W O R L D W I D E

wwPDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 17, 2024 – 01:01 AM EDT

PDB ID	:	5LM7
Title	:	Crystal structure of the lambda N-Nus factor complex
Authors	:	Said, N.; Santos, K.; Weber, G.; Wahl, M.C.
Deposited on	:	2016-07-29
Resolution	:	3.35 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:

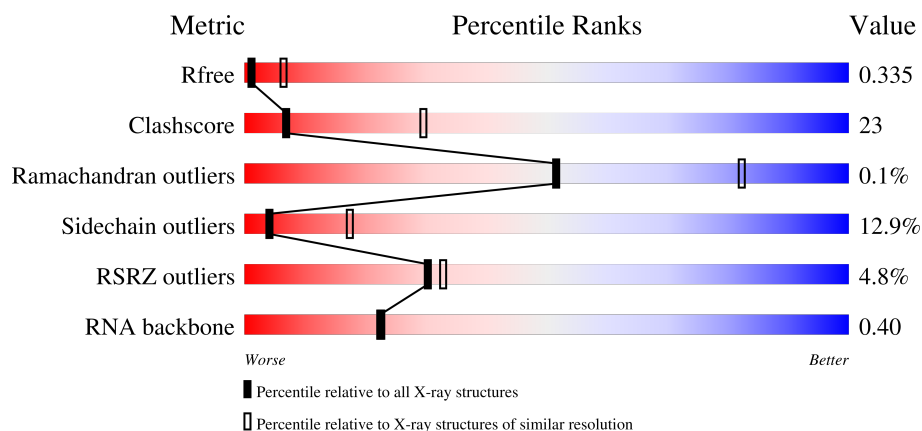|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.35 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	Percentile Ranks	Value
Rfree		0.335
Clashscore		23
Ramachandran outliers		0.1%
Sidechain outliers		12.9%
RSRZ outliers		4.8%
RNA backbone		0.40

Worse ... *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)
RNA backbone	3102	1023 (3.80-2.92)

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 <=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	428	3% / 50% / 42% / 7%
1	C	428	4% / 56% / 37% / 6% ·
2	B	141	6% / 33% / 51% / 11% / 5%
2	D	141	6% / 50% / 39% / · / 6%

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Mol	Chain	Length	Quality of chain
3	E	108	6% 37% 39% 8% 16%
3	J	108	6% 51% 31% 6% • 11%
4	F	89	9% 43% 44% 7% • 6%
4	N	89	10% 51% 36% 9% •
5	G	30	37% 37% 13% • 10%
5	R	30	20% 40% 27% 10% •

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 12834 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 Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3345	2082	585	668	10			
1	C	423	Total	C	N	O	S	0	0	0
			3308	2061	580	657	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P0AFF8
A	0	ALA	-	expression tag	UNP P0AFF8
C	-1	GLY	-	expression tag	UNP P0AFF8
C	0	ALA	-	expression tag	UNP P0AFF8

- Molecule 2 is a protein called N utilization substance protein B homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	134	Total	C	N	O	S	0	0	0
			1063	677	183	201	2			
2	D	132	Total	C	N	O	S	0	0	0
			1050	670	180	198	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP B7MD74
B	0	ALA	-	expression tag	UNP B7MD74
D	-1	GLY	-	expression tag	UNP B7MD74
D	0	ALA	-	expression tag	UNP B7MD74

- Molecule 3 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	J	96	Total 771	C 482	N 147	O 141	S 1	0	0	0
3	E	91	Total 733	C 459	N 139	O 134	S 1	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-4	GLY	-	expression tag	UNP B7MCT6
J	-3	PRO	-	expression tag	UNP B7MCT6
J	-2	LEU	-	expression tag	UNP B7MCT6
J	-1	GLY	-	expression tag	UNP B7MCT6
J	0	SER	-	expression tag	UNP B7MCT6
E	-4	GLY	-	expression tag	UNP B7MCT6
E	-3	PRO	-	expression tag	UNP B7MCT6
E	-2	LEU	-	expression tag	UNP B7MCT6
E	-1	GLY	-	expression tag	UNP B7MCT6
E	0	SER	-	expression tag	UNP B7MCT6

- Molecule 4 is a protein called Antitermination protein N.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	N	85	Total 693	C 428	N 141	O 123	S 1	0	0	0
4	F	84	Total 679	C 417	N 139	O 122	S 1	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	-4	GLY	-	expression tag	UNP P03045
N	-3	PRO	-	expression tag	UNP P03045
N	-2	LEU	-	expression tag	UNP P03045
N	-1	GLY	-	expression tag	UNP P03045
N	0	SER	-	expression tag	UNP P03045
F	-4	GLY	-	expression tag	UNP P03045
F	-3	PRO	-	expression tag	UNP P03045
F	-2	LEU	-	expression tag	UNP P03045
F	-1	GLY	-	expression tag	UNP P03045
F	0	SER	-	expression tag	UNP P03045

- Molecule 5 is a RNA chain called RNA (29-MER).

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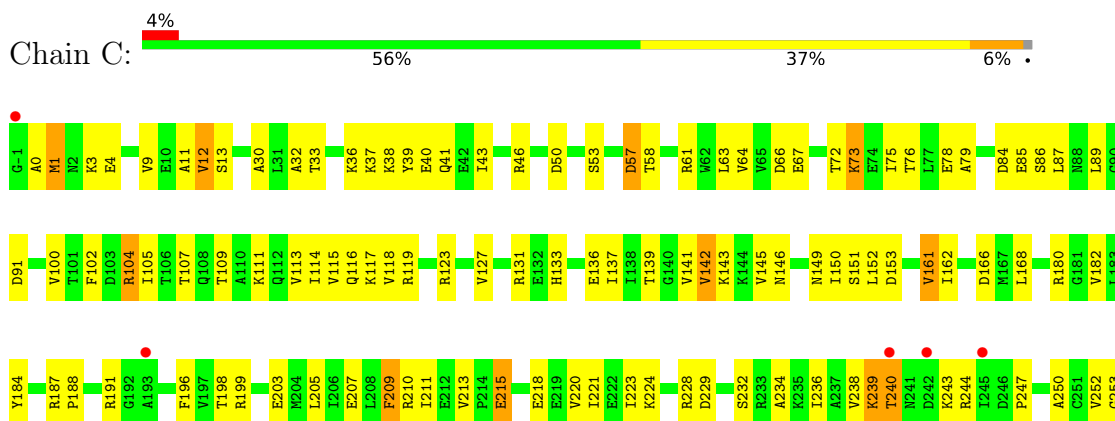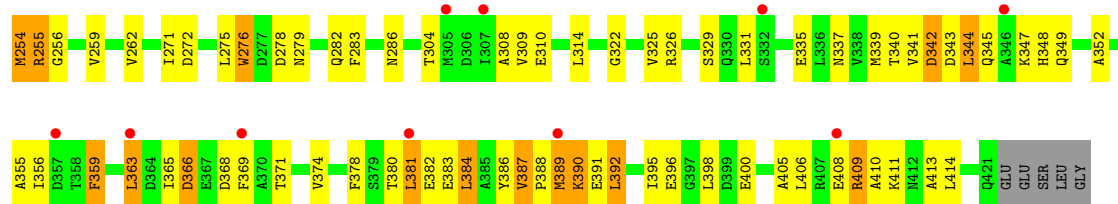| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	R	29	Total	C	N	O	P	0	0	0
			616	276	110	201	29			
5	G	27	Total	C	N	O	P	0	0	0
			576	258	105	186	27			

3 Residue-property plots ⓘ

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.

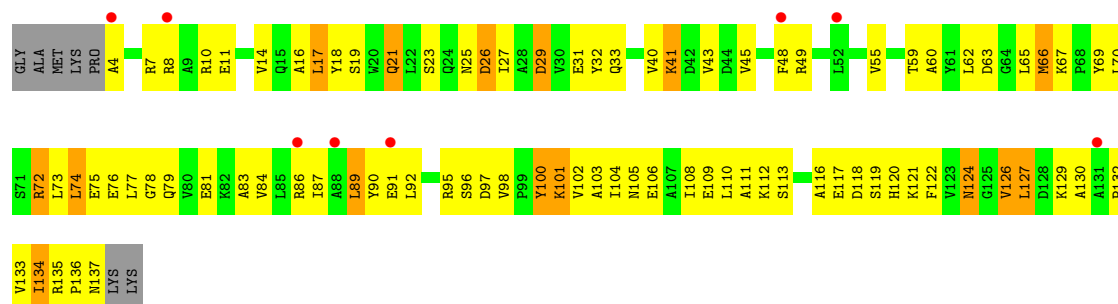• Molecule 1: Transcription termination/antitermination protein NusA

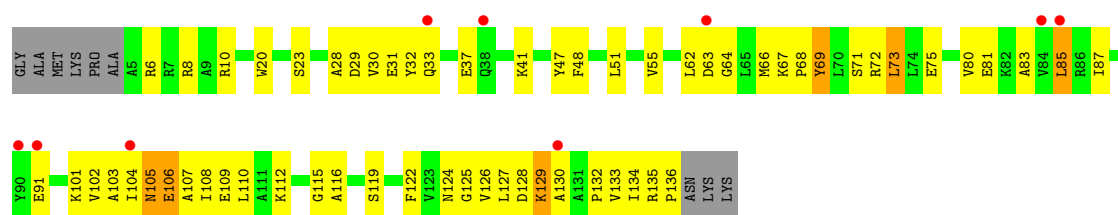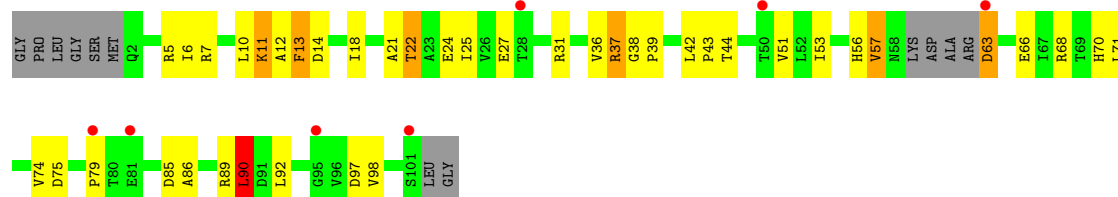• Molecule 1: Transcription termination/antitermination protein NusA

M254 R255 G256 V259 V262 I271 D272 L275 W276 D277 D278 N279 Q282 F283 N286 T304 M305 D306 I307 A308 V309 E310 L314 G322 V325 R326 S329 Q330 L331 S332 E335 L336 N337 V338 M339 T340 V341 D342 L343 A344 Q345 A346 K347 H348 Q349 A352

A355 I356 D357 T358 F359 L363 D364 I365 D366 E367 D368 F369 A370 T371 V374 F378 S379 T380 L381 E382 E383 L384 A385 Y386 V387 P388 M389 K390 E391 L392 I395 E396 G397 L398 D399 E400 A405 L406 R407 E408 R409 A410 K411 N412 A413 L414 Q421 GLU SER LEU GLY

- Molecule 2: N utilization substance protein B homolog

Chain B:

6%
33%　51%　11%　5%

GLY ALA MET LYS PRO A4 R7 R8 A9 R10 E11 V14 Q15 A16 L17 Y18 S19 W20 Q21 L22 S23 Q24 N25 D26 I27 A28 D29 V30 E31 Y32 Q33 V40 K41 D42 V43 D44 V45 F48 R49 L52 V55 T59 A60 Y61 L62 D63 G64 L65 M66 K67 P68 Y69 L70

S71 R72 L73 L74 E75 E76 L77 G78 Q79 V80 E81 K82 A83 V84 L85 R86 I87 A88 L89 Y90 E91 L92 R95 S96 D97 V98 P99 Y100 K101 V102 A103 I104 N105 E106 A107 I108 E109 L110 A111 K112 S113 A116 E117 D118 S119 H120 K121 F122 V123 N124 G125 V126 L127 D128 K129 A130 A131 P132

V133 I134 R135 P136 N137 LYS LYS

- Molecule 2: N utilization substance protein B homolog

Chain D:

6%
50%　39%　·　6%

GLY ALA MET LYS PRO ALA A5 R6 R7 R8 A9 R10 W20 S23 A28 D29 V30 E31 Y32 Q33 E37 Q38 K41 Y47 F48 L51 V55 L62 D63 G64 L65 M66 K67 P68 Y69 L70 S71 R72 L73 L74 E75 V80 E81 K82 A83 V84 L85 R86 I87

Y90 E91 K101 V102 A103 I104 N105 E106 A107 I108 E109 L110 A111 K112 G115 A116 S119 F122 V123 N124 G125 V126 L127 D128 K129 A130 A131 P132 V133 I134 R135 P136 ASN LYS LYS

- Molecule 3: 30S ribosomal protein S10

Chain J:

6%
51%　31%　6%　·　11%

GLY PRO LEU GLY SER MET Q2 R5 I6 R7 L10 K11 A12 F13 D14 I18 A21 T22 A23 E24 I25 V26 E27 T28 R31 V36 R37 G38 P39 L42 P43 T44 T50 V51 L52 I53 H56 V57 N58 LYS ASP ALA ARG D63 E66 I67 R68 T69 H70 L71

V74 D75 P79 T80 E81 D85 A86 R89 L90 D91 L92 G95 V96 D97 V98 S101 LEU GLY

- Molecule 3: 30S ribosomal protein S10

Chain E:

6%
37%　39%　8%　16%

GLY PRO LEU GLY SER MET Q2 N3 Q4 R5 I6 R7 I8 R9 L10 K11 A12 F13 D14 H15 R16 L17 I18 A21 T22 A23 E24 I25 V26 E27 T28 R31 T32 Q35 V36 R37 G38 P39 I40 P41 L42 P43 T44 R45 K46 E47 R48 F49 T50 I53 SER PRO HIS VAL ASN LYS

ASP ALA ARG D63 Q64 I67 R68 T69 H70 L71 R72 L73 V74 D75 I76 V77 E78 T83 A86 L92 V96 D97 V98 Q99 I100 S101 LEU GLY

• Molecule 4: Antitermination protein N

Chain N:

10%

51% 36% 9%

GLY PRO L-2 Q4 R7 R8 R11 Q15 K19 A20 A21 N22 P23 L24 K31 P32 V33 N34 R35 P36 I37 L40 N41 R42 K43 P44 K45 S46 R47 V48 A51 L52 D56 L57 T58 E62 Y63 H64 K65 Q66 I67 E68 S69 N70 L71 Q72 R73 I74 E75 R76

K77 N78 Q79 R80 T81 W82 TYR SER

• Molecule 4: Antitermination protein N

Chain F:

9%

43% 44% 7% 6%

GLY PRO L-2 A3 R6 R7 R8 E9 R10 R11 A12 E13 K14 Q15 A16 Q17 W18 K19 A20 A21 N22 P23 L24 L25 V26 S29 A30 V33 N34 R35 P36 I37 L38 S39 R42 K43 P44 K45 S46 R47 V48 E49 S50 A51 L52 N53 P54 I55 A61 E62 Y63 H64 K65 Q66

I67 E68 S69 N70 L71 Q72 R73 I74 E75 R76 K77 N78 Q79 R80 T81 TRP TYR SER

• Molecule 5: RNA (29-MER)

Chain R:

20% 40% 27% 10%

C3 U4 C5 U6 U7 U8 A9 A10 C11 A12 U13 U14 A15 A16 G17 C18 C19 C20 U21 A24 G25 A26 G28 G29 G30 C31 C

• Molecule 5: RNA (29-MER)

Chain G:

37% 37% 13% 10%

C U C5 U6 U7 U8 A9 A10 C11 A12 U13 U14 A15 A16 G17 C18 C19 C20 A23 A24 G25 C31 C

4   Data and refinement statistics   ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	95.78Å 101.80Å 279.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.52 – 3.35 48.33 – 3.35	Depositor EDS
% Data completeness (in resolution range)	99.4 (39.52-3.35) 99.4 (48.33-3.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) >$ [1]	1.14 (at 3.33Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.297 , 0.335 0.298 , 0.335	Depositor DCC
R_{free} test set	2004 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	117.5	Xtriage
Anisotropy	0.662	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 110.7	EDS
L-test for twinning[2]	$< |L| > = 0.45, < L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	12834	wwPDB-VP
Average B, all atoms (Å^2)	142.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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 ⓘ

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	0.27	0/3385	0.51	2/4578 (0.0%)
1	C	0.28	0/3348	0.49	1/4530 (0.0%)
2	B	0.34	0/1080	0.56	0/1462
2	D	0.27	0/1067	0.46	0/1444
3	E	0.28	0/740	0.49	0/999
3	J	0.26	0/780	0.56	1/1055 (0.1%)
4	F	0.26	0/687	0.56	1/923 (0.1%)
4	N	0.28	0/703	0.52	0/946
5	G	0.31	0/644	1.06	2/1001 (0.2%)
5	R	0.46	0/688	1.24	6/1069 (0.6%)
All	All	0.29	0/13122	0.62	13/18007 (0.1%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	R	3	C	N1-C2-O2	9.01	124.30	118.90
5	R	7	U	N1-C2-O2	7.61	128.13	122.80
5	R	7	U	N3-C2-O2	-7.04	117.28	122.20
3	J	90	LEU	CA-CB-CG	6.85	131.04	115.30
5	G	7	U	C2-N1-C1'	6.80	125.86	117.70

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	3345	0	3346	180	0
1	C	3308	0	3315	148	0
2	B	1063	0	1071	87	0
2	D	1050	0	1060	45	0
3	E	733	0	769	42	0
3	J	771	0	803	33	0
4	F	679	0	719	45	0
4	N	693	0	729	44	0
5	G	576	0	292	19	0
5	R	616	0	313	38	0
All	All	12834	0	12417	581	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 23.

The worst 5 of 581 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)
3:J:85:ASP:O	3:J:89:ARG:HB2	1.54	1.07
2:B:62:LEU:HD13	2:B:89:LEU:HB3	1.41	1.01
1:A:244:ARG:HG3	1:A:245:ILE:HG13	1.50	0.91
2:B:92:LEU:HD21	2:B:133:VAL:HG11	1.49	0.91
4:N:24:LEU:HD22	4:N:24:LEU:H	1.36	0.90

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	426/428 (100%)	395 (93%)	30 (7%)	1 (0%)	47	78
1	C	421/428 (98%)	391 (93%)	30 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	132/141 (94%)	126 (96%)	6 (4%)	0	100	100
2	D	130/141 (92%)	122 (94%)	8 (6%)	0	100	100
3	E	87/108 (81%)	82 (94%)	5 (6%)	0	100	100
3	J	92/108 (85%)	81 (88%)	11 (12%)	0	100	100
4	F	82/89 (92%)	76 (93%)	5 (6%)	1 (1%)	13	44
4	N	83/89 (93%)	76 (92%)	7 (8%)	0	100	100
All	All	1453/1532 (95%)	1349 (93%)	102 (7%)	2 (0%)	51	82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	23	PRO
1	A	19	PRO

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	357/357 (100%)	313 (88%)	44 (12%)	4	19
1	C	353/357 (99%)	313 (89%)	40 (11%)	6	23
2	B	111/116 (96%)	90 (81%)	21 (19%)	1	6
2	D	110/116 (95%)	97 (88%)	13 (12%)	5	21
3	E	80/93 (86%)	66 (82%)	14 (18%)	2	8
3	J	85/93 (91%)	75 (88%)	10 (12%)	5	21
4	F	74/78 (95%)	66 (89%)	8 (11%)	6	25
4	N	75/78 (96%)	64 (85%)	11 (15%)	3	13
All	All	1245/1288 (97%)	1084 (87%)	161 (13%)	4	17

5 of 161 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	366	ASP
3	E	32	THR
1	C	384	LEU
2	D	80	VAL
3	E	92	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	421	GLN
4	F	22	ASN
1	A	286	ASN
2	B	120	HIS
1	C	133	HIS

5.3.3   RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	G	26/30 (86%)	10 (38%)	0
5	R	29/30 (96%)	15 (51%)	5 (17%)
All	All	55/60 (91%)	25 (45%)	5 (9%)

5 of 25 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	R	4	U
5	R	5	C
5	R	6	U
5	R	7	U
5	R	8	U

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	R	3	C
5	R	9	A
5	R	10	A
5	R	11	C
5	R	14	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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(Å²)	Q<0.9
1	A	428/428 (100%)	0.16	12 (2%)	53	55	52, 111, 223, 267	0
1	C	423/428 (98%)	0.20	15 (3%)	44	46	54, 110, 252, 312	0
2	B	134/141 (95%)	0.30	8 (5%)	21	24	108, 183, 227, 237	0
2	D	132/141 (93%)	0.30	9 (6%)	17	20	123, 172, 211, 233	0
3	E	91/108 (84%)	0.47	6 (6%)	18	21	81, 136, 176, 207	0
3	J	96/108 (88%)	0.61	7 (7%)	15	17	92, 136, 207, 226	0
4	F	84/89 (94%)	0.25	8 (9%)	8	10	86, 158, 221, 253	0
4	N	85/89 (95%)	0.36	9 (10%)	6	7	69, 146, 236, 282	0
5	G	27/30 (90%)	-0.08	0	100	100	104, 141, 174, 180	0
5	R	29/30 (96%)	-0.09	0	100	100	91, 123, 239, 243	0
All	All	1529/1592 (96%)	0.25	74 (4%)	30	33	52, 135, 229, 312	0

The worst 5 of 74 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	48	PHE	6.6
1	C	305	MET	5.3
2	D	130	ALA	4.5
1	A	406	LEU	4.4
1	A	308	ALA	4.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.