



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:04 PM UTC

PDB ID : 7B27 / pdb_00007b27
Title : RBD domain SARS-CoV2 in complex with neutralizing nanobody NM1230
Authors : Ostertag, E.; Zocher, G.; Stehle, T.
Deposited on : 2020-11-26
Resolution : 2.90 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)
Xtrriage (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

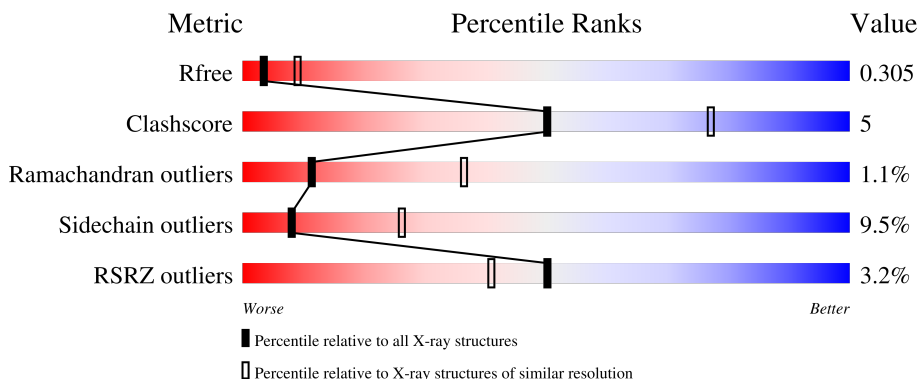
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

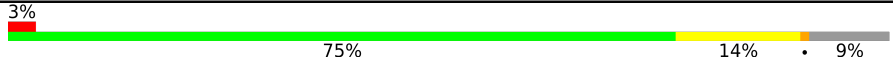



The reported resolution of this entry is 2.90 Å.

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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	AAA	222	 3% 75% 14% • 9%
1	aba	222	 2% 70% 10% • 18%
2	CCC	141	 % 74% 15% 11%
2	DDD	141	 5% 69% 13% • 13%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4859 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.

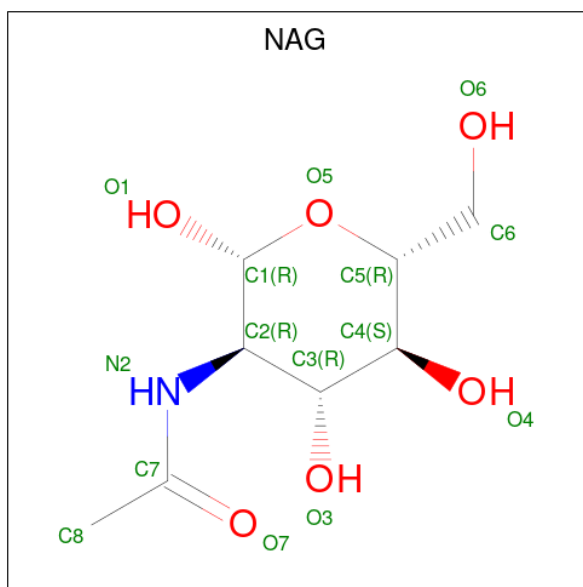
- Molecule 1 is a protein called Surface glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	202	Total 1571	C 1006	N 260	O 296	S 9	0	0	0
1	aba	181	Total 1435	C 920	N 239	O 269	S 7	0	0	0

- Molecule 2 is a protein called neutralizing nanobody NM1230.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	CCC	125	Total 934	C 577	N 170	O 182	S 5	0	0	0
2	DDD	122	Total 891	C 553	N 164	O 169	S 5	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	AAA	1	Total	C	N	O	0	0
			14	8	1	5		
3	aba	1	Total	C	N	O	0	0
			14	8	1	5		

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	63.29Å 63.29Å 411.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 30.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	93.4 (30.00-2.90) 93.4 (30.00-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.91Å)	Xtrriage
Refinement program	REFMAC 5.8.0232 2018/13/08	Depositor
R, R_{free}	0.266 , 0.305 0.266 , 0.305	Depositor DCC
R_{free} test set	1295 reflections (7.00%)	wwPDB-VP
Wilson B-factor (Å ²)	65.1	Xtrriage
Anisotropy	0.727	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 22.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4859	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	AAA	1.02	0/1613	1.32	0/2196
1	aba	1.01	0/1475	1.33	0/2005
2	CCC	1.06	0/951	1.29	2/1287 (0.2%)
2	DDD	1.07	0/908	1.30	0/1232
All	All	1.03	0/4947	1.32	2/6720 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	CCC	49	ALA	CA-C-N	5.22	125.20	121.65
2	CCC	49	ALA	C-N-CA	5.22	125.20	121.65

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	AAA	1571	0	1476	16	0
1	aba	1435	0	1352	11	0
2	CCC	934	0	903	7	0
2	DDD	891	0	858	12	0
3	AAA	14	0	13	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	aba	14	0	13	0	0
All	All	4859	0	4615	45	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 5.

The worst 5 of 45 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:AAA:324:CYS:HG	1:AAA:349:CYS:HG	1.09	0.86
1:AAA:367:CYS:HG	1:AAA:420:CYS:HG	0.86	0.81
1:AAA:348:ASN:N	1:AAA:511:THR:OG1	2.12	0.81
1:AAA:348:ASN:H	1:AAA:511:THR:HG1	1.29	0.77
1:AAA:468:CYS:HG	1:AAA:476:CYS:HG	1.32	0.76

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	AAA	198/222 (89%)	177 (89%)	20 (10%)	1 (0%)	24	54
1	aba	179/222 (81%)	158 (88%)	21 (12%)	0	100	100
2	CCC	123/141 (87%)	110 (89%)	12 (10%)	1 (1%)	16	44
2	DDD	120/141 (85%)	111 (92%)	4 (3%)	5 (4%)	2	9
All	All	620/726 (85%)	556 (90%)	57 (9%)	7 (1%)	11	36

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	408	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	CCC	65	LYS
2	DDD	53	ASN
2	DDD	91	THR
2	DDD	108	ARG

5.3.2 Protein sidechains [i](#)

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	AAA	168/195 (86%)	152 (90%)	16 (10%)	8	26
1	aba	154/195 (79%)	142 (92%)	12 (8%)	11	35
2	CCC	96/114 (84%)	89 (93%)	7 (7%)	13	38
2	DDD	89/114 (78%)	76 (85%)	13 (15%)	3	10
All	All	507/618 (82%)	459 (90%)	48 (10%)	8	26

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	CCC	2	VAL
2	DDD	2	VAL
2	CCC	18	LEU
2	CCC	75	ASP
2	DDD	4	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

2 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	NAG	AAA	601	1	14,14,15	0.35	0	17,19,21	1.37	3 (17%)
3	NAG	aba	601	1	14,14,15	0.44	0	17,19,21	1.42	2 (11%)

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	NAG	AAA	601	1	-	2/6/23/26	0/1/1/1
3	NAG	aba	601	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	aba	601	NAG	C1-O5-C5	4.20	117.82	112.19
3	AAA	601	NAG	C1-O5-C5	3.33	116.64	112.19
3	AAA	601	NAG	O5-C1-C2	3.05	116.02	111.29
3	aba	601	NAG	O5-C1-C2	2.66	115.40	111.29
3	AAA	601	NAG	C3-C4-C5	2.36	114.51	110.23

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	AAA	601	NAG	C4-C5-C6-O6
3	AAA	601	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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	AAA	202/222 (90%)	0.58	7 (3%) 47 38	47, 71, 114, 134	0
1	aba	181/222 (81%)	0.55	4 (2%) 62 53	45, 73, 104, 120	0
2	CCC	125/141 (88%)	0.43	2 (1%) 70 62	43, 63, 93, 115	0
2	DDD	122/141 (86%)	0.72	7 (5%) 29 23	60, 81, 103, 113	0
All	All	630/726 (86%)	0.57	20 (3%) 50 41	43, 72, 106, 134	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	522	VAL	3.8
2	CCC	55	GLY	3.8
2	DDD	10	GLY	3.3
1	AAA	493	TYR	3.1
2	DDD	34	MET	3.1

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](#)

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(\AA^2)	Q<0.9
3	NAG	aba	601	14/15	0.67	0.17	97,113,120,125	0
3	NAG	AAA	601	14/15	0.71	0.17	87,106,112,113	0

6.5 Other polymers [i](#)

There are no such residues in this entry.