



wwPDB EM Validation Summary Report ⓘ

Apr 20, 2026 – 04:17 PM EDT

PDB ID : 9ZZY / pdb_00009zzy
EMDB ID : EMD-75020
Title : ssRNA phage PRR1 virion with 3' gRNA
Authors : Lill, Z.R.; Zhang, J.
Deposited on : 2026-01-08
Resolution : 3.45 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

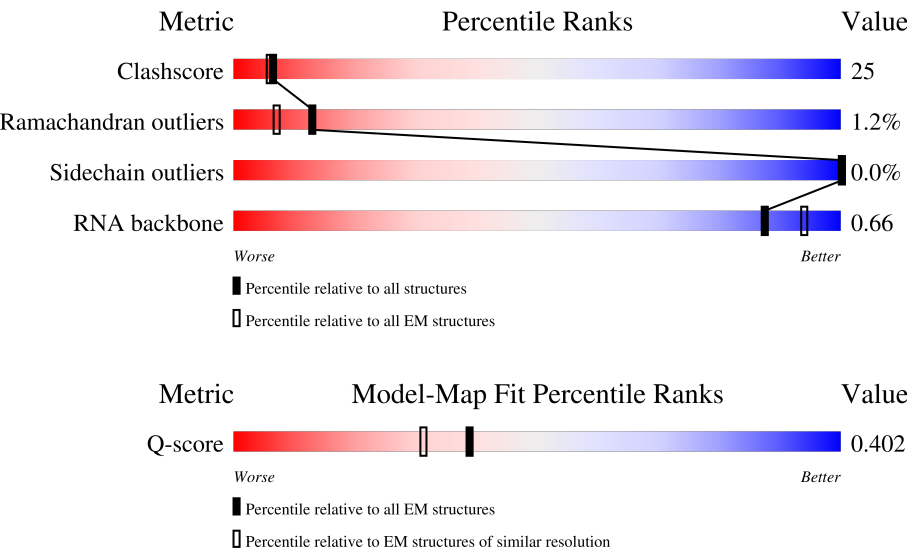
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.45 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13836 (2.95 - 3.95)

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

Mol	Chain	Length	Quality of chain
1	F	406	 97% 98% •
2	AE	132	 84% 83% 15% •
3	0	131	 12% 46% 54%

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Mol	Chain	Length	Quality of chain
3	1	131	
3	2	131	
3	3	131	
3	4	131	
3	5	131	
3	6	131	
3	7	131	
3	8	131	
3	9	131	
3	A	131	
3	A0	131	
3	A1	131	
3	A2	131	
3	A3	131	
3	A4	131	
3	A5	131	
3	A6	131	
3	A7	131	
3	A8	131	
3	A9	131	
3	AA	131	
3	AB	131	
3	AC	131	
3	AD	131	
3	AO	131	

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Mol	Chain	Length	Quality of chain
3	AP	131	
3	AQ	131	
3	AR	131	
3	AS	131	
3	AT	131	
3	AU	131	
3	AV	131	
3	AW	131	
3	AX	131	
3	AY	131	
3	AZ	131	
3	Aa	131	
3	Ab	131	
3	Ac	131	
3	Ad	131	
3	Ae	131	
3	Af	131	
3	Ag	131	
3	Ah	131	
3	Ai	131	
3	Aj	131	
3	Ak	131	
3	Al	131	
3	Am	131	
3	An	131	

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Mol	Chain	Length	Quality of chain
3	Ao	131	
3	Ap	131	
3	Aq	131	
3	Ar	131	
3	As	131	
3	At	131	
3	Au	131	
3	Av	131	
3	Aw	131	
3	Ax	131	
3	Ay	131	
3	Az	131	
3	B	131	
3	B0	131	
3	B1	131	
3	B2	131	
3	B3	131	
3	B4	131	
3	B5	131	
3	B6	131	
3	B7	131	
3	B8	131	
3	B9	131	
3	BA	131	
3	BB	131	

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Mol	Chain	Length	Quality of chain
3	BC	131	
3	BD	131	
3	BE	131	
3	BF	131	
3	BG	131	
3	BH	131	
3	BI	131	
3	BJ	131	
3	BK	131	
3	BL	131	
3	BM	131	
3	BN	131	
3	BO	131	
3	BP	131	
3	BQ	131	
3	BR	131	
3	BS	131	
3	BV	131	
3	BY	131	
3	BZ	131	
3	Bb	131	
3	Bc	131	
3	Bd	131	
3	Bg	131	
3	Bh	131	

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Mol	Chain	Length	Quality of chain
3	Bi	131	
3	Bj	131	
3	Bk	131	
3	Bl	131	
3	Bm	131	
3	Bn	131	
3	Bu	131	
3	Bv	131	
3	Bw	131	
3	Bx	131	
3	By	131	
3	Bz	131	
3	C	131	
3	CA	131	
3	CB	131	
3	CC	131	
3	CD	131	
3	CH	131	
3	CI	131	
3	CK	131	
3	CL	131	
3	CM	131	
3	CN	131	
3	CO	131	
3	CP	131	

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Mol	Chain	Length	Quality of chain
3	CQ	131	
3	CR	131	
3	CS	131	
3	CT	131	
3	D	131	
3	E	131	
3	G	131	
3	H	131	
3	I	131	
3	J	131	
3	K	131	
3	L	131	
3	M	131	
3	N	131	
3	O	131	
3	P	131	
3	Q	131	
3	R	131	
3	S	131	
3	T	131	
3	U	131	
3	V	131	
3	W	131	
3	X	131	
3	Y	131	

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Mol	Chain	Length	Quality of chain
3	Z	131	<div> <div>5%</div> <div>56%</div> <div>44%</div> </div>
3	a	131	<div> <div>8%</div> <div>59%</div> <div>41%</div> </div>
3	b	131	<div> <div>11%</div> <div>43%</div> <div>56%</div> </div>
3	c	131	<div> <div>6%</div> <div>60%</div> <div>40%</div> </div>
3	d	131	<div> <div>9%</div> <div>65%</div> <div>35%</div> </div>
3	e	131	<div> <div>6%</div> <div>56%</div> <div>44%</div> </div>
3	f	131	<div> <div>9%</div> <div>47%</div> <div>53%</div> </div>
3	g	131	<div> <div>8%</div> <div>55%</div> <div>45%</div> </div>
3	h	131	<div> <div>6%</div> <div>51%</div> <div>49%</div> </div>
3	i	131	<div> <div>8%</div> <div>44%</div> <div>54%</div> </div>
3	j	131	<div> <div>8%</div> <div>44%</div> <div>55%</div> </div>
3	k	131	<div> <div>8%</div> <div>60%</div> <div>40%</div> </div>
3	l	131	<div> <div>9%</div> <div>53%</div> <div>47%</div> </div>
3	m	131	<div> <div>5%</div> <div>49%</div> <div>50%</div> </div>
3	n	131	<div> <div>11%</div> <div>49%</div> <div>51%</div> </div>
3	o	131	<div> <div>6%</div> <div>56%</div> <div>44%</div> </div>
3	p	131	<div> <div>10%</div> <div>52%</div> <div>48%</div> </div>
3	q	131	<div> <div>11%</div> <div>51%</div> <div>48%</div> </div>
3	r	131	<div> <div>11%</div> <div>44%</div> <div>56%</div> </div>
3	s	131	<div> <div>11%</div> <div>51%</div> <div>49%</div> </div>
3	t	131	<div> <div>10%</div> <div>50%</div> <div>50%</div> </div>
3	u	131	<div> <div>8%</div> <div>51%</div> <div>48%</div> </div>
3	v	131	<div> <div>11%</div> <div>48%</div> <div>52%</div> </div>
3	w	131	<div> <div>11%</div> <div>57%</div> <div>43%</div> </div>
3	x	131	<div> <div>11%</div> <div>58%</div> <div>42%</div> </div>

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Mol	Chain	Length	Quality of chain
3	y	131	<div><div>5%</div><div><div></div><div>50%</div><div>48%</div></div><div></div></div>
3	z	131	<div><div>10%</div><div><div></div><div>50%</div><div>50%</div></div><div></div></div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 192962 atoms, of which 4643 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 Maturation Protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	406	Total	C	H	N	O	S	
			6461	2072	3222	566	590	11	0

- Molecule 2 is a RNA chain called 3' gRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AE	132	Total	C	H	N	O	P	
			4225	1252	1421	493	927	132	0

- Molecule 3 is a protein called Coat Protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	1	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	2	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	3	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	4	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	5	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	6	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	7	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	8	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	9	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0
3	A	131	Total	C	N	O	S		
			1024	640	182	200	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	C	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	D	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	E	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	O	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	P	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Q	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	R	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	S	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	T	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	U	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	V	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	W	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	X	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Y	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Z	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	a	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	b	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	c	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	d	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	e	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	f	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	g	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	h	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	i	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	j	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	k	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	l	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	m	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	n	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	o	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	p	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	q	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	r	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	s	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	t	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	u	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	v	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	w	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	x	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	y	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	z	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	H	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	I	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	J	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	K	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	L	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	M	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	N	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AA	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AB	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AC	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AD	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AO	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AP	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AQ	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AR	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AS	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AT	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AU	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AV	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AW	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	AX	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AY	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	AZ	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Aa	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ab	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ac	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ad	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ae	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Af	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ag	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ah	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ai	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Aj	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ak	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Al	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Am	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	An	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ao	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ap	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Aq	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Ar	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	As	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	At	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	Au	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	Av	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	Aw	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	Ax	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	Ay	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	Az	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A1	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A2	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A3	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A4	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A5	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A6	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A7	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A8	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A9	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	A0	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BA	131	Total 1028	C 642	N 182	O 202	S 2	1	0
3	BB	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BC	131	Total 1024	C 640	N 182	O 200	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	BD	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BE	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BF	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BG	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BH	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BI	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BJ	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BK	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BL	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BM	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BN	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BO	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BP	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BQ	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BR	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BS	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BV	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BY	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	BZ	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	Bb	131	Total 1024	C 640	N 182	O 200	S 2	0	0
3	Bc	131	Total 1024	C 640	N 182	O 200	S 2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Bd	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bg	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bh	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bi	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bj	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bk	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bl	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bm	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bn	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bu	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bv	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bw	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bx	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	By	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	Bz	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	B1	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	B2	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	B3	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	B4	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	B5	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	B6	131	Total	C	N	O	S	0	0
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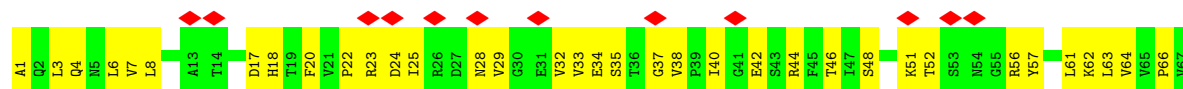
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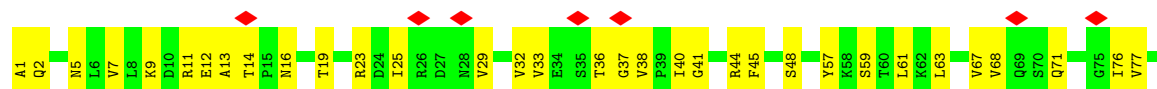
Mol	Chain	Residues	Atoms					AltConf	Trace
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			1024	640	182	200	2		
3	B9	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	B0	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CA	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CB	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CC	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CD	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CH	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CI	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CK	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CL	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CM	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CN	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CO	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CP	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CQ	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CR	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
3	CS	131	Total	C	N	O	S	0	0
			1024	640	182	200	2		
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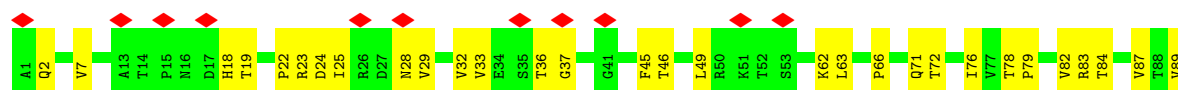
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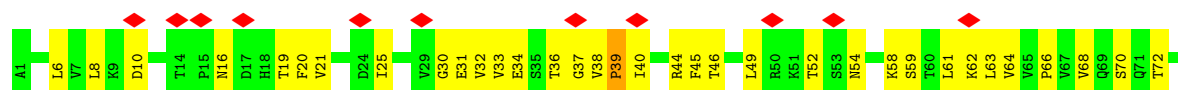
• Molecule 3: Coat Protein



• Molecule 3: Coat Protein

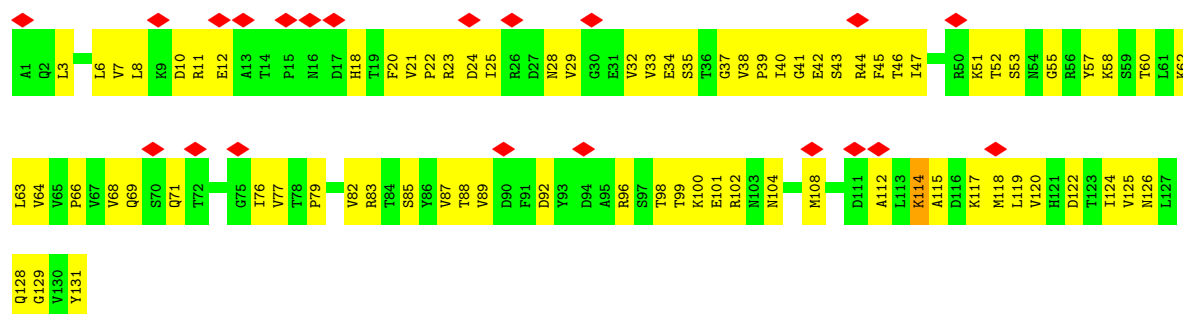
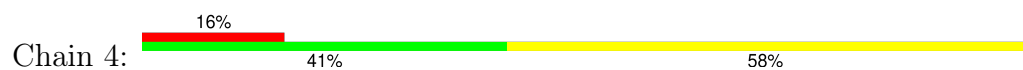


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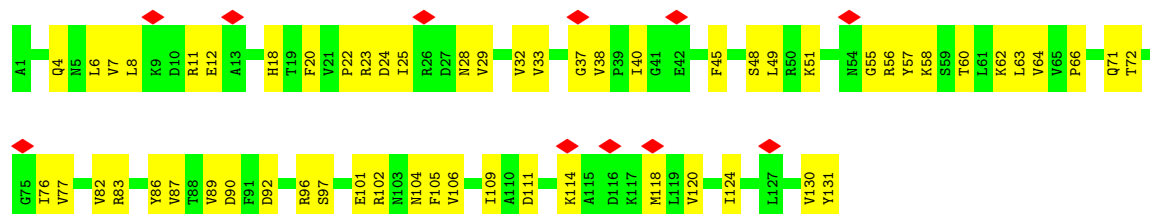




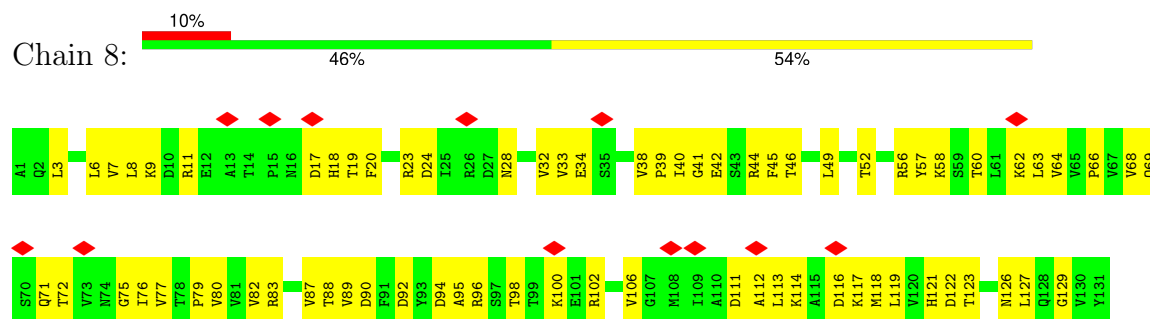
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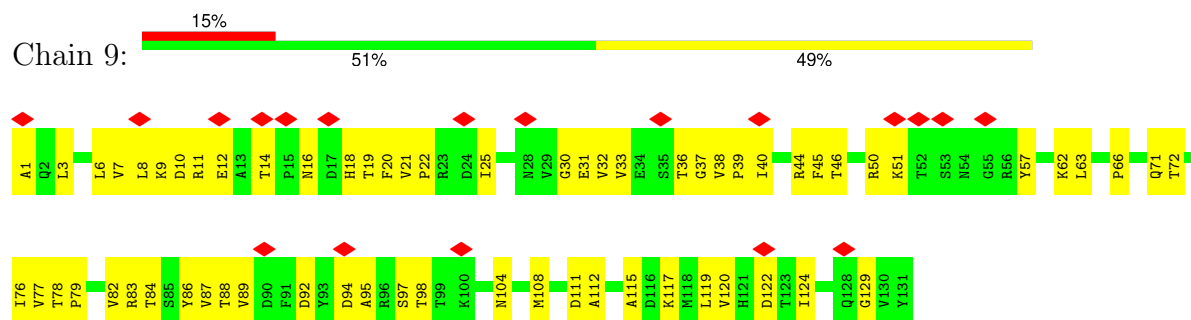
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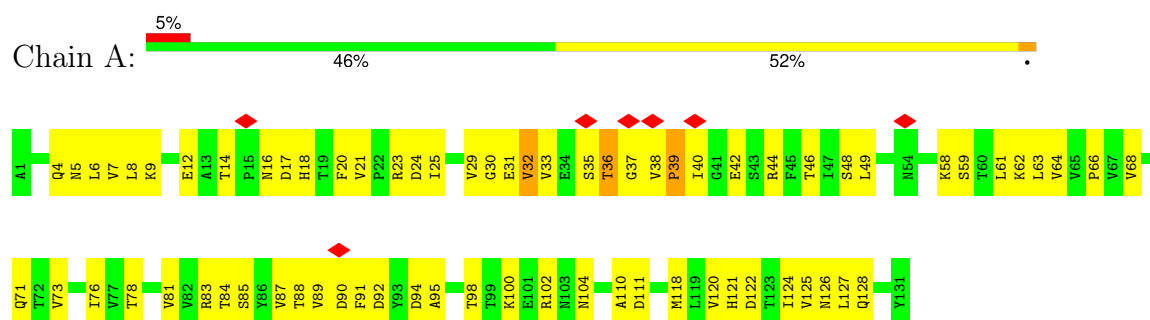
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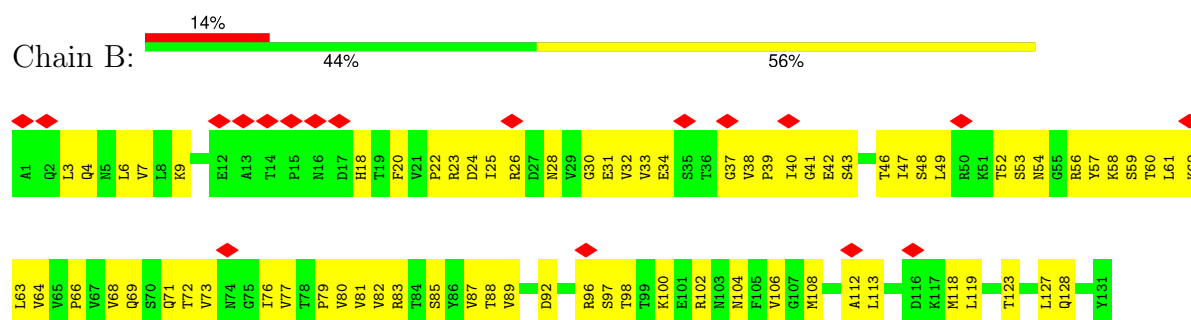
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- Molecule 3: Coat Protein

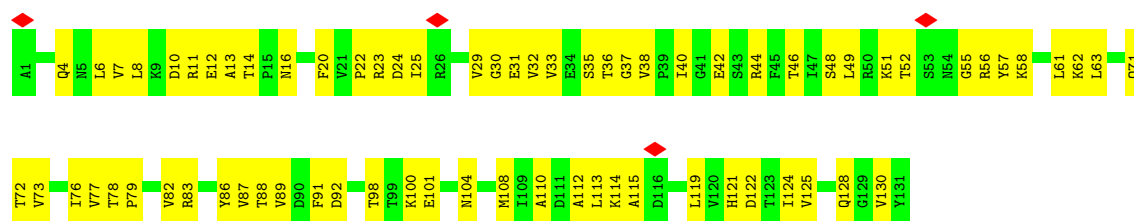


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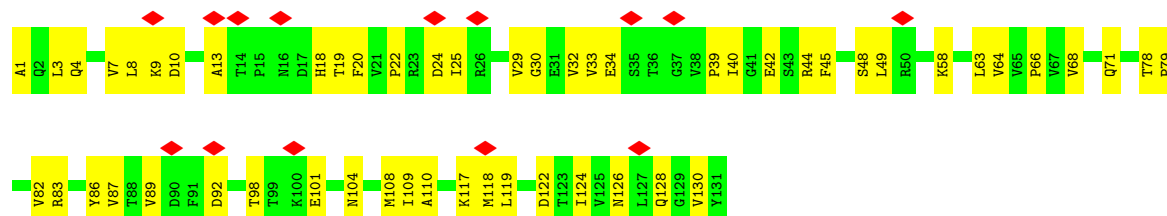


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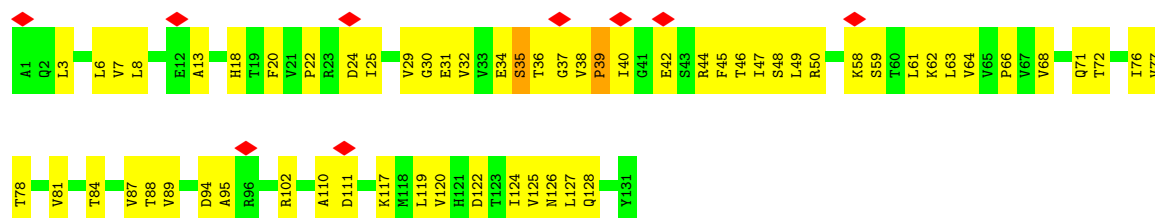




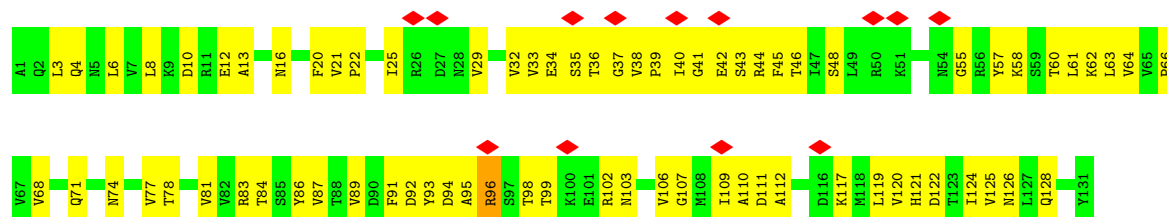
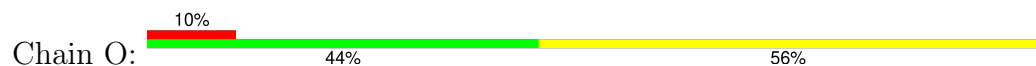
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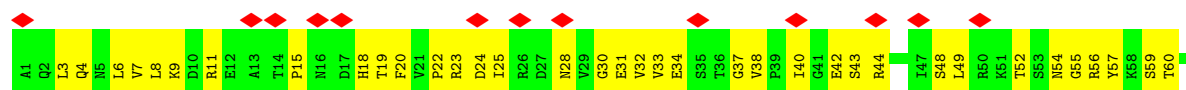
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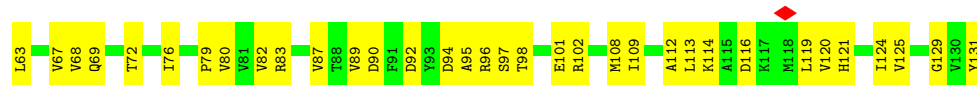


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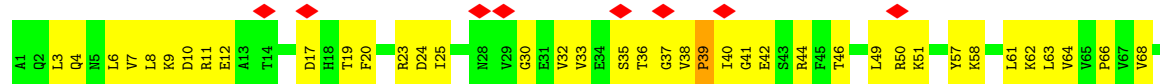


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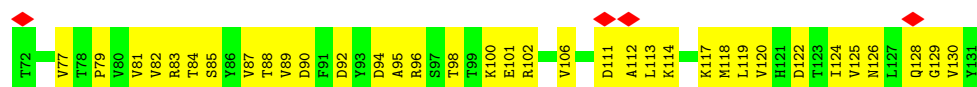
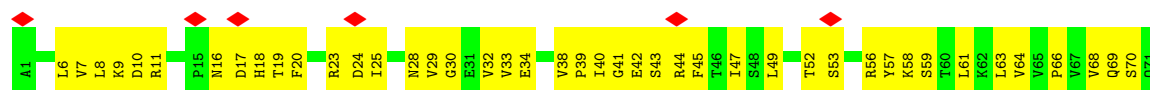




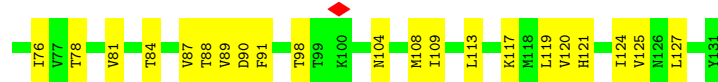
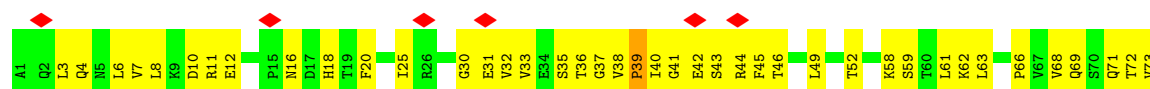
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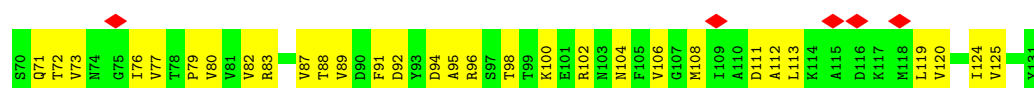
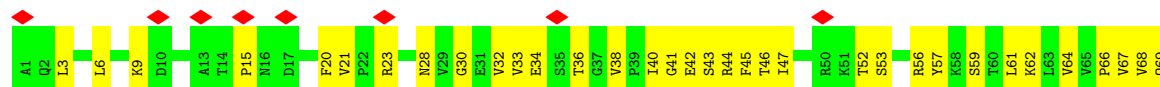
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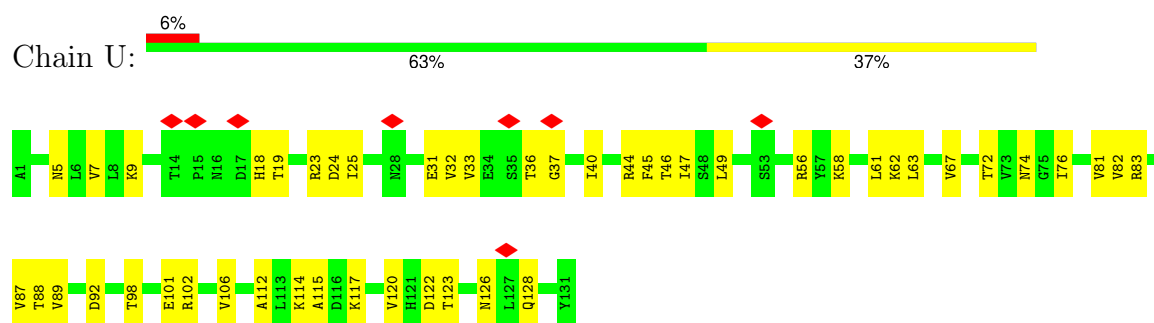
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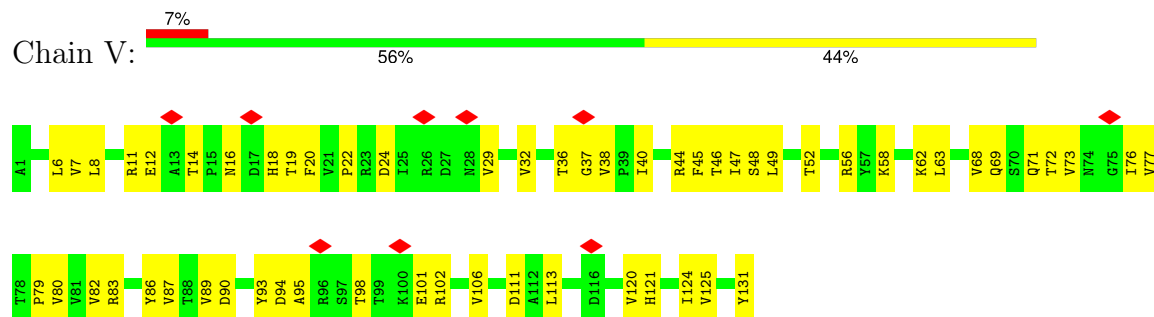
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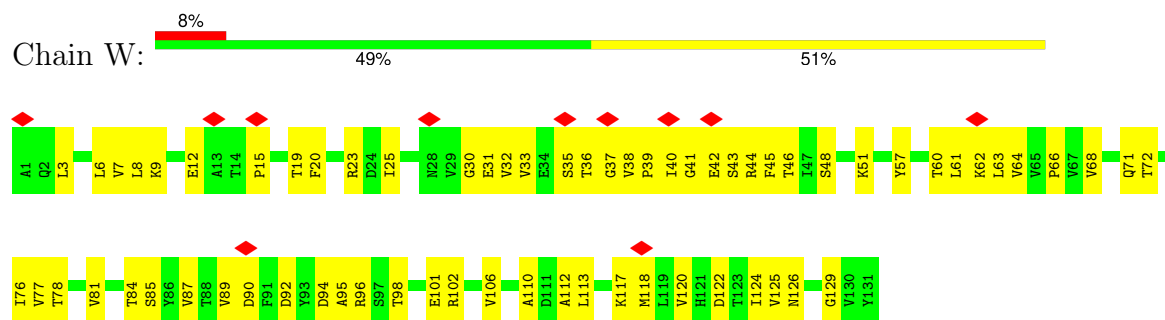
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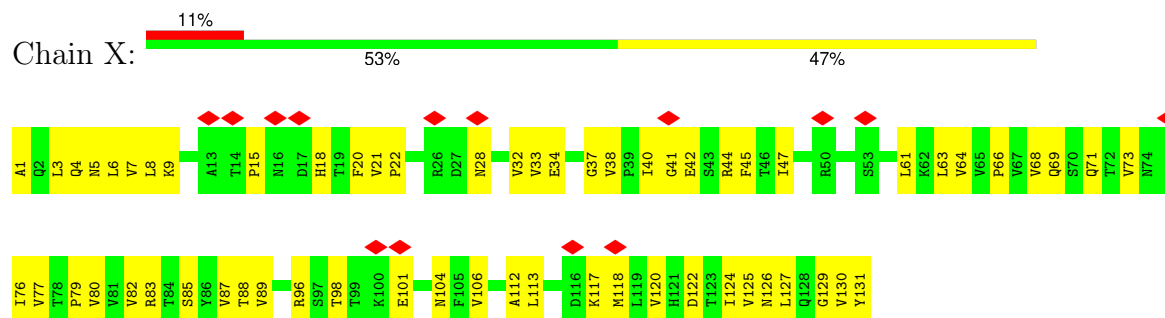
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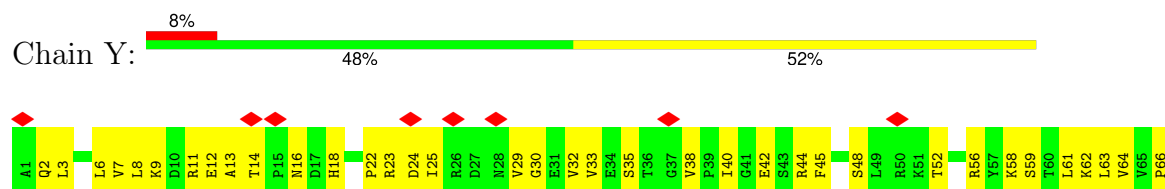
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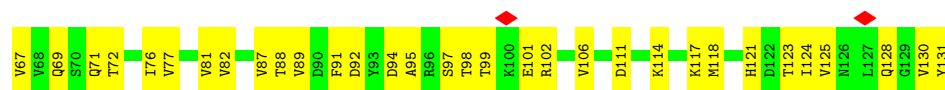


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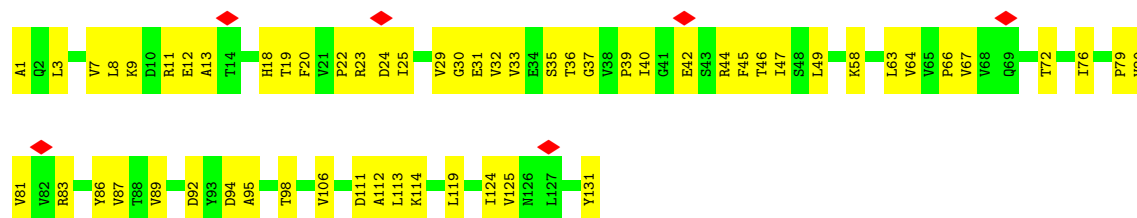


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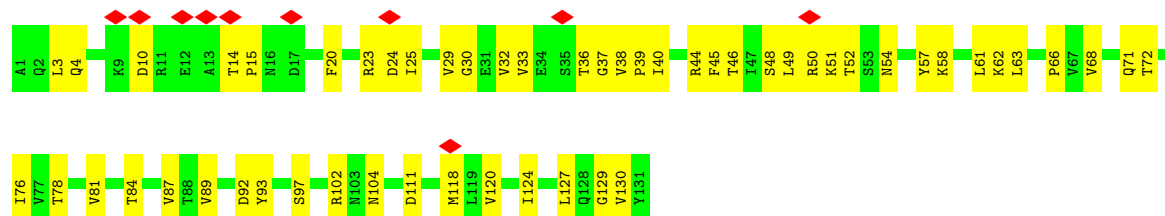




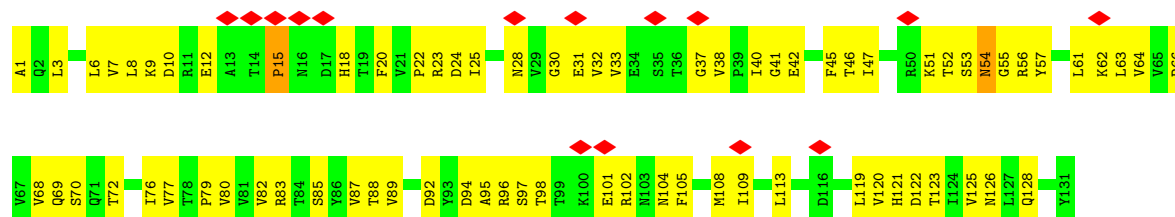
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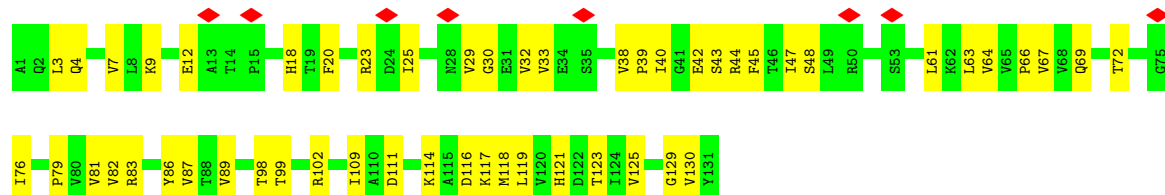
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• Molecule 3: Coat Protein

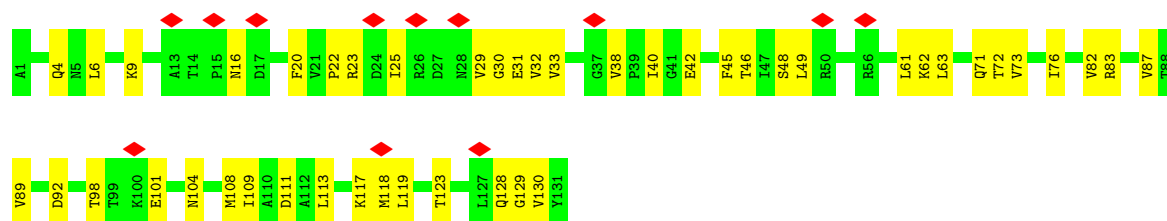


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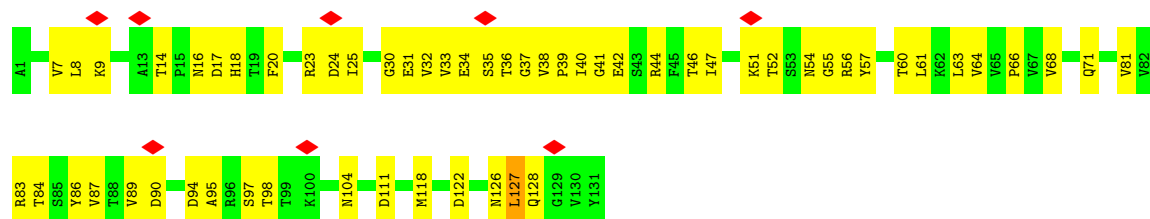


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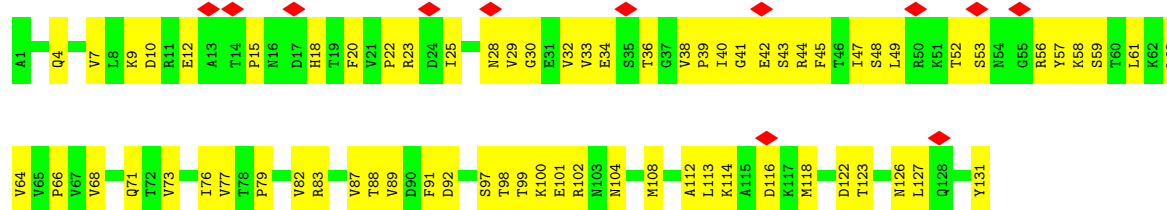




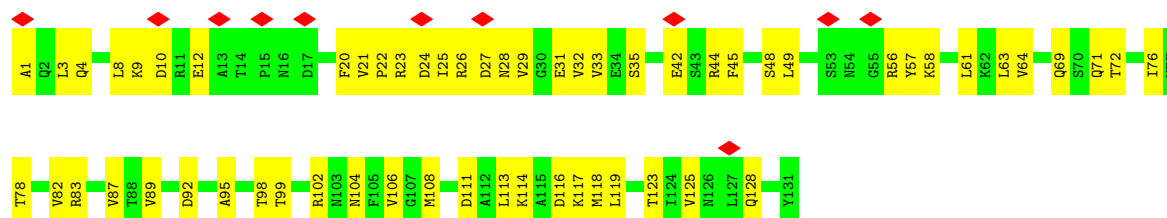
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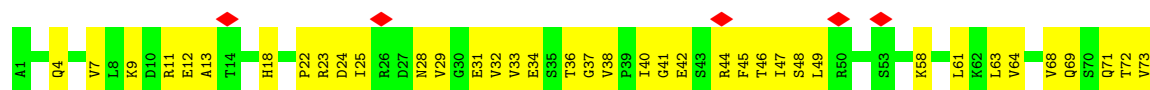
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• Molecule 3: Coat Protein

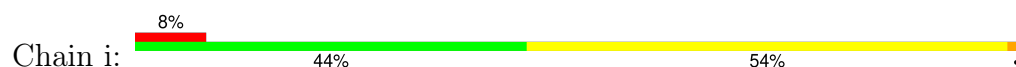


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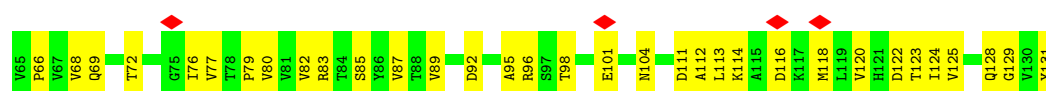
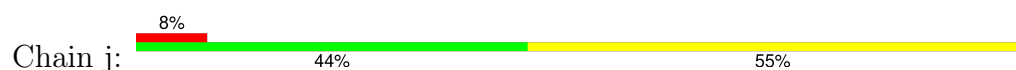




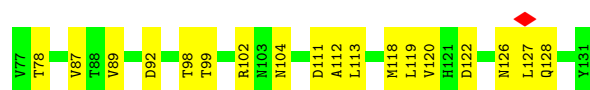
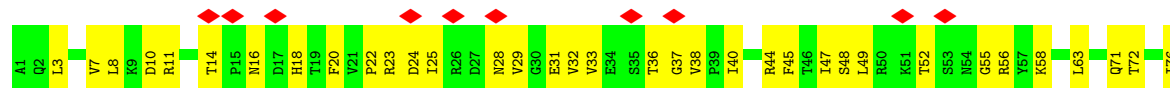
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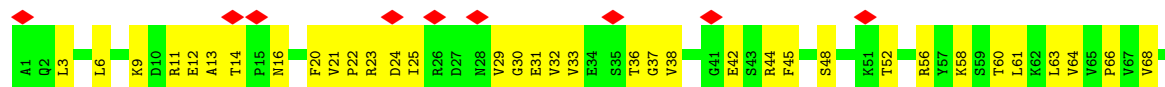
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• Molecule 3: Coat Protein

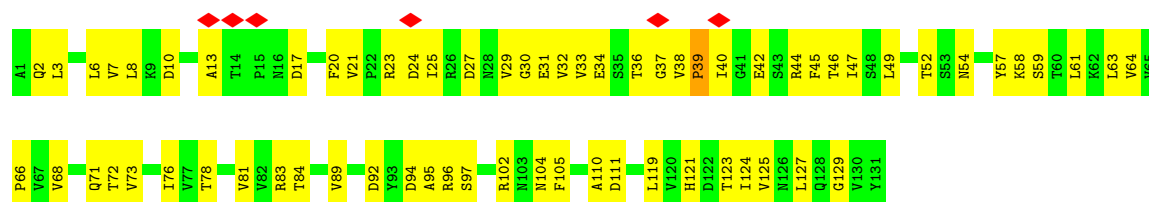


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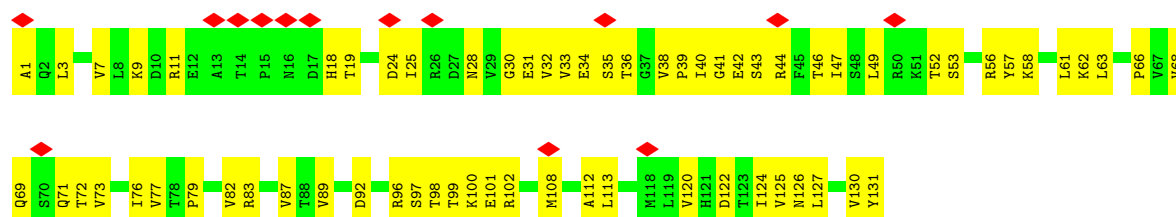


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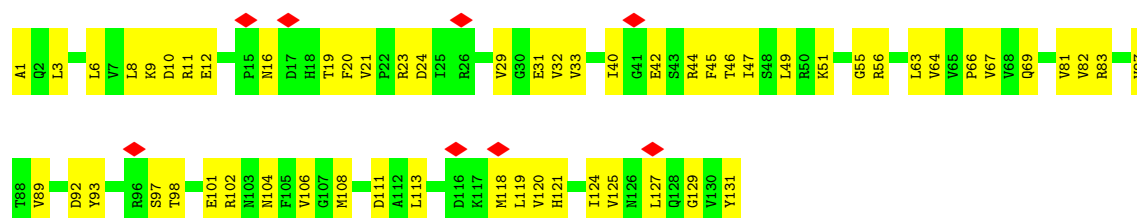




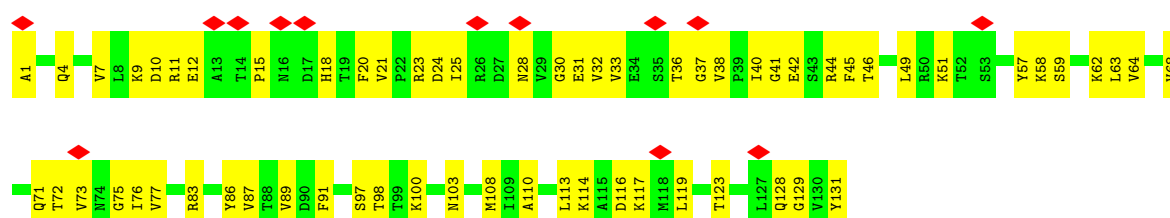
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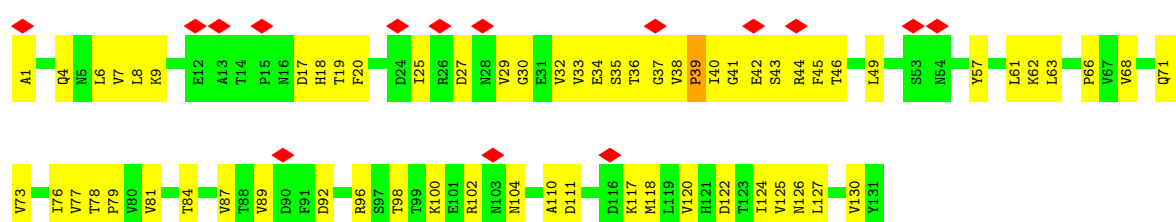
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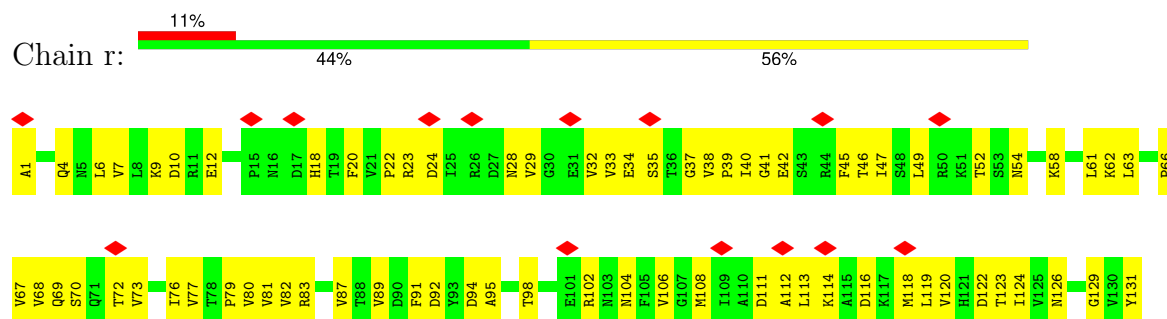
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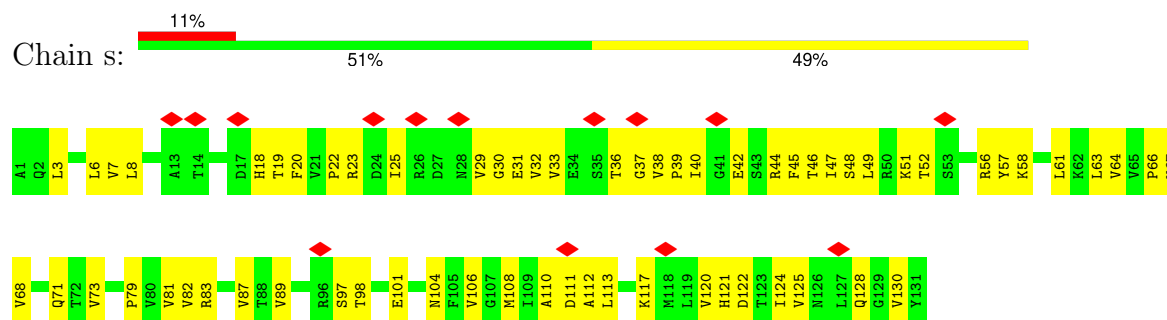
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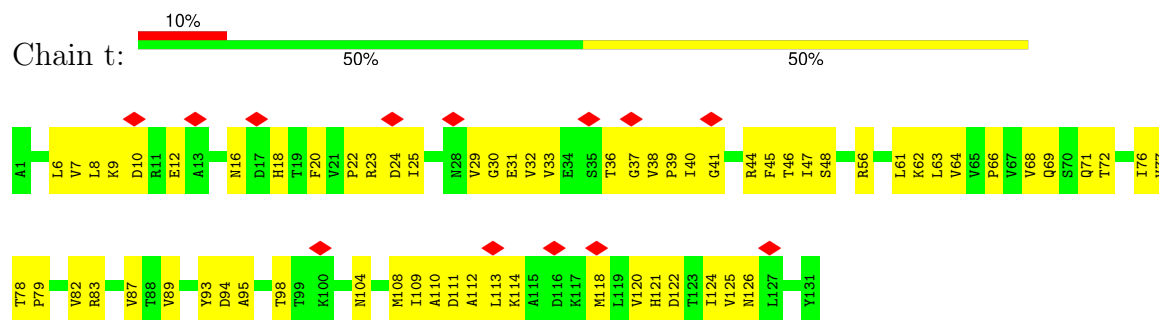
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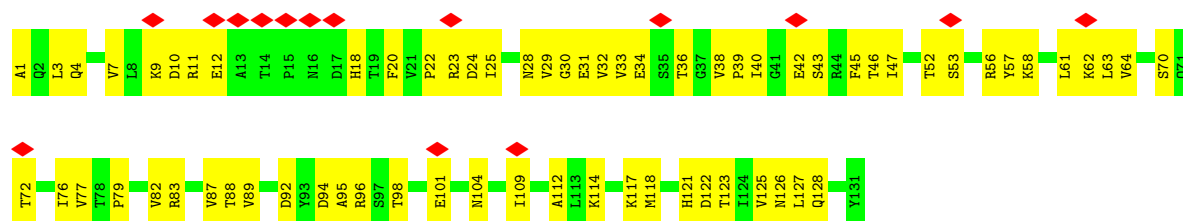


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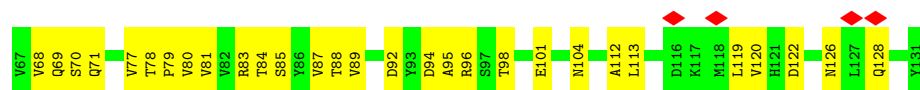


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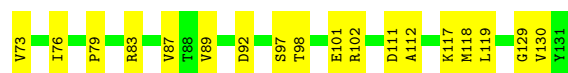
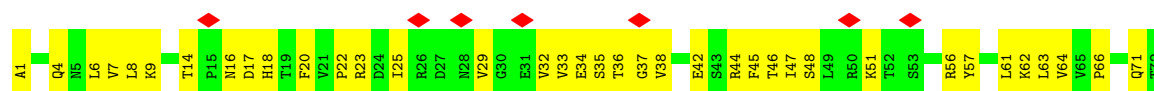


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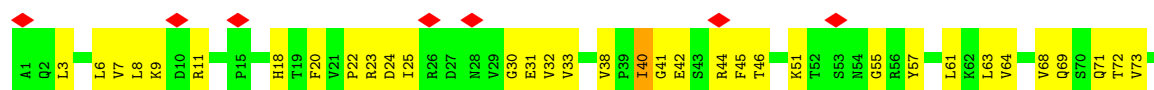




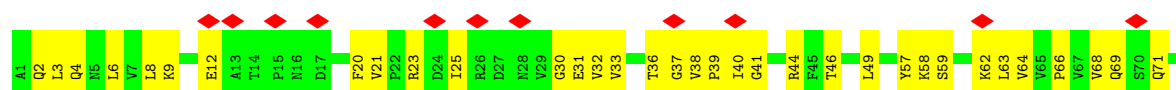
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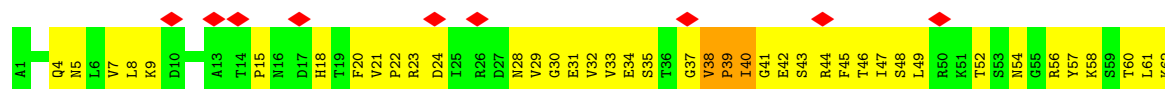
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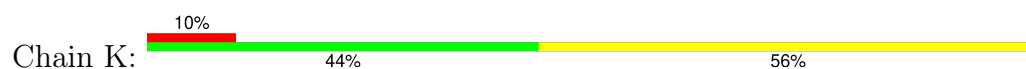
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• Molecule 3: Coat Protein

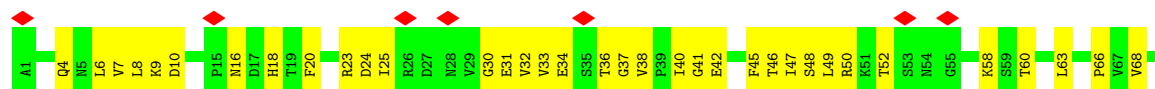


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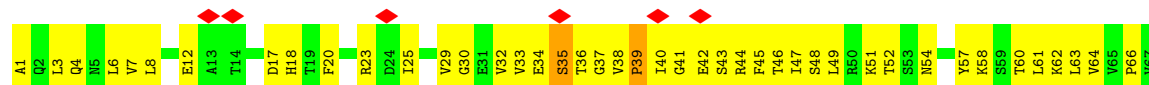




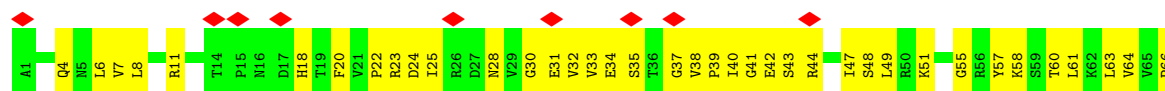
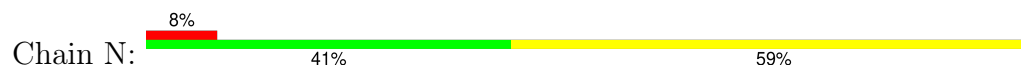
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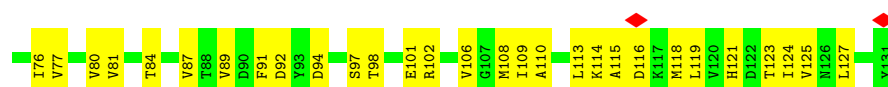
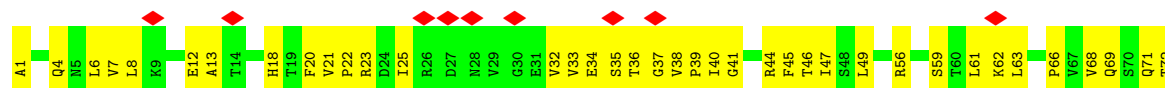
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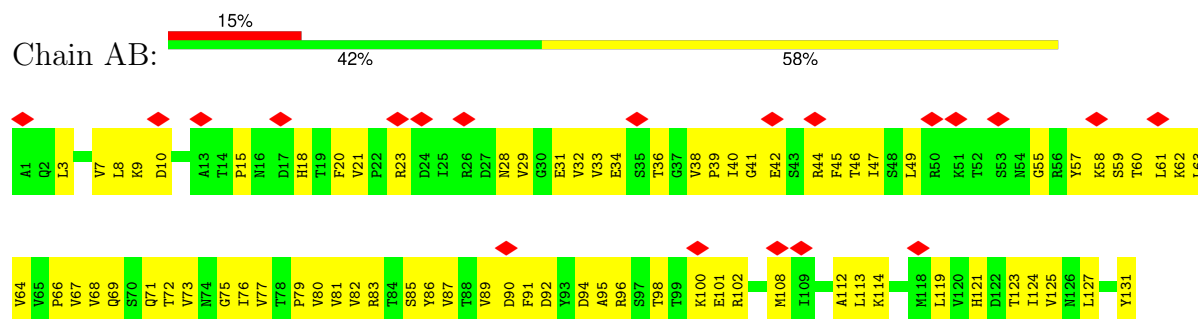
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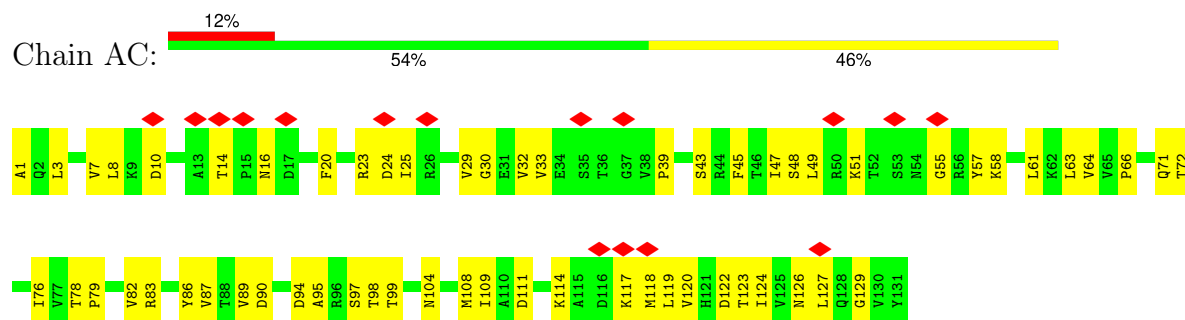
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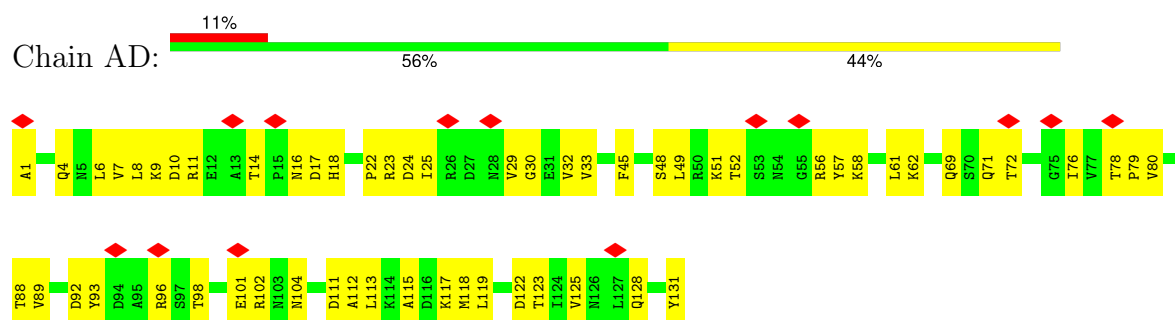
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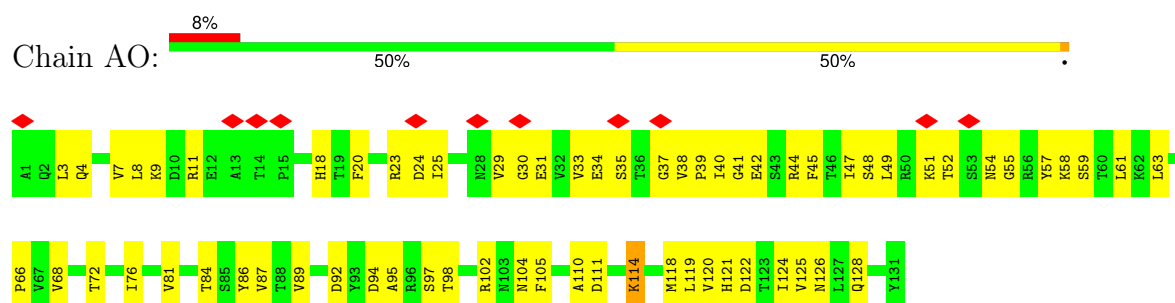
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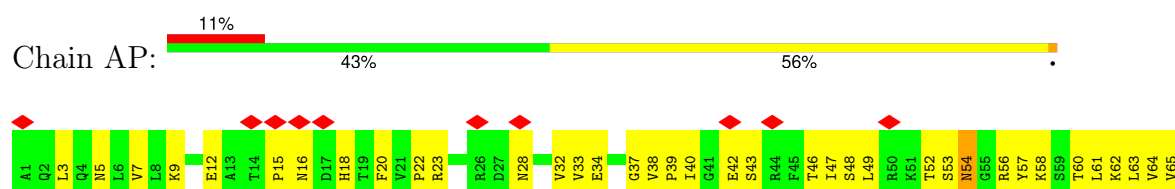
• Molecule 3: Coat Protein

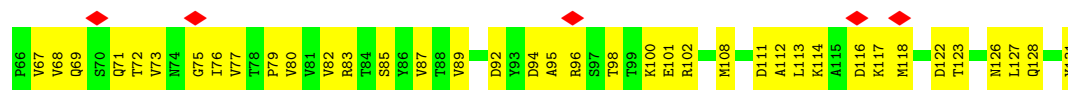


• Molecule 3: Coat Protein



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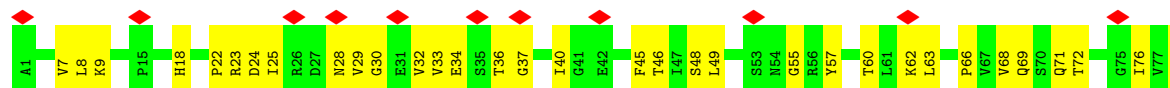




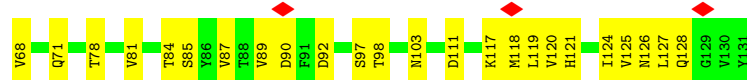
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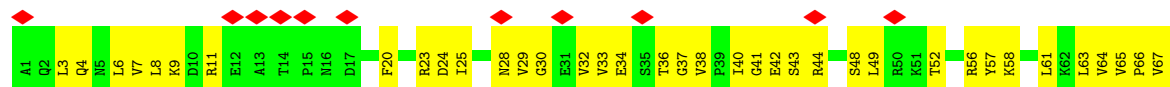
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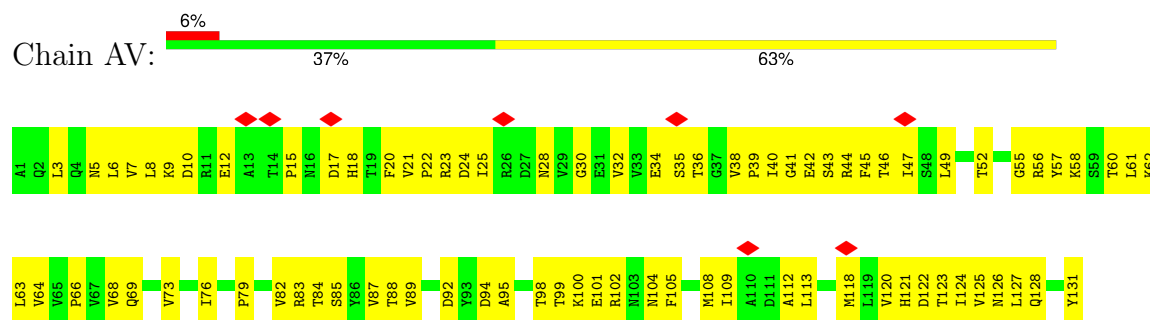
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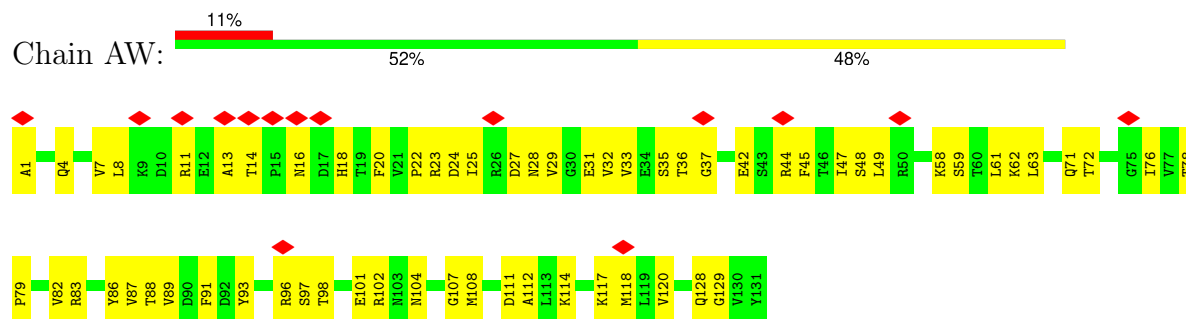
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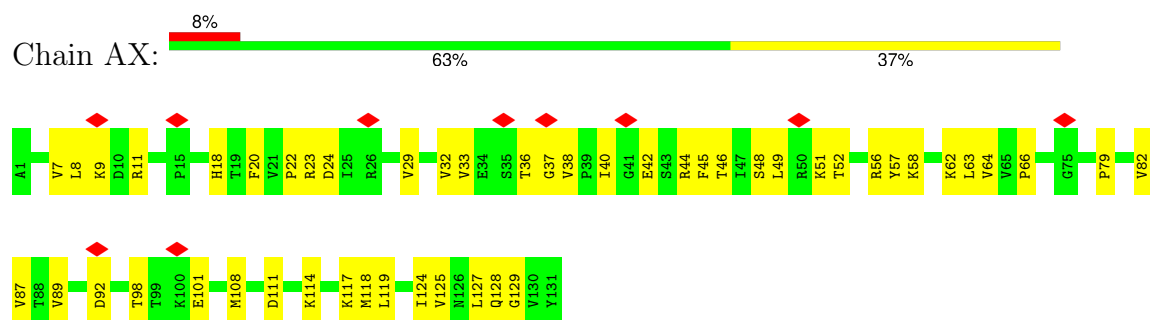
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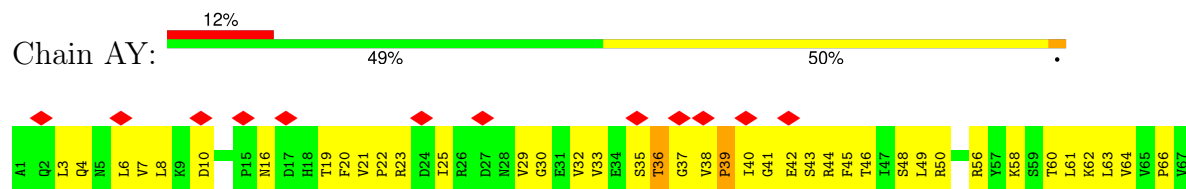
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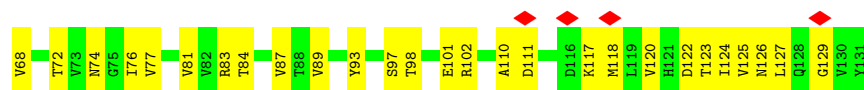


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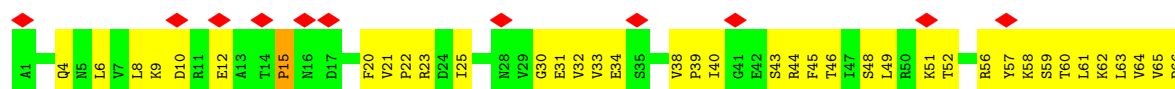


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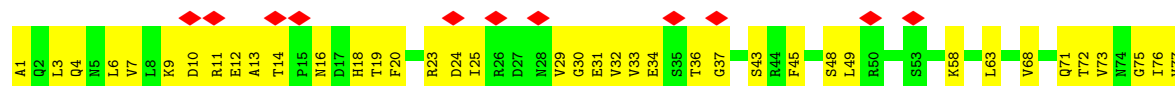
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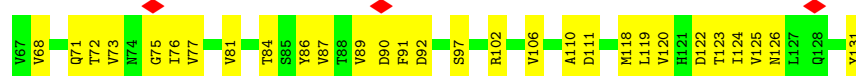
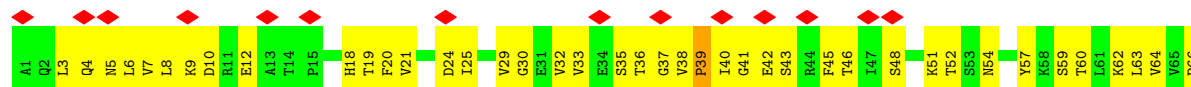
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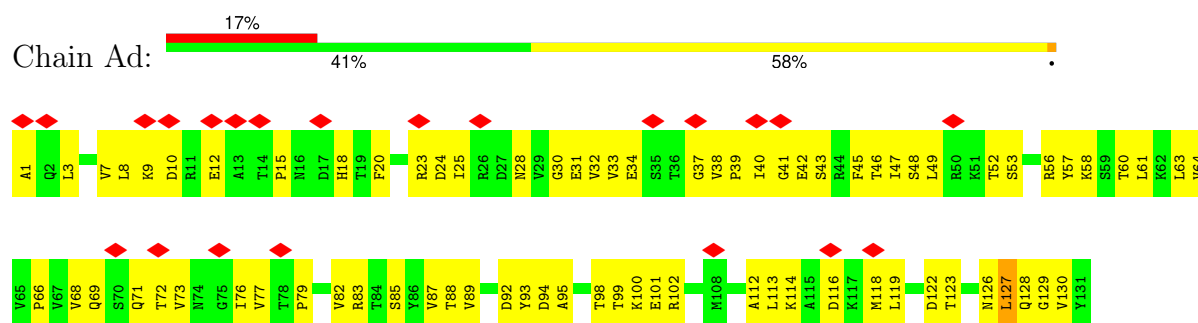
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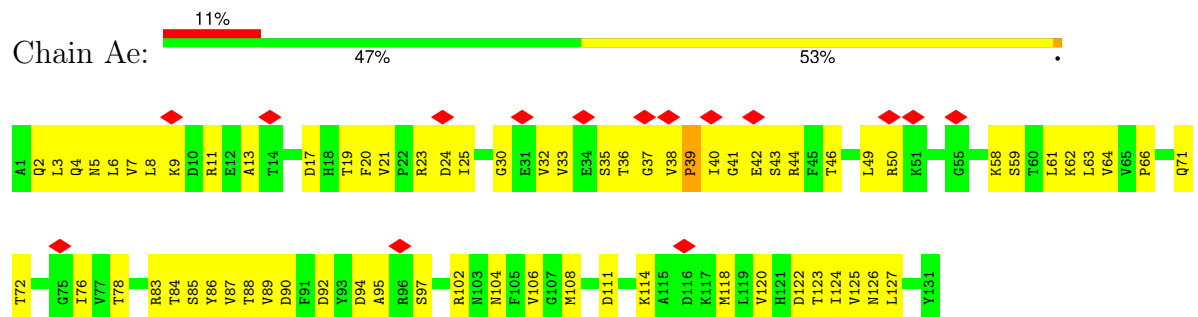
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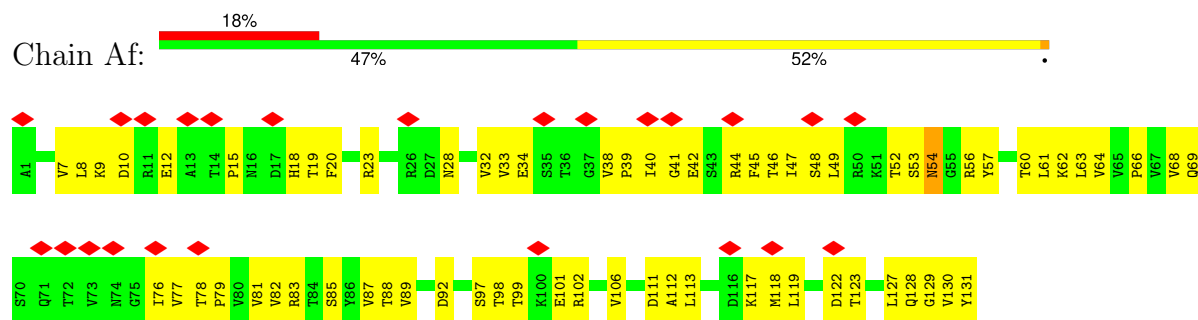
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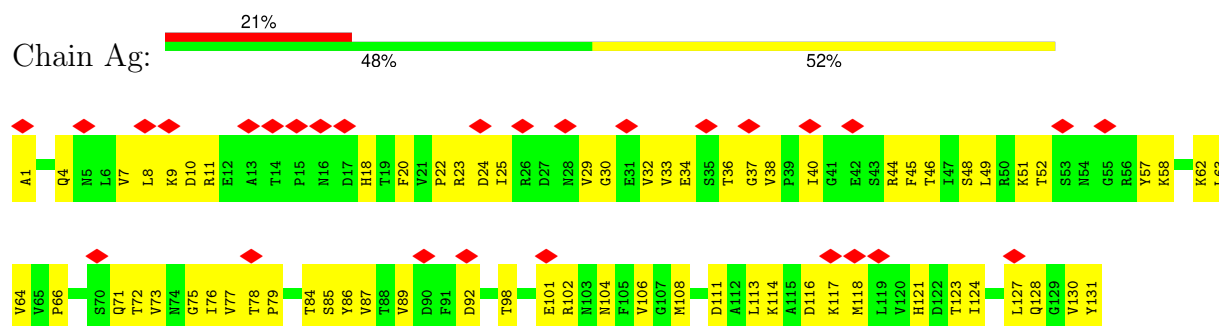
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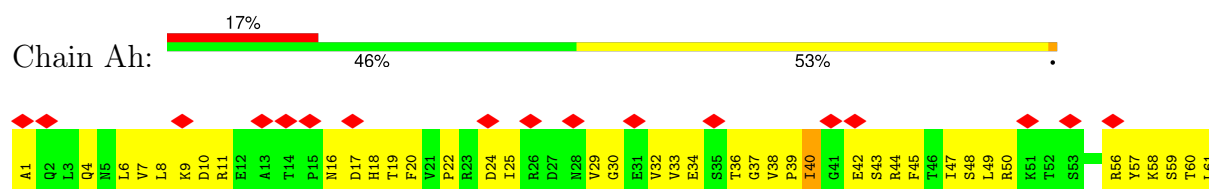
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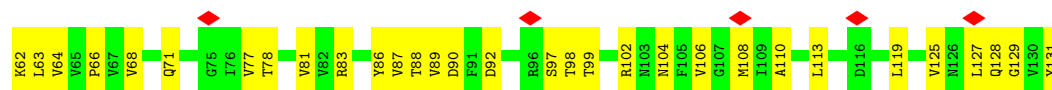


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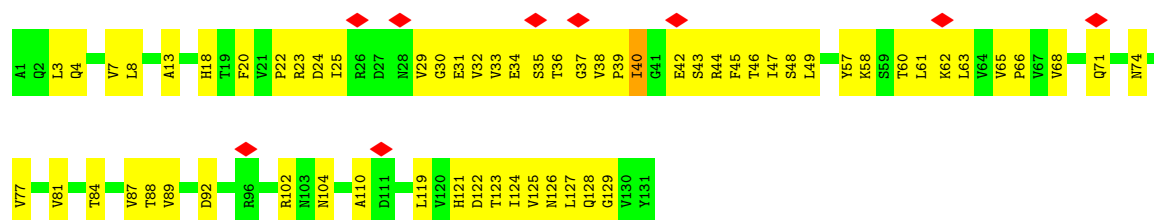


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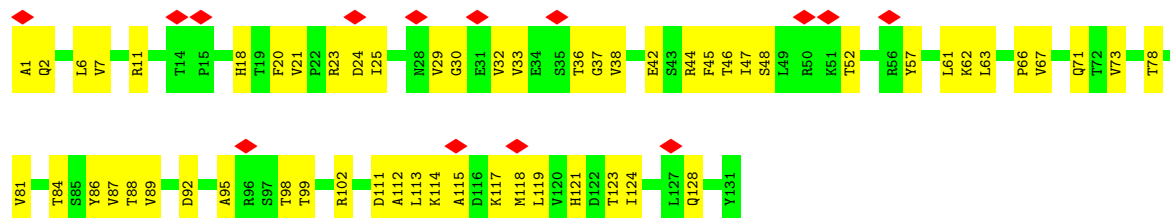
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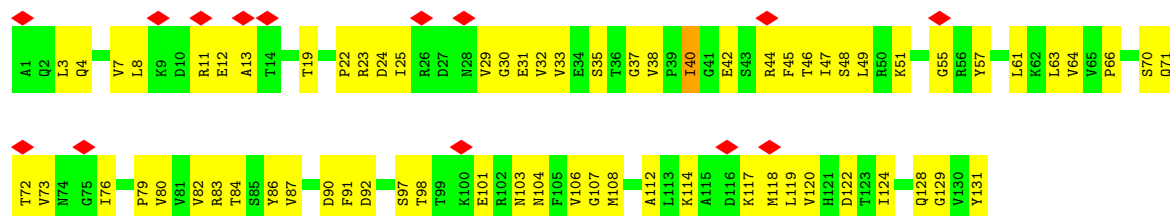
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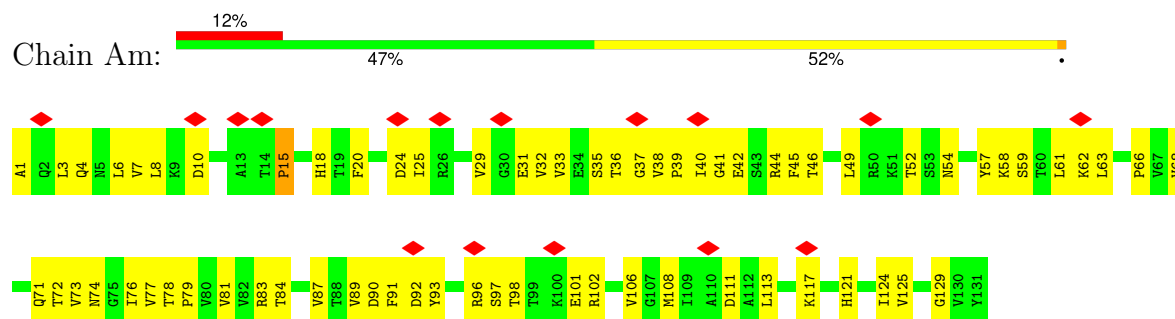
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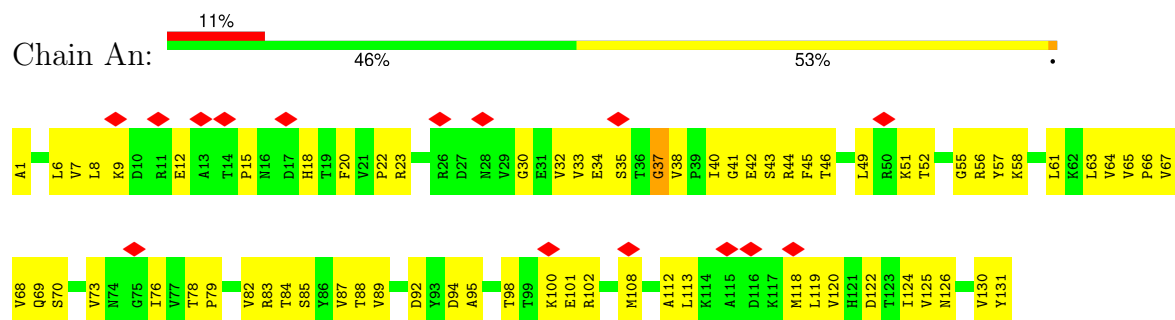
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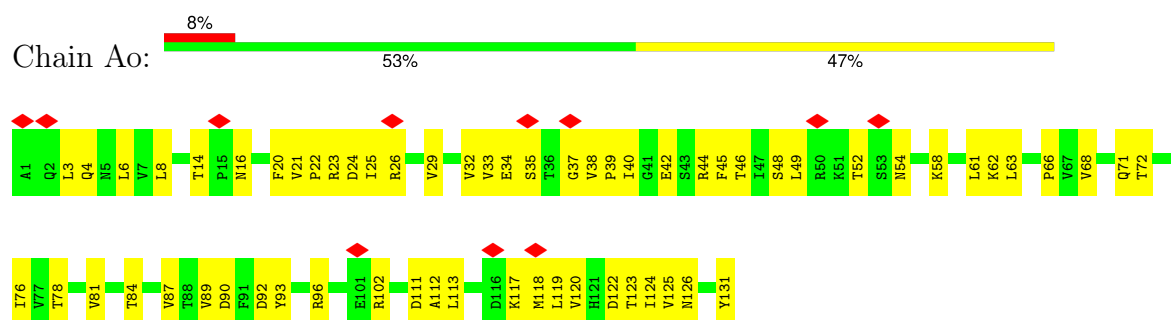
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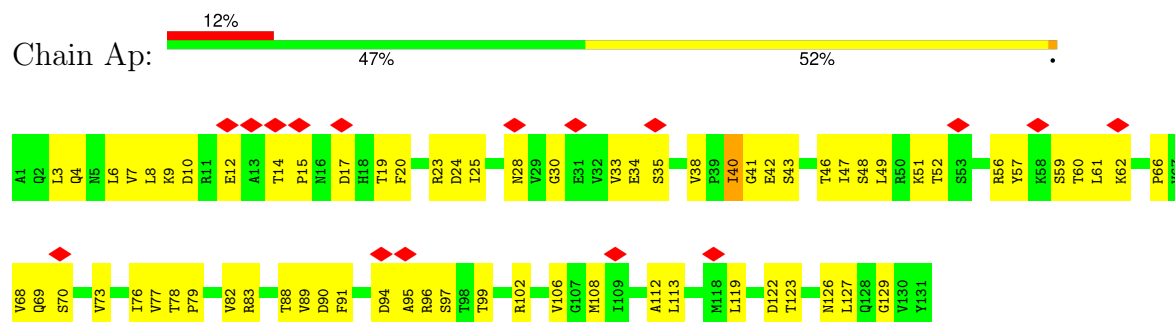
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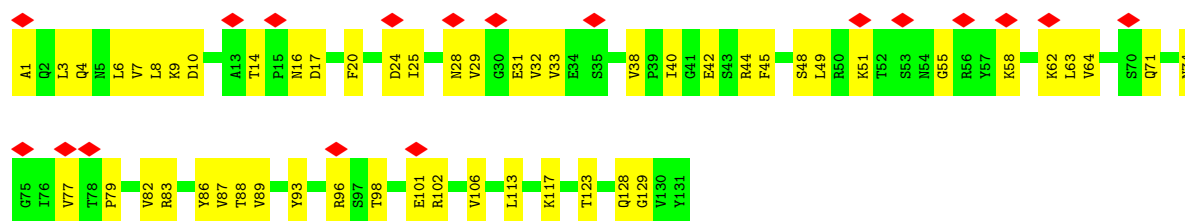


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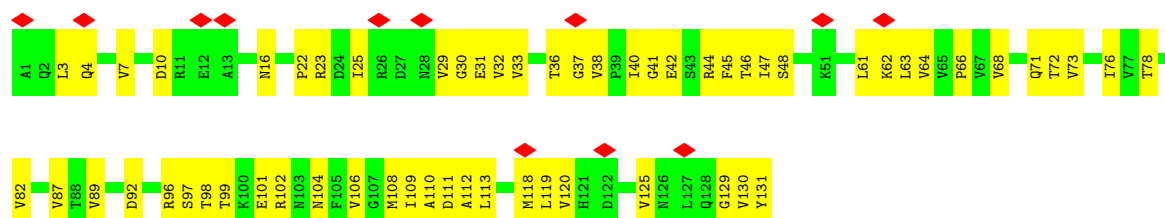


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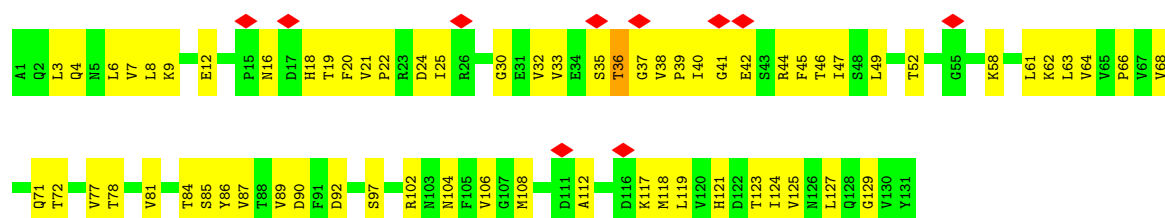




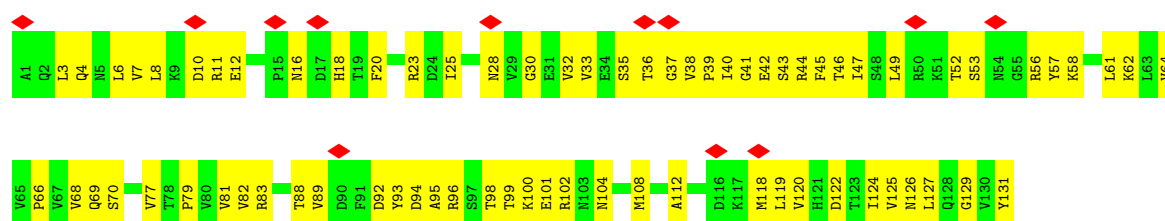
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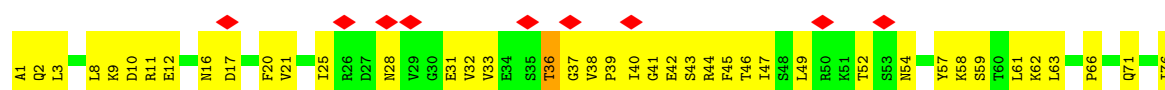
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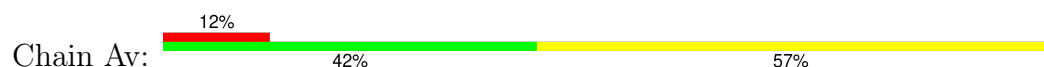


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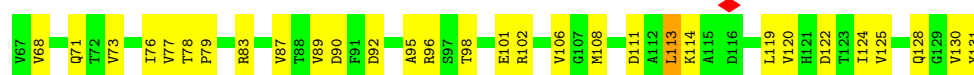
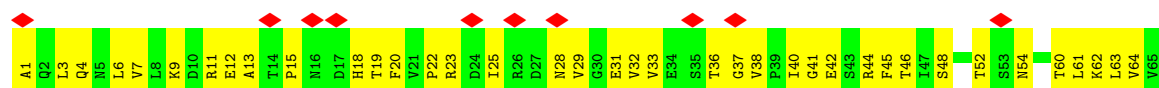
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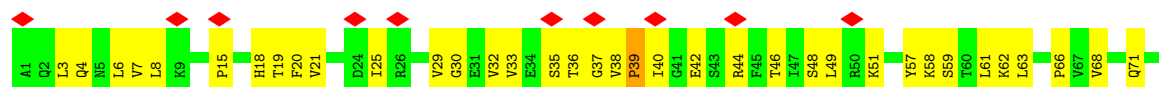
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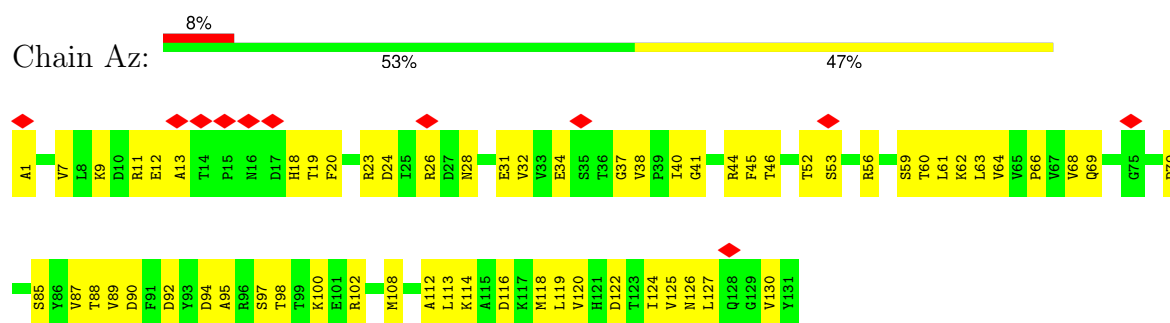
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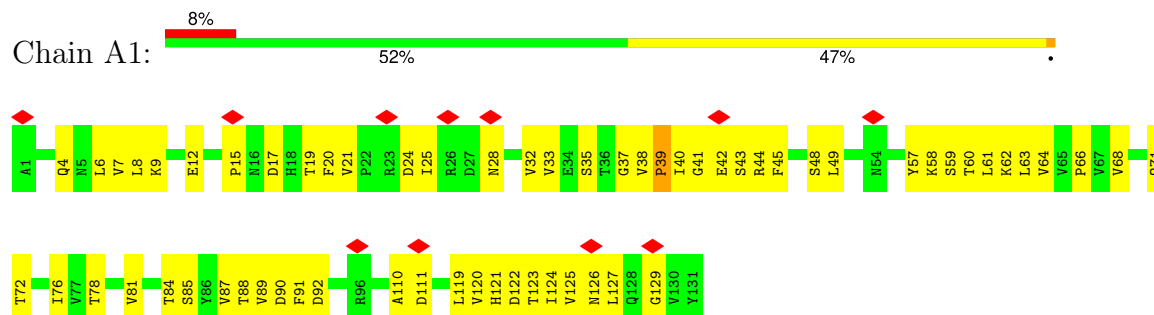
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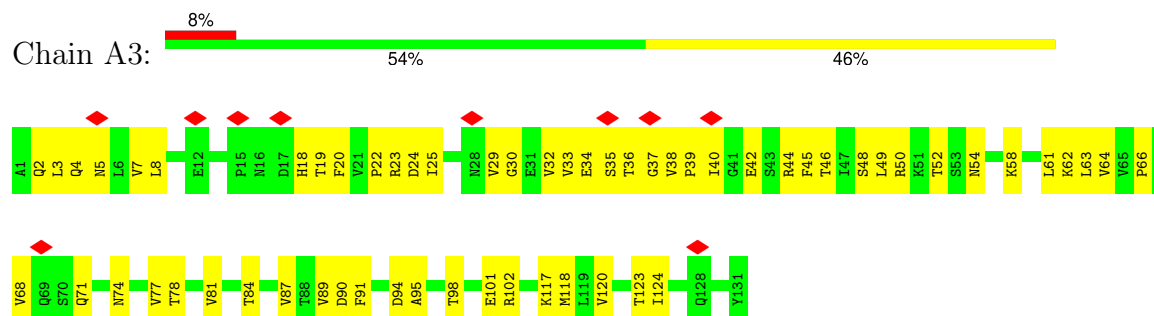
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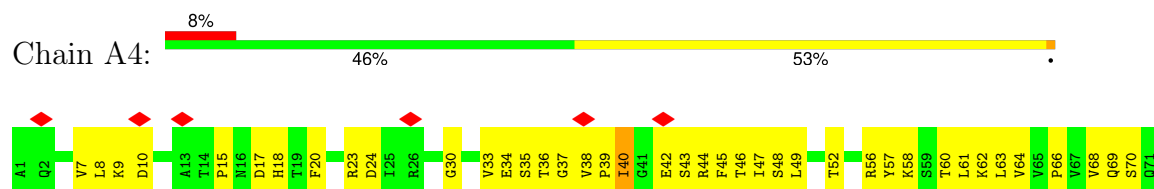
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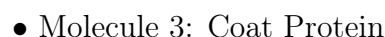


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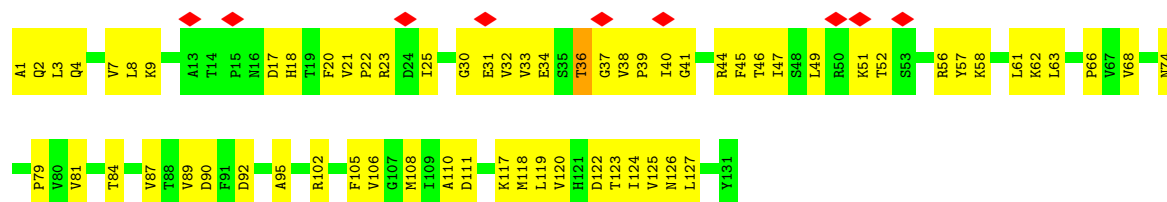


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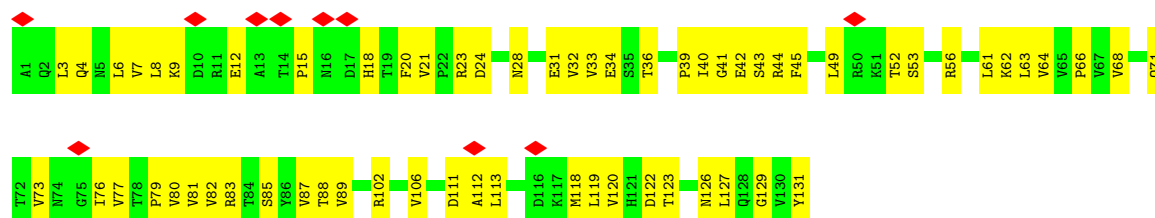


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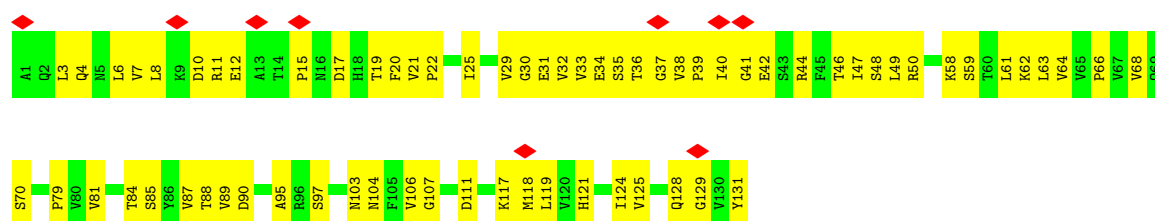
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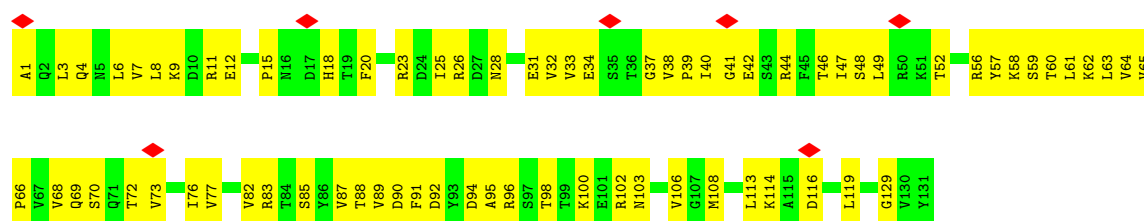
• Molecule 3: Coat Protein

Chain BA: 



• Molecule 3: Coat Protein

Chain BB: 



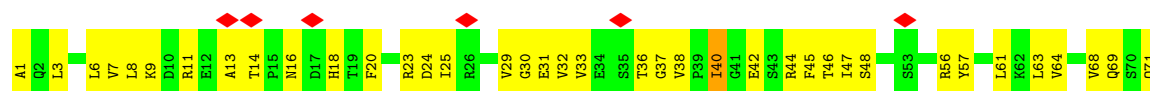
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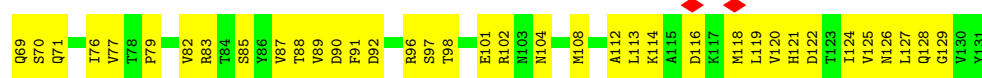
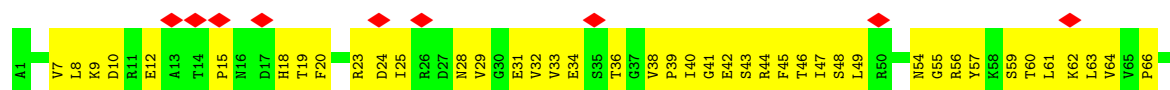
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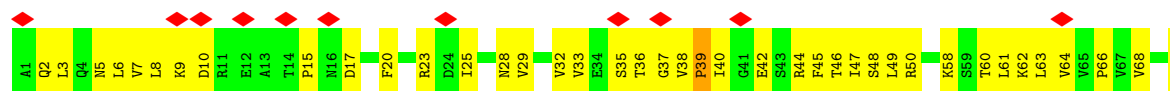
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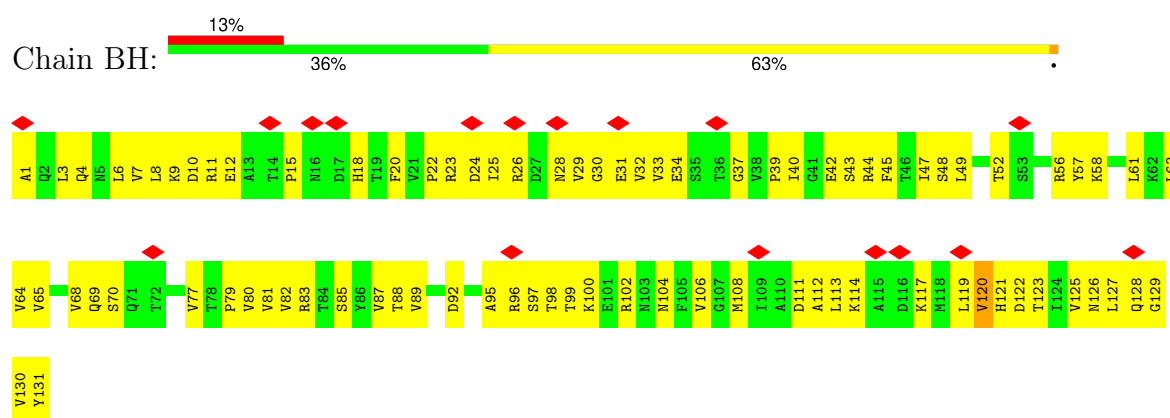
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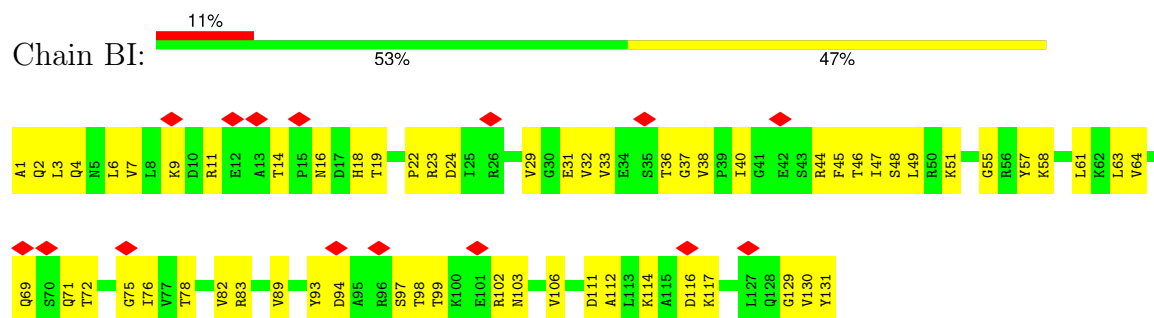
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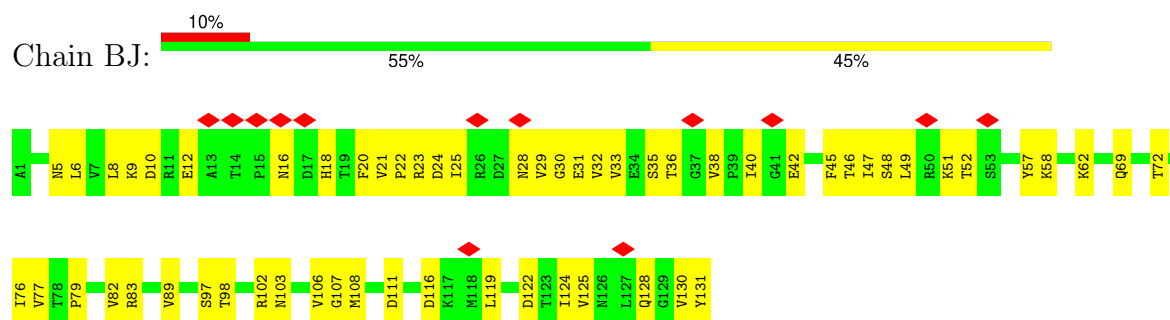
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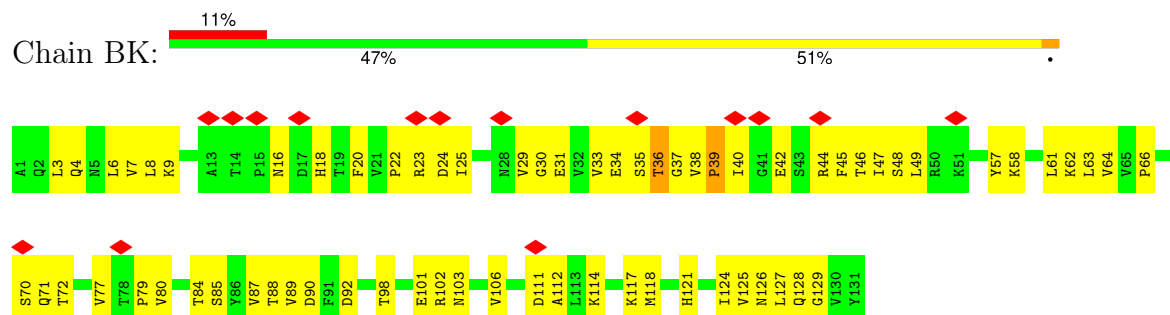
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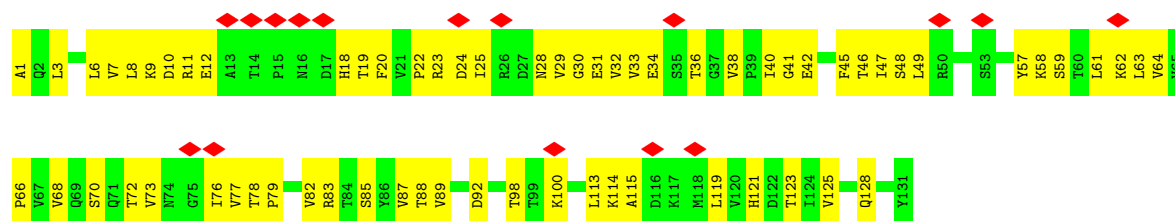


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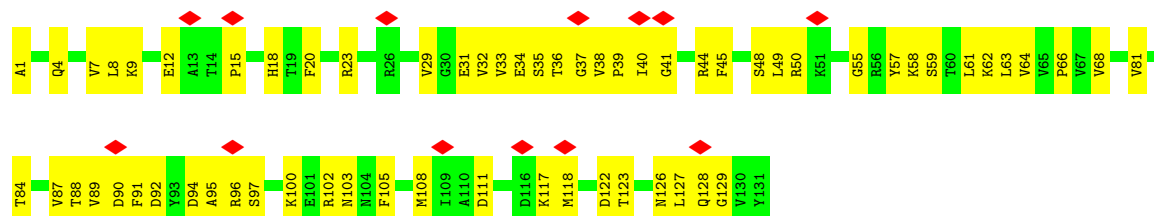


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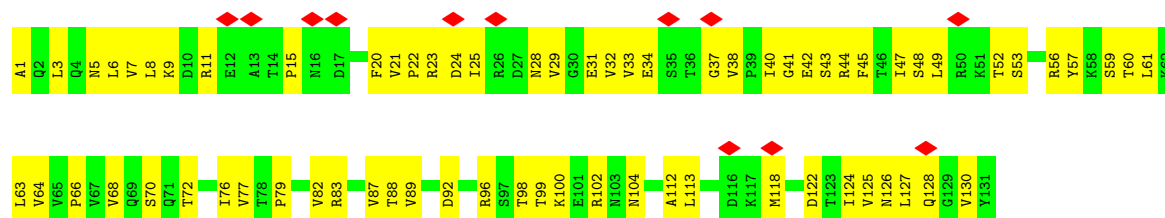




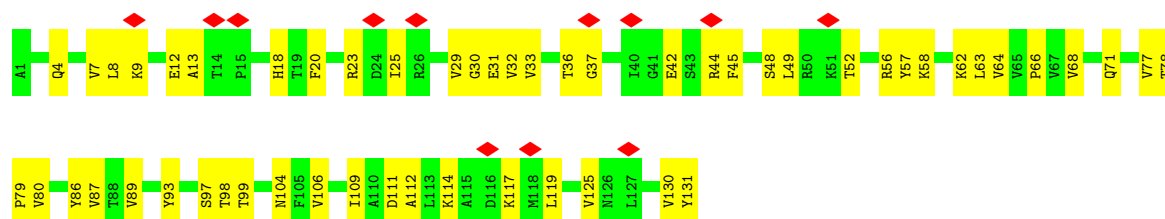
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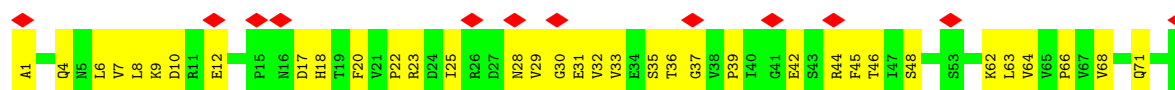
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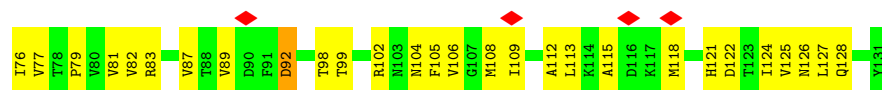


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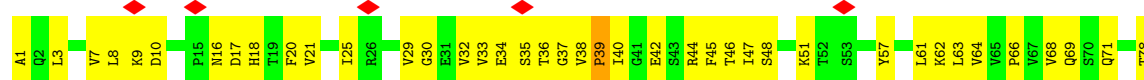


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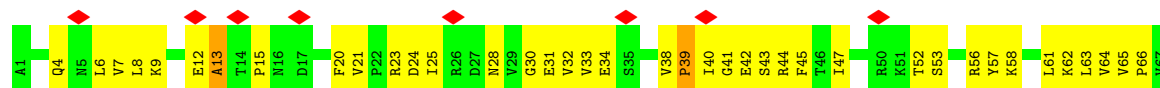




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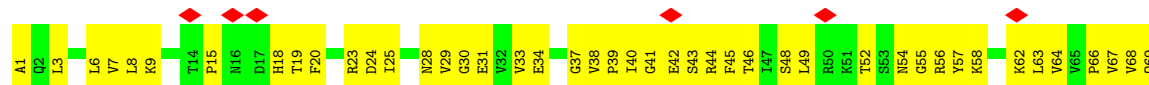
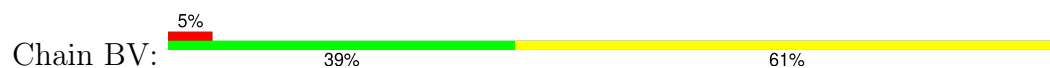
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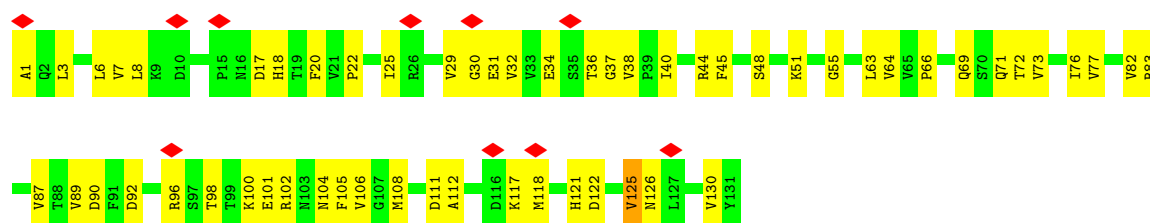
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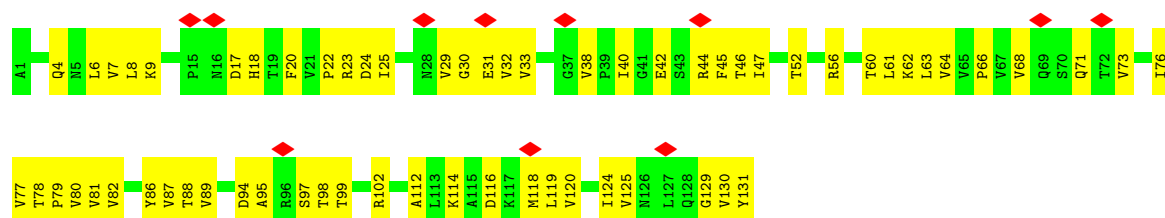
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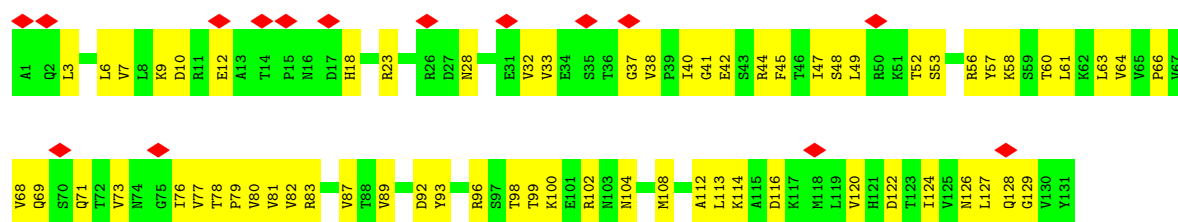
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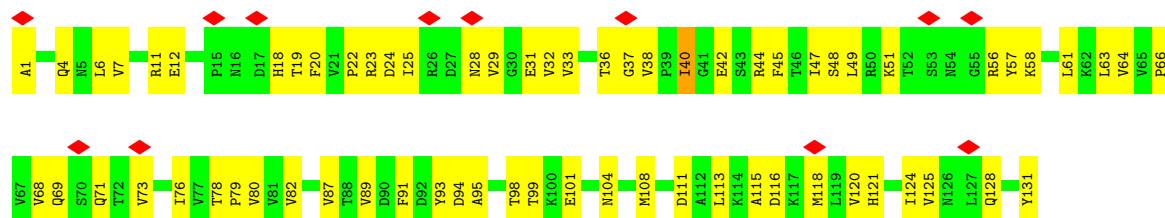
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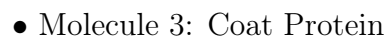


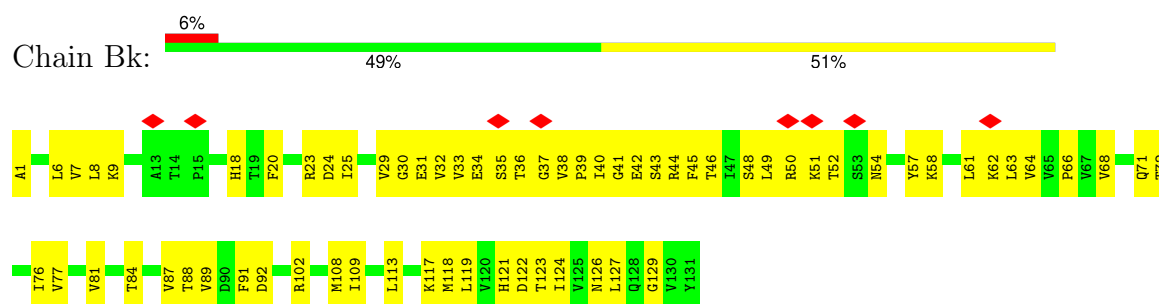
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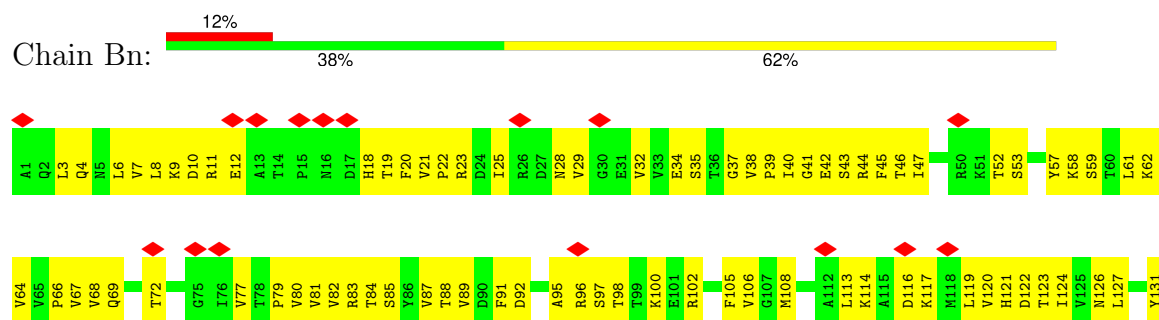
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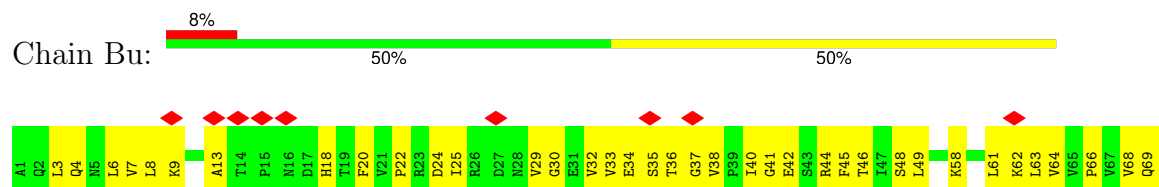
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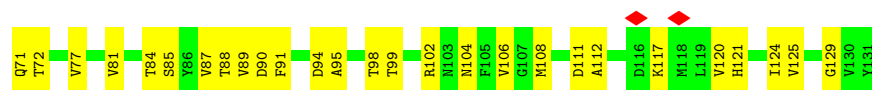


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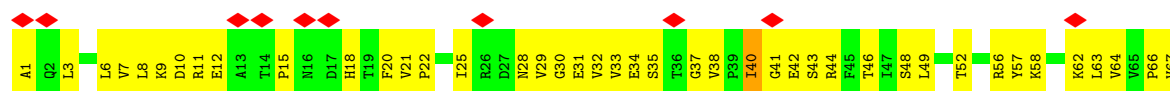
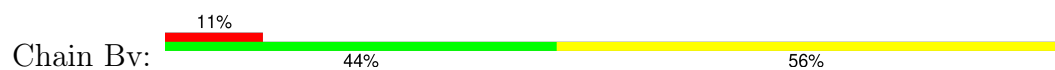


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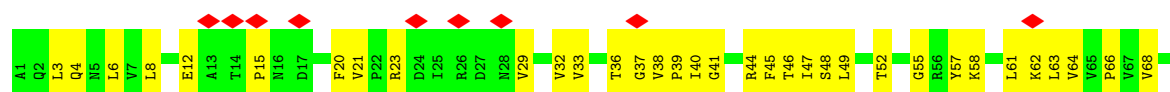




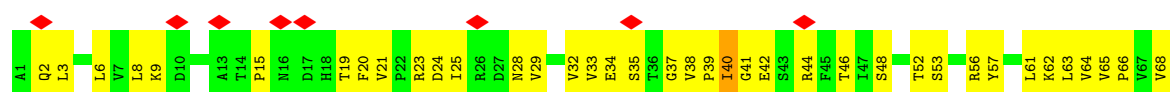
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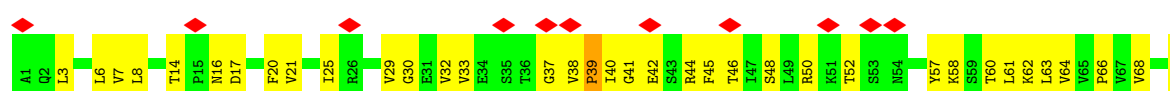
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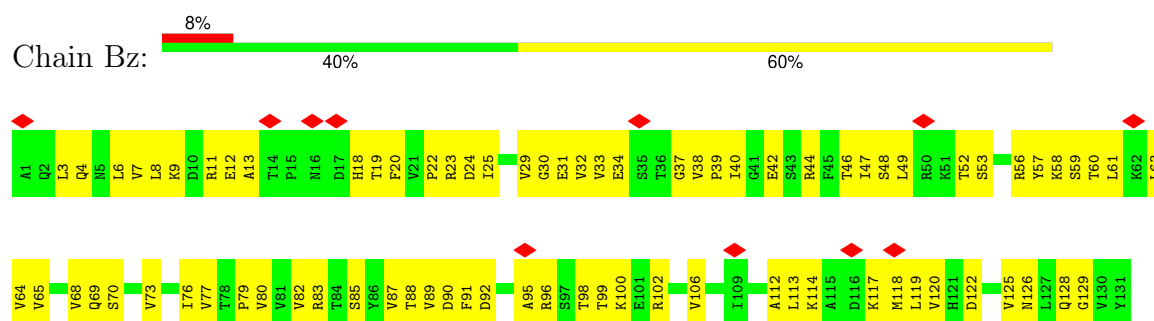


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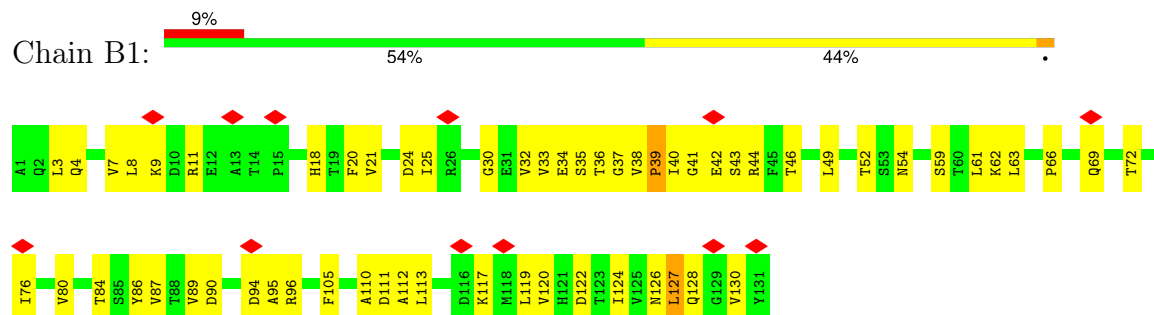


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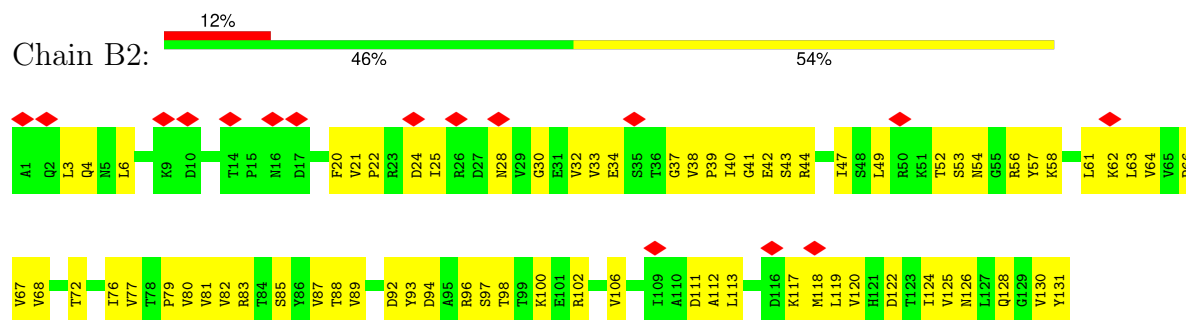




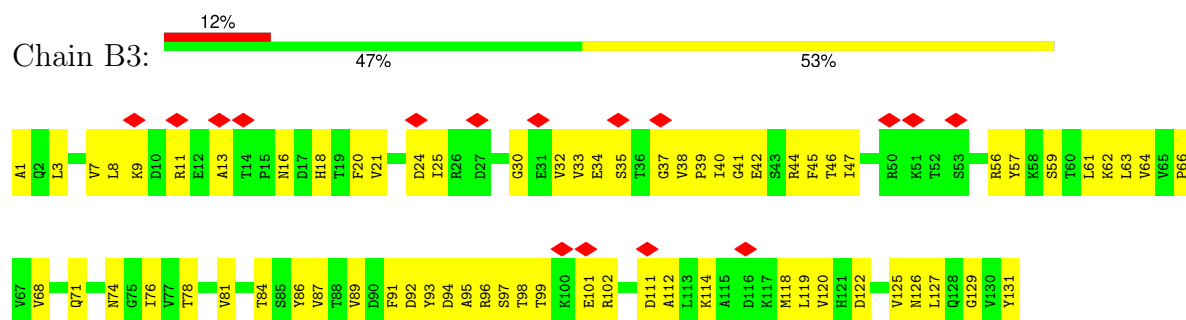
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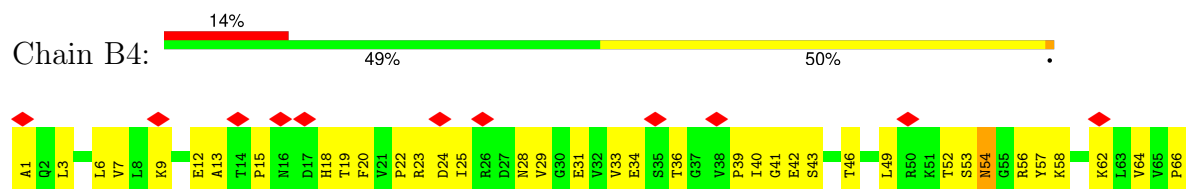
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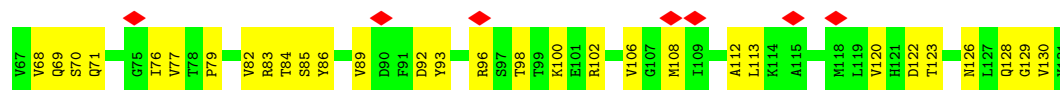


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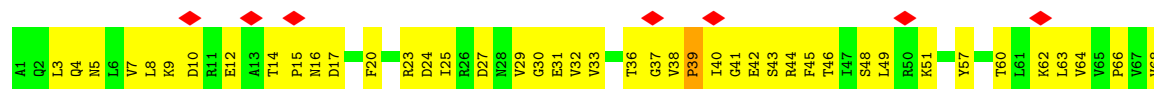


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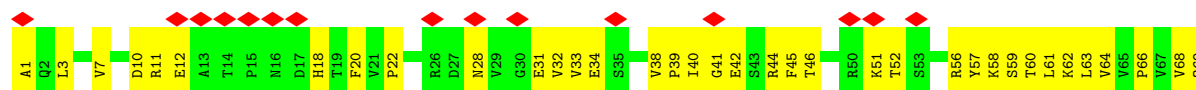




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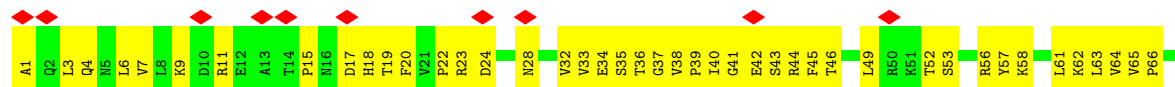
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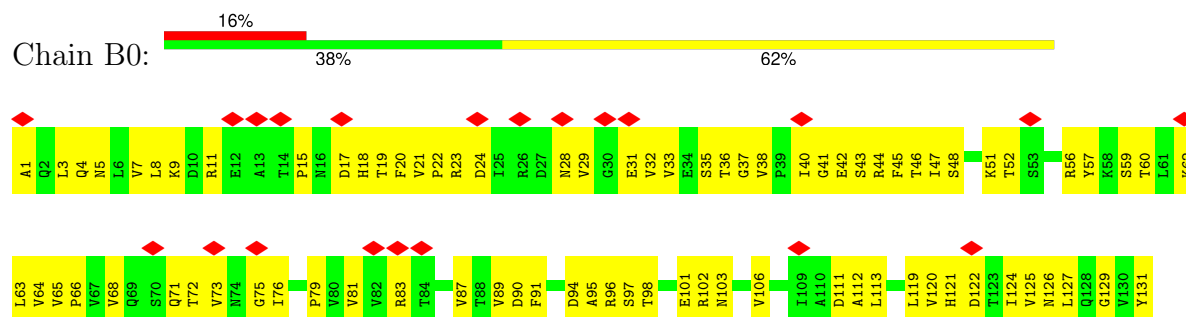


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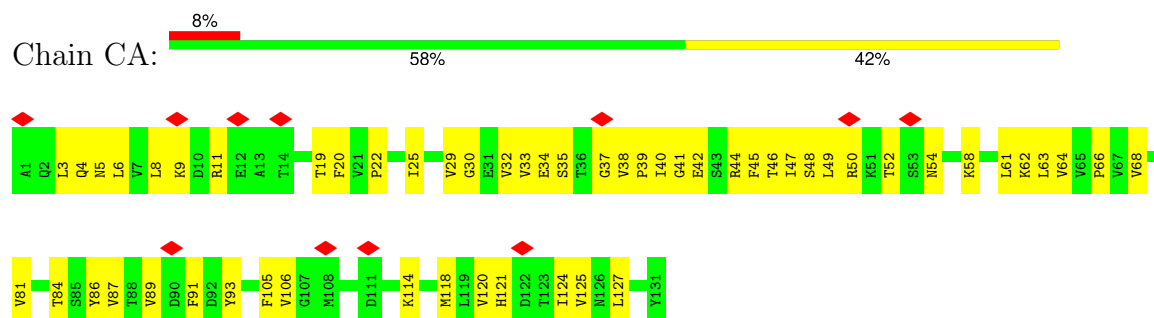




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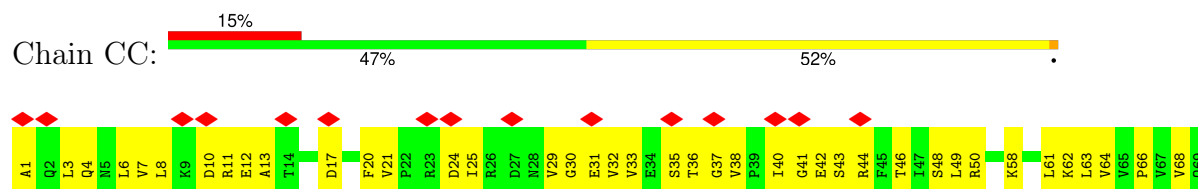
- Molecule 3: Coat Protein

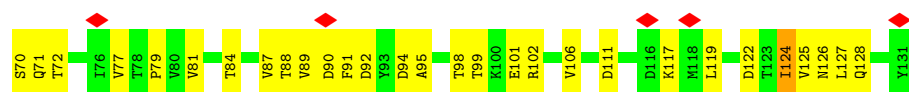


- Molecule 3: Coat Protein

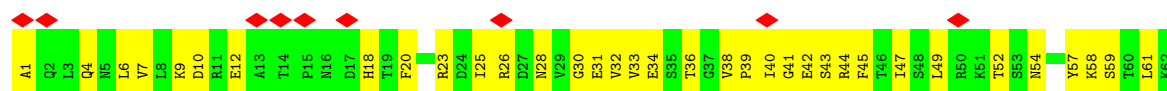


- Molecule 3: Coat Protein





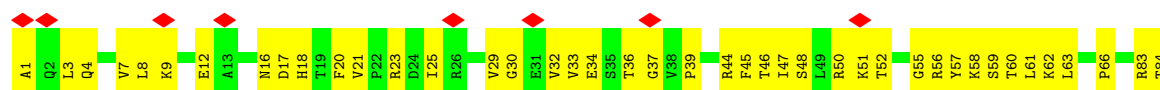
• Molecule 3: Coat Protein



• Molecule 3: Coat Protein



• Molecule 3: Coat Protein

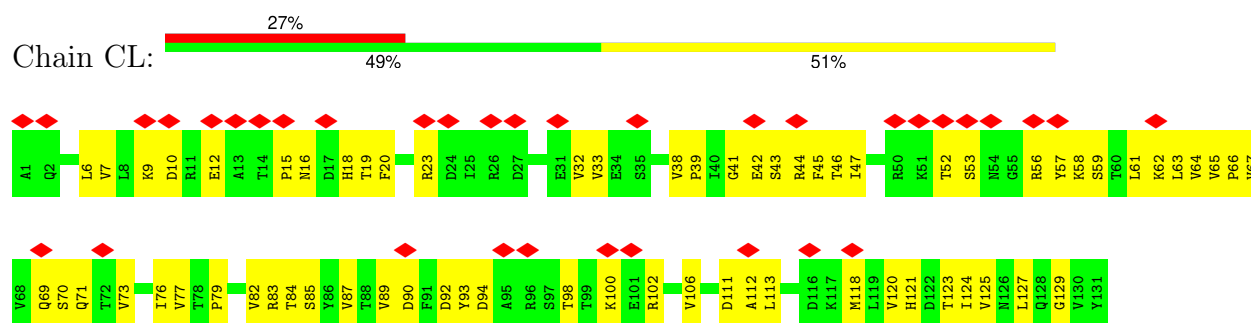


• Molecule 3: Coat Protein

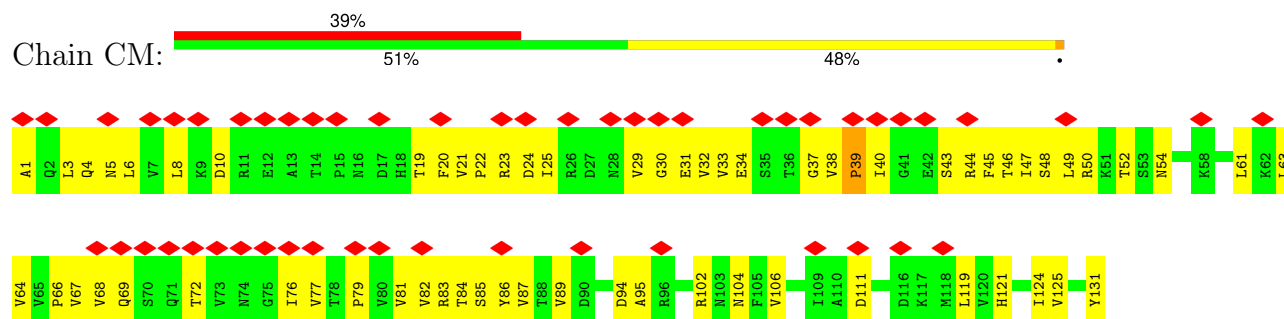


• Molecule 3: Coat Protein

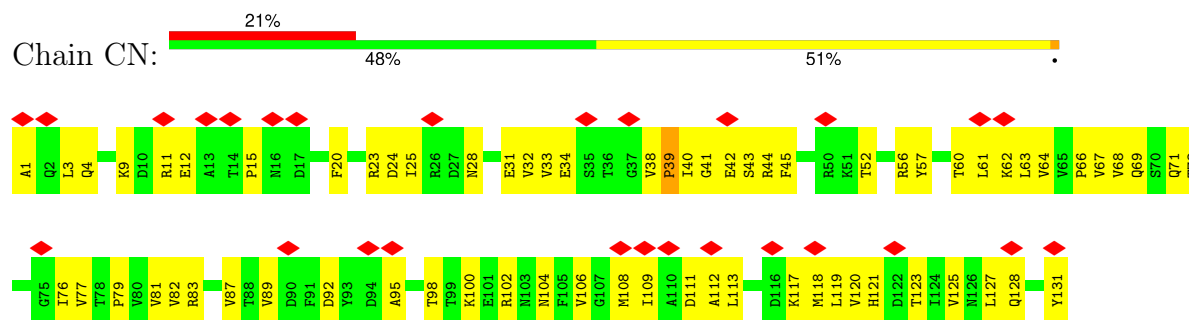




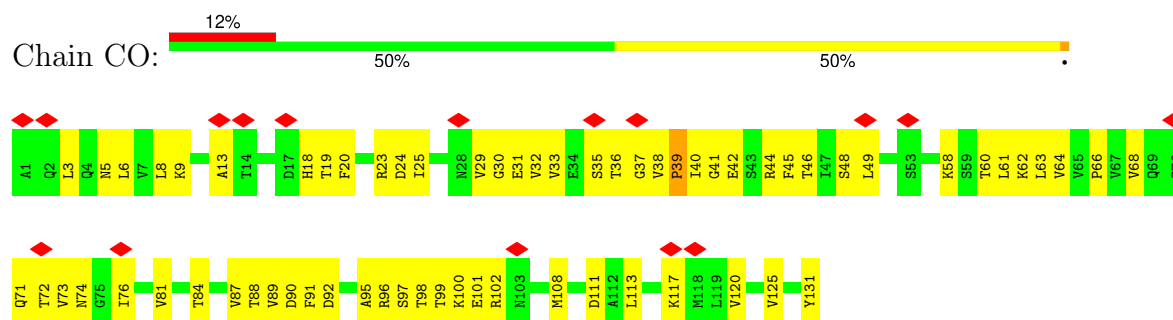
• Molecule 3: Coat Protein



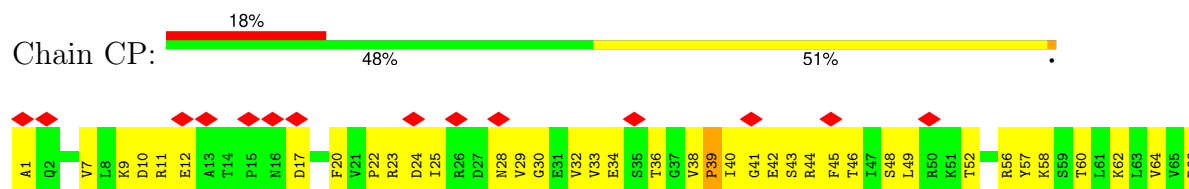
• Molecule 3: Coat Protein

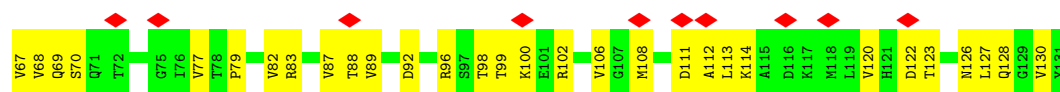


• Molecule 3: Coat Protein

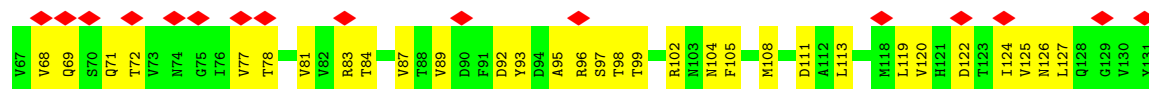
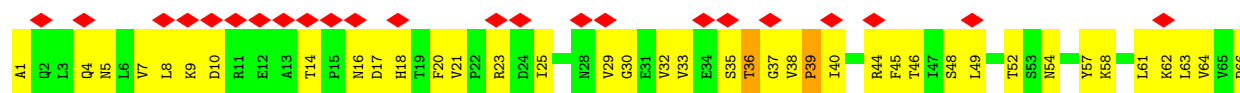


• Molecule 3: Coat Protein

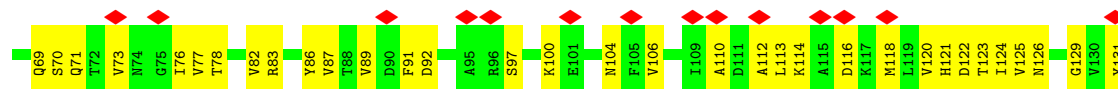
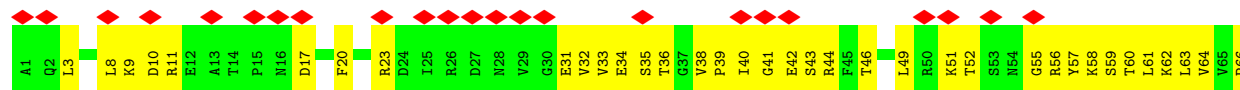




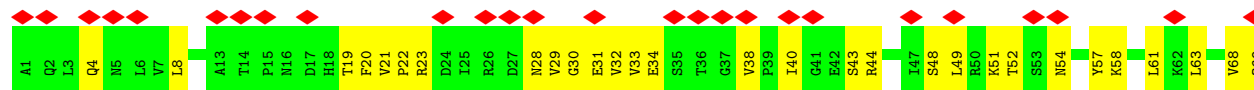
• Molecule 3: Coat Protein



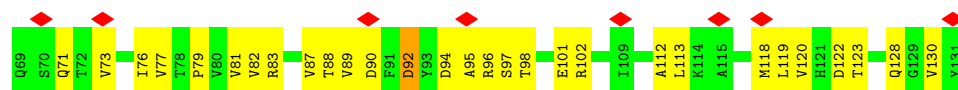
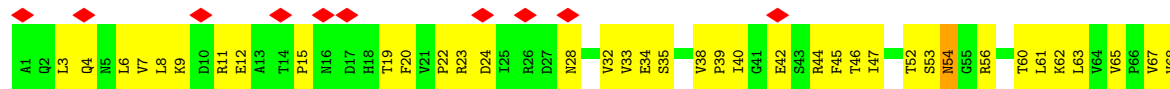
• Molecule 3: Coat Protein



• Molecule 3: Coat Protein



• Molecule 3: Coat Protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30437	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.471	Depositor
Minimum map value	-0.229	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	510.0, 510.0, 510.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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	F	0.06	0/3323	0.14	0/4515
2	AE	0.13	0/3131	0.11	0/4876
3	0	0.05	0/1038	0.15	0/1410
3	1	0.06	0/1038	0.14	0/1410
3	2	0.05	0/1038	0.12	0/1410
3	3	0.05	0/1038	0.15	0/1410
3	4	0.05	0/1038	0.13	0/1410
3	5	0.05	0/1038	0.14	0/1410
3	6	0.05	0/1038	0.13	0/1410
3	7	0.05	0/1038	0.17	0/1410
3	8	0.05	0/1038	0.14	0/1410
3	9	0.06	0/1038	0.19	0/1410
3	A	0.04	0/1038	0.12	0/1410
3	A0	0.05	0/1038	0.13	0/1410
3	A1	0.05	0/1038	0.13	0/1410
3	A2	0.05	0/1038	0.13	0/1410
3	A3	0.05	0/1038	0.12	0/1410
3	A4	0.05	0/1038	0.16	0/1410
3	A5	0.07	0/1038	0.14	0/1410
3	A6	0.05	0/1038	0.16	0/1410
3	A7	0.06	0/1038	0.18	0/1410
3	A8	0.05	0/1038	0.13	0/1410
3	A9	0.06	0/1038	0.14	0/1410
3	AA	0.05	0/1038	0.13	0/1410
3	AB	0.06	0/1038	0.17	0/1410
3	AC	0.05	0/1038	0.13	0/1410
3	AD	0.04	0/1038	0.12	0/1410
3	AO	0.05	0/1038	0.13	0/1410
3	AP	0.05	0/1038	0.13	0/1410
3	AQ	0.06	0/1038	0.14	0/1410
3	AR	0.05	0/1038	0.13	0/1410
3	AS	0.05	0/1038	0.12	0/1410
3	AT	0.05	0/1038	0.14	0/1410
3	AU	0.05	0/1038	0.15	0/1410

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	AV	0.05	0/1038	0.12	0/1410
3	AW	0.05	0/1038	0.13	0/1410
3	AX	0.05	0/1038	0.14	0/1410
3	AY	0.06	0/1038	0.18	0/1410
3	AZ	0.05	0/1038	0.14	0/1410
3	Aa	0.07	0/1038	0.17	0/1410
3	Ab	0.07	0/1038	0.16	0/1410
3	Ac	0.05	0/1038	0.13	0/1410
3	Ad	0.05	0/1038	0.13	0/1410
3	Ae	0.05	0/1038	0.13	0/1410
3	Af	0.04	0/1038	0.12	0/1410
3	Ag	0.04	0/1038	0.12	0/1410
3	Ah	0.06	0/1038	0.15	0/1410
3	Ai	0.06	0/1038	0.15	0/1410
3	Aj	0.05	0/1038	0.14	0/1410
3	Ak	0.07	0/1038	0.19	0/1410
3	Al	0.05	0/1038	0.13	0/1410
3	Am	0.05	0/1038	0.13	0/1410
3	An	0.05	0/1038	0.13	0/1410
3	Ao	0.05	0/1038	0.13	0/1410
3	Ap	0.08	0/1038	0.22	0/1410
3	Aq	0.06	0/1038	0.15	0/1410
3	Ar	0.06	0/1038	0.16	0/1410
3	As	0.05	0/1038	0.13	0/1410
3	At	0.05	0/1038	0.13	0/1410
3	Au	0.06	0/1038	0.14	0/1410
3	Av	0.05	0/1038	0.14	0/1410
3	Aw	0.06	0/1038	0.17	0/1410
3	Ax	0.05	0/1038	0.14	0/1410
3	Ay	0.05	0/1038	0.12	0/1410
3	Az	0.04	0/1038	0.14	0/1410
3	B	0.05	0/1038	0.14	0/1410
3	B0	0.05	0/1038	0.13	0/1410
3	B1	0.05	0/1038	0.13	0/1410
3	B2	0.06	0/1038	0.15	0/1410
3	B3	0.06	0/1038	0.17	0/1410
3	B4	0.06	0/1038	0.18	0/1410
3	B5	0.05	0/1038	0.16	0/1410
3	B6	0.05	0/1038	0.14	0/1410
3	B7	0.05	0/1038	0.13	0/1410
3	B8	0.06	0/1038	0.15	0/1410
3	B9	0.05	0/1038	0.13	0/1410
3	BA	0.05	0/1046	0.15	0/1421

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	BB	0.05	0/1038	0.13	0/1410
3	BC	0.05	0/1038	0.12	0/1410
3	BD	0.05	0/1038	0.13	0/1410
3	BE	0.05	0/1038	0.13	0/1410
3	BF	0.05	0/1038	0.13	0/1410
3	BG	0.05	0/1038	0.14	0/1410
3	BH	0.05	0/1038	0.14	0/1410
3	BI	0.05	0/1038	0.17	0/1410
3	BJ	0.06	0/1038	0.14	0/1410
3	BK	0.06	0/1038	0.14	0/1410
3	BL	0.05	0/1038	0.13	0/1410
3	BM	0.04	0/1038	0.12	0/1410
3	BN	0.05	0/1038	0.13	0/1410
3	BO	0.04	0/1038	0.13	0/1410
3	BP	0.08	0/1038	0.23	0/1410
3	BQ	0.05	0/1038	0.18	0/1410
3	BR	0.05	0/1038	0.13	0/1410
3	BS	0.06	0/1038	0.15	0/1410
3	BV	0.05	0/1038	0.16	0/1410
3	BY	0.06	0/1038	0.16	0/1410
3	BZ	0.05	0/1038	0.13	0/1410
3	Bb	0.07	0/1038	0.16	0/1410
3	Bc	0.05	0/1038	0.13	0/1410
3	Bd	0.05	0/1038	0.18	0/1410
3	Bg	0.05	0/1038	0.13	0/1410
3	Bh	0.06	0/1038	0.16	0/1410
3	Bi	0.05	0/1038	0.16	0/1410
3	Bj	0.05	0/1038	0.20	0/1410
3	Bk	0.05	0/1038	0.16	0/1410
3	Bl	0.05	0/1038	0.13	0/1410
3	Bm	0.05	0/1038	0.17	0/1410
3	Bn	0.06	0/1038	0.18	0/1410
3	Bu	0.06	0/1038	0.19	0/1410
3	Bv	0.06	0/1038	0.17	0/1410
3	Bw	0.06	0/1038	0.19	0/1410
3	Bx	0.06	0/1038	0.17	0/1410
3	By	0.06	0/1038	0.18	0/1410
3	Bz	0.05	0/1038	0.16	0/1410
3	C	0.06	0/1038	0.19	0/1410
3	CA	0.05	0/1038	0.13	0/1410
3	CB	0.07	0/1038	0.18	0/1410
3	CC	0.05	0/1038	0.12	0/1410
3	CD	0.06	0/1038	0.19	0/1410

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	CH	0.05	0/1038	0.13	0/1410
3	CI	0.05	0/1038	0.13	0/1410
3	CK	0.05	0/1038	0.14	0/1410
3	CL	0.05	0/1038	0.13	0/1410
3	CM	0.05	0/1038	0.14	0/1410
3	CN	0.05	0/1038	0.15	0/1410
3	CO	0.06	0/1038	0.15	0/1410
3	CP	0.06	0/1038	0.17	0/1410
3	CQ	0.05	0/1038	0.13	0/1410
3	CR	0.06	0/1038	0.15	0/1410
3	CS	0.05	0/1038	0.16	0/1410
3	CT	0.05	0/1038	0.13	0/1410
3	D	0.05	0/1038	0.14	0/1410
3	E	0.05	0/1038	0.13	0/1410
3	G	0.05	0/1038	0.17	0/1410
3	H	0.06	0/1038	0.18	0/1410
3	I	0.05	0/1038	0.15	0/1410
3	J	0.05	0/1038	0.14	0/1410
3	K	0.05	0/1038	0.16	0/1410
3	L	0.06	0/1038	0.15	0/1410
3	M	0.05	0/1038	0.15	0/1410
3	N	0.07	0/1038	0.18	0/1410
3	O	0.05	0/1038	0.15	0/1410
3	P	0.05	0/1038	0.13	0/1410
3	Q	0.05	0/1038	0.14	0/1410
3	R	0.05	0/1038	0.13	0/1410
3	S	0.05	0/1038	0.12	0/1410
3	T	0.05	0/1038	0.15	0/1410
3	U	0.05	0/1038	0.13	0/1410
3	V	0.05	0/1038	0.14	0/1410
3	W	0.06	0/1038	0.16	0/1410
3	X	0.05	0/1038	0.14	0/1410
3	Y	0.05	0/1038	0.13	0/1410
3	Z	0.06	0/1038	0.14	0/1410
3	a	0.05	0/1038	0.14	0/1410
3	b	0.05	0/1038	0.13	0/1410
3	c	0.05	0/1038	0.13	0/1410
3	d	0.05	0/1038	0.12	0/1410
3	e	0.05	0/1038	0.14	0/1410
3	f	0.05	0/1038	0.13	0/1410
3	g	0.06	0/1038	0.13	0/1410
3	h	0.05	0/1038	0.13	0/1410
3	i	0.05	0/1038	0.14	0/1410

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	j	0.06	0/1038	0.16	0/1410
3	k	0.05	0/1038	0.14	0/1410
3	l	0.05	0/1038	0.14	0/1410
3	m	0.05	0/1038	0.13	0/1410
3	n	0.05	0/1038	0.13	0/1410
3	o	0.05	0/1038	0.13	0/1410
3	p	0.06	0/1038	0.14	0/1410
3	q	0.05	0/1038	0.15	0/1410
3	r	0.06	0/1038	0.16	0/1410
3	s	0.05	0/1038	0.13	0/1410
3	t	0.04	0/1038	0.12	0/1410
3	u	0.06	0/1038	0.15	0/1410
3	v	0.08	0/1038	0.23	0/1410
3	w	0.05	0/1038	0.13	0/1410
3	x	0.04	0/1038	0.12	0/1410
3	y	0.05	0/1038	0.13	0/1410
3	z	0.05	0/1038	0.13	0/1410
All	All	0.06	0/191226	0.15	0/260382

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	3239	3222	3221	6	0
2	AE	2804	1421	1422	5	0
3	0	1024	0	1043	80	0
3	1	1024	0	1043	44	0
3	2	1024	0	1043	40	0
3	3	1024	0	1043	61	0
3	4	1024	0	1043	70	0
3	5	1024	0	1043	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	6	1024	0	1043	63	0
3	7	1024	0	1043	61	0
3	8	1024	0	1043	74	0
3	9	1024	0	1043	71	0
3	A	1024	0	1043	67	0
3	A0	1024	0	1043	64	0
3	A1	1024	0	1043	67	0
3	A2	1024	0	1043	65	0
3	A3	1024	0	1043	60	0
3	A4	1024	0	1043	64	0
3	A5	1024	0	1043	71	0
3	A6	1024	0	1043	68	0
3	A7	1024	0	1043	64	0
3	A8	1024	0	1043	74	0
3	A9	1024	0	1043	62	0
3	AA	1024	0	1043	66	0
3	AB	1024	0	1043	75	0
3	AC	1024	0	1043	59	0
3	AD	1024	0	1043	55	0
3	AO	1024	0	1043	58	0
3	AP	1024	0	1043	74	0
3	AQ	1024	0	1043	47	0
3	AR	1024	0	1043	50	0
3	AS	1024	0	1043	60	0
3	AT	1024	0	1043	71	0
3	AU	1024	0	1043	70	0
3	AV	1024	0	1043	82	0
3	AW	1024	0	1043	60	0
3	AX	1024	0	1043	48	0
3	AY	1024	0	1043	64	0
3	AZ	1024	0	1043	66	0
3	Aa	1024	0	1043	70	0
3	Ab	1024	0	1043	60	0
3	Ac	1024	0	1043	64	0
3	Ad	1024	0	1043	78	0
3	Ae	1024	0	1043	75	0
3	Af	1024	0	1043	78	0
3	Ag	1024	0	1043	70	0
3	Ah	1024	0	1043	76	0
3	Ai	1024	0	1043	67	0
3	Aj	1024	0	1043	79	0
3	Ak	1024	0	1043	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	Al	1024	0	1043	67	0
3	Am	1024	0	1043	67	0
3	An	1024	0	1043	73	0
3	Ao	1024	0	1043	62	0
3	Ap	1024	0	1043	76	0
3	Aq	1024	0	1043	51	0
3	Ar	1024	0	1043	62	0
3	As	1024	0	1043	65	0
3	At	1024	0	1043	73	0
3	Au	1024	0	1043	65	0
3	Av	1024	0	1043	70	0
3	Aw	1024	0	1043	59	0
3	Ax	1024	0	1043	65	0
3	Ay	1024	0	1043	56	0
3	Az	1024	0	1043	69	0
3	B	1024	0	1043	76	0
3	B0	1024	0	1043	84	0
3	B1	1024	0	1043	62	0
3	B2	1024	0	1043	75	0
3	B3	1024	0	1043	62	0
3	B4	1024	0	1043	74	0
3	B5	1024	0	1043	68	0
3	B6	1024	0	1043	72	0
3	B7	1024	0	1043	62	0
3	B8	1024	0	1043	83	0
3	B9	1024	0	1043	67	0
3	BA	1028	0	1043	68	0
3	BB	1024	0	1043	73	0
3	BC	1024	0	1043	68	0
3	BD	1024	0	1043	61	0
3	BE	1024	0	1043	65	0
3	BF	1024	0	1043	85	0
3	BG	1024	0	1043	81	0
3	BH	1024	0	1043	82	0
3	BI	1024	0	1043	61	0
3	BJ	1024	0	1043	57	0
3	BK	1024	0	1043	64	0
3	BL	1024	0	1043	60	0
3	BM	1024	0	1043	61	0
3	BN	1024	0	1043	72	0
3	BO	1024	0	1043	54	0
3	BP	1024	0	1043	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BQ	1024	0	1043	58	0
3	BR	1024	0	1043	72	0
3	BS	1024	0	1043	72	0
3	BV	1024	0	1043	85	0
3	BY	1024	0	1043	52	0
3	BZ	1024	0	1043	69	0
3	Bb	1024	0	1043	66	0
3	Bc	1024	0	1043	64	0
3	Bd	1024	0	1043	69	0
3	Bg	1024	0	1043	66	0
3	Bh	1024	0	1043	63	0
3	Bi	1024	0	1043	49	0
3	Bj	1024	0	1043	68	0
3	Bk	1024	0	1043	65	0
3	Bl	1024	0	1043	67	0
3	Bm	1024	0	1043	66	0
3	Bn	1024	0	1043	81	0
3	Bu	1024	0	1043	50	0
3	Bv	1024	0	1043	77	0
3	Bw	1024	0	1043	68	0
3	Bx	1024	0	1043	82	0
3	By	1024	0	1043	70	0
3	Bz	1024	0	1043	88	0
3	C	1024	0	1043	67	0
3	CA	1024	0	1043	54	0
3	CB	1024	0	1043	64	0
3	CC	1024	0	1043	69	0
3	CD	1024	0	1043	79	0
3	CH	1024	0	1043	68	0
3	CI	1024	0	1043	60	0
3	CK	1024	0	1043	63	0
3	CL	1024	0	1043	66	0
3	CM	1024	0	1043	65	0
3	CN	1024	0	1043	69	0
3	CO	1024	0	1043	63	0
3	CP	1024	0	1043	67	0
3	CQ	1024	0	1043	74	0
3	CR	1024	0	1043	68	0
3	CS	1024	0	1043	58	0
3	CT	1024	0	1043	80	0
3	D	1024	0	1043	58	0
3	E	1024	0	1043	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	1024	0	1043	49	0
3	H	1024	0	1043	56	0
3	I	1024	0	1043	56	0
3	J	1024	0	1043	81	0
3	K	1024	0	1043	67	0
3	L	1024	0	1043	49	0
3	M	1024	0	1043	71	0
3	N	1024	0	1043	75	0
3	O	1024	0	1043	77	0
3	P	1024	0	1043	74	0
3	Q	1024	0	1043	74	0
3	R	1024	0	1043	78	0
3	S	1024	0	1043	62	0
3	T	1024	0	1043	72	0
3	U	1024	0	1043	44	0
3	V	1024	0	1043	55	0
3	W	1024	0	1043	73	0
3	X	1024	0	1043	55	0
3	Y	1024	0	1043	63	0
3	Z	1024	0	1043	58	0
3	a	1024	0	1043	49	0
3	b	1024	0	1043	65	0
3	c	1024	0	1043	53	0
3	d	1024	0	1043	54	0
3	e	1024	0	1043	58	0
3	f	1024	0	1043	69	0
3	g	1024	0	1043	60	0
3	h	1024	0	1043	62	0
3	i	1024	0	1043	67	0
3	j	1024	0	1043	78	0
3	k	1024	0	1043	47	0
3	l	1024	0	1043	52	0
3	m	1024	0	1043	72	0
3	n	1024	0	1043	67	0
3	o	1024	0	1043	58	0
3	p	1024	0	1043	67	0
3	q	1024	0	1043	72	0
3	r	1024	0	1043	77	0
3	s	1024	0	1043	60	0
3	t	1024	0	1043	67	0
3	u	1024	0	1043	64	0
3	v	1024	0	1043	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	w	1024	0	1043	53	0
3	x	1024	0	1043	48	0
3	y	1024	0	1043	65	0
3	z	1024	0	1043	70	0
All	All	188319	4643	190297	9542	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

The worst 5 of 9542 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BZ:52:THR:HG22	3:BZ:56:ARG:O	1.58	1.02
3:8:41:GLY:HA2	3:8:66:PRO:HG2	1.45	0.99
3:CR:71:GLN:HB2	3:CR:78:THR:HB	1.43	0.97
3:Ak:6:LEU:HD12	3:Al:119:LEU:HD23	1.44	0.97
3:A:6:LEU:HB3	3:A:20:PHE:HB2	1.43	0.97

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	404/406 (100%)	372 (92%)	30 (7%)	2 (0%)	24	57
3	0	129/131 (98%)	107 (83%)	21 (16%)	1 (1%)	16	49
3	1	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	2	129/131 (98%)	106 (82%)	23 (18%)	0	100	100
3	3	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	4	129/131 (98%)	105 (81%)	21 (16%)	3 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	5	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
3	6	129/131 (98%)	112 (87%)	17 (13%)	0	100	100
3	7	129/131 (98%)	109 (84%)	17 (13%)	3 (2%)	5	30
3	8	129/131 (98%)	107 (83%)	22 (17%)	0	100	100
3	9	129/131 (98%)	109 (84%)	20 (16%)	0	100	100
3	A	129/131 (98%)	106 (82%)	21 (16%)	2 (2%)	7	36
3	A0	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	A1	129/131 (98%)	106 (82%)	21 (16%)	2 (2%)	7	36
3	A2	129/131 (98%)	107 (83%)	18 (14%)	4 (3%)	3	25
3	A3	129/131 (98%)	112 (87%)	16 (12%)	1 (1%)	16	49
3	A4	129/131 (98%)	113 (88%)	15 (12%)	1 (1%)	16	49
3	A5	129/131 (98%)	110 (85%)	16 (12%)	3 (2%)	5	30
3	A6	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	A7	129/131 (98%)	107 (83%)	21 (16%)	1 (1%)	16	49
3	A8	129/131 (98%)	108 (84%)	19 (15%)	2 (2%)	7	36
3	A9	129/131 (98%)	113 (88%)	13 (10%)	3 (2%)	5	30
3	AA	129/131 (98%)	107 (83%)	20 (16%)	2 (2%)	7	36
3	AB	129/131 (98%)	107 (83%)	20 (16%)	2 (2%)	7	36
3	AC	129/131 (98%)	107 (83%)	22 (17%)	0	100	100
3	AD	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	AO	129/131 (98%)	108 (84%)	19 (15%)	2 (2%)	7	36
3	AP	129/131 (98%)	104 (81%)	22 (17%)	3 (2%)	5	30
3	AQ	129/131 (98%)	114 (88%)	15 (12%)	0	100	100
3	AR	129/131 (98%)	111 (86%)	18 (14%)	0	100	100
3	AS	129/131 (98%)	108 (84%)	19 (15%)	2 (2%)	7	36
3	AT	129/131 (98%)	114 (88%)	13 (10%)	2 (2%)	7	36
3	AU	129/131 (98%)	110 (85%)	17 (13%)	2 (2%)	7	36
3	AV	129/131 (98%)	103 (80%)	24 (19%)	2 (2%)	7	36
3	AW	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	AX	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	AY	129/131 (98%)	108 (84%)	18 (14%)	3 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AZ	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36
3	Aa	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
3	Ab	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36
3	Ac	129/131 (98%)	108 (84%)	19 (15%)	2 (2%)	7	36
3	Ad	129/131 (98%)	107 (83%)	19 (15%)	3 (2%)	5	30
3	Ae	129/131 (98%)	112 (87%)	14 (11%)	3 (2%)	5	30
3	Af	129/131 (98%)	106 (82%)	21 (16%)	2 (2%)	7	36
3	Ag	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
3	Ah	129/131 (98%)	113 (88%)	15 (12%)	1 (1%)	16	49
3	Ai	129/131 (98%)	108 (84%)	18 (14%)	3 (2%)	5	30
3	Aj	129/131 (98%)	110 (85%)	17 (13%)	2 (2%)	7	36
3	Ak	129/131 (98%)	109 (84%)	20 (16%)	0	100	100
3	Al	129/131 (98%)	113 (88%)	14 (11%)	2 (2%)	7	36
3	Am	129/131 (98%)	105 (81%)	22 (17%)	2 (2%)	7	36
3	An	129/131 (98%)	112 (87%)	16 (12%)	1 (1%)	16	49
3	Ao	129/131 (98%)	107 (83%)	21 (16%)	1 (1%)	16	49
3	Ap	129/131 (98%)	110 (85%)	18 (14%)	1 (1%)	16	49
3	Aq	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
3	Ar	129/131 (98%)	112 (87%)	17 (13%)	0	100	100
3	As	129/131 (98%)	110 (85%)	17 (13%)	2 (2%)	7	36
3	At	129/131 (98%)	110 (85%)	16 (12%)	3 (2%)	5	30
3	Au	129/131 (98%)	107 (83%)	19 (15%)	3 (2%)	5	30
3	Av	129/131 (98%)	100 (78%)	27 (21%)	2 (2%)	7	36
3	Aw	129/131 (98%)	108 (84%)	20 (16%)	1 (1%)	16	49
3	Ax	129/131 (98%)	109 (84%)	18 (14%)	2 (2%)	7	36
3	Ay	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36
3	Az	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36
3	B	129/131 (98%)	106 (82%)	21 (16%)	2 (2%)	7	36
3	B0	129/131 (98%)	110 (85%)	19 (15%)	0	100	100
3	B1	129/131 (98%)	110 (85%)	16 (12%)	3 (2%)	5	30
3	B2	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B3	129/131 (98%)	115 (89%)	12 (9%)	2 (2%)	7	36
3	B4	129/131 (98%)	104 (81%)	22 (17%)	3 (2%)	5	30
3	B5	129/131 (98%)	111 (86%)	15 (12%)	3 (2%)	5	30
3	B6	129/131 (98%)	107 (83%)	21 (16%)	1 (1%)	16	49
3	B7	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36
3	B8	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	B9	129/131 (98%)	104 (81%)	22 (17%)	3 (2%)	5	30
3	BA	130/131 (99%)	106 (82%)	22 (17%)	2 (2%)	8	37
3	BB	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36
3	BC	129/131 (98%)	114 (88%)	14 (11%)	1 (1%)	16	49
3	BD	129/131 (98%)	115 (89%)	12 (9%)	2 (2%)	7	36
3	BE	129/131 (98%)	110 (85%)	17 (13%)	2 (2%)	7	36
3	BF	129/131 (98%)	108 (84%)	19 (15%)	2 (2%)	7	36
3	BG	129/131 (98%)	115 (89%)	13 (10%)	1 (1%)	16	49
3	BH	129/131 (98%)	117 (91%)	10 (8%)	2 (2%)	7	36
3	BI	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
3	BJ	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	BK	129/131 (98%)	108 (84%)	18 (14%)	3 (2%)	5	30
3	BL	129/131 (98%)	104 (81%)	23 (18%)	2 (2%)	7	36
3	BM	129/131 (98%)	105 (81%)	22 (17%)	2 (2%)	7	36
3	BN	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	BO	129/131 (98%)	110 (85%)	17 (13%)	2 (2%)	7	36
3	BP	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	BQ	129/131 (98%)	114 (88%)	14 (11%)	1 (1%)	16	49
3	BR	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36
3	BS	129/131 (98%)	107 (83%)	20 (16%)	2 (2%)	7	36
3	BV	129/131 (98%)	110 (85%)	18 (14%)	1 (1%)	16	49
3	BY	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	BZ	129/131 (98%)	116 (90%)	13 (10%)	0	100	100
3	Bb	129/131 (98%)	112 (87%)	17 (13%)	0	100	100
3	Bc	129/131 (98%)	109 (84%)	18 (14%)	2 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Bd	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	Bg	129/131 (98%)	108 (84%)	21 (16%)	0	100	100
3	Bh	129/131 (98%)	110 (85%)	18 (14%)	1 (1%)	16	49
3	Bi	129/131 (98%)	108 (84%)	19 (15%)	2 (2%)	7	36
3	Bj	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	Bk	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	Bl	129/131 (98%)	108 (84%)	20 (16%)	1 (1%)	16	49
3	Bm	129/131 (98%)	112 (87%)	14 (11%)	3 (2%)	5	30
3	Bn	129/131 (98%)	103 (80%)	24 (19%)	2 (2%)	7	36
3	Bu	129/131 (98%)	107 (83%)	19 (15%)	3 (2%)	5	30
3	Bv	129/131 (98%)	109 (84%)	17 (13%)	3 (2%)	5	30
3	Bw	129/131 (98%)	114 (88%)	12 (9%)	3 (2%)	5	30
3	Bx	129/131 (98%)	108 (84%)	18 (14%)	3 (2%)	5	30
3	By	129/131 (98%)	112 (87%)	15 (12%)	2 (2%)	7	36
3	Bz	129/131 (98%)	112 (87%)	15 (12%)	2 (2%)	7	36
3	C	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
3	CA	129/131 (98%)	114 (88%)	14 (11%)	1 (1%)	16	49
3	CB	129/131 (98%)	110 (85%)	16 (12%)	3 (2%)	5	30
3	CC	129/131 (98%)	106 (82%)	20 (16%)	3 (2%)	5	30
3	CD	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	CH	129/131 (98%)	106 (82%)	18 (14%)	5 (4%)	2	20
3	CI	129/131 (98%)	117 (91%)	10 (8%)	2 (2%)	7	36
3	CK	129/131 (98%)	107 (83%)	20 (16%)	2 (2%)	7	36
3	CL	129/131 (98%)	102 (79%)	27 (21%)	0	100	100
3	CM	129/131 (98%)	113 (88%)	15 (12%)	1 (1%)	16	49
3	CN	129/131 (98%)	110 (85%)	18 (14%)	1 (1%)	16	49
3	CO	129/131 (98%)	107 (83%)	19 (15%)	3 (2%)	5	30
3	CP	129/131 (98%)	108 (84%)	19 (15%)	2 (2%)	7	36
3	CQ	129/131 (98%)	110 (85%)	17 (13%)	2 (2%)	7	36
3	CR	129/131 (98%)	113 (88%)	15 (12%)	1 (1%)	16	49
3	CS	129/131 (98%)	117 (91%)	12 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CT	129/131 (98%)	106 (82%)	21 (16%)	2 (2%)	7	36
3	D	129/131 (98%)	110 (85%)	18 (14%)	1 (1%)	16	49
3	E	129/131 (98%)	108 (84%)	18 (14%)	3 (2%)	5	30
3	G	129/131 (98%)	113 (88%)	16 (12%)	0	100	100
3	H	129/131 (98%)	112 (87%)	16 (12%)	1 (1%)	16	49
3	I	129/131 (98%)	106 (82%)	21 (16%)	2 (2%)	7	36
3	J	129/131 (98%)	110 (85%)	16 (12%)	3 (2%)	5	30
3	K	129/131 (98%)	109 (84%)	20 (16%)	0	100	100
3	L	129/131 (98%)	109 (84%)	20 (16%)	0	100	100
3	M	129/131 (98%)	106 (82%)	19 (15%)	4 (3%)	3	25
3	N	129/131 (98%)	106 (82%)	22 (17%)	1 (1%)	16	49
3	O	129/131 (98%)	106 (82%)	18 (14%)	5 (4%)	2	20
3	P	129/131 (98%)	110 (85%)	17 (13%)	2 (2%)	7	36
3	Q	129/131 (98%)	110 (85%)	17 (13%)	2 (2%)	7	36
3	R	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	S	129/131 (98%)	109 (84%)	18 (14%)	2 (2%)	7	36
3	T	129/131 (98%)	107 (83%)	21 (16%)	1 (1%)	16	49
3	U	129/131 (98%)	114 (88%)	15 (12%)	0	100	100
3	V	129/131 (98%)	110 (85%)	19 (15%)	0	100	100
3	W	129/131 (98%)	108 (84%)	20 (16%)	1 (1%)	16	49
3	X	129/131 (98%)	113 (88%)	15 (12%)	1 (1%)	16	49
3	Y	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49
3	Z	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	a	129/131 (98%)	107 (83%)	21 (16%)	1 (1%)	16	49
3	b	129/131 (98%)	104 (81%)	20 (16%)	5 (4%)	2	20
3	c	129/131 (98%)	111 (86%)	18 (14%)	0	100	100
3	d	129/131 (98%)	114 (88%)	15 (12%)	0	100	100
3	e	129/131 (98%)	107 (83%)	20 (16%)	2 (2%)	7	36
3	f	129/131 (98%)	112 (87%)	15 (12%)	2 (2%)	7	36
3	g	129/131 (98%)	114 (88%)	14 (11%)	1 (1%)	16	49
3	h	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	i	129/131 (98%)	113 (88%)	12 (9%)	4 (3%)	3	25
3	j	129/131 (98%)	105 (81%)	23 (18%)	1 (1%)	16	49
3	k	129/131 (98%)	113 (88%)	15 (12%)	1 (1%)	16	49
3	l	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	m	129/131 (98%)	106 (82%)	21 (16%)	2 (2%)	7	36
3	n	129/131 (98%)	111 (86%)	17 (13%)	1 (1%)	16	49
3	o	129/131 (98%)	105 (81%)	24 (19%)	0	100	100
3	p	129/131 (98%)	109 (84%)	20 (16%)	0	100	100
3	q	129/131 (98%)	101 (78%)	26 (20%)	2 (2%)	7	36
3	r	129/131 (98%)	110 (85%)	18 (14%)	1 (1%)	16	49
3	s	129/131 (98%)	112 (87%)	17 (13%)	0	100	100
3	t	129/131 (98%)	112 (87%)	17 (13%)	0	100	100
3	u	129/131 (98%)	110 (85%)	18 (14%)	1 (1%)	16	49
3	v	129/131 (98%)	112 (87%)	16 (12%)	1 (1%)	16	49
3	w	129/131 (98%)	112 (87%)	16 (12%)	1 (1%)	16	49
3	x	129/131 (98%)	114 (88%)	15 (12%)	0	100	100
3	y	129/131 (98%)	111 (86%)	16 (12%)	2 (2%)	7	36
3	z	129/131 (98%)	108 (84%)	20 (16%)	1 (1%)	16	49
All	All	23367/23724 (98%)	19879 (85%)	3212 (14%)	276 (1%)	13	41

5 of 276 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	1	13	ALA
3	O	96	ARG
3	Y	13	ALA
3	Z	13	ALA
3	b	15	PRO

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	354/354 (100%)	354 (100%)	0	100	100
3	0	118/118 (100%)	118 (100%)	0	100	100
3	1	118/118 (100%)	118 (100%)	0	100	100
3	2	118/118 (100%)	118 (100%)	0	100	100
3	3	118/118 (100%)	118 (100%)	0	100	100
3	4	118/118 (100%)	118 (100%)	0	100	100
3	5	118/118 (100%)	118 (100%)	0	100	100
3	6	118/118 (100%)	118 (100%)	0	100	100
3	7	118/118 (100%)	118 (100%)	0	100	100
3	8	118/118 (100%)	118 (100%)	0	100	100
3	9	118/118 (100%)	118 (100%)	0	100	100
3	A	118/118 (100%)	117 (99%)	1 (1%)	73	77
3	A0	118/118 (100%)	118 (100%)	0	100	100
3	A1	118/118 (100%)	118 (100%)	0	100	100
3	A2	118/118 (100%)	118 (100%)	0	100	100
3	A3	118/118 (100%)	117 (99%)	1 (1%)	73	77
3	A4	118/118 (100%)	117 (99%)	1 (1%)	73	77
3	A5	118/118 (100%)	118 (100%)	0	100	100
3	A6	118/118 (100%)	118 (100%)	0	100	100
3	A7	118/118 (100%)	118 (100%)	0	100	100
3	A8	118/118 (100%)	118 (100%)	0	100	100
3	A9	118/118 (100%)	118 (100%)	0	100	100
3	AA	118/118 (100%)	118 (100%)	0	100	100
3	AB	118/118 (100%)	118 (100%)	0	100	100
3	AC	118/118 (100%)	118 (100%)	0	100	100
3	AD	118/118 (100%)	118 (100%)	0	100	100
3	AO	118/118 (100%)	118 (100%)	0	100	100
3	AP	118/118 (100%)	118 (100%)	0	100	100
3	AQ	118/118 (100%)	118 (100%)	0	100	100
3	AR	118/118 (100%)	118 (100%)	0	100	100
3	AS	118/118 (100%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AT	118/118 (100%)	118 (100%)	0	100	100
3	AU	118/118 (100%)	118 (100%)	0	100	100
3	AV	118/118 (100%)	118 (100%)	0	100	100
3	AW	118/118 (100%)	118 (100%)	0	100	100
3	AX	118/118 (100%)	118 (100%)	0	100	100
3	AY	118/118 (100%)	118 (100%)	0	100	100
3	AZ	118/118 (100%)	118 (100%)	0	100	100
3	Aa	118/118 (100%)	118 (100%)	0	100	100
3	Ab	118/118 (100%)	118 (100%)	0	100	100
3	Ac	118/118 (100%)	118 (100%)	0	100	100
3	Ad	118/118 (100%)	118 (100%)	0	100	100
3	Ae	118/118 (100%)	118 (100%)	0	100	100
3	Af	118/118 (100%)	118 (100%)	0	100	100
3	Ag	118/118 (100%)	118 (100%)	0	100	100
3	Ah	118/118 (100%)	118 (100%)	0	100	100
3	Ai	118/118 (100%)	118 (100%)	0	100	100
3	Aj	118/118 (100%)	118 (100%)	0	100	100
3	Ak	118/118 (100%)	118 (100%)	0	100	100
3	Al	118/118 (100%)	118 (100%)	0	100	100
3	Am	118/118 (100%)	118 (100%)	0	100	100
3	An	118/118 (100%)	118 (100%)	0	100	100
3	Ao	118/118 (100%)	118 (100%)	0	100	100
3	Ap	118/118 (100%)	118 (100%)	0	100	100
3	Aq	118/118 (100%)	118 (100%)	0	100	100
3	Ar	118/118 (100%)	118 (100%)	0	100	100
3	As	118/118 (100%)	118 (100%)	0	100	100
3	At	118/118 (100%)	118 (100%)	0	100	100
3	Au	118/118 (100%)	118 (100%)	0	100	100
3	Av	118/118 (100%)	118 (100%)	0	100	100
3	Aw	118/118 (100%)	118 (100%)	0	100	100
3	Ax	118/118 (100%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Ay	118/118 (100%)	118 (100%)	0	100	100
3	Az	118/118 (100%)	118 (100%)	0	100	100
3	B	118/118 (100%)	118 (100%)	0	100	100
3	B0	118/118 (100%)	118 (100%)	0	100	100
3	B1	118/118 (100%)	118 (100%)	0	100	100
3	B2	118/118 (100%)	118 (100%)	0	100	100
3	B3	118/118 (100%)	118 (100%)	0	100	100
3	B4	118/118 (100%)	118 (100%)	0	100	100
3	B5	118/118 (100%)	118 (100%)	0	100	100
3	B6	118/118 (100%)	118 (100%)	0	100	100
3	B7	118/118 (100%)	117 (99%)	1 (1%)	73	77
3	B8	118/118 (100%)	118 (100%)	0	100	100
3	B9	118/118 (100%)	118 (100%)	0	100	100
3	BA	119/118 (101%)	119 (100%)	0	100	100
3	BB	118/118 (100%)	118 (100%)	0	100	100
3	BC	118/118 (100%)	118 (100%)	0	100	100
3	BD	118/118 (100%)	118 (100%)	0	100	100
3	BE	118/118 (100%)	118 (100%)	0	100	100
3	BF	118/118 (100%)	118 (100%)	0	100	100
3	BG	118/118 (100%)	118 (100%)	0	100	100
3	BH	118/118 (100%)	117 (99%)	1 (1%)	73	77
3	BI	118/118 (100%)	118 (100%)	0	100	100
3	BJ	118/118 (100%)	118 (100%)	0	100	100
3	BK	118/118 (100%)	118 (100%)	0	100	100
3	BL	118/118 (100%)	118 (100%)	0	100	100
3	BM	118/118 (100%)	118 (100%)	0	100	100
3	BN	118/118 (100%)	118 (100%)	0	100	100
3	BO	118/118 (100%)	118 (100%)	0	100	100
3	BP	118/118 (100%)	118 (100%)	0	100	100
3	BQ	118/118 (100%)	118 (100%)	0	100	100
3	BR	118/118 (100%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	BS	118/118 (100%)	118 (100%)	0	100	100
3	BV	118/118 (100%)	118 (100%)	0	100	100
3	BY	118/118 (100%)	118 (100%)	0	100	100
3	BZ	118/118 (100%)	118 (100%)	0	100	100
3	Bb	118/118 (100%)	118 (100%)	0	100	100
3	Bc	118/118 (100%)	118 (100%)	0	100	100
3	Bd	118/118 (100%)	118 (100%)	0	100	100
3	Bg	118/118 (100%)	118 (100%)	0	100	100
3	Bh	118/118 (100%)	118 (100%)	0	100	100
3	Bi	118/118 (100%)	118 (100%)	0	100	100
3	Bj	118/118 (100%)	118 (100%)	0	100	100
3	Bk	118/118 (100%)	118 (100%)	0	100	100
3	Bl	118/118 (100%)	118 (100%)	0	100	100
3	Bm	118/118 (100%)	118 (100%)	0	100	100
3	Bn	118/118 (100%)	118 (100%)	0	100	100
3	Bu	118/118 (100%)	118 (100%)	0	100	100
3	Bv	118/118 (100%)	118 (100%)	0	100	100
3	Bw	118/118 (100%)	118 (100%)	0	100	100
3	Bx	118/118 (100%)	118 (100%)	0	100	100
3	By	118/118 (100%)	118 (100%)	0	100	100
3	Bz	118/118 (100%)	117 (99%)	1 (1%)	73	77
3	C	118/118 (100%)	118 (100%)	0	100	100
3	CA	118/118 (100%)	118 (100%)	0	100	100
3	CB	118/118 (100%)	118 (100%)	0	100	100
3	CC	118/118 (100%)	118 (100%)	0	100	100
3	CD	118/118 (100%)	118 (100%)	0	100	100
3	CH	118/118 (100%)	118 (100%)	0	100	100
3	CI	118/118 (100%)	118 (100%)	0	100	100
3	CK	118/118 (100%)	118 (100%)	0	100	100
3	CL	118/118 (100%)	117 (99%)	1 (1%)	73	77
3	CM	118/118 (100%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CN	118/118 (100%)	118 (100%)	0	100	100
3	CO	118/118 (100%)	118 (100%)	0	100	100
3	CP	118/118 (100%)	118 (100%)	0	100	100
3	CQ	118/118 (100%)	118 (100%)	0	100	100
3	CR	118/118 (100%)	118 (100%)	0	100	100
3	CS	118/118 (100%)	118 (100%)	0	100	100
3	CT	118/118 (100%)	118 (100%)	0	100	100
3	D	118/118 (100%)	118 (100%)	0	100	100
3	E	118/118 (100%)	118 (100%)	0	100	100
3	G	118/118 (100%)	118 (100%)	0	100	100
3	H	118/118 (100%)	118 (100%)	0	100	100
3	I	118/118 (100%)	118 (100%)	0	100	100
3	J	118/118 (100%)	116 (98%)	2 (2%)	53	70
3	K	118/118 (100%)	118 (100%)	0	100	100
3	L	118/118 (100%)	118 (100%)	0	100	100
3	M	118/118 (100%)	118 (100%)	0	100	100
3	N	118/118 (100%)	118 (100%)	0	100	100
3	O	118/118 (100%)	118 (100%)	0	100	100
3	P	118/118 (100%)	118 (100%)	0	100	100
3	Q	118/118 (100%)	118 (100%)	0	100	100
3	R	118/118 (100%)	118 (100%)	0	100	100
3	S	118/118 (100%)	118 (100%)	0	100	100
3	T	118/118 (100%)	118 (100%)	0	100	100
3	U	118/118 (100%)	118 (100%)	0	100	100
3	V	118/118 (100%)	118 (100%)	0	100	100
3	W	118/118 (100%)	118 (100%)	0	100	100
3	X	118/118 (100%)	118 (100%)	0	100	100
3	Y	118/118 (100%)	118 (100%)	0	100	100
3	Z	118/118 (100%)	118 (100%)	0	100	100
3	a	118/118 (100%)	118 (100%)	0	100	100
3	b	118/118 (100%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	c	118/118 (100%)	118 (100%)	0	100	100
3	d	118/118 (100%)	118 (100%)	0	100	100
3	e	118/118 (100%)	118 (100%)	0	100	100
3	f	118/118 (100%)	118 (100%)	0	100	100
3	g	118/118 (100%)	118 (100%)	0	100	100
3	h	118/118 (100%)	118 (100%)	0	100	100
3	i	118/118 (100%)	118 (100%)	0	100	100
3	j	118/118 (100%)	118 (100%)	0	100	100
3	k	118/118 (100%)	118 (100%)	0	100	100
3	l	118/118 (100%)	118 (100%)	0	100	100
3	m	118/118 (100%)	118 (100%)	0	100	100
3	n	118/118 (100%)	118 (100%)	0	100	100
3	o	118/118 (100%)	118 (100%)	0	100	100
3	p	118/118 (100%)	118 (100%)	0	100	100
3	q	118/118 (100%)	118 (100%)	0	100	100
3	r	118/118 (100%)	118 (100%)	0	100	100
3	s	118/118 (100%)	118 (100%)	0	100	100
3	t	118/118 (100%)	118 (100%)	0	100	100
3	u	118/118 (100%)	118 (100%)	0	100	100
3	v	118/118 (100%)	118 (100%)	0	100	100
3	w	118/118 (100%)	118 (100%)	0	100	100
3	x	118/118 (100%)	118 (100%)	0	100	100
3	y	118/118 (100%)	118 (100%)	0	100	100
3	z	118/118 (100%)	118 (100%)	0	100	100
All	All	21359/21358 (100%)	21350 (100%)	9 (0%)	100	100

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B7	40	ILE
3	CL	65	VAL
3	A3	2	GLN
3	A4	40	ILE
3	BH	65	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 350 such sidechains are listed below:

Mol	Chain	Res	Type
3	BG	69	GLN
3	Bw	69	GLN
3	BK	2	GLN
3	Bc	104	ASN
3	B4	54	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	AE	131/132 (99%)	18 (13%)	1 (0%)

5 of 18 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	AE	558	C
2	AE	561	A
2	AE	563	A
2	AE	570	U
2	AE	583	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	AE	609	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

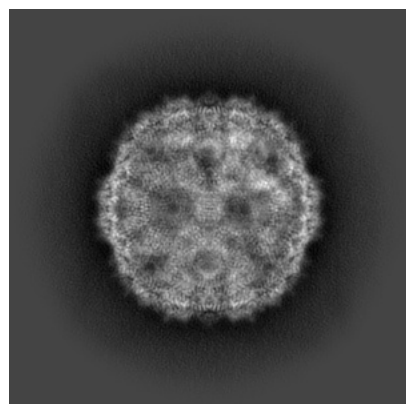
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75020. These allow visual inspection of the internal detail of the map and identification of artifacts.

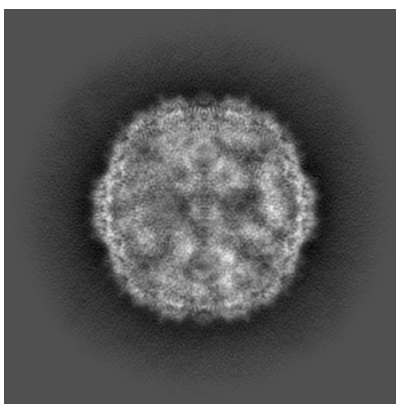
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

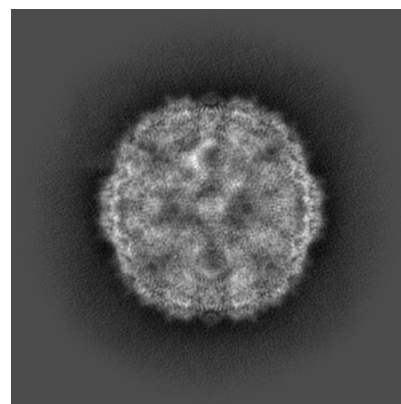
6.1.1 Primary map



X

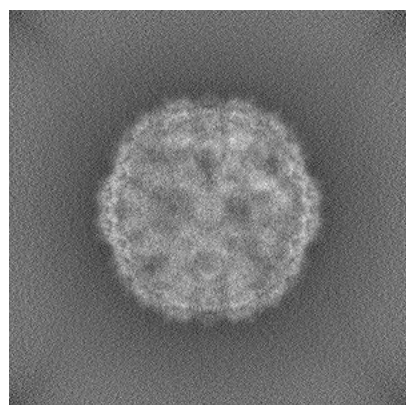


Y

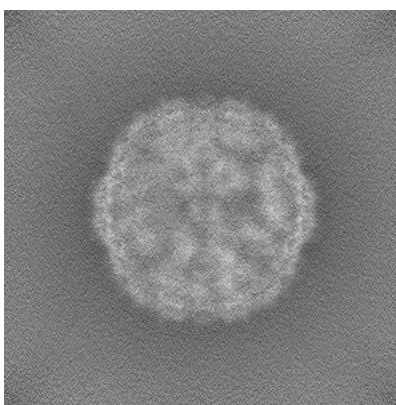


Z

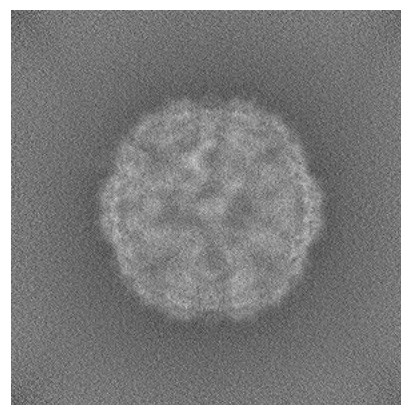
6.1.2 Raw map



X



Y

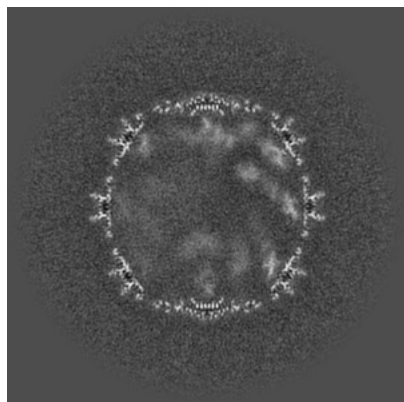


Z

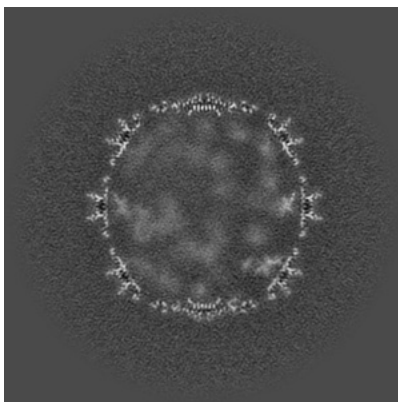
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

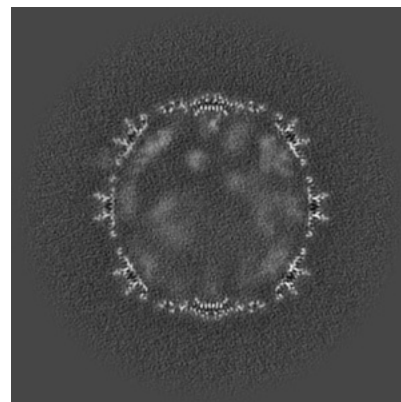
6.2.1 Primary map



X Index: 300

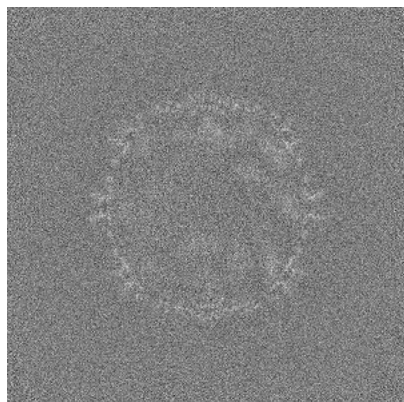


Y Index: 300

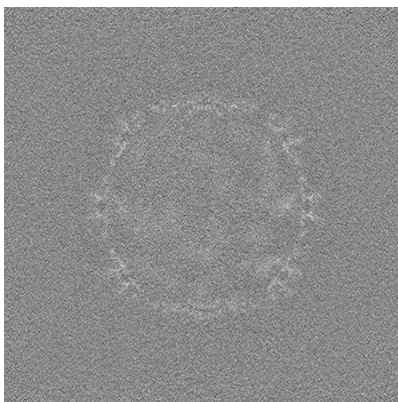


Z Index: 300

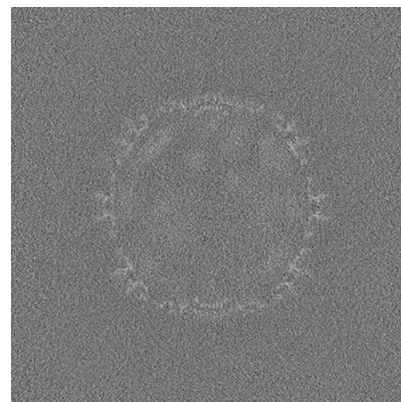
6.2.2 Raw map



X Index: 300



Y Index: 300

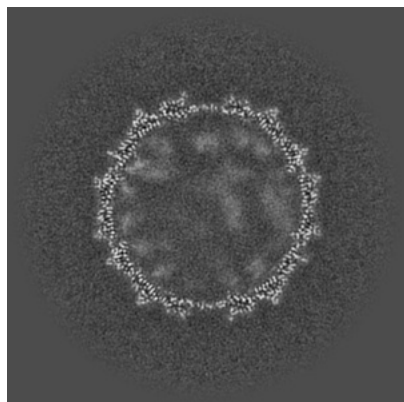


Z Index: 300

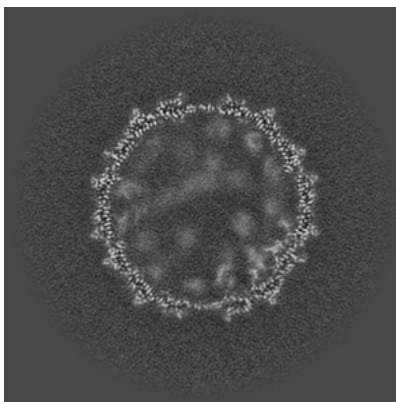
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

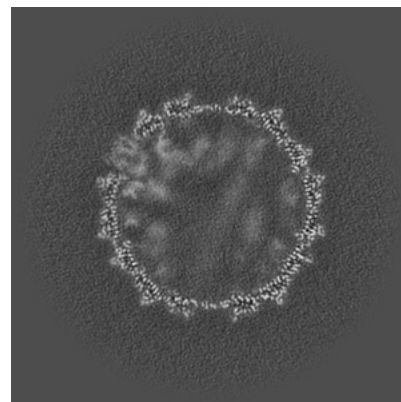
6.3.1 Primary map



X Index: 338

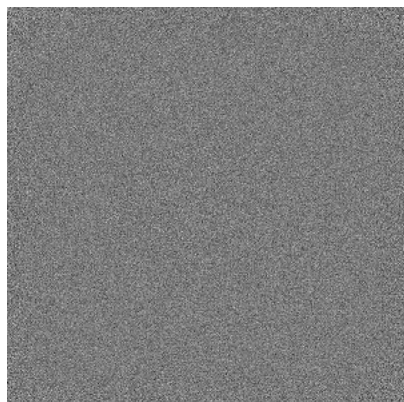


Y Index: 338

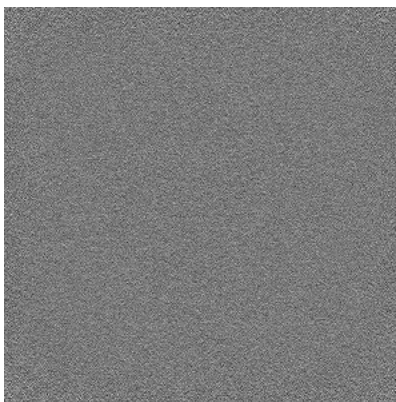


Z Index: 338

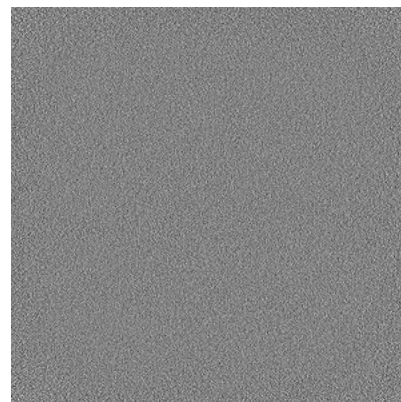
6.3.2 Raw map



X Index: 0



Y Index: 0

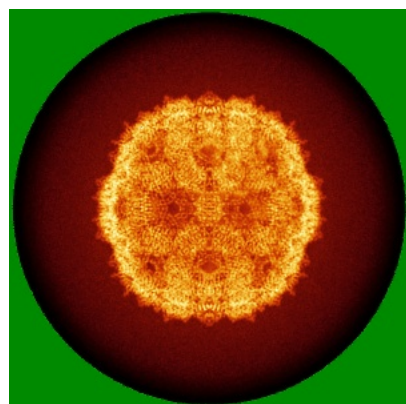


Z Index: 0

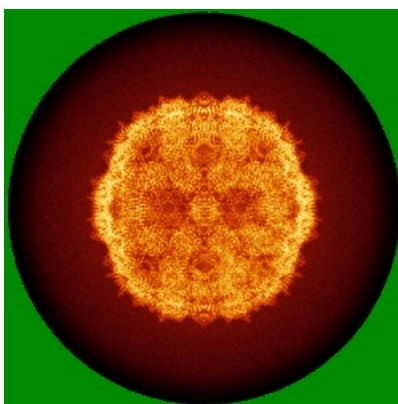
The images above show the largest variance slices of the map in three orthogonal directions.

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

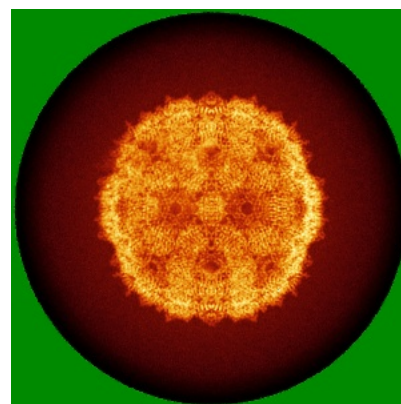
6.4.1 Primary map



X

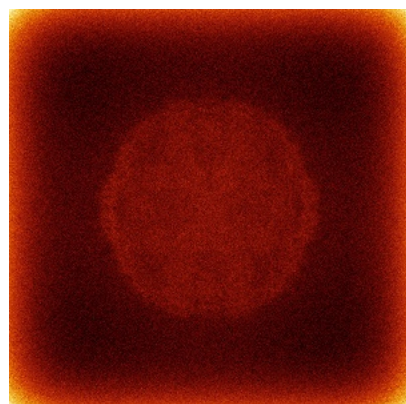


Y

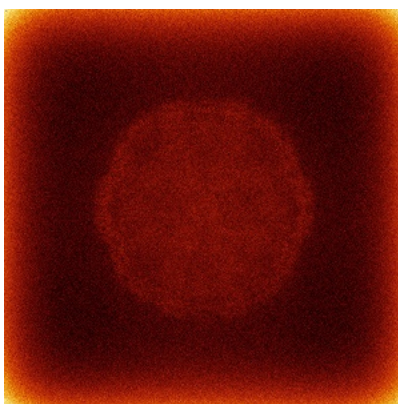


Z

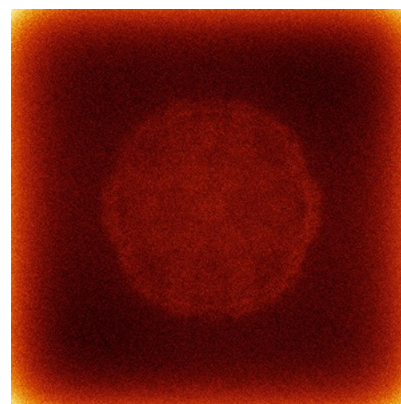
6.4.2 Raw map



X



Y

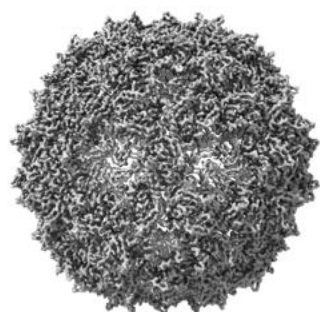


Z

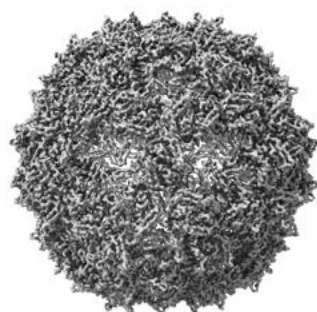
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

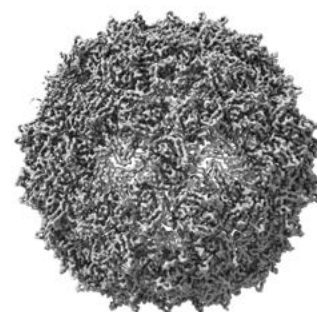
6.5.1 Primary map



X



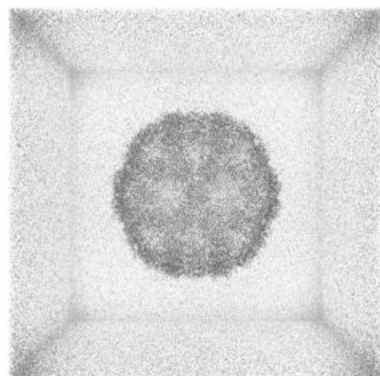
Y



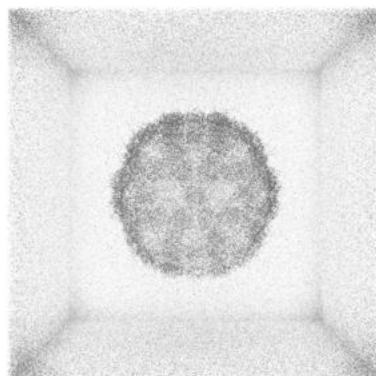
Z

The images above show the 3D surface view of the map at the recommended contour level 0.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

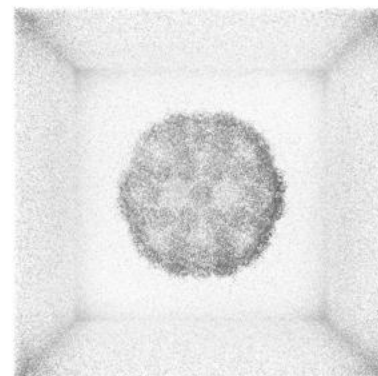
6.5.2 Raw map



X



Y



Z

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

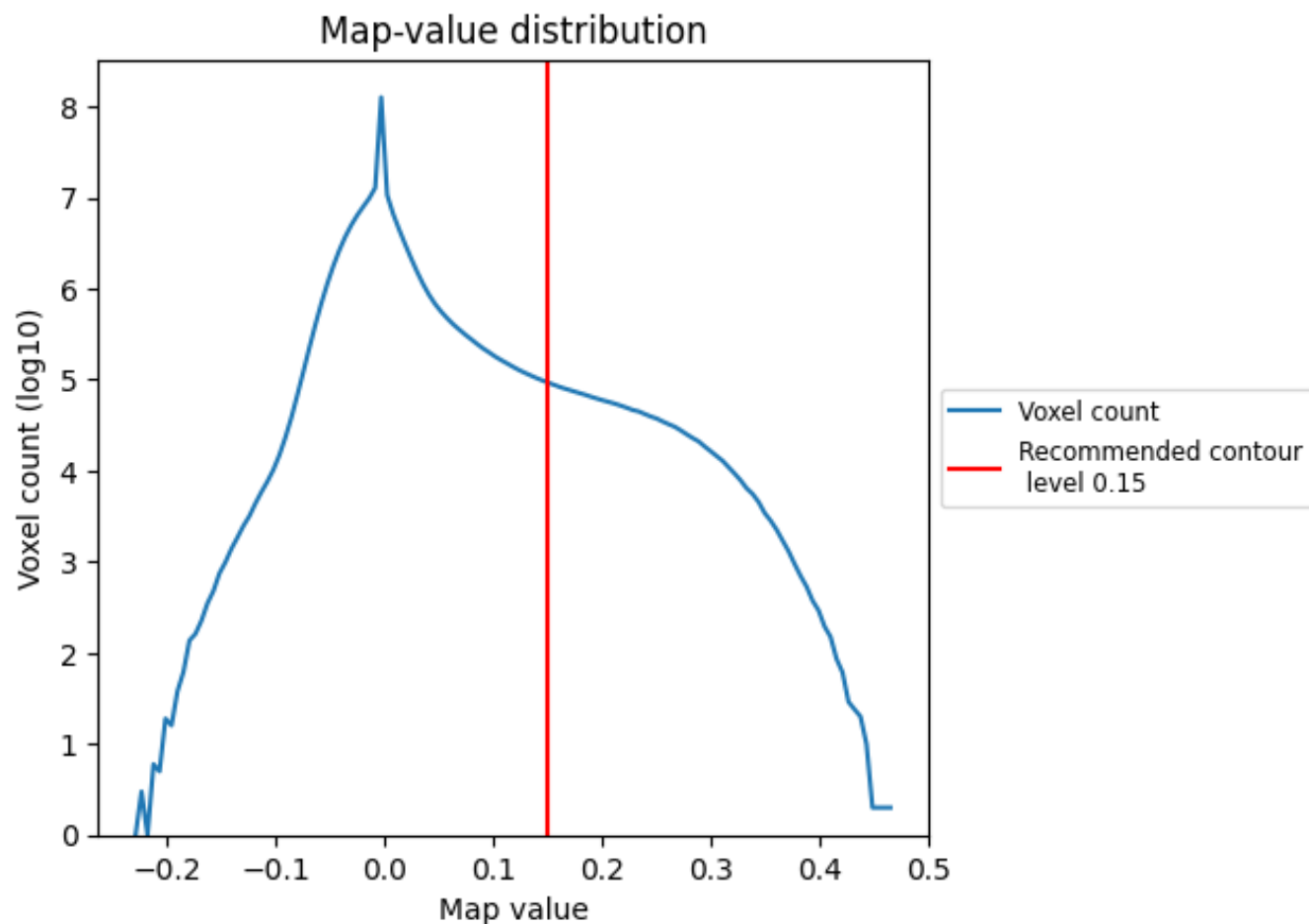
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

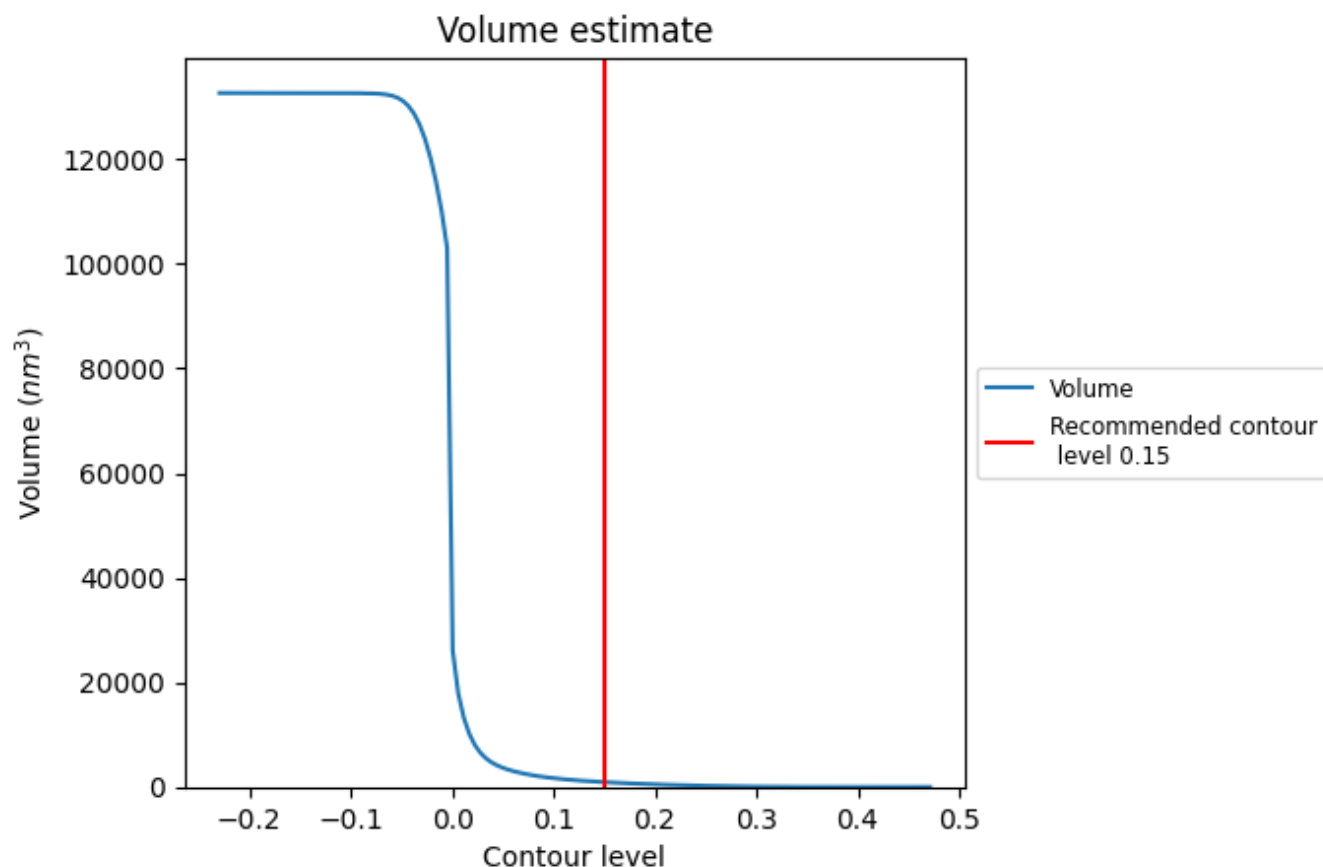
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

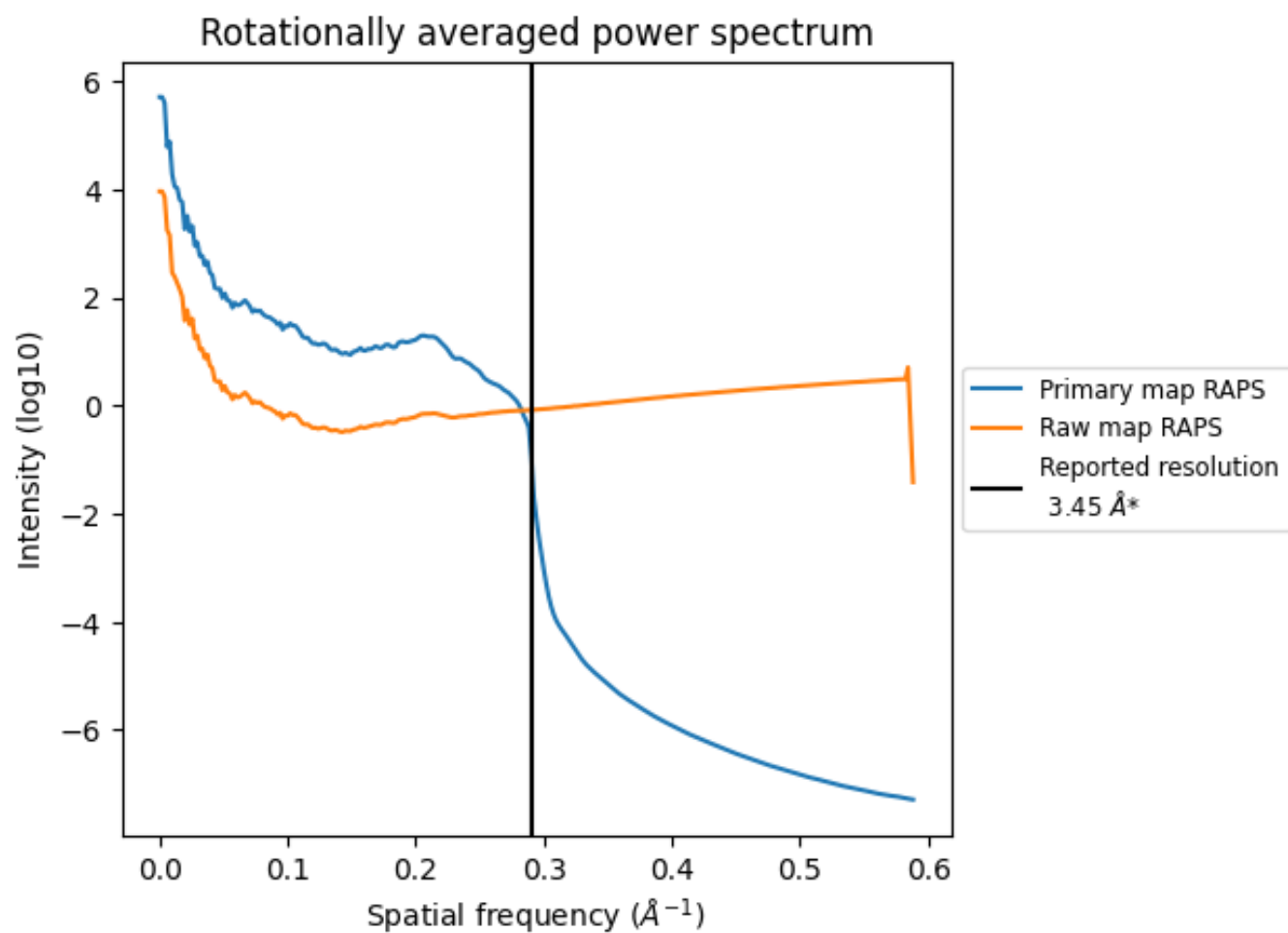
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 924 nm^3 ; this corresponds to an approximate mass of 835 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

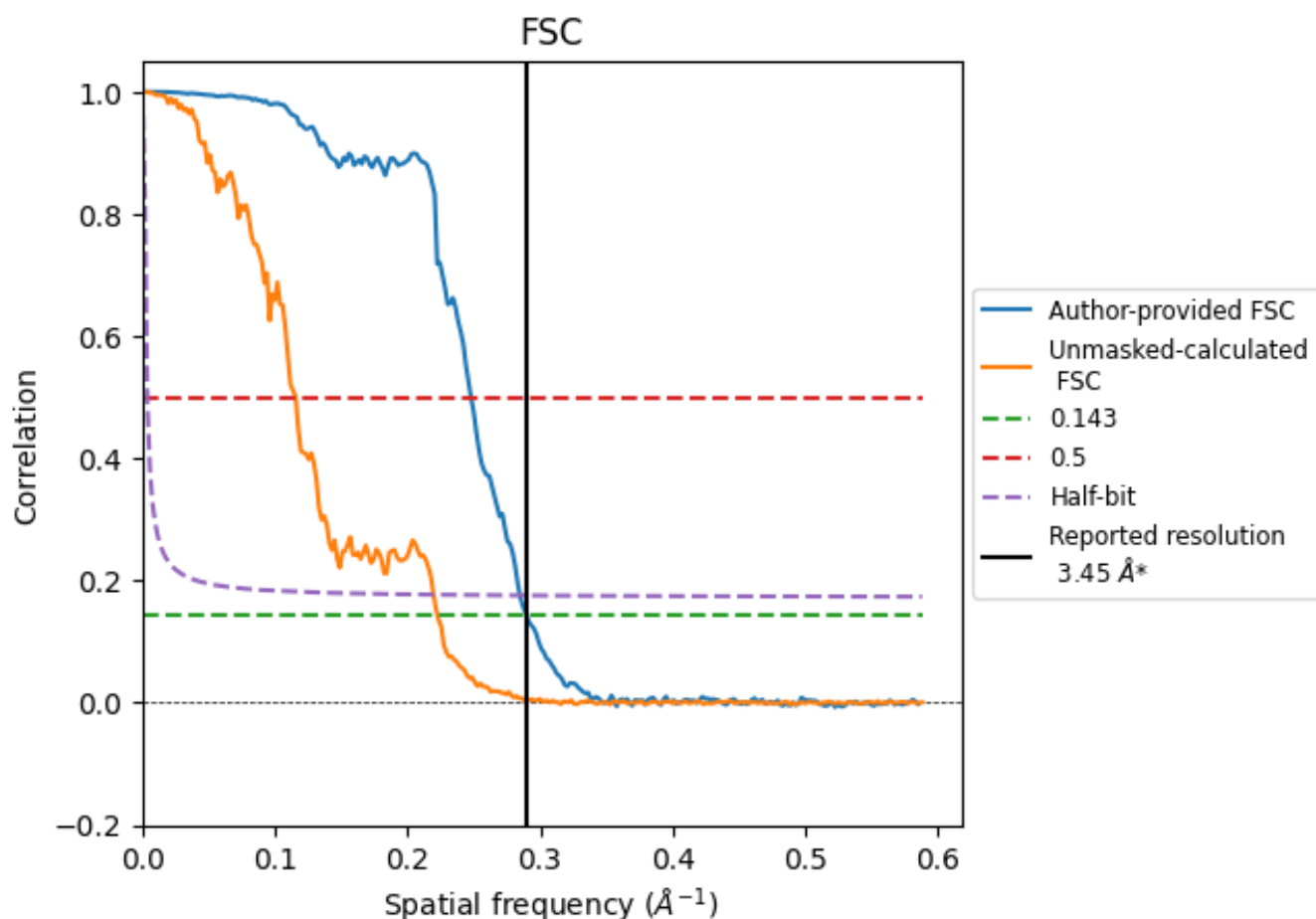


*Reported resolution corresponds to spatial frequency of 0.290 \AA^{-1}

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 0.290 Å⁻¹

8.2 Resolution estimates [i](#)

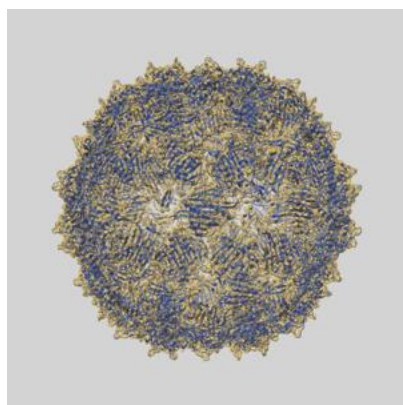
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.45	-	-
Author-provided FSC curve	3.45	4.03	3.51
Unmasked-calculated*	4.49	8.64	4.55

*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 4.49 differs from the reported value 3.45 by more than 10 %

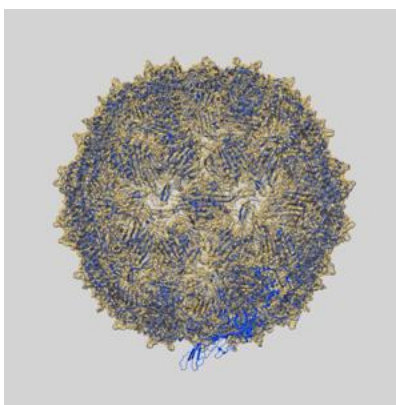
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75020 and PDB model 9ZZY. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

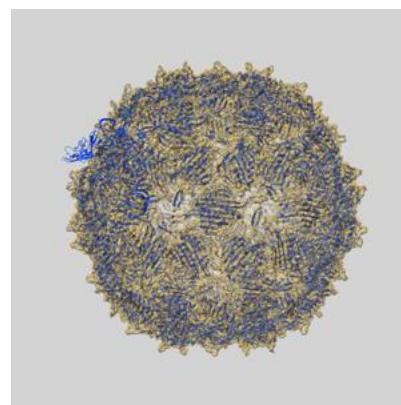
9.1 Map-model overlay [i](#)



X



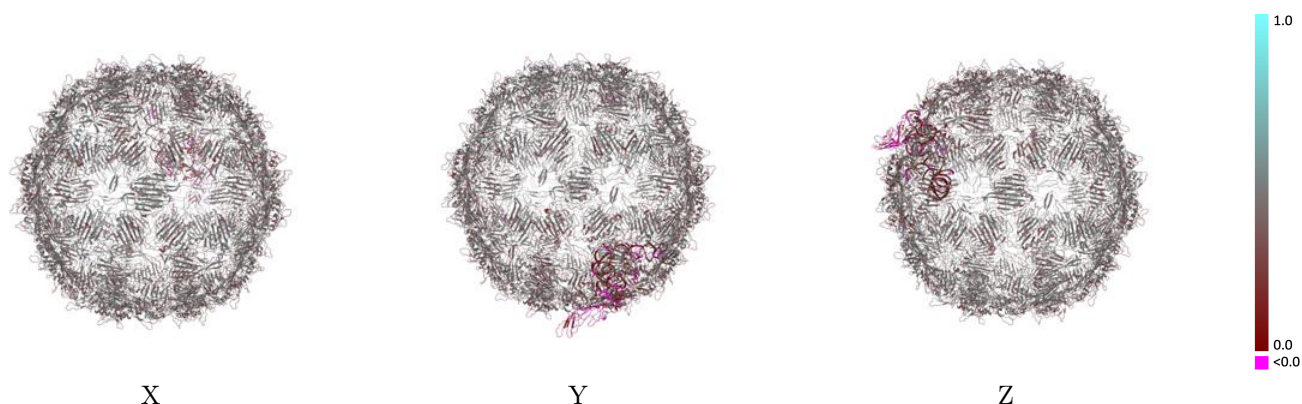
Y



Z

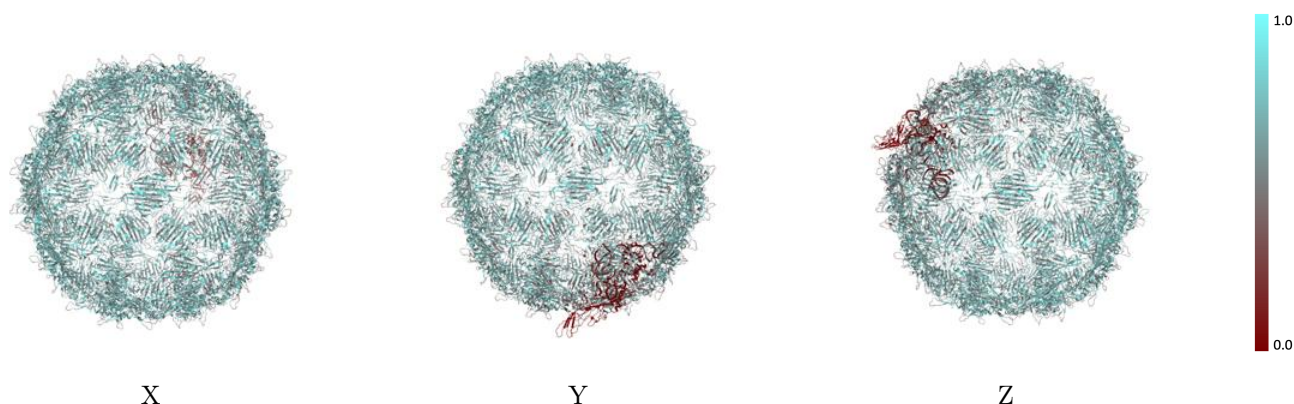
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



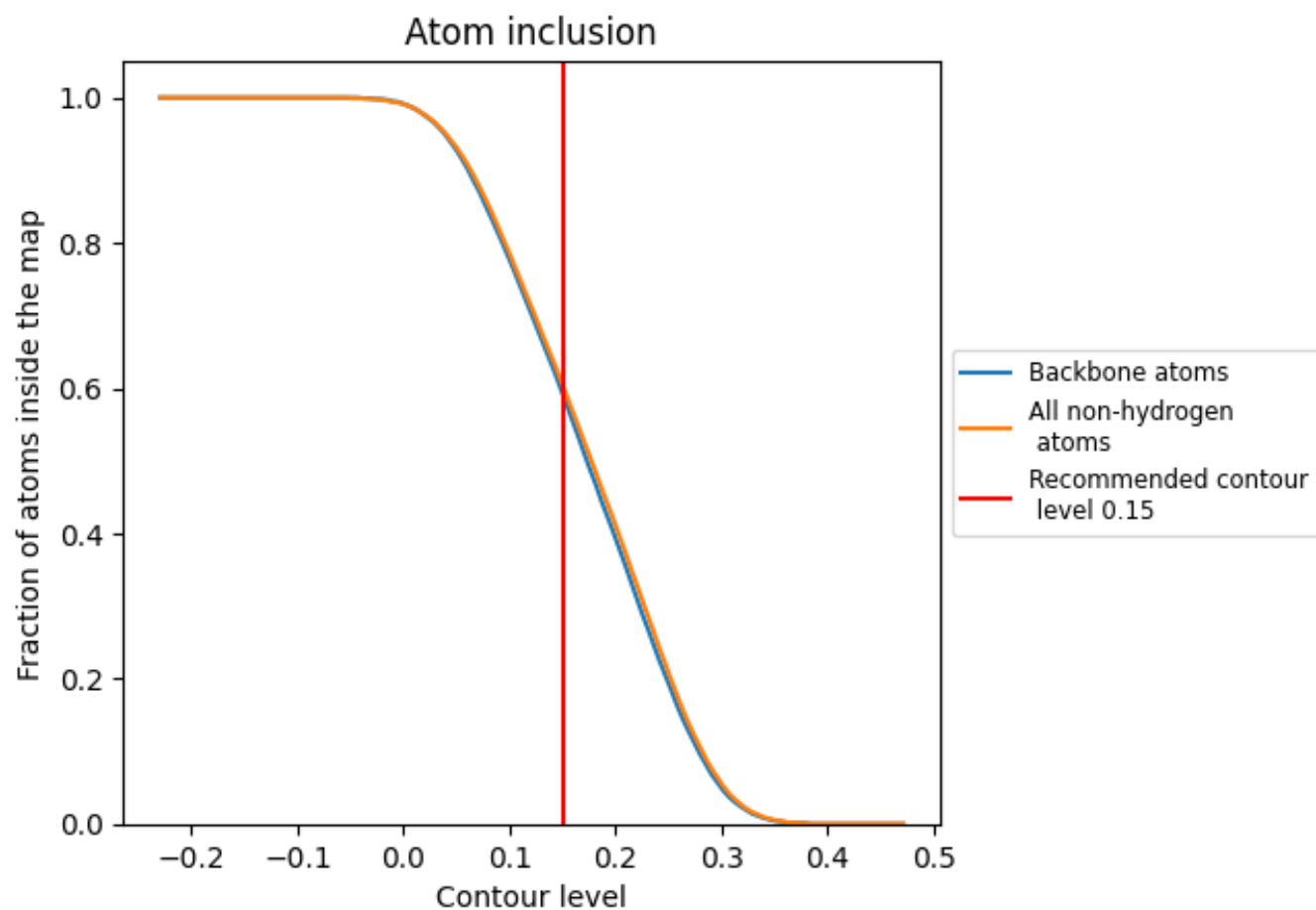
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6050	 0.4020
0	 0.6000	 0.4110
1	 0.6520	 0.4520
2	 0.6180	 0.4280
3	 0.6070	 0.4090
4	 0.5890	 0.3940
5	 0.6440	 0.4260
6	 0.6400	 0.4300
7	 0.6020	 0.4080
8	 0.6070	 0.3870
9	 0.6000	 0.4050
A	 0.6510	 0.4190
A0	 0.6580	 0.4150
A1	 0.6340	 0.4180
A2	 0.6000	 0.3950
A3	 0.6190	 0.4150
A4	 0.6250	 0.3920
A5	 0.6270	 0.4080
A6	 0.6520	 0.4370
A7	 0.6510	 0.4330
A8	 0.6170	 0.3880
A9	 0.6470	 0.4260
AA	 0.6290	 0.4230
AB	 0.6120	 0.3860
AC	 0.6220	 0.4280
AD	 0.6250	 0.4190
AE	 0.2160	 0.1120
AO	 0.6290	 0.4060
AP	 0.6190	 0.3850
AQ	 0.6240	 0.4360
AR	 0.6440	 0.4300
AS	 0.6370	 0.4250
AT	 0.6130	 0.3960
AU	 0.6520	 0.4340
AV	 0.6360	 0.4090























































































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Chain	Atom inclusion	Q-score
AW	 0.6340	 0.4180
AX	 0.6450	 0.4270
AY	 0.6110	 0.4080
AZ	 0.6090	 0.3900
Aa	 0.6130	 0.4120
Ab	 0.6180	 0.4350
Ac	 0.5950	 0.4020
Ad	 0.5890	 0.3940
Ae	 0.6030	 0.4260
Af	 0.5780	 0.3830
Ag	 0.5450	 0.4020
Ah	 0.5800	 0.4080
Ai	 0.6050	 0.4270
Aj	 0.6020	 0.3980
Ak	 0.6100	 0.3940
Al	 0.6200	 0.4240
Am	 0.6090	 0.4080
An	 0.6070	 0.4010
Ao	 0.5980	 0.4060
Ap	 0.5790	 0.3670
Aq	 0.5760	 0.4070
Ar	 0.6200	 0.4220
As	 0.6350	 0.4220
At	 0.6450	 0.4180
Au	 0.6310	 0.4070
Av	 0.6250	 0.4030
Aw	 0.6280	 0.4290
Ax	 0.6330	 0.4350
Ay	 0.6430	 0.4310
Az	 0.6490	 0.4030
B	 0.6190	 0.3760
B0	 0.5670	 0.3580
B1	 0.6310	 0.4230
B2	 0.6240	 0.3990
B3	 0.5990	 0.4060
B4	 0.6020	 0.3940
B5	 0.6260	 0.4050
B6	 0.6130	 0.3910
B7	 0.6200	 0.4240
B8	 0.6050	 0.3970
B9	 0.5800	 0.3840
BA	 0.6730	 0.4280





















































































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Chain	Atom inclusion	Q-score
BB	 0.6490	 0.3920
BC	 0.6840	 0.4510
BD	 0.6570	 0.4440
BE	 0.6610	 0.4220
BF	 0.6350	 0.4020
BG	 0.6070	 0.4080
BH	 0.5850	 0.3930
BI	 0.5980	 0.4160
BJ	 0.6040	 0.4080
BK	 0.6180	 0.4100
BL	 0.6290	 0.4150
BM	 0.6210	 0.4120
BN	 0.6120	 0.3950
BO	 0.6350	 0.4200
BP	 0.6320	 0.4250
BQ	 0.6440	 0.4310
BR	 0.6270	 0.3940
BS	 0.6260	 0.4160
BV	 0.6390	 0.4000
BY	 0.6510	 0.4410
BZ	 0.6240	 0.4310
Bb	 0.6030	 0.3900
Bc	 0.6400	 0.4220
Bd	 0.6230	 0.4220
Bg	 0.6180	 0.4190
Bh	 0.6170	 0.4180
Bi	 0.6310	 0.4270
Bj	 0.6380	 0.4010
Bk	 0.6480	 0.4200
Bl	 0.6560	 0.4100
Bm	 0.6350	 0.4200
Bn	 0.6240	 0.3780
Bu	 0.6490	 0.4250
Bv	 0.6360	 0.4200
Bw	 0.6520	 0.4290
Bx	 0.6200	 0.4140
By	 0.6600	 0.4320
Bz	 0.6360	 0.3870
C	 0.6740	 0.4370
CA	 0.6400	 0.4310
CB	 0.6200	 0.3940
CC	 0.5850	 0.4070









































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Chain	Atom inclusion	Q-score
CD	 0.6120	 0.3870
CH	 0.6190	 0.3990
CI	 0.6310	 0.4260
CK	 0.5140	 0.3640
CL	 0.5090	 0.3850
CM	 0.4550	 0.3660
CN	 0.5430	 0.3820
CO	 0.5760	 0.3960
CP	 0.5620	 0.3760
CQ	 0.4870	 0.3880
CR	 0.5070	 0.3820
CS	 0.4580	 0.3710
CT	 0.5680	 0.3850
D	 0.6400	 0.4240
E	 0.6420	 0.4310
F	 0.0340	 0.0810
G	 0.6580	 0.4460
H	 0.6620	 0.4390
I	 0.6230	 0.4150
J	 0.6090	 0.3890
K	 0.6260	 0.4260
L	 0.6630	 0.4410
M	 0.6550	 0.4290
N	 0.6330	 0.3850
O	 0.6330	 0.3860
P	 0.6390	 0.3990
Q	 0.6590	 0.4310
R	 0.6460	 0.4210
S	 0.6550	 0.4340
T	 0.6520	 0.4040
U	 0.6720	 0.4500
V	 0.6490	 0.4410
W	 0.6540	 0.4240
X	 0.6180	 0.3920
Y	 0.6330	 0.4330
Z	 0.6600	 0.4420
a	 0.6410	 0.4270
b	 0.6290	 0.3920
c	 0.6340	 0.4450
d	 0.6440	 0.4340
e	 0.6430	 0.4240
f	 0.6430	 0.4080

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Chain	Atom inclusion	Q-score
g	 0.6540	 0.4340
h	 0.6450	 0.4310
i	 0.6490	 0.4200
j	 0.6310	 0.4010
k	 0.6470	 0.4300
l	 0.6540	 0.4320
m	 0.6730	 0.4230
n	 0.6420	 0.4090
o	 0.6410	 0.4180
p	 0.6600	 0.4210
q	 0.6110	 0.4160
r	 0.6050	 0.3850
s	 0.6350	 0.4300
t	 0.6280	 0.4300
u	 0.6240	 0.4200
v	 0.6120	 0.4090
w	 0.6120	 0.4330
x	 0.6240	 0.4390
y	 0.6390	 0.4370
z	 0.6280	 0.4050