



wwPDB X-ray Structure Validation Summary Report ⓘ

May 28, 2020 – 08:57 pm BST

PDB ID : 1RHI
Title : HUMAN RHINOVIRUS 3 COAT PROTEIN
Authors : Zhao, R.; Rossmann, M.G.
Deposited on : 1996-06-17
Resolution : 3.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

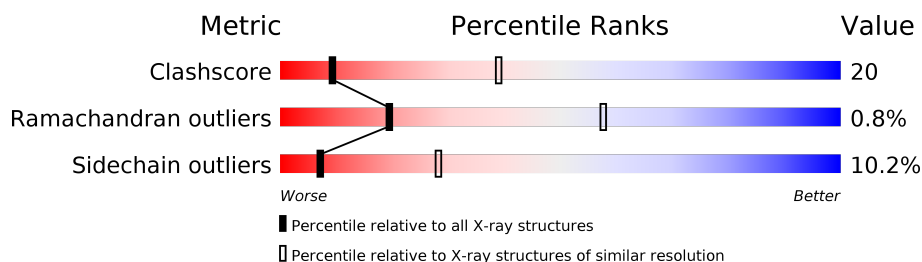
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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 on 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	1	288	
2	2	262	
3	3	236	
4	4	68	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6288 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 HUMAN RHINOVIRUS 3 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	273	Total	C	N	O	S	0	0	0
			2163	1366	379	412	6			

- Molecule 2 is a protein called HUMAN RHINOVIRUS 3 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	255	Total	C	N	O	S	0	0	0
			1964	1239	335	377	13			

- Molecule 3 is a protein called HUMAN RHINOVIRUS 3 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	3	236	Total	C	N	O	S	0	0	0
			1835	1175	299	354	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	142	LYS	ARG	CONFLICT	UNP Q82081
3	144	GLU	LYS	CONFLICT	UNP Q82081

- Molecule 4 is a protein called HUMAN RHINOVIRUS 3 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	4	43	Total	C	N	O	S	0	0	0
			325	206	50	67	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	26	TYR	PHE	CONFLICT	UNP Q82081

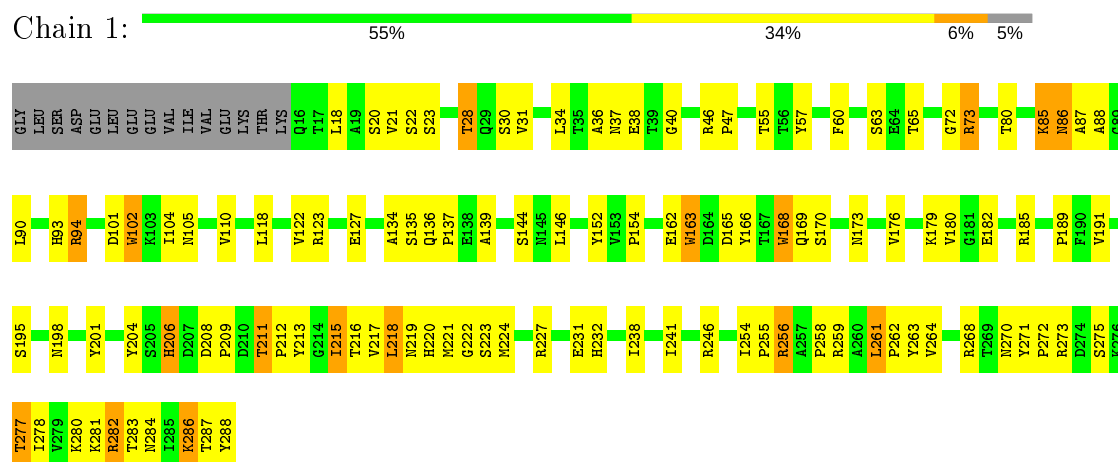
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	1	1	Total	Ca	0	0
			1	1		

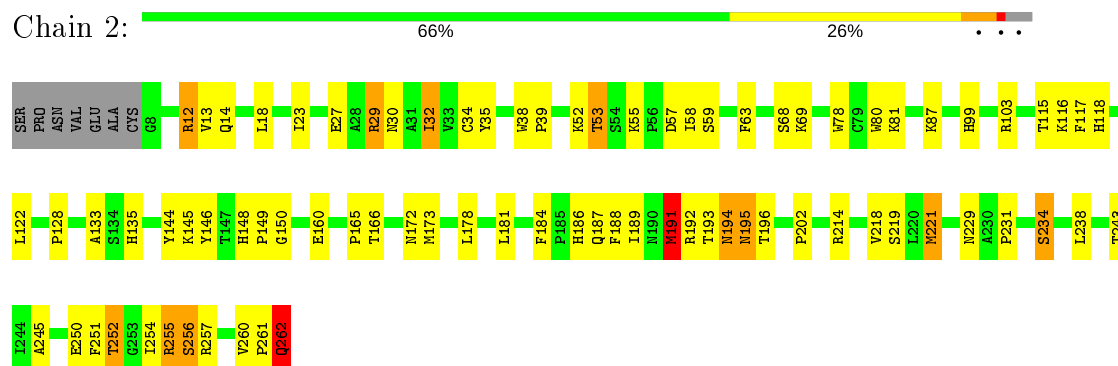
3 Residue-property plots

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.

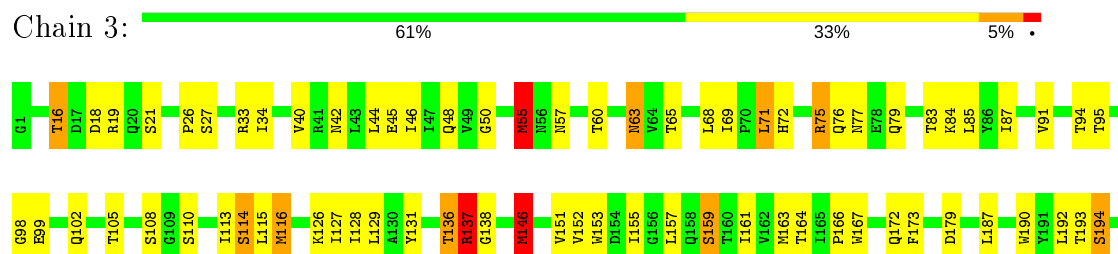
• Molecule 1: HUMAN RHINOVIRUS 3 COAT PROTEIN

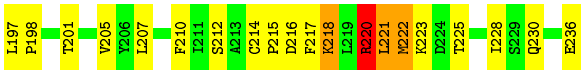


• Molecule 2: HUMAN RHINOVIRUS 3 COAT PROTEIN



• Molecule 3: HUMAN RHINOVIRUS 3 COAT PROTEIN





● Molecule 4: HUMAN RHINOVIRUS 3 COAT PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	397.90Å 341.80Å 301.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 3.00 29.78 – 2.98	Depositor EDS
% Data completeness (in resolution range)	64.0 (5.00-3.00) 78.6 (29.78-2.98)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.54 (at 3.00Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.284 , 0.288 0.475 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	14.8	Xtriage
Anisotropy	0.671	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.14 , 0.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.07	EDS
Total number of atoms	6288	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.49 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.7949e-03.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.64	3/2222 (0.1%)	0.97	7/3027 (0.2%)
2	2	0.65	2/2012 (0.1%)	0.99	7/2748 (0.3%)
3	3	0.57	1/1882 (0.1%)	0.99	9/2574 (0.3%)
4	4	0.57	0/332	0.91	1/447 (0.2%)
All	All	0.62	6/6448 (0.1%)	0.98	24/8796 (0.3%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	262	GLN	C-OXT	14.61	1.51	1.23
1	1	102	TRP	NE1-CE2	-5.62	1.30	1.37
3	3	167	TRP	NE1-CE2	-5.46	1.30	1.37
1	1	163	TRP	NE1-CE2	-5.41	1.30	1.37
1	1	168	TRP	NE1-CE2	-5.37	1.30	1.37

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	220	ARG	NE-CZ-NH2	8.02	124.31	120.30
2	2	214	ARG	NE-CZ-NH2	7.50	124.05	120.30
1	1	282	ARG	NE-CZ-NH2	7.50	124.05	120.30
2	2	257	ARG	NE-CZ-NH2	7.49	124.05	120.30
3	3	137	ARG	NE-CZ-NH2	7.47	124.04	120.30

There are no chirality outliers.

There are no planarity outliers.

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	1	2163	0	2100	106	0
2	2	1964	0	1930	100	0
3	3	1835	0	1832	83	0
4	4	325	0	315	12	0
5	1	1	0	0	0	0
All	All	6288	0	6177	247	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 247 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)
1:1:36:ALA:CB	2:2:29:ARG:HH21	1.60	1.14
2:2:194:ASN:ND2	2:2:196:THR:O	1.81	1.12
2:2:53:THR:HG21	2:2:250:GLU:HG2	1.36	1.07
1:1:36:ALA:HB2	2:2:29:ARG:HH21	0.88	1.05
1:1:36:ALA:HB2	2:2:29:ARG:NH2	1.72	1.04

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 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	1	271/288 (94%)	249 (92%)	19 (7%)	3 (1%)	14 50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	2	253/262 (97%)	232 (92%)	19 (8%)	2 (1%)	19	57
3	3	234/236 (99%)	219 (94%)	14 (6%)	1 (0%)	34	72
4	4	41/68 (60%)	35 (85%)	6 (15%)	0	100	100
All	All	799/854 (94%)	735 (92%)	58 (7%)	6 (1%)	19	57

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	2	58	ILE
1	1	139	ALA
2	2	116	LYS
3	3	194	SER
1	1	231	GLU

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	1	239/253 (94%)	215 (90%)	24 (10%)	7	29
2	2	223/229 (97%)	204 (92%)	19 (8%)	10	38
3	3	207/207 (100%)	182 (88%)	25 (12%)	5	21
4	4	36/57 (63%)	32 (89%)	4 (11%)	6	25
All	All	705/746 (94%)	633 (90%)	72 (10%)	7	28

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	194	ASN
2	2	255	ARG
3	3	228	ILE
2	2	195	ASN
2	2	234	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
2	2	135	HIS
2	2	172	ASN
3	3	204	GLN
1	1	219	ASN
2	2	229	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.