



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 08:13 AM UTC

PDB ID : 1GAV / pdb_00001gav
Title : BACTERIOPHAGE GA PROTEIN CAPSID
Authors : Tars, K.; Bundule, M.; Liljas, L.
Deposited on : 1997-01-28
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

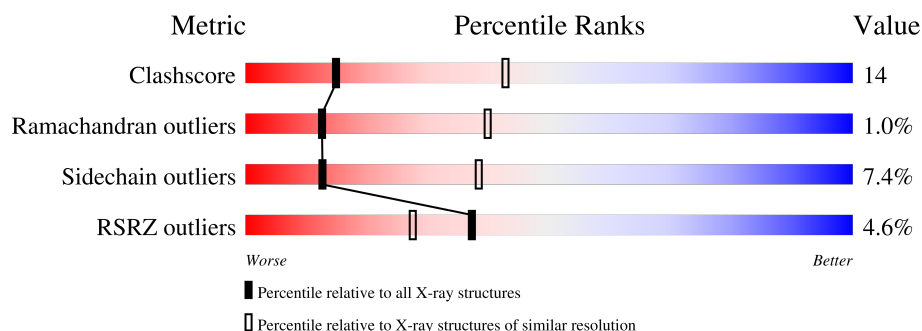
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	129	2% 72% 25% ..
1	1	129	2% 67% 28% .
1	2	129	4% 64% 29% 6%
1	3	129	5% 57% 34% 9%
1	4	129	5% 70% 26% ..
1	5	129	5% 64% 29% 6%

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Mol	Chain	Length	Quality of chain
1	6	129	
1	7	129	
1	8	129	
1	9	129	
1	A	129	
1	B	129	
1	C	129	
1	D	129	
1	E	129	
1	F	129	
1	G	129	
1	H	129	
1	I	129	
1	J	129	
1	K	129	
1	L	129	
1	M	129	
1	N	129	
1	O	129	
1	P	129	
1	Q	129	
1	R	129	
1	S	129	
1	T	129	
1	U	129	

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Mol	Chain	Length	Quality of chain
1	V	129	 6% 64% 30% 6%
1	W	129	 3% 59% 33% 8%
1	X	129	 3% 73% 24% ..
1	Y	129	 3% 64% 29% 6%
1	Z	129	 6% 57% 34% 9%
1	a	129	 7% 65% 29% 6%
1	b	129	 5% 58% 33% 9%
1	c	129	 5% 74% 23% ..
1	d	129	 5% 64% 30% 6%
1	e	129	 3% 58% 33% 9%
1	f	129	 2% 67% 29% ..
1	g	129	 9% 65% 28% 7%
1	h	129	 2% 59% 33% 8%
1	i	129	 5% 71% 26% ..

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 43335 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 BACTERIOPHAGE GA PROTEIN CAPSID.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	B	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	C	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	D	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	E	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	F	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	G	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	H	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	I	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	J	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	K	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	L	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	M	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	N	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	O	129	Total	C	N	O	0	0	0
			963	612	164	187			
1	P	129	Total	C	N	O	0	0	0
			963	612	164	187			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	Q	129	Total 963	C 612	N 164	O 187	0	0	0
1	R	129	Total 963	C 612	N 164	O 187	0	0	0
1	S	129	Total 963	C 612	N 164	O 187	0	0	0
1	T	129	Total 963	C 612	N 164	O 187	0	0	0
1	U	129	Total 963	C 612	N 164	O 187	0	0	0
1	V	129	Total 963	C 612	N 164	O 187	0	0	0
1	W	129	Total 963	C 612	N 164	O 187	0	0	0
1	X	129	Total 963	C 612	N 164	O 187	0	0	0
1	Y	129	Total 963	C 612	N 164	O 187	0	0	0
1	Z	129	Total 963	C 612	N 164	O 187	0	0	0
1	1	129	Total 963	C 612	N 164	O 187	0	0	0
1	2	129	Total 963	C 612	N 164	O 187	0	0	0
1	3	129	Total 963	C 612	N 164	O 187	0	0	0
1	4	129	Total 963	C 612	N 164	O 187	0	0	0
1	5	129	Total 963	C 612	N 164	O 187	0	0	0
1	6	129	Total 963	C 612	N 164	O 187	0	0	0
1	7	129	Total 963	C 612	N 164	O 187	0	0	0
1	8	129	Total 963	C 612	N 164	O 187	0	0	0
1	9	129	Total 963	C 612	N 164	O 187	0	0	0
1	0	129	Total 963	C 612	N 164	O 187	0	0	0
1	a	129	Total 963	C 612	N 164	O 187	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	b	129	Total 963	C 612	N 164	O 187	0	0	0
1	c	129	Total 963	C 612	N 164	O 187	0	0	0
1	d	129	Total 963	C 612	N 164	O 187	0	0	0
1	e	129	Total 963	C 612	N 164	O 187	0	0	0
1	f	129	Total 963	C 612	N 164	O 187	0	0	0
1	g	129	Total 963	C 612	N 164	O 187	0	0	0
1	h	129	Total 963	C 612	N 164	O 187	0	0	0
1	i	129	Total 963	C 612	N 164	O 187	0	0	0

There are 90 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	59	THR	ALA	variant	UNP P07234
A	79	VAL	GLY	variant	UNP P07234
B	59	THR	ALA	variant	UNP P07234
B	79	VAL	GLY	variant	UNP P07234
C	59	THR	ALA	variant	UNP P07234
C	79	VAL	GLY	variant	UNP P07234
D	59	THR	ALA	variant	UNP P07234
D	79	VAL	GLY	variant	UNP P07234
E	59	THR	ALA	variant	UNP P07234
E	79	VAL	GLY	variant	UNP P07234
F	59	THR	ALA	variant	UNP P07234
F	79	VAL	GLY	variant	UNP P07234
G	59	THR	ALA	variant	UNP P07234
G	79	VAL	GLY	variant	UNP P07234
H	59	THR	ALA	variant	UNP P07234
H	79	VAL	GLY	variant	UNP P07234
I	59	THR	ALA	variant	UNP P07234
I	79	VAL	GLY	variant	UNP P07234
J	59	THR	ALA	variant	UNP P07234
J	79	VAL	GLY	variant	UNP P07234
K	59	THR	ALA	variant	UNP P07234
K	79	VAL	GLY	variant	UNP P07234
L	59	THR	ALA	variant	UNP P07234

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Chain	Residue	Modelled	Actual	Comment	Reference
L	79	VAL	GLY	variant	UNP P07234
M	59	THR	ALA	variant	UNP P07234
M	79	VAL	GLY	variant	UNP P07234
N	59	THR	ALA	variant	UNP P07234
N	79	VAL	GLY	variant	UNP P07234
O	59	THR	ALA	variant	UNP P07234
O	79	VAL	GLY	variant	UNP P07234
P	59	THR	ALA	variant	UNP P07234
P	79	VAL	GLY	variant	UNP P07234
Q	59	THR	ALA	variant	UNP P07234
Q	79	VAL	GLY	variant	UNP P07234
R	59	THR	ALA	variant	UNP P07234
R	79	VAL	GLY	variant	UNP P07234
S	59	THR	ALA	variant	UNP P07234
S	79	VAL	GLY	variant	UNP P07234
T	59	THR	ALA	variant	UNP P07234
T	79	VAL	GLY	variant	UNP P07234
U	59	THR	ALA	variant	UNP P07234
U	79	VAL	GLY	variant	UNP P07234
V	59	THR	ALA	variant	UNP P07234
V	79	VAL	GLY	variant	UNP P07234
W	59	THR	ALA	variant	UNP P07234
W	79	VAL	GLY	variant	UNP P07234
X	59	THR	ALA	variant	UNP P07234
X	79	VAL	GLY	variant	UNP P07234
Y	59	THR	ALA	variant	UNP P07234
Y	79	VAL	GLY	variant	UNP P07234
Z	59	THR	ALA	variant	UNP P07234
Z	79	VAL	GLY	variant	UNP P07234
1	59	THR	ALA	variant	UNP P07234
1	79	VAL	GLY	variant	UNP P07234
2	59	THR	ALA	variant	UNP P07234
2	79	VAL	GLY	variant	UNP P07234
3	59	THR	ALA	variant	UNP P07234
3	79	VAL	GLY	variant	UNP P07234
4	59	THR	ALA	variant	UNP P07234
4	79	VAL	GLY	variant	UNP P07234
5	59	THR	ALA	variant	UNP P07234
5	79	VAL	GLY	variant	UNP P07234
6	59	THR	ALA	variant	UNP P07234
6	79	VAL	GLY	variant	UNP P07234
7	59	THR	ALA	variant	UNP P07234

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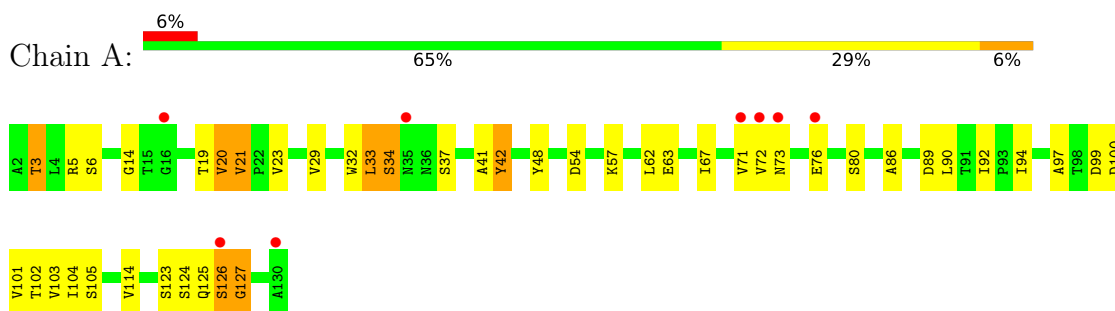
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Chain	Residue	Modelled	Actual	Comment	Reference
7	79	VAL	GLY	variant	UNP P07234
8	59	THR	ALA	variant	UNP P07234
8	79	VAL	GLY	variant	UNP P07234
9	59	THR	ALA	variant	UNP P07234
9	79	VAL	GLY	variant	UNP P07234
0	59	THR	ALA	variant	UNP P07234
0	79	VAL	GLY	variant	UNP P07234
a	59	THR	ALA	variant	UNP P07234
a	79	VAL	GLY	variant	UNP P07234
b	59	THR	ALA	variant	UNP P07234
b	79	VAL	GLY	variant	UNP P07234
c	59	THR	ALA	variant	UNP P07234
c	79	VAL	GLY	variant	UNP P07234
d	59	THR	ALA	variant	UNP P07234
d	79	VAL	GLY	variant	UNP P07234
e	59	THR	ALA	variant	UNP P07234
e	79	VAL	GLY	variant	UNP P07234
f	59	THR	ALA	variant	UNP P07234
f	79	VAL	GLY	variant	UNP P07234
g	59	THR	ALA	variant	UNP P07234
g	79	VAL	GLY	variant	UNP P07234
h	59	THR	ALA	variant	UNP P07234
h	79	VAL	GLY	variant	UNP P07234
i	59	THR	ALA	variant	UNP P07234
i	79	VAL	GLY	variant	UNP P07234

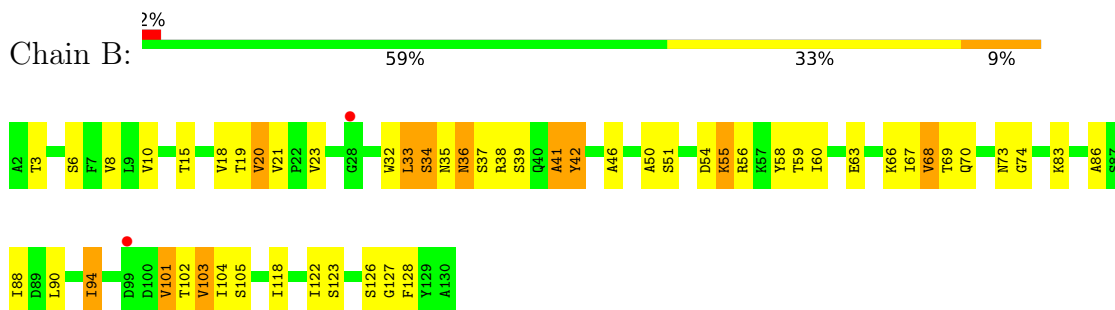
3 Residue-property plots [i](#)

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

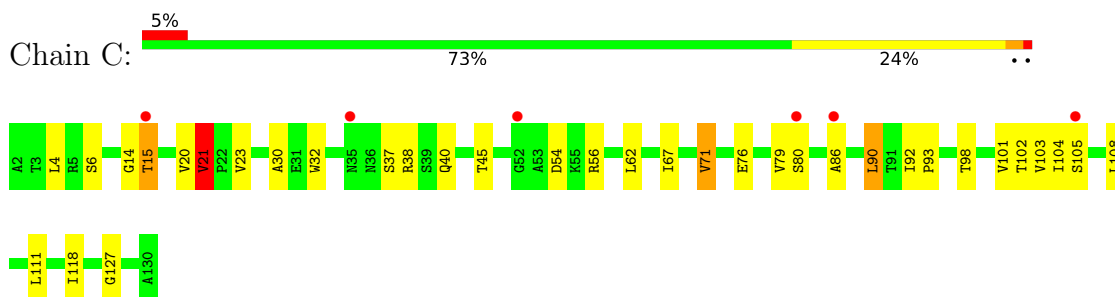
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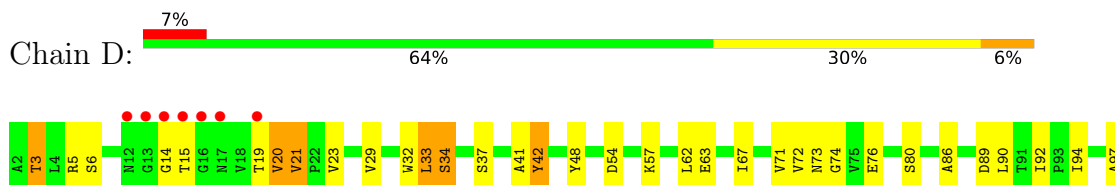
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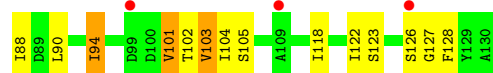


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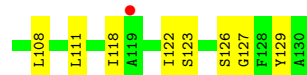




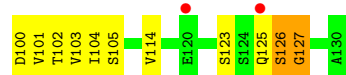
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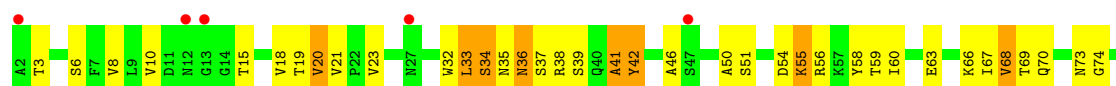
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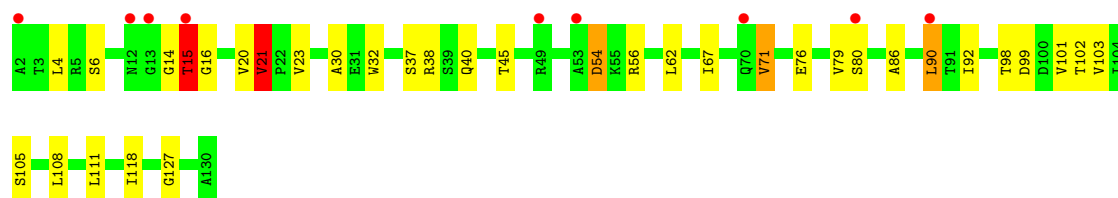


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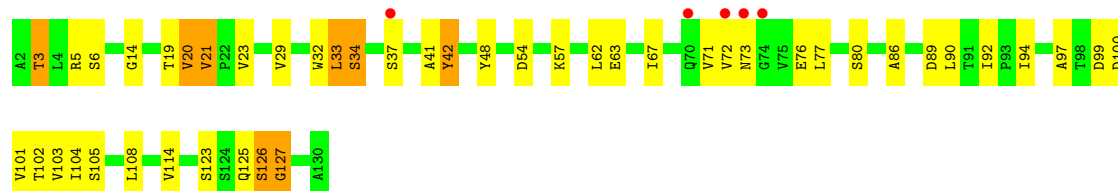


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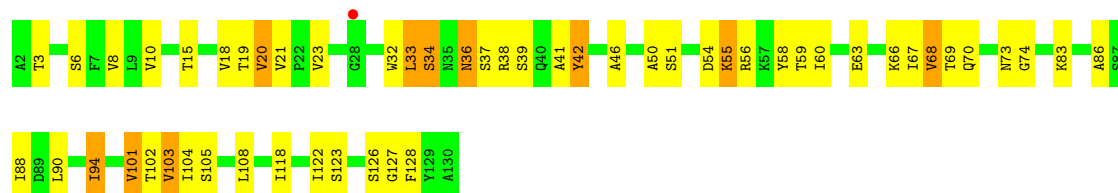




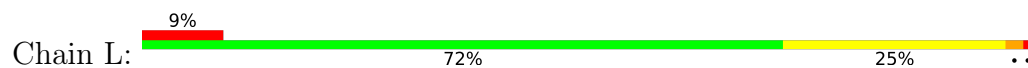
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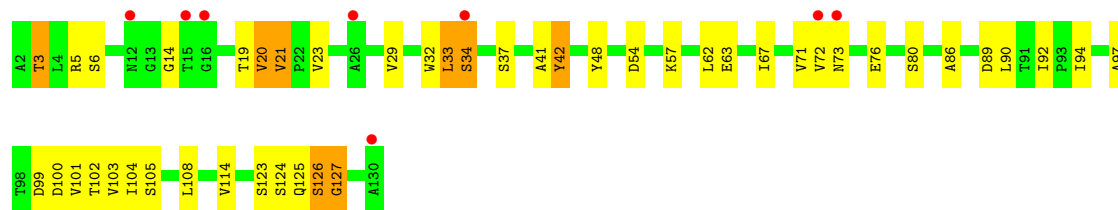
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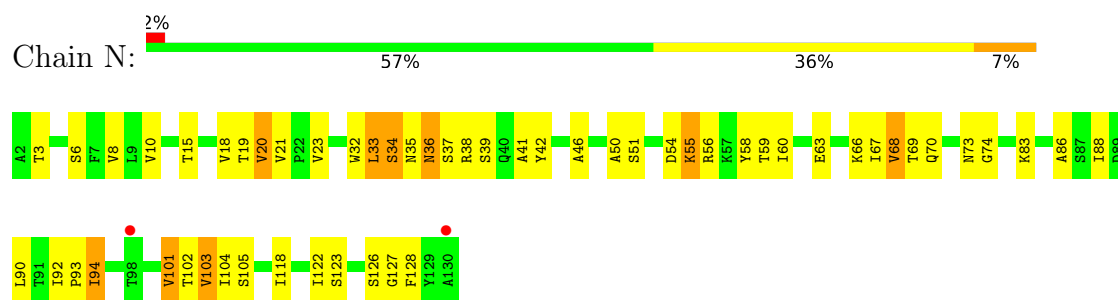
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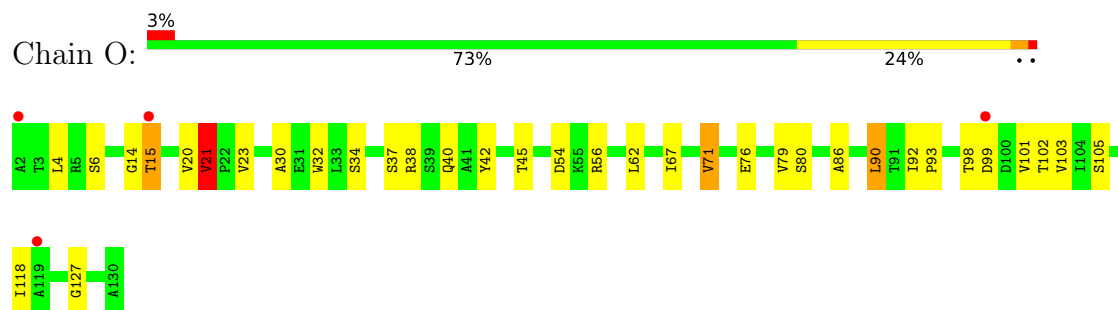
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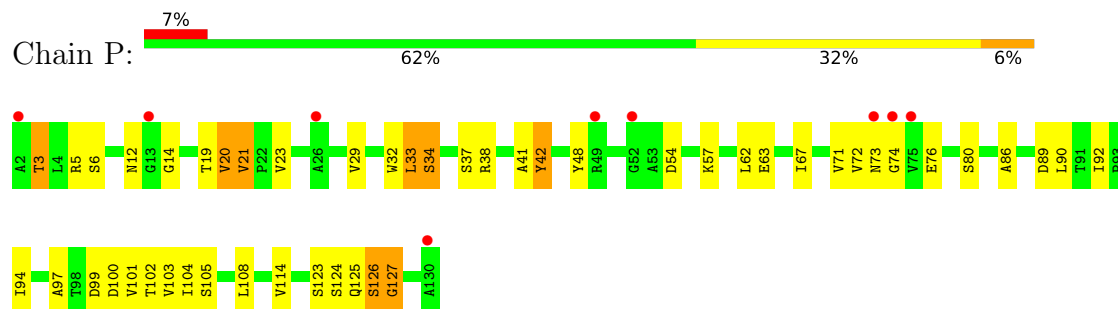
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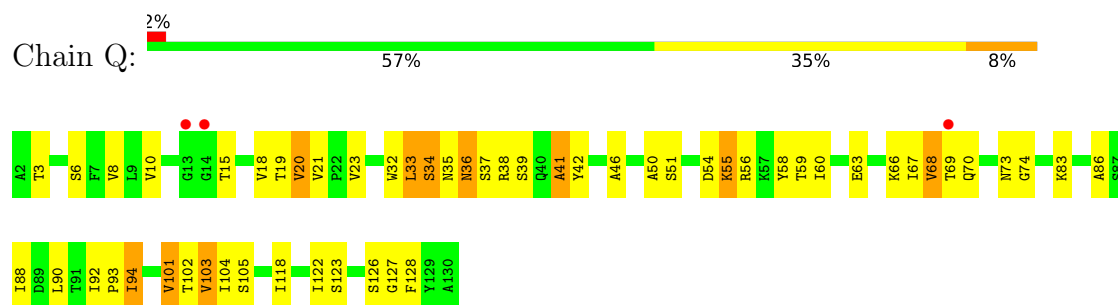
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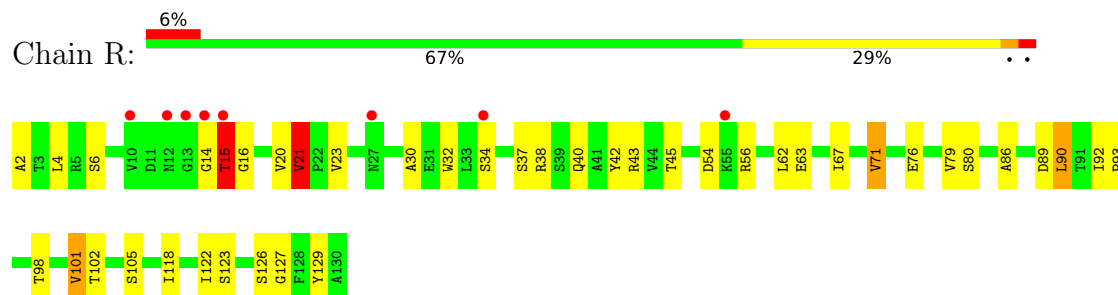
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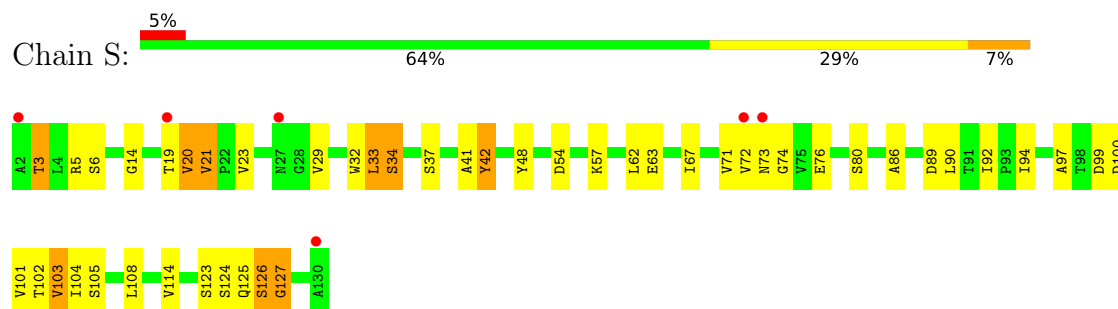
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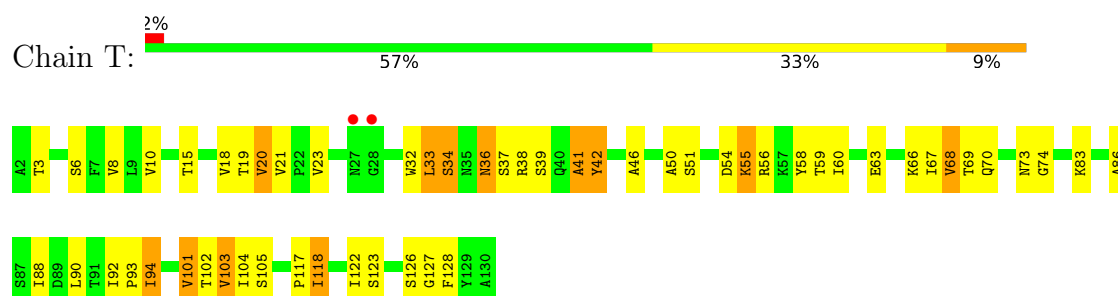
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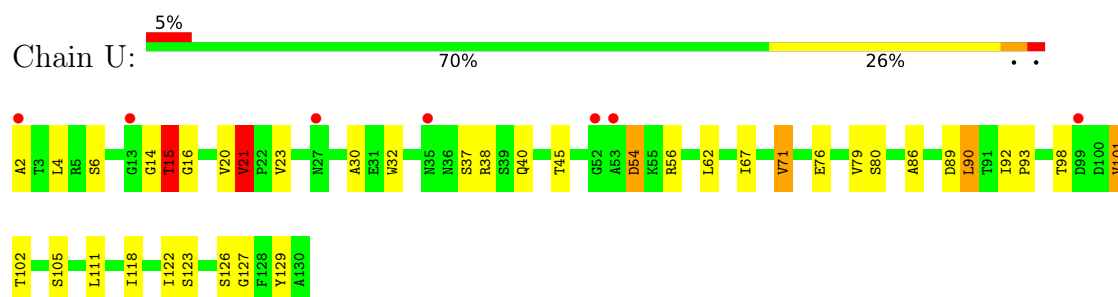
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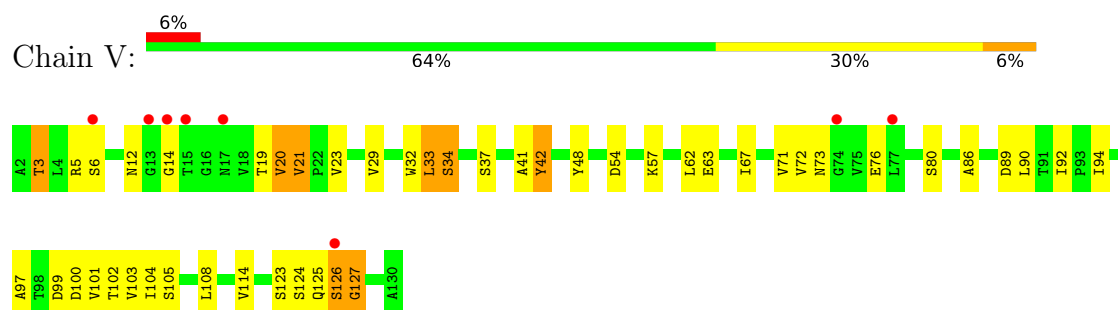
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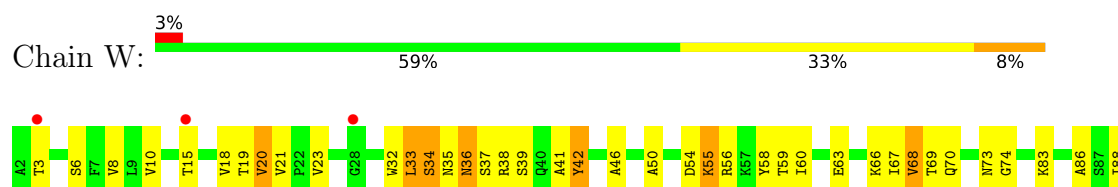
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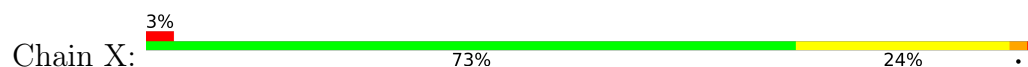


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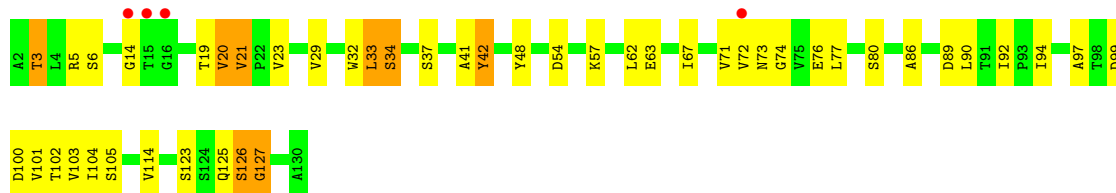




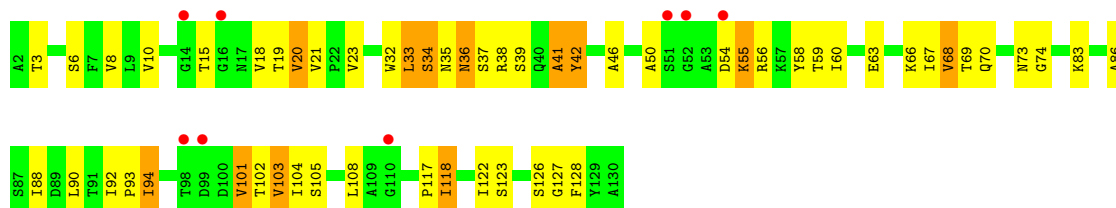
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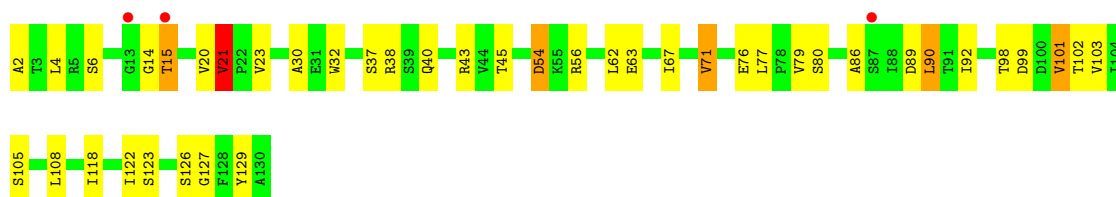
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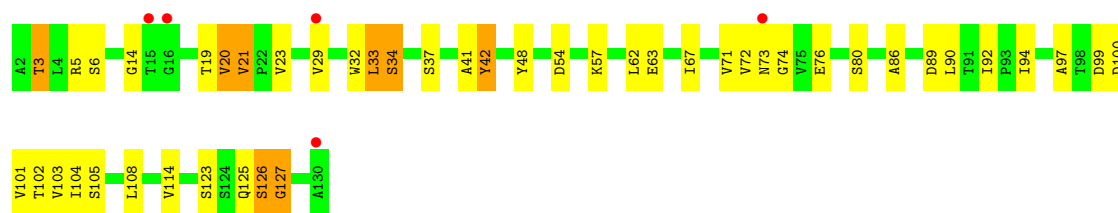


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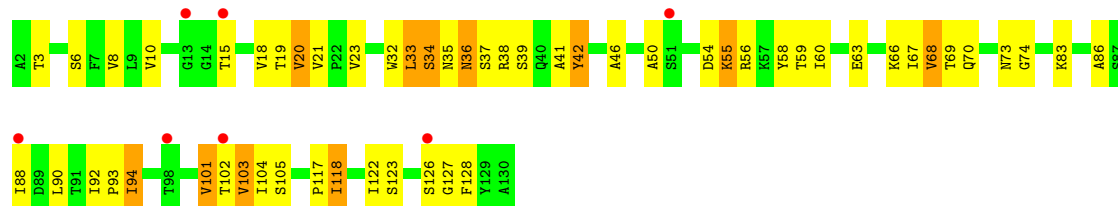


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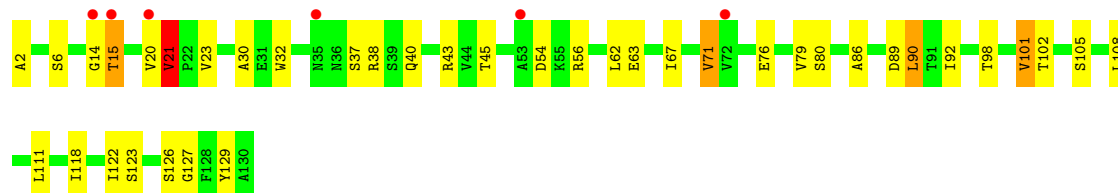




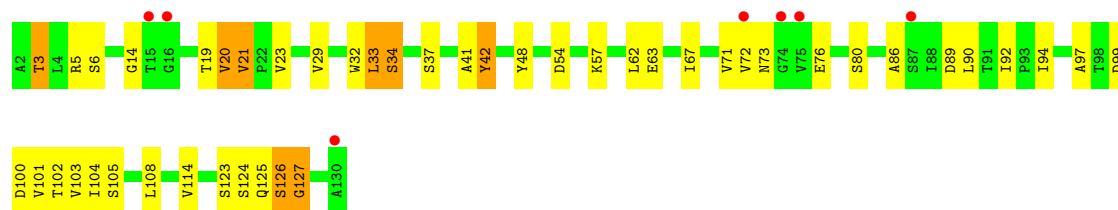
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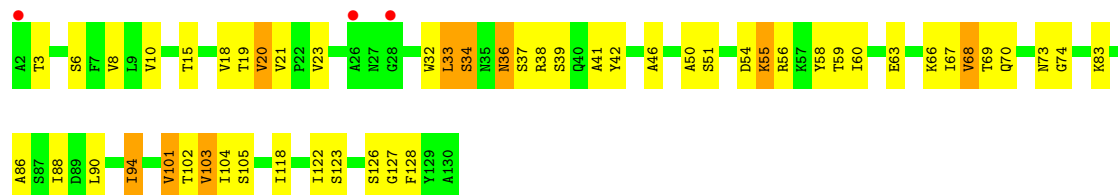
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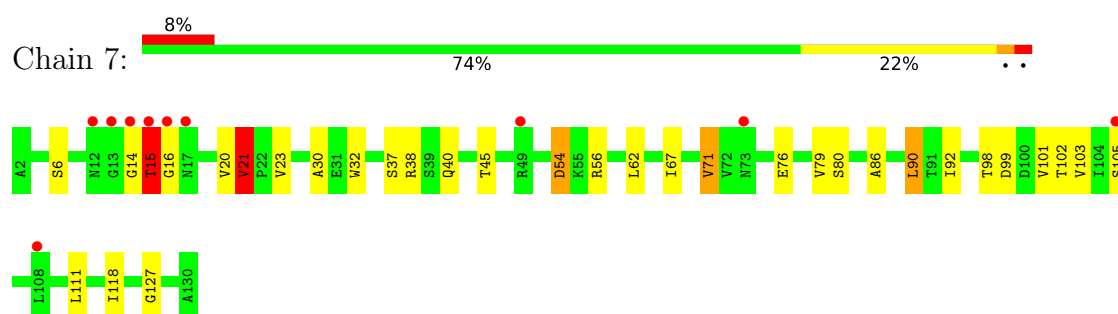
● Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



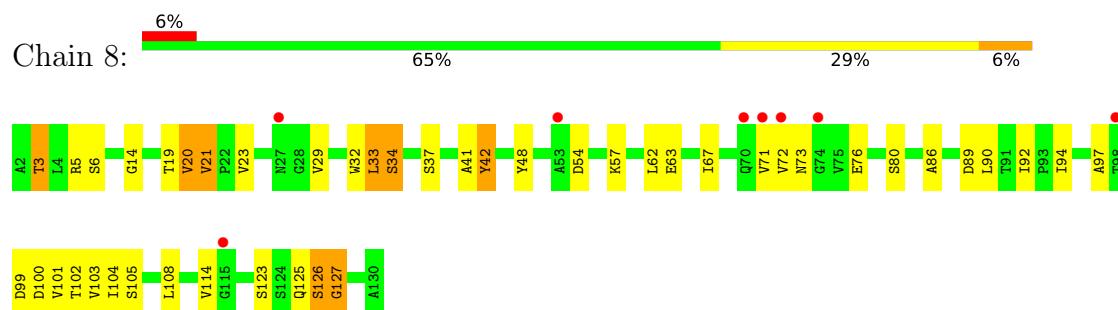
● Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



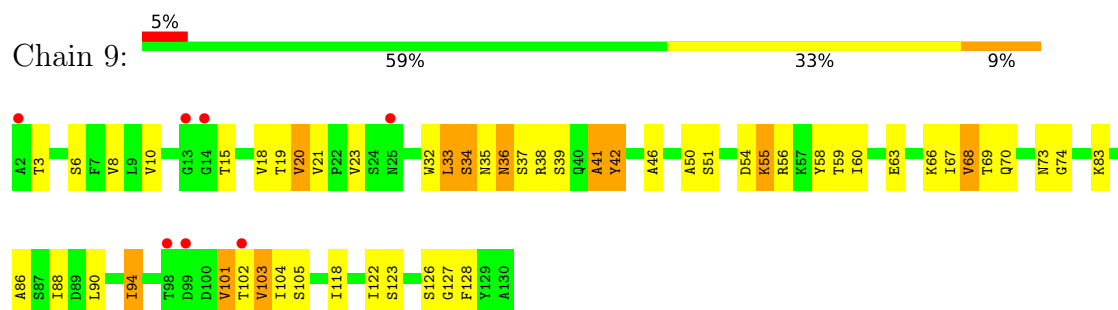
● Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



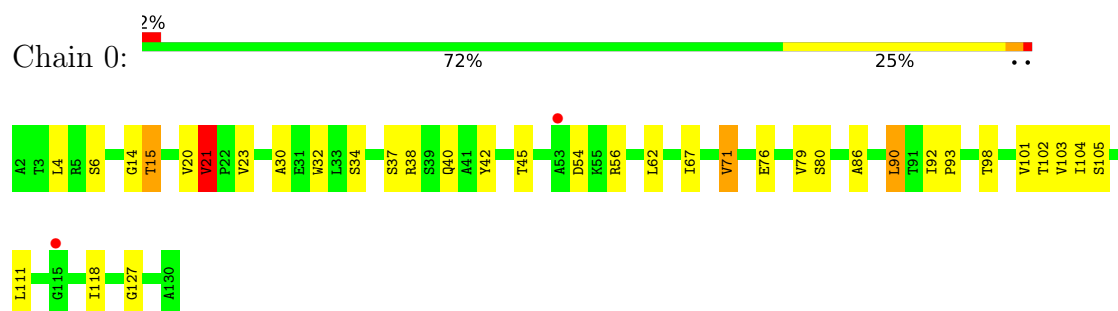
• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



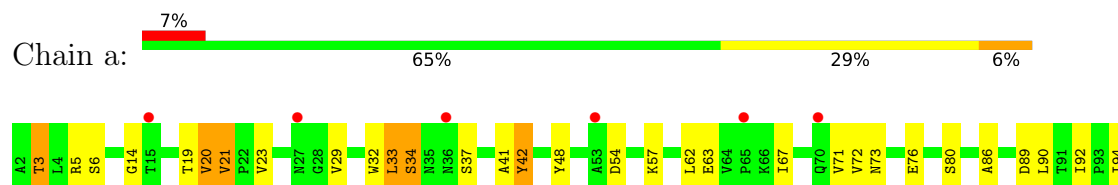
• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

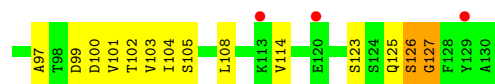


• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

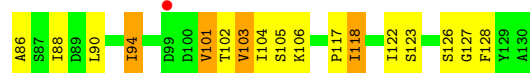
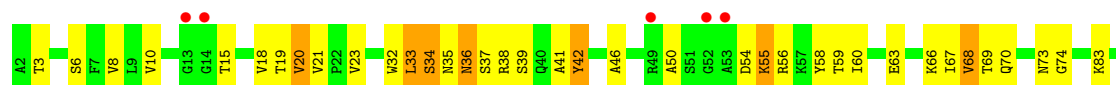


• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID





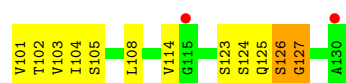
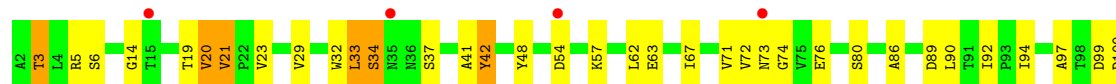
• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



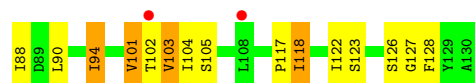
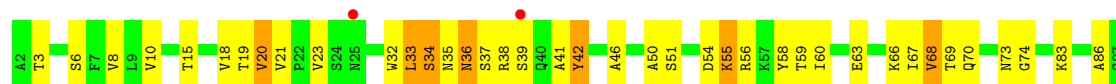
• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

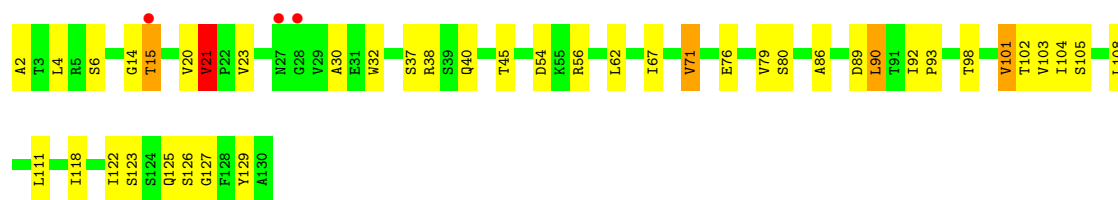


• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

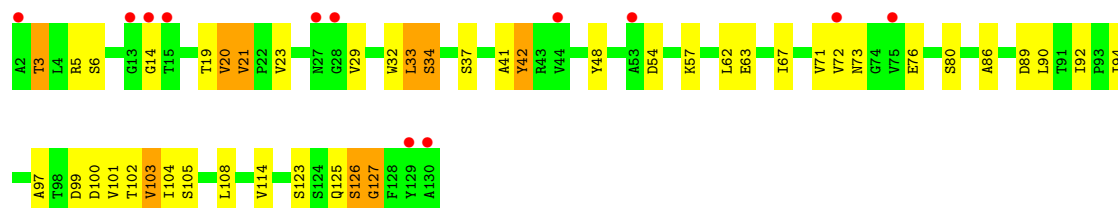


• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

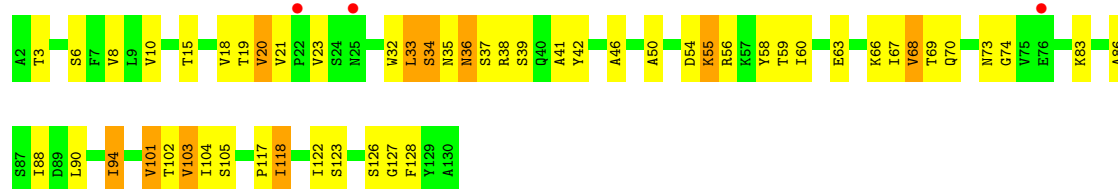




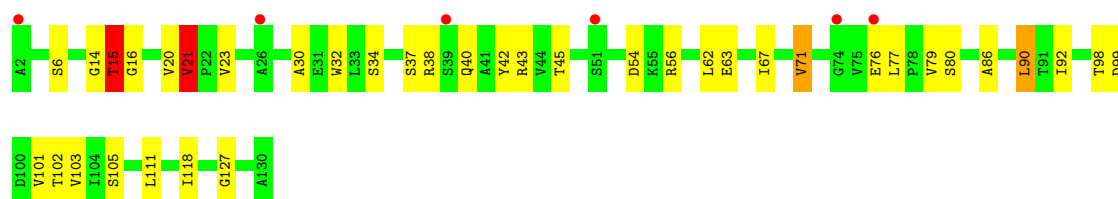
• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



• Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	272.70Å 293.50Å 339.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.40 30.00 – 3.40	Depositor EDS
% Data completeness (in resolution range)	66.0 (30.00-3.40) 65.9 (30.00-3.40)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.02 (at 3.40Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.279 , (Not available) 0.245 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 53.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	43335	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	1	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	2	1.08	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	3	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	4	1.07	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	5	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	6	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	7	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	8	1.08	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	9	1.14	4/980 (0.4%)	1.28	11/1336 (0.8%)
1	A	1.08	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	B	1.14	4/980 (0.4%)	1.28	11/1336 (0.8%)
1	C	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	D	1.08	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	E	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	F	1.07	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	G	1.08	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	H	1.14	4/980 (0.4%)	1.28	11/1336 (0.8%)
1	I	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	J	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	K	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	L	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	M	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	N	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	O	1.07	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	P	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	Q	1.14	4/980 (0.4%)	1.28	11/1336 (0.8%)
1	R	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	S	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	T	1.14	4/980 (0.4%)	1.28	11/1336 (0.8%)
1	U	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	V	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	W	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	X	1.07	3/980 (0.3%)	1.22	6/1336 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Y	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	Z	1.14	4/980 (0.4%)	1.28	11/1336 (0.8%)
1	a	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	b	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	c	1.06	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	d	1.08	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	e	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	f	1.07	3/980 (0.3%)	1.22	6/1336 (0.4%)
1	g	1.09	3/980 (0.3%)	1.27	10/1336 (0.7%)
1	h	1.14	4/980 (0.4%)	1.28	10/1336 (0.7%)
1	i	1.07	3/980 (0.3%)	1.22	6/1336 (0.4%)
All	All	1.10	150/44100 (0.3%)	1.26	396/60120 (0.7%)

The worst 5 of 150 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	103	VAL	CA-CB	-7.33	1.46	1.54
1	5	103	VAL	CA-CB	-7.33	1.46	1.54
1	a	103	VAL	CA-CB	-7.33	1.46	1.54
1	D	103	VAL	CA-CB	-7.31	1.46	1.54
1	2	103	VAL	CA-CB	-7.31	1.46	1.54

The worst 5 of 396 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	3	THR	N-CA-C	-8.97	102.84	113.88
1	2	3	THR	N-CA-C	-8.97	102.84	113.88
1	d	3	THR	N-CA-C	-8.97	102.84	113.88
1	P	3	THR	N-CA-C	-8.96	102.86	113.88
1	S	3	THR	N-CA-C	-8.96	102.86	113.88

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	963	0	976	19	0
1	1	963	0	976	38	0
1	2	963	0	976	35	0
1	3	963	0	976	40	0
1	4	963	0	976	35	0
1	5	963	0	976	32	0
1	6	963	0	976	36	0
1	7	963	0	976	18	0
1	8	963	0	976	31	0
1	9	963	0	976	37	0
1	A	963	0	976	31	0
1	B	963	0	976	40	0
1	C	963	0	976	19	0
1	D	963	0	976	34	2
1	E	963	0	976	38	0
1	F	963	0	976	36	0
1	G	963	0	976	30	0
1	H	963	0	976	39	0
1	I	963	0	976	19	0
1	J	963	0	976	32	0
1	K	963	0	976	39	0
1	L	963	0	976	20	0
1	M	963	0	976	32	0
1	N	963	0	976	38	0
1	O	963	0	976	18	0
1	P	963	0	976	38	0
1	Q	963	0	976	40	0
1	R	963	0	976	38	0
1	S	963	0	976	37	0
1	T	963	0	976	40	0
1	U	963	0	976	36	0
1	V	963	0	976	33	2
1	W	963	0	976	38	0
1	X	963	0	976	18	0
1	Y	963	0	976	35	0
1	Z	963	0	976	40	0
1	a	963	0	976	31	0
1	b	963	0	976	39	0
1	c	963	0	976	17	0
1	d	963	0	976	36	0
1	e	963	0	976	40	0
1	f	963	0	976	40	0
1	g	963	0	976	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	h	963	0	976	37	0
1	i	963	0	976	21	0
All	All	43335	0	43920	1202	2

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 14.

The worst 5 of 1202 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:U:101:VAL:HG12	1:4:123:SER:HA	1.42	1.01
1:F:101:VAL:HG12	1:1:123:SER:HA	1.42	1.00
1:R:101:VAL:HG12	1:f:123:SER:HA	1.42	1.00
1:R:123:SER:HA	1:f:101:VAL:HG12	1.42	1.00
1:F:123:SER:HA	1:1:101:VAL:HG12	1.42	0.99

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:15:THR:CG2	1:V:6:SER:O[8_554]	1.49	0.71
1:D:15:THR:CB	1:V:6:SER:O[8_554]	2.15	0.05

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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	1	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	2	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	4	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	5	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	6	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	7	127/129 (98%)	116 (91%)	9 (7%)	2 (2%)	7	29
1	8	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	9	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	A	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	B	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	C	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	D	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	E	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	F	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	G	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	H	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	I	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	J	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	K	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	L	127/129 (98%)	116 (91%)	9 (7%)	2 (2%)	7	29
1	M	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	N	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	O	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	P	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	Q	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	R	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	S	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	T	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	U	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	V	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	W	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	X	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	Z	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	a	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	b	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	c	127/129 (98%)	116 (91%)	9 (7%)	2 (2%)	7	29
1	d	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	e	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	f	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
1	g	127/129 (98%)	111 (87%)	15 (12%)	1 (1%)	16	44
1	h	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	44
1	i	127/129 (98%)	117 (92%)	8 (6%)	2 (2%)	7	29
All	All	5715/5805 (98%)	5172 (90%)	483 (8%)	60 (1%)	12	40

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	15	THR
1	C	14	GLY
1	C	15	THR
1	E	15	THR
1	F	14	GLY

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 X-ray entries followed by that with respect to entries of similar resolution.

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	0	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	1	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	2	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	3	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	4	104/104 (100%)	96 (92%)	8 (8%)	12	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	5	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	6	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	7	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	8	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	9	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	A	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	B	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	C	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	D	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	E	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	F	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	G	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	H	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	I	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	J	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	K	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	L	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	M	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	N	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	O	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	P	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	Q	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	R	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	S	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	T	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	U	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	V	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	W	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	X	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	Y	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	Z	104/104 (100%)	95 (91%)	9 (9%)	9	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	b	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	c	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	d	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	e	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	f	104/104 (100%)	96 (92%)	8 (8%)	12	37
1	g	104/104 (100%)	98 (94%)	6 (6%)	18	45
1	h	104/104 (100%)	95 (91%)	9 (9%)	9	32
1	i	104/104 (100%)	96 (92%)	8 (8%)	12	37
All	All	4680/4680 (100%)	4335 (93%)	345 (7%)	13	38

5 of 345 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	5	20	VAL
1	b	55	LYS
1	6	33	LEU
1	9	20	VAL
1	d	20	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 106 such sidechains are listed below:

Mol	Chain	Res	Type
1	Y	73	ASN
1	5	73	ASN
1	g	12	ASN
1	Z	70	GLN
1	3	36	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	129/129 (100%)	0.49	2 (1%) 70 56	4, 19, 52, 83	0
1	1	129/129 (100%)	0.40	3 (2%) 61 46	4, 19, 52, 83	0
1	2	129/129 (100%)	0.54	5 (3%) 43 31	2, 18, 56, 81	0
1	3	129/129 (100%)	0.62	7 (5%) 31 24	3, 15, 50, 77	0
1	4	129/129 (100%)	0.50	6 (4%) 36 27	4, 19, 52, 83	0
1	5	129/129 (100%)	0.54	7 (5%) 31 24	2, 18, 56, 81	0
1	6	129/129 (100%)	0.40	3 (2%) 61 46	3, 15, 50, 77	0
1	7	129/129 (100%)	0.75	10 (7%) 19 16	4, 19, 52, 83	0
1	8	129/129 (100%)	0.62	8 (6%) 26 21	2, 18, 56, 81	0
1	9	129/129 (100%)	0.51	7 (5%) 31 24	3, 15, 50, 77	0
1	A	129/129 (100%)	0.38	8 (6%) 26 21	2, 18, 56, 81	0
1	B	129/129 (100%)	0.28	2 (1%) 70 56	3, 15, 50, 77	0
1	C	129/129 (100%)	0.41	6 (4%) 36 27	4, 19, 52, 83	0
1	D	129/129 (100%)	0.57	9 (6%) 22 18	2, 18, 56, 81	0
1	E	129/129 (100%)	0.49	6 (4%) 36 27	3, 15, 50, 77	0
1	F	129/129 (100%)	0.32	6 (4%) 36 27	4, 19, 52, 83	0
1	G	129/129 (100%)	0.43	6 (4%) 36 27	2, 18, 56, 81	0
1	H	129/129 (100%)	0.46	6 (4%) 36 27	3, 15, 50, 77	0
1	I	129/129 (100%)	0.62	9 (6%) 22 18	4, 19, 52, 83	0
1	J	129/129 (100%)	0.38	5 (3%) 43 31	2, 18, 56, 81	0
1	K	129/129 (100%)	0.42	1 (0%) 82 71	3, 15, 50, 77	0
1	L	129/129 (100%)	0.83	11 (8%) 16 15	4, 19, 52, 83	0
1	M	129/129 (100%)	0.49	8 (6%) 26 21	2, 18, 56, 81	0
1	N	129/129 (100%)	0.39	2 (1%) 70 56	3, 15, 50, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	O	129/129 (100%)	0.47	4 (3%) 51 38	4, 19, 52, 83	0
1	P	129/129 (100%)	0.50	9 (6%) 22 18	2, 18, 56, 81	0
1	Q	129/129 (100%)	0.38	3 (2%) 61 46	3, 15, 50, 77	0
1	R	129/129 (100%)	0.50	8 (6%) 26 21	4, 19, 52, 83	0
1	S	129/129 (100%)	0.53	6 (4%) 36 27	2, 18, 56, 81	0
1	T	129/129 (100%)	0.40	2 (1%) 70 56	3, 15, 50, 77	0
1	U	129/129 (100%)	0.61	7 (5%) 31 24	4, 19, 52, 83	0
1	V	129/129 (100%)	0.57	8 (6%) 26 21	2, 18, 56, 81	0
1	W	129/129 (100%)	0.39	4 (3%) 51 38	3, 15, 50, 77	0
1	X	129/129 (100%)	0.45	4 (3%) 51 38	4, 19, 52, 83	0
1	Y	129/129 (100%)	0.34	4 (3%) 51 38	2, 18, 56, 81	0
1	Z	129/129 (100%)	0.41	8 (6%) 26 21	3, 15, 50, 77	0
1	a	129/129 (100%)	0.59	9 (6%) 22 18	2, 18, 56, 81	0
1	b	129/129 (100%)	0.34	6 (4%) 36 27	3, 15, 50, 77	0
1	c	129/129 (100%)	0.44	7 (5%) 31 24	4, 19, 52, 83	0
1	d	129/129 (100%)	0.49	6 (4%) 36 27	2, 18, 56, 81	0
1	e	129/129 (100%)	0.35	4 (3%) 51 38	3, 15, 50, 77	0
1	f	129/129 (100%)	0.42	3 (2%) 61 46	4, 19, 52, 83	0
1	g	129/129 (100%)	0.62	12 (9%) 14 14	2, 18, 56, 81	0
1	h	129/129 (100%)	0.46	3 (2%) 61 46	3, 15, 50, 77	0
1	i	129/129 (100%)	0.53	6 (4%) 36 27	4, 19, 52, 83	0
All	All	5805/5805 (100%)	0.48	266 (4%) 37 27	2, 17, 55, 83	0

The worst 5 of 266 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	7	14	GLY	8.1
1	7	15	THR	7.7
1	L	16	GLY	6.6
1	V	13	GLY	6.2
1	L	15	THR	6.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.