



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 27, 2026 – 06:06 AM EDT

PDB ID : 9Q4F / pdb_00009q4f
Title : Measles Virus Fusion Glycoprotein Postfusion Core (Wild-type Variant)
Authors : Vithanage, N.; Outlaw, V.K.
Deposited on : 2025-08-20
Resolution : 1.95 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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

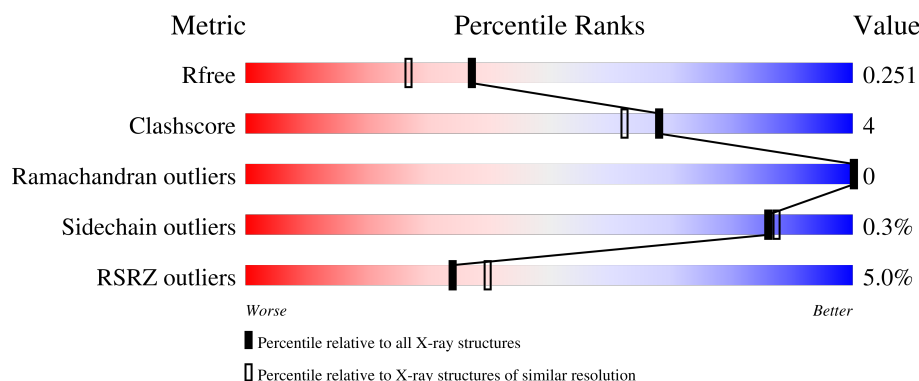
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	50	
1	C	50	
1	E	50	
1	G	50	
1	H	50	

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Mol	Chain	Length	Quality of chain
1	I	50	8% 76% 14% 10%
2	B	38	5% 87% 5% 8%
2	D	38	3% 84% 8% 8%
2	F	38	3% 84% 8% 8%
2	J	38	3% 89% 8%
2	K	38	8% 79% 8% 13%
2	L	38	82% 11% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7464 atoms, of which 3647 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 F1 N-terminal heptad repeat (HR1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	48	Total	C	H	N	O	0	0	1
			713	217	354	65	77			
1	C	48	Total	C	H	N	O	0	1	1
			726	221	361	66	78			
1	E	47	Total	C	H	N	O	0	0	0
			717	220	357	64	76			
1	G	46	Total	C	H	N	O	0	0	0
			677	210	332	62	73			
1	H	45	Total	C	H	N	O	0	0	0
			684	209	339	62	74			
1	I	45	Total	C	H	N	O	0	0	0
			665	205	326	61	73			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	ACE	-	acetylation	UNP P69358
A	171	THR	MET	variant	UNP P69358
A	190	NH2	-	amidation	UNP P69358
C	141	ACE	-	acetylation	UNP P69358
C	171	THR	MET	variant	UNP P69358
C	190	NH2	-	amidation	UNP P69358
E	141	ACE	-	acetylation	UNP P69358
E	171	THR	MET	variant	UNP P69358
E	190	NH2	-	amidation	UNP P69358
G	141	ACE	-	acetylation	UNP P69358
G	171	THR	MET	variant	UNP P69358
G	190	NH2	-	amidation	UNP P69358
H	141	ACE	-	acetylation	UNP P69358
H	171	THR	MET	variant	UNP P69358
H	190	NH2	-	amidation	UNP P69358
I	141	ACE	-	acetylation	UNP P69358
I	171	THR	MET	variant	UNP P69358

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Chain	Residue	Modelled	Actual	Comment	Reference
I	190	NH2	-	amidation	UNP P69358

- Molecule 2 is a protein called Fusion glycoprotein F1 C-terminal heptad repeat (HR2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	35	Total	C	H	N	O	0	0	0
			528	160	265	46	57			
2	D	35	Total	C	H	N	O	0	0	1
			531	160	270	46	55			
2	F	35	Total	C	H	N	O	0	0	1
			531	160	270	46	55			
2	J	35	Total	C	H	N	O	0	0	1
			519	157	261	46	55			
2	K	33	Total	C	H	N	O	0	1	0
			501	152	251	45	53			
2	L	35	Total	C	H	N	O	0	0	1
			519	157	261	46	55			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	451	ACE	-	acetylation	UNP P69358
B	487	NLE	MET	engineered mutation	UNP P69358
B	488	NH2	-	amidation	UNP P69358
D	451	ACE	-	acetylation	UNP P69358
D	487	NLE	MET	engineered mutation	UNP P69358
D	488	NH2	-	amidation	UNP P69358
F	451	ACE	-	acetylation	UNP P69358
F	487	NLE	MET	engineered mutation	UNP P69358
F	488	NH2	-	amidation	UNP P69358
J	451	ACE	-	acetylation	UNP P69358
J	487	NLE	MET	engineered mutation	UNP P69358
J	488	NH2	-	amidation	UNP P69358
K	451	ACE	-	acetylation	UNP P69358
K	487	NLE	MET	engineered mutation	UNP P69358
K	488	NH2	-	amidation	UNP P69358
L	451	ACE	-	acetylation	UNP P69358
L	487	NLE	MET	engineered mutation	UNP P69358
L	488	NH2	-	amidation	UNP P69358

- Molecule 3 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Br 1	0	0
3	H	1	Total 1	Br 1	0	0

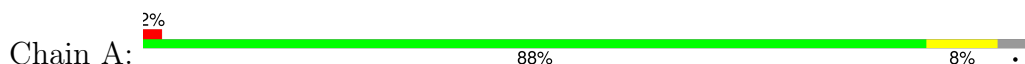
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	20	Total 20	O 20	0	0
4	B	17	Total 17	O 17	0	0
4	C	20	Total 20	O 20	0	0
4	D	15	Total 15	O 15	0	0
4	E	18	Total 18	O 18	0	0
4	F	13	Total 13	O 13	0	0
4	G	9	Total 9	O 9	0	0
4	H	13	Total 13	O 13	0	0
4	I	11	Total 11	O 11	0	0
4	J	2	Total 2	O 2	0	0
4	K	8	Total 8	O 8	0	0
4	L	5	Total 5	O 5	0	0

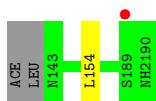
3 Residue-property plots [i](#)

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.

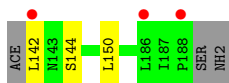
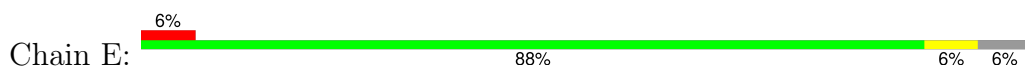
- Molecule 1: Fusion glycoprotein F1 N-terminal heptad repeat (HR1)



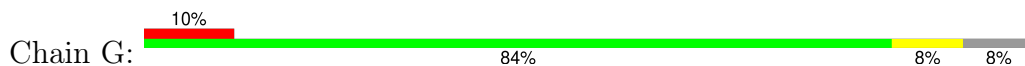
- Molecule 1: Fusion glycoprotein F1 N-terminal heptad repeat (HR1)



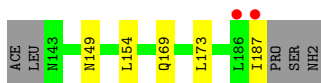
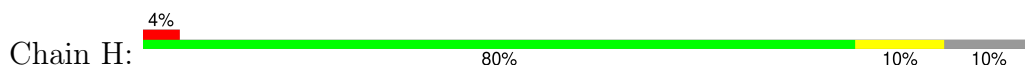
- Molecule 1: Fusion glycoprotein F1 N-terminal heptad repeat (HR1)



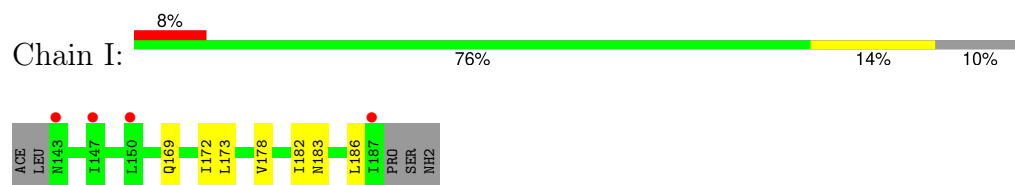
- Molecule 1: Fusion glycoprotein F1 N-terminal heptad repeat (HR1)



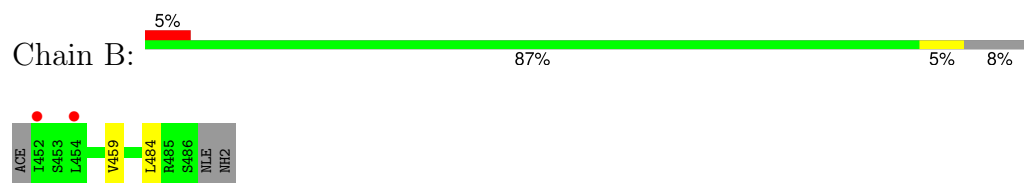
- Molecule 1: Fusion glycoprotein F1 N-terminal heptad repeat (HR1)



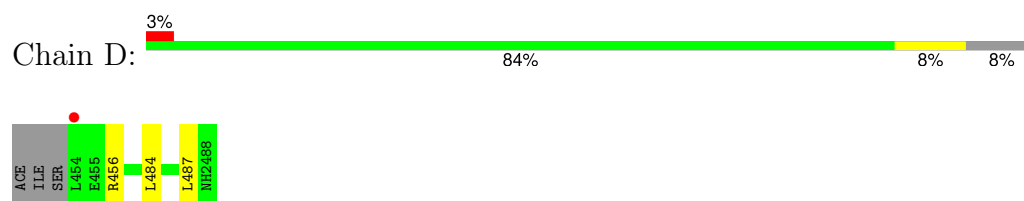
- Molecule 1: Fusion glycoprotein F1 N-terminal heptad repeat (HR1)



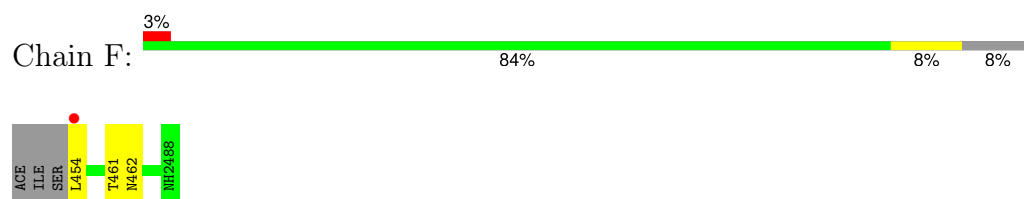
- Molecule 2: Fusion glycoprotein F1 C-terminal heptad repeat (HR2)



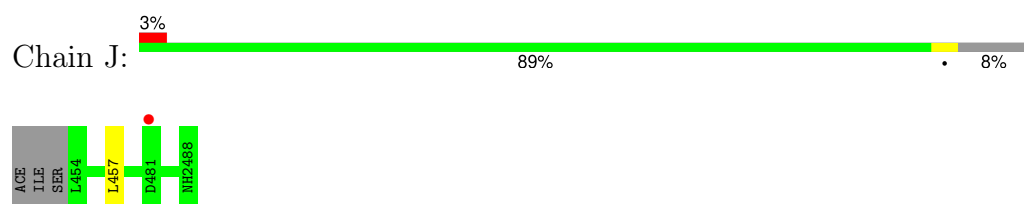
- Molecule 2: Fusion glycoprotein F1 C-terminal heptad repeat (HR2)



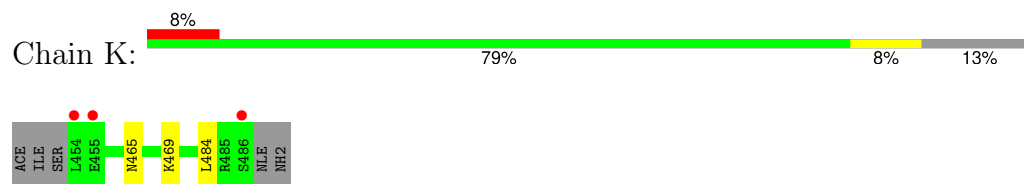
- Molecule 2: Fusion glycoprotein F1 C-terminal heptad repeat (HR2)



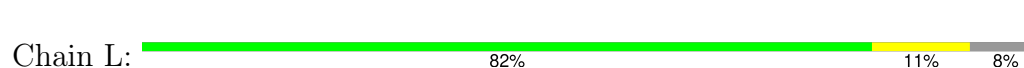
- Molecule 2: Fusion glycoprotein F1 C-terminal heptad repeat (HR2)



- Molecule 2: Fusion glycoprotein F1 C-terminal heptad repeat (HR2)



- Molecule 2: Fusion glycoprotein F1 C-terminal heptad repeat (HR2)





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.55Å 53.98Å 70.96Å 90.00° 92.72° 90.00°	Depositor
Resolution (Å)	32.91 – 1.95 32.91 – 1.95	Depositor EDS
% Data completeness (in resolution range)	77.9 (32.91-1.95) 77.9 (32.91-1.95)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.195 , 0.251 0.197 , 0.251	Depositor DCC
R_{free} test set	2001 reflections (7.28%)	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 61.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.031 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7464	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.29% 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: BR, NH2, NLE

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	0.31	0/359	0.37	0/488
1	C	0.29	0/368	0.38	0/500
1	E	0.28	0/361	0.33	0/491
1	G	0.24	0/345	0.29	0/469
1	H	0.22	0/345	0.30	0/468
1	I	0.20	0/339	0.30	0/460
2	B	0.28	0/262	0.37	0/351
2	D	0.28	0/251	0.38	0/336
2	F	0.26	0/251	0.33	0/336
2	J	0.22	0/248	0.30	0/332
2	K	0.21	0/252	0.27	0/338
2	L	0.24	0/251	0.34	0/336
All	All	0.26	0/3632	0.33	0/4905

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	359	354	351	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	365	361	359	1	0
1	E	360	357	357	4	0
1	G	345	332	332	4	0
1	H	345	339	339	5	0
1	I	339	326	326	6	0
2	B	263	265	265	2	0
2	D	261	270	268	3	0
2	F	261	270	268	3	0
2	J	258	261	259	1	0
2	K	250	251	251	3	0
2	L	258	261	259	4	0
3	A	1	0	0	0	0
3	H	1	0	0	0	0
4	A	20	0	0	1	0
4	B	17	0	0	0	0
4	C	20	0	0	0	0
4	D	15	0	0	0	0
4	E	18	0	0	0	0
4	F	13	0	0	0	0
4	G	9	0	0	0	0
4	H	13	0	0	1	0
4	I	11	0	0	0	0
4	J	2	0	0	0	0
4	K	8	0	0	0	0
4	L	5	0	0	0	0
All	All	3817	3647	3634	26	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 4.

All (26) 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:186:LEU:HD12	2:F:454:LEU:HD21	1.60	0.83
1:G:186:LEU:HD11	1:H:187:ILE:HD11	1.65	0.76
1:I:182:ILE:HA	1:I:186:LEU:HD12	1.80	0.64
1:H:154:LEU:HG	2:K:484:LEU:HD11	1.83	0.60
1:E:142:LEU:HD21	1:E:144:SER:OG	2.04	0.57
1:G:186:LEU:CD1	1:H:187:ILE:HD11	2.35	0.57
1:I:172:ILE:HG21	2:L:467:ILE:HD11	1.89	0.54
1:A:179:GLN:OE1	2:B:459:VAL:HG22	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:LEU:HD23	2:B:484:LEU:HD21	1.91	0.53
2:D:487:NLE:HE1	1:E:150:LEU:HD21	1.91	0.53
2:L:478:GLU:O	2:L:482:GLN:HG2	2.12	0.50
1:G:142:LEU:HD12	1:G:143:ASN:N	2.28	0.49
2:D:487:NLE:HE1	1:E:150:LEU:CD2	2.44	0.48
1:G:166:GLN:HB2	2:K:469:LYS:HD3	1.97	0.47
1:A:145:GLN:NE2	4:A:301:HOH:O	2.46	0.46
1:I:183:ASN:HB3	2:L:456:ARG:HH21	1.81	0.46
1:I:172:ILE:HD13	2:L:467:ILE:HD13	1.98	0.45
1:E:142:LEU:O	1:E:142:LEU:HD23	2.15	0.45
1:I:178:VAL:HG22	2:J:457:LEU:HD21	2.00	0.44
1:H:169:GLN:O	1:H:173:LEU:HD23	2.19	0.43
1:H:149:ASN:ND2	4:H:302:HOH:O	2.53	0.42
2:K:465[A]:ASN:OD1	2:K:469:LYS:HE2	2.19	0.42
1:C:154:LEU:HD23	2:D:484:LEU:HD21	2.03	0.41
1:A:186:LEU:CD1	2:F:454:LEU:HD21	2.40	0.41
2:F:461:THR:HG23	2:F:462:ASN:N	2.36	0.41
1:I:169:GLN:O	1:I:173:LEU:HD13	2.20	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	46/50 (92%)	45 (98%)	1 (2%)	0	100	100
1	C	47/50 (94%)	46 (98%)	1 (2%)	0	100	100
1	E	45/50 (90%)	43 (96%)	2 (4%)	0	100	100
1	G	44/50 (88%)	44 (100%)	0	0	100	100
1	H	43/50 (86%)	41 (95%)	2 (5%)	0	100	100
1	I	43/50 (86%)	42 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	33/38 (87%)	33 (100%)	0	0	100	100
2	D	32/38 (84%)	32 (100%)	0	0	100	100
2	F	32/38 (84%)	31 (97%)	1 (3%)	0	100	100
2	J	32/38 (84%)	32 (100%)	0	0	100	100
2	K	32/38 (84%)	32 (100%)	0	0	100	100
2	L	32/38 (84%)	31 (97%)	1 (3%)	0	100	100
All	All	461/528 (87%)	452 (98%)	9 (2%)	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	39/40 (98%)	39 (100%)	0	100	100
1	C	40/40 (100%)	40 (100%)	0	100	100
1	E	39/40 (98%)	39 (100%)	0	100	100
1	G	35/40 (88%)	35 (100%)	0	100	100
1	H	37/40 (92%)	37 (100%)	0	100	100
1	I	35/40 (88%)	35 (100%)	0	100	100
2	B	29/30 (97%)	29 (100%)	0	100	100
2	D	28/30 (93%)	27 (96%)	1 (4%)	31	21
2	F	28/30 (93%)	28 (100%)	0	100	100
2	J	27/30 (90%)	27 (100%)	0	100	100
2	K	27/30 (90%)	27 (100%)	0	100	100
2	L	28/30 (93%)	28 (100%)	0	100	100
All	All	392/420 (93%)	391 (100%)	1 (0%)	86	87

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	456	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	145	GLN
1	E	169	GLN
1	H	166	GLN
2	J	482	GLN
2	K	462	ASN
2	L	462	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
2	NLE	J	487	2	6,7,8	0.49	0	2,7,9	0.29	0
2	NLE	D	487	2	6,7,8	0.40	0	2,7,9	0.17	0
2	NLE	F	487	2	6,7,8	0.44	0	2,7,9	0.11	0
2	NLE	L	487	2	3,4,8	0.72	0	2,4,9	1.15	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
2	NLE	J	487	2	-	3/5/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NLE	D	487	2	-	0/5/6/8	-
2	NLE	F	487	2	-	0/5/6/8	-
2	NLE	L	487	2	-	0/1/2/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	J	487	NLE	CA-CB-CG-CD
2	J	487	NLE	C-CA-CB-CG
2	J	487	NLE	CE-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	487	NLE	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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](#)

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	47/50 (94%)	0.14	1 (2%) 63 70	17, 30, 67, 74	0
1	C	47/50 (94%)	-0.12	1 (2%) 63 70	12, 25, 57, 74	1 (2%)
1	E	47/50 (94%)	0.08	3 (6%) 25 29	14, 28, 64, 93	0
1	G	46/50 (92%)	0.32	5 (10%) 10 12	20, 34, 64, 88	0
1	H	45/50 (90%)	0.28	2 (4%) 39 45	21, 37, 64, 74	0
1	I	45/50 (90%)	0.42	4 (8%) 15 17	21, 36, 71, 102	0
2	B	35/38 (92%)	-0.06	2 (5%) 29 34	15, 25, 66, 83	0
2	D	33/38 (86%)	-0.21	1 (3%) 52 59	14, 27, 49, 67	0
2	F	33/38 (86%)	-0.02	1 (3%) 52 59	18, 34, 73, 88	0
2	J	33/38 (86%)	0.16	1 (3%) 52 59	21, 34, 61, 72	0
2	K	33/38 (86%)	0.45	3 (9%) 15 17	17, 35, 81, 92	1 (3%)
2	L	33/38 (86%)	0.32	0 100 100	24, 39, 63, 74	0
All	All	477/528 (90%)	0.15	24 (5%) 34 40	12, 32, 71, 102	2 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	187	ILE	4.7
1	G	187	ILE	4.5
1	I	143	ASN	4.1
1	H	186	LEU	3.8
2	K	455	GLU	3.8
2	K	454	LEU	3.7
2	K	486	SER	3.5
2	D	454	LEU	3.3
2	F	454	LEU	3.1
1	E	188	PRO	3.1
2	B	452	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	G	144	SER	3.0
1	H	187	ILE	2.9
1	G	143	ASN	2.8
1	C	189	SER	2.8
1	E	186	LEU	2.5
2	J	481	ASP	2.5
1	A	186	LEU	2.4
2	B	454	LEU	2.3
1	I	147	ILE	2.3
1	E	142	LEU	2.3
1	G	142	LEU	2.3
1	I	150	LEU	2.2
1	G	147	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
2	NLE	J	487	8/9	0.67	0.20	79,96,111,111	0
2	NLE	L	487	5/9	0.67	0.18	61,62,63,74	0
2	NLE	F	487	8/9	0.84	0.13	46,55,60,60	0
2	NLE	D	487	8/9	0.85	0.10	39,48,59,59	0

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(Å ²)	Q<0.9
3	BR	H	201	1/1	0.84	0.11	115,115,115,115	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	BR	A	201	1/1	0.89	0.15	100,100,100,100	0

6.5 Other polymers [i](#)

There are no such residues in this entry.