



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 8BG3 / pdb_00008bg3
Title : Crystal structure of the SARS-CoV-2 S RBD in complex with pT1610 scFV
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Deposited on : 2022-10-27
Resolution : 1.90 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)
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

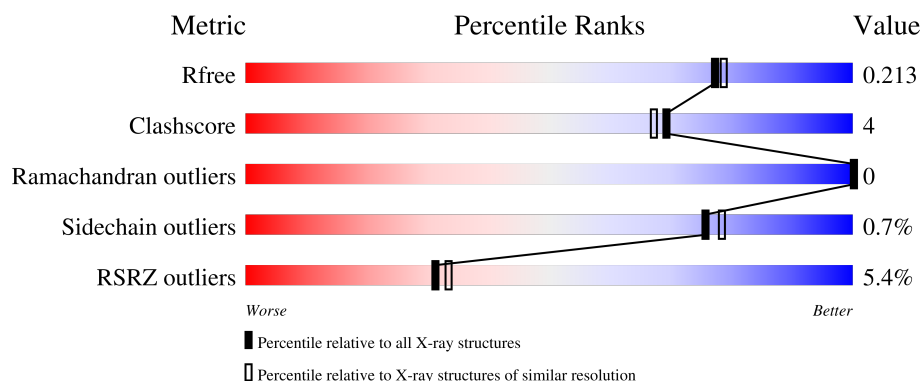
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	A	252	0% 81% 8% 11%
1	C	252	2% 81% 8% 11%
2	B	199	7% 88% 8% •
2	D	199	12% 90% 5% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13019 atoms, of which 6103 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 pT1610 single-chain Fv.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	225	Total	C	H	N	O	S	0	0	0
			3293	1053	1609	289	335	7			
1	C	225	Total	C	H	N	O	S	0	0	0
			3293	1053	1609	289	335	7			

- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	191	Total	C	H	N	O	S	0	0	0
			2952	974	1435	252	283	8			
2	D	190	Total	C	H	N	O	S	0	0	0
			2933	968	1424	251	282	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	195	ASP	-	expression tag	UNP P0DTC2
B	196	ASP	-	expression tag	UNP P0DTC2
B	197	ASP	-	expression tag	UNP P0DTC2
B	198	ASP	-	expression tag	UNP P0DTC2
B	199	LYS	-	expression tag	UNP P0DTC2
D	195	ASP	-	expression tag	UNP P0DTC2
D	196	ASP	-	expression tag	UNP P0DTC2
D	197	ASP	-	expression tag	UNP P0DTC2
D	198	ASP	-	expression tag	UNP P0DTC2
D	199	LYS	-	expression tag	UNP P0DTC2

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

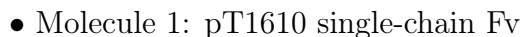


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	D	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	153	Total	O	0	0
			153	153		
4	B	128	Total	O	0	0
			128	128		
4	C	113	Total	O	0	0
			113	113		
4	D	100	Total	O	0	0
			100	100		

- Molecule 1: pT1610 single-chain Fv



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.99Å 60.17Å 113.13Å 90.00° 105.40° 90.00°	Depositor
Resolution (Å)	45.46 – 1.90 45.46 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.6 (45.46-1.90) 96.6 (45.46-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.185 , 0.214 0.183 , 0.213	Depositor DCC
R_{free} test set	1878 reflections (2.06%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.297	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13019	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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	A	0.36	0/1723	0.60	0/2337
1	C	0.34	0/1723	0.60	0/2337
2	B	0.32	0/1560	0.53	0/2123
2	D	0.32	0/1552	0.54	0/2112
All	All	0.34	0/6558	0.57	0/8909

There are no bond length outliers.

There are no bond angle outliers.

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	1684	1609	1611	11	0
1	C	1684	1609	1611	18	0
2	B	1517	1435	1436	10	0
2	D	1509	1424	1425	7	0
3	B	14	13	13	0	0
3	D	14	13	13	0	0
4	A	153	0	0	0	5
4	B	128	0	0	2	4
4	C	113	0	0	8	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	100	0	0	2	0
All	All	6916	6103	6109	44	5

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 4.

The worst 5 of 44 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:C:22:CYS:SG	4:C:410:HOH:O	1.99	1.17
2:B:97:THR:O	4:B:601:HOH:O	1.97	0.82
1:C:20:LEU:HG	1:C:82:MET:HE2	1.65	0.77
1:A:102:GLU:OE1	2:B:120:TYR:OH	2.03	0.76
2:D:60:THR:O	2:D:190:THR:HG22	1.84	0.76

All (5) 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)
4:A:440:HOH:O	4:B:642:HOH:O[2_546]	1.81	0.39
4:A:440:HOH:O	4:B:652:HOH:O[2_546]	1.84	0.36
4:A:427:HOH:O	4:B:714:HOH:O[2_446]	1.86	0.34
4:A:384:HOH:O	4:B:662:HOH:O[2_446]	1.95	0.25
4:A:422:HOH:O	4:C:405:HOH:O[1_455]	2.01	0.19

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	A	221/252 (88%)	213 (96%)	8 (4%)	0	100	100
1	C	221/252 (88%)	210 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	189/199 (95%)	183 (97%)	6 (3%)	0	100	100
2	D	188/199 (94%)	179 (95%)	9 (5%)	0	100	100
All	All	819/902 (91%)	785 (96%)	34 (4%)	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 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	182/194 (94%)	180 (99%)	2 (1%)	65	67
1	C	182/194 (94%)	182 (100%)	0	100	100
2	B	165/172 (96%)	165 (100%)	0	100	100
2	D	164/172 (95%)	161 (98%)	3 (2%)	51	50
All	All	693/732 (95%)	688 (99%)	5 (1%)	76	78

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ILE
1	A	165	ASP
2	D	26	SER
2	D	40	SER
2	D	50	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	81	GLN
1	C	83	ASN
1	C	177	GLN
1	C	176	GLN

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Mol	Chain	Res	Type
1	C	39	GLN

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	D	500	2	14,14,15	0.41	0	17,19,21	1.22	1 (5%)
3	NAG	B	500	2	14,14,15	0.43	0	17,19,21	0.68	1 (5%)

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	D	500	2	-	2/6/23/26	0/1/1/1
3	NAG	B	500	2	-	2/6/23/26	0/1/1/1

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	D	500	NAG	C1-O5-C5	4.61	118.37	112.19
3	B	500	NAG	C1-O5-C5	2.20	115.13	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	500	NAG	C8-C7-N2-C2
3	D	500	NAG	O7-C7-N2-C2
3	B	500	NAG	O5-C5-C6-O6
3	B	500	NAG	C4-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	A	225/252 (89%)	-0.27	3 (1%) 75 78	23, 32, 49, 67	0
1	C	225/252 (89%)	0.08	6 (2%) 56 60	28, 39, 60, 80	0
2	B	191/199 (95%)	0.09	13 (6%) 23 24	25, 36, 69, 90	0
2	D	190/199 (95%)	0.37	23 (12%) 8 9	28, 40, 87, 106	0
All	All	831/902 (92%)	0.05	45 (5%) 31 33	23, 37, 71, 106	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	36	TYR	4.9
2	D	29	VAL	4.4
1	A	247	LEU	4.1
2	D	190	THR	4.0
1	C	117	SER	4.0

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($\text{\AA}^2$)	Q<0.9
3	NAG	D	500	14/15	0.72	0.13	50,74,102,104	0
3	NAG	B	500	14/15	0.86	0.10	39,52,61,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.