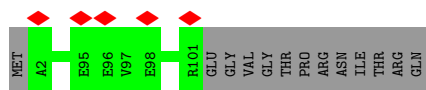
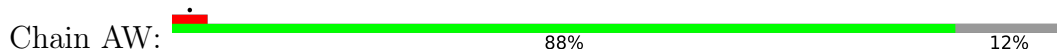
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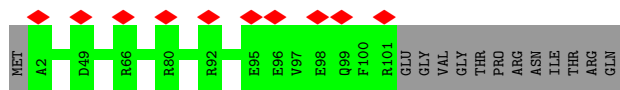
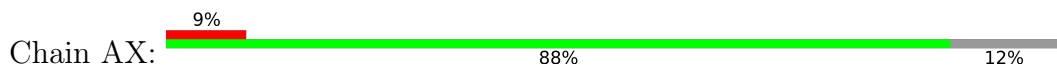
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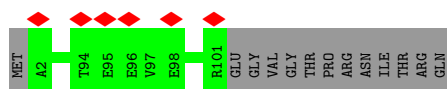
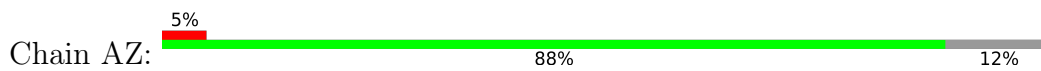
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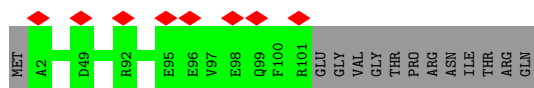
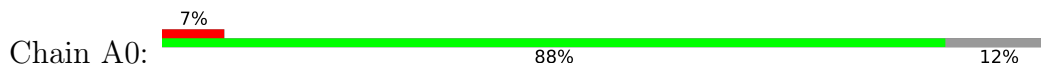
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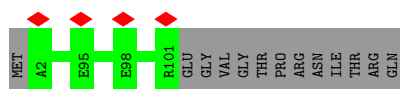
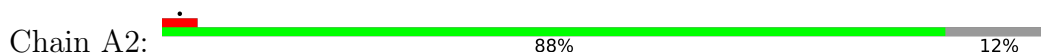
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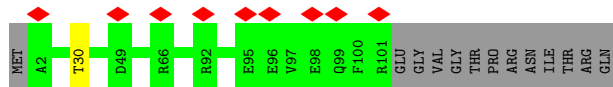
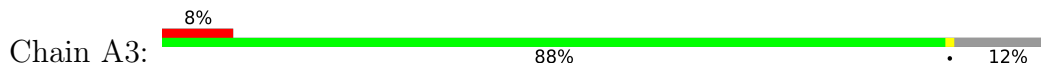
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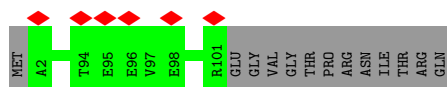
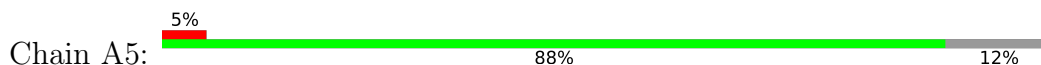
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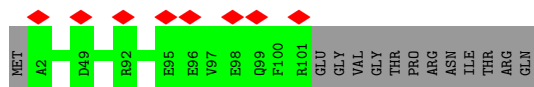
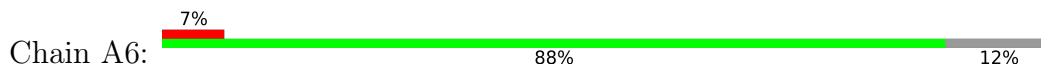
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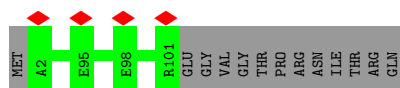
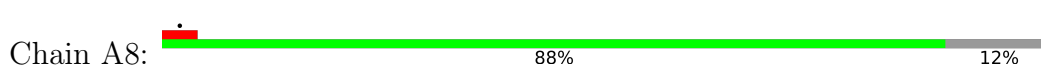
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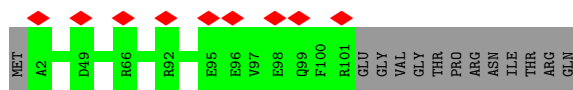
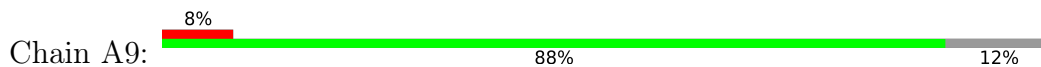
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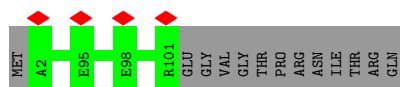
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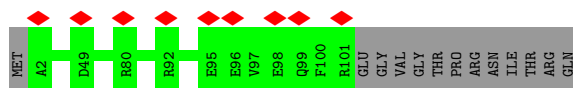
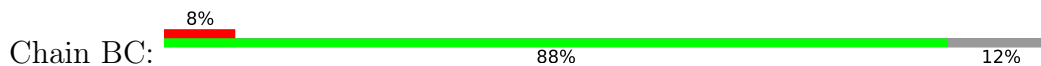
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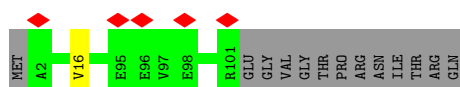
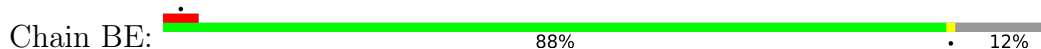
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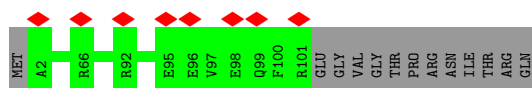
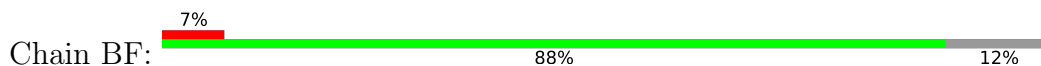
• Molecule 1: Microcompartments protein



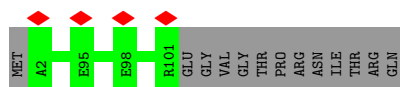
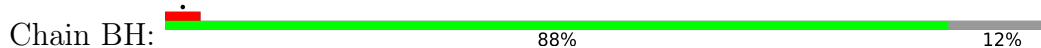
• Molecule 1: Microcompartments protein



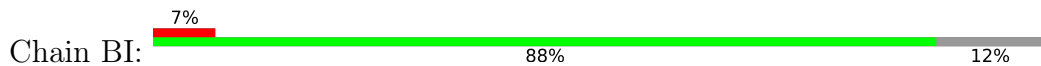
• Molecule 1: Microcompartments protein

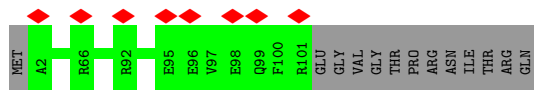


• Molecule 1: Microcompartments protein

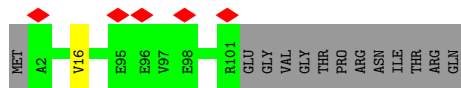
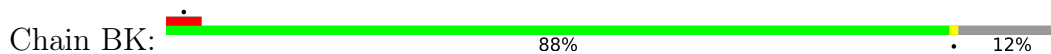


• Molecule 1: Microcompartments protein

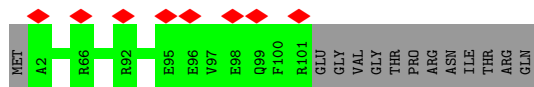
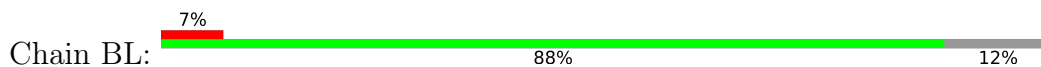




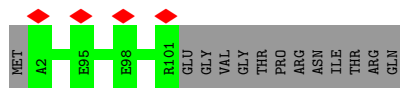
• Molecule 1: Microcompartments protein



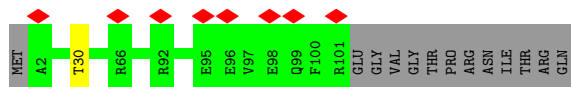
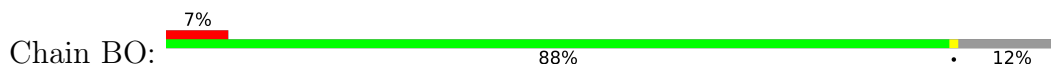
• Molecule 1: Microcompartments protein



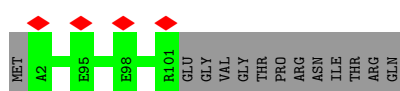
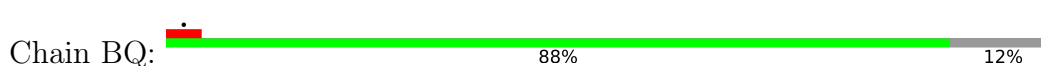
• Molecule 1: Microcompartments protein



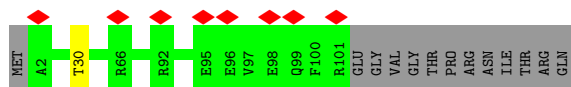
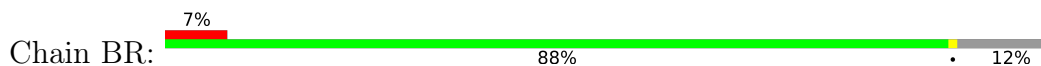
• Molecule 1: Microcompartments protein



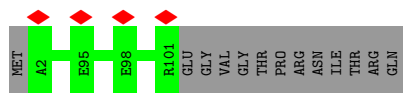
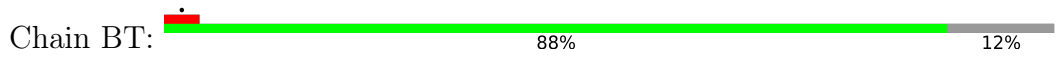
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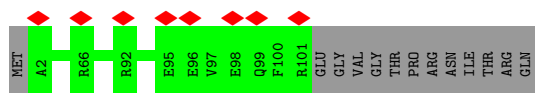
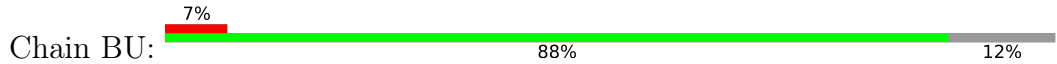
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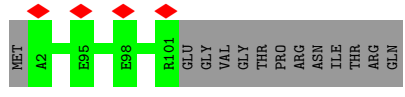
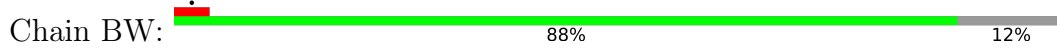
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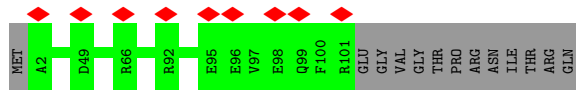
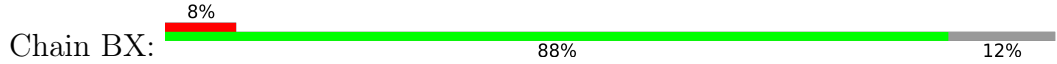
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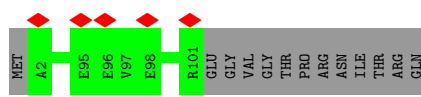
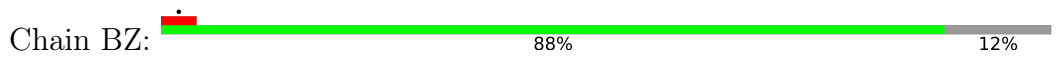
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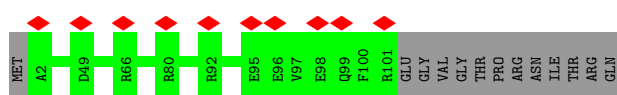
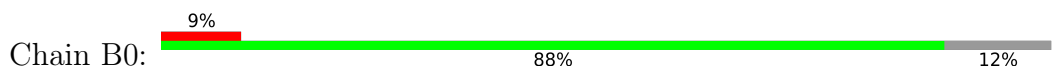
• Molecule 1: Microcompartments protein



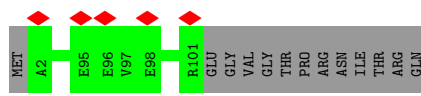
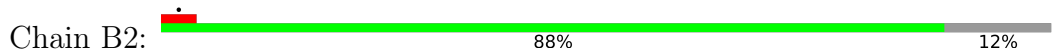
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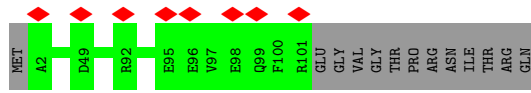
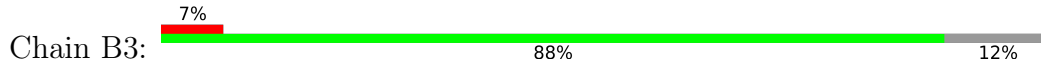
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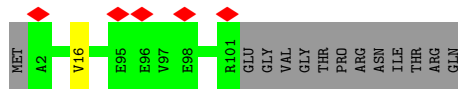
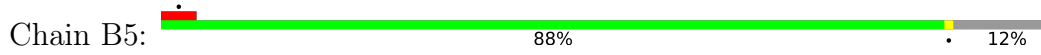
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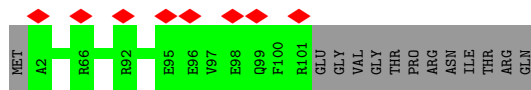
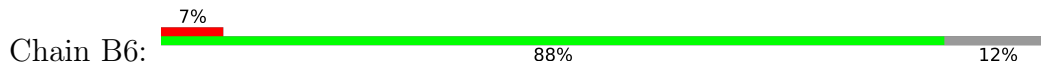
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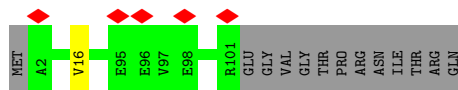
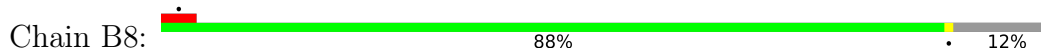
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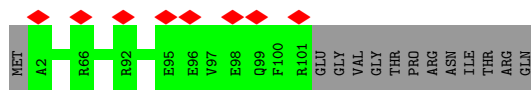
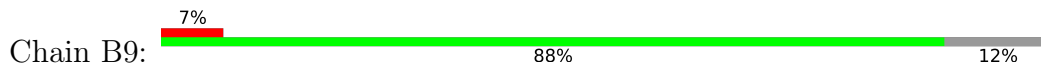
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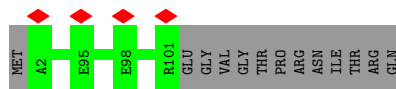
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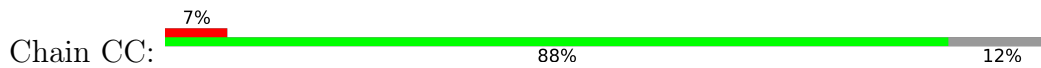
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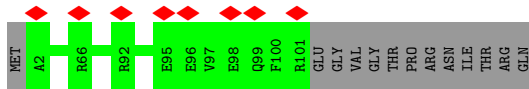


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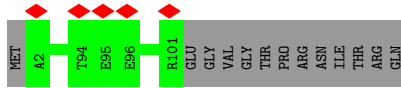
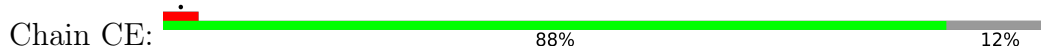


• Molecule 1: Microcompartments protein

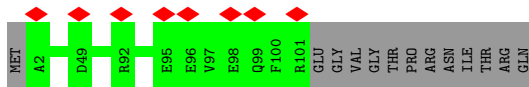
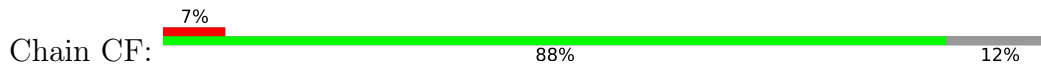




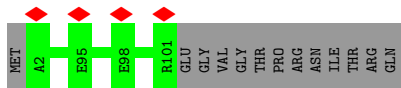
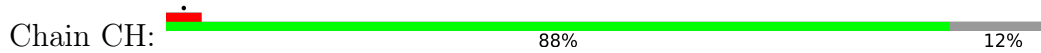
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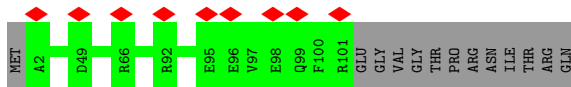
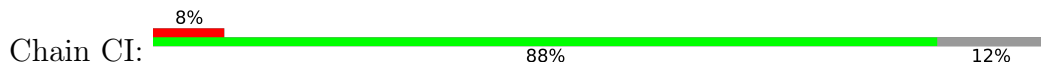
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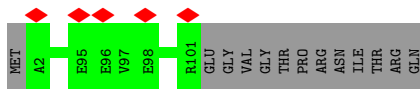
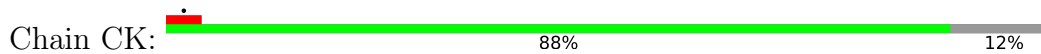
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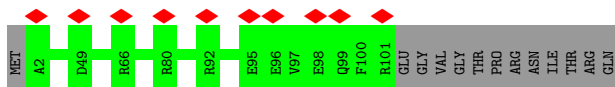
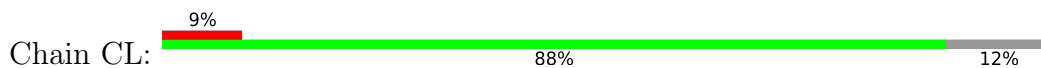
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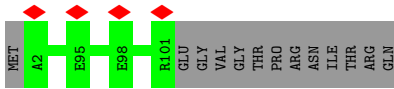


- Molecule 1: Microcompartments protein




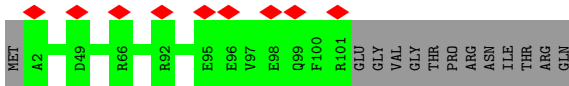
- Molecule 1: Microcompartments protein

Chain CN:  88% 12%




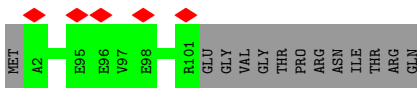
- Molecule 1: Microcompartments protein

Chain CO:  8% 88% 12%




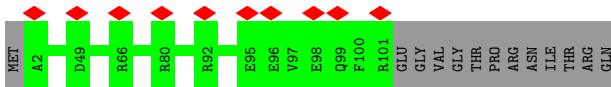
- Molecule 1: Microcompartments protein

Chain CQ:  88% 12%




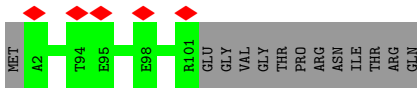
- Molecule 1: Microcompartments protein

Chain CR:  9% 88% 12%

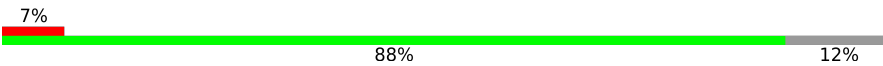


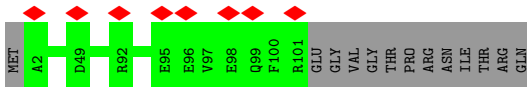
- Molecule 1: Microcompartments protein

Chain CT:  88% 12%



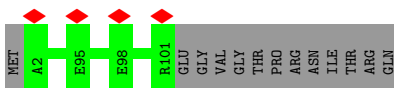
- Molecule 1: Microcompartments protein

Chain CU:  7% 88% 12%

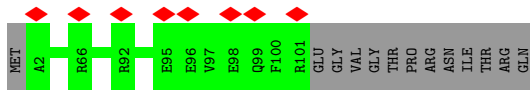
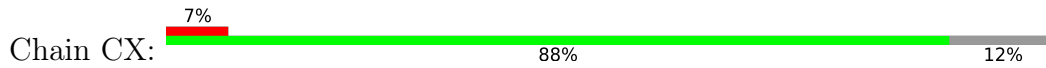


- Molecule 1: Microcompartments protein

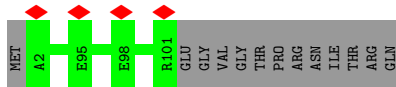
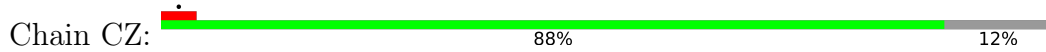
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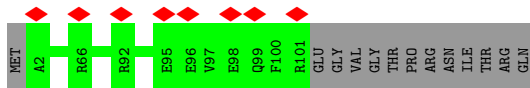
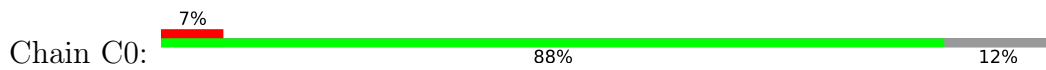
- Molecule 1: Microcompartments protein



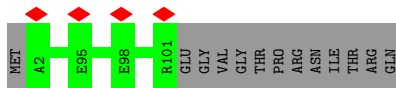
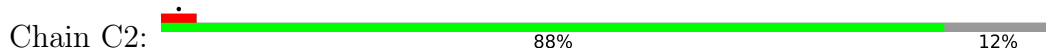
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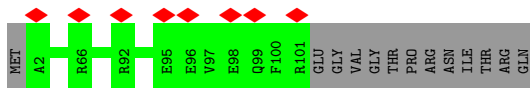
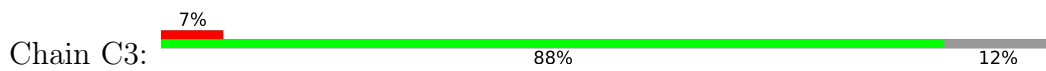
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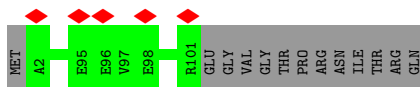
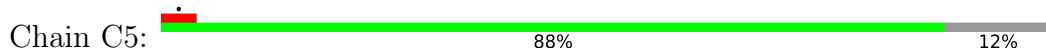
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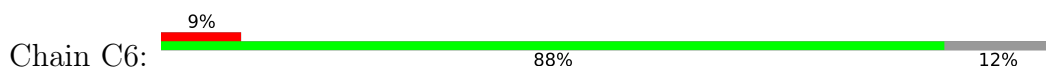
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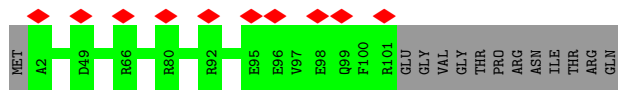


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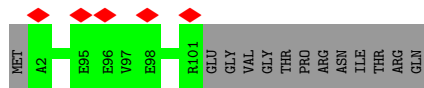
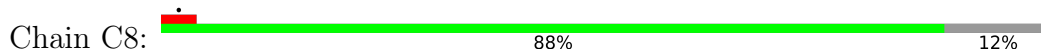


- Molecule 1: Microcompartments protein

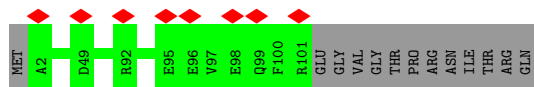
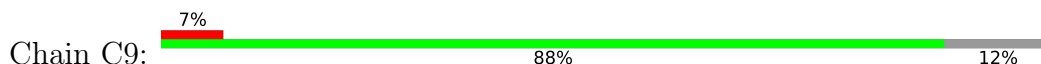




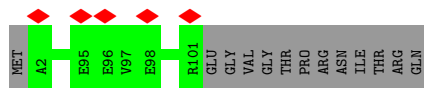
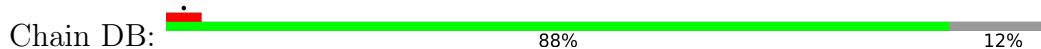
• Molecule 1: Microcompartments protein



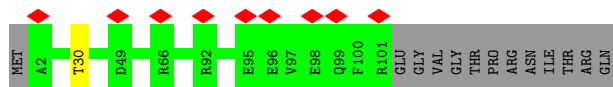
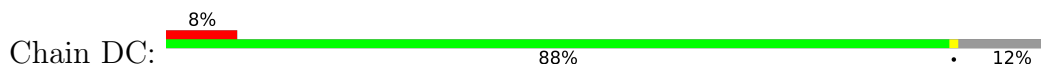
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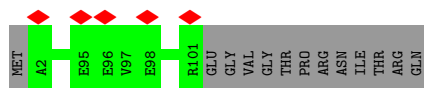
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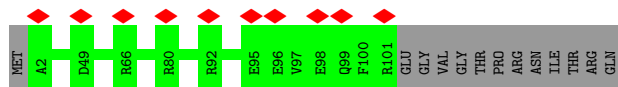
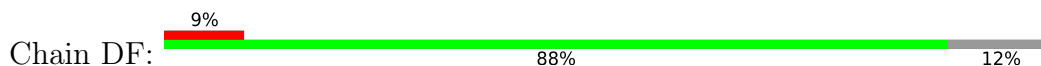
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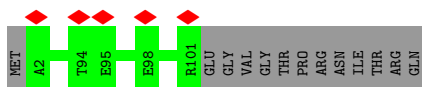
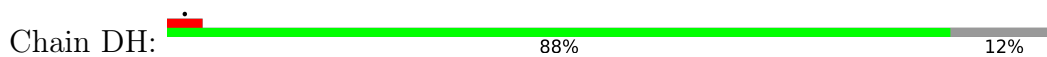
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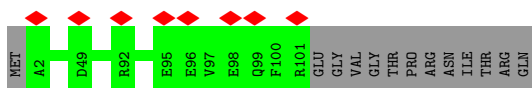
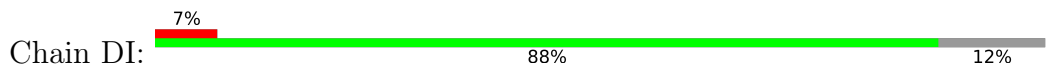
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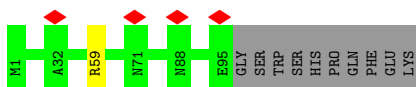
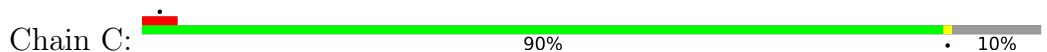
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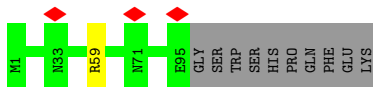
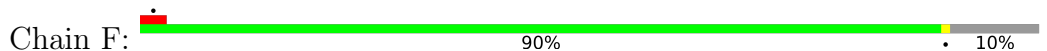
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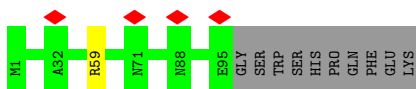
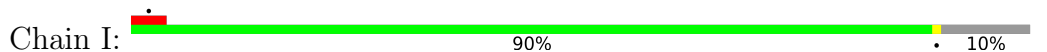
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



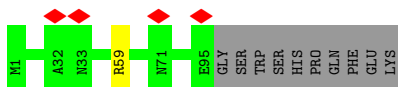
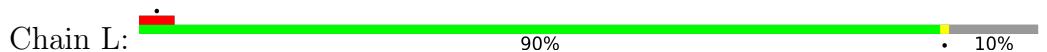
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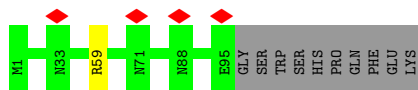


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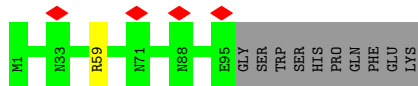
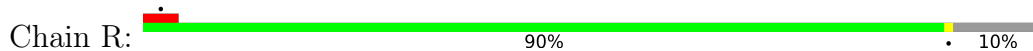


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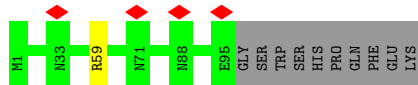
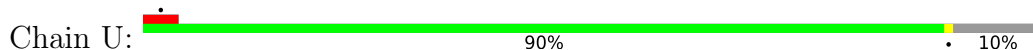




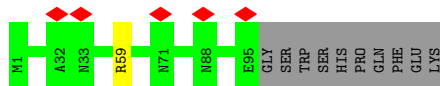
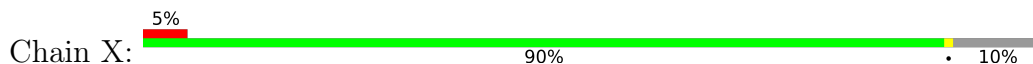
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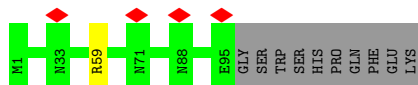
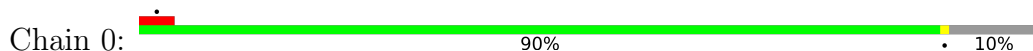
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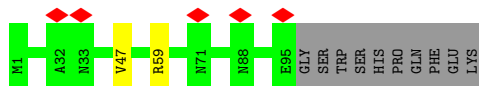
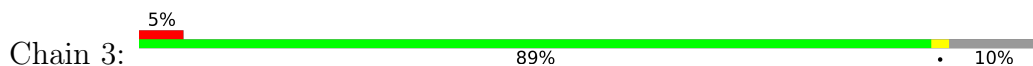
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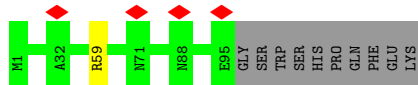
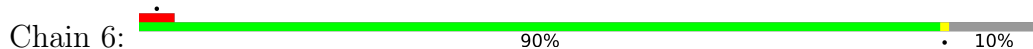
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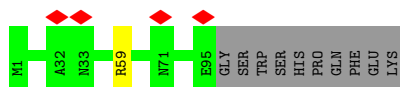
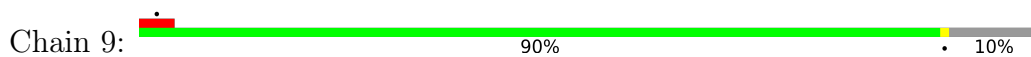
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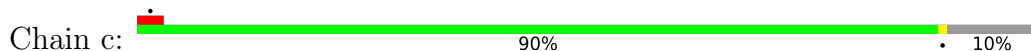
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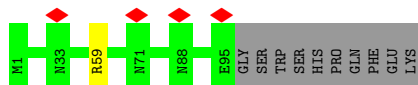
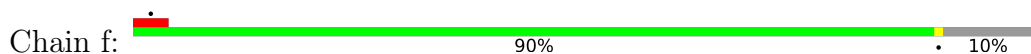
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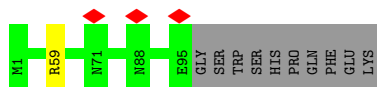
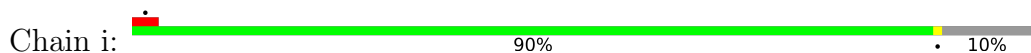
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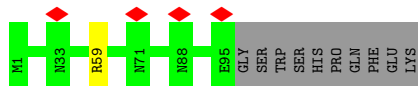
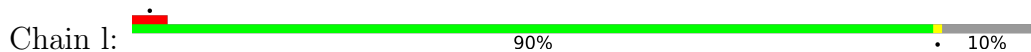
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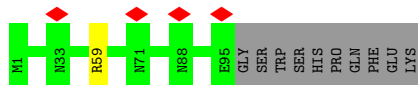
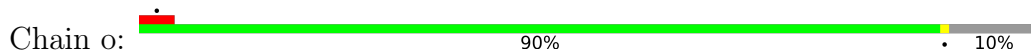
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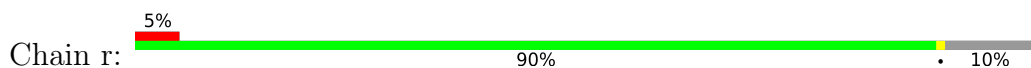
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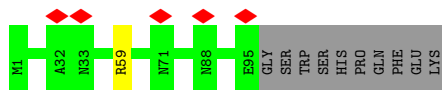


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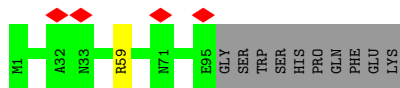
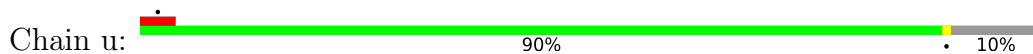


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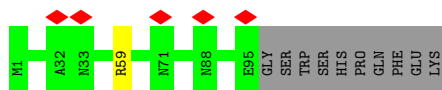
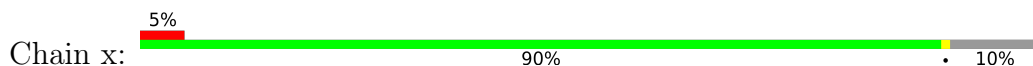




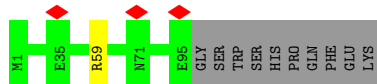
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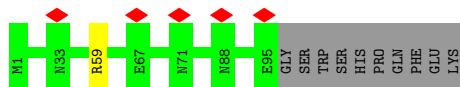
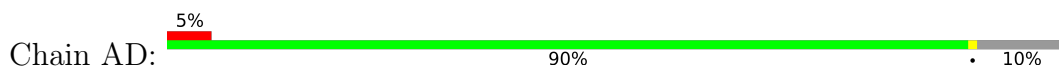
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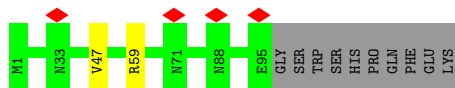
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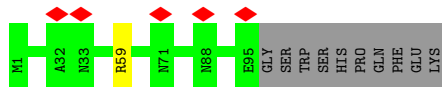
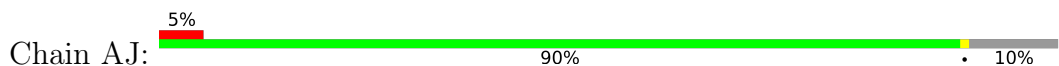
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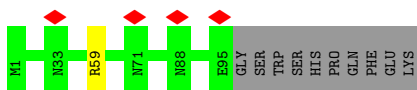
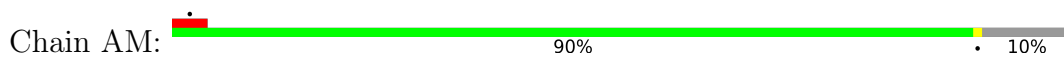
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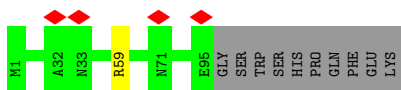
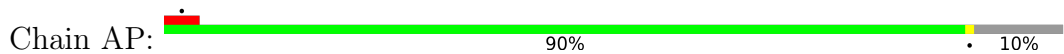
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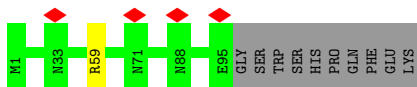
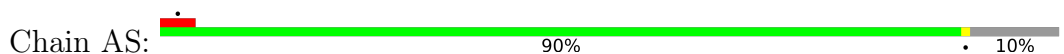
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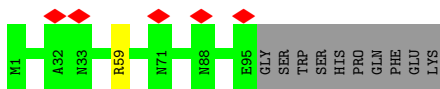
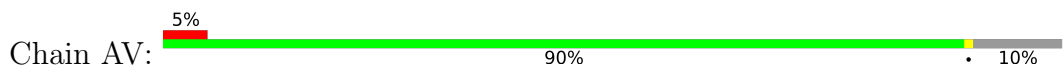
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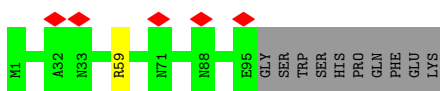
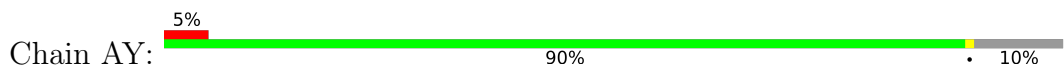
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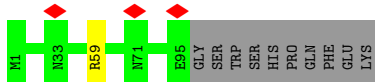
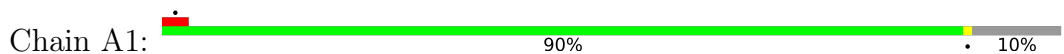
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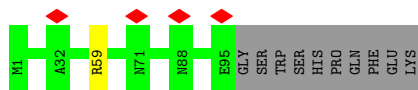


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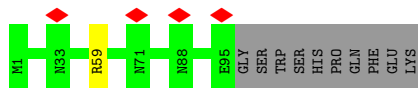
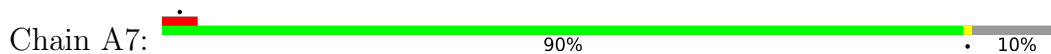


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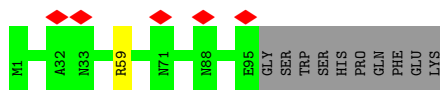




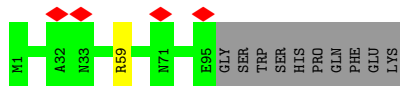
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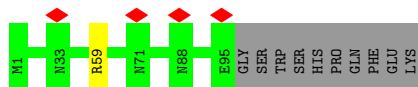
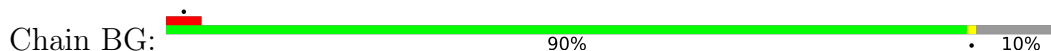
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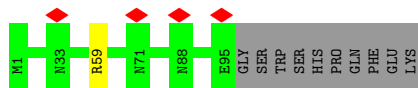
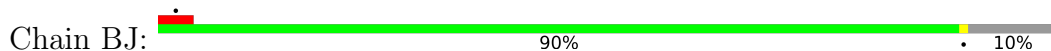
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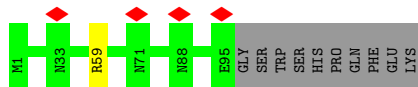
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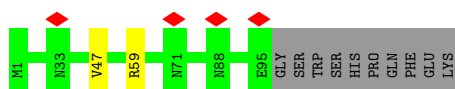
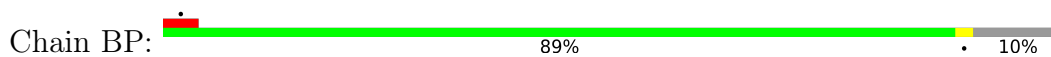
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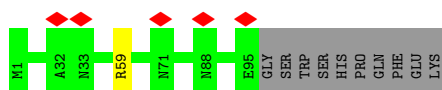
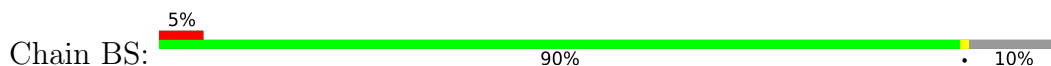
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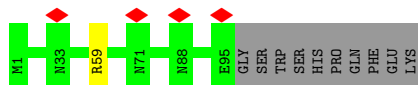
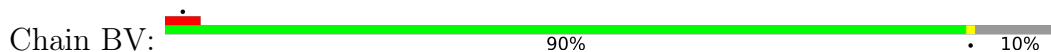
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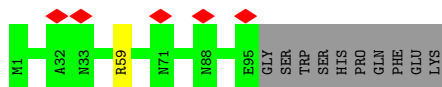
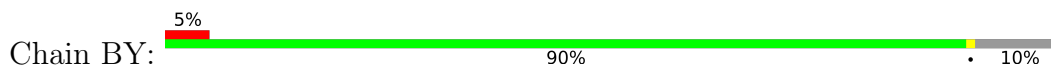
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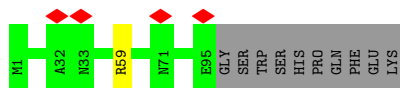
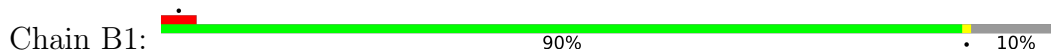
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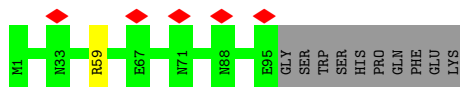
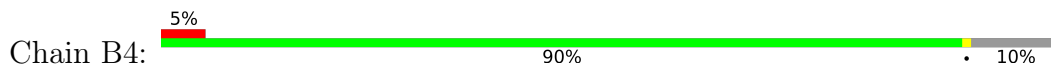
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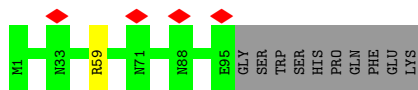


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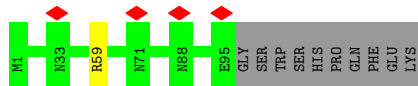
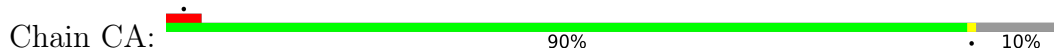


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

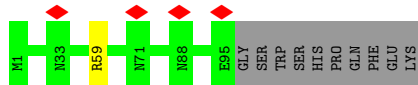
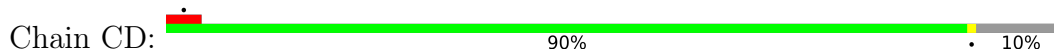




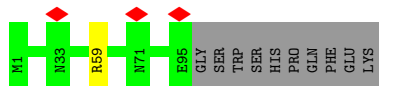
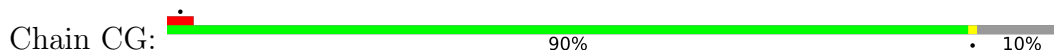
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



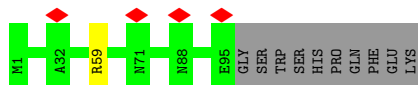
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



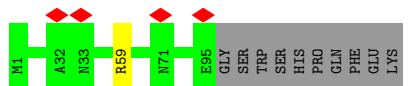
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



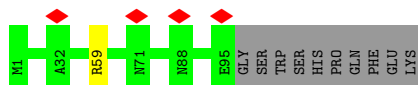
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



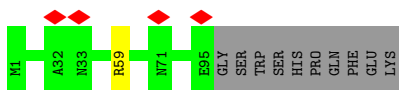
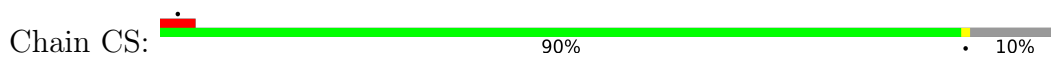
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



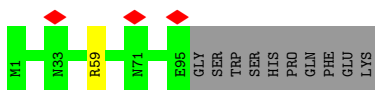
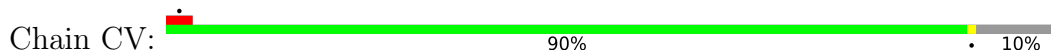
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



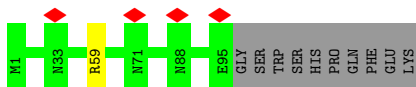
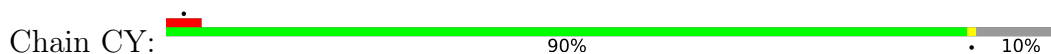
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



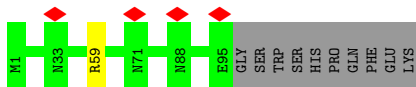
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



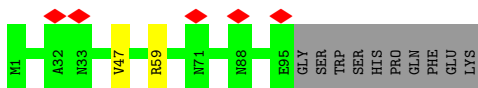
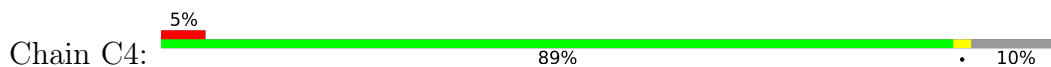
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



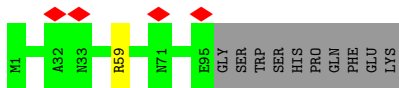
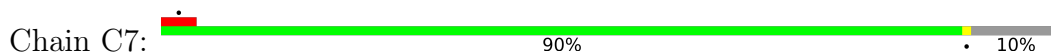
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



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

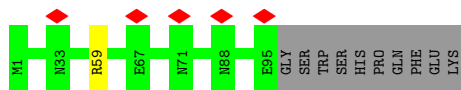


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

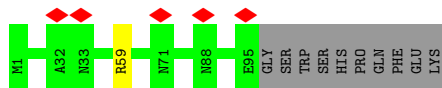


- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

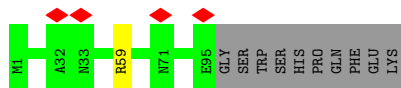
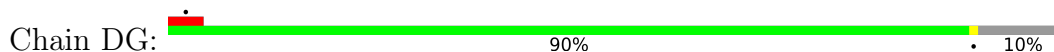




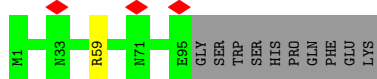
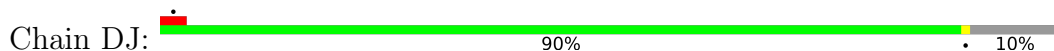
- Molecule 2: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



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



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	1586	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)	2000	Depositor
Maximum defocus (nm)	Not provided	
Magnification	56000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	8.607	Depositor
Minimum map value	-4.295	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.7	Depositor
Map size (Å)	222.7, 222.7, 222.7	wwPDB
Map dimensions	250, 250, 250	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	1	0.34	0/761	0.52	0/1033
1	2	0.33	0/761	0.51	0/1033
1	4	0.33	0/761	0.51	0/1033
1	5	0.33	0/761	0.51	0/1033
1	7	0.34	0/761	0.51	0/1033
1	8	0.32	0/761	0.50	0/1033
1	A	0.34	0/761	0.51	0/1033
1	A0	0.33	0/761	0.51	0/1033
1	A2	0.34	0/761	0.51	0/1033
1	A3	0.33	0/761	0.50	0/1033
1	A5	0.35	0/761	0.51	0/1033
1	A6	0.33	0/761	0.51	0/1033
1	A8	0.33	0/761	0.52	0/1033
1	A9	0.33	0/761	0.51	0/1033
1	AB	0.34	0/761	0.52	0/1033
1	AC	0.33	0/761	0.50	0/1033
1	AE	0.34	0/761	0.52	0/1033
1	AF	0.32	0/761	0.51	0/1033
1	AH	0.35	0/761	0.52	0/1033
1	AI	0.33	0/761	0.52	0/1033
1	AK	0.35	0/761	0.52	0/1033
1	AL	0.33	0/761	0.51	0/1033
1	AN	0.34	0/761	0.51	0/1033
1	AO	0.33	0/761	0.50	0/1033
1	AQ	0.34	0/761	0.51	0/1033
1	AR	0.34	0/761	0.51	0/1033
1	AT	0.33	0/761	0.51	0/1033
1	AU	0.32	0/761	0.50	0/1033
1	AW	0.34	0/761	0.50	0/1033
1	AX	0.32	0/761	0.51	0/1033
1	AZ	0.34	0/761	0.52	0/1033
1	B	0.33	0/761	0.50	0/1033
1	B0	0.32	0/761	0.50	0/1033
1	B2	0.35	0/761	0.52	0/1033

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B3	0.34	0/761	0.50	0/1033
1	B5	0.34	0/761	0.52	0/1033
1	B6	0.33	0/761	0.52	0/1033
1	B8	0.34	0/761	0.52	0/1033
1	B9	0.33	0/761	0.51	0/1033
1	BB	0.35	0/761	0.51	0/1033
1	BC	0.33	0/761	0.50	0/1033
1	BE	0.34	0/761	0.51	0/1033
1	BF	0.33	0/761	0.52	0/1033
1	BH	0.34	0/761	0.51	0/1033
1	BI	0.33	0/761	0.51	0/1033
1	BK	0.34	0/761	0.52	0/1033
1	BL	0.33	0/761	0.52	0/1033
1	BN	0.34	0/761	0.52	0/1033
1	BO	0.33	0/761	0.51	0/1033
1	BQ	0.34	0/761	0.51	0/1033
1	BR	0.33	0/761	0.51	0/1033
1	BT	0.35	0/761	0.52	0/1033
1	BU	0.33	0/761	0.52	0/1033
1	BW	0.33	0/761	0.51	0/1033
1	BX	0.33	0/761	0.50	0/1033
1	BZ	0.34	0/761	0.51	0/1033
1	C0	0.33	0/761	0.51	0/1033
1	C2	0.34	0/761	0.52	0/1033
1	C3	0.33	0/761	0.51	0/1033
1	C5	0.34	0/761	0.50	0/1033
1	C6	0.33	0/761	0.50	0/1033
1	C8	0.35	0/761	0.52	0/1033
1	C9	0.33	0/761	0.50	0/1033
1	CB	0.34	0/761	0.51	0/1033
1	CC	0.33	0/761	0.51	0/1033
1	CE	0.35	0/761	0.52	0/1033
1	CF	0.34	0/761	0.51	0/1033
1	CH	0.34	0/761	0.51	0/1033
1	CI	0.33	0/761	0.50	0/1033
1	CK	0.34	0/761	0.50	0/1033
1	CL	0.32	0/761	0.50	0/1033
1	CN	0.34	0/761	0.51	0/1033
1	CO	0.33	0/761	0.50	0/1033
1	CQ	0.35	0/761	0.50	0/1033
1	CR	0.33	0/761	0.50	0/1033
1	CT	0.35	0/761	0.52	0/1033
1	CU	0.34	0/761	0.51	0/1033

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CW	0.34	0/761	0.52	0/1033
1	CX	0.33	0/761	0.52	0/1033
1	CZ	0.34	0/761	0.52	0/1033
1	D	0.35	0/761	0.52	0/1033
1	DB	0.34	0/761	0.52	0/1033
1	DC	0.33	0/761	0.50	0/1033
1	DE	0.34	0/761	0.50	0/1033
1	DF	0.32	0/761	0.50	0/1033
1	DH	0.35	0/761	0.52	0/1033
1	DI	0.34	0/761	0.51	0/1033
1	E	0.34	0/761	0.51	0/1033
1	G	0.34	0/761	0.51	0/1033
1	H	0.33	0/761	0.50	0/1033
1	J	0.35	0/761	0.51	0/1033
1	K	0.32	0/761	0.51	0/1033
1	M	0.34	0/761	0.52	0/1033
1	N	0.33	0/761	0.52	0/1033
1	P	0.34	0/761	0.52	0/1033
1	Q	0.33	0/761	0.52	0/1033
1	S	0.34	0/761	0.52	0/1033
1	T	0.33	0/761	0.52	0/1033
1	V	0.34	0/761	0.51	0/1033
1	W	0.33	0/761	0.52	0/1033
1	Y	0.35	0/761	0.52	0/1033
1	Z	0.33	0/761	0.51	0/1033
1	a	0.35	0/761	0.52	0/1033
1	b	0.34	0/761	0.50	0/1033
1	d	0.34	0/761	0.51	0/1033
1	e	0.33	0/761	0.52	0/1033
1	g	0.34	0/761	0.51	0/1033
1	h	0.33	0/761	0.52	0/1033
1	j	0.35	0/761	0.52	0/1033
1	k	0.33	0/761	0.52	0/1033
1	m	0.35	0/761	0.51	0/1033
1	n	0.34	0/761	0.51	0/1033
1	p	0.34	0/761	0.51	0/1033
1	q	0.33	0/761	0.51	0/1033
1	s	0.34	0/761	0.51	0/1033
1	t	0.33	0/761	0.50	0/1033
1	v	0.33	0/761	0.52	0/1033
1	w	0.33	0/761	0.51	0/1033
1	y	0.35	0/761	0.51	0/1033
1	z	0.32	0/761	0.50	0/1033

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	0	0.31	0/731	0.49	0/992
2	3	0.31	0/731	0.50	0/992
2	6	0.32	0/731	0.51	0/992
2	9	0.32	0/731	0.50	0/992
2	A1	0.32	0/731	0.49	0/992
2	A4	0.32	0/731	0.50	0/992
2	A7	0.32	0/731	0.50	0/992
2	AA	0.31	0/731	0.50	0/992
2	AD	0.32	0/731	0.50	0/992
2	AG	0.31	0/731	0.49	0/992
2	AJ	0.32	0/731	0.50	0/992
2	AM	0.31	0/731	0.49	0/992
2	AP	0.32	0/731	0.51	0/992
2	AS	0.31	0/731	0.50	0/992
2	AV	0.33	0/731	0.51	0/992
2	AY	0.31	0/731	0.50	0/992
2	B1	0.31	0/731	0.50	0/992
2	B4	0.32	0/731	0.50	0/992
2	B7	0.32	0/731	0.50	0/992
2	BA	0.33	0/731	0.51	0/992
2	BD	0.32	0/731	0.51	0/992
2	BG	0.32	0/731	0.51	0/992
2	BJ	0.32	0/731	0.50	0/992
2	BM	0.32	0/731	0.50	0/992
2	BP	0.31	0/731	0.49	0/992
2	BS	0.31	0/731	0.50	0/992
2	BV	0.31	0/731	0.49	0/992
2	BY	0.31	0/731	0.50	0/992
2	C	0.32	0/731	0.51	0/992
2	C1	0.32	0/731	0.50	0/992
2	C4	0.31	0/731	0.50	0/992
2	C7	0.31	0/731	0.50	0/992
2	CA	0.32	0/731	0.51	0/992
2	CD	0.32	0/731	0.50	0/992
2	CG	0.31	0/731	0.50	0/992
2	CJ	0.31	0/731	0.50	0/992
2	CM	0.32	0/731	0.50	0/992
2	CP	0.31	0/731	0.50	0/992
2	CS	0.31	0/731	0.50	0/992
2	CV	0.31	0/731	0.51	0/992
2	CY	0.31	0/731	0.50	0/992
2	DA	0.32	0/731	0.50	0/992
2	DD	0.33	0/731	0.51	0/992

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	DG	0.31	0/731	0.50	0/992
2	DJ	0.32	0/731	0.50	0/992
2	F	0.32	0/731	0.49	0/992
2	I	0.31	0/731	0.50	0/992
2	L	0.32	0/731	0.50	0/992
2	O	0.31	0/731	0.50	0/992
2	R	0.31	0/731	0.50	0/992
2	U	0.31	0/731	0.50	0/992
2	X	0.32	0/731	0.50	0/992
2	c	0.32	0/731	0.49	0/992
2	f	0.32	0/731	0.50	0/992
2	i	0.32	0/731	0.51	0/992
2	l	0.32	0/731	0.50	0/992
2	o	0.32	0/731	0.50	0/992
2	r	0.33	0/731	0.51	0/992
2	u	0.32	0/731	0.51	0/992
2	x	0.32	0/731	0.49	0/992
All	All	0.33	0/135180	0.51	0/183480

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	1	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	2	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	4	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	5	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	7	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	8	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	A	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	A0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	A2	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	A3	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	A5	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	A6	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	A8	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	A9	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	AB	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AC	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	AE	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AF	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	AH	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	AI	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	AK	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AL	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	AN	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AO	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	AQ	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AR	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	AT	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AU	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	AW	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	AX	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	AZ	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	B	98/113 (87%)	93 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B0	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	B2	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	B3	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	B5	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	B6	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	B8	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	B9	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	BB	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BC	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	BE	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BF	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	BH	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BI	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	BK	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BL	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	BN	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BO	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	BQ	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BR	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	BT	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	BU	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	BW	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	BX	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	BZ	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	C0	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	C2	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	C3	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	C5	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	C6	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	C8	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	C9	98/113 (87%)	94 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CB	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CC	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	CE	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CF	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	CH	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CI	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	CK	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CL	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	CN	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CO	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	CQ	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CR	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	CT	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	CU	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	CW	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	CX	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	CZ	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	D	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	DB	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	DC	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	DE	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	DF	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	DH	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	DI	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	E	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	G	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	H	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	J	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	K	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	M	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	N	98/113 (87%)	93 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	P	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	Q	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	S	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	T	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	V	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	W	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	Y	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	Z	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	a	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	b	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	d	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	e	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	g	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	h	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	j	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	k	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	m	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	n	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	p	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	q	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	s	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	t	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
1	v	98/113 (87%)	96 (98%)	2 (2%)	0	100	100
1	w	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
1	y	98/113 (87%)	95 (97%)	3 (3%)	0	100	100
1	z	98/113 (87%)	94 (96%)	4 (4%)	0	100	100
2	0	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	3	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	6	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	9	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
2	A1	93/105 (89%)	90 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A4	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	A7	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	AA	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	AD	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	AG	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	AJ	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	AM	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	AP	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	AS	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	AV	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	AY	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
2	B1	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	B4	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	B7	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	BA	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	BD	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	BG	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	BJ	93/105 (89%)	85 (91%)	8 (9%)	0	100	100
2	BM	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	BP	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	BS	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	BV	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	BY	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	C	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	C1	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	C4	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	C7	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	CA	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	CD	93/105 (89%)	85 (91%)	8 (9%)	0	100	100
2	CG	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	CJ	93/105 (89%)	89 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	CM	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
2	CP	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	CS	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	CV	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	CY	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	DA	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	DD	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	DG	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	DJ	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	F	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	I	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	L	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
2	O	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	R	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	U	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	X	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	c	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	f	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
2	i	93/105 (89%)	85 (91%)	8 (9%)	0	100	100
2	l	93/105 (89%)	86 (92%)	7 (8%)	0	100	100
2	o	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	r	93/105 (89%)	88 (95%)	5 (5%)	0	100	100
2	u	93/105 (89%)	89 (96%)	4 (4%)	0	100	100
2	x	93/105 (89%)	87 (94%)	6 (6%)	0	100	100
All	All	17340/19860 (87%)	16611 (96%)	729 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	80/91 (88%)	80 (100%)	0	100	100
1	2	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	4	80/91 (88%)	80 (100%)	0	100	100
1	5	80/91 (88%)	80 (100%)	0	100	100
1	7	80/91 (88%)	80 (100%)	0	100	100
1	8	80/91 (88%)	80 (100%)	0	100	100
1	A	80/91 (88%)	80 (100%)	0	100	100
1	A0	80/91 (88%)	80 (100%)	0	100	100
1	A2	80/91 (88%)	80 (100%)	0	100	100
1	A3	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	A5	80/91 (88%)	80 (100%)	0	100	100
1	A6	80/91 (88%)	80 (100%)	0	100	100
1	A8	80/91 (88%)	80 (100%)	0	100	100
1	A9	80/91 (88%)	80 (100%)	0	100	100
1	AB	80/91 (88%)	80 (100%)	0	100	100
1	AC	80/91 (88%)	80 (100%)	0	100	100
1	AE	80/91 (88%)	80 (100%)	0	100	100
1	AF	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	AH	80/91 (88%)	80 (100%)	0	100	100
1	AI	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	AK	80/91 (88%)	80 (100%)	0	100	100
1	AL	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	AN	80/91 (88%)	80 (100%)	0	100	100
1	AO	80/91 (88%)	80 (100%)	0	100	100
1	AQ	80/91 (88%)	80 (100%)	0	100	100
1	AR	80/91 (88%)	80 (100%)	0	100	100
1	AT	80/91 (88%)	80 (100%)	0	100	100
1	AU	80/91 (88%)	80 (100%)	0	100	100
1	AW	80/91 (88%)	80 (100%)	0	100	100
1	AX	80/91 (88%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AZ	80/91 (88%)	80 (100%)	0	100	100
1	B	80/91 (88%)	80 (100%)	0	100	100
1	B0	80/91 (88%)	80 (100%)	0	100	100
1	B2	80/91 (88%)	80 (100%)	0	100	100
1	B3	80/91 (88%)	80 (100%)	0	100	100
1	B5	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	B6	80/91 (88%)	80 (100%)	0	100	100
1	B8	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	B9	80/91 (88%)	80 (100%)	0	100	100
1	BB	80/91 (88%)	80 (100%)	0	100	100
1	BC	80/91 (88%)	80 (100%)	0	100	100
1	BE	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	BF	80/91 (88%)	80 (100%)	0	100	100
1	BH	80/91 (88%)	80 (100%)	0	100	100
1	BI	80/91 (88%)	80 (100%)	0	100	100
1	BK	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	BL	80/91 (88%)	80 (100%)	0	100	100
1	BN	80/91 (88%)	80 (100%)	0	100	100
1	BO	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	BQ	80/91 (88%)	80 (100%)	0	100	100
1	BR	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	BT	80/91 (88%)	80 (100%)	0	100	100
1	BU	80/91 (88%)	80 (100%)	0	100	100
1	BW	80/91 (88%)	80 (100%)	0	100	100
1	BX	80/91 (88%)	80 (100%)	0	100	100
1	BZ	80/91 (88%)	80 (100%)	0	100	100
1	C0	80/91 (88%)	80 (100%)	0	100	100
1	C2	80/91 (88%)	80 (100%)	0	100	100
1	C3	80/91 (88%)	80 (100%)	0	100	100
1	C5	80/91 (88%)	80 (100%)	0	100	100
1	C6	80/91 (88%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C8	80/91 (88%)	80 (100%)	0	100	100
1	C9	80/91 (88%)	80 (100%)	0	100	100
1	CB	80/91 (88%)	80 (100%)	0	100	100
1	CC	80/91 (88%)	80 (100%)	0	100	100
1	CE	80/91 (88%)	80 (100%)	0	100	100
1	CF	80/91 (88%)	80 (100%)	0	100	100
1	CH	80/91 (88%)	80 (100%)	0	100	100
1	CI	80/91 (88%)	80 (100%)	0	100	100
1	CK	80/91 (88%)	80 (100%)	0	100	100
1	CL	80/91 (88%)	80 (100%)	0	100	100
1	CN	80/91 (88%)	80 (100%)	0	100	100
1	CO	80/91 (88%)	80 (100%)	0	100	100
1	CQ	80/91 (88%)	80 (100%)	0	100	100
1	CR	80/91 (88%)	80 (100%)	0	100	100
1	CT	80/91 (88%)	80 (100%)	0	100	100
1	CU	80/91 (88%)	80 (100%)	0	100	100
1	CW	80/91 (88%)	80 (100%)	0	100	100
1	CX	80/91 (88%)	80 (100%)	0	100	100
1	CZ	80/91 (88%)	80 (100%)	0	100	100
1	D	80/91 (88%)	80 (100%)	0	100	100
1	DB	80/91 (88%)	80 (100%)	0	100	100
1	DC	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	DE	80/91 (88%)	80 (100%)	0	100	100
1	DF	80/91 (88%)	80 (100%)	0	100	100
1	DH	80/91 (88%)	80 (100%)	0	100	100
1	DI	80/91 (88%)	80 (100%)	0	100	100
1	E	80/91 (88%)	80 (100%)	0	100	100
1	G	80/91 (88%)	80 (100%)	0	100	100
1	H	80/91 (88%)	80 (100%)	0	100	100
1	J	80/91 (88%)	80 (100%)	0	100	100
1	K	80/91 (88%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	N	80/91 (88%)	80 (100%)	0	100	100
1	P	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	Q	80/91 (88%)	80 (100%)	0	100	100
1	S	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	T	80/91 (88%)	80 (100%)	0	100	100
1	V	80/91 (88%)	80 (100%)	0	100	100
1	W	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	Y	80/91 (88%)	80 (100%)	0	100	100
1	Z	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	a	80/91 (88%)	80 (100%)	0	100	100
1	b	80/91 (88%)	80 (100%)	0	100	100
1	d	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	e	80/91 (88%)	80 (100%)	0	100	100
1	g	80/91 (88%)	80 (100%)	0	100	100
1	h	80/91 (88%)	80 (100%)	0	100	100
1	j	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	k	80/91 (88%)	80 (100%)	0	100	100
1	m	80/91 (88%)	80 (100%)	0	100	100
1	n	80/91 (88%)	80 (100%)	0	100	100
1	p	80/91 (88%)	80 (100%)	0	100	100
1	q	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	s	80/91 (88%)	80 (100%)	0	100	100
1	t	80/91 (88%)	80 (100%)	0	100	100
1	v	80/91 (88%)	80 (100%)	0	100	100
1	w	80/91 (88%)	79 (99%)	1 (1%)	69	89
1	y	80/91 (88%)	80 (100%)	0	100	100
1	z	80/91 (88%)	80 (100%)	0	100	100
2	0	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	3	77/86 (90%)	75 (97%)	2 (3%)	46	78
2	6	77/86 (90%)	76 (99%)	1 (1%)	69	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	9	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	A1	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	A4	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	A7	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	AA	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	AD	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	AG	77/86 (90%)	75 (97%)	2 (3%)	46	78
2	AJ	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	AM	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	AP	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	AS	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	AV	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	AY	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	B1	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	B4	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	B7	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	BA	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	BD	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	BG	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	BJ	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	BM	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	BP	77/86 (90%)	75 (97%)	2 (3%)	46	78
2	BS	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	BV	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	BY	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	C	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	C1	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	C4	77/86 (90%)	75 (97%)	2 (3%)	46	78
2	C7	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	CA	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	CD	77/86 (90%)	76 (99%)	1 (1%)	69	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	CG	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	CJ	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	CM	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	CP	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	CS	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	CV	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	CY	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	DA	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	DD	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	DG	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	DJ	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	F	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	I	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	L	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	O	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	R	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	U	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	X	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	c	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	f	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	i	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	l	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	o	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	r	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	u	77/86 (90%)	76 (99%)	1 (1%)	69	89
2	x	77/86 (90%)	76 (99%)	1 (1%)	69	89
All	All	14220/16080 (88%)	14135 (99%)	85 (1%)	86	95

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	59	ARG
2	F	59	ARG

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Mol	Chain	Res	Type
2	I	59	ARG
2	L	59	ARG
1	M	16	VAL
2	O	59	ARG
1	P	16	VAL
2	R	59	ARG
1	S	16	VAL
2	U	59	ARG
1	W	30	THR
2	X	59	ARG
1	Z	30	THR
2	0	59	ARG
1	2	30	THR
2	3	47	VAL
2	3	59	ARG
2	6	59	ARG
2	9	59	ARG
2	c	59	ARG
1	d	16	VAL
2	f	59	ARG
2	i	59	ARG
1	j	16	VAL
2	l	59	ARG
2	o	59	ARG
1	q	30	THR
2	r	59	ARG
2	u	59	ARG
1	w	30	THR
2	x	59	ARG
2	AA	59	ARG
2	AD	59	ARG
1	AF	30	THR
2	AG	47	VAL
2	AG	59	ARG
1	AI	30	THR
2	AJ	59	ARG
1	AL	30	THR
2	AM	59	ARG
2	AP	59	ARG
2	AS	59	ARG
2	AV	59	ARG
2	AY	59	ARG

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Mol	Chain	Res	Type
2	A1	59	ARG
1	A3	30	THR
2	A4	59	ARG
2	A7	59	ARG
2	BA	59	ARG
2	BD	59	ARG
1	BE	16	VAL
2	BG	59	ARG
2	BJ	59	ARG
1	BK	16	VAL
2	BM	59	ARG
1	BO	30	THR
2	BP	47	VAL
2	BP	59	ARG
1	BR	30	THR
2	BS	59	ARG
2	BV	59	ARG
2	BY	59	ARG
2	B1	59	ARG
2	B4	59	ARG
1	B5	16	VAL
2	B7	59	ARG
1	B8	16	VAL
2	CA	59	ARG
2	CD	59	ARG
2	CG	59	ARG
2	CJ	59	ARG
2	CM	59	ARG
2	CP	59	ARG
2	CS	59	ARG
2	CV	59	ARG
2	CY	59	ARG
2	C1	59	ARG
2	C4	47	VAL
2	C4	59	ARG
2	C7	59	ARG
2	DA	59	ARG
1	DC	30	THR
2	DD	59	ARG
2	DG	59	ARG
2	DJ	59	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (71)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	D	54	GLN
1	G	54	GLN
1	J	54	GLN
1	M	54	GLN
1	P	54	GLN
1	S	54	GLN
1	V	54	GLN
1	V	84	ASN
1	Y	54	GLN
1	Y	84	ASN
1	1	54	GLN
1	4	54	GLN
1	7	54	GLN
1	a	54	GLN
1	d	54	GLN
1	g	54	GLN
1	h	84	ASN
1	j	54	GLN
1	k	84	ASN
1	m	54	GLN
2	o	2	GLN
1	p	54	GLN
1	s	54	GLN
1	v	54	GLN
1	y	54	GLN
1	AE	54	GLN
1	AH	54	GLN
1	AH	84	ASN
1	AK	54	GLN
1	AK	84	ASN
1	AN	54	GLN
1	AQ	54	GLN
1	AT	54	GLN
1	AW	54	GLN
1	A2	54	GLN
1	A5	54	GLN
1	A8	54	GLN
1	BB	54	GLN
1	BE	54	GLN
1	BH	54	GLN
1	BI	84	ASN

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Mol	Chain	Res	Type
1	BK	54	GLN
1	BL	84	ASN
1	BN	54	GLN
1	BQ	54	GLN
1	BQ	84	ASN
1	BT	54	GLN
1	BT	84	ASN
1	BW	54	GLN
1	BZ	54	GLN
1	B5	54	GLN
1	B6	84	ASN
1	CB	54	GLN
1	CC	84	ASN
1	CE	54	GLN
1	CH	54	GLN
1	CK	54	GLN
1	CN	54	GLN
1	CQ	54	GLN
1	CT	54	GLN
1	CW	54	GLN
1	CW	84	ASN
1	CZ	54	GLN
1	CZ	84	ASN
1	C2	54	GLN
1	C2	84	ASN
1	C5	54	GLN
1	DB	54	GLN
1	DE	54	GLN
1	DH	54	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

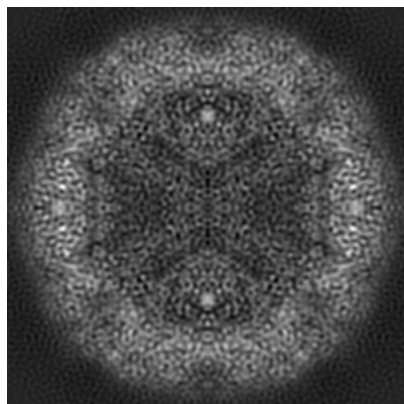
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20208. These allow visual inspection of the internal detail of the map and identification of artifacts.

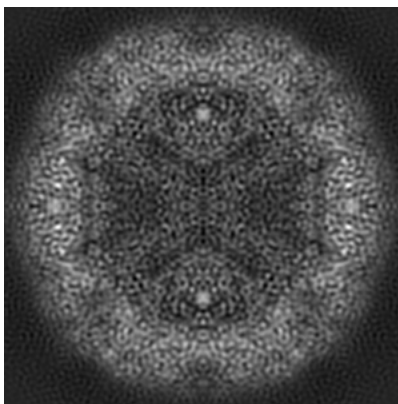
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

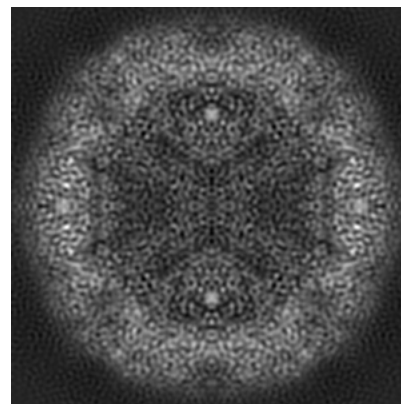
6.1.1 Primary map



X

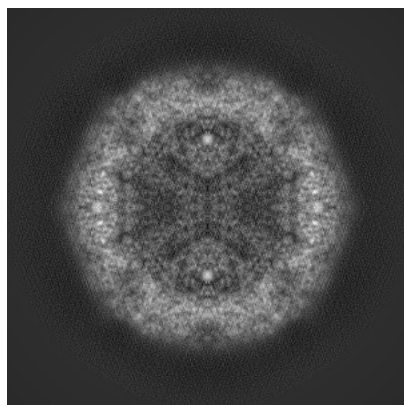


Y

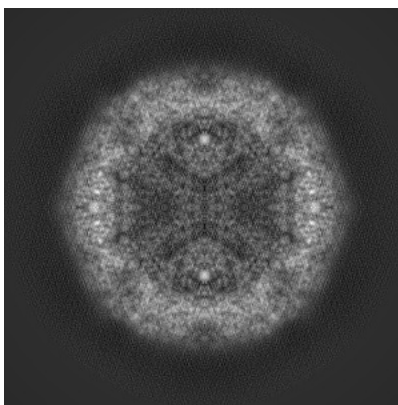


Z

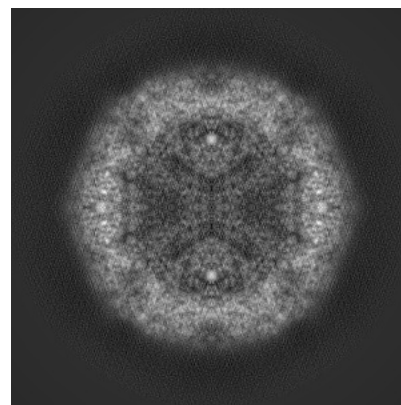
6.1.2 Raw map



X



Y

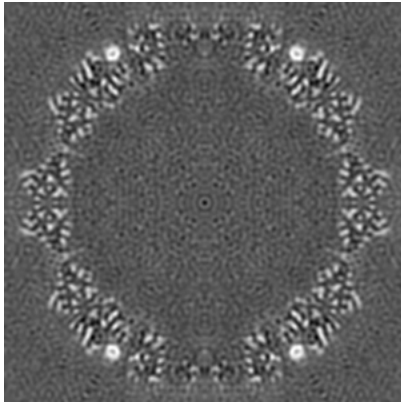


Z

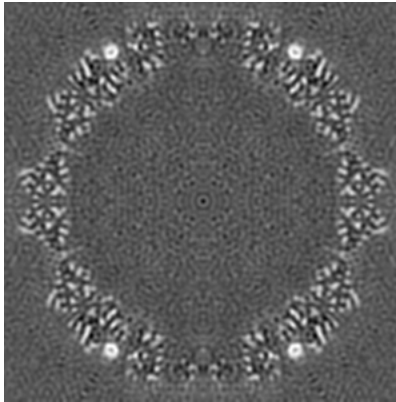
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

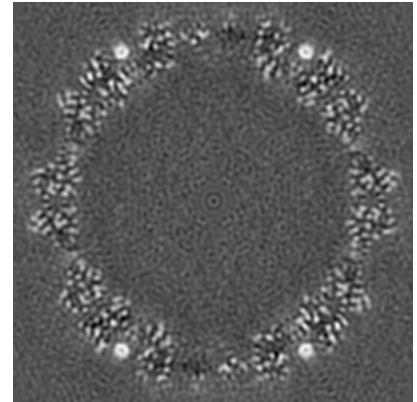
6.2.1 Primary map



X Index: 125

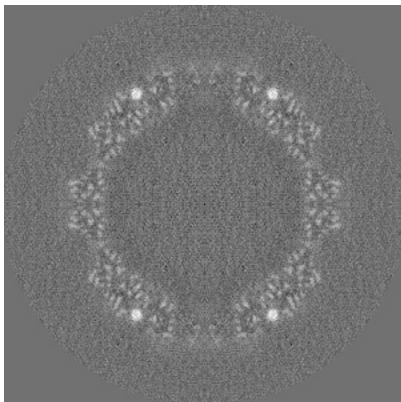


Y Index: 125

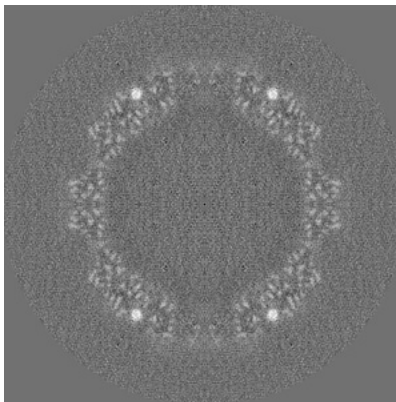


Z Index: 125

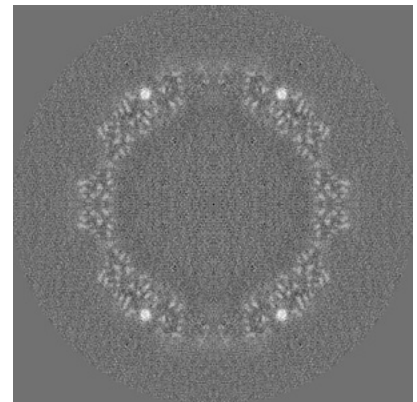
6.2.2 Raw map



X Index: 169



Y Index: 169

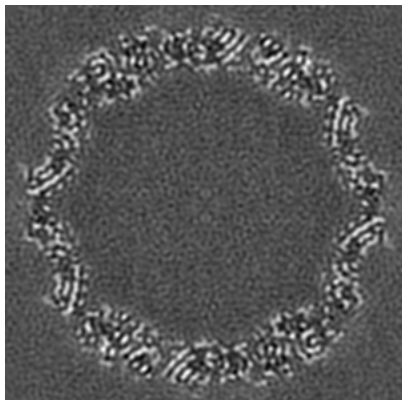


Z Index: 169

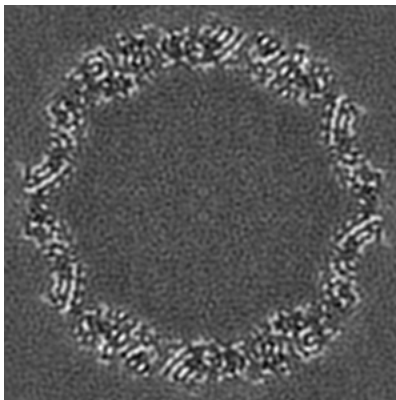
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

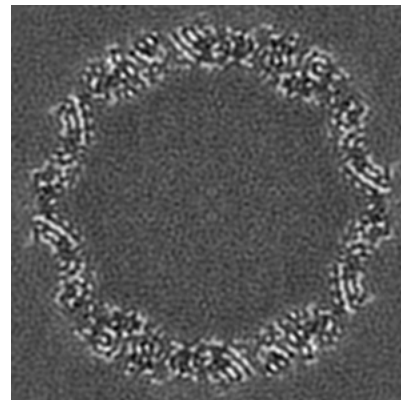
6.3.1 Primary map



X Index: 112

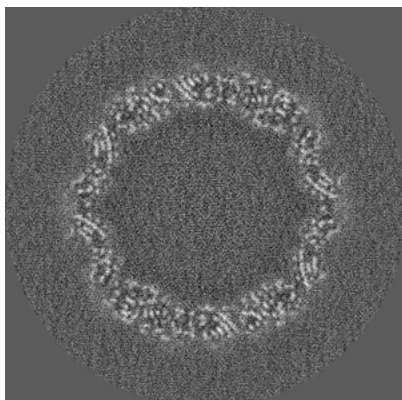


Y Index: 112

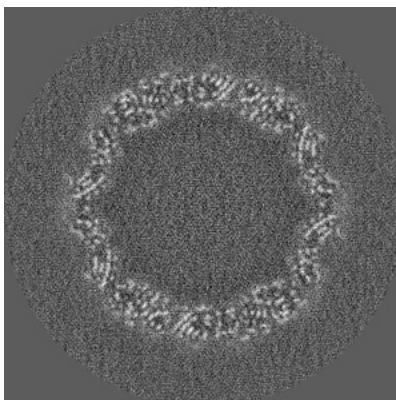


Z Index: 137

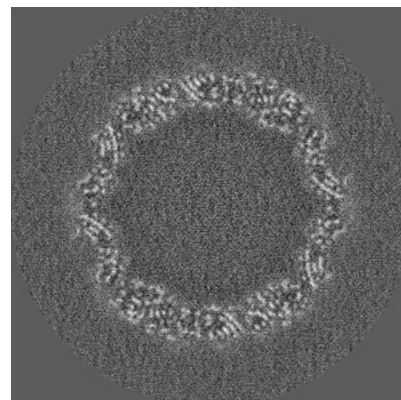
6.3.2 Raw map



X Index: 156



Y Index: 182

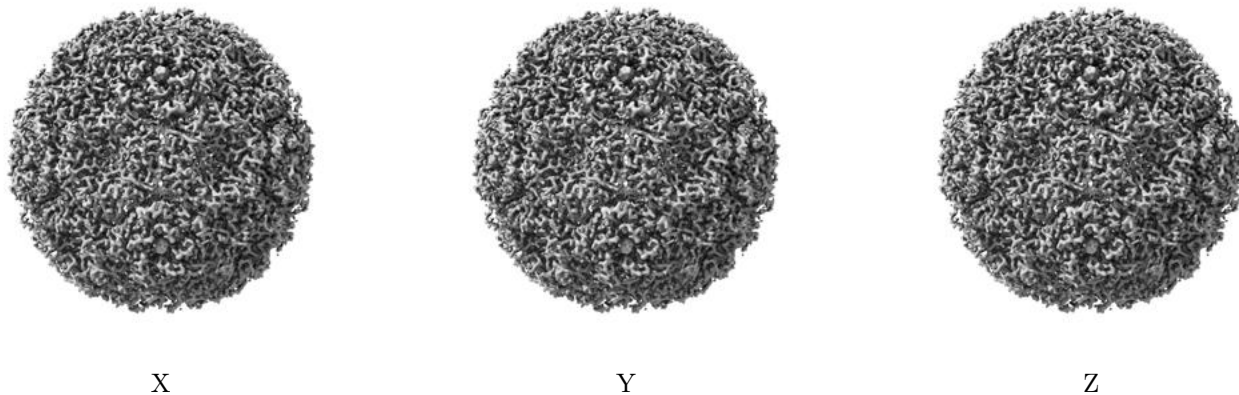


Z Index: 156

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

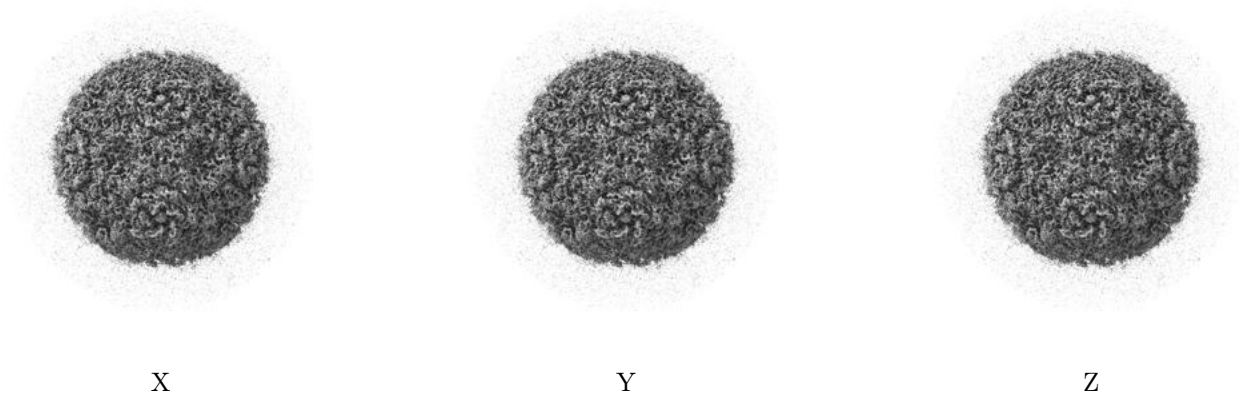
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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

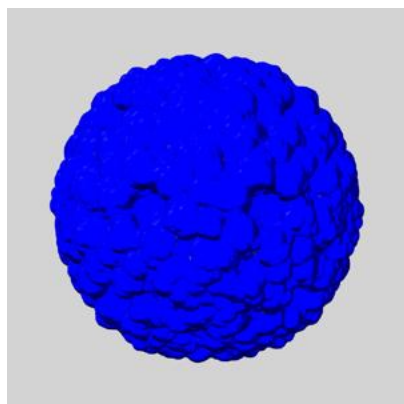
6.5 Mask visualisation [i](#)

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

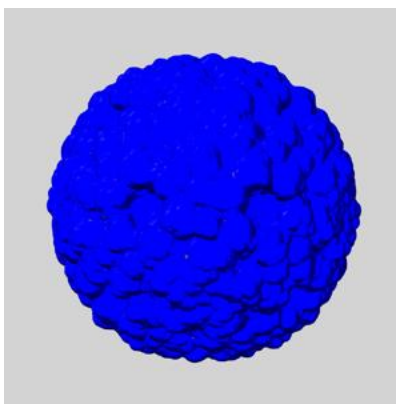
A mask typically either:

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

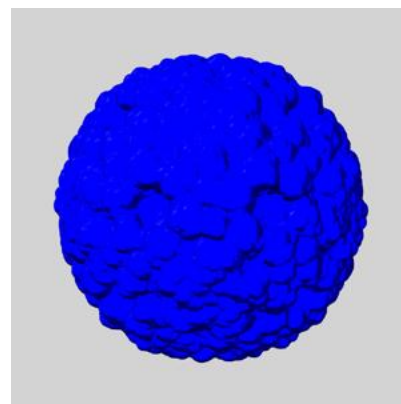
6.5.1 emd_20208_msk_1.map [i](#)



X



Y

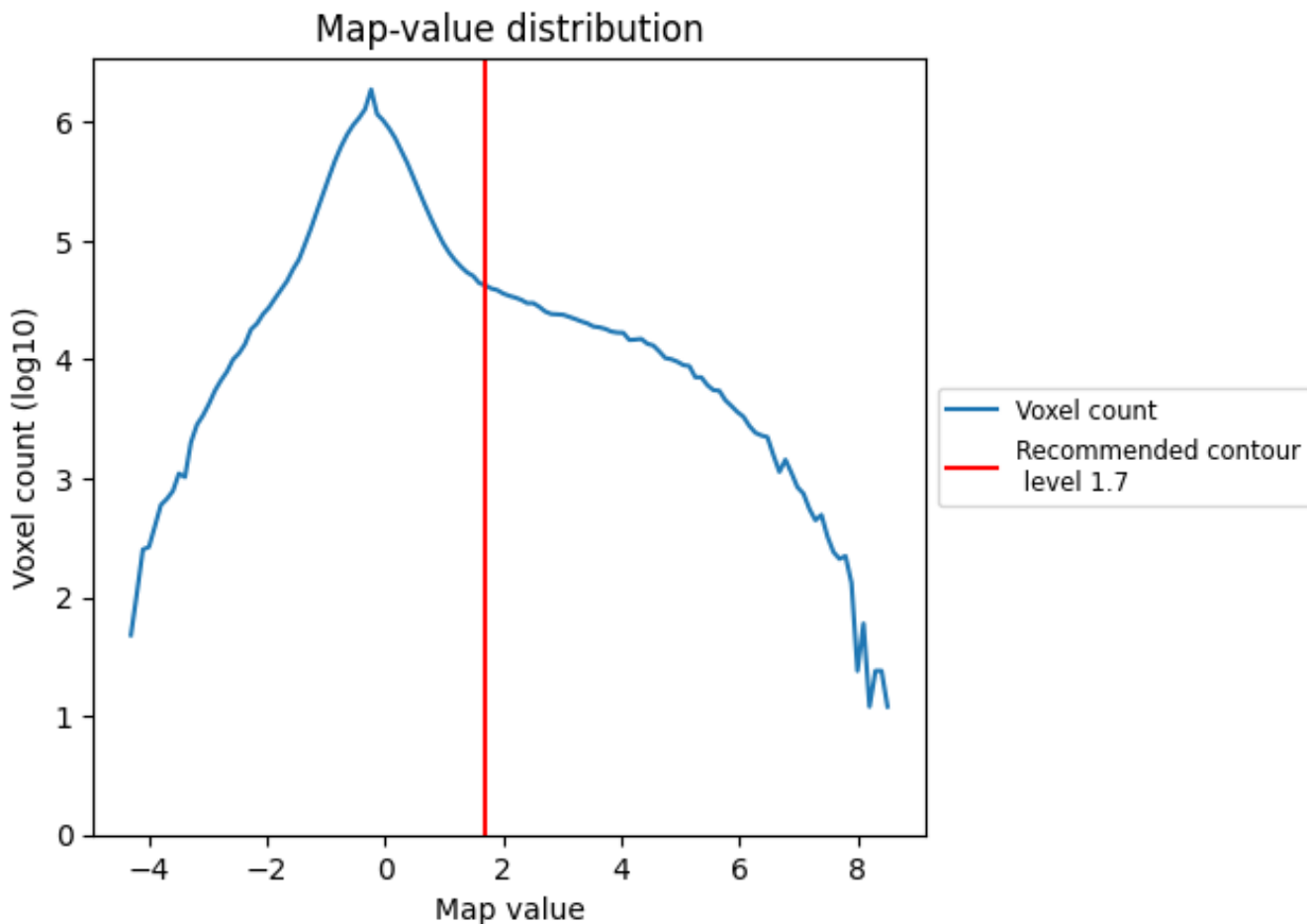


Z

7 Map analysis [i](#)

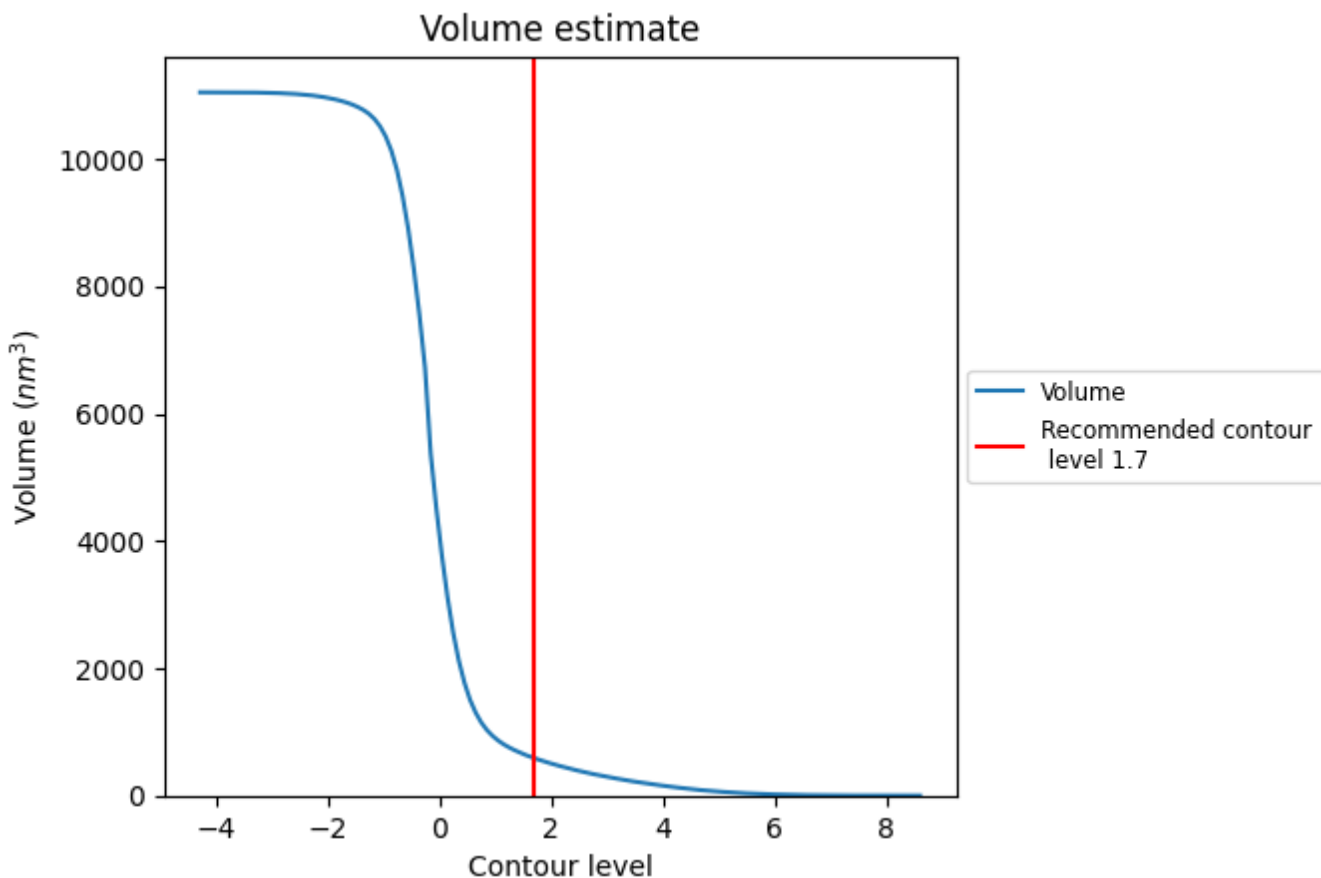
This section contains the results of statistical analysis of the map.

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.

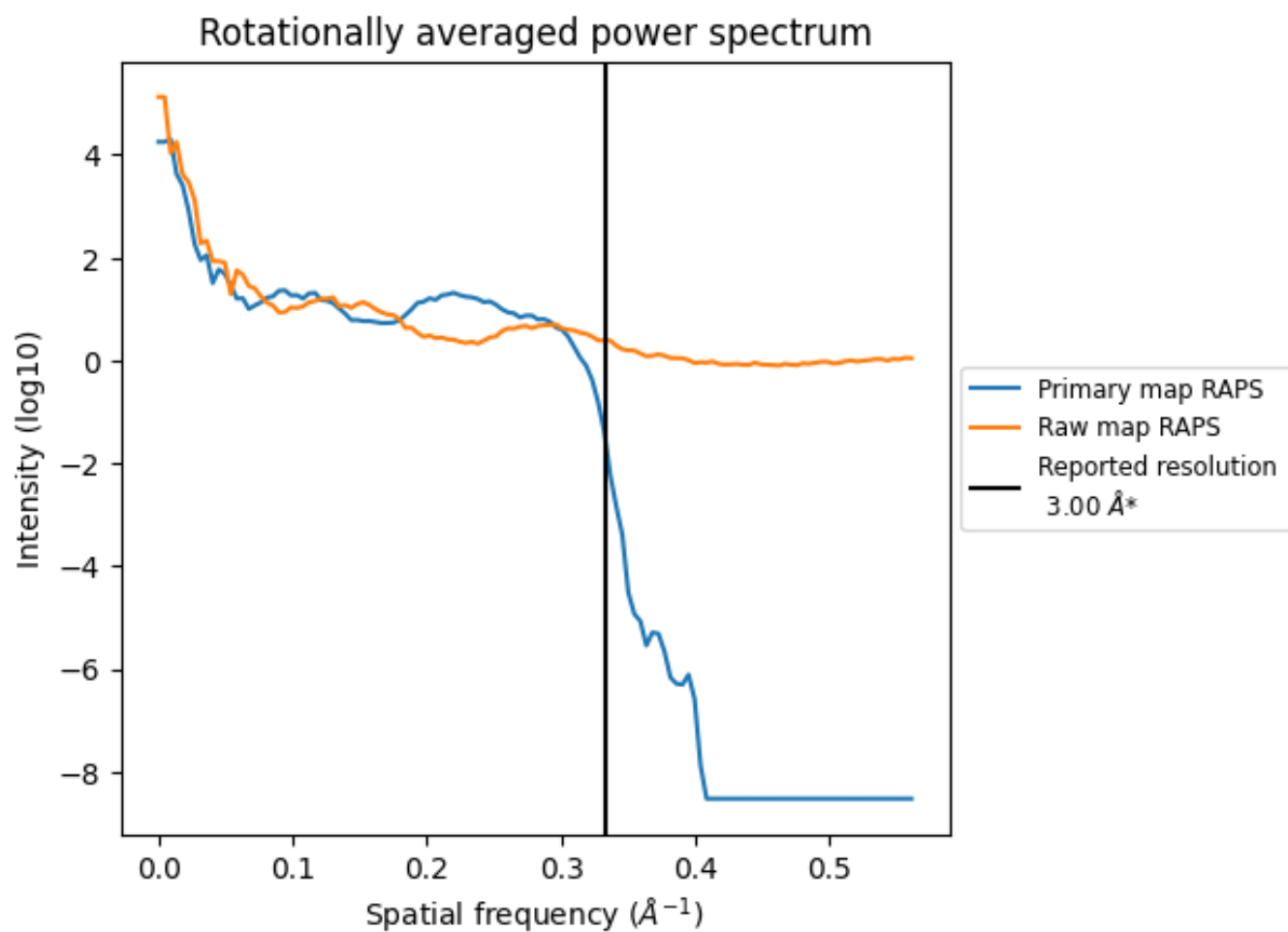
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 586 nm³; this corresponds to an approximate mass of 529 kDa.

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

7.3 Rotationally averaged power spectrum i

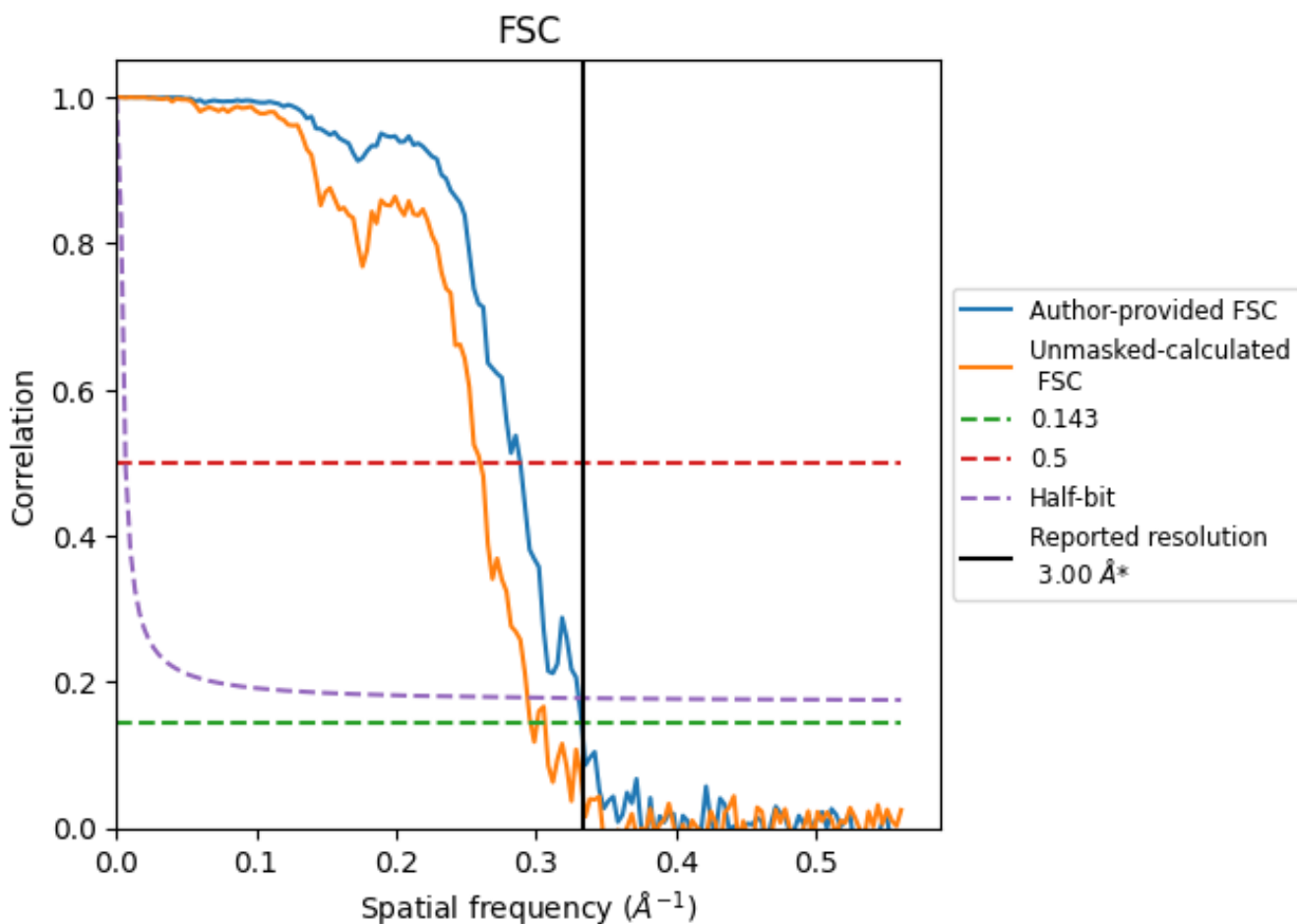


*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

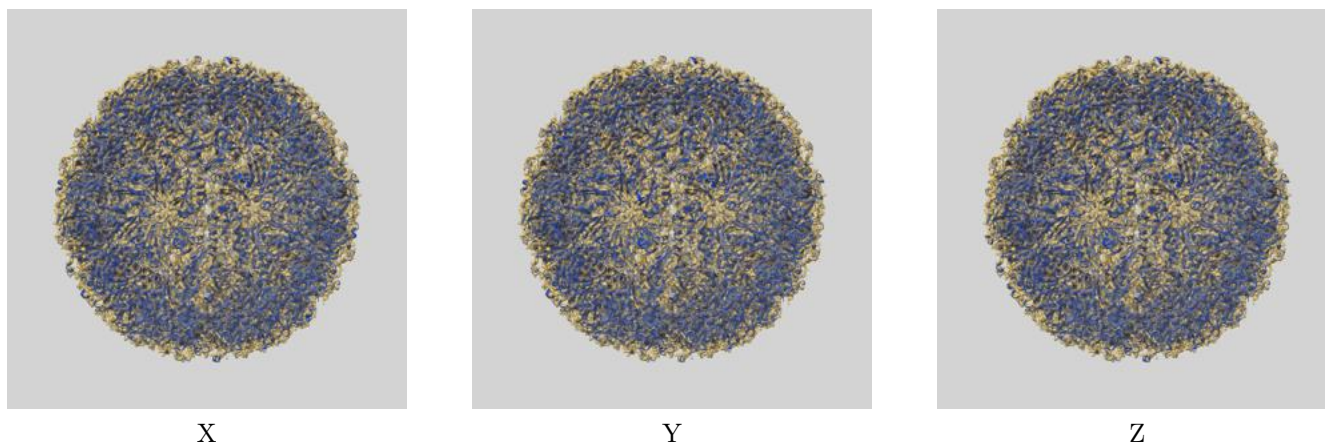
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.01	3.46	3.02
Unmasked-calculated*	3.37	3.84	3.40

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.37 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20208 and PDB model 6OWF. Per-residue inclusion information can be found in section [3](#) on page [34](#).

9.1 Map-model overlay [i](#)

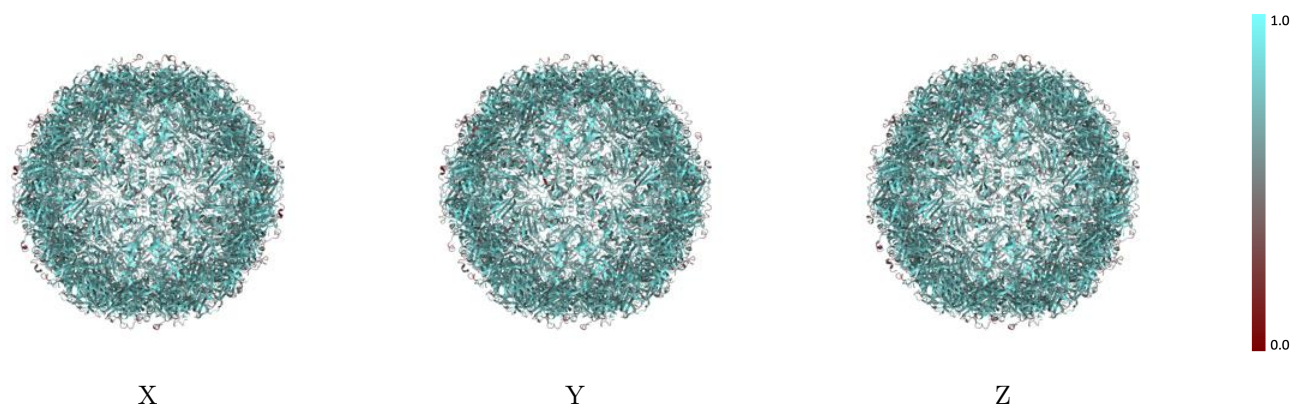


The images above show the 3D surface view of the map at the recommended contour level 1.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

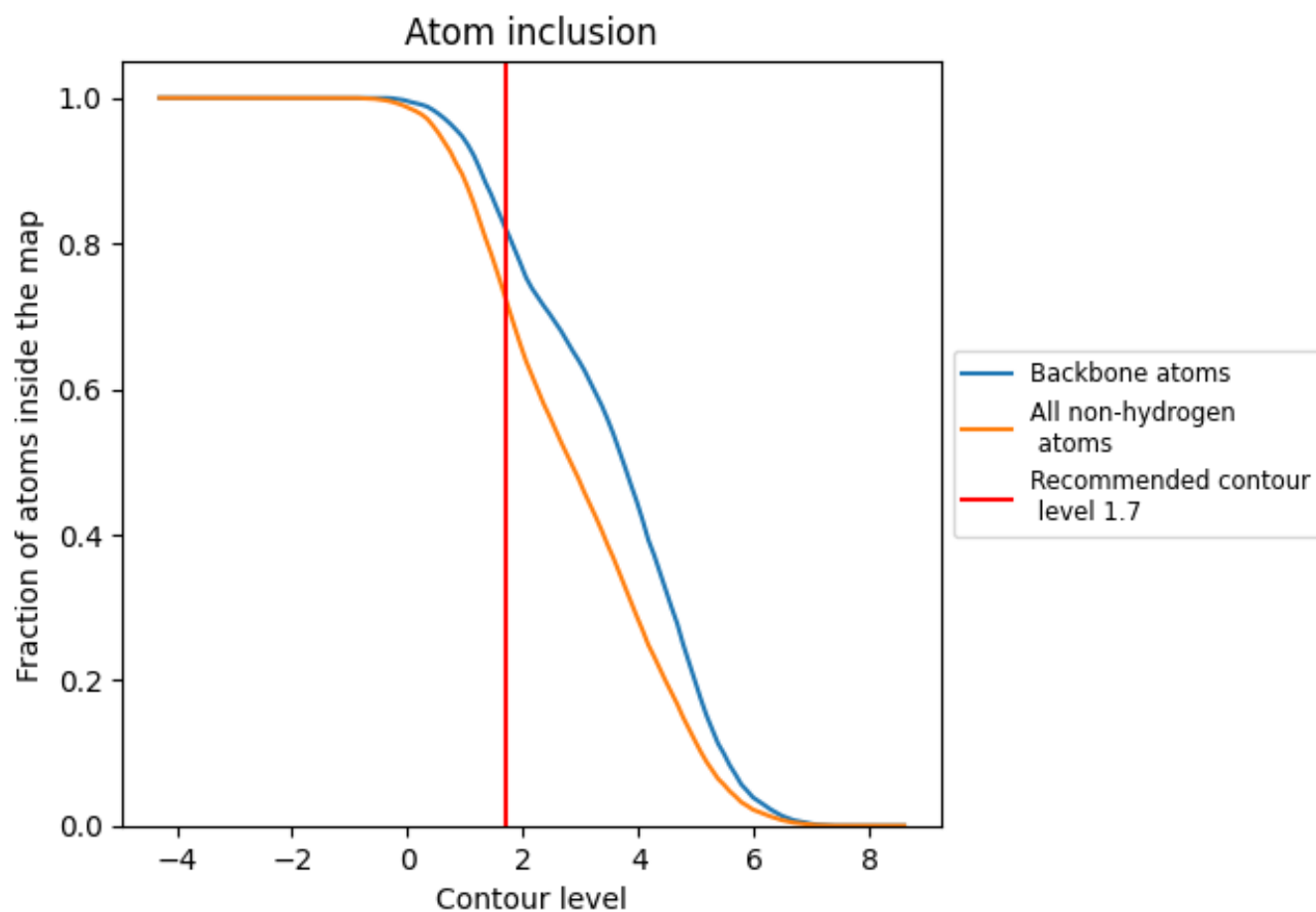
This section was not generated.

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 (1.7).




































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (1.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	 0.7239
0	 0.7482
1	 0.7361
2	 0.6952
3	 0.7511
4	 0.7279
5	 0.6925
6	 0.7610
7	 0.7279
8	 0.7048
9	 0.7426
A	 0.7333
A0	 0.6939
A1	 0.7341
A2	 0.7293
A3	 0.6912
A4	 0.7539
A5	 0.7306
A6	 0.7020
A7	 0.7355
A8	 0.7293
A9	 0.6925
AA	 0.7468
AB	 0.7293
AC	 0.6925
AD	 0.7327
AE	 0.7306
AF	 0.6925
AG	 0.7496
AH	 0.7374
AI	 0.6952
AJ	 0.7511
AK	 0.7361
AL	 0.6966
AM	 0.7468













































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Chain	Atom inclusion
AN	0.7252
AO	0.7075
AP	0.7397
AQ	0.7279
AR	0.7007
AS	0.7369
AT	0.7279
AU	0.6925
AV	0.7511
AW	0.7293
AX	0.7075
AY	0.7426
AZ	0.7252
B	0.6925
B0	0.7075
B1	0.7454
B2	0.7320
B3	0.6952
B4	0.7355
B5	0.7224
B6	0.6966
B7	0.7454
B8	0.7279
B9	0.6993
BA	0.7525
BB	0.7252
BC	0.7075
BD	0.7397
BE	0.7197
BF	0.6966
BG	0.7454
BH	0.7211
BI	0.6952
BJ	0.7468
BK	0.7238
BL	0.6952
BM	0.7468
BN	0.7374
BO	0.6925
BP	0.7482
BQ	0.7347
BR	0.6966

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Chain	Atom inclusion
BS	 0.7496
BT	 0.7388
BU	 0.6980
BV	 0.7468
BW	 0.7320
BX	 0.6966
BY	 0.7511
BZ	 0.7293
C	 0.7553
C0	 0.6993
C1	 0.7496
C2	 0.7374
C3	 0.7020
C4	 0.7468
C5	 0.7265
C6	 0.7088
C7	 0.7426
C8	 0.7279
C9	 0.6939
CA	 0.7412
CB	 0.7224
CC	 0.6952
CD	 0.7440
CE	 0.7320
CF	 0.7034
CG	 0.7369
CH	 0.7333
CI	 0.6952
CJ	 0.7539
CK	 0.7252
CL	 0.7075
CM	 0.7440
CN	 0.7333
CO	 0.6939
CP	 0.7539
CQ	 0.7293
CR	 0.7075
CS	 0.7397
CT	 0.7279
CU	 0.6993
CV	 0.7454
CW	 0.7401





















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Chain	Atom inclusion
CX	0.6993
CY	0.7496
CZ	0.7388
D	0.7279
DA	0.7355
DB	0.7197
DC	0.6871
DD	0.7511
DE	0.7265
DF	0.7075
DG	0.7426
DH	0.7265
DI	0.6980
DJ	0.7355
E	0.6925
F	0.7341
G	0.7320
H	0.6952
I	0.7553
J	0.7238
K	0.7061
L	0.7397
M	0.7252
N	0.6939
O	0.7454
P	0.7279
Q	0.6939
R	0.7440
S	0.7306
T	0.6952
U	0.7440
V	0.7361
W	0.6993
X	0.7482
Y	0.7374
Z	0.6952
a	0.7333
b	0.6912
c	0.7355
d	0.7252
e	0.6993
f	0.7468

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Chain	Atom inclusion
g	 0.7238
h	 0.6952
i	 0.7440
j	 0.7320
k	 0.6966
l	 0.7482
m	 0.7293
n	 0.6966
o	 0.7397
p	 0.7293
q	 0.6898
r	 0.7511
s	 0.7224
t	 0.7088
u	 0.7412
v	 0.7265
w	 0.6898
x	 0.7511
y	 0.7265
z	 0.7075