



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 06:04 PM UTC

PDB ID : 4RR3 / pdb_00004rr3
Title : Crystal structure of a recombinant EV71 virus particle
Authors : Chen, R.; Lyu, K.
Deposited on : 2014-11-06
Resolution : 3.10 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
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

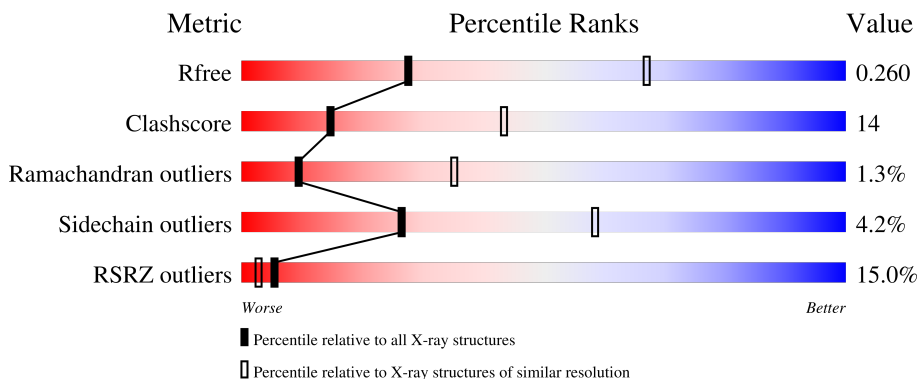
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



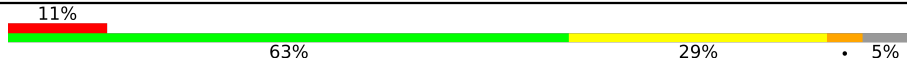

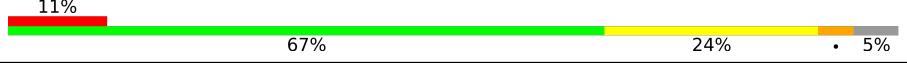
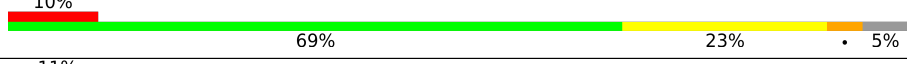

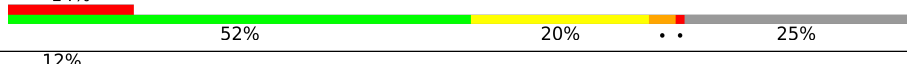
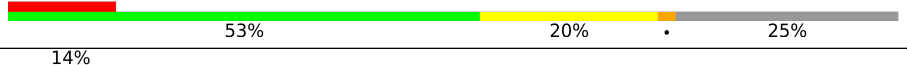

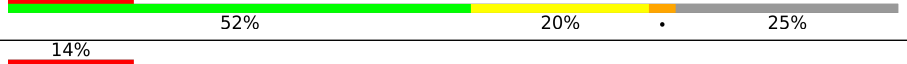

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	303	
1	E	303	
1	I	303	
1	M	303	
1	Q	303	

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Mol	Chain	Length	Quality of chain
2	B	242	
2	F	242	
2	J	242	
2	N	242	
2	R	242	
3	C	323	
3	G	323	
3	K	323	
3	O	323	
3	S	323	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 27390 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 Capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	232	1844	1179	316	338	11	0	0	0
1	Q	232	1844	1179	316	338	11	0	0	0
1	I	232	1844	1179	316	338	11	0	0	0
1	M	232	1844	1179	316	338	11	0	0	0
1	A	232	1844	1179	316	338	11	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	101	GLU	-	expression tag	UNP F6KTB0
E	102	ARG	-	expression tag	UNP F6KTB0
E	103	LYS	-	expression tag	UNP F6KTB0
E	104	ARG	-	expression tag	UNP F6KTB0
E	105	ALA	-	expression tag	UNP F6KTB0
E	106	ARG	-	expression tag	UNP F6KTB0
E	107	LEU	-	expression tag	UNP F6KTB0
E	?	-	ASN	deletion	UNP F6KTB0
Q	101	GLU	-	expression tag	UNP F6KTB0
Q	102	ARG	-	expression tag	UNP F6KTB0
Q	103	LYS	-	expression tag	UNP F6KTB0
Q	104	ARG	-	expression tag	UNP F6KTB0
Q	105	ALA	-	expression tag	UNP F6KTB0
Q	106	ARG	-	expression tag	UNP F6KTB0
Q	107	LEU	-	expression tag	UNP F6KTB0
Q	?	-	ASN	deletion	UNP F6KTB0
I	101	GLU	-	expression tag	UNP F6KTB0
I	102	ARG	-	expression tag	UNP F6KTB0
I	103	LYS	-	expression tag	UNP F6KTB0

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Chain	Residue	Modelled	Actual	Comment	Reference
I	104	ARG	-	expression tag	UNP F6KTB0
I	105	ALA	-	expression tag	UNP F6KTB0
I	106	ARG	-	expression tag	UNP F6KTB0
I	107	LEU	-	expression tag	UNP F6KTB0
I	?	-	ASN	deletion	UNP F6KTB0
M	101	GLU	-	expression tag	UNP F6KTB0
M	102	ARG	-	expression tag	UNP F6KTB0
M	103	LYS	-	expression tag	UNP F6KTB0
M	104	ARG	-	expression tag	UNP F6KTB0
M	105	ALA	-	expression tag	UNP F6KTB0
M	106	ARG	-	expression tag	UNP F6KTB0
M	107	LEU	-	expression tag	UNP F6KTB0
M	?	-	ASN	deletion	UNP F6KTB0
A	101	GLU	-	expression tag	UNP F6KTB0
A	102	ARG	-	expression tag	UNP F6KTB0
A	103	LYS	-	expression tag	UNP F6KTB0
A	104	ARG	-	expression tag	UNP F6KTB0
A	105	ALA	-	expression tag	UNP F6KTB0
A	106	ARG	-	expression tag	UNP F6KTB0
A	107	LEU	-	expression tag	UNP F6KTB0
A	?	-	ASN	deletion	UNP F6KTB0

- Molecule 2 is a protein called Capsid protein VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	230	Total	C	N	O	S	0	0	0
			1762	1133	291	327	11			
2	R	230	Total	C	N	O	S	0	0	0
			1762	1133	291	327	11			
2	J	230	Total	C	N	O	S	0	0	0
			1762	1133	291	327	11			
2	N	230	Total	C	N	O	S	0	0	0
			1762	1133	291	327	11			
2	B	230	Total	C	N	O	S	0	0	0
			1762	1133	291	327	11			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	227	GLN	LYS	engineered mutation	UNP F6KTB0
R	227	GLN	LYS	engineered mutation	UNP F6KTB0
J	227	GLN	LYS	engineered mutation	UNP F6KTB0

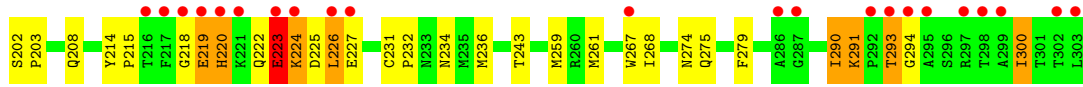
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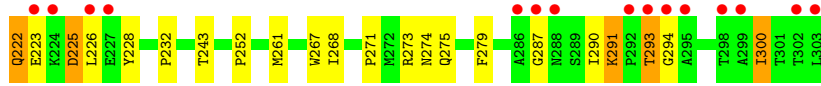
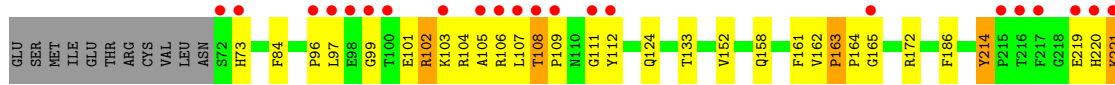
Chain	Residue	Modelled	Actual	Comment	Reference
N	227	GLN	LYS	engineered mutation	UNP F6KTB0
B	227	GLN	LYS	engineered mutation	UNP F6KTB0

- Molecule 3 is a protein called Capsid protein VP0.

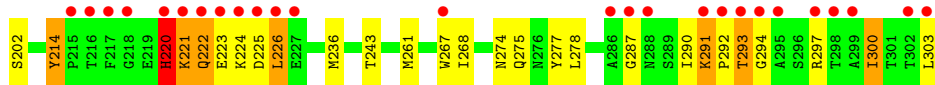
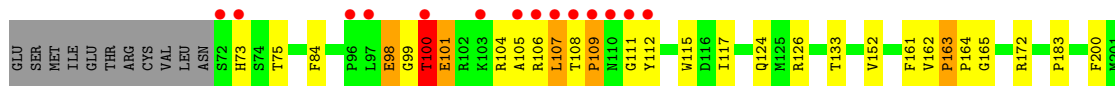
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	242	Total	C	N	O	S	0	0	0
			1872	1201	310	353	8			
3	S	242	Total	C	N	O	S	0	0	0
			1872	1201	310	353	8			
3	K	242	Total	C	N	O	S	0	0	0
			1872	1201	310	353	8			
3	O	242	Total	C	N	O	S	0	0	0
			1872	1201	310	353	8			
3	C	242	Total	C	N	O	S	0	0	0
			1872	1201	310	353	8			



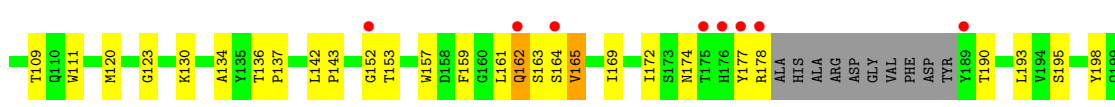
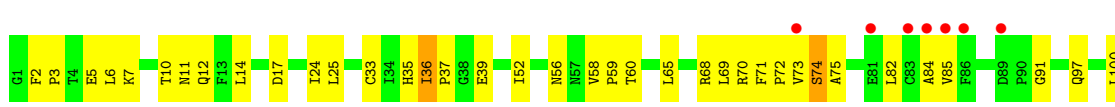
• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1

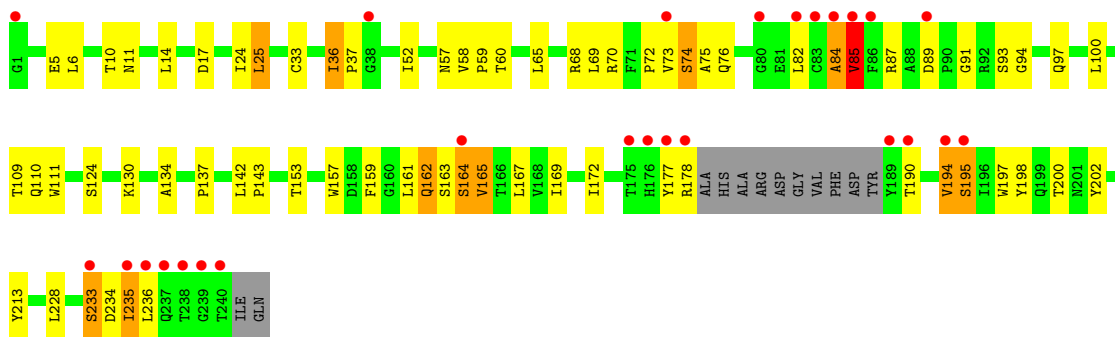


• Molecule 2: Capsid protein VP3

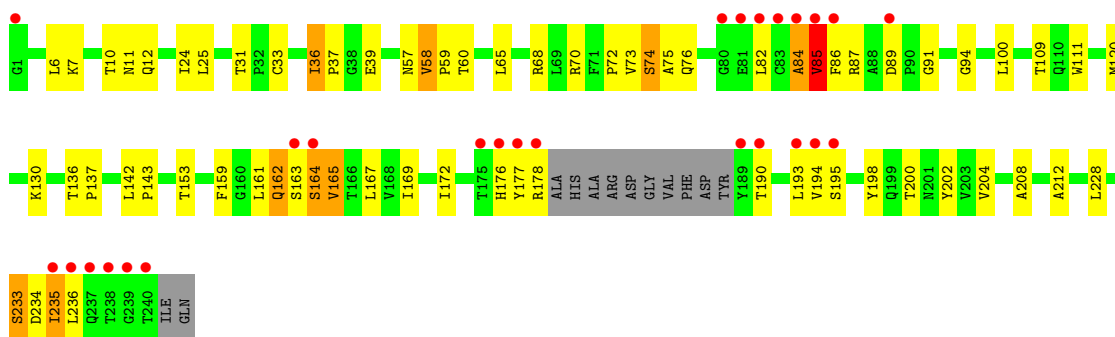


• Molecule 2: Capsid protein VP3

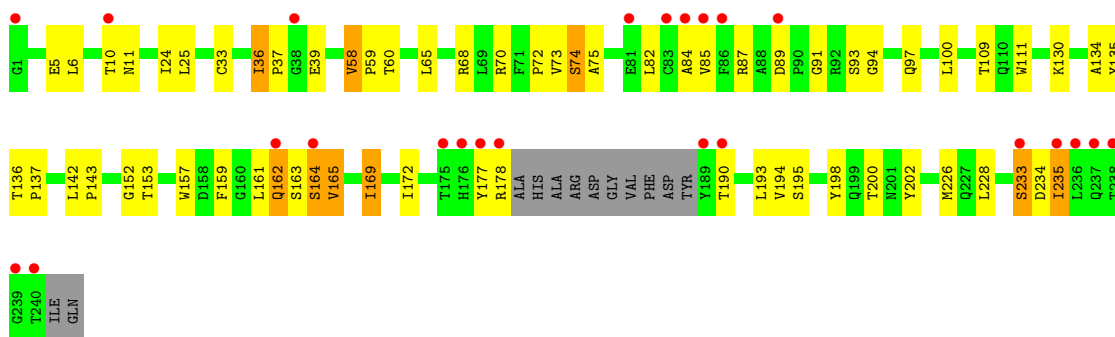




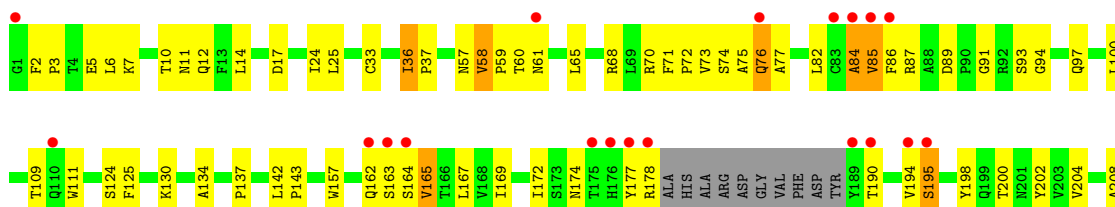
• Molecule 2: Capsid protein VP3



• Molecule 2: Capsid protein VP3



• Molecule 2: Capsid protein VP3



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 3 2	Depositor
Cell constants a, b, c, α , β , γ	350.60Å 350.60Å 350.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.44 – 3.10 46.44 – 3.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (46.44-3.10) 90.5 (46.44-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 3.12Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.235 , 0.265 0.235 , 0.260	Depositor DCC
R_{free} test set	2000 reflections (1.52%)	wwPDB-VP
Wilson B-factor (Å ²)	59.5	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 29.0	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	0.90	EDS
Total number of atoms	27390	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.18% 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	0.47	0/1899	1.05	15/2584 (0.6%)
1	E	0.53	3/1899 (0.2%)	0.95	3/2584 (0.1%)
1	I	0.45	0/1899	1.01	11/2584 (0.4%)
1	M	0.43	0/1899	0.95	9/2584 (0.3%)
1	Q	0.49	0/1899	0.98	14/2584 (0.5%)
2	B	0.45	0/1810	0.96	14/2477 (0.6%)
2	F	0.40	0/1810	0.90	5/2477 (0.2%)
2	J	0.45	0/1810	0.96	13/2477 (0.5%)
2	N	0.39	0/1810	0.89	9/2477 (0.4%)
2	R	0.45	1/1810 (0.1%)	0.95	13/2477 (0.5%)
3	C	0.46	0/1927	0.89	4/2644 (0.2%)
3	G	0.38	0/1927	0.87	2/2644 (0.1%)
3	K	0.41	0/1927	0.89	4/2644 (0.2%)
3	O	0.40	0/1927	0.89	3/2644 (0.1%)
3	S	0.42	1/1927 (0.1%)	0.87	2/2644 (0.1%)
All	All	0.44	5/28180 (0.0%)	0.94	121/38525 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	I	0	1
1	Q	0	2
3	C	0	2
3	G	0	2
3	K	0	2
3	O	0	1
All	All	0	10

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	220	HIS	ND1-CE1	-8.79	1.23	1.32
1	E	220	HIS	CE1-NE2	8.13	1.40	1.32
1	E	220	HIS	CG-ND1	6.54	1.45	1.38
2	R	194	VAL	CA-C	5.47	1.59	1.52
3	S	178	HIS	CD2-NE2	5.40	1.43	1.37

The worst 5 of 121 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	214	TYR	CA-C-N	10.00	130.15	119.05
1	I	214	TYR	C-N-CA	10.00	130.15	119.05
2	B	85	VAL	N-CA-C	9.41	121.91	108.17
1	A	101	GLU	N-CA-C	9.38	123.12	109.14
2	R	85	VAL	N-CA-C	8.43	120.47	108.17

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	G	121	LYS	Peptide
3	G	95	GLN	Peptide
1	I	219	GLU	Peptide
1	Q	225	ASP	Peptide
1	Q	226	LEU	Peptide

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	1844	0	1803	61	0
1	E	1844	0	1803	47	0
1	I	1844	0	1803	56	0
1	M	1844	0	1803	69	0
1	Q	1844	0	1803	69	0
2	B	1762	0	1746	70	0
2	F	1762	0	1746	70	0
2	J	1762	0	1746	65	0
2	N	1762	0	1746	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	R	1762	0	1746	65	0
3	C	1872	0	1811	59	0
3	G	1872	0	1811	55	0
3	K	1872	0	1811	47	0
3	O	1872	0	1811	65	0
3	S	1872	0	1811	67	0
All	All	27390	0	26800	752	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 14.

The worst 5 of 752 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:I:98:GLU:HA	1:I:104:ARG:HH12	1.19	1.04
2:R:85:VAL:HG21	2:R:195:SER:HA	1.40	1.02
3:C:295:GLN:HE21	3:C:295:GLN:HA	1.19	1.00
1:M:105:ALA:HA	1:M:108:THR:HA	1.44	0.99
1:I:105:ALA:HA	1:I:108:THR:HA	1.43	0.98

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	230/303 (76%)	207 (90%)	19 (8%)	4 (2%)	7	30
1	E	230/303 (76%)	207 (90%)	18 (8%)	5 (2%)	5	24
1	I	230/303 (76%)	208 (90%)	17 (7%)	5 (2%)	5	24
1	M	230/303 (76%)	208 (90%)	19 (8%)	3 (1%)	9	35
1	Q	230/303 (76%)	208 (90%)	18 (8%)	4 (2%)	7	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	226/242 (93%)	206 (91%)	18 (8%)	2 (1%)	14	44
2	F	226/242 (93%)	204 (90%)	20 (9%)	2 (1%)	14	44
2	J	226/242 (93%)	204 (90%)	20 (9%)	2 (1%)	14	44
2	N	226/242 (93%)	204 (90%)	20 (9%)	2 (1%)	14	44
2	R	226/242 (93%)	204 (90%)	20 (9%)	2 (1%)	14	44
3	C	240/323 (74%)	218 (91%)	19 (8%)	3 (1%)	9	35
3	G	240/323 (74%)	221 (92%)	16 (7%)	3 (1%)	9	35
3	K	240/323 (74%)	221 (92%)	16 (7%)	3 (1%)	9	35
3	O	240/323 (74%)	225 (94%)	11 (5%)	4 (2%)	7	30
3	S	240/323 (74%)	223 (93%)	15 (6%)	2 (1%)	16	47
All	All	3480/4340 (80%)	3168 (91%)	266 (8%)	46 (1%)	9	35

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	121	LYS
3	G	317	LEU
1	Q	226	LEU
1	I	226	LEU
1	M	221	LYS

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	199/256 (78%)	190 (96%)	9 (4%)	24	56
1	E	199/256 (78%)	190 (96%)	9 (4%)	24	56
1	I	199/256 (78%)	189 (95%)	10 (5%)	22	53
1	M	199/256 (78%)	193 (97%)	6 (3%)	36	65
1	Q	199/256 (78%)	193 (97%)	6 (3%)	36	65
2	B	193/202 (96%)	186 (96%)	7 (4%)	31	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	193/202 (96%)	187 (97%)	6 (3%)	35	64
2	J	193/202 (96%)	185 (96%)	8 (4%)	27	59
2	N	193/202 (96%)	186 (96%)	7 (4%)	31	62
2	R	193/202 (96%)	185 (96%)	8 (4%)	27	59
3	C	205/272 (75%)	194 (95%)	11 (5%)	20	50
3	G	205/272 (75%)	197 (96%)	8 (4%)	28	60
3	K	205/272 (75%)	196 (96%)	9 (4%)	25	56
3	O	205/272 (75%)	195 (95%)	10 (5%)	22	53
3	S	205/272 (75%)	195 (95%)	10 (5%)	22	53
All	All	2985/3650 (82%)	2861 (96%)	124 (4%)	26	58

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	R	162	GLN
3	O	259	CYS
2	N	70	ARG
3	O	239	ILE
3	C	218	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
3	S	280	ASN
3	O	188	GLN
3	K	280	ASN
3	O	280	ASN
2	R	61	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	232/303 (76%)	0.52	40 (17%) 4 2	25, 40, 140, 156	0
1	E	232/303 (76%)	0.45	36 (15%) 5 2	27, 41, 140, 154	0
1	I	232/303 (76%)	0.60	37 (15%) 5 2	30, 41, 142, 157	0
1	M	232/303 (76%)	0.55	37 (15%) 5 2	28, 41, 142, 156	0
1	Q	232/303 (76%)	0.46	33 (14%) 6 3	29, 42, 140, 156	0
2	B	230/242 (95%)	0.50	26 (11%) 10 5	27, 41, 73, 147	0
2	F	230/242 (95%)	0.33	20 (8%) 16 9	32, 44, 80, 142	0
2	J	230/242 (95%)	0.43	26 (11%) 10 5	31, 44, 79, 145	0
2	N	230/242 (95%)	0.40	24 (10%) 11 6	28, 44, 76, 149	0
2	R	230/242 (95%)	0.39	26 (11%) 10 5	30, 45, 81, 145	0
3	C	242/323 (74%)	0.72	46 (19%) 3 1	25, 47, 130, 150	0
3	G	242/323 (74%)	0.55	40 (16%) 4 2	31, 50, 131, 149	0
3	K	242/323 (74%)	0.64	46 (19%) 3 1	29, 50, 130, 148	0
3	O	242/323 (74%)	0.57	44 (18%) 3 1	31, 52, 131, 148	0
3	S	242/323 (74%)	0.67	46 (19%) 3 1	31, 52, 133, 148	0
All	All	3520/4340 (81%)	0.52	527 (14%) 5 3	25, 44, 129, 157	0

The worst 5 of 527 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	107	LEU	8.8
1	E	107	LEU	8.5
1	I	107	LEU	8.5
1	A	107	LEU	8.0
1	Q	107	LEU	7.8

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.