



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Apr 27, 2019 – 01:20 PM EDT

PDB ID : 6N4V
EMDB ID: : EMD-0344
Title : CryoEM structure of Leviviridae PP7 WT coat protein dimer capsid (PP7PP7-WT)
Authors : Liangjun, Z.; Kopylov, M.; Potter, C.S.; Carragher, B.; Finn, M.G.
Deposited on : 2018-11-20
Resolution : 3.00 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB 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.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031633

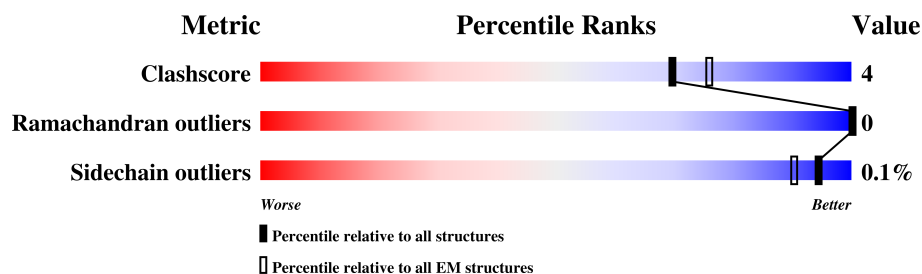
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain	
1	A	258	91%	9%
1	AA	258	89%	11%
1	AB	258	87%	13%
1	AC	258	90%	10%
1	AD	258	89%	11%
1	Af	258	100%	
1	B	258	90%	10%
1	BA	258	88%	12%
1	BB	258	88%	12%

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Mol	Chain	Length	Quality of chain	
1	BC	258	<div><div></div></div>	90% 10%
1	BD	258	<div><div></div></div>	83% 17%
1	C	258	<div><div></div></div>	88% 12%
1	CA	258	<div><div></div></div>	89% 11%
1	CB	258	<div><div></div></div>	87% 13%
1	CC	258	<div><div></div></div>	90% 10%
1	CD	258	<div><div></div></div>	84% 16%
1	D	258	<div><div></div></div>	89% 11%
1	DA	258	<div><div></div></div>	90% 10%
1	DB	258	<div><div></div></div>	88% 12%
1	DC	258	<div><div></div></div>	89% 11%
1	DD	258	<div><div></div></div>	84% 16%
1	E	258	<div><div></div></div>	89% 11%
1	EA	258	<div><div></div></div>	90% 10%
1	EB	258	<div><div></div></div>	88% 12%
1	EC	258	<div><div></div></div>	90% 10%
1	ED	258	<div><div></div></div>	89% 11%
1	F	258	<div><div></div></div>	87% 13%
1	FA	258	<div><div></div></div>	90% 10%
1	FB	258	<div><div></div></div>	88% 12%
1	FC	258	<div><div></div></div>	90% 10%
1	FD	258	<div><div></div></div>	87% 13%
1	G	258	<div><div></div></div>	86% 14%
1	GA	258	<div><div></div></div>	90% 10%
1	GB	258	<div><div></div></div>	88% 12%

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Mol	Chain	Length	Quality of chain	
1	GC	258	<div><div></div></div>	90% 10%
1	GD	258	<div><div></div></div>	87% 13%
1	H	258	<div><div></div></div>	85% 15%
1	HA	258	<div><div></div></div>	91% 9%
1	HB	258	<div><div></div></div>	89% 11%
1	HC	258	<div><div></div></div>	88% 12%
1	HD	258	<div><div></div></div>	86% 14%
1	I	258	<div><div></div></div>	90% 10%
1	IA	258	<div><div></div></div>	92% 8%
1	IB	258	<div><div></div></div>	89% 11%
1	IC	258	<div><div></div></div>	87% 13%
1	ID	258	<div><div></div></div>	85% 15%
1	J	258	<div><div></div></div>	90% 10%
1	JA	258	<div><div></div></div>	88% 12%
1	JB	258	<div><div></div></div>	91% 9%
1	JC	258	<div><div></div></div>	86% 14%
1	JD	258	<div><div></div></div>	84% 16%
1	K	258	<div><div></div></div>	88% 12%
1	KA	258	<div><div></div></div>	89% 11%
1	KB	258	<div><div></div></div>	92% 8%
1	KC	258	<div><div></div></div>	84% 16%
1	KD	258	<div><div></div></div>	86% 14%
1	L	258	<div><div></div></div>	88% 12%
1	LA	258	<div><div></div></div>	89% 11%
1	LB	258	<div><div></div></div>	91% 9%

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Mol	Chain	Length	Quality of chain	
1	LC	258	<div><div></div></div>	88% 12%
1	LD	258	<div><div></div></div>	84% 16%
1	M	258	<div><div></div></div>	89% 11%
1	MA	258	<div><div></div></div>	87% 13%
1	MB	258	<div><div></div></div>	91% 9%
1	MC	258	<div><div></div></div>	88% 12%
1	MD	258	<div><div></div></div>	84% 16%
1	N	258	<div><div></div></div>	90% 10%
1	NA	258	<div><div></div></div>	87% 13%
1	NB	258	<div><div></div></div>	91% 9%
1	NC	258	<div><div></div></div>	90% 10%
1	ND	258	<div><div></div></div>	88% 12%
1	O	258	<div><div></div></div>	91% 9%
1	OA	258	<div><div></div></div>	87% 13%
1	OB	258	<div><div></div></div>	90% 10%
1	OC	258	<div><div></div></div>	90% 10%
1	OD	258	<div><div></div></div>	88% 12%
1	P	258	<div><div></div></div>	88% 12%
1	PA	258	<div><div></div></div>	86% 13%
1	PB	258	<div><div></div></div>	88% 12%
1	PC	258	<div><div></div></div>	90% 10%
1	PD	258	<div><div></div></div>	89% 11%
1	Q	258	<div><div></div></div>	93% 7%
1	QA	258	<div><div></div></div>	88% 12%
1	QB	258	<div><div></div></div>	89% 11%

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Mol	Chain	Length	Quality of chain	
1	QC	258	<div><div></div></div>	90% 10%
1	R	258	<div><div></div></div>	90% 10%
1	RA	258	<div><div></div></div>	88% 12%
1	RB	258	<div><div></div></div>	88% 12%
1	RC	258	<div><div></div></div>	89% 11%
1	S	258	<div><div></div></div>	90% 10%
1	SA	258	<div><div></div></div>	89% 11%
1	SB	258	<div><div></div></div>	88% 12%
1	SC	258	<div><div></div></div>	83% 17%
1	T	258	<div><div></div></div>	90% 10%
1	TA	258	<div><div></div></div>	90% 10%
1	TB	258	<div><div></div></div>	83% 17%
1	TC	258	<div><div></div></div>	86% 14%
1	UA	258	<div><div></div></div>	90% 10%
1	UB	258	<div><div></div></div>	87% 13%
1	UC	258	<div><div></div></div>	84% 16%
1	V	258	<div><div></div></div>	86% 13%
1	VA	258	<div><div></div></div>	91% 9%
1	VB	258	<div><div></div></div>	89% 11%
1	VC	258	<div><div></div></div>	87% 13%
1	W	258	<div><div></div></div>	88% 12%
1	WA	258	<div><div></div></div>	89% 11%
1	WB	258	<div><div></div></div>	87% 13%
1	WC	258	<div><div></div></div>	88% 12%
1	X	258	<div><div></div></div>	85% 15%

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Mol	Chain	Length	Quality of chain	
1	XA	258		92% 8%
1	XB	258		88% 12%
1	XC	258		89% 11%
1	Y	258		87% 13%
1	YA	258		91% 9%
1	YB	258		90% 10%
1	YC	258		88% 12%
1	Z	258		87% 13%
1	ZA	258		89% 11%
1	ZB	258		90% 10%
1	ZC	258		88% 12%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 236760 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Coat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Af	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	A	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	B	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	C	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	D	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	E	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	F	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	G	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	H	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	I	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	J	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	K	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	L	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	M	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	N	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	O	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	P	258	Total 1973	C 1226	N 352	O 391	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Q	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	R	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	S	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	T	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	V	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	W	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	X	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	Y	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	Z	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	AA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	BA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	CA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	DA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	EA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	FA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	GA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	HA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	IA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	JA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	KA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	LA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	MA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	NA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	OA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	PA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	QA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	RA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	SA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	TA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	UA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	VA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	WA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	XA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	YA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	ZA	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	AB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	BB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	CB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	DB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	EB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	FB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	GB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	HB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	IB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	JB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	KB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	LB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	MB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	NB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	OB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	PB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	QB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	RB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	SB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	TB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	UB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	VB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	WB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	XB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	YB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	ZB	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	AC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	BC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	DC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	EC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	FC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	GC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	HC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	IC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	JC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	KC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	LC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	MC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	NC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	OC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	PC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	QC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	RC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	SC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	TC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	UC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	VC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	WC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	XC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	YC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	ZC	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	AD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	BD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	CD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	DD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	ED	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	FD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	GD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	HD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	ID	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	JD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	KD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	LD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	MD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	ND	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	OD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0
1	PD	258	Total 1973	C 1226	N 352	O 391	S 4	0	0

There are 480 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Af	128	ALA	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
Af	129	TYR	-	linker	UNP Q38062
Af	130	GLY	-	linker	UNP Q38062
Af	131	GLY	-	linker	UNP Q38062
A	128	ALA	-	linker	UNP Q38062
A	129	TYR	-	linker	UNP Q38062
A	130	GLY	-	linker	UNP Q38062
A	131	GLY	-	linker	UNP Q38062
B	128	ALA	-	linker	UNP Q38062
B	129	TYR	-	linker	UNP Q38062
B	130	GLY	-	linker	UNP Q38062
B	131	GLY	-	linker	UNP Q38062
C	128	ALA	-	linker	UNP Q38062
C	129	TYR	-	linker	UNP Q38062
C	130	GLY	-	linker	UNP Q38062
C	131	GLY	-	linker	UNP Q38062
D	128	ALA	-	linker	UNP Q38062
D	129	TYR	-	linker	UNP Q38062
D	130	GLY	-	linker	UNP Q38062
D	131	GLY	-	linker	UNP Q38062
E	128	ALA	-	linker	UNP Q38062
E	129	TYR	-	linker	UNP Q38062
E	130	GLY	-	linker	UNP Q38062
E	131	GLY	-	linker	UNP Q38062
F	128	ALA	-	linker	UNP Q38062
F	129	TYR	-	linker	UNP Q38062
F	130	GLY	-	linker	UNP Q38062
F	131	GLY	-	linker	UNP Q38062
G	128	ALA	-	linker	UNP Q38062
G	129	TYR	-	linker	UNP Q38062
G	130	GLY	-	linker	UNP Q38062
G	131	GLY	-	linker	UNP Q38062
H	128	ALA	-	linker	UNP Q38062
H	129	TYR	-	linker	UNP Q38062
H	130	GLY	-	linker	UNP Q38062
H	131	GLY	-	linker	UNP Q38062
I	128	ALA	-	linker	UNP Q38062
I	129	TYR	-	linker	UNP Q38062
I	130	GLY	-	linker	UNP Q38062
I	131	GLY	-	linker	UNP Q38062
J	128	ALA	-	linker	UNP Q38062
J	129	TYR	-	linker	UNP Q38062
J	130	GLY	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
J	131	GLY	-	linker	UNP Q38062
K	128	ALA	-	linker	UNP Q38062
K	129	TYR	-	linker	UNP Q38062
K	130	GLY	-	linker	UNP Q38062
K	131	GLY	-	linker	UNP Q38062
L	128	ALA	-	linker	UNP Q38062
L	129	TYR	-	linker	UNP Q38062
L	130	GLY	-	linker	UNP Q38062
L	131	GLY	-	linker	UNP Q38062
M	128	ALA	-	linker	UNP Q38062
M	129	TYR	-	linker	UNP Q38062
M	130	GLY	-	linker	UNP Q38062
M	131	GLY	-	linker	UNP Q38062
N	128	ALA	-	linker	UNP Q38062
N	129	TYR	-	linker	UNP Q38062
N	130	GLY	-	linker	UNP Q38062
N	131	GLY	-	linker	UNP Q38062
O	128	ALA	-	linker	UNP Q38062
O	129	TYR	-	linker	UNP Q38062
O	130	GLY	-	linker	UNP Q38062
O	131	GLY	-	linker	UNP Q38062
P	128	ALA	-	linker	UNP Q38062
P	129	TYR	-	linker	UNP Q38062
P	130	GLY	-	linker	UNP Q38062
P	131	GLY	-	linker	UNP Q38062
Q	128	ALA	-	linker	UNP Q38062
Q	129	TYR	-	linker	UNP Q38062
Q	130	GLY	-	linker	UNP Q38062
Q	131	GLY	-	linker	UNP Q38062
R	128	ALA	-	linker	UNP Q38062
R	129	TYR	-	linker	UNP Q38062
R	130	GLY	-	linker	UNP Q38062
R	131	GLY	-	linker	UNP Q38062
S	128	ALA	-	linker	UNP Q38062
S	129	TYR	-	linker	UNP Q38062
S	130	GLY	-	linker	UNP Q38062
S	131	GLY	-	linker	UNP Q38062
T	128	ALA	-	linker	UNP Q38062
T	129	TYR	-	linker	UNP Q38062
T	130	GLY	-	linker	UNP Q38062
T	131	GLY	-	linker	UNP Q38062
V	128	ALA	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
V	129	TYR	-	linker	UNP Q38062
V	130	GLY	-	linker	UNP Q38062
V	131	GLY	-	linker	UNP Q38062
W	128	ALA	-	linker	UNP Q38062
W	129	TYR	-	linker	UNP Q38062
W	130	GLY	-	linker	UNP Q38062
W	131	GLY	-	linker	UNP Q38062
X	128	ALA	-	linker	UNP Q38062
X	129	TYR	-	linker	UNP Q38062
X	130	GLY	-	linker	UNP Q38062
X	131	GLY	-	linker	UNP Q38062
Y	128	ALA	-	linker	UNP Q38062
Y	129	TYR	-	linker	UNP Q38062
Y	130	GLY	-	linker	UNP Q38062
Y	131	GLY	-	linker	UNP Q38062
Z	128	ALA	-	linker	UNP Q38062
Z	129	TYR	-	linker	UNP Q38062
Z	130	GLY	-	linker	UNP Q38062
Z	131	GLY	-	linker	UNP Q38062
AA	128	ALA	-	linker	UNP Q38062
AA	129	TYR	-	linker	UNP Q38062
AA	130	GLY	-	linker	UNP Q38062
AA	131	GLY	-	linker	UNP Q38062
BA	128	ALA	-	linker	UNP Q38062
BA	129	TYR	-	linker	UNP Q38062
BA	130	GLY	-	linker	UNP Q38062
BA	131	GLY	-	linker	UNP Q38062
CA	128	ALA	-	linker	UNP Q38062
CA	129	TYR	-	linker	UNP Q38062
CA	130	GLY	-	linker	UNP Q38062
CA	131	GLY	-	linker	UNP Q38062
DA	128	ALA	-	linker	UNP Q38062
DA	129	TYR	-	linker	UNP Q38062
DA	130	GLY	-	linker	UNP Q38062
DA	131	GLY	-	linker	UNP Q38062
EA	128	ALA	-	linker	UNP Q38062
EA	129	TYR	-	linker	UNP Q38062
EA	130	GLY	-	linker	UNP Q38062
EA	131	GLY	-	linker	UNP Q38062
FA	128	ALA	-	linker	UNP Q38062
FA	129	TYR	-	linker	UNP Q38062
FA	130	GLY	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
FA	131	GLY	-	linker	UNP Q38062
GA	128	ALA	-	linker	UNP Q38062
GA	129	TYR	-	linker	UNP Q38062
GA	130	GLY	-	linker	UNP Q38062
GA	131	GLY	-	linker	UNP Q38062
HA	128	ALA	-	linker	UNP Q38062
HA	129	TYR	-	linker	UNP Q38062
HA	130	GLY	-	linker	UNP Q38062
HA	131	GLY	-	linker	UNP Q38062
IA	128	ALA	-	linker	UNP Q38062
IA	129	TYR	-	linker	UNP Q38062
IA	130	GLY	-	linker	UNP Q38062
IA	131	GLY	-	linker	UNP Q38062
JA	128	ALA	-	linker	UNP Q38062
JA	129	TYR	-	linker	UNP Q38062
JA	130	GLY	-	linker	UNP Q38062
JA	131	GLY	-	linker	UNP Q38062
KA	128	ALA	-	linker	UNP Q38062
KA	129	TYR	-	linker	UNP Q38062
KA	130	GLY	-	linker	UNP Q38062
KA	131	GLY	-	linker	UNP Q38062
LA	128	ALA	-	linker	UNP Q38062
LA	129	TYR	-	linker	UNP Q38062
LA	130	GLY	-	linker	UNP Q38062
LA	131	GLY	-	linker	UNP Q38062
MA	128	ALA	-	linker	UNP Q38062
MA	129	TYR	-	linker	UNP Q38062
MA	130	GLY	-	linker	UNP Q38062
MA	131	GLY	-	linker	UNP Q38062
NA	128	ALA	-	linker	UNP Q38062
NA	129	TYR	-	linker	UNP Q38062
NA	130	GLY	-	linker	UNP Q38062
NA	131	GLY	-	linker	UNP Q38062
OA	128	ALA	-	linker	UNP Q38062
OA	129	TYR	-	linker	UNP Q38062
OA	130	GLY	-	linker	UNP Q38062
OA	131	GLY	-	linker	UNP Q38062
PA	128	ALA	-	linker	UNP Q38062
PA	129	TYR	-	linker	UNP Q38062
PA	130	GLY	-	linker	UNP Q38062
PA	131	GLY	-	linker	UNP Q38062
QA	128	ALA	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
QA	129	TYR	-	linker	UNP Q38062
QA	130	GLY	-	linker	UNP Q38062
QA	131	GLY	-	linker	UNP Q38062
RA	128	ALA	-	linker	UNP Q38062
RA	129	TYR	-	linker	UNP Q38062
RA	130	GLY	-	linker	UNP Q38062
RA	131	GLY	-	linker	UNP Q38062
SA	128	ALA	-	linker	UNP Q38062
SA	129	TYR	-	linker	UNP Q38062
SA	130	GLY	-	linker	UNP Q38062
SA	131	GLY	-	linker	UNP Q38062
TA	128	ALA	-	linker	UNP Q38062
TA	129	TYR	-	linker	UNP Q38062
TA	130	GLY	-	linker	UNP Q38062
TA	131	GLY	-	linker	UNP Q38062
UA	128	ALA	-	linker	UNP Q38062
UA	129	TYR	-	linker	UNP Q38062
UA	130	GLY	-	linker	UNP Q38062
UA	131	GLY	-	linker	UNP Q38062
VA	128	ALA	-	linker	UNP Q38062
VA	129	TYR	-	linker	UNP Q38062
VA	130	GLY	-	linker	UNP Q38062
VA	131	GLY	-	linker	UNP Q38062
WA	128	ALA	-	linker	UNP Q38062
WA	129	TYR	-	linker	UNP Q38062
WA	130	GLY	-	linker	UNP Q38062
WA	131	GLY	-	linker	UNP Q38062
XA	128	ALA	-	linker	UNP Q38062
XA	129	TYR	-	linker	UNP Q38062
XA	130	GLY	-	linker	UNP Q38062
XA	131	GLY	-	linker	UNP Q38062
YA	128	ALA	-	linker	UNP Q38062
YA	129	TYR	-	linker	UNP Q38062
YA	130	GLY	-	linker	UNP Q38062
YA	131	GLY	-	linker	UNP Q38062
ZA	128	ALA	-	linker	UNP Q38062
ZA	129	TYR	-	linker	UNP Q38062
ZA	130	GLY	-	linker	UNP Q38062
ZA	131	GLY	-	linker	UNP Q38062
AB	128	ALA	-	linker	UNP Q38062
AB	129	TYR	-	linker	UNP Q38062
AB	130	GLY	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
AB	131	GLY	-	linker	UNP Q38062
BB	128	ALA	-	linker	UNP Q38062
BB	129	TYR	-	linker	UNP Q38062
BB	130	GLY	-	linker	UNP Q38062
BB	131	GLY	-	linker	UNP Q38062
CB	128	ALA	-	linker	UNP Q38062
CB	129	TYR	-	linker	UNP Q38062
CB	130	GLY	-	linker	UNP Q38062
CB	131	GLY	-	linker	UNP Q38062
DB	128	ALA	-	linker	UNP Q38062
DB	129	TYR	-	linker	UNP Q38062
DB	130	GLY	-	linker	UNP Q38062
DB	131	GLY	-	linker	UNP Q38062
EB	128	ALA	-	linker	UNP Q38062
EB	129	TYR	-	linker	UNP Q38062
EB	130	GLY	-	linker	UNP Q38062
EB	131	GLY	-	linker	UNP Q38062
FB	128	ALA	-	linker	UNP Q38062
FB	129	TYR	-	linker	UNP Q38062
FB	130	GLY	-	linker	UNP Q38062
FB	131	GLY	-	linker	UNP Q38062
GB	128	ALA	-	linker	UNP Q38062
GB	129	TYR	-	linker	UNP Q38062
GB	130	GLY	-	linker	UNP Q38062
GB	131	GLY	-	linker	UNP Q38062
HB	128	ALA	-	linker	UNP Q38062
HB	129	TYR	-	linker	UNP Q38062
HB	130	GLY	-	linker	UNP Q38062
HB	131	GLY	-	linker	UNP Q38062
IB	128	ALA	-	linker	UNP Q38062
IB	129	TYR	-	linker	UNP Q38062
IB	130	GLY	-	linker	UNP Q38062
IB	131	GLY	-	linker	UNP Q38062
JB	128	ALA	-	linker	UNP Q38062
JB	129	TYR	-	linker	UNP Q38062
JB	130	GLY	-	linker	UNP Q38062
JB	131	GLY	-	linker	UNP Q38062
KB	128	ALA	-	linker	UNP Q38062
KB	129	TYR	-	linker	UNP Q38062
KB	130	GLY	-	linker	UNP Q38062
KB	131	GLY	-	linker	UNP Q38062
LB	128	ALA	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
LB	129	TYR	-	linker	UNP Q38062
LB	130	GLY	-	linker	UNP Q38062
LB	131	GLY	-	linker	UNP Q38062
MB	128	ALA	-	linker	UNP Q38062
MB	129	TYR	-	linker	UNP Q38062
MB	130	GLY	-	linker	UNP Q38062
MB	131	GLY	-	linker	UNP Q38062
NB	128	ALA	-	linker	UNP Q38062
NB	129	TYR	-	linker	UNP Q38062
NB	130	GLY	-	linker	UNP Q38062
NB	131	GLY	-	linker	UNP Q38062
OB	128	ALA	-	linker	UNP Q38062
OB	129	TYR	-	linker	UNP Q38062
OB	130	GLY	-	linker	UNP Q38062
OB	131	GLY	-	linker	UNP Q38062
PB	128	ALA	-	linker	UNP Q38062
PB	129	TYR	-	linker	UNP Q38062
PB	130	GLY	-	linker	UNP Q38062
PB	131	GLY	-	linker	UNP Q38062
QB	128	ALA	-	linker	UNP Q38062
QB	129	TYR	-	linker	UNP Q38062
QB	130	GLY	-	linker	UNP Q38062
QB	131	GLY	-	linker	UNP Q38062
RB	128	ALA	-	linker	UNP Q38062
RB	129	TYR	-	linker	UNP Q38062
RB	130	GLY	-	linker	UNP Q38062
RB	131	GLY	-	linker	UNP Q38062
SB	128	ALA	-	linker	UNP Q38062
SB	129	TYR	-	linker	UNP Q38062
SB	130	GLY	-	linker	UNP Q38062
SB	131	GLY	-	linker	UNP Q38062
TB	128	ALA	-	linker	UNP Q38062
TB	129	TYR	-	linker	UNP Q38062
TB	130	GLY	-	linker	UNP Q38062
TB	131	GLY	-	linker	UNP Q38062
UB	128	ALA	-	linker	UNP Q38062
UB	129	TYR	-	linker	UNP Q38062
UB	130	GLY	-	linker	UNP Q38062
UB	131	GLY	-	linker	UNP Q38062
VB	128	ALA	-	linker	UNP Q38062
VB	129	TYR	-	linker	UNP Q38062
VB	130	GLY	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
VB	131	GLY	-	linker	UNP Q38062
WB	128	ALA	-	linker	UNP Q38062
WB	129	TYR	-	linker	UNP Q38062
WB	130	GLY	-	linker	UNP Q38062
WB	131	GLY	-	linker	UNP Q38062
XB	128	ALA	-	linker	UNP Q38062
XB	129	TYR	-	linker	UNP Q38062
XB	130	GLY	-	linker	UNP Q38062
XB	131	GLY	-	linker	UNP Q38062
YB	128	ALA	-	linker	UNP Q38062
YB	129	TYR	-	linker	UNP Q38062
YB	130	GLY	-	linker	UNP Q38062
YB	131	GLY	-	linker	UNP Q38062
ZB	128	ALA	-	linker	UNP Q38062
ZB	129	TYR	-	linker	UNP Q38062
ZB	130	GLY	-	linker	UNP Q38062
ZB	131	GLY	-	linker	UNP Q38062
AC	128	ALA	-	linker	UNP Q38062
AC	129	TYR	-	linker	UNP Q38062
AC	130	GLY	-	linker	UNP Q38062
AC	131	GLY	-	linker	UNP Q38062
BC	128	ALA	-	linker	UNP Q38062
BC	129	TYR	-	linker	UNP Q38062
BC	130	GLY	-	linker	UNP Q38062
BC	131	GLY	-	linker	UNP Q38062
CC	128	ALA	-	linker	UNP Q38062
CC	129	TYR	-	linker	UNP Q38062
CC	130	GLY	-	linker	UNP Q38062
CC	131	GLY	-	linker	UNP Q38062
DC	128	ALA	-	linker	UNP Q38062
DC	129	TYR	-	linker	UNP Q38062
DC	130	GLY	-	linker	UNP Q38062
DC	131	GLY	-	linker	UNP Q38062
EC	128	ALA	-	linker	UNP Q38062
EC	129	TYR	-	linker	UNP Q38062
EC	130	GLY	-	linker	UNP Q38062
EC	131	GLY	-	linker	UNP Q38062
FC	128	ALA	-	linker	UNP Q38062
FC	129	TYR	-	linker	UNP Q38062
FC	130	GLY	-	linker	UNP Q38062
FC	131	GLY	-	linker	UNP Q38062
GC	128	ALA	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
GC	129	TYR	-	linker	UNP Q38062
GC	130	GLY	-	linker	UNP Q38062
GC	131	GLY	-	linker	UNP Q38062
HC	128	ALA	-	linker	UNP Q38062
HC	129	TYR	-	linker	UNP Q38062
HC	130	GLY	-	linker	UNP Q38062
HC	131	GLY	-	linker	UNP Q38062
IC	128	ALA	-	linker	UNP Q38062
IC	129	TYR	-	linker	UNP Q38062
IC	130	GLY	-	linker	UNP Q38062
IC	131	GLY	-	linker	UNP Q38062
JC	128	ALA	-	linker	UNP Q38062
JC	129	TYR	-	linker	UNP Q38062
JC	130	GLY	-	linker	UNP Q38062
JC	131	GLY	-	linker	UNP Q38062
KC	128	ALA	-	linker	UNP Q38062
KC	129	TYR	-	linker	UNP Q38062
KC	130	GLY	-	linker	UNP Q38062
KC	131	GLY	-	linker	UNP Q38062
LC	128	ALA	-	linker	UNP Q38062
LC	129	TYR	-	linker	UNP Q38062
LC	130	GLY	-	linker	UNP Q38062
LC	131	GLY	-	linker	UNP Q38062
MC	128	ALA	-	linker	UNP Q38062
MC	129	TYR	-	linker	UNP Q38062
MC	130	GLY	-	linker	UNP Q38062
MC	131	GLY	-	linker	UNP Q38062
NC	128	ALA	-	linker	UNP Q38062
NC	129	TYR	-	linker	UNP Q38062
NC	130	GLY	-	linker	UNP Q38062
NC	131	GLY	-	linker	UNP Q38062
OC	128	ALA	-	linker	UNP Q38062
OC	129	TYR	-	linker	UNP Q38062
OC	130	GLY	-	linker	UNP Q38062
OC	131	GLY	-	linker	UNP Q38062
PC	128	ALA	-	linker	UNP Q38062
PC	129	TYR	-	linker	UNP Q38062
PC	130	GLY	-	linker	UNP Q38062
PC	131	GLY	-	linker	UNP Q38062
QC	128	ALA	-	linker	UNP Q38062
QC	129	TYR	-	linker	UNP Q38062
QC	130	GLY	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
QC	131	GLY	-	linker	UNP Q38062
RC	128	ALA	-	linker	UNP Q38062
RC	129	TYR	-	linker	UNP Q38062
RC	130	GLY	-	linker	UNP Q38062
RC	131	GLY	-	linker	UNP Q38062
SC	128	ALA	-	linker	UNP Q38062
SC	129	TYR	-	linker	UNP Q38062
SC	130	GLY	-	linker	UNP Q38062
SC	131	GLY	-	linker	UNP Q38062
TC	128	ALA	-	linker	UNP Q38062
TC	129	TYR	-	linker	UNP Q38062
TC	130	GLY	-	linker	UNP Q38062
TC	131	GLY	-	linker	UNP Q38062
UC	128	ALA	-	linker	UNP Q38062
UC	129	TYR	-	linker	UNP Q38062
UC	130	GLY	-	linker	UNP Q38062
UC	131	GLY	-	linker	UNP Q38062
VC	128	ALA	-	linker	UNP Q38062
VC	129	TYR	-	linker	UNP Q38062
VC	130	GLY	-	linker	UNP Q38062
VC	131	GLY	-	linker	UNP Q38062
WC	128	ALA	-	linker	UNP Q38062
WC	129	TYR	-	linker	UNP Q38062
WC	130	GLY	-	linker	UNP Q38062
WC	131	GLY	-	linker	UNP Q38062
XC	128	ALA	-	linker	UNP Q38062
XC	129	TYR	-	linker	UNP Q38062
XC	130	GLY	-	linker	UNP Q38062
XC	131	GLY	-	linker	UNP Q38062
YC	128	ALA	-	linker	UNP Q38062
YC	129	TYR	-	linker	UNP Q38062
YC	130	GLY	-	linker	UNP Q38062
YC	131	GLY	-	linker	UNP Q38062
ZC	128	ALA	-	linker	UNP Q38062
ZC	129	TYR	-	linker	UNP Q38062
ZC	130	GLY	-	linker	UNP Q38062
ZC	131	GLY	-	linker	UNP Q38062
AD	128	ALA	-	linker	UNP Q38062
AD	129	TYR	-	linker	UNP Q38062
AD	130	GLY	-	linker	UNP Q38062
AD	131	GLY	-	linker	UNP Q38062
BD	128	ALA	-	linker	UNP Q38062

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Chain	Residue	Modelled	Actual	Comment	Reference
BD	129	TYR	-	linker	UNP Q38062
BD	130	GLY	-	linker	UNP Q38062
BD	131	GLY	-	linker	UNP Q38062
CD	128	ALA	-	linker	UNP Q38062
CD	129	TYR	-	linker	UNP Q38062
CD	130	GLY	-	linker	UNP Q38062
CD	131	GLY	-	linker	UNP Q38062
DD	128	ALA	-	linker	UNP Q38062
DD	129	TYR	-	linker	UNP Q38062
DD	130	GLY	-	linker	UNP Q38062
DD	131	GLY	-	linker	UNP Q38062
ED	128	ALA	-	linker	UNP Q38062
ED	129	TYR	-	linker	UNP Q38062
ED	130	GLY	-	linker	UNP Q38062
ED	131	GLY	-	linker	UNP Q38062
FD	128	ALA	-	linker	UNP Q38062
FD	129	TYR	-	linker	UNP Q38062
FD	130	GLY	-	linker	UNP Q38062
FD	131	GLY	-	linker	UNP Q38062
GD	128	ALA	-	linker	UNP Q38062
GD	129	TYR	-	linker	UNP Q38062
GD	130	GLY	-	linker	UNP Q38062
GD	131	GLY	-	linker	UNP Q38062
HD	128	ALA	-	linker	UNP Q38062
HD	129	TYR	-	linker	UNP Q38062
HD	130	GLY	-	linker	UNP Q38062
HD	131	GLY	-	linker	UNP Q38062
ID	128	ALA	-	linker	UNP Q38062
ID	129	TYR	-	linker	UNP Q38062
ID	130	GLY	-	linker	UNP Q38062
ID	131	GLY	-	linker	UNP Q38062
JD	128	ALA	-	linker	UNP Q38062
JD	129	TYR	-	linker	UNP Q38062
JD	130	GLY	-	linker	UNP Q38062
JD	131	GLY	-	linker	UNP Q38062
KD	128	ALA	-	linker	UNP Q38062
KD	129	TYR	-	linker	UNP Q38062
KD	130	GLY	-	linker	UNP Q38062
KD	131	GLY	-	linker	UNP Q38062
LD	128	ALA	-	linker	UNP Q38062
LD	129	TYR	-	linker	UNP Q38062
LD	130	GLY	-	linker	UNP Q38062

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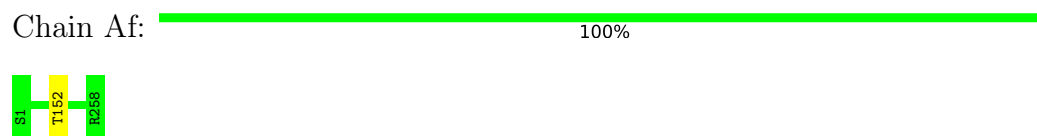
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Chain	Residue	Modelled	Actual	Comment	Reference
LD	131	GLY	-	linker	UNP Q38062
MD	128	ALA	-	linker	UNP Q38062
MD	129	TYR	-	linker	UNP Q38062
MD	130	GLY	-	linker	UNP Q38062
MD	131	GLY	-	linker	UNP Q38062
ND	128	ALA	-	linker	UNP Q38062
ND	129	TYR	-	linker	UNP Q38062
ND	130	GLY	-	linker	UNP Q38062
ND	131	GLY	-	linker	UNP Q38062
OD	128	ALA	-	linker	UNP Q38062
OD	129	TYR	-	linker	UNP Q38062
OD	130	GLY	-	linker	UNP Q38062
OD	131	GLY	-	linker	UNP Q38062
PD	128	ALA	-	linker	UNP Q38062
PD	129	TYR	-	linker	UNP Q38062
PD	130	GLY	-	linker	UNP Q38062
PD	131	GLY	-	linker	UNP Q38062

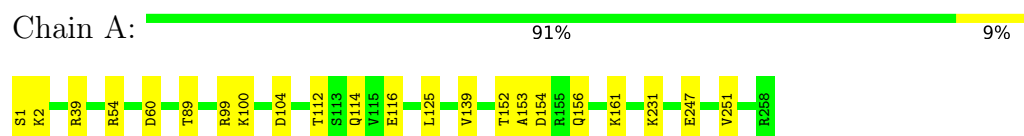
3 Residue-property plots

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

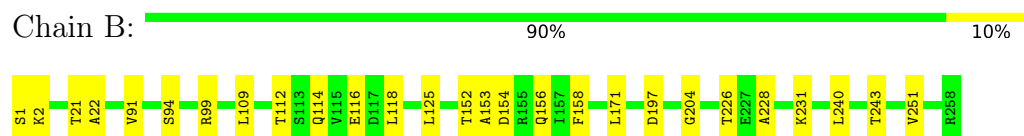
- Molecule 1: Coat protein



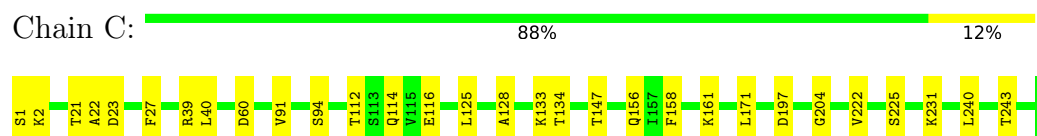
- Molecule 1: Coat protein



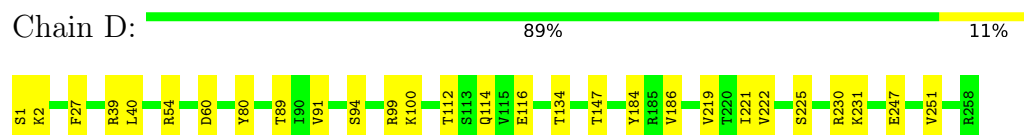
- Molecule 1: Coat protein



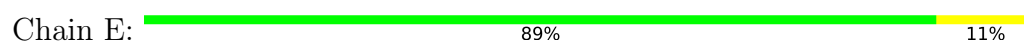
- Molecule 1: Coat protein



- Molecule 1: Coat protein



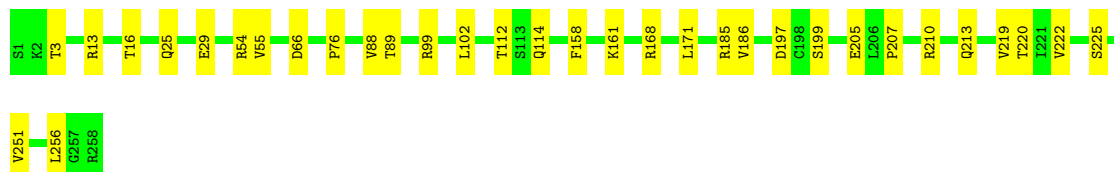
- Molecule 1: Coat protein





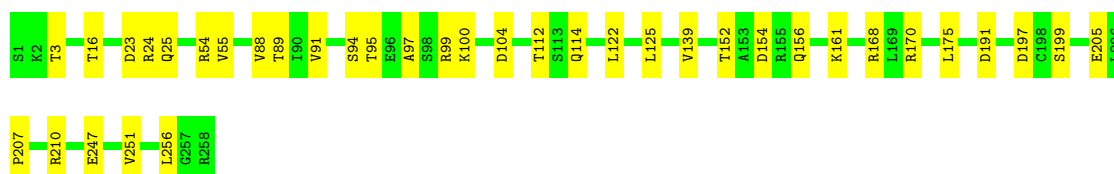
- Molecule 1: Coat protein

Chain F: 87% 13%



- Molecule 1: Coat protein

Chain G: 86% 14%



- Molecule 1: Coat protein

Chain H: 85% 15%



- Molecule 1: Coat protein

Chain I: 90% 10%



- Molecule 1: Coat protein

Chain J: 90% 10%



- Molecule 1: Coat protein

Chain K: 88% 12%



- Molecule 1: Coat protein

Chain L: 88% 12%



- Molecule 1: Coat protein

Chain M: 89% 11%



- Molecule 1: Coat protein

Chain N: 90% 10%



- Molecule 1: Coat protein

Chain O: 91% 9%



- Molecule 1: Coat protein

Chain P: 88% 12%



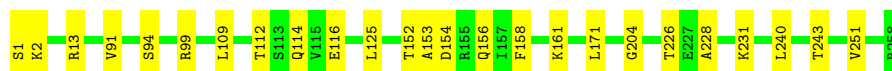
- Molecule 1: Coat protein


Chain Q: 93% 7%



- Molecule 1: Coat protein

Chain R: 90% 10%



- Chain Y:  87% 13%
- | Chain | Node | Value |
|---------|--------|--------|
| Chain Y | S1 | 0.0000 |
| | K2 | 0.0000 |
| | T3 | 0.0000 |
| | T16 | 0.0000 |
| | Q25 | 0.0000 |
| | V55 | 0.0000 |
| | D63 | 0.0000 |
| | R79 | 0.0000 |
| | V88 | 0.0000 |
| | T99 | 0.0000 |
| | I90 | 0.0000 |
| | V91 | 0.0000 |
| | S94 | 0.0000 |
| | R99 | 0.0000 |
| | K100 | 0.0000 |
| | D104 | 0.0000 |
| | T112 | 0.0000 |
| | S113 | 0.0000 |
| | Q114 | 0.0000 |
| | L122 | 0.0000 |
| L125 | 0.0000 | |
| V139 | 0.0000 | |
| T152 | 0.0000 | |
| A153 | 0.0000 | |
| D154 | 0.0000 | |
| R155 | 0.0000 | |
| Q156 | 0.0000 | |
| K161 | 0.0000 | |
| R168 | 0.0000 | |
| L169 | 0.0000 | |
| R170 | 0.0000 | |
| L175 | 0.0000 | |
| D191 | 0.0000 | |
| D197 | 0.0000 | |
| C198 | 0.0000 | |
| S199 | 0.0000 | |
| E205 | 0.0000 | |
| L206 | 0.0000 | |
| P207 | 0.0000 | |



- Molecule 1: Coat protein

Chain Z: 87% 13%



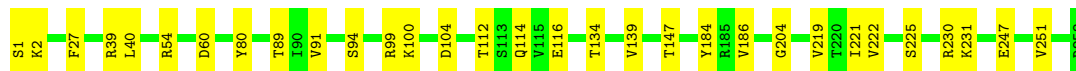
- Molecule 1: Coat protein

Chain AA: 89% 11%



- Molecule 1: Coat protein

Chain BA: 88% 12%



- Molecule 1: Coat protein

Chain CA: 89% 11%



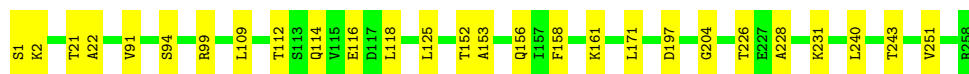
- Molecule 1: Coat protein

Chain DA: 90% 10%



- Molecule 1: Coat protein

Chain EA: 90% 10%



- Molecule 1: Coat protein

Chain FA: 90% 10%



- Molecule 1: Coat protein

Chain GA: 90% 10%



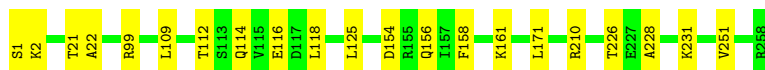
- Molecule 1: Coat protein

Chain HA: 91% 9%



- Molecule 1: Coat protein

Chain IA: 92% 8%



- Molecule 1: Coat protein

Chain JA: 88% 12%



- Molecule 1: Coat protein

Chain KA: 89% 11%



- Molecule 1: Coat protein

Chain LA: 89% 11%



- Molecule 1: Coat protein

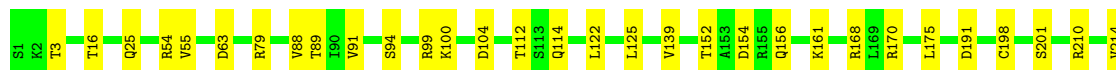
Chain MA: 87% 13%





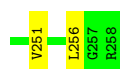
- Molecule 1: Coat protein

Chain NA: 87% 13%



- Molecule 1: Coat protein

Chain OA: 87% 13%



- Molecule 1: Coat protein

Chain PA: 86% 13%



- Molecule 1: Coat protein

Chain QA: 88% 12%



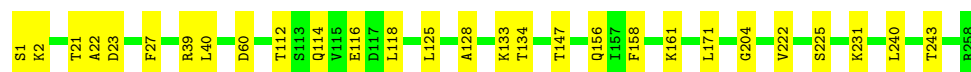
- Molecule 1: Coat protein

Chain RA: 88% 12%



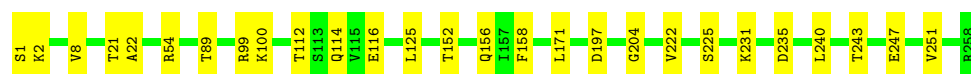
- Molecule 1: Coat protein

Chain SA:  89% 11%



- Molecule 1: Coat protein

Chain TA:  90% 10%



- Molecule 1: Coat protein

Chain UA:  90% 10%



- Molecule 1: Coat protein

Chain VA:  91% 9%



- Molecule 1: Coat protein

Chain WA:  89% 11%



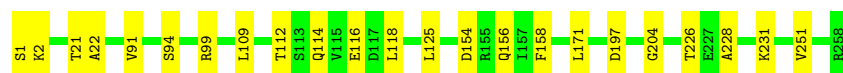
- Molecule 1: Coat protein

Chain XA:  92% 8%



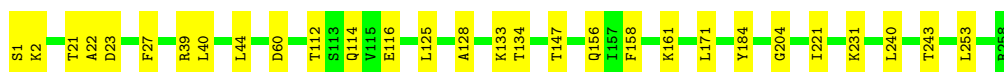
- Molecule 1: Coat protein

Chain YA:  91% 9%



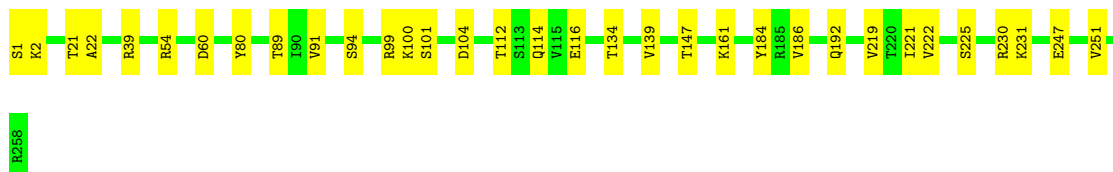
- Molecule 1: Coat protein

Chain ZA:  89% 11%



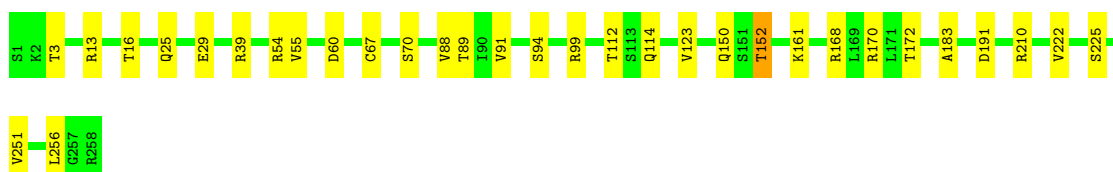
- Molecule 1: Coat protein

Chain AB: 87% 13%



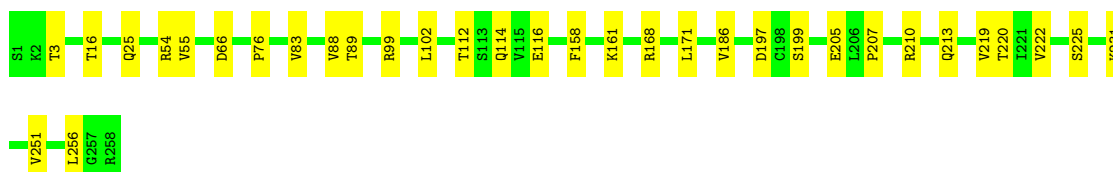
- Molecule 1: Coat protein

Chain BB: 88% 12%



- Molecule 1: Coat protein

Chain CB: 87% 13%



- Molecule 1: Coat protein

Chain DB: 88% 12%



- Molecule 1: Coat protein

Chain EB: 88% 12%





- Molecule 1: Coat protein

Chain FB: 88% 12%



- Molecule 1: Coat protein

Chain GB: 88% 12%



- Molecule 1: Coat protein

Chain HB: 89% 11%



- Molecule 1: Coat protein

Chain IB: 89% 11%



- Molecule 1: Coat protein

Chain JB: 91% 9%



- Molecule 1: Coat protein

Chain KB: 92% 8%



- Molecule 1: Coat protein

Chain LB:  91% 9%



- Molecule 1: Coat protein

Chain MB:  91% 9%



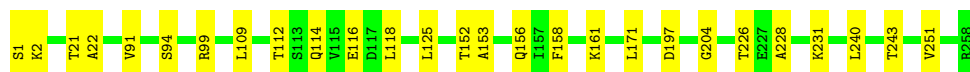
- Molecule 1: Coat protein

Chain NB:  91% 9%



- Molecule 1: Coat protein

Chain OB:  90% 10%



- Molecule 1: Coat protein

Chain PB:  88% 12%



- Molecule 1: Coat protein

Chain QB:  89% 11%




- Molecule 1: Coat protein

Chain RB:  88% 12%




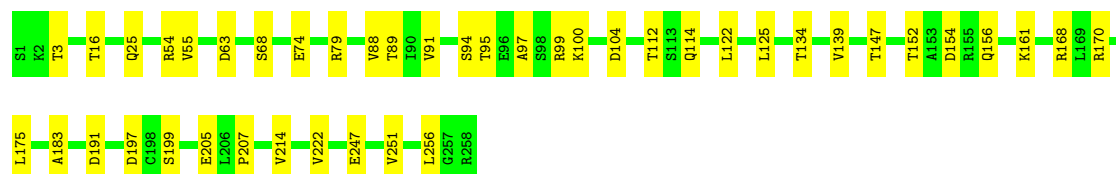
- Molecule 1: Coat protein

Chain SB:  88% 12%



- Molecule 1: Coat protein

Chain TB:  83% 17%



- Molecule 1: Coat protein

Chain UB:  87% 13%



- Molecule 1: Coat protein

Chain VB:  89% 11%



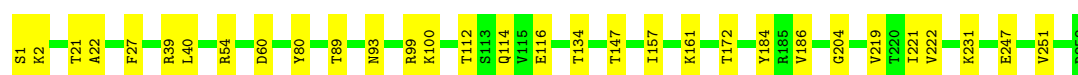
- Molecule 1: Coat protein

Chain WB:  87% 13%

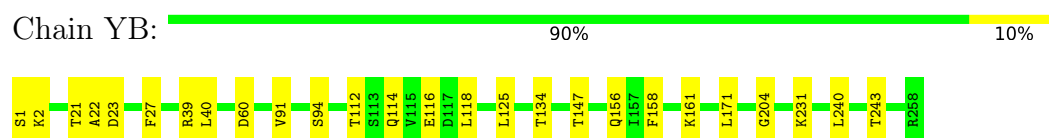


- Molecule 1: Coat protein

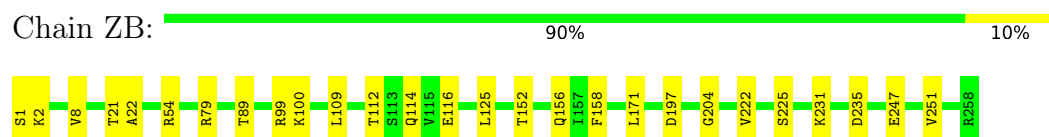
Chain XB:  88% 12%



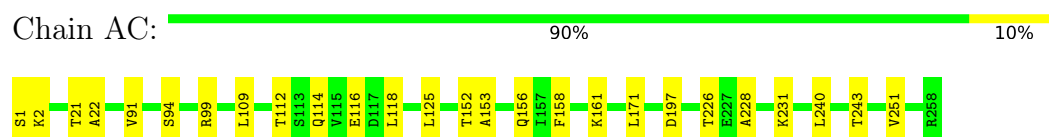
- Molecule 1: Coat protein



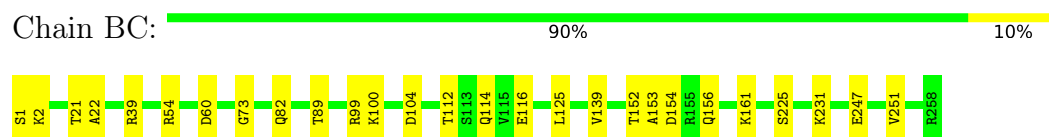
- Molecule 1: Coat protein



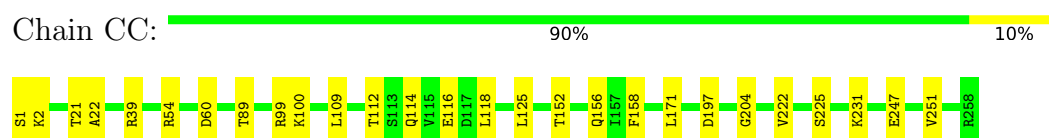
- Molecule 1: Coat protein



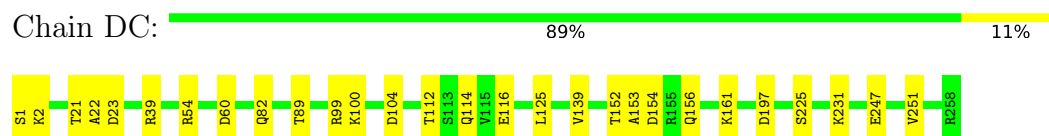
- Molecule 1: Coat protein



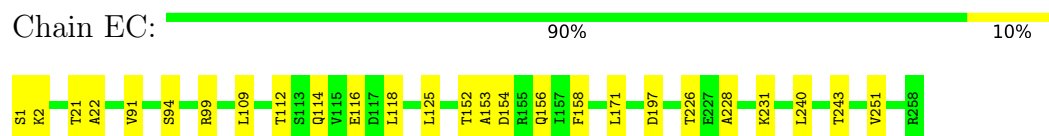
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein

Chain FC:  90% 10%



- Molecule 1: Coat protein

Chain GC:  90% 10%




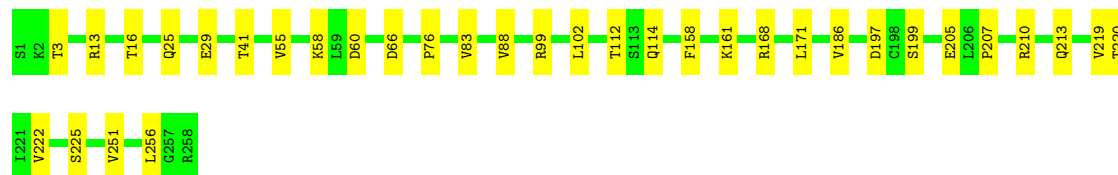
- Molecule 1: Coat protein

Chain HC:  88% 12%




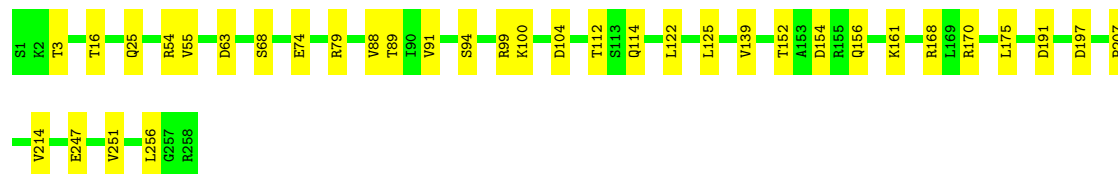
- Molecule 1: Coat protein

Chain IC:  87% 13%




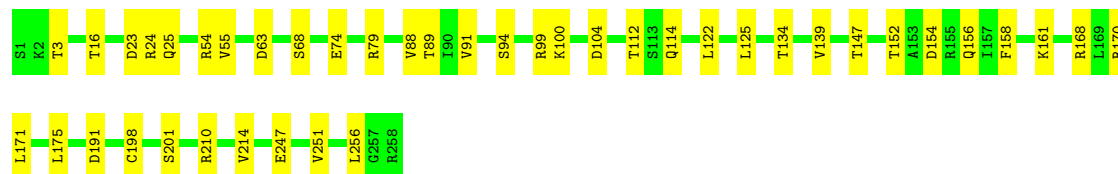
- Molecule 1: Coat protein

Chain JC:  86% 14%

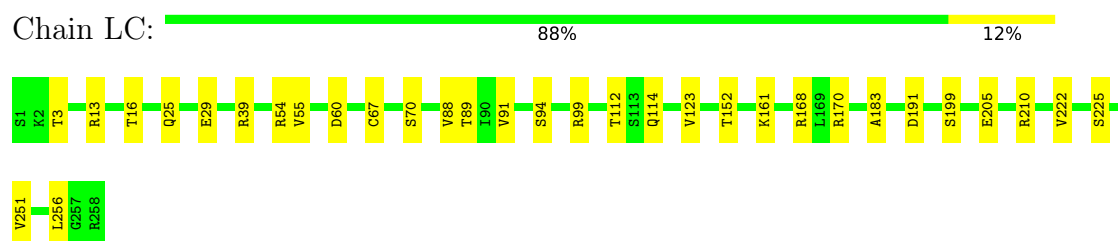


- Molecule 1: Coat protein

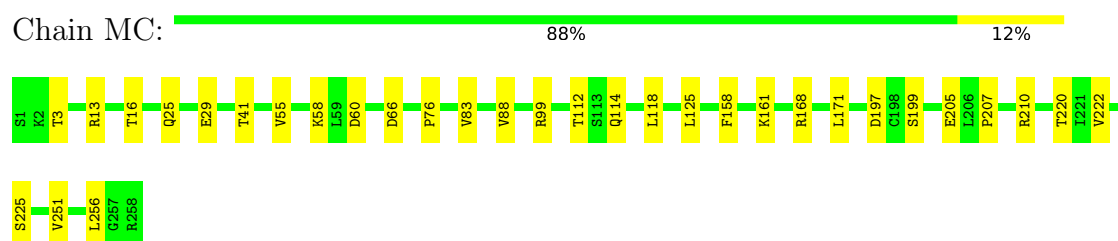
Chain KC:  84% 16%



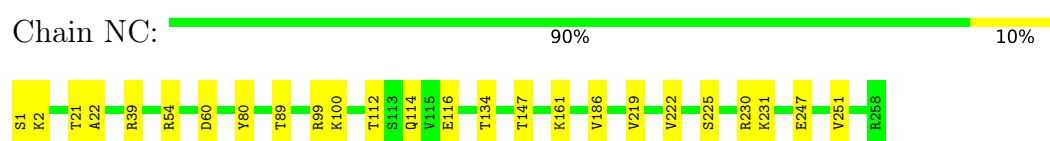
- Molecule 1: Coat protein



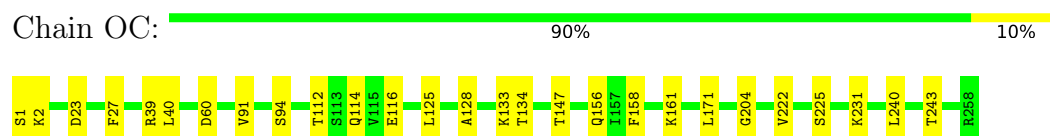
- Molecule 1: Coat protein



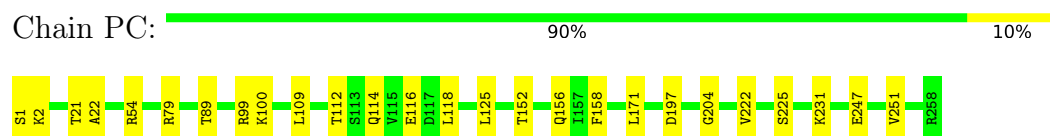
- Molecule 1: Coat protein



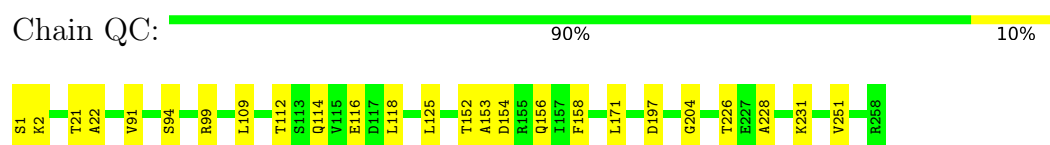
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein





- Molecule 1: Coat protein

Chain SC: 83% 17%



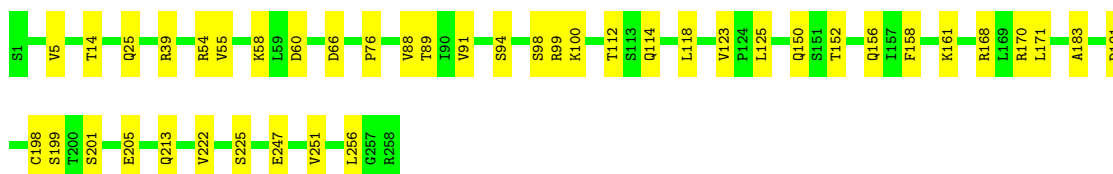
- Molecule 1: Coat protein

Chain TC: 86% 14%



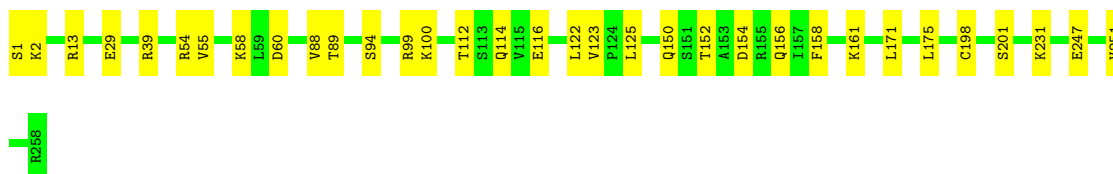
- Molecule 1: Coat protein

Chain UC: 84% 16%



- Molecule 1: Coat protein

Chain VC: 87% 13%




- Molecule 1: Coat protein

Chain WC: 88% 12%




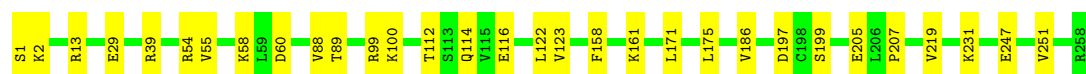
- Molecule 1: Coat protein

Chain XC:  89% 11%




- Molecule 1: Coat protein

Chain YC:  88% 12%



- Molecule 1: Coat protein

Chain ZC:  88% 12%




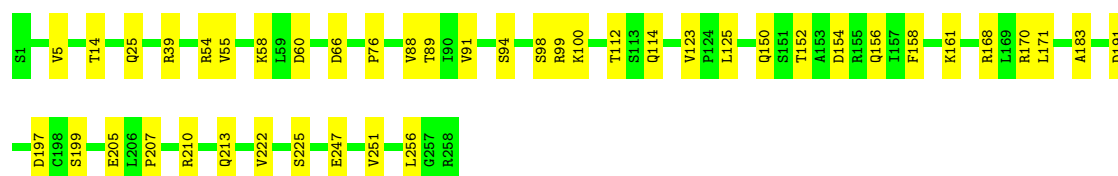
- Molecule 1: Coat protein

Chain AD:  89% 11%




- Molecule 1: Coat protein

Chain BD:  83% 17%




- Molecule 1: Coat protein

Chain CD:  84% 16%



- Molecule 1: Coat protein

Chain DD:  84% 16%



- Molecule 1: Coat protein

Chain ED: 89% 11%



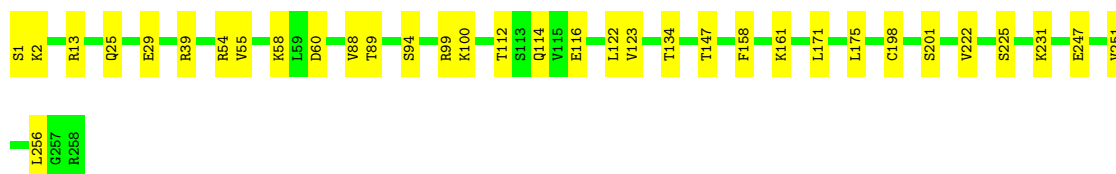
- Molecule 1: Coat protein

Chain FD: 87% 13%



- Molecule 1: Coat protein

Chain GD: 87% 13%



- Molecule 1: Coat protein

Chain HD: 86% 14%



- Molecule 1: Coat protein

Chain ID: 85% 15%





- Molecule 1: Coat protein

Chain JD: 84% 16%



- Molecule 1: Coat protein

Chain KD: 86% 14%



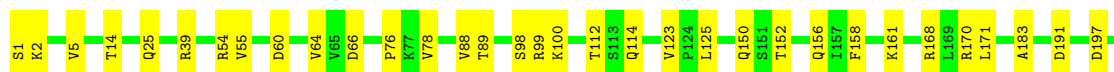
- Molecule 1: Coat protein

Chain LD: 84% 16%



- Molecule 1: Coat protein

Chain MD: 84% 16%



- Molecule 1: Coat protein

Chain ND: 88% 12%

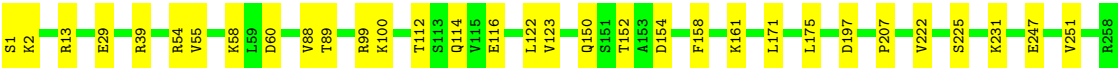


- Molecule 1: Coat protein

Chain OD:

88%

12%



● Molecule 1: Coat protein

Chain PD:

89%

11%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	33224	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	2	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.30	0/1993	0.53	0/2708
1	AA	0.28	0/1993	0.51	0/2708
1	AB	0.30	0/1993	0.53	0/2708
1	AC	0.29	0/1993	0.52	0/2708
1	AD	0.28	0/1993	0.52	0/2708
1	Af	0.30	0/1993	0.52	0/2708
1	B	0.29	0/1993	0.52	0/2708
1	BA	0.30	0/1993	0.52	0/2708
1	BB	0.28	0/1993	0.53	0/2708
1	BC	0.30	0/1993	0.53	0/2708
1	BD	0.28	0/1993	0.52	0/2708
1	C	0.30	0/1993	0.52	0/2708
1	CA	0.30	0/1993	0.52	0/2708
1	CB	0.28	0/1993	0.52	0/2708
1	CC	0.29	0/1993	0.52	0/2708
1	CD	0.28	0/1993	0.52	0/2708
1	D	0.30	0/1993	0.52	0/2708
1	DA	0.30	0/1993	0.52	0/2708
1	DB	0.28	0/1993	0.53	0/2708
1	DC	0.30	0/1993	0.53	0/2708
1	DD	0.28	0/1993	0.52	0/2708
1	E	0.28	0/1993	0.53	0/2708
1	EA	0.30	0/1993	0.52	0/2708
1	EB	0.29	0/1993	0.53	0/2708
1	EC	0.29	0/1993	0.51	0/2708
1	ED	0.28	0/1993	0.52	0/2708
1	F	0.28	0/1993	0.52	0/2708
1	FA	0.30	0/1993	0.53	0/2708
1	FB	0.28	0/1993	0.52	0/2708
1	FC	0.29	0/1993	0.52	0/2708
1	FD	0.28	0/1993	0.51	0/2708
1	G	0.28	0/1993	0.53	0/2708
1	GA	0.30	0/1993	0.52	0/2708
1	GB	0.28	0/1993	0.52	0/2708

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	GC	0.30	0/1993	0.52	0/2708
1	GD	0.28	0/1993	0.52	0/2708
1	H	0.29	0/1993	0.53	0/2708
1	HA	0.30	0/1993	0.53	0/2708
1	HB	0.30	0/1993	0.52	0/2708
1	HC	0.28	0/1993	0.54	0/2708
1	HD	0.28	0/1993	0.52	0/2708
1	I	0.28	0/1993	0.53	0/2708
1	IA	0.29	0/1993	0.51	0/2708
1	IB	0.29	0/1993	0.52	0/2708
1	IC	0.28	0/1993	0.52	0/2708
1	ID	0.28	0/1993	0.52	0/2708
1	J	0.28	0/1993	0.51	0/2708
1	JA	0.30	0/1993	0.53	0/2708
1	JB	0.30	0/1993	0.52	0/2708
1	JC	0.28	0/1993	0.53	0/2708
1	JD	0.28	0/1993	0.52	0/2708
1	K	0.29	0/1993	0.53	0/2708
1	KA	0.30	0/1993	0.52	0/2708
1	KB	0.29	0/1993	0.52	0/2708
1	KC	0.28	0/1993	0.53	0/2708
1	KD	0.28	0/1993	0.52	0/2708
1	L	0.29	0/1993	0.52	0/2708
1	LA	0.28	0/1993	0.53	0/2708
1	LB	0.30	0/1993	0.53	0/2708
1	LC	0.28	0/1993	0.52	0/2708
1	LD	0.28	0/1993	0.52	0/2708
1	M	0.30	0/1993	0.52	0/2708
1	MA	0.28	0/1993	0.52	0/2708
1	MB	0.29	0/1993	0.52	0/2708
1	MC	0.28	0/1993	0.52	0/2708
1	MD	0.28	0/1993	0.52	0/2708
1	N	0.30	0/1993	0.52	0/2708
1	NA	0.29	0/1993	0.53	0/2708
1	NB	0.30	0/1993	0.53	0/2708
1	NC	0.30	0/1993	0.52	0/2708
1	ND	0.28	0/1993	0.52	0/2708
1	O	0.30	0/1993	0.53	0/2708
1	OA	0.29	0/1993	0.53	0/2708
1	OB	0.29	0/1993	0.51	0/2708
1	OC	0.30	0/1993	0.52	0/2708
1	OD	0.28	0/1993	0.52	0/2708
1	P	0.30	0/1993	0.52	0/2708

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	PA	0.28	0/1993	0.53	0/2708
1	PB	0.30	0/1993	0.53	0/2708
1	PC	0.30	0/1993	0.52	0/2708
1	PD	0.28	0/1993	0.52	0/2708
1	Q	0.30	0/1993	0.53	0/2708
1	QA	0.28	0/1993	0.52	0/2708
1	QB	0.30	0/1993	0.52	0/2708
1	QC	0.29	0/1993	0.52	0/2708
1	R	0.30	0/1993	0.52	0/2708
1	RA	0.30	0/1993	0.52	0/2708
1	RB	0.28	0/1993	0.53	0/2708
1	RC	0.29	0/1993	0.53	0/2708
1	S	0.30	0/1993	0.52	0/2708
1	SA	0.30	0/1993	0.52	0/2708
1	SB	0.28	0/1993	0.51	0/2708
1	SC	0.28	0/1993	0.52	0/2708
1	T	0.30	0/1993	0.52	0/2708
1	TA	0.30	0/1993	0.52	0/2708
1	TB	0.28	0/1993	0.53	0/2708
1	TC	0.28	0/1993	0.52	0/2708
1	UA	0.30	0/1993	0.52	0/2708
1	UB	0.28	0/1993	0.53	0/2708
1	UC	0.28	0/1993	0.52	0/2708
1	V	0.28	0/1993	0.52	0/2708
1	VA	0.30	0/1993	0.53	0/2708
1	VB	0.28	0/1993	0.53	0/2708
1	VC	0.28	0/1993	0.51	0/2708
1	W	0.28	0/1993	0.51	0/2708
1	WA	0.30	0/1993	0.52	0/2708
1	WB	0.28	0/1993	0.52	0/2708
1	WC	0.28	0/1993	0.52	0/2708
1	X	0.29	0/1993	0.52	0/2708
1	XA	0.29	0/1993	0.53	0/2708
1	XB	0.30	0/1993	0.52	0/2708
1	XC	0.28	0/1993	0.52	0/2708
1	Y	0.28	0/1993	0.53	0/2708
1	YA	0.29	0/1993	0.51	0/2708
1	YB	0.29	0/1993	0.52	0/2708
1	YC	0.28	0/1993	0.51	0/2708
1	Z	0.28	0/1993	0.53	0/2708
1	ZA	0.30	0/1993	0.53	0/2708
1	ZB	0.30	0/1993	0.52	0/2708
1	ZC	0.28	0/1993	0.51	0/2708

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
All	All	0.29	0/239160	0.52	0/324960

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1973	0	2041	12	0
1	AA	1973	0	2039	16	0
1	AB	1973	0	2041	17	0
1	AC	1973	0	2041	15	0
1	AD	1973	0	2039	16	0
1	Af	1973	0	2041	0	0
1	B	1973	0	2041	16	0
1	BA	1973	0	2041	16	0
1	BB	1973	0	2039	18	0
1	BC	1973	0	2041	15	0
1	BD	1973	0	2039	25	0
1	C	1973	0	2041	17	0
1	CA	1973	0	2041	16	0
1	CB	1973	0	2039	18	0
1	CC	1973	0	2041	15	0
1	CD	1973	0	2039	24	0
1	D	1973	0	2041	14	0
1	DA	1973	0	2041	15	0
1	DB	1973	0	2039	17	0
1	DC	1973	0	2041	16	0
1	DD	1973	0	2039	23	0
1	E	1973	0	2039	16	0
1	EA	1973	0	2041	16	0
1	EB	1973	0	2039	17	0
1	EC	1973	0	2041	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	ED	1973	0	2039	16	0
1	F	1973	0	2039	18	0
1	FA	1973	0	2041	15	0
1	FB	1973	0	2039	18	0
1	FC	1973	0	2041	16	0
1	FD	1973	0	2039	18	0
1	G	1973	0	2039	19	0
1	GA	1973	0	2041	14	0
1	GB	1973	0	2039	17	0
1	GC	1973	0	2041	13	0
1	GD	1973	0	2039	19	0
1	H	1973	0	2039	21	0
1	HA	1973	0	2041	13	0
1	HB	1973	0	2041	15	0
1	HC	1973	0	2039	17	0
1	HD	1973	0	2039	23	0
1	I	1973	0	2039	15	0
1	IA	1973	0	2041	12	0
1	IB	1973	0	2041	16	0
1	IC	1973	0	2039	19	0
1	ID	1973	0	2039	22	0
1	J	1973	0	2039	15	0
1	JA	1973	0	2041	17	0
1	JB	1973	0	2041	12	0
1	JC	1973	0	2039	18	0
1	JD	1973	0	2039	23	0
1	K	1973	0	2041	16	0
1	KA	1973	0	2041	15	0
1	KB	1973	0	2041	12	0
1	KC	1973	0	2039	22	0
1	KD	1973	0	2039	21	0
1	L	1973	0	2041	18	0
1	LA	1973	0	2039	16	0
1	LB	1973	0	2041	13	0
1	LC	1973	0	2039	18	0
1	LD	1973	0	2039	23	0
1	M	1973	0	2041	16	0
1	MA	1973	0	2039	19	0
1	MB	1973	0	2041	13	0
1	MC	1973	0	2039	18	0
1	MD	1973	0	2039	23	0
1	N	1973	0	2041	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	NA	1973	0	2039	18	0
1	NB	1973	0	2041	13	0
1	NC	1973	0	2041	13	0
1	ND	1973	0	2039	17	0
1	O	1973	0	2041	12	0
1	OA	1973	0	2039	17	0
1	OB	1973	0	2041	16	0
1	OC	1973	0	2041	15	0
1	OD	1973	0	2039	18	0
1	P	1973	0	2041	18	0
1	PA	1973	0	2039	20	0
1	PB	1973	0	2041	17	0
1	PC	1973	0	2041	15	0
1	PD	1973	0	2039	16	0
1	Q	1973	0	2041	11	0
1	QA	1973	0	2039	18	0
1	QB	1973	0	2041	15	0
1	QC	1973	0	2041	15	0
1	R	1973	0	2041	15	0
1	RA	1973	0	2041	16	0
1	RB	1973	0	2039	17	0
1	RC	1973	0	2041	16	0
1	S	1973	0	2041	16	0
1	SA	1973	0	2041	16	0
1	SB	1973	0	2039	18	0
1	SC	1973	0	2039	24	0
1	T	1973	0	2041	14	0
1	TA	1973	0	2041	14	0
1	TB	1973	0	2039	22	0
1	TC	1973	0	2039	21	0
1	UA	1973	0	2041	15	0
1	UB	1973	0	2039	18	0
1	UC	1973	0	2039	24	0
1	V	1973	0	2039	19	0
1	VA	1973	0	2041	12	0
1	VB	1973	0	2039	16	0
1	VC	1973	0	2039	19	0
1	W	1973	0	2039	17	0
1	WA	1973	0	2041	15	0
1	WB	1973	0	2039	19	0
1	WC	1973	0	2039	17	0
1	X	1973	0	2039	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	XA	1973	0	2041	11	0
1	XB	1973	0	2041	17	0
1	XC	1973	0	2039	16	0
1	Y	1973	0	2039	17	0
1	YA	1973	0	2041	14	0
1	YB	1973	0	2041	15	0
1	YC	1973	0	2039	17	0
1	Z	1973	0	2039	19	0
1	ZA	1973	0	2041	16	0
1	ZB	1973	0	2041	15	0
1	ZC	1973	0	2039	17	0
All	All	236760	0	244800	1929	0

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

The worst 5 of 1929 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MB:204:GLY:HA2	1:WB:210:ARG:HH21	1.60	0.67
1:SB:210:ARG:HH21	1:ZB:204:GLY:HA2	1.60	0.67
1:W:210:ARG:HH21	1:DA:204:GLY:HA2	1.61	0.66
1:CB:210:ARG:HH21	1:JB:204:GLY:HA2	1.60	0.66
1:MA:210:ARG:HH21	1:TA:204:GLY:HA2	1.60	0.66

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	256/258 (99%)	243 (95%)	13 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	256/258 (99%)	239 (93%)	17 (7%)	0	100	100
1	AB	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	AC	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	AD	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	Af	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	B	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	BA	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	BB	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	BC	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	BD	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	C	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	CA	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	CB	256/258 (99%)	238 (93%)	18 (7%)	0	100	100
1	CC	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	CD	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	D	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	DA	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	DB	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	DC	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	DD	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	E	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	EA	256/258 (99%)	245 (96%)	11 (4%)	0	100	100
1	EB	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	EC	256/258 (99%)	245 (96%)	11 (4%)	0	100	100
1	ED	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	F	256/258 (99%)	240 (94%)	16 (6%)	0	100	100
1	FA	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	FB	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	FC	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	FD	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	G	256/258 (99%)	241 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GA	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	GB	256/258 (99%)	239 (93%)	17 (7%)	0	100	100
1	GC	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	GD	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	H	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	HA	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	HB	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	HC	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	HD	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	I	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	IA	256/258 (99%)	245 (96%)	11 (4%)	0	100	100
1	IB	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	IC	256/258 (99%)	239 (93%)	17 (7%)	0	100	100
1	ID	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	J	256/258 (99%)	238 (93%)	18 (7%)	0	100	100
1	JA	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	JB	256/258 (99%)	245 (96%)	11 (4%)	0	100	100
1	JC	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	JD	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	K	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	KA	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	KB	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	KC	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	KD	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	L	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	LA	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	LB	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	LC	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	LD	256/258 (99%)	240 (94%)	16 (6%)	0	100	100
1	M	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	MA	256/258 (99%)	241 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	MB	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	MC	256/258 (99%)	239 (93%)	17 (7%)	0	100	100
1	MD	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	N	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	NA	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	NB	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	NC	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	ND	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	O	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	OA	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	OB	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	OC	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	OD	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	P	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	PA	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	PB	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	PC	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	PD	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	Q	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	QA	256/258 (99%)	239 (93%)	17 (7%)	0	100	100
1	QB	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	QC	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	R	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	RA	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	RB	256/258 (99%)	240 (94%)	16 (6%)	0	100	100
1	RC	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	S	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	SA	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	SB	256/258 (99%)	240 (94%)	16 (6%)	0	100	100
1	SC	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	T	256/258 (99%)	243 (95%)	13 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	TA	256/258 (99%)	245 (96%)	11 (4%)	0	100	100
1	TB	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	TC	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	UA	256/258 (99%)	245 (96%)	11 (4%)	0	100	100
1	UB	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	UC	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	V	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	VA	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	VB	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	VC	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	W	256/258 (99%)	238 (93%)	18 (7%)	0	100	100
1	WA	256/258 (99%)	245 (96%)	11 (4%)	0	100	100
1	WB	256/258 (99%)	240 (94%)	16 (6%)	0	100	100
1	WC	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	X	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	XA	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	XB	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	XC	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	Y	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	YA	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	YB	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	YC	256/258 (99%)	243 (95%)	13 (5%)	0	100	100
1	Z	256/258 (99%)	242 (94%)	14 (6%)	0	100	100
1	ZA	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
1	ZB	256/258 (99%)	244 (95%)	12 (5%)	0	100	100
1	ZC	256/258 (99%)	241 (94%)	15 (6%)	0	100	100
All	All	30720/30960 (99%)	29056 (95%)	1664 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	225/225 (100%)	225 (100%)	0	100	100
1	AA	225/225 (100%)	225 (100%)	0	100	100
1	AB	225/225 (100%)	225 (100%)	0	100	100
1	AC	225/225 (100%)	225 (100%)	0	100	100
1	AD	225/225 (100%)	225 (100%)	0	100	100
1	Af	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	B	225/225 (100%)	225 (100%)	0	100	100
1	BA	225/225 (100%)	225 (100%)	0	100	100
1	BB	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	BC	225/225 (100%)	225 (100%)	0	100	100
1	BD	225/225 (100%)	225 (100%)	0	100	100
1	C	225/225 (100%)	225 (100%)	0	100	100
1	CA	225/225 (100%)	225 (100%)	0	100	100
1	CB	225/225 (100%)	225 (100%)	0	100	100
1	CC	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	CD	225/225 (100%)	225 (100%)	0	100	100
1	D	225/225 (100%)	225 (100%)	0	100	100
1	DA	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	DB	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	DC	225/225 (100%)	225 (100%)	0	100	100
1	DD	225/225 (100%)	225 (100%)	0	100	100
1	E	225/225 (100%)	225 (100%)	0	100	100
1	EA	225/225 (100%)	225 (100%)	0	100	100
1	EB	225/225 (100%)	225 (100%)	0	100	100
1	EC	225/225 (100%)	225 (100%)	0	100	100
1	ED	225/225 (100%)	225 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	225/225 (100%)	225 (100%)	0	100	100
1	FA	225/225 (100%)	225 (100%)	0	100	100
1	FB	225/225 (100%)	225 (100%)	0	100	100
1	FC	225/225 (100%)	225 (100%)	0	100	100
1	FD	225/225 (100%)	225 (100%)	0	100	100
1	G	225/225 (100%)	225 (100%)	0	100	100
1	GA	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	GB	225/225 (100%)	225 (100%)	0	100	100
1	GC	225/225 (100%)	225 (100%)	0	100	100
1	GD	225/225 (100%)	225 (100%)	0	100	100
1	H	225/225 (100%)	225 (100%)	0	100	100
1	HA	225/225 (100%)	225 (100%)	0	100	100
1	HB	225/225 (100%)	225 (100%)	0	100	100
1	HC	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	HD	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	I	225/225 (100%)	225 (100%)	0	100	100
1	IA	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	IB	225/225 (100%)	225 (100%)	0	100	100
1	IC	225/225 (100%)	225 (100%)	0	100	100
1	ID	225/225 (100%)	225 (100%)	0	100	100
1	J	225/225 (100%)	225 (100%)	0	100	100
1	JA	225/225 (100%)	225 (100%)	0	100	100
1	JB	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	JC	225/225 (100%)	225 (100%)	0	100	100
1	JD	225/225 (100%)	225 (100%)	0	100	100
1	K	225/225 (100%)	225 (100%)	0	100	100
1	KA	225/225 (100%)	225 (100%)	0	100	100
1	KB	225/225 (100%)	225 (100%)	0	100	100
1	KC	225/225 (100%)	225 (100%)	0	100	100
1	KD	225/225 (100%)	225 (100%)	0	100	100
1	L	225/225 (100%)	225 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	225/225 (100%)	225 (100%)	0	100	100
1	LB	225/225 (100%)	225 (100%)	0	100	100
1	LC	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	LD	225/225 (100%)	225 (100%)	0	100	100
1	M	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	MA	225/225 (100%)	225 (100%)	0	100	100
1	MB	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	MC	225/225 (100%)	225 (100%)	0	100	100
1	MD	225/225 (100%)	225 (100%)	0	100	100
1	N	225/225 (100%)	225 (100%)	0	100	100
1	NA	225/225 (100%)	225 (100%)	0	100	100
1	NB	225/225 (100%)	225 (100%)	0	100	100
1	NC	225/225 (100%)	225 (100%)	0	100	100
1	ND	225/225 (100%)	225 (100%)	0	100	100
1	O	225/225 (100%)	225 (100%)	0	100	100
1	OA	225/225 (100%)	225 (100%)	0	100	100
1	OB	225/225 (100%)	225 (100%)	0	100	100
1	OC	225/225 (100%)	225 (100%)	0	100	100
1	OD	225/225 (100%)	225 (100%)	0	100	100
1	P	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	PA	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	PB	225/225 (100%)	225 (100%)	0	100	100
1	PC	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	PD	225/225 (100%)	225 (100%)	0	100	100
1	Q	225/225 (100%)	225 (100%)	0	100	100
1	QA	225/225 (100%)	225 (100%)	0	100	100
1	QB	225/225 (100%)	225 (100%)	0	100	100
1	QC	225/225 (100%)	225 (100%)	0	100	100
1	R	225/225 (100%)	225 (100%)	0	100	100
1	RA	225/225 (100%)	225 (100%)	0	100	100
1	RB	225/225 (100%)	225 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	RC	225/225 (100%)	225 (100%)	0	100	100
1	S	225/225 (100%)	225 (100%)	0	100	100
1	SA	225/225 (100%)	225 (100%)	0	100	100
1	SB	225/225 (100%)	225 (100%)	0	100	100
1	SC	225/225 (100%)	225 (100%)	0	100	100
1	T	225/225 (100%)	225 (100%)	0	100	100
1	TA	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	TB	225/225 (100%)	225 (100%)	0	100	100
1	TC	225/225 (100%)	225 (100%)	0	100	100
1	UA	225/225 (100%)	225 (100%)	0	100	100
1	UB	225/225 (100%)	225 (100%)	0	100	100
1	UC	225/225 (100%)	225 (100%)	0	100	100
1	V	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	VA	225/225 (100%)	225 (100%)	0	100	100
1	VB	225/225 (100%)	225 (100%)	0	100	100
1	VC	225/225 (100%)	225 (100%)	0	100	100
1	W	225/225 (100%)	225 (100%)	0	100	100
1	WA	225/225 (100%)	224 (100%)	1 (0%)	92	97
1	WB	225/225 (100%)	225 (100%)	0	100	100
1	WC	225/225 (100%)	225 (100%)	0	100	100
1	X	225/225 (100%)	225 (100%)	0	100	100
1	XA	225/225 (100%)	225 (100%)	0	100	100
1	XB	225/225 (100%)	225 (100%)	0	100	100
1	XC	225/225 (100%)	225 (100%)	0	100	100
1	Y	225/225 (100%)	225 (100%)	0	100	100
1	YA	225/225 (100%)	225 (100%)	0	100	100
1	YB	225/225 (100%)	225 (100%)	0	100	100
1	YC	225/225 (100%)	225 (100%)	0	100	100
1	Z	225/225 (100%)	225 (100%)	0	100	100
1	ZA	225/225 (100%)	225 (100%)	0	100	100
1	ZB	225/225 (100%)	224 (100%)	1 (0%)	92	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	ZC	225/225 (100%)	225 (100%)	0	100	100
All	All	27000/27000 (100%)	26980 (100%)	20 (0%)	94	99

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	WA	152	THR
1	BB	152	THR
1	HC	152	THR
1	PA	152	THR
1	TA	152	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	SA	213	GLN
1	DB	82	GLN
1	VC	150	GLN
1	VA	82	GLN
1	ZA	82	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.