



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 02:22 AM UTC

PDB ID : 9V0N / pdb_00009v0n
EMDB ID : EMD-64666
Title : Cryo-EM structure of RSV pre-F in complex with antibody CNR2042
Authors : Zhai, H.; Deng, J.; Yu, W.
Deposited on : 2025-05-18
Resolution : 3.75 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : **FAILED**
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

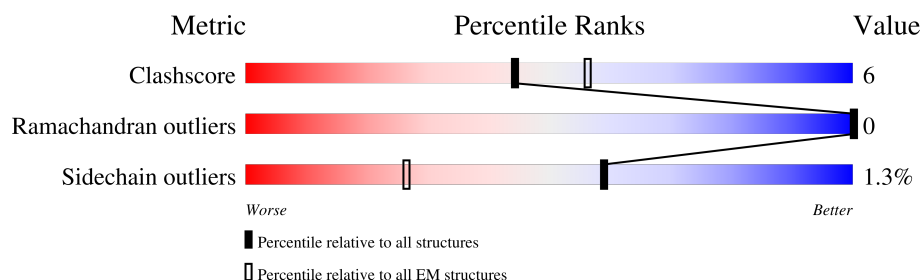
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	553	67% 11% 23%
1	D	553	65% 12% 23%
1	E	553	64% 13% 23%
2	C	124	83% 16% .
2	H	124	84% 15% .
2	I	124	83% 17%
3	B	110	82% 17% .
3	F	110	85% 15%
3	G	110	86% 13% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15225 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 RSV Pre-fusion Protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	427	Total	C	N	O	S	0	0
			3305	2089	543	651	22		
1	D	427	Total	C	N	O	S	0	0
			3305	2089	543	651	22		
1	E	427	Total	C	N	O	S	0	0
			3305	2089	543	651	22		

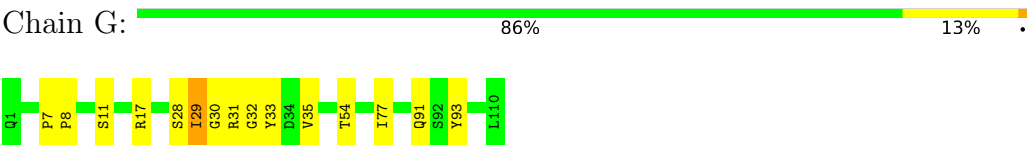
- Molecule 2 is a protein called CNR2042 Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	124	Total	C	N	O	S	0	0
			952	599	163	186	4		
2	H	124	Total	C	N	O	S	0	0
			952	599	163	186	4		
2	I	124	Total	C	N	O	S	0	0
			952	599	163	186	4		

- Molecule 3 is a protein called CNR2042 Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	110	Total	C	N	O	S	0	0
			818	509	140	166	3		
3	F	110	Total	C	N	O	S	0	0
			818	509	140	166	3		
3	G	110	Total	C	N	O	S	0	0
			818	509	140	166	3		

● Molecule 3: CNR2042 Light Chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42798	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
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 > 5$	RMSZ	# $ Z > 5$
1	A	0.14	0/3352	0.33	0/4545
1	D	0.14	0/3352	0.32	0/4545
1	E	0.14	0/3352	0.34	0/4545
2	C	0.17	0/975	0.47	0/1317
2	H	0.17	0/975	0.46	0/1317
2	I	0.18	0/975	0.47	0/1317
3	B	0.16	0/837	0.49	2/1140 (0.2%)
3	F	0.15	0/837	0.45	0/1140
3	G	0.17	0/837	0.44	0/1140
All	All	0.15	0/15492	0.38	2/21006 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	33	TYR	CA-C-N	5.68	132.38	121.54
3	B	33	TYR	C-N-CA	5.68	132.38	121.54

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	A	3305	0	3337	37	0
1	D	3305	0	3337	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	3305	0	3337	48	0
2	C	952	0	905	17	0
2	H	952	0	905	15	0
2	I	952	0	905	16	0
3	B	818	0	788	15	0
3	F	818	0	788	13	0
3	G	818	0	788	13	0
All	All	15225	0	15090	194	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 6.

The worst 5 of 194 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)
2:I:111:PHE:HE2	3:G:91:GLN:HE22	1.32	0.76
1:A:86:TYR:HB2	1:A:227:ASN:HD21	1.54	0.72
1:D:86:TYR:HB2	1:D:227:ASN:HD21	1.54	0.72
2:H:29:PHE:HE1	2:H:34:MET:HE2	1.55	0.72
1:D:320:PRO:HA	1:D:335:THR:HG22	1.71	0.71

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	421/553 (76%)	403 (96%)	18 (4%)	0	100	100
1	D	421/553 (76%)	405 (96%)	16 (4%)	0	100	100
1	E	421/553 (76%)	403 (96%)	18 (4%)	0	100	100
2	C	122/124 (98%)	107 (88%)	15 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	122/124 (98%)	108 (88%)	14 (12%)	0	100	100
2	I	122/124 (98%)	108 (88%)	14 (12%)	0	100	100
3	B	108/110 (98%)	94 (87%)	14 (13%)	0	100	100
3	F	108/110 (98%)	94 (87%)	14 (13%)	0	100	100
3	G	108/110 (98%)	95 (88%)	13 (12%)	0	100	100
All	All	1953/2361 (83%)	1817 (93%)	136 (7%)	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	390/498 (78%)	385 (99%)	5 (1%)	61	71
1	D	390/498 (78%)	386 (99%)	4 (1%)	68	73
1	E	390/498 (78%)	385 (99%)	5 (1%)	61	71
2	C	103/103 (100%)	101 (98%)	2 (2%)	50	65
2	H	103/103 (100%)	100 (97%)	3 (3%)	37	56
2	I	103/103 (100%)	102 (99%)	1 (1%)	68	73
3	B	90/90 (100%)	89 (99%)	1 (1%)	65	72
3	F	90/90 (100%)	90 (100%)	0	100	100
3	G	90/90 (100%)	88 (98%)	2 (2%)	45	62
All	All	1749/2073 (84%)	1726 (99%)	23 (1%)	59	71

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	111	PHE
1	E	274	MET
1	E	247	VAL
1	E	290	CYS

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Mol	Chain	Res	Type
2	C	111	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	454	ASN
3	G	1	GLN
1	D	227	ASN
1	D	270	GLN
1	D	380	ASN

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 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.