



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:57 AM UTC

PDB ID : 3RRT / pdb_00003rrt
Title : Structure of the RSV F protein in the post-fusion conformation
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Deposited on : 2011-04-30
Resolution : 3.20 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
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

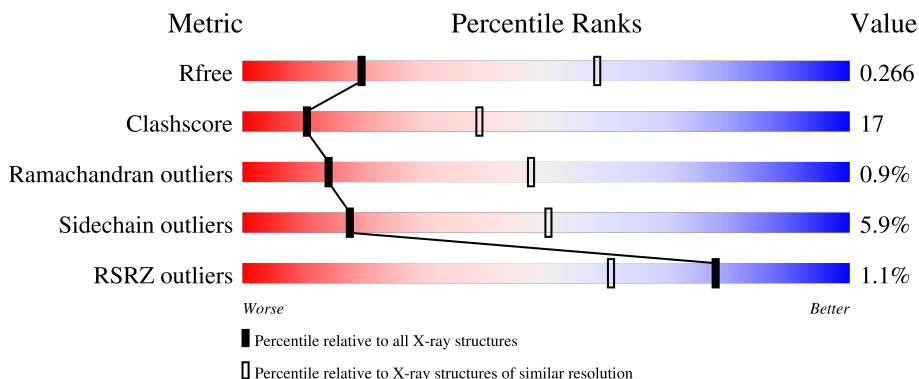
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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.



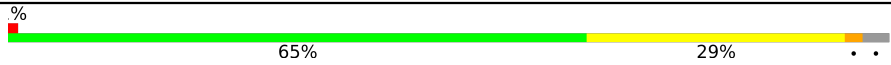
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	84	 67% 17% 14%
1	C	84	 62% 21% 14%
1	E	84	 65% 18% 14%
2	B	374	 64% 30% 5%
2	D	374	 62% 32% ...

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Mol	Chain	Length	Quality of chain
2	F	374	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into segments: a small red segment at the start, followed by a large green segment labeled '65%', then a yellow segment labeled '29%', and finally a small grey segment at the end. Above the bar is a '%' symbol, and below the bar are two dots '...'.</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 20264 atoms, of which 10200 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 Fusion glycoprotein F0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	72	1152	361	581	93	114	3	0	0	0
1	C	72	1152	361	581	93	114	3	0	0	0
1	E	72	1152	361	581	93	114	3	0	0	0

- Molecule 2 is a protein called Fusion glycoprotein F0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	B	356	5545	1738	2790	456	543	18	0	0	0
2	D	360	5605	1757	2821	460	549	18	0	0	0
2	F	364	5658	1772	2846	465	557	18	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	342	TYR	PHE	SEE REMARK 999	UNP Q84850
B	514	GLY	-	expression tag	UNP Q84850
B	515	LEU	-	expression tag	UNP Q84850
B	516	GLU	-	expression tag	UNP Q84850
B	517	VAL	-	expression tag	UNP Q84850
B	518	LEU	-	expression tag	UNP Q84850
B	519	PHE	-	expression tag	UNP Q84850
B	520	GLN	-	expression tag	UNP Q84850
D	342	TYR	PHE	SEE REMARK 999	UNP Q84850
D	514	GLY	-	expression tag	UNP Q84850
D	515	LEU	-	expression tag	UNP Q84850
D	516	GLU	-	expression tag	UNP Q84850

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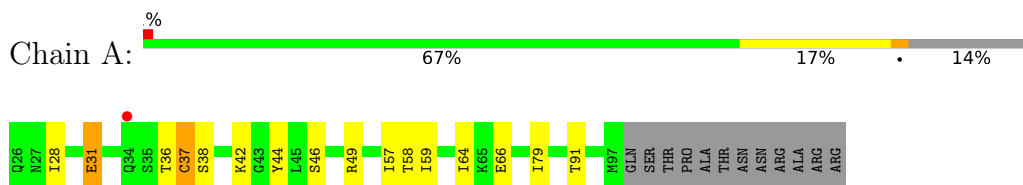
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Chain	Residue	Modelled	Actual	Comment	Reference
D	517	VAL	-	expression tag	UNP Q84850
D	518	LEU	-	expression tag	UNP Q84850
D	519	PHE	-	expression tag	UNP Q84850
D	520	GLN	-	expression tag	UNP Q84850
F	342	TYR	PHE	SEE REMARK 999	UNP Q84850
F	514	GLY	-	expression tag	UNP Q84850
F	515	LEU	-	expression tag	UNP Q84850
F	516	GLU	-	expression tag	UNP Q84850
F	517	VAL	-	expression tag	UNP Q84850
F	518	LEU	-	expression tag	UNP Q84850
F	519	PHE	-	expression tag	UNP Q84850
F	520	GLN	-	expression tag	UNP Q84850

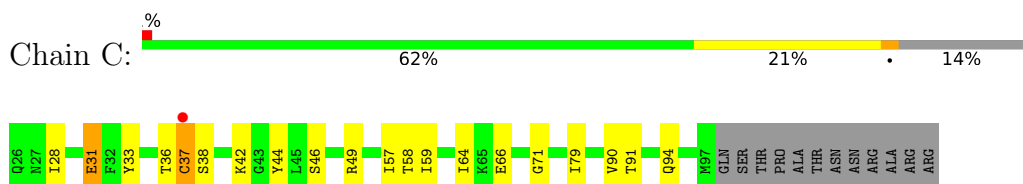
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

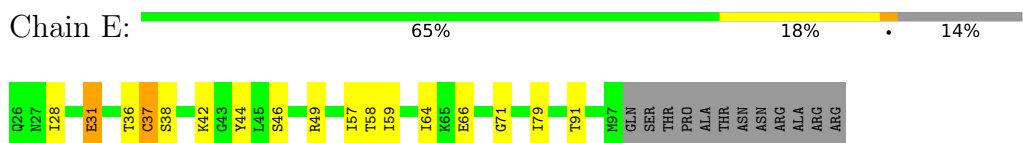
- Molecule 1: Fusion glycoprotein F0



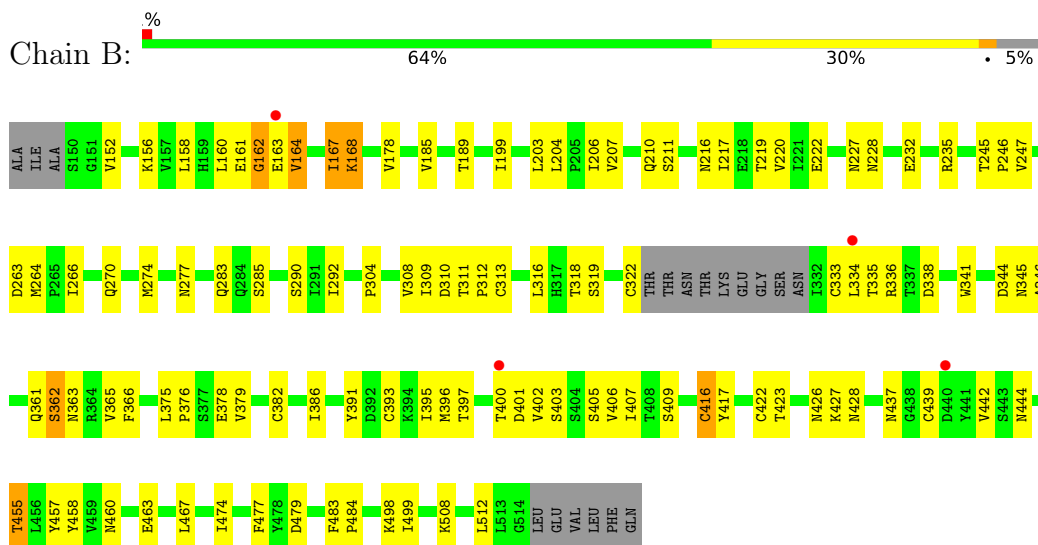
- Molecule 1: Fusion glycoprotein F0



- Molecule 1: Fusion glycoprotein F0



- Molecule 2: Fusion glycoprotein F0



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.02Å 81.88Å 271.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.17 – 3.20 46.17 – 3.20	Depositor EDS
% Data completeness (in resolution range)	91.5 (46.17-3.20) 93.3 (46.17-3.20)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	0.21	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 3.12Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.253 , 0.282 0.236 , 0.266	Depositor DCC
R_{free} test set	1331 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	64.9	Xtrriage
Anisotropy	0.620	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	20264	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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](#)

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	0.51	0/577	0.82	0/777
1	C	0.53	0/577	0.82	0/777
1	E	0.57	0/577	0.82	0/777
2	B	0.55	0/2795	0.79	1/3789 (0.0%)
2	D	0.56	0/2824	0.82	2/3829 (0.1%)
2	F	0.62	0/2852	0.86	4/3868 (0.1%)
All	All	0.57	0/10202	0.82	7/13817 (0.1%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	322	CYS	N-CA-C	8.13	121.75	107.61
2	F	161	GLU	N-CA-C	-7.71	102.88	111.28
2	F	152	VAL	CB-CA-C	-5.89	104.19	112.14
2	F	288	ILE	N-CA-C	5.39	114.51	106.85
2	D	161	GLU	N-CA-C	-5.38	99.34	110.80

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	571	581	581	19	0
1	C	571	581	581	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	571	581	581	22	0
2	B	2755	2790	2788	109	0
2	D	2784	2821	2819	126	0
2	F	2812	2846	2844	117	0
All	All	10064	10200	10194	341	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 17.

The worst 5 of 341 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:F:150:SER:HB2	2:F:154:VAL:HG21	1.53	0.90
2:B:311:THR:HG21	2:B:344:ASP:O	1.81	0.80
2:D:264:MET:HE1	2:D:274:MET:SD	2.21	0.79
2:F:246:PRO:HB3	2:F:283:GLN:HA	1.65	0.78
2:D:261:ILE:HA	2:D:264:MET:HE2	1.65	0.78

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	70/84 (83%)	67 (96%)	2 (3%)	1 (1%)	9	39
1	C	70/84 (83%)	67 (96%)	2 (3%)	1 (1%)	9	39
1	E	70/84 (83%)	67 (96%)	2 (3%)	1 (1%)	9	39
2	B	352/374 (94%)	329 (94%)	20 (6%)	3 (1%)	14	47
2	D	356/374 (95%)	336 (94%)	17 (5%)	3 (1%)	16	50
2	F	360/374 (96%)	341 (95%)	16 (4%)	3 (1%)	16	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1278/1374 (93%)	1207 (94%)	59 (5%)	12 (1%)	14 47

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	346	ALA
2	D	346	ALA
2	F	346	ALA
1	A	37	CYS
2	B	162	GLY

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	65/75 (87%)	63 (97%)	2 (3%)	35 66
1	C	65/75 (87%)	63 (97%)	2 (3%)	35 66
1	E	65/75 (87%)	63 (97%)	2 (3%)	35 66
2	B	329/344 (96%)	310 (94%)	19 (6%)	18 51
2	D	332/344 (96%)	310 (93%)	22 (7%)	15 47
2	F	336/344 (98%)	313 (93%)	23 (7%)	14 46
All	All	1192/1257 (95%)	1122 (94%)	70 (6%)	18 50

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	323	THR
2	F	401	ASP
2	F	442	VAL
2	D	160	LEU
2	D	150	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	34	GLN
2	F	331	ASN
1	E	81	GLN
2	F	240	ASN
2	F	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.

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	72/84 (85%)	0.15	1 (1%) 73 54	48, 78, 127, 169	0
1	C	72/84 (85%)	0.20	1 (1%) 73 54	45, 72, 141, 161	0
1	E	72/84 (85%)	0.14	0 100 100	49, 74, 136, 157	0
2	B	356/374 (95%)	0.07	5 (1%) 73 54	42, 73, 115, 180	0
2	D	360/374 (96%)	0.02	2 (0%) 85 73	26, 74, 114, 153	0
2	F	364/374 (97%)	0.07	5 (1%) 73 54	36, 69, 102, 137	0
All	All	1296/1374 (94%)	0.07	14 (1%) 78 61	26, 72, 115, 180	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	163	GLU	5.6
2	B	163	GLU	4.5
2	B	356	GLU	3.5
2	D	167	ILE	2.7
2	F	428	ASN	2.6

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.