WORLDWIDE
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Feb 15, 2017 – 01:20 am GMT

PDB ID	:	5HBU
Title	:	Structure of the E. coli nucleoid occlusion protein SlmA bound to DNA and the C-terminal tail of the cytoskeletal cell division protein FtsZ
Authors	:	Schumacher, M.A.; Zeng, W.
Deposited on	:	2016-01-02
Resolution	:	2.60 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

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 2.60 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.
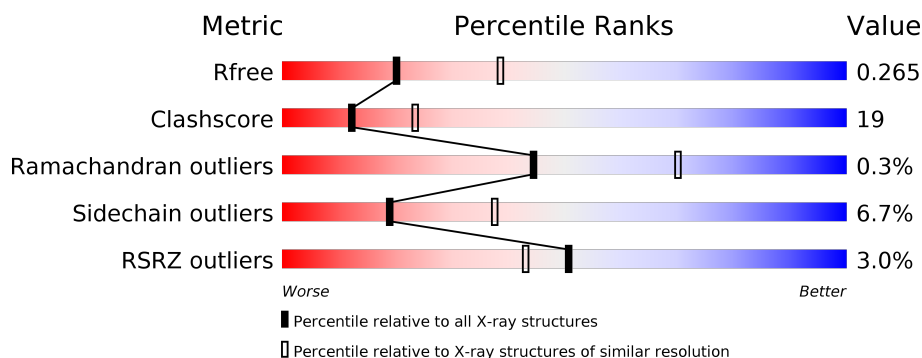
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	196	6% / 54% / 41% / · · ·
1	B	196	9% / 60% / 35% / 5%
1	C	196	% / 62% / 33% / · ·
1	D	196	63% / 30% / · ·
1	E	196	% / 59% / 34% / · ·
1	F	196	% / 68% / 24% / 5% ·

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Mol	Chain	Length	Quality of chain
1	G	196	3% / 65% / 28%
1	H	196	2% / 61% / 33%
2	R	12	42% / 58%
2	T	12	42% / 58%
2	W	12	33% / 67%
2	Z	12	33% / 67%
3	K	10	60% / 70% / 10% / 20%

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 13710 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 Nucleoid occlusion factor SlmA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	0	0
			1543	970	281	286	6			
1	B	196	Total	C	N	O	S	0	0	0
			1589	998	290	295	6			
1	C	190	Total	C	N	O	S	0	0	0
			1543	970	281	286	6			
1	D	189	Total	C	N	O	S	0	0	0
			1532	964	277	285	6			
1	E	190	Total	C	N	O	S	0	0	0
			1543	970	281	286	6			
1	F	189	Total	C	N	O	S	0	0	0
			1532	964	277	285	6			
1	G	190	Total	C	N	O	S	0	0	0
			1543	970	281	286	6			
1	H	190	Total	C	N	O	S	0	0	0
			1543	970	281	286	6			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3	ALA	-	expression tag	UNP P0C093
A	4	GLU	-	expression tag	UNP P0C093
A	5	LYS	-	expression tag	UNP P0C093
A	6	GLN	-	expression tag	UNP P0C093
B	3	ALA	-	expression tag	UNP P0C093
B	4	GLU	-	expression tag	UNP P0C093
B	5	LYS	-	expression tag	UNP P0C093
B	6	GLN	-	expression tag	UNP P0C093
C	3	ALA	-	expression tag	UNP P0C093
C	4	GLU	-	expression tag	UNP P0C093
C	5	LYS	-	expression tag	UNP P0C093
C	6	GLN	-	expression tag	UNP P0C093
D	3	ALA	-	expression tag	UNP P0C093

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Chain	Residue	Modelled	Actual	Comment	Reference
D	4	GLU	-	expression tag	UNP P0C093
D	5	LYS	-	expression tag	UNP P0C093
D	6	GLN	-	expression tag	UNP P0C093
E	3	ALA	-	expression tag	UNP P0C093
E	4	GLU	-	expression tag	UNP P0C093
E	5	LYS	-	expression tag	UNP P0C093
E	6	GLN	-	expression tag	UNP P0C093
F	3	ALA	-	expression tag	UNP P0C093
F	4	GLU	-	expression tag	UNP P0C093
F	5	LYS	-	expression tag	UNP P0C093
F	6	GLN	-	expression tag	UNP P0C093
G	3	ALA	-	expression tag	UNP P0C093
G	4	GLU	-	expression tag	UNP P0C093
G	5	LYS	-	expression tag	UNP P0C093
G	6	GLN	-	expression tag	UNP P0C093
H	3	ALA	-	expression tag	UNP P0C093
H	4	GLU	-	expression tag	UNP P0C093
H	5	LYS	-	expression tag	UNP P0C093
H	6	GLN	-	expression tag	UNP P0C093

- Molecule 2 is a DNA chain called DNA (5'-D(*GP*TP*GP*AP*GP*TP*AP*CP*TP*CP*AP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	W	12	Total 243	C 117	N 45	O 70	P 11	0	0	0
2	Z	12	Total 243	C 117	N 45	O 70	P 11	0	0	0
2	R	12	Total 243	C 117	N 45	O 70	P 11	0	0	0
2	T	12	Total 243	C 117	N 45	O 70	P 11	0	0	0

- Molecule 3 is a protein called FtsZ CTT peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	K	8	Total 67	C 45	N 11	O 11	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	17	Total 17	O 17	0	0
4	B	10	Total 10	O 10	0	0
4	C	58	Total 58	O 58	0	0
4	D	48	Total 48	O 48	0	0
4	E	28	Total 28	O 28	0	0
4	F	29	Total 29	O 29	0	0
4	G	50	Total 50	O 50	0	0
4	H	36	Total 36	O 36	0	0
4	W	9	Total 9	O 9	0	0
4	Z	7	Total 7	O 7	0	0
4	R	7	Total 7	O 7	0	0
4	T	2	Total 2	O 2	0	0
4	K	2	Total 2	O 2	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the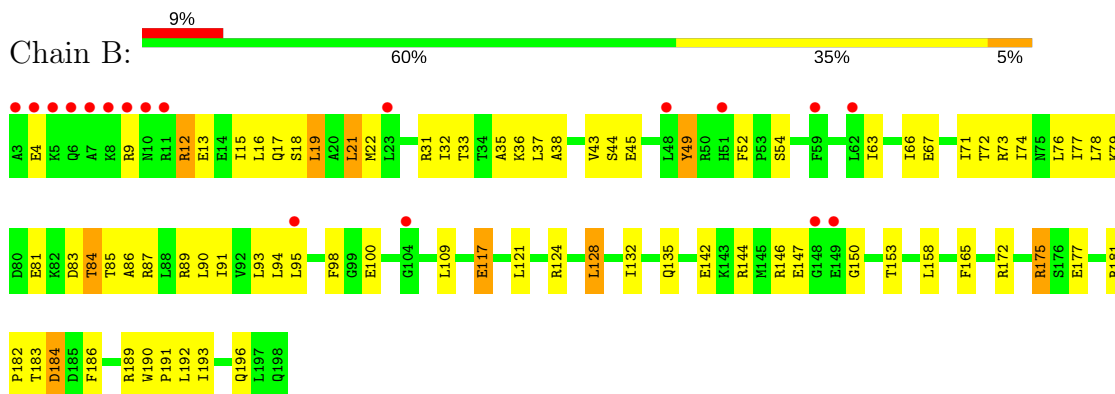 second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot 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.
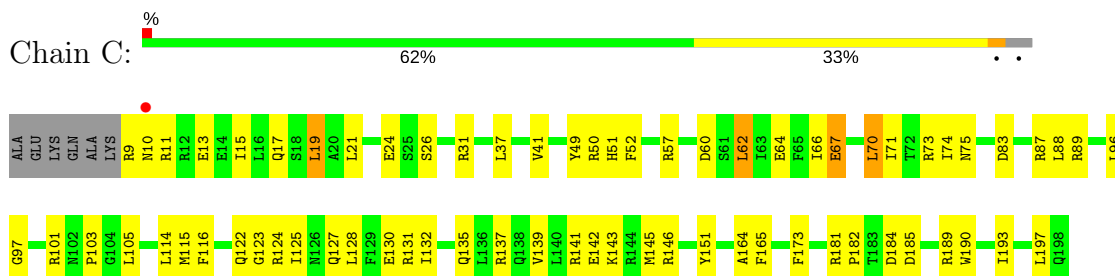
- Molecule 1: Nucleoid occlusion factor SlmA

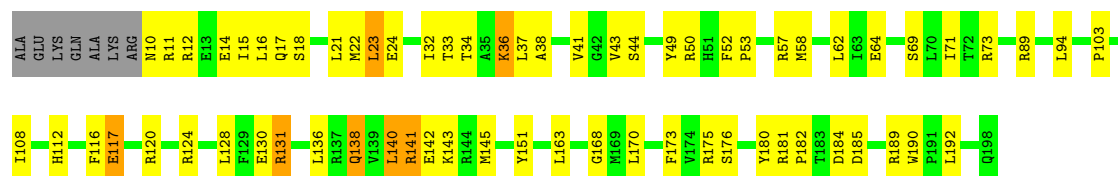- Molecule 1: Nucleoid occlusion factor SlmA
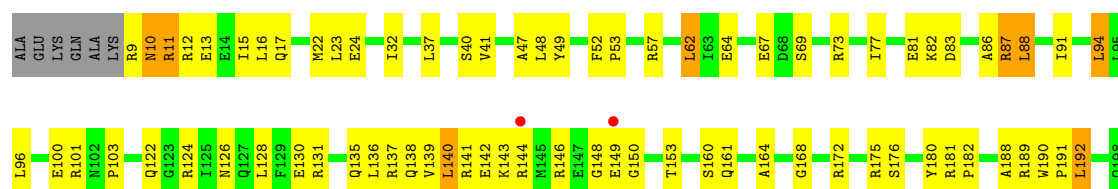

- Molecule 1: Nucleoid occlusion factor SlmA

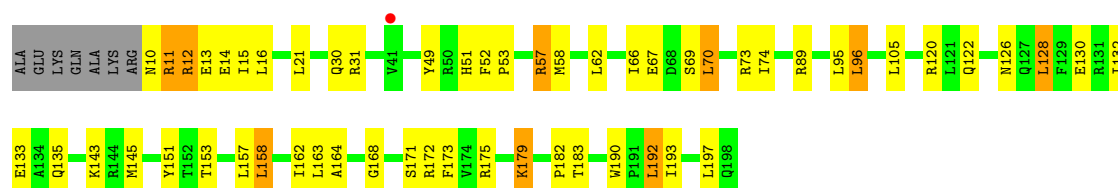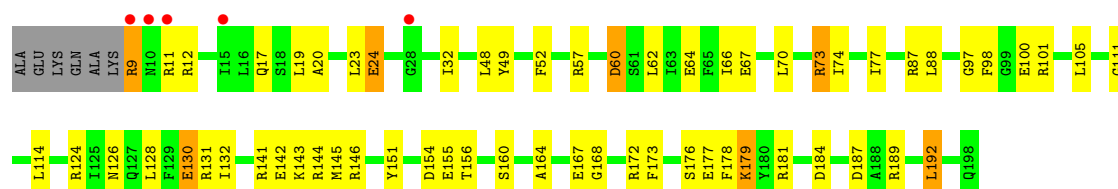- Molecule 1: Nucleoid occlusion factor SlmA

Chain D:

63%　　　　30%

ALA GLU LYS GLN ALA LYS ARG N10 R11 R12 E13 E14 I15 L16 Q17 S18 L21 M22 L23 E24 I32 T33 T34 A35 K36 L37 A38 V41 G42 V43 S44 Y49 R50 H51 F52 P53 R57 M58 L62 I63 E64 S69 L70 I71 T72 R73 R89 L94 P103

I108 H112 F116 E117 R120 R124 L128 F129 E130 R131 L136 R137 Q138 V139 L140 R141 E142 K143 R144 M145 Y151 L163 G168 M169 L170 F173 V174 R175 S176 Y180 R181 P182 T183 D184 D185 R189 W190 P191 L192 Q198

• Molecule 1: Nucleoid occlusion factor SlmA

%

Chain E:

59%　　　　34%

ALA GLU LYS GLN ALA LYS R9 N10 R11 R12 E13 E14 I15 L16 Q17 M22 L23 E24 I32 L37 S40 V41 A47 L48 Y49 F52 P53 R57 L62 I63 E64 E67 D68 S69 R73 I77 E81 K82 D83 A86 R87 L88 I91 L94 L95

L96 E100 R101 N102 P103 Q122 G123 R124 I125 N126 Q127 L128 F129 E130 R131 Q135 L136 R137 Q138 V139 L140 R141 E142 K143 R144 M145 R146 E147 G148 E149 G150 T153 S160 Q161 A164 G168 R172 R175 S176 Y180 R181 P182 A188 R189 W190 P191 L192 Q198

• Molecule 1: Nucleoid occlusion factor SlmA

%

Chain F:

68%　　　　24%　　5%

ALA GLU LYS GLN ALA LYS ARG N10 R11 R12 E13 E14 I15 L16 L21 Q30 R31 V41 Y49 R50 H51 F52 P53 R57 M58 L62 I66 E67 D68 S69 L70 R73 I74 R89 L95 L96 L105 R120 L121 Q122 N126 Q127 L128 F129 E130 R131 I132

E133 A134 Q135 K143 R144 M145 Y151 T152 T153 L157 L158 I162 L163 A164 G168 S171 R172 F173 V174 R175 K179 P182 T183 W190 P191 L192 I193 L197 Q198

• Molecule 1: Nucleoid occlusion factor SlmA

3%

Chain G:

65%　　　　28%

ALA GLU LYS GLN ALA LYS R9 N10 R11 R12 I15 L16 Q17 S18 L19 A20 L23 E24 G28 I32 L48 Y49 F52 R57 D60 S61 L62 I63 E64 F65 I66 E67 L70 R73 I74 I77 R87 L88 G97 F98 Q99 E100 R101 L105 G111

L114 R124 I125 N126 Q127 L128 F129 E130 R131 I132 R141 E142 K143 R144 M145 R146 Y151 D154 E155 T156 S160 A164 E167 G168 R172 F173 S176 E177 F178 K179 Y180 R181 D184 D187 A188 R189 L192 Q198

• Molecule 1: Nucleoid occlusion factor SlmA

2%

Chain H:

61%　　　　33%

ALA GLU LYS GLN ALA LYS R9 N10 R11 R12 I15 L16 L23 E24 R31 I32 T33 T34 A35 K36 L37 A38 A39 S40 L48 Y49 R50 H51 F52 P53 S54 R57 M58 F59 L62 I63 I66 S69 L70 R73 I74 I77 L78 D83 A86 R87 L88 R89

L90 I91 L94 L95 P103 R107 I108 L109 F116 E117 Q118 R124 L128 I132 Q135 L136 R137 Q138 E142 K143 G148 E149 G150 Y151 T152 T153 L163 A164 F165 G168 S171 R172 F173 V174 R175 S176 Y180 R181 P182 R189 W190 P191 L192 I193

Q198

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• Molecule 2: DNA (5'-D(*GP*TP*GP*AP*GP*TP*AP*CP*TP*CP*AP*C)-3')

Chain W:

33%   67%

G2 T3   G6 T7 A8   C11 A12 C13

• Molecule 2: DNA (5'-D(*GP*TP*GP*AP*GP*TP*AP*CP*TP*CP*AP*C)-3')

Chain Z:

33%   67%

G23 T24 G25 A26 G27 T28 A29   C32 A33 C34

• Molecule 2: DNA (5'-D(*GP*TP*GP*AP*GP*TP*AP*CP*TP*CP*AP*C)-3')

Chain R:

42%   58%

G2 T3   G6 T7   C11 A12 C13

• Molecule 2: DNA (5'-D(*GP*TP*GP*AP*GP*TP*AP*CP*TP*CP*AP*C)-3')

Chain T:

42%   58%

G23 T24 G25 A26 G27 T28 A29   C34

• Molecule 3: FtsZ CTT peptide

Chain K:

60%

70%   10%   20%

ASP TYR L372   P375 A376 F377 L378 R379
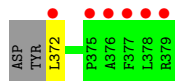
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	70.11Å 158.89Å 200.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.10 – 2.60 100.10 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (100.10-2.60) 99.7 (100.10-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	2.21 (at 2.62Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.226 , 0.270 0.220 , 0.265	Depositor DCC
R_{free} test set	3805 reflections (2.88%)	DCC
Wilson B-factor (Å^2)	37.3	Xtriage
Anisotropy	0.808	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 58.0	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13710	wwPDB-VP
Average B, all atoms (Å^2)	55.0	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 36.13 % 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 5.2397e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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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	0.24	0/1563	0.42	1/2098 (0.0%)
1	B	0.25	0/1609	0.44	0/2158
1	C	0.21	0/1563	0.36	0/2098
1	D	0.26	0/1552	0.41	0/2084
1	E	0.22	0/1563	0.37	0/2098
1	F	0.21	0/1552	0.37	0/2084
1	G	0.23	0/1563	0.38	0/2098
1	H	0.22	0/1563	0.38	0/2098
2	R	0.44	0/272	0.97	0/418
2	T	0.42	0/272	1.00	0/418
2	W	0.42	0/272	0.99	0/418
2	Z	0.42	0/272	1.04	0/418
3	K	0.21	0/68	0.48	0/90
All	All	0.25	0/13684	0.48	1/18578 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	140	LEU	CB-CG-CD2	-5.03	102.46	111.00

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	1543	0	1579	84	0
1	B	1589	0	1629	87	0
1	C	1543	0	1579	58	0
1	D	1532	0	1566	67	0
1	E	1543	0	1579	68	0
1	F	1532	0	1566	46	0
1	G	1543	0	1579	47	0
1	H	1543	0	1579	59	0
2	R	243	0	137	9	0
2	T	243	0	137	8	0
2	W	243	0	137	6	0
2	Z	243	0	137	13	0
3	K	67	0	70	2	0
4	A	17	0	0	10	0
4	B	10	0	0	2	0
4	C	58	0	0	7	0
4	D	48	0	0	3	0
4	E	28	0	0	2	0
4	F	29	0	0	1	0
4	G	50	0	0	4	0
4	H	36	0	0	2	0
4	K	2	0	0	0	0
4	R	7	0	0	2	0
4	T	2	0	0	0	0
4	W	9	0	0	0	0
4	Z	7	0	0	0	0
All	All	13710	0	13274	505	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 19.

The worst 5 of 505 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:140:LEU:CD2	1:A:158:LEU:HD11	1.75	1.16
1:D:36:LYS:HB2	1:D:36:LYS:HZ3	1.08	1.11
1:A:140:LEU:HD21	1:A:158:LEU:CD1	1.86	1.05
1:D:64:GLU:HG3	1:D:124:ARG:HH22	1.25	1.01
1:C:73:ARG:HH12	1:C:101:ARG:HH12	1.07	1.00

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	188/196 (96%)	176 (94%)	11 (6%)	1 (0%)	32	58
1	B	194/196 (99%)	171 (88%)	21 (11%)	2 (1%)	18	37
1	C	188/196 (96%)	181 (96%)	7 (4%)	0	100	100
1	D	187/196 (95%)	184 (98%)	3 (2%)	0	100	100
1	E	188/196 (96%)	180 (96%)	7 (4%)	1 (0%)	32	58
1	F	187/196 (95%)	185 (99%)	2 (1%)	0	100	100
1	G	188/196 (96%)	181 (96%)	7 (4%)	0	100	100
1	H	188/196 (96%)	181 (96%)	7 (4%)	0	100	100
3	K	6/10 (60%)	5 (83%)	1 (17%)	0	100	100
All	All	1514/1578 (96%)	1444 (95%)	66 (4%)	4 (0%)	44	70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	12	ARG
1	E	10	ASN
1	A	53	PRO
1	B	84	THR

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	166/170 (98%)	162 (98%)	4 (2%)	54	80
1	B	170/170 (100%)	160 (94%)	10 (6%)	23	45
1	C	166/170 (98%)	156 (94%)	10 (6%)	22	44
1	D	165/170 (97%)	152 (92%)	13 (8%)	14	28
1	E	166/170 (98%)	152 (92%)	14 (8%)	13	25
1	F	165/170 (97%)	153 (93%)	12 (7%)	16	33
1	G	166/170 (98%)	150 (90%)	16 (10%)	10	18
1	H	166/170 (98%)	156 (94%)	10 (6%)	22	44
3	K	7/9 (78%)	7 (100%)	0	100	100
All	All	1337/1369 (98%)	1248 (93%)	89 (7%)	19	38

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	48	LEU
1	E	140	LEU
1	H	48	LEU
1	E	62	LEU
1	E	96	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	118	GLN
1	D	127	GLN
1	E	122	GLN
1	G	10	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 carbohydrates 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	190/196 (96%)	0.45	11 (5%)	24	18	27, 67, 132, 150	0
1	B	196/196 (100%)	0.74	18 (9%)	10	6	32, 73, 115, 192	0
1	C	190/196 (96%)	-0.05	1 (0%)	90	89	13, 36, 70, 138	0
1	D	189/196 (96%)	-0.00	0	100	100	12, 36, 86, 104	0
1	E	190/196 (96%)	0.01	2 (1%)	80	77	25, 46, 87, 127	0
1	F	189/196 (96%)	0.09	1 (0%)	90	89	27, 49, 95, 116	0
1	G	190/196 (96%)	-0.00	5 (2%)	56	49	20, 41, 79, 110	0
1	H	190/196 (96%)	0.07	4 (2%)	64	58	21, 43, 85, 118	0
2	R	12/12 (100%)	-0.27	0	100	100	43, 59, 84, 88	0
2	T	12/12 (100%)	-0.30	0	100	100	41, 54, 80, 82	0
2	W	12/12 (100%)	-0.07	0	100	100	35, 55, 89, 94	0
2	Z	12/12 (100%)	-0.20	0	100	100	48, 58, 83, 84	0
3	K	8/10 (80%)	2.33	6 (75%)	0	0	83, 117, 127, 132	0
All	All	1580/1626 (97%)	0.16	48 (3%)	51	43	12, 49, 102, 192	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	ALA	13.4
1	B	5	LYS	5.4
1	B	7	ALA	5.2
1	B	8	LYS	5.2
1	B	4	GLU	5.0

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 carbohydrates 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.