



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 05:11 PM UTC

PDB ID : 3NG9 / pdb_00003ng9
Title : Structure to Function Correlations for Adeno-associated Virus Serotype 1
Authors : Govindasamy, L.; Miller, E.B.; Gurda, B.; McKenna, R.; Zolotukhin, S.; Muzy-
czka, N.; Agbandje-McKenna, M.
Deposited on : 2010-06-11
Resolution : 2.50 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

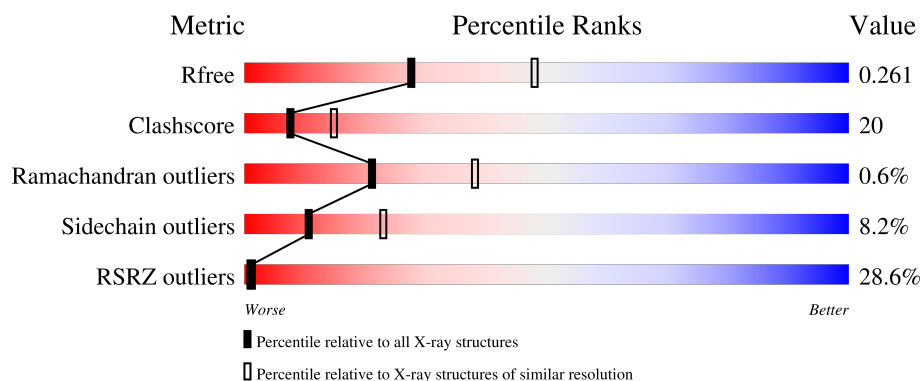
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	A	736	7% 46% 20% • • 29%
1	B	736	15% 46% 20% • 29%
1	C	736	20% 47% 20% • 29%
1	D	736	12% 45% 21% • • 29%
1	E	736	30% 46% 21% • 29%

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Mol	Chain	Length	Quality of chain
1	F	736	16% 45% 22% • 29%
1	G	736	24% 45% 22% • 29%
1	H	736	12% 46% 20% • • 29%
1	I	736	24% 45% 21% • 29%
1	J	736	42% 49% 18% • 29%

2 Entry composition

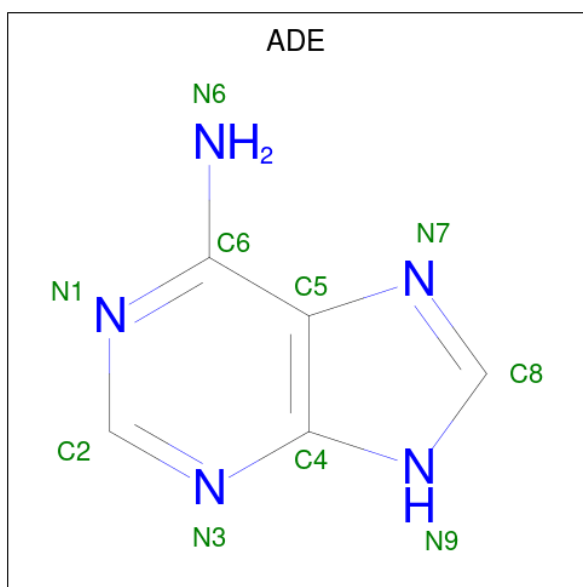
There are 4 unique types of molecules in this entry. The entry contains 42680 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Capsid protein.

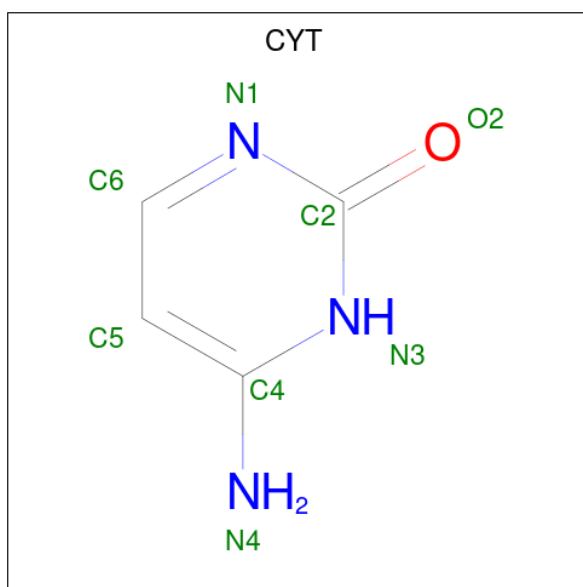
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	B	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	C	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	D	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	E	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	F	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	G	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	H	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	I	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			
1	J	520	Total	C	N	O	S	0	0	0
			4120	2606	710	788	16			

- Molecule 2 is ADENINE (CCD ID: ADE) (formula: C₅H₅N₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			10	5	5		
2	B	1	Total	C	N	0	0
			10	5	5		
2	C	1	Total	C	N	0	0
			10	5	5		
2	D	1	Total	C	N	0	0
			10	5	5		
2	E	1	Total	C	N	0	0
			10	5	5		
2	F	1	Total	C	N	0	0
			10	5	5		
2	G	1	Total	C	N	0	0
			10	5	5		
2	H	1	Total	C	N	0	0
			10	5	5		
2	I	1	Total	C	N	0	0
			10	5	5		
2	J	1	Total	C	N	0	0
			10	5	5		

- Molecule 3 is 6-AMINOPYRIMIDIN-2(1H)-ONE (CCD ID: CYT) (formula: C₄H₅N₃O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	3	1		
3	B	1	Total	C	N	O	0	0
			8	4	3	1		
3	B	1	Total	C	N	O	0	0
			8	4	3	1		
3	C	1	Total	C	N	O	0	0
			8	4	3	1		
3	D	1	Total	C	N	O	0	0
			8	4	3	1		
3	E	1	Total	C	N	O	0	0
			8	4	3	1		
3	F	1	Total	C	N	O	0	0
			8	4	3	1		
3	H	1	Total	C	N	O	0	0
			8	4	3	1		
3	I	1	Total	C	N	O	0	0
			8	4	3	1		
3	J	1	Total	C	N	O	0	0
			8	4	3	1		

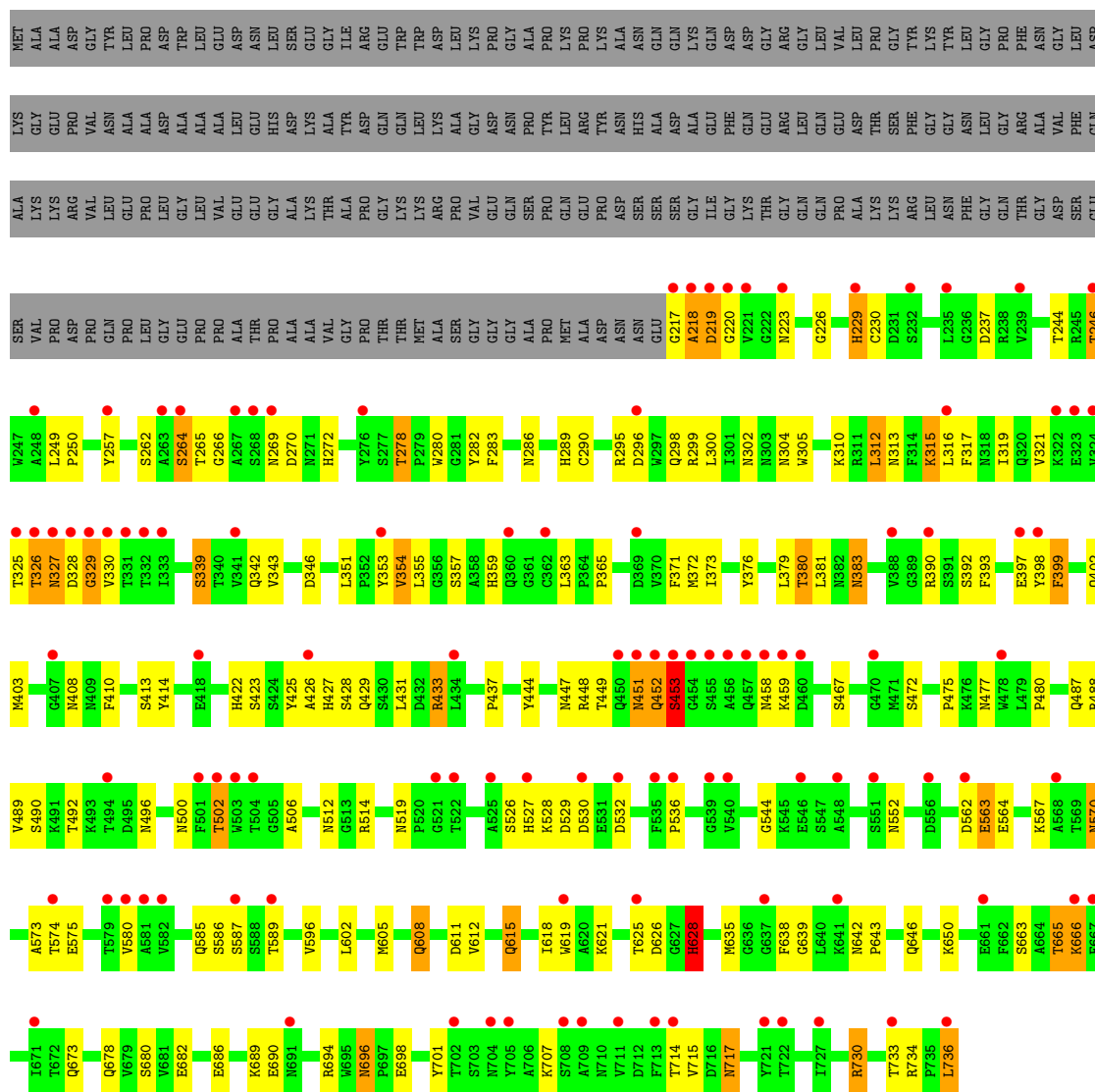
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	131	Total	O	0	0
			131	131		
4	B	130	Total	O	0	0
			130	130		

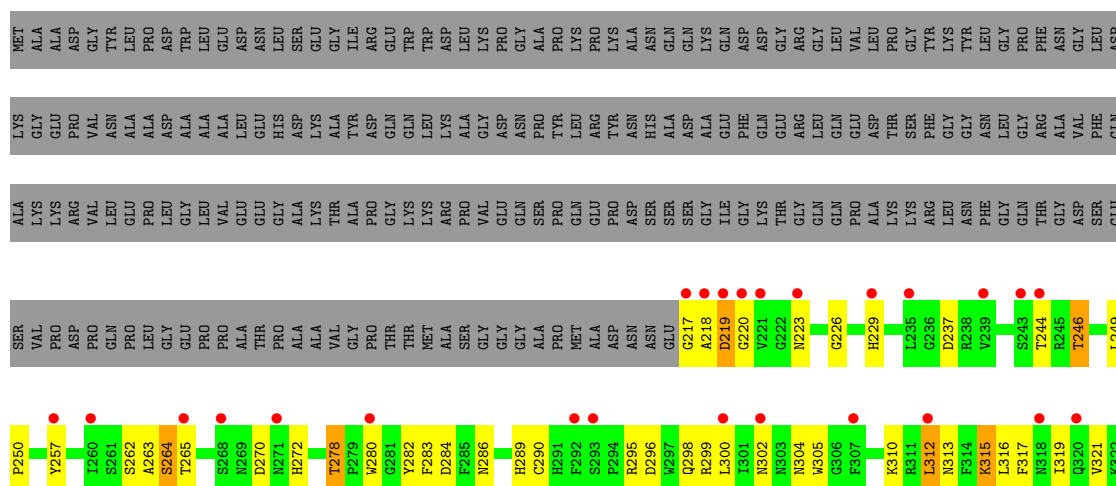
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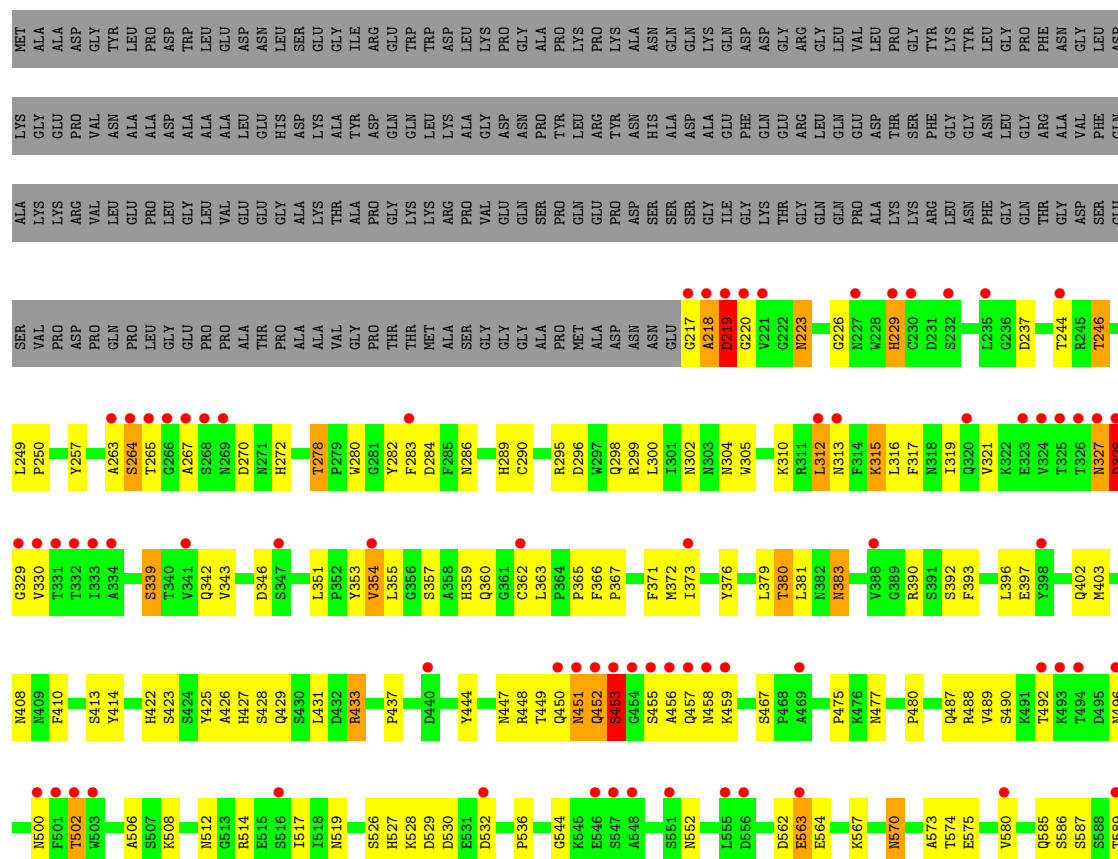
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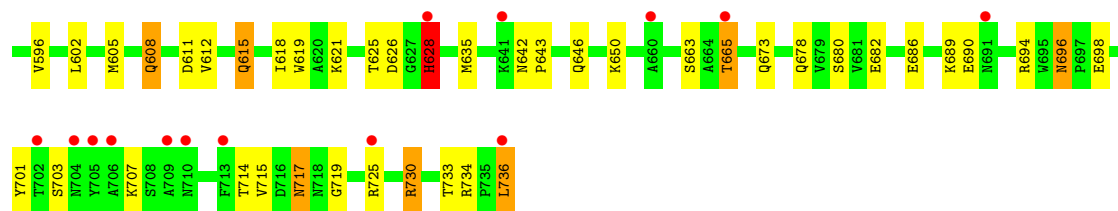
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	128	Total 128	O 128	0	0
4	D	131	Total 131	O 131	0	0
4	E	133	Total 133	O 133	0	0
4	F	131	Total 131	O 131	0	0
4	G	127	Total 127	O 127	0	0
4	H	130	Total 130	O 130	0	0
4	I	130	Total 130	O 130	0	0
4	J	129	Total 129	O 129	0	0



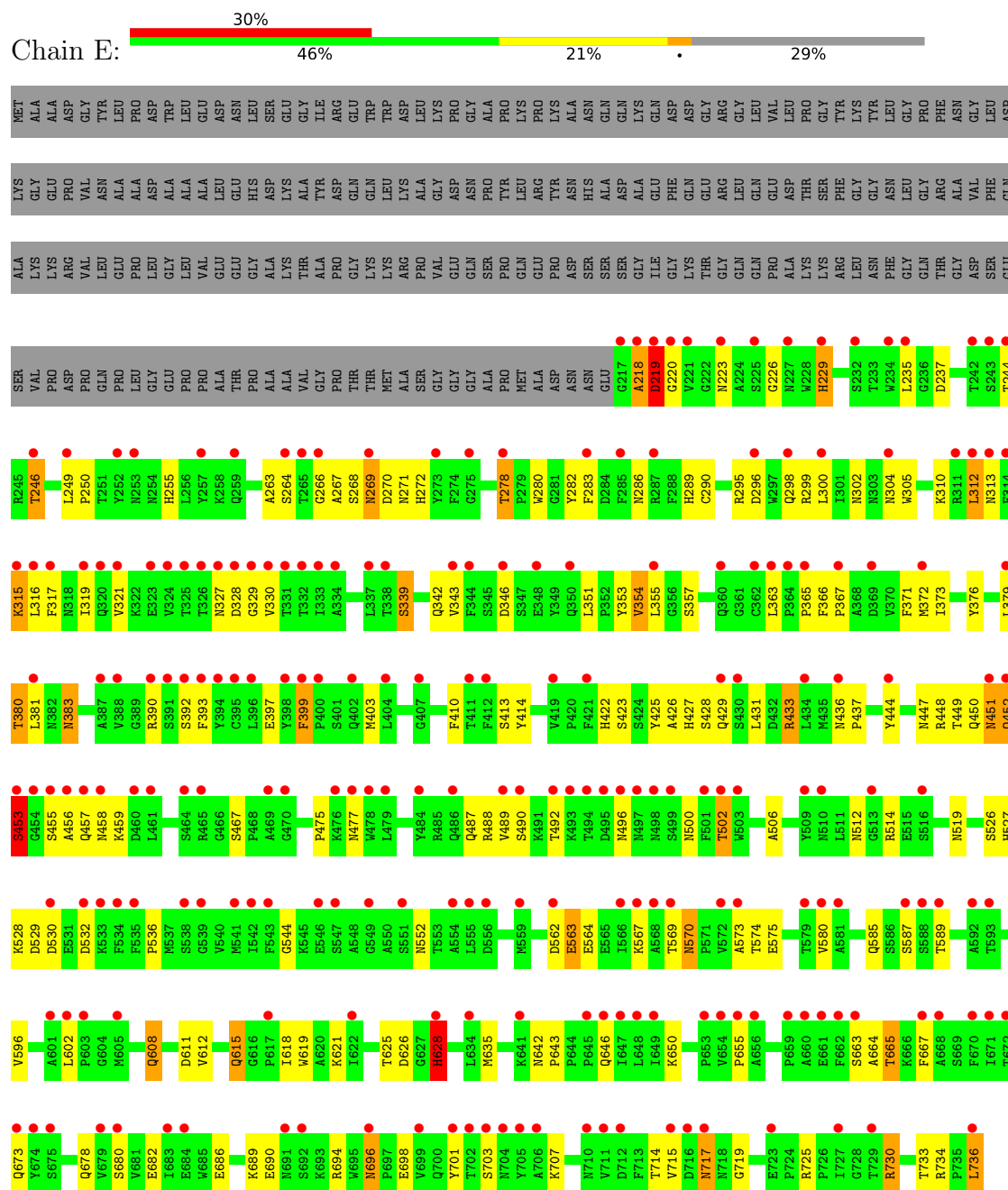
● Molecule 1: Capsid protein





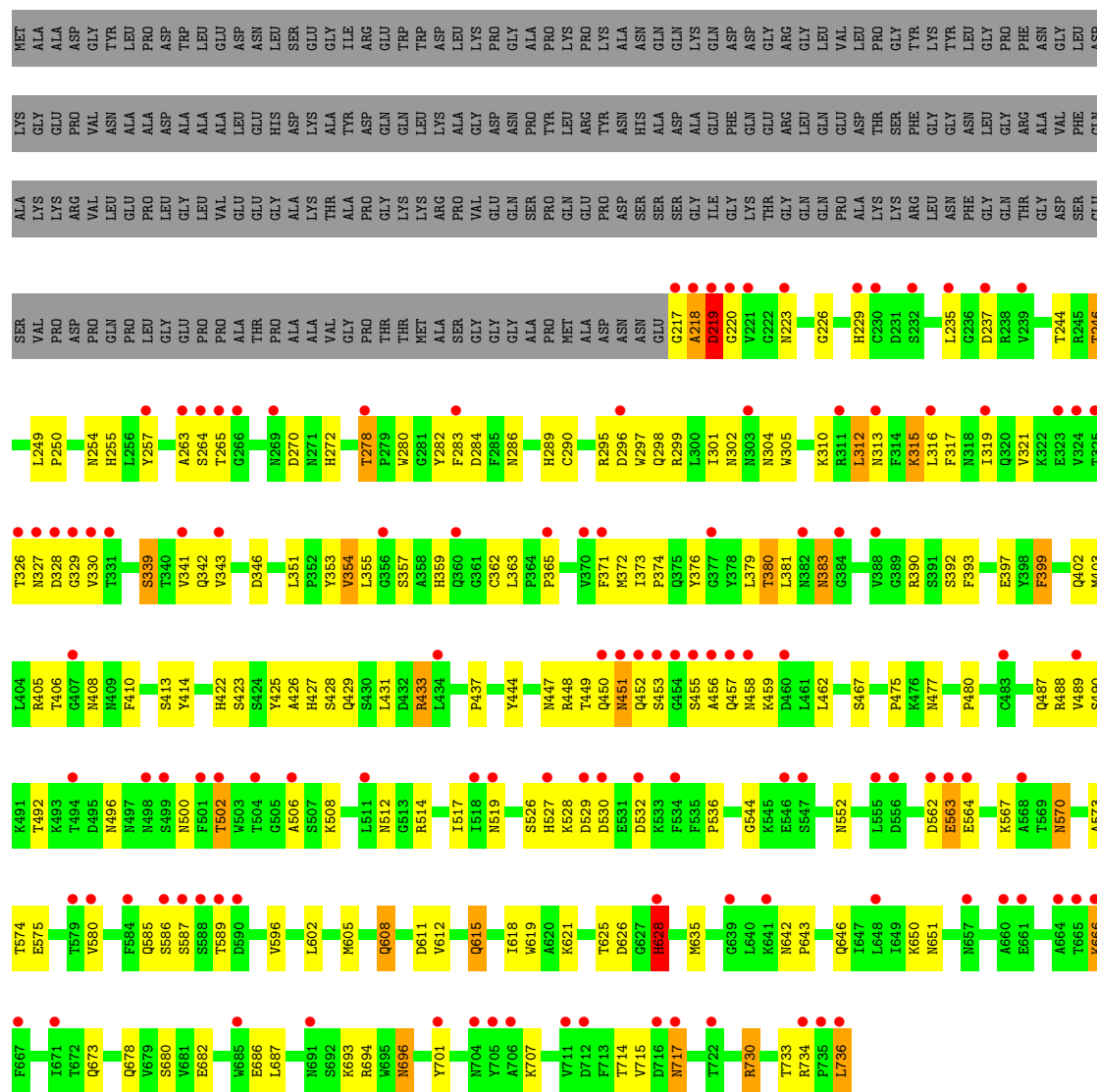


• Molecule 1: Capsid protein

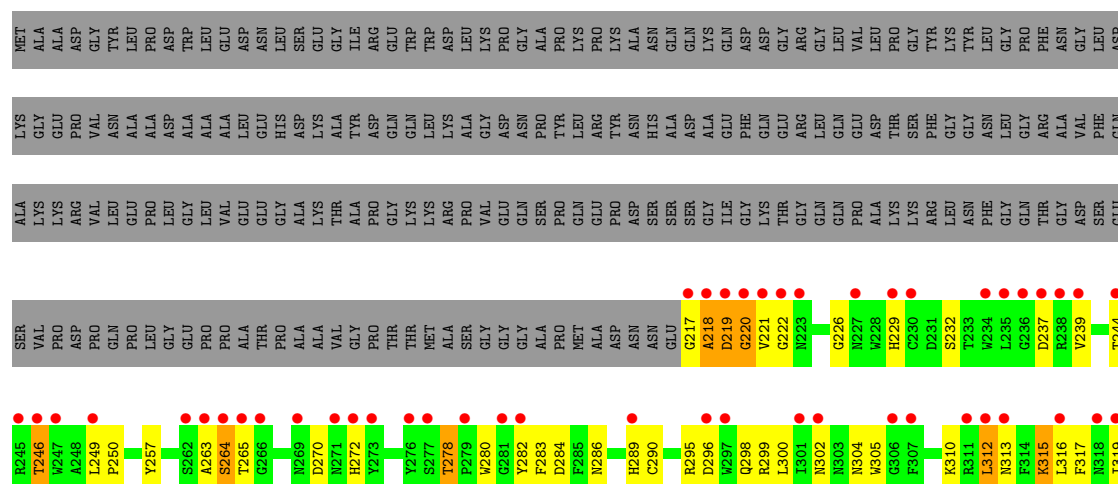


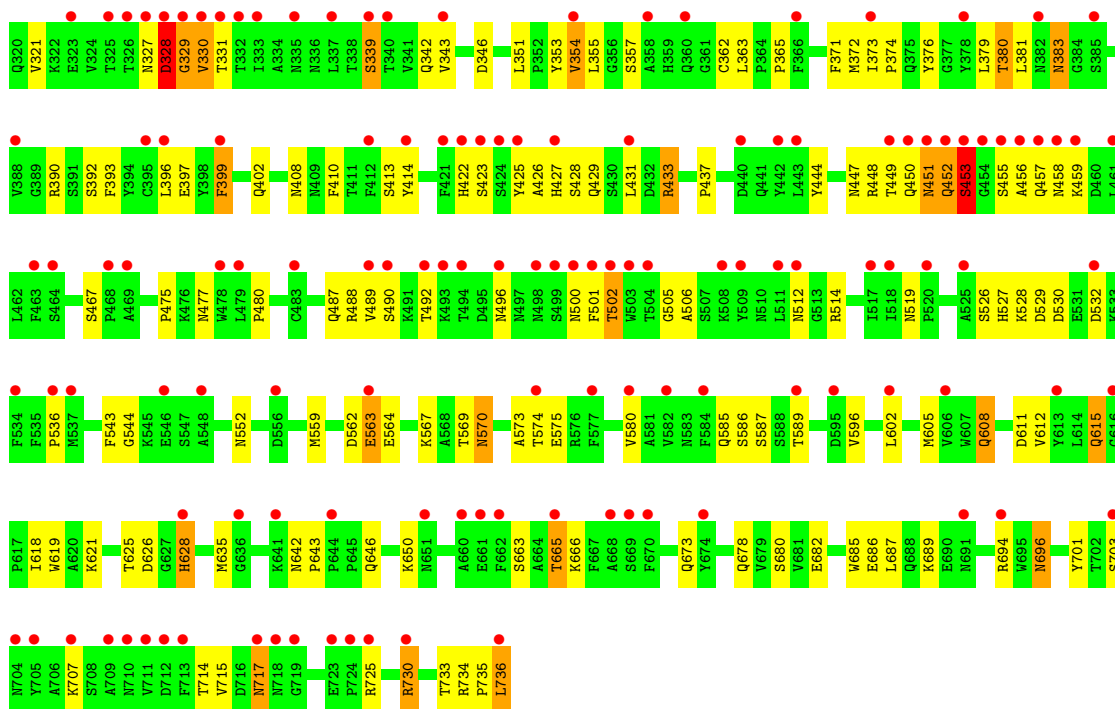
• Molecule 1: Capsid protein



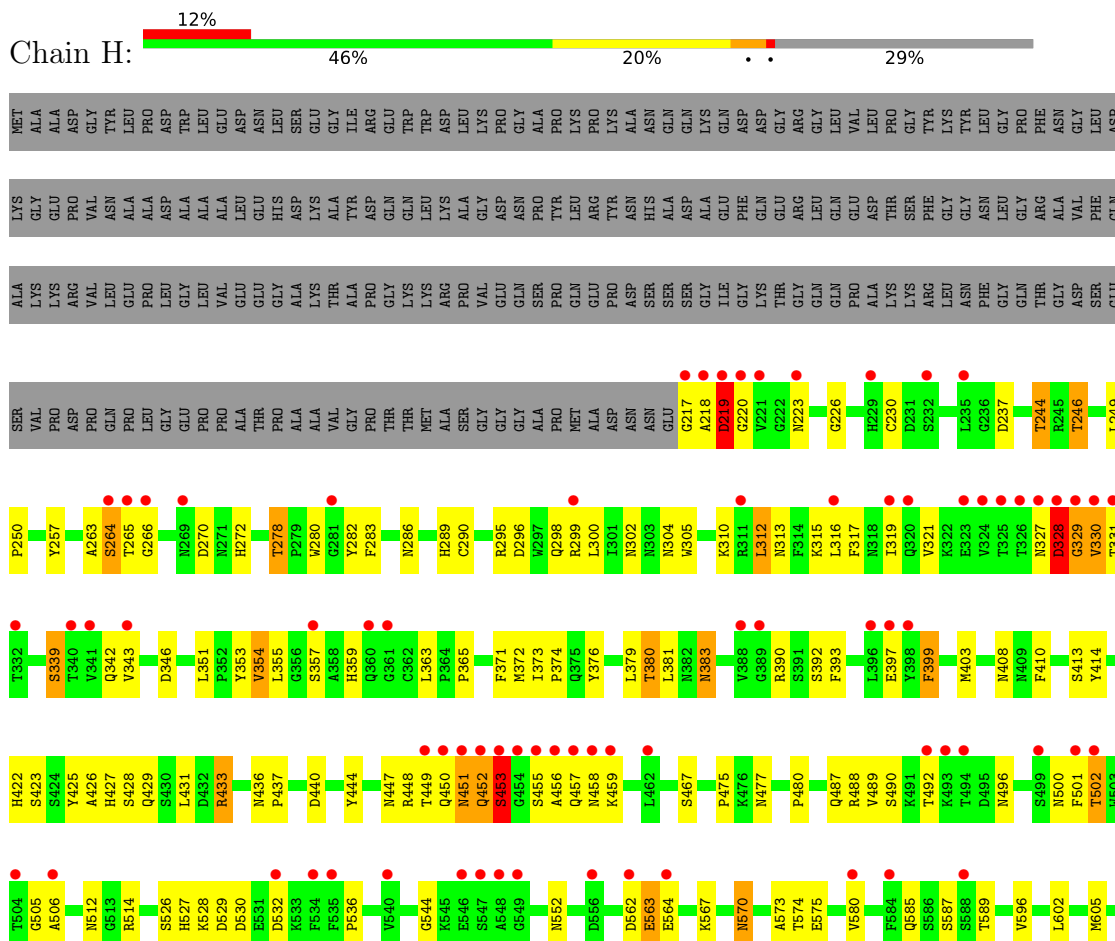


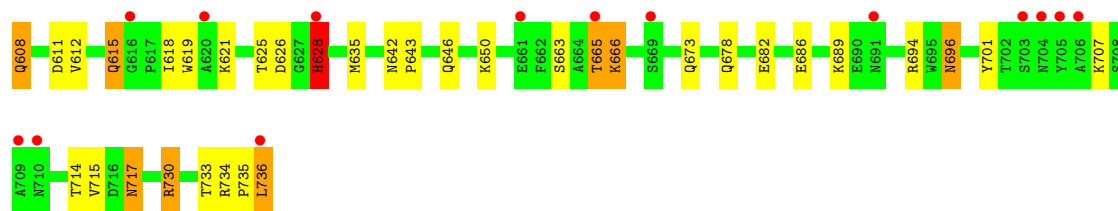
● Molecule 1: Capsid protein



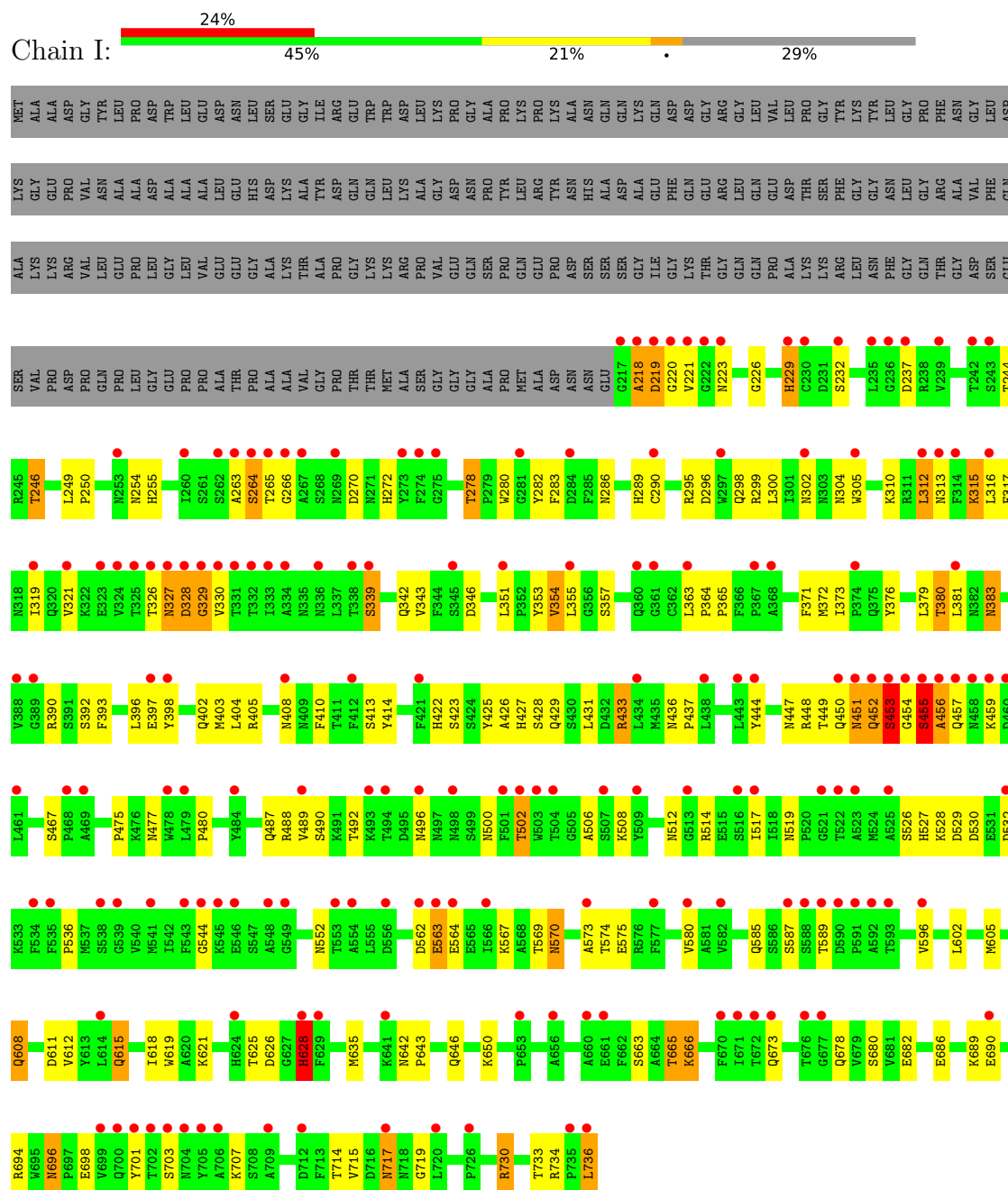


- Molecule 1: Capsid protein





● Molecule 1: Capsid protein



● Molecule 1: Capsid protein





4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	262.70Å 262.70Å 612.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.50 50.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	89.0 (50.00-2.50) 89.0 (50.00-2.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.74 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.230 , 0.250 0.257 , 0.261	Depositor DCC
R_{free} test set	12421 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.686	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 28.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.004 for -h,1/3*h-1/3*k-1/3*l,-4/3*h-8/3*k +1/3*l 0.009 for -1/3*h+1/3*k+1/3*l,-k,8/3*h+4/ 3*k+1/3*l 0.017 for -2/3*h-1/3*k-1/3*l,-1/3*h-2/3*k+ 1/3*l,-4/3*h+4/3*k+1/3*l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	42680	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.69% 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

Bond lengths and bond angles in the following residue types are not validated in this section: ADE, CYT

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	A	0.94	0/4246	1.04	11/5790 (0.2%)
1	B	0.94	0/4246	1.05	14/5790 (0.2%)
1	C	0.95	0/4246	1.04	10/5790 (0.2%)
1	D	0.94	0/4246	1.04	10/5790 (0.2%)
1	E	0.94	0/4246	1.05	12/5790 (0.2%)
1	F	0.93	0/4246	1.02	8/5790 (0.1%)
1	G	0.93	0/4246	1.04	12/5790 (0.2%)
1	H	0.95	0/4246	1.05	12/5790 (0.2%)
1	I	0.93	0/4246	1.03	10/5790 (0.2%)
1	J	0.94	0/4246	1.03	10/5790 (0.2%)
All	All	0.94	0/42460	1.04	109/57900 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8
1	B	0	8
1	C	0	8
1	D	0	7
1	E	0	5
1	F	0	8
1	G	0	6
1	H	0	6
1	I	0	10
1	J	0	6
All	All	0	72

There are no bond length outliers.

The worst 5 of 109 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	327	ASN	CA-C-N	-6.18	113.44	122.65
1	B	327	ASN	C-N-CA	-6.18	113.44	122.65
1	B	399	PHE	CA-C-N	-5.81	113.56	119.83
1	B	399	PHE	C-N-CA	-5.81	113.56	119.83
1	H	399	PHE	CA-C-N	-5.80	113.56	119.83

There are no chirality outliers.

5 of 72 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	217	GLY	Peptide
1	A	219	ASP	Peptide
1	A	263	ALA	Peptide
1	A	328	ASP	Peptide
1	A	329	GLY	Peptide

5.2 Too-close contacts [i](#)

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	4120	0	3884	207	0
1	B	4120	0	3884	196	0
1	C	4120	0	3884	177	0
1	D	4120	0	3884	194	0
1	E	4120	0	3884	189	0
1	F	4120	0	3884	196	0
1	G	4120	0	3884	197	0
1	H	4120	0	3884	192	0
1	I	4120	0	3884	211	0
1	J	4120	0	3884	130	0
2	A	10	0	4	0	0
2	B	10	0	4	3	0
2	C	10	0	4	0	0
2	D	10	0	4	0	0
2	E	10	0	4	0	0
2	F	10	0	4	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	10	0	4	0	0
2	H	10	0	4	0	0
2	I	10	0	4	0	0
2	J	10	0	4	0	0
3	A	8	0	4	3	0
3	B	16	0	8	1	0
3	C	8	0	4	3	0
3	D	8	0	4	3	0
3	E	8	0	4	1	0
3	F	8	0	4	2	0
3	H	8	0	4	3	0
3	I	8	0	4	2	0
3	J	8	0	4	1	0
4	A	131	0	0	6	0
4	B	130	0	0	7	0
4	C	128	0	0	4	0
4	D	131	0	0	9	0
4	E	133	0	0	9	0
4	F	131	0	0	4	0
4	G	127	0	0	7	0
4	H	130	0	0	5	0
4	I	130	0	0	6	0
4	J	129	0	0	5	0
All	All	42680	0	38920	1620	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 20.

The worst 5 of 1620 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:G:328:ASP:HB3	1:G:329:GLY:C	1.41	1.45
1:C:328:ASP:HB3	1:C:329:GLY:C	1.41	1.44
1:H:328:ASP:HB3	1:H:329:GLY:C	1.41	1.42
1:D:328:ASP:CB	1:D:329:GLY:HA3	1.42	1.29
1:B:328:ASP:OD1	1:B:329:GLY:HA2	1.28	1.28

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	A	518/736 (70%)	499 (96%)	15 (3%)	4 (1%)	16	31
1	B	518/736 (70%)	500 (96%)	17 (3%)	1 (0%)	43	63
1	C	518/736 (70%)	498 (96%)	18 (4%)	2 (0%)	30	49
1	D	518/736 (70%)	498 (96%)	16 (3%)	4 (1%)	16	31
1	E	518/736 (70%)	500 (96%)	16 (3%)	2 (0%)	30	49
1	F	518/736 (70%)	501 (97%)	14 (3%)	3 (1%)	21	38
1	G	518/736 (70%)	498 (96%)	16 (3%)	4 (1%)	16	31
1	H	518/736 (70%)	498 (96%)	17 (3%)	3 (1%)	21	38
1	I	518/736 (70%)	501 (97%)	12 (2%)	5 (1%)	12	24
1	J	518/736 (70%)	497 (96%)	18 (4%)	3 (1%)	21	38
All	All	5180/7360 (70%)	4990 (96%)	159 (3%)	31 (1%)	21	38

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	ALA
1	A	219	ASP
1	C	328	ASP
1	E	219	ASP
1	F	218	ALA

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	A	451/617 (73%)	413 (92%)	38 (8%)	10	22
1	B	451/617 (73%)	412 (91%)	39 (9%)	10	21
1	C	451/617 (73%)	413 (92%)	38 (8%)	10	22
1	D	451/617 (73%)	415 (92%)	36 (8%)	11	24
1	E	451/617 (73%)	414 (92%)	37 (8%)	10	23
1	F	451/617 (73%)	414 (92%)	37 (8%)	10	23
1	G	451/617 (73%)	415 (92%)	36 (8%)	11	24
1	H	451/617 (73%)	413 (92%)	38 (8%)	10	22
1	I	451/617 (73%)	415 (92%)	36 (8%)	11	24
1	J	451/617 (73%)	414 (92%)	37 (8%)	10	23
All	All	4510/6170 (73%)	4138 (92%)	372 (8%)	10	23

5 of 372 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	315	LYS
1	H	570	ASN
1	G	380	THR
1	G	736	LEU
1	I	229	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 348 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	510	ASN
1	I	298	GLN
1	G	624	HIS
1	H	429	GLN
1	I	512	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](#)

20 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	CYT	B	738	-	7,8,8	2.12	3 (42%)	7,10,10	5.54	4 (57%)
2	ADE	E	737	-	11,11,11	1.03	1 (9%)	15,15,15	2.46	7 (46%)
2	ADE	F	737	-	11,11,11	1.02	1 (9%)	15,15,15	2.46	7 (46%)
3	CYT	F	738	-	7,8,8	2.13	3 (42%)	7,10,10	5.53	4 (57%)
2	ADE	I	737	-	11,11,11	1.03	1 (9%)	15,15,15	2.46	7 (46%)
2	ADE	B	737	-	11,11,11	1.05	1 (9%)	15,15,15	2.45	7 (46%)
3	CYT	B	739	-	7,8,8	2.14	3 (42%)	7,10,10	5.53	4 (57%)
2	ADE	H	737	-	11,11,11	1.01	1 (9%)	15,15,15	2.46	7 (46%)
2	ADE	D	737	-	11,11,11	1.04	1 (9%)	15,15,15	2.46	7 (46%)
3	CYT	J	738	-	7,8,8	2.11	3 (42%)	7,10,10	5.56	4 (57%)
2	ADE	A	737	-	11,11,11	1.03	1 (9%)	15,15,15	2.46	7 (46%)
2	ADE	G	737	-	11,11,11	1.03	1 (9%)	15,15,15	2.47	7 (46%)
2	ADE	C	737	-	11,11,11	1.02	1 (9%)	15,15,15	2.47	7 (46%)
2	ADE	J	737	-	11,11,11	1.03	1 (9%)	15,15,15	2.46	7 (46%)
3	CYT	A	738	-	7,8,8	2.12	3 (42%)	7,10,10	5.57	4 (57%)
3	CYT	C	738	-	7,8,8	2.12	3 (42%)	7,10,10	5.57	4 (57%)
3	CYT	E	738	-	7,8,8	2.11	3 (42%)	7,10,10	5.57	4 (57%)
3	CYT	I	738	-	7,8,8	2.12	3 (42%)	7,10,10	5.58	4 (57%)
3	CYT	H	738	-	7,8,8	2.13	3 (42%)	7,10,10	5.57	4 (57%)
3	CYT	D	738	-	7,8,8	2.12	3 (42%)	7,10,10	5.57	4 (57%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CYT	B	738	-	-	-	0/1/1/1
2	ADE	E	737	-	-	-	0/2/2/2
2	ADE	F	737	-	-	-	0/2/2/2
3	CYT	F	738	-	-	-	0/1/1/1
2	ADE	I	737	-	-	-	0/2/2/2
2	ADE	B	737	-	-	-	0/2/2/2
3	CYT	B	739	-	-	-	0/1/1/1
2	ADE	H	737	-	-	-	0/2/2/2
2	ADE	D	737	-	-	-	0/2/2/2
3	CYT	J	738	-	-	-	0/1/1/1
2	ADE	A	737	-	-	-	0/2/2/2
2	ADE	G	737	-	-	-	0/2/2/2
2	ADE	C	737	-	-	-	0/2/2/2
2	ADE	J	737	-	-	-	0/2/2/2
3	CYT	A	738	-	-	-	0/1/1/1
3	CYT	C	738	-	-	-	0/1/1/1
3	CYT	E	738	-	-	-	0/1/1/1
3	CYT	I	738	-	-	-	0/1/1/1
3	CYT	H	738	-	-	-	0/1/1/1
3	CYT	D	738	-	-	-	0/1/1/1

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	739	CYT	C4-N3	-3.22	1.32	1.37
3	H	738	CYT	C4-N3	-3.21	1.32	1.37
3	A	738	CYT	C4-N3	-3.19	1.32	1.37
3	B	738	CYT	C4-N3	-3.19	1.32	1.37
3	J	738	CYT	C4-N3	-3.18	1.32	1.37

The worst 5 of 110 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	738	CYT	C5-C4-N3	12.66	125.25	118.04
3	H	738	CYT	C5-C4-N3	12.63	125.23	118.04
3	D	738	CYT	C5-C4-N3	12.61	125.22	118.04
3	A	738	CYT	C5-C4-N3	12.61	125.22	118.04
3	E	738	CYT	C5-C4-N3	12.59	125.21	118.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	738	CYT	2	0
2	B	737	ADE	3	0
3	B	739	CYT	1	0
3	J	738	CYT	1	0
3	A	738	CYT	3	0
3	C	738	CYT	3	0
3	E	738	CYT	1	0
3	I	738	CYT	2	0
3	H	738	CYT	3	0
3	D	738	CYT	3	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	A	520/736 (70%)	0.95	54 (10%) 11 10	25, 34, 55, 92	0
1	B	520/736 (70%)	1.52	109 (20%) 2 2	25, 34, 55, 92	0
1	C	520/736 (70%)	1.74	147 (28%) 1 1	25, 34, 55, 92	0
1	D	520/736 (70%)	1.42	86 (16%) 4 3	25, 34, 55, 92	0
1	E	520/736 (70%)	2.02	224 (43%) 0 0	25, 34, 55, 92	0
1	F	520/736 (70%)	1.57	117 (22%) 2 2	25, 34, 55, 92	0
1	G	520/736 (70%)	1.88	178 (34%) 1 1	25, 34, 55, 92	0
1	H	520/736 (70%)	1.37	88 (16%) 4 3	25, 34, 55, 92	0
1	I	520/736 (70%)	1.87	173 (33%) 1 1	25, 34, 55, 92	0
1	J	520/736 (70%)	2.36	309 (59%) 0 0	25, 34, 55, 92	0
All	All	5200/7360 (70%)	1.67	1485 (28%) 1 1	25, 34, 55, 92	0

The worst 5 of 1485 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	217	GLY	10.7
1	H	453	SER	10.2
1	E	217	GLY	10.1
1	F	456	ALA	10.0
1	B	218	ALA	9.5

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	CYT	H	738	8/8	0.60	0.32	63,67,68,70	0
3	CYT	F	738	8/8	0.65	0.27	63,67,68,70	0
3	CYT	E	738	8/8	0.65	0.25	63,67,68,70	0
3	CYT	D	738	8/8	0.66	0.28	63,67,68,70	0
2	ADE	F	737	10/10	0.70	0.32	78,81,82,83	0
3	CYT	B	739	8/8	0.70	0.25	63,67,68,70	0
3	CYT	C	738	8/8	0.71	0.27	63,67,68,70	0
3	CYT	J	738	8/8	0.71	0.23	63,67,68,70	0
3	CYT	I	738	8/8	0.77	0.23	63,67,68,70	0
3	CYT	B	738	8/8	0.79	0.22	63,67,68,70	0
2	ADE	E	737	10/10	0.79	0.29	78,81,82,83	0
3	CYT	A	738	8/8	0.79	0.26	63,67,68,70	0
2	ADE	I	737	10/10	0.80	0.25	78,81,82,83	0
2	ADE	D	737	10/10	0.82	0.25	78,81,82,83	0
2	ADE	C	737	10/10	0.83	0.24	78,81,82,83	0
2	ADE	A	737	10/10	0.84	0.21	78,81,82,83	0
2	ADE	J	737	10/10	0.84	0.24	78,81,82,83	0
2	ADE	G	737	10/10	0.84	0.24	78,81,82,83	0
2	ADE	H	737	10/10	0.85	0.21	78,81,82,83	0
2	ADE	B	737	10/10	0.86	0.20	78,81,82,83	0

6.5 Other polymers ⓘ

There are no such residues in this entry.