



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 8BG2 / pdb_00008bg2
Title : Crystal structure of the SARS-CoV-2 S RBD in complex with pT1580 scFV
Authors : Hansen, G.; Ssebyatika, G.L.; Krey, T.
Deposited on : 2022-10-27
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

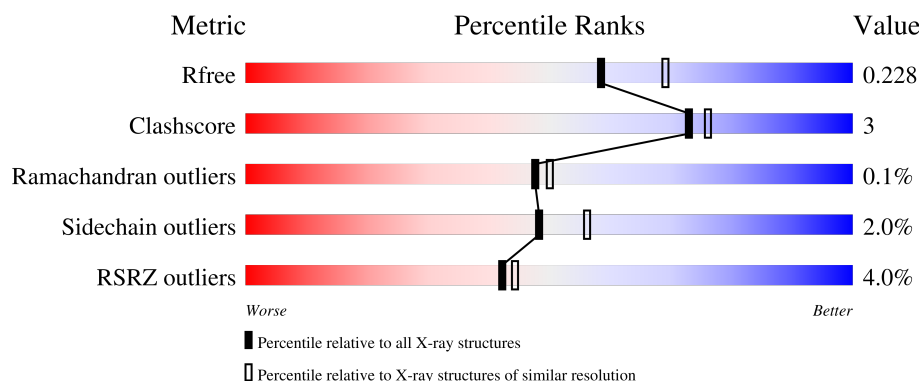
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	251	2% 80% 10% 10%
1	C	251	4% 81% 9% 10%
2	B	199	5% 89% 7% ..
2	D	199	5% 87% 10% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6975 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 pT1375 single-chain Fv.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	0	0
			1725	1087	291	341	6			
1	C	227	Total	C	N	O	S	0	0	0
			1725	1087	291	341	6			

- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	193	Total	C	N	O	S	0	0	0
			1528	981	254	285	8			
2	D	193	Total	C	N	O	S	0	0	0
			1528	981	254	285	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	528	ASP	-	expression tag	UNP P0DTC2
B	529	ASP	-	expression tag	UNP P0DTC2
B	530	ASP	-	expression tag	UNP P0DTC2
B	531	ASP	-	expression tag	UNP P0DTC2
B	532	LYS	-	expression tag	UNP P0DTC2
D	528	ASP	-	expression tag	UNP P0DTC2
D	529	ASP	-	expression tag	UNP P0DTC2
D	530	ASP	-	expression tag	UNP P0DTC2
D	531	ASP	-	expression tag	UNP P0DTC2
D	532	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	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	111	Total	O	0	0
			111	111		
4	B	99	Total	O	0	0
			99	99		
4	C	122	Total	O	0	0
			122	122		
4	D	109	Total	O	0	0
			109	109		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.05Å 85.90Å 88.20Å 90.00° 117.04° 90.00°	Depositor
Resolution (Å)	45.76 – 2.10 45.76 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.1 (45.76-2.10) 94.1 (45.76-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.43 (at 1.73Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.189 , 0.227 0.189 , 0.228	Depositor DCC
R_{free} test set	2003 reflections (1.90%)	wwPDB-VP
Wilson B-factor (Å ²)	23.2	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.011 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6975	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 4.28% 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	0.33	0/1763	0.54	0/2390
1	C	0.32	0/1763	0.54	0/2390
2	B	0.31	0/1572	0.50	0/2140
2	D	0.32	0/1572	0.47	0/2140
All	All	0.32	0/6670	0.52	0/9060

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	1725	0	1668	11	0
1	C	1725	0	1668	15	0
2	B	1528	0	1446	9	0
2	D	1528	0	1446	10	0
3	B	14	0	13	0	0
3	D	14	0	13	0	0
4	A	111	0	0	0	0
4	B	99	0	0	0	0
4	C	122	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	109	0	0	0	0
All	All	6975	0	6254	41	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 3.

All (41) 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:39:GLN:HE22	1:C:177:GLN:HE22	1.14	0.89
1:A:20:LEU:HG	1:A:82:MET:HE2	1.64	0.79
1:C:146:PRO:HG2	1:C:149:LEU:HD21	1.83	0.60
1:A:72:ASP:OD1	1:A:75:LYS:HD2	2.03	0.59
2:B:484:GLU:HG3	2:B:485:GLY:N	2.17	0.59
1:A:12:ILE:HG21	1:A:85:LEU:HD13	1.88	0.55
1:C:39:GLN:NE2	1:C:177:GLN:HE22	1.95	0.55
1:A:167:VAL:HG13	1:A:231:ASP:HB2	1.90	0.53
2:D:484:GLU:HG3	2:D:485:GLY:N	2.25	0.52
1:A:152:SER:O	1:A:155:GLU:HG3	2.11	0.51
2:B:385:THR:HB	2:B:386:LYS:HE3	1.92	0.50
1:C:39:GLN:HE22	1:C:177:GLN:NE2	1.97	0.49
1:A:14:PRO:HG3	1:A:118:SER:O	2.13	0.48
1:C:156:ARG:HG3	1:C:215:SER:HA	1.96	0.48
1:A:168:SER:CB	2:B:502:GLY:H	2.26	0.48
1:C:12:ILE:HG21	1:C:85:LEU:HD13	1.96	0.48
2:B:517:LEU:HB2	2:D:517:LEU:HB2	1.96	0.47
1:A:156:ARG:HG3	1:A:215:SER:HA	1.96	0.47
1:C:82:MET:HE1	1:C:115:VAL:HG21	1.97	0.47
1:C:159:LEU:HD22	1:C:241:THR:HG21	1.96	0.47
1:C:176:GLN:HB2	1:C:186:LEU:HD11	1.96	0.46
2:D:395:VAL:HA	2:D:514:SER:O	2.17	0.45
1:C:20:LEU:HG	1:C:82:MET:HE2	2.00	0.44
1:C:150:SER:C	1:C:151:LEU:HD23	2.43	0.44
1:A:176:GLN:HB2	1:A:186:LEU:HD11	2.00	0.43
1:C:18:LEU:HD12	1:C:19:ARG:N	2.33	0.43
2:D:388:ASN:HB3	2:D:527:PRO:HD2	2.01	0.43
1:A:218:GLU:O	1:A:245:ILE:HD13	2.19	0.42
2:B:393:THR:HG21	2:B:520:ALA:HB3	2.02	0.42
2:D:357:ARG:NH2	2:D:396:TYR:OH	2.53	0.42
1:C:64:LYS:HE3	1:C:64:LYS:HB2	1.77	0.42
2:D:376:THR:HB	2:D:435:ALA:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:517:LEU:HD22	2:D:430:THR:HG21	2.02	0.42
1:C:85:LEU:HD23	1:C:85:LEU:HA	1.83	0.42
1:A:198:SER:OG	1:A:200:ARG:HG2	2.20	0.41
1:C:168:SER:CB	2:D:502:GLY:H	2.33	0.41
2:D:399:SER:HA	2:D:510:VAL:O	2.21	0.41
2:B:451:TYR:C	2:B:452:LEU:HD23	2.46	0.41
2:B:376:THR:HB	2:B:435:ALA:HB3	2.03	0.40
2:D:518:LEU:C	2:D:520:ALA:H	2.29	0.40
2:B:364:ASP:HB3	2:B:367:VAL:HB	2.03	0.40

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	A	223/251 (89%)	218 (98%)	4 (2%)	1 (0%)	30	28
1	C	223/251 (89%)	216 (97%)	7 (3%)	0	100	100
2	B	191/199 (96%)	186 (97%)	5 (3%)	0	100	100
2	D	191/199 (96%)	183 (96%)	8 (4%)	0	100	100
All	All	828/900 (92%)	803 (97%)	24 (3%)	1 (0%)	48	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	104	HIS

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	A	187/197 (95%)	184 (98%)	3 (2%)	55	64
1	C	187/197 (95%)	183 (98%)	4 (2%)	47	54
2	B	166/172 (96%)	163 (98%)	3 (2%)	51	60
2	D	166/172 (96%)	162 (98%)	4 (2%)	43	49
All	All	706/738 (96%)	692 (98%)	14 (2%)	48	56

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	145	SER
1	A	150	SER
1	A	172	LEU
2	B	385	THR
2	B	483	VAL
2	B	517	LEU
1	C	18	LEU
1	C	74	SER
1	C	145	SER
1	C	152	SER
2	D	373	SER
2	D	477	SER
2	D	483	VAL
2	D	517	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	111	GLN
1	A	181	GLN
2	B	354	ASN
2	B	493	GLN
1	C	39	GLN
1	C	81	GLN
1	C	170	ASN
2	D	360	ASN

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Mol	Chain	Res	Type
2	D	493	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	B	1000	2	14,14,15	0.62	0	17,19,21	0.63	0
3	NAG	D	1000	2	14,14,15	0.77	1 (7%)	17,19,21	0.69	0

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	B	1000	2	-	2/6/23/26	0/1/1/1
3	NAG	D	1000	2	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1000	NAG	C1-C2	2.52	1.55	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1000	NAG	C4-C5-C6-O6
3	B	1000	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	227/251 (90%)	0.06	5 (2%) 62 65	27, 36, 65, 75	0
1	C	227/251 (90%)	0.12	10 (4%) 39 41	27, 36, 65, 73	0
2	B	193/199 (96%)	0.10	9 (4%) 36 38	26, 37, 61, 65	0
2	D	193/199 (96%)	0.19	10 (5%) 33 35	27, 38, 62, 69	0
All	All	840/900 (93%)	0.12	34 (4%) 42 44	26, 37, 63, 75	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	482	GLY	6.2
2	B	482	GLY	6.1
2	D	486	PHE	4.8
2	D	335	LEU	3.9
2	D	481	ASN	3.9
2	D	483	VAL	3.8
2	D	485	GLY	3.8
1	C	245	ILE	3.6
1	C	138	GLY	3.6
2	B	369	TYR	3.4
1	A	41	PRO	3.0
2	B	486	PHE	3.0
2	B	496	GLY	2.7
1	C	73	SER	2.6
1	A	245	ILE	2.6
2	B	483	VAL	2.6
2	D	484	GLU	2.6
1	C	1	GLU	2.5
2	B	481	ASN	2.4
2	B	371	SER	2.4
1	C	41	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	138	GLY	2.3
1	C	220	GLU	2.3
1	A	119	SER	2.2
1	A	1	GLU	2.2
1	C	118	SER	2.2
2	B	346	ARG	2.2
1	C	119	SER	2.2
2	B	480	CYS	2.1
2	D	372	ALA	2.1
1	C	150	SER	2.1
2	D	393	THR	2.1
1	C	151	LEU	2.1
2	D	369	TYR	2.0

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	1000	14/15	0.79	0.12	51,59,65,67	0
3	NAG	B	1000	14/15	0.81	0.12	51,61,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.