



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2026 – 10:35 AM UTC

PDB ID : 1EBO / pdb\_00001ebo  
Title : CRYSTAL STRUCTURE OF THE EBOLA VIRUS MEMBRANE-FUSION SUBUNIT, GP2, FROM THE ENVELOPE GLYCOPROTEIN ECTODOMAIN  
Authors : Weissenhorn, W.; Carfi, A.; Lee, K.H.; Skehel, J.J.; Wiley, D.C.  
Deposited on : 1998-11-03  
Resolution : 3.00 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](mailto: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>.

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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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

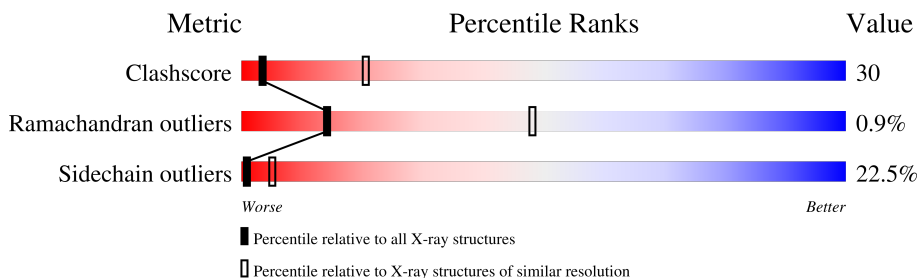
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)

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  $\geq 3$ , 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  $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	131	
1	B	131	
1	C	131	
1	D	131	
1	E	131	
1	F	131	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5331 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 EBOLA VIRUS ENVELOPE PROTEIN CHIMERA CONSISTING OF A FRAGMENT OF GCN4 ZIPPER CLONED N-TERMINAL TO A FRAGMENT OF GP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	112	Total 901	C 571	N 159	O 169	S 2	0	0	0
1	B	112	Total 881	C 559	N 151	O 169	S 2	0	0	0
1	C	111	Total 893	C 567	N 158	O 166	S 2	0	0	0
1	D	112	Total 876	C 556	N 149	O 169	S 2	0	0	0
1	E	111	Total 881	C 560	N 153	O 166	S 2	0	0	0
1	F	113	Total 894	C 568	N 154	O 170	S 2	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	deletion	UNP Q913A3
B	?	-	GLU	deletion	gb 4389202
C	?	-	GLU	deletion	GB 4389203
D	?	-	GLU	deletion	GB 4389204
E	?	-	GLU	deletion	GB 4389205
F	?	-	GLU	deletion	GB 4389206

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	D	1	Total	Cl	0	0
			1	1		

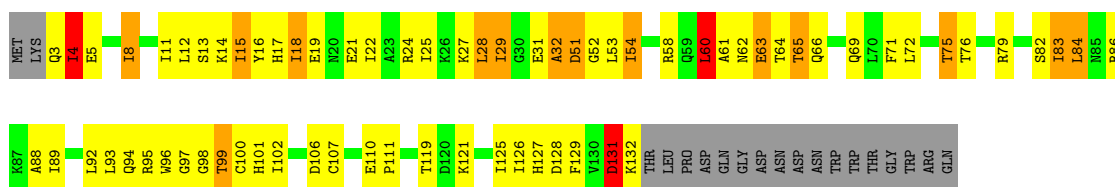
### 3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

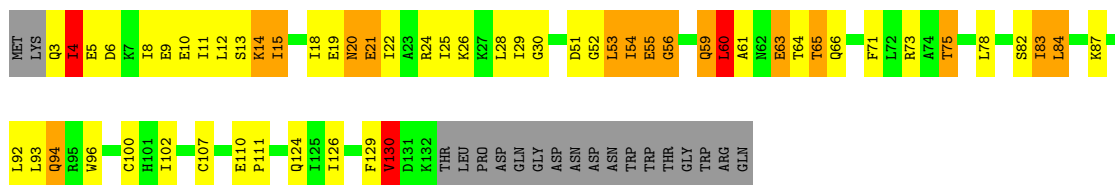
- Molecule 1: EBOLA VIRUS ENVELOPE PROTEIN CHIMERA CONSISTING OF A FRAGMENT OF GCN4 ZIPPER CLONED N-TERMINAL TO A FRAGMENT OF GP2

Chain A: 



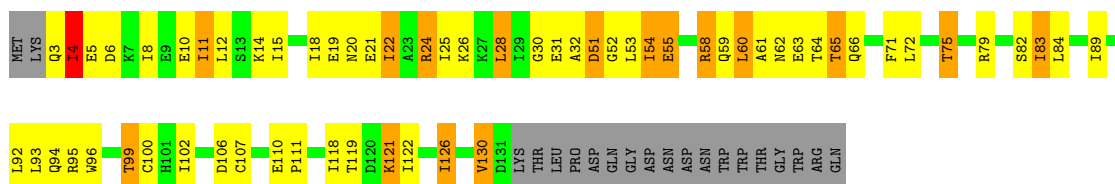
- Molecule 1: EBOLA VIRUS ENVELOPE PROTEIN CHIMERA CONSISTING OF A FRAGMENT OF GCN4 ZIPPER CLONED N-TERMINAL TO A FRAGMENT OF GP2

Chain B: 



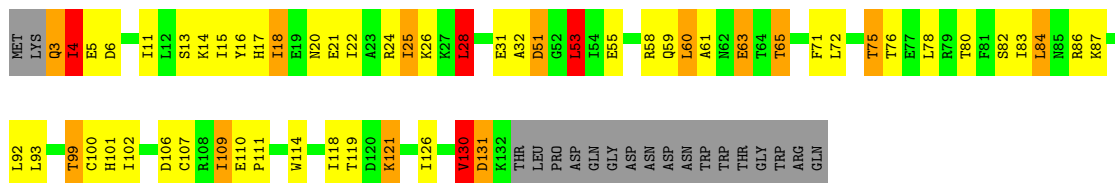
- Molecule 1: EBOLA VIRUS ENVELOPE PROTEIN CHIMERA CONSISTING OF A FRAGMENT OF GCN4 ZIPPER CLONED N-TERMINAL TO A FRAGMENT OF GP2

Chain C: 

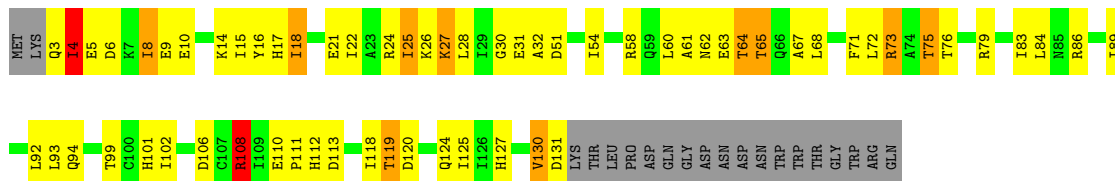
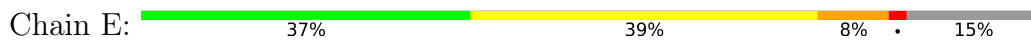


- Molecule 1: EBOLA VIRUS ENVELOPE PROTEIN CHIMERA CONSISTING OF A FRAGMENT OF GCN4 ZIPPER CLONED N-TERMINAL TO A FRAGMENT OF GP2

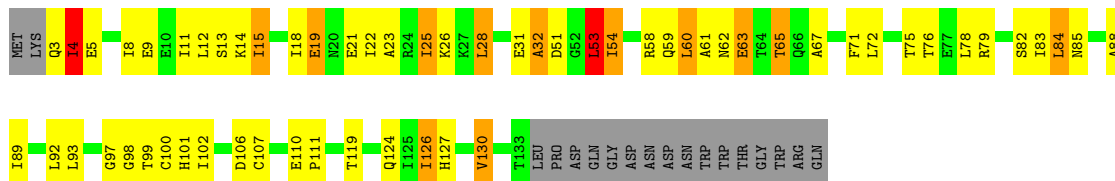
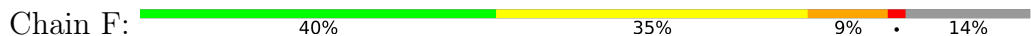
Chain D: 



- Molecule 1: EBOLA VIRUS ENVELOPE PROTEIN CHIMERA CONSISTING OF A FRAGMENT OF GCN4 ZIPPER CLONED N-TERMINAL TO A FRAGMENT OF GP2



- Molecule 1: EBOLA VIRUS ENVELOPE PROTEIN CHIMERA CONSISTING OF A FRAGMENT OF GCN4 ZIPPER CLONED N-TERMINAL TO A FRAGMENT OF GP2



## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	171.70Å 32.69Å 168.86Å 90.00° 119.23° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00	Depositor
% Data completeness (in resolution range)	99.3 (20.00-3.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.239 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	5331	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

## 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: CL, ZN

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	0.79	2/915 (0.2%)	1.23	8/1237 (0.6%)
1	B	0.79	2/895 (0.2%)	1.19	8/1215 (0.7%)
1	C	0.57	0/907	1.11	3/1226 (0.2%)
1	D	0.66	0/890	1.26	9/1208 (0.7%)
1	E	0.91	3/895 (0.3%)	1.16	4/1211 (0.3%)
1	F	0.59	0/908	1.21	6/1230 (0.5%)
All	All	0.73	7/5410 (0.1%)	1.19	38/7327 (0.5%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	108	ARG	CD-NE	-19.48	1.19	1.46
1	B	73	ARG	CD-NE	-14.67	1.25	1.46
1	A	131	ASP	C-N	-13.59	1.14	1.33
1	A	27	LYS	CA-CB	-7.30	1.41	1.53
1	E	27	LYS	CB-CG	-6.99	1.31	1.52

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	73	ARG	CD-NE-CZ	13.41	143.18	124.40
1	D	51	ASP	CA-CB-CG	-12.25	100.35	112.60
1	A	52	GLY	N-CA-C	-12.07	95.78	115.46
1	D	55	GLU	CA-CB-CG	10.87	135.84	114.10
1	C	4	ILE	N-CA-C	-10.80	100.13	111.58

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	901	0	894	77	0
1	B	881	0	851	66	0
1	C	893	0	891	86	0
1	D	876	0	842	64	0
1	E	881	0	869	62	0
1	F	894	0	875	59	0
2	A	1	0	0	0	0
2	D	1	0	0	0	0
2	F	1	0	0	0	0
3	B	1	0	0	1	0
3	D	1	0	0	1	0
All	All	5331	0	5222	314	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 30.

The worst 5 of 314 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:A:53:LEU:HD23	1:C:53:LEU:HD22	1.42	0.99
1:C:126:ILE:HA	1:C:130:VAL:CG1	1.98	0.93
1:F:32:ALA:O	1:F:53:LEU:HG	1.67	0.93
1:F:3:GLN:O	1:F:3:GLN:HG2	1.65	0.92
1:E:26:LYS:HG3	1:F:25:ILE:HD11	1.49	0.92

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	110/131 (84%)	103 (94%)	5 (4%)	2 (2%)	6	31
1	B	110/131 (84%)	99 (90%)	10 (9%)	1 (1%)	14	48
1	C	109/131 (83%)	102 (94%)	6 (6%)	1 (1%)	14	48
1	D	110/131 (84%)	103 (94%)	6 (6%)	1 (1%)	14	48
1	E	109/131 (83%)	102 (94%)	7 (6%)	0	100	100
1	F	111/131 (85%)	101 (91%)	9 (8%)	1 (1%)	14	48
All	All	659/786 (84%)	610 (93%)	43 (6%)	6 (1%)	14	48

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	32	ALA
1	D	32	ALA
1	A	29	ILE
1	F	31	GLU
1	B	29	ILE

### 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	96/117 (82%)	76 (79%)	20 (21%)	1	7
1	B	92/117 (79%)	71 (77%)	21 (23%)	1	5
1	C	95/117 (81%)	72 (76%)	23 (24%)	1	4
1	D	91/117 (78%)	68 (75%)	23 (25%)	0	3
1	E	93/117 (80%)	73 (78%)	20 (22%)	1	6
1	F	94/117 (80%)	75 (80%)	19 (20%)	1	7
All	All	561/702 (80%)	435 (78%)	126 (22%)	1	5

5 of 126 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	84	LEU
1	F	14	LYS
1	D	26	LYS
1	F	13	SER
1	F	65	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	62	ASN
1	F	69	GLN
1	C	20	ASN
1	B	124	GLN
1	F	101	HIS

### 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](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	131:ASP	C	132:LYS	N	1.14

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.