



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 03:23 PM UTC

PDB ID : 9LV3 / pdb_00009lv3
Title : Crystal structure of mutant H1 Haemagglutinin HN/18-HA FPP from Influenza A virus
Authors : Deng, G.; Wei, X.; Sun, H.
Deposited on : 2025-02-11
Resolution : 2.70 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
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

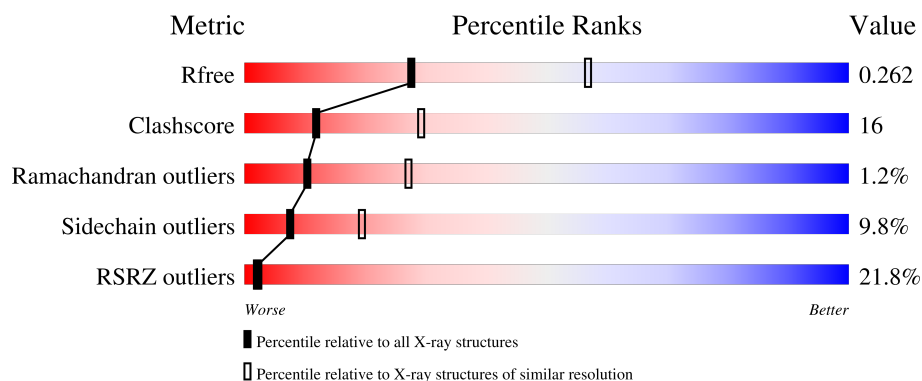
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	321	<div> <div>17%</div> <div>69%</div> <div>27%</div> <div>.</div> </div>
1	C	321	<div> <div>17%</div> <div>75%</div> <div>20%</div> <div>.</div> </div>
1	E	321	<div> <div>14%</div> <div>72%</div> <div>26%</div> <div>..</div> </div>
1	G	321	<div> <div>11%</div> <div>70%</div> <div>25%</div> <div>5% .</div> </div>
1	I	321	<div> <div>11%</div> <div>75%</div> <div>22%</div> <div>.</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	K	321	
2	B	156	
2	D	156	
2	F	156	
2	H	156	
2	J	156	
2	L	156	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	E	402	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22926 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			
1	I	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			
1	K	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			
1	A	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			
1	C	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			
1	E	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	5	ILE	VAL	conflict	UNP A0A6G5UYK1
G	321	VAL	ILE	conflict	UNP A0A6G5UYK1
I	5	ILE	VAL	conflict	UNP A0A6G5UYK1
I	321	VAL	ILE	conflict	UNP A0A6G5UYK1
K	5	ILE	VAL	conflict	UNP A0A6G5UYK1
K	321	VAL	ILE	conflict	UNP A0A6G5UYK1
A	5	ILE	VAL	conflict	UNP A0A6G5UYK1
A	321	VAL	ILE	conflict	UNP A0A6G5UYK1
C	5	ILE	VAL	conflict	UNP A0A6G5UYK1
C	321	VAL	ILE	conflict	UNP A0A6G5UYK1
E	5	ILE	VAL	conflict	UNP A0A6G5UYK1
E	321	VAL	ILE	conflict	UNP A0A6G5UYK1

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	156	Total	C	N	O	S	0	0	0
			1250	786	212	245	7			
2	J	156	Total	C	N	O	S	0	0	0
			1250	786	212	245	7			
2	L	156	Total	C	N	O	S	0	0	0
			1250	786	212	245	7			
2	B	156	Total	C	N	O	S	0	0	0
			1250	786	212	245	7			
2	D	156	Total	C	N	O	S	0	0	0
			1250	786	212	245	7			
2	F	156	Total	C	N	O	S	0	0	0
			1250	786	212	245	7			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	38	LEU	GLN	conflict	UNP A0A6G5UYL6
H	110	TYR	PHE	conflict	UNP A0A6G5UYL6
H	113	SER	LEU	conflict	UNP A0A6G5UYL6
J	38	LEU	GLN	conflict	UNP A0A6G5UYL6
J	110	TYR	PHE	conflict	UNP A0A6G5UYL6
J	113	SER	LEU	conflict	UNP A0A6G5UYL6
L	38	LEU	GLN	conflict	UNP A0A6G5UYL6
L	110	TYR	PHE	conflict	UNP A0A6G5UYL6
L	113	SER	LEU	conflict	UNP A0A6G5UYL6
B	38	LEU	GLN	conflict	UNP A0A6G5UYL6
B	110	TYR	PHE	conflict	UNP A0A6G5UYL6
B	113	SER	LEU	conflict	UNP A0A6G5UYL6
D	38	LEU	GLN	conflict	UNP A0A6G5UYL6
D	110	TYR	PHE	conflict	UNP A0A6G5UYL6
D	113	SER	LEU	conflict	UNP A0A6G5UYL6
F	38	LEU	GLN	conflict	UNP A0A6G5UYL6
F	110	TYR	PHE	conflict	UNP A0A6G5UYL6
F	113	SER	LEU	conflict	UNP A0A6G5UYL6

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	I	1	Total	C	N	O	0	0
			14	8	1	5		
3	I	1	Total	C	N	O	0	0
			14	8	1	5		
3	I	1	Total	C	N	O	0	0
			14	8	1	5		
3	K	1	Total	C	N	O	0	0
			14	8	1	5		
3	K	1	Total	C	N	O	0	0
			14	8	1	5		
3	K	1	Total	C	N	O	0	0
			14	8	1	5		
3	K	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

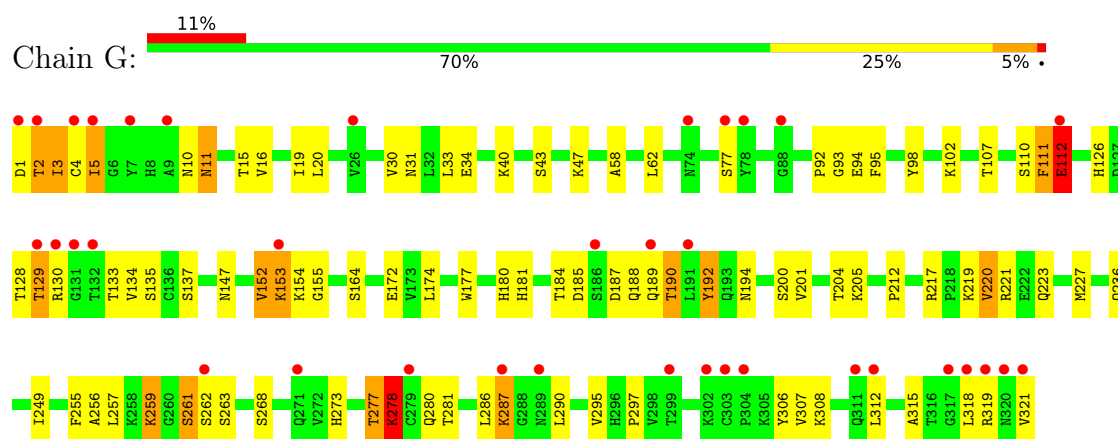
Continued from previous page...

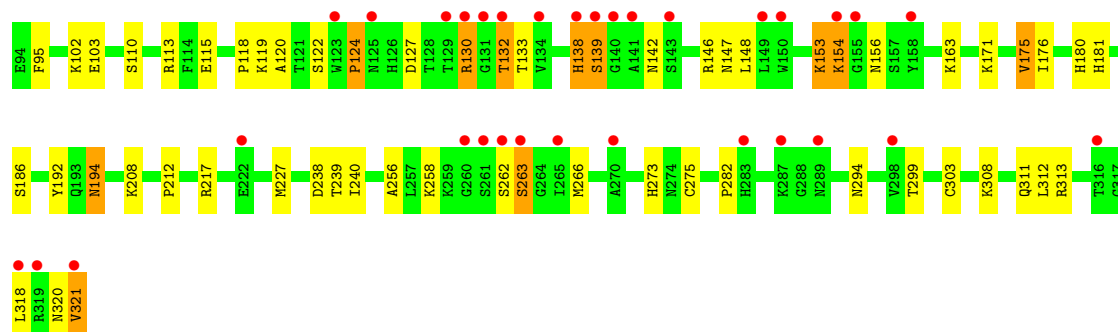
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		

3 Residue-property plots [i](#)

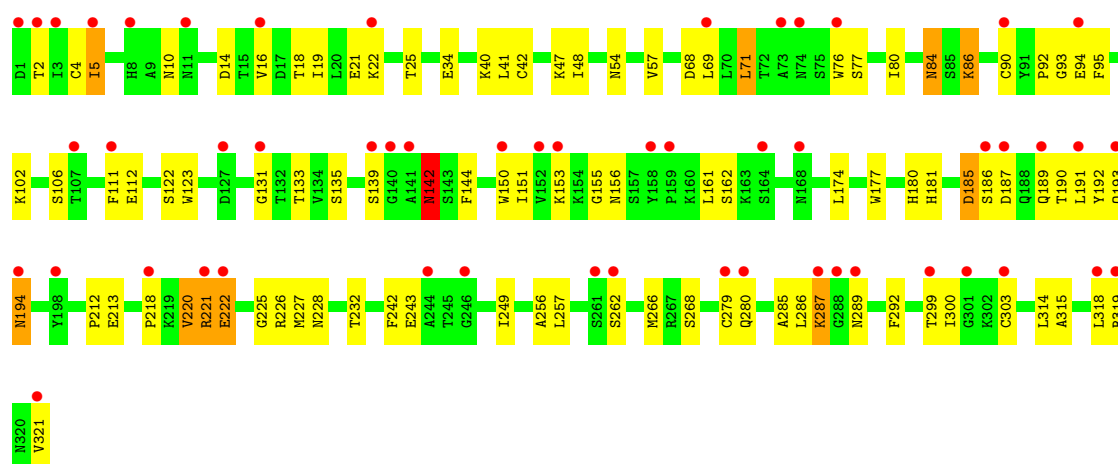
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Hemagglutinin

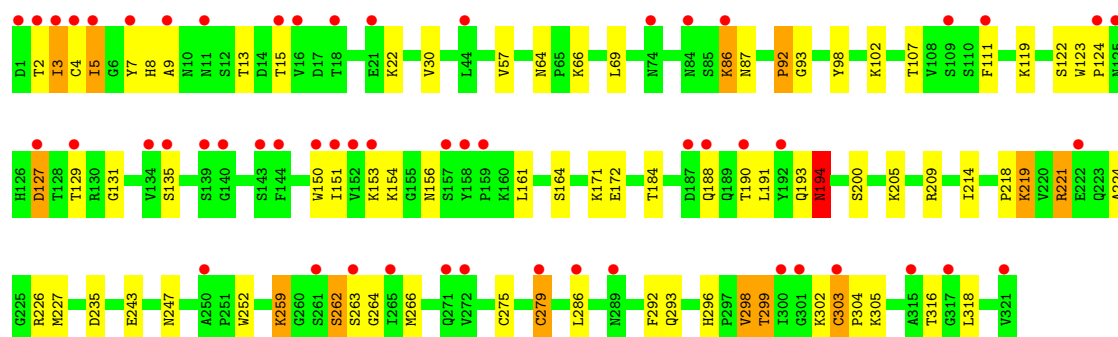
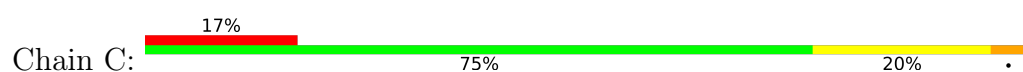




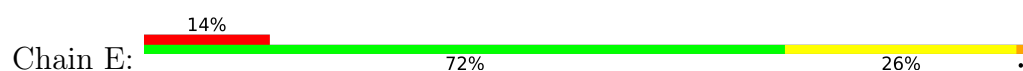
• Molecule 1: Hemagglutinin

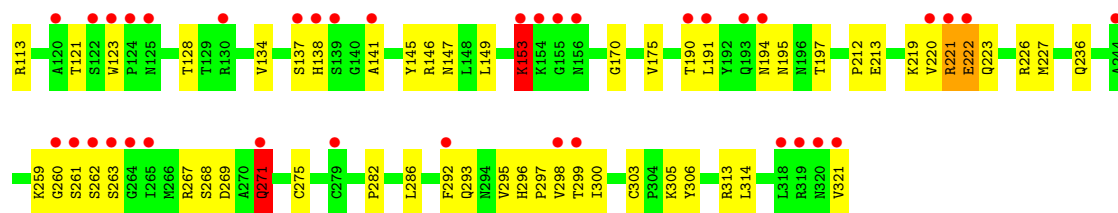


• Molecule 1: Hemagglutinin

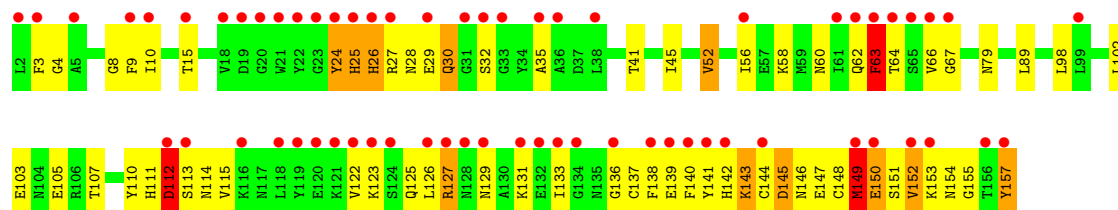
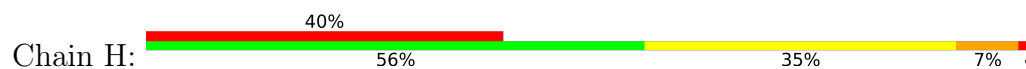


• Molecule 1: Hemagglutinin

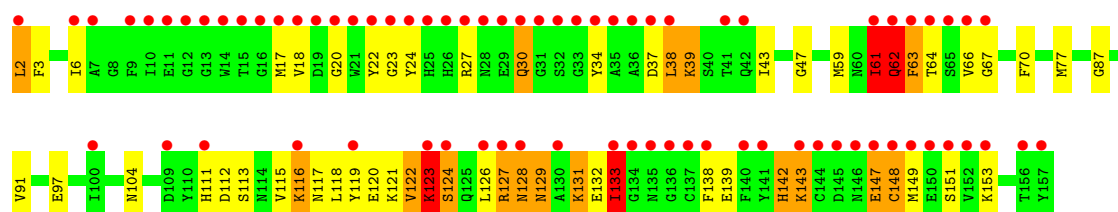




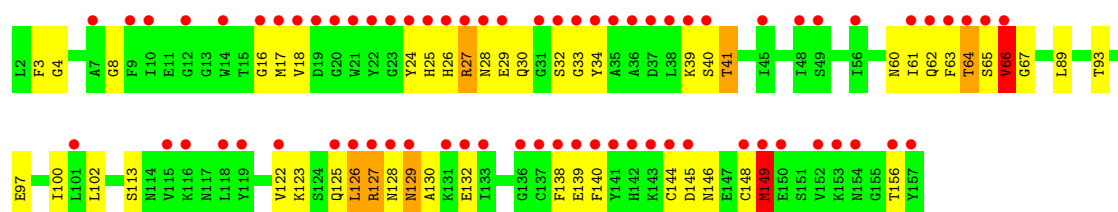
• Molecule 2: Hemagglutinin



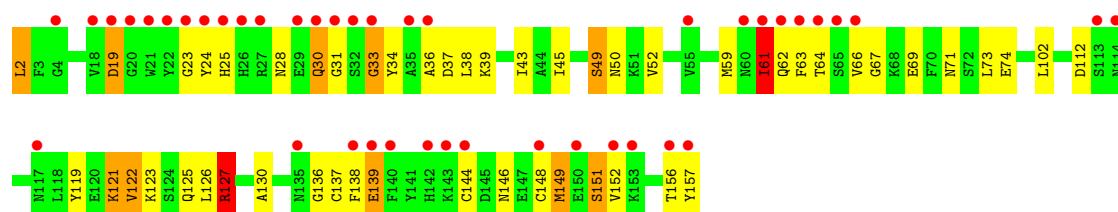
• Molecule 2: Hemagglutinin



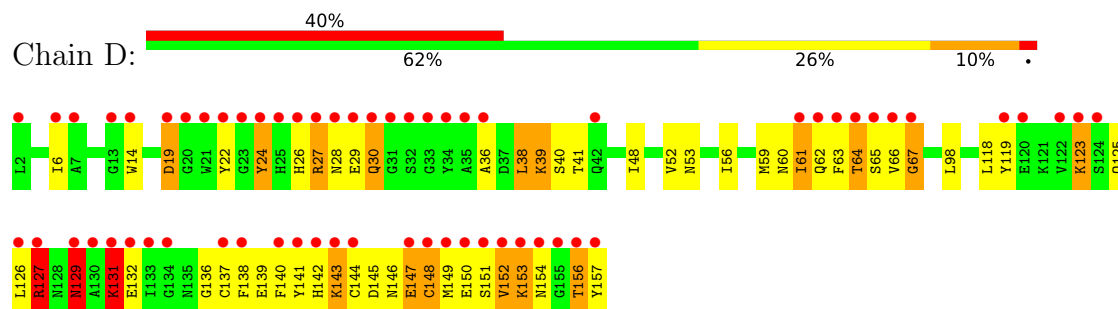
• Molecule 2: Hemagglutinin



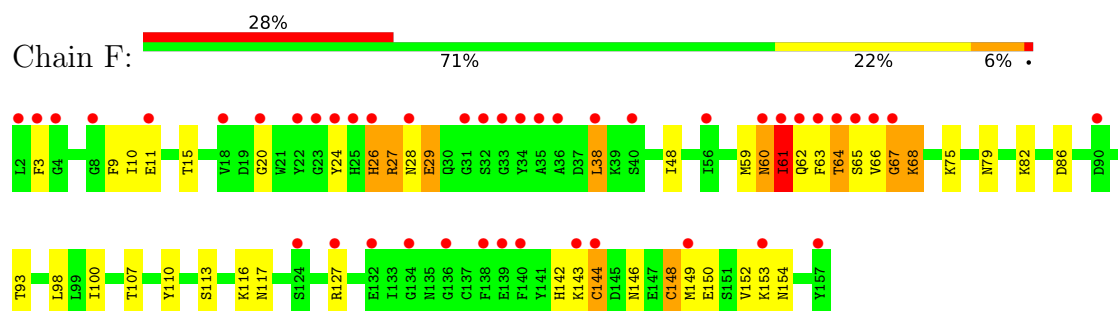
• Molecule 2: Hemagglutinin



- Molecule 2: Hemagglutinin



- Molecule 2: Hemagglutinin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.78Å 251.37Å 113.10Å 90.00° 90.50° 90.00°	Depositor
Resolution (Å)	43.61 – 2.70 43.61 – 2.70	Depositor EDS
% Data completeness (in resolution range)	86.4 (43.61-2.70) 87.0 (43.61-2.70)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0218	Depositor
R, R_{free}	0.234 , 0.253 0.244 , 0.262	Depositor DCC
R_{free} test set	4557 reflections (4.36%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.031 for h,-k,-l	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	22926	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 67.01 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.5136e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 ⓘ

5.1 Standard geometry ⓘ

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	0.54	0/2577	0.73	6/3506 (0.2%)
1	C	0.51	2/2577 (0.1%)	0.73	8/3506 (0.2%)
1	E	0.47	0/2577	0.67	4/3506 (0.1%)
1	G	0.58	1/2577 (0.0%)	0.68	6/3506 (0.2%)
1	I	0.46	1/2577 (0.0%)	0.67	3/3506 (0.1%)
1	K	0.45	0/2577	0.64	4/3506 (0.1%)
2	B	0.69	1/1274 (0.1%)	0.88	8/1713 (0.5%)
2	D	0.51	0/1274	0.83	4/1713 (0.2%)
2	F	0.51	0/1274	0.74	2/1713 (0.1%)
2	H	0.63	0/1274	0.86	3/1713 (0.2%)
2	J	0.59	0/1274	0.79	5/1713 (0.3%)
2	L	0.56	0/1274	0.82	3/1713 (0.2%)
All	All	0.53	5/23106 (0.0%)	0.73	56/31314 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	69	GLU	C-O	-5.70	1.16	1.24
1	C	259	LYS	CA-C	-5.67	1.47	1.53
1	I	284	GLY	C-O	-5.50	1.17	1.24
1	C	266	MET	C-O	-5.42	1.17	1.23
1	G	133	THR	C-O	-5.07	1.17	1.23

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	122	VAL	N-CA-C	-9.92	100.19	111.00
2	D	147	GLU	N-CA-C	-9.13	102.65	113.88
1	A	142	ASN	N-CA-C	9.03	121.97	110.24
1	C	86	LYS	N-CA-C	8.84	120.68	111.14
2	L	41	THR	N-CA-C	-8.81	102.66	113.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2515	0	2454	73	0
1	C	2515	0	2452	65	0
1	E	2515	0	2452	74	0
1	G	2515	0	2452	69	0
1	I	2515	0	2452	54	0
1	K	2515	0	2452	70	0
2	B	1250	0	1188	68	0
2	D	1250	0	1190	64	0
2	F	1250	0	1188	64	0
2	H	1250	0	1190	81	0
2	J	1250	0	1188	77	0
2	L	1250	0	1190	77	0
3	A	56	0	52	4	0
3	C	56	0	52	0	0
3	E	56	0	52	0	0
3	G	56	0	52	0	0
3	I	56	0	52	1	0
3	K	56	0	52	1	0
All	All	22926	0	22160	709	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 16.

The worst 5 of 709 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:279:CYS:SG	1:C:286:LEU:HB2	1.63	1.38
2:F:9:PHE:CE1	2:F:10:ILE:CD1	2.14	1.29
2:F:9:PHE:CE1	2:F:10:ILE:HD11	1.68	1.28
2:F:9:PHE:CD1	2:F:10:ILE:HD12	1.70	1.27
1:E:305:LYS:CE	2:F:61:ILE:HD11	1.64	1.25

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	319/321 (99%)	298 (93%)	21 (7%)	0	100	100
1	C	319/321 (99%)	302 (95%)	16 (5%)	1 (0%)	36	60
1	E	319/321 (99%)	297 (93%)	20 (6%)	2 (1%)	21	44
1	G	319/321 (99%)	303 (95%)	14 (4%)	2 (1%)	21	44
1	I	319/321 (99%)	300 (94%)	16 (5%)	3 (1%)	14	35
1	K	319/321 (99%)	299 (94%)	19 (6%)	1 (0%)	36	60
2	B	154/156 (99%)	146 (95%)	5 (3%)	3 (2%)	6	17
2	D	154/156 (99%)	136 (88%)	11 (7%)	7 (4%)	2	4
2	F	154/156 (99%)	137 (89%)	15 (10%)	2 (1%)	9	25
2	H	154/156 (99%)	136 (88%)	13 (8%)	5 (3%)	3	7
2	J	154/156 (99%)	137 (89%)	13 (8%)	4 (3%)	4	11
2	L	154/156 (99%)	136 (88%)	14 (9%)	4 (3%)	4	11
All	All	2838/2862 (99%)	2627 (93%)	177 (6%)	34 (1%)	10	27

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	150	GLU
1	I	261	SER
2	J	63	PHE
2	L	128	ASN
2	D	127	ARG

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	282/282 (100%)	260 (92%)	22 (8%)	11	29
1	C	282/282 (100%)	259 (92%)	23 (8%)	10	27
1	E	282/282 (100%)	261 (93%)	21 (7%)	13	32
1	G	282/282 (100%)	250 (89%)	32 (11%)	5	14
1	I	282/282 (100%)	258 (92%)	24 (8%)	10	25
1	K	282/282 (100%)	262 (93%)	20 (7%)	13	33
2	B	134/134 (100%)	120 (90%)	14 (10%)	7	17
2	D	134/134 (100%)	114 (85%)	20 (15%)	3	8
2	F	134/134 (100%)	119 (89%)	15 (11%)	6	15
2	H	134/134 (100%)	115 (86%)	19 (14%)	3	8
2	J	134/134 (100%)	112 (84%)	22 (16%)	2	6
2	L	134/134 (100%)	121 (90%)	13 (10%)	8	20
All	All	2496/2496 (100%)	2251 (90%)	245 (10%)	7	19

5 of 245 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	263	SER
1	E	138	HIS
1	A	213	GLU
1	E	128	THR
2	F	60	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	156	ASN
1	E	125	ASN
1	C	188	GLN
2	D	50	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	236	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](#)

24 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	E	402	1	14,14,15	0.41	0	17,19,21	0.75	0
3	NAG	G	403	1	14,14,15	0.27	0	17,19,21	0.70	0
3	NAG	I	402	1	14,14,15	0.32	0	17,19,21	0.86	0
3	NAG	C	404	1	14,14,15	0.28	0	17,19,21	0.71	0
3	NAG	K	403	1	14,14,15	0.31	0	17,19,21	0.78	0
3	NAG	C	401	1	14,14,15	0.26	0	17,19,21	0.73	0
3	NAG	A	401	1	14,14,15	0.29	0	17,19,21	0.73	0
3	NAG	E	403	1	14,14,15	0.31	0	17,19,21	0.71	0
3	NAG	I	403	1	14,14,15	0.29	0	17,19,21	0.69	0
3	NAG	G	401	1	14,14,15	0.32	0	17,19,21	0.76	0
3	NAG	E	401	1	14,14,15	0.32	0	17,19,21	0.75	0
3	NAG	K	402	1	14,14,15	0.32	0	17,19,21	0.70	0
3	NAG	A	404	1	14,14,15	0.29	0	17,19,21	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	K	404	1	14,14,15	0.28	0	17,19,21	0.63	0
3	NAG	A	403	1	14,14,15	0.28	0	17,19,21	0.68	0
3	NAG	K	401	1	14,14,15	0.27	0	17,19,21	0.95	0
3	NAG	G	402	1	14,14,15	0.26	0	17,19,21	0.49	0
3	NAG	I	401	1	14,14,15	0.29	0	17,19,21	0.68	0
3	NAG	C	402	1	14,14,15	0.28	0	17,19,21	0.83	0
3	NAG	G	404	1	14,14,15	0.28	0	17,19,21	0.58	0
3	NAG	C	403	1	14,14,15	0.26	0	17,19,21	0.83	0
3	NAG	E	404	1	14,14,15	0.29	0	17,19,21	0.61	0
3	NAG	I	404	1	14,14,15	0.29	0	17,19,21	0.92	1 (5%)
3	NAG	A	402	1	14,14,15	0.35	0	17,19,21	1.10	1 (5%)

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	E	402	1	-	1/6/23/26	0/1/1/1
3	NAG	G	403	1	-	4/6/23/26	0/1/1/1
3	NAG	I	402	1	-	0/6/23/26	0/1/1/1
3	NAG	C	404	1	-	0/6/23/26	0/1/1/1
3	NAG	K	403	1	-	4/6/23/26	0/1/1/1
3	NAG	C	401	1	-	0/6/23/26	0/1/1/1
3	NAG	A	401	1	-	0/6/23/26	0/1/1/1
3	NAG	E	403	1	-	2/6/23/26	0/1/1/1
3	NAG	I	403	1	-	2/6/23/26	0/1/1/1
3	NAG	G	401	1	-	2/6/23/26	0/1/1/1
3	NAG	E	401	1	-	2/6/23/26	0/1/1/1
3	NAG	K	402	1	-	2/6/23/26	0/1/1/1
3	NAG	A	404	1	-	2/6/23/26	0/1/1/1
3	NAG	K	404	1	-	2/6/23/26	0/1/1/1
3	NAG	A	403	1	-	2/6/23/26	0/1/1/1
3	NAG	K	401	1	-	2/6/23/26	0/1/1/1
3	NAG	G	402	1	-	4/6/23/26	0/1/1/1
3	NAG	I	401	1	-	4/6/23/26	0/1/1/1
3	NAG	C	402	1	-	0/6/23/26	0/1/1/1
3	NAG	G	404	1	-	2/6/23/26	0/1/1/1
3	NAG	C	403	1	-	0/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	404	1	-	2/6/23/26	0/1/1/1
3	NAG	I	404	1	-	2/6/23/26	0/1/1/1
3	NAG	A	402	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	NAG	C2-N2-C7	-2.65	119.35	122.90
3	I	404	NAG	O5-C1-C2	-2.02	108.17	111.29

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	401	NAG	C8-C7-N2-C2
3	G	401	NAG	O7-C7-N2-C2
3	G	402	NAG	C8-C7-N2-C2
3	G	402	NAG	O7-C7-N2-C2
3	G	404	NAG	C8-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	402	NAG	1	0
3	K	403	NAG	1	0
3	A	404	NAG	1	0
3	A	402	NAG	3	0

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	321/321 (100%)	1.21	53 (16%) 4 4	18, 46, 70, 104	0
1	C	321/321 (100%)	1.16	55 (17%) 4 3	14, 48, 76, 105	0
1	E	321/321 (100%)	1.12	45 (14%) 6 5	16, 48, 69, 88	0
1	G	321/321 (100%)	0.87	36 (11%) 10 8	15, 38, 69, 112	0
1	I	321/321 (100%)	0.94	35 (10%) 10 9	14, 45, 70, 110	0
1	K	321/321 (100%)	1.05	43 (13%) 7 6	15, 45, 73, 102	0
2	B	156/156 (100%)	1.51	42 (26%) 1 1	15, 60, 98, 130	0
2	D	156/156 (100%)	1.86	62 (39%) 1 0	16, 66, 128, 140	0
2	F	156/156 (100%)	1.45	44 (28%) 1 1	17, 60, 94, 115	0
2	H	156/156 (100%)	1.73	63 (40%) 0 0	16, 73, 111, 130	0
2	J	156/156 (100%)	1.90	74 (47%) 0 0	17, 73, 118, 135	0
2	L	156/156 (100%)	1.86	71 (45%) 0 0	13, 69, 111, 120	0
All	All	2862/2862 (100%)	1.27	623 (21%) 2 2	13, 50, 97, 140	0

The worst 5 of 623 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	157	TYR	6.4
2	H	63	PHE	6.3
2	F	64	THR	6.3
1	C	4	CYS	6.1
2	L	35	ALA	5.9

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	NAG	E	402	14/15	0.05	0.51	30,30,30,30	0
3	NAG	G	404	14/15	0.34	0.31	30,30,30,30	0
3	NAG	A	404	14/15	0.35	0.27	30,30,30,30	0
3	NAG	G	401	14/15	0.39	0.38	30,30,30,30	0
3	NAG	G	402	14/15	0.46	0.30	30,30,30,30	0
3	NAG	K	402	14/15	0.52	0.33	30,30,30,30	0
3	NAG	K	403	14/15	0.52	0.33	30,30,30,30	0
3	NAG	C	401	14/15	0.53	0.32	30,30,30,30	0
3	NAG	K	401	14/15	0.53	0.23	30,30,30,30	0
3	NAG	C	402	14/15	0.55	0.23	30,30,30,30	0
3	NAG	A	402	14/15	0.56	0.37	30,30,30,30	0
3	NAG	C	403	14/15	0.57	0.23	30,30,30,30	0
3	NAG	I	401	14/15	0.57	0.26	30,30,30,30	0
3	NAG	E	401	14/15	0.59	0.24	30,30,30,30	0
3	NAG	A	401	14/15	0.59	0.28	30,30,30,30	0
3	NAG	E	403	14/15	0.61	0.23	30,30,30,30	0
3	NAG	K	404	14/15	0.63	0.23	30,30,30,30	0
3	NAG	I	404	14/15	0.63	0.26	30,30,30,30	0
3	NAG	E	404	14/15	0.63	0.31	30,30,30,30	0
3	NAG	I	402	14/15	0.66	0.28	30,30,30,30	0
3	NAG	C	404	14/15	0.66	0.28	30,30,30,30	0
3	NAG	I	403	14/15	0.68	0.25	30,30,30,30	0
3	NAG	G	403	14/15	0.71	0.21	30,30,30,30	0
3	NAG	A	403	14/15	0.72	0.27	30,30,30,30	0

6.5 Other polymers ⓘ

There are no such residues in this entry.