



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 17, 2021 – 07:28 AM EDT

PDB ID : 1L8I  
Title : Dna Protection and Binding by E. Coli DPS Protein  
Authors : Luo, J.; Liu, D.; White, M.A.; Fox, R.O.  
Deposited on : 2002-03-20  
Resolution : 3.00 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
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) : 2.23.2

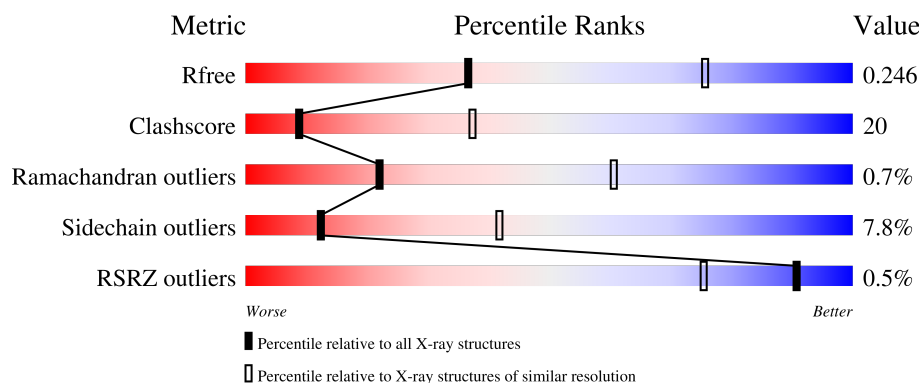
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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  $\geq 3$ , 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	167	<div> <div>55%</div> <div>34%</div> <div>5%</div> <div>7%</div> </div>
1	B	167	<div> <div>57%</div> <div>33%</div> <div>•</div> <div>7%</div> </div>
1	C	167	<div> <div>%</div> <div>59%</div> <div>32%</div> <div>•</div> <div>7%</div> </div>
1	D	167	<div> <div>%</div> <div>57%</div> <div>33%</div> <div>•</div> <div>7%</div> </div>
1	E	167	<div> <div>%</div> <div>58%</div> <div>31%</div> <div>•</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	167	<div><div><div>%</div><div><div></div><div></div><div></div><div></div></div><div>60%29%5%6%</div></div></div>
1	G	167	<div><div><div></div><div></div><div></div><div></div></div><div>58%32%• 7%</div></div>
1	H	167	<div><div><div></div><div></div><div></div><div></div></div><div>62%30%• 7%</div></div>
1	I	167	<div><div><div>%</div><div><div></div><div></div><div></div><div></div></div><div>57%34%• 7%</div></div></div>
1	J	167	<div><div><div>%</div><div><div></div><div></div><div></div><div></div></div><div>58%33%• 6%</div></div></div>
1	K	167	<div><div><div>%</div><div><div></div><div></div><div></div><div></div></div><div>54%37%• • 7%</div></div></div>
1	L	167	<div><div><div>%</div><div><div></div><div></div><div></div><div></div></div><div>59%32%• 7%</div></div></div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14968 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 DNA PROTECTION DURING STARVATION PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	B	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	C	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	D	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	E	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	F	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	G	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	H	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	I	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	J	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	K	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	L	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	CYS	ASP	engineered mutation	UNP P0ABT2
A	78	ALA	ASP	engineered mutation	UNP P0ABT2
B	75	CYS	ASP	engineered mutation	UNP P0ABT2
B	78	ALA	ASP	engineered mutation	UNP P0ABT2
C	75	CYS	ASP	engineered mutation	UNP P0ABT2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	78	ALA	ASP	engineered mutation	UNP P0ABT2
D	75	CYS	ASP	engineered mutation	UNP P0ABT2
D	78	ALA	ASP	engineered mutation	UNP P0ABT2
E	75	CYS	ASP	engineered mutation	UNP P0ABT2
E	78	ALA	ASP	engineered mutation	UNP P0ABT2
F	75	CYS	ASP	engineered mutation	UNP P0ABT2
F	78	ALA	ASP	engineered mutation	UNP P0ABT2
G	75	CYS	ASP	engineered mutation	UNP P0ABT2
G	78	ALA	ASP	engineered mutation	UNP P0ABT2
H	75	CYS	ASP	engineered mutation	UNP P0ABT2
H	78	ALA	ASP	engineered mutation	UNP P0ABT2
I	75	CYS	ASP	engineered mutation	UNP P0ABT2
I	78	ALA	ASP	engineered mutation	UNP P0ABT2
J	75	CYS	ASP	engineered mutation	UNP P0ABT2
J	78	ALA	ASP	engineered mutation	UNP P0ABT2
K	75	CYS	ASP	engineered mutation	UNP P0ABT2
K	78	ALA	ASP	engineered mutation	UNP P0ABT2
L	75	CYS	ASP	engineered mutation	UNP P0ABT2
L	78	ALA	ASP	engineered mutation	UNP P0ABT2

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

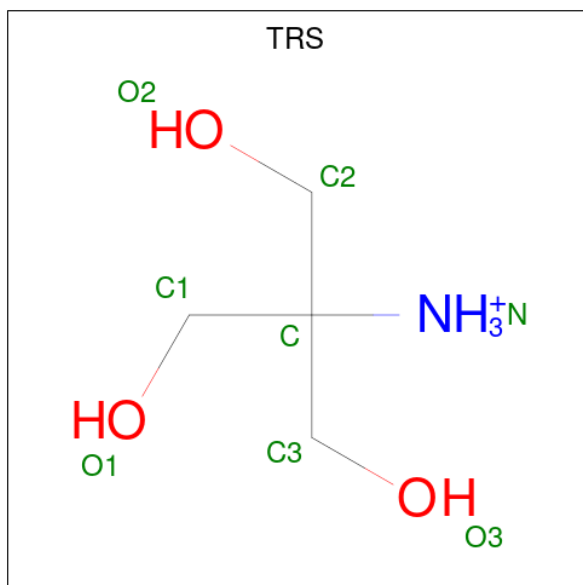
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total K 1 1	0	0
2	B	1	Total K 1 1	0	0
2	C	1	Total K 1 1	0	0
2	D	1	Total K 1 1	0	0
2	E	2	Total K 2 2	0	0
2	F	1	Total K 1 1	0	0
2	G	1	Total K 1 1	0	0
2	H	1	Total K 1 1	0	0
2	I	1	Total K 1 1	0	0
2	J	1	Total K 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	L	1	Total	K	0	0
			1	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula:  $C_4H_{12}NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	B	1	Total	C	N	O	0	0
			8	4	1	3		
3	B	1	Total	C	N	O	0	0
			8	4	1	3		
3	C	1	Total	C	N	O	0	0
			8	4	1	3		
3	C	1	Total	C	N	O	0	0
			8	4	1	3		
3	C	1	Total	C	N	O	0	0
			8	4	1	3		
3	D	1	Total	C	N	O	0	0
			8	4	1	3		
3	D	1	Total	C	N	O	0	0
			8	4	1	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	G	1	Total	C	N	O	0	0
			8	4	1	3		
3	L	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is water.

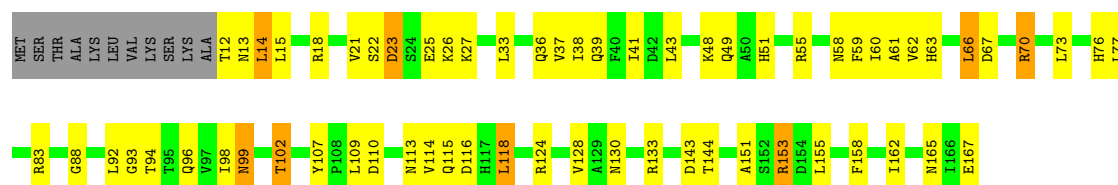
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	10	Total	O	0	0
			10	10		
4	C	6	Total	O	0	0
			6	6		
4	D	10	Total	O	0	0
			10	10		
4	E	8	Total	O	0	0
			8	8		
4	F	3	Total	O	0	0
			3	3		
4	G	14	Total	O	0	0
			14	14		
4	H	10	Total	O	0	0
			10	10		
4	I	6	Total	O	0	0
			6	6		
4	J	9	Total	O	0	0
			9	9		
4	K	7	Total	O	0	0
			7	7		
4	L	8	Total	O	0	0
			8	8		

### 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.

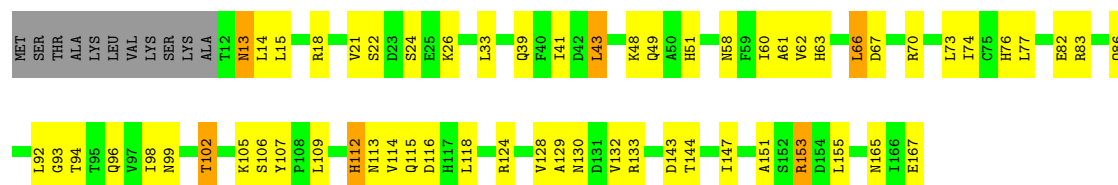
#### • Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain A: 



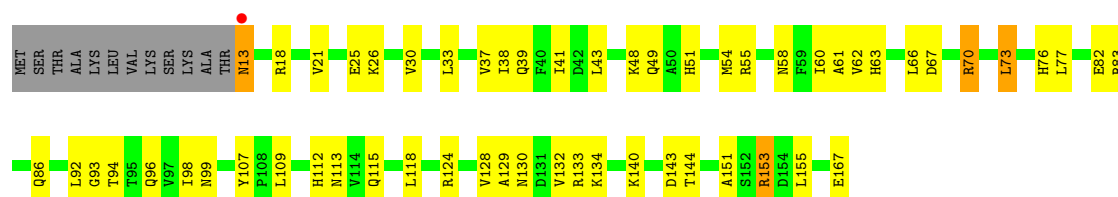
#### • Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain B: 



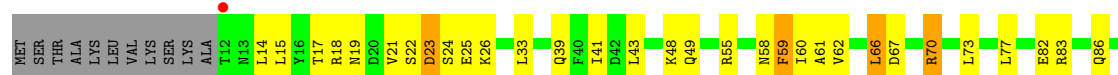
#### • Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain C: 

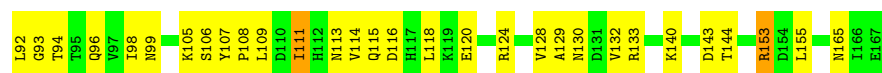


#### • Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

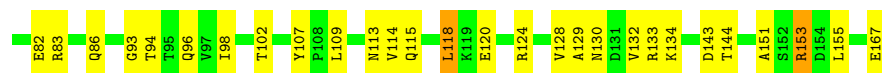
Chain D: 



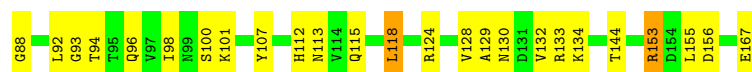
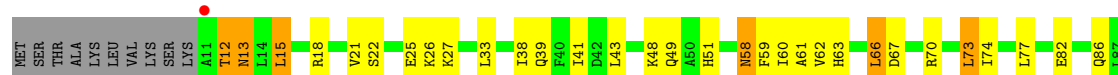




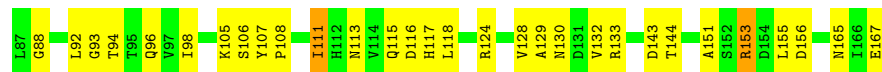
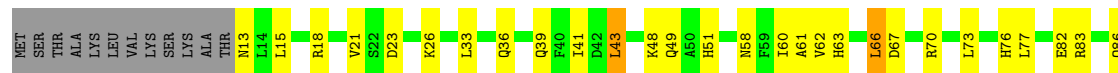
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



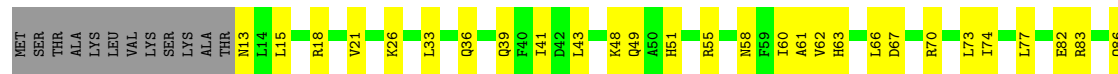
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

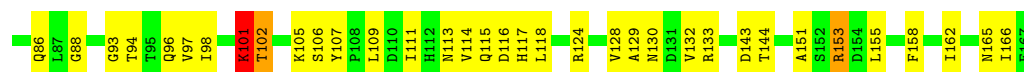




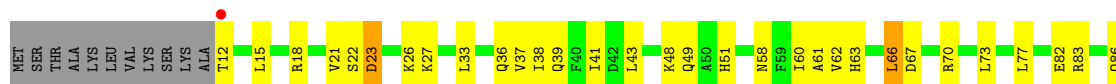
- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.54Å 90.54Å 226.08Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.86 – 3.00 29.86 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.0 (29.86-3.00) 98.0 (29.86-3.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.25 (at 3.00Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.202 , 0.250 0.198 , 0.246	Depositor DCC
$R_{free}$ test set	2074 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	61.8	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 62.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l 0.045 for h,-h-k,-l 0.029 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	14968	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: TRS, K

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	0.42	0/1249	0.75	3/1691 (0.2%)
1	B	0.44	0/1249	0.64	0/1691
1	C	0.39	0/1242	0.75	3/1681 (0.2%)
1	D	0.40	0/1249	0.73	3/1691 (0.2%)
1	E	0.41	0/1249	0.62	0/1691
1	F	0.39	0/1254	0.62	0/1698
1	G	0.43	0/1242	0.64	0/1681
1	H	0.41	0/1242	0.63	0/1681
1	I	0.40	0/1249	0.61	0/1691
1	J	0.38	0/1254	0.60	0/1698
1	K	0.40	0/1249	0.63	0/1691
1	L	0.40	0/1249	0.61	0/1691
All	All	0.41	0/14977	0.66	9/20276 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	70	ARG	NE-CZ-NH1	-11.74	114.43	120.30
1	C	70	ARG	NE-CZ-NH2	11.72	126.16	120.30
1	D	70	ARG	NE-CZ-NH1	-11.66	114.47	120.30
1	D	70	ARG	NE-CZ-NH2	11.52	126.06	120.30
1	C	70	ARG	NE-CZ-NH1	-11.46	114.57	120.30

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	1231	0	1234	67	0
1	B	1231	0	1234	60	0
1	C	1224	0	1227	65	0
1	D	1231	0	1234	62	0
1	E	1231	0	1234	64	0
1	F	1236	0	1239	53	0
1	G	1224	0	1227	52	0
1	H	1224	0	1227	47	0
1	I	1231	0	1234	54	0
1	J	1236	0	1239	64	0
1	K	1231	0	1234	61	0
1	L	1231	0	1234	56	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	2	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	L	1	0	0	0	0
3	A	24	0	36	2	0
3	B	16	0	24	0	0
3	C	24	0	36	3	0
3	D	16	0	24	1	0
3	G	8	0	12	0	0
3	L	8	0	12	4	0
4	A	8	0	0	0	0
4	B	10	0	0	1	0
4	C	6	0	0	0	0
4	D	10	0	0	0	0
4	E	8	0	0	0	0
4	F	3	0	0	0	0
4	G	14	0	0	1	0
4	H	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	6	0	0	0	0
4	J	9	0	0	1	0
4	K	7	0	0	0	0
4	L	8	0	0	0	0
All	All	14968	0	14941	608	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 20.

The worst 5 of 608 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:130:ASN:ND2	1:C:133:ARG:HH22	1.64	0.95
1:L:108:PRO:HG2	1:L:111:ILE:HD11	1.49	0.95
1:J:130:ASN:ND2	1:J:133:ARG:HH22	1.66	0.93
1:J:130:ASN:HD22	1:J:133:ARG:HH22	1.16	0.93
1:G:49:GLN:HE21	1:H:93:GLY:H	1.17	0.91

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	154/167 (92%)	140 (91%)	12 (8%)	2 (1%)	12	45
1	B	154/167 (92%)	145 (94%)	9 (6%)	0	100	100
1	C	153/167 (92%)	141 (92%)	12 (8%)	0	100	100
1	D	154/167 (92%)	141 (92%)	11 (7%)	2 (1%)	12	45
1	E	154/167 (92%)	147 (96%)	6 (4%)	1 (1%)	25	64
1	F	155/167 (93%)	144 (93%)	9 (6%)	2 (1%)	12	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	153/167 (92%)	142 (93%)	11 (7%)	0	100	100
1	H	153/167 (92%)	145 (95%)	8 (5%)	0	100	100
1	I	154/167 (92%)	143 (93%)	9 (6%)	2 (1%)	12	45
1	J	155/167 (93%)	144 (93%)	9 (6%)	2 (1%)	12	45
1	K	154/167 (92%)	139 (90%)	13 (8%)	2 (1%)	12	45
1	L	154/167 (92%)	141 (92%)	13 (8%)	0	100	100
All	All	1847/2004 (92%)	1712 (93%)	122 (7%)	13 (1%)	22	60

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	12	THR
1	J	14	LEU
1	K	101	LYS
1	A	14	LEU
1	I	101	LYS

### 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	133/142 (94%)	119 (90%)	14 (10%)	7	27
1	B	133/142 (94%)	121 (91%)	12 (9%)	9	35
1	C	132/142 (93%)	123 (93%)	9 (7%)	16	48
1	D	133/142 (94%)	123 (92%)	10 (8%)	13	43
1	E	133/142 (94%)	122 (92%)	11 (8%)	11	39
1	F	133/142 (94%)	122 (92%)	11 (8%)	11	39
1	G	132/142 (93%)	121 (92%)	11 (8%)	11	39
1	H	132/142 (93%)	124 (94%)	8 (6%)	18	53
1	I	133/142 (94%)	124 (93%)	9 (7%)	16	48
1	J	133/142 (94%)	124 (93%)	9 (7%)	16	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	133/142 (94%)	123 (92%)	10 (8%)	13	43
1	L	133/142 (94%)	122 (92%)	11 (8%)	11	39
All	All	1593/1704 (94%)	1468 (92%)	125 (8%)	12	42

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	15	LEU
1	K	101	LYS
1	G	66	LEU
1	K	96	GLN
1	L	67	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 131 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	63	HIS
1	K	130	ASN
1	L	165	ASN
1	E	58	ASN
1	E	51	HIS

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 12 are monoatomic - leaving 12 for Mogul analysis.



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	TRS	A	301	-	7,7,7	0.46	0	9,9,9	0.98	0
3	TRS	D	311	-	7,7,7	0.46	0	9,9,9	0.90	0
3	TRS	A	306	-	7,7,7	0.17	0	9,9,9	0.92	0
3	TRS	L	309	-	7,7,7	0.21	0	9,9,9	0.95	0
3	TRS	B	310	-	7,7,7	0.32	0	9,9,9	0.92	0
3	TRS	C	304	-	7,7,7	0.55	0	9,9,9	1.06	0
3	TRS	C	303	-	7,7,7	0.41	0	9,9,9	0.93	0
3	TRS	A	305	-	7,7,7	0.45	0	9,9,9	0.90	0
3	TRS	C	302	-	7,7,7	0.46	0	9,9,9	0.91	0
3	TRS	D	312	-	7,7,7	0.25	0	9,9,9	0.91	0
3	TRS	G	307	-	7,7,7	0.39	0	9,9,9	0.94	0
3	TRS	B	308	-	7,7,7	0.32	0	9,9,9	0.96	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
3	TRS	A	301	-	-	2/9/9/9	-
3	TRS	D	311	-	-	0/9/9/9	-
3	TRS	A	306	-	-	1/9/9/9	-
3	TRS	L	309	-	-	0/9/9/9	-
3	TRS	B	310	-	-	2/9/9/9	-
3	TRS	C	304	-	-	3/9/9/9	-
3	TRS	C	303	-	-	1/9/9/9	-
3	TRS	A	305	-	-	0/9/9/9	-
3	TRS	C	302	-	-	0/9/9/9	-
3	TRS	D	312	-	-	1/9/9/9	-
3	TRS	G	307	-	-	3/9/9/9	-
3	TRS	B	308	-	-	0/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	TRS	N-C-C2-O2
3	B	310	TRS	N-C-C2-O2
3	C	304	TRS	N-C-C2-O2
3	G	307	TRS	N-C-C2-O2
3	A	301	TRS	C3-C-C2-O2

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	306	TRS	2	0
3	L	309	TRS	4	0
3	C	303	TRS	3	0
3	D	312	TRS	1	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	156/167 (93%)	-0.65	0 100 100	27, 48, 65, 86	0
1	B	156/167 (93%)	-0.62	0 100 100	25, 48, 69, 85	0
1	C	155/167 (92%)	-0.54	1 (0%) 89 72	36, 54, 76, 88	0
1	D	156/167 (93%)	-0.58	1 (0%) 89 72	36, 57, 70, 80	0
1	E	156/167 (93%)	-0.63	1 (0%) 89 72	31, 50, 78, 94	0
1	F	157/167 (94%)	-0.55	1 (0%) 89 72	39, 59, 76, 100	0
1	G	155/167 (92%)	-0.75	0 100 100	26, 48, 74, 86	0
1	H	155/167 (92%)	-0.66	0 100 100	33, 52, 68, 76	0
1	I	156/167 (93%)	-0.55	1 (0%) 89 72	34, 59, 75, 89	0
1	J	157/167 (94%)	-0.49	2 (1%) 77 51	40, 58, 77, 108	0
1	K	156/167 (93%)	-0.64	1 (0%) 89 72	32, 51, 72, 91	0
1	L	156/167 (93%)	-0.66	1 (0%) 89 72	33, 52, 73, 87	0
All	All	1871/2004 (93%)	-0.61	9 (0%) 91 75	25, 53, 74, 108	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	11	ALA	5.2
1	K	12	THR	3.6
1	E	12	THR	3.4
1	J	12	THR	3.3
1	F	11	ALA	2.9

### 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 monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	K	E	207	1/1	0.71	0.21	67,67,67,67	0
2	K	I	204	1/1	0.76	0.17	67,67,67,67	0
3	TRS	D	311	8/8	0.78	0.30	106,107,107,108	0
2	K	G	201	1/1	0.81	0.18	79,79,79,79	0
2	K	E	208	1/1	0.84	0.13	55,55,55,55	0
3	TRS	C	302	8/8	0.86	0.26	95,97,99,101	0
3	TRS	C	303	8/8	0.87	0.23	61,66,67,69	0
3	TRS	A	305	8/8	0.87	0.31	99,100,100,102	0
2	K	J	202	1/1	0.88	0.10	64,64,64,64	0
2	K	H	205	1/1	0.88	0.18	52,52,52,52	0
3	TRS	B	308	8/8	0.88	0.31	95,95,96,99	0
2	K	A	209	1/1	0.89	0.18	61,61,61,61	0
3	TRS	D	312	8/8	0.89	0.22	69,70,71,72	0
2	K	D	203	1/1	0.90	0.24	76,76,76,76	0
2	K	L	210	1/1	0.90	0.16	60,60,60,60	0
3	TRS	A	306	8/8	0.92	0.18	51,52,53,54	0
3	TRS	A	301	8/8	0.93	0.21	54,56,57,60	0
3	TRS	C	304	8/8	0.93	0.18	52,54,54,55	0
3	TRS	B	310	8/8	0.94	0.21	64,65,66,67	0
2	K	F	211	1/1	0.95	0.07	49,49,49,49	0
3	TRS	L	309	8/8	0.95	0.17	47,49,51,52	0
2	K	B	206	1/1	0.97	0.25	62,62,62,62	0
3	TRS	G	307	8/8	0.97	0.12	30,31,33,34	0
2	K	C	212	1/1	0.97	0.17	52,52,52,52	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.