



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:41 PM UTC

PDB ID : 1JRE / pdb_00001jre
Title : DNA PROTECTION AND BINDING BY E. COLI DPS PROTEIN
Authors : Luo, J.; Liu, D.; White, M.A.; Fox, R.O.
Deposited on : 2001-08-13
Resolution : 2.65 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

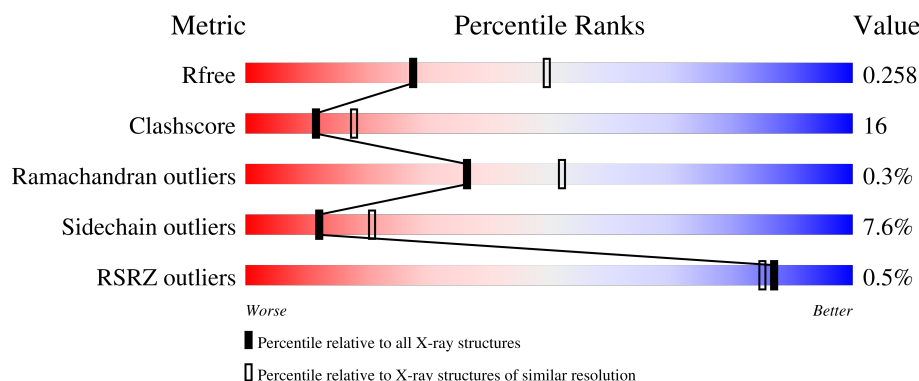
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	167	% 59% 29% 5% 6%
1	B	167	60% 30% • 6%
1	C	167	% 60% 26% 5% 7%
1	D	167	% 62% 28% • 6%
1	E	167	63% 26% • 7%

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Mol	Chain	Length	Quality of chain
1	F	167	% 62% 27% 7%
1	G	167	% 62% 27% 7%
1	H	167	63% 26% 6%
1	I	167	% 62% 27% 7%
1	J	167	% 59% 30% 7%
1	K	167	62% 27% 7%
1	L	167	63% 26% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15083 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	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	B	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	C	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	D	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	E	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	F	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	G	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	H	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	I	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	J	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	K	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	L	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	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 CADMIUM ION (CCD ID: CD) (formula: Cd).

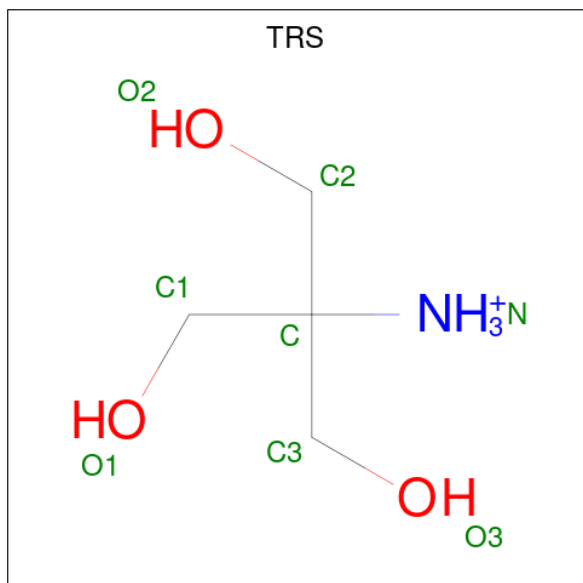
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cd 1 1	0	0
2	B	1	Total Cd 1 1	0	0
2	C	1	Total Cd 1 1	0	0
2	D	1	Total Cd 1 1	0	0
2	E	1	Total Cd 1 1	0	0
2	F	1	Total Cd 1 1	0	0
2	G	2	Total Cd 2 2	0	0
2	H	1	Total Cd 1 1	0	0
2	I	1	Total Cd 1 1	0	0
2	J	1	Total Cd 1 1	0	0

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

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: 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	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	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	E	1	Total	C	N	O	0	0
			8	4	1	3		
3	H	1	Total	C	N	O	0	0
			8	4	1	3		
3	K	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total	O	0	0
			32	32		
4	B	23	Total	O	0	0
			23	23		
4	C	16	Total	O	0	0
			16	16		
4	D	9	Total	O	0	0
			9	9		
4	E	20	Total	O	0	0
			20	20		
4	F	11	Total	O	0	0
			11	11		
4	G	31	Total	O	0	0
			31	31		
4	H	20	Total	O	0	0
			20	20		
4	I	15	Total	O	0	0
			15	15		
4	J	11	Total	O	0	0
			11	11		
4	K	15	Total	O	0	0
			15	15		
4	L	14	Total	O	0	0
			14	14		

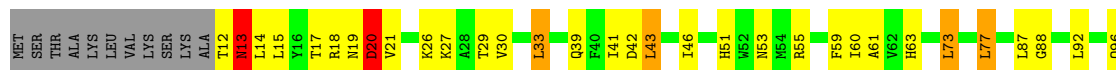
- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN





● Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain E: 63% 26% 7%



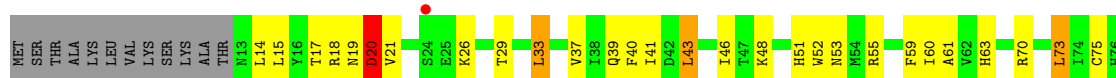
● Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain F: % 62% 27% 7%



● Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain G: % 62% 27% 7%



● Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain H: 63% 26% 6%

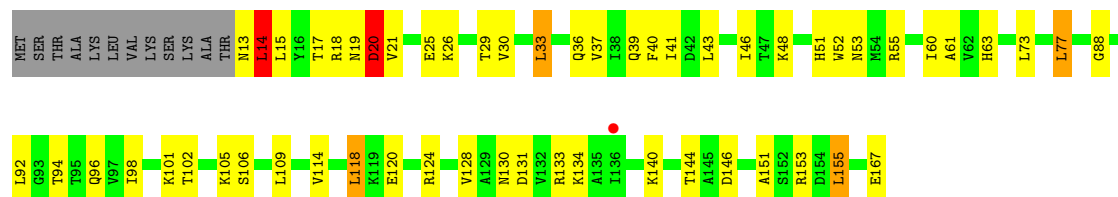


● Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

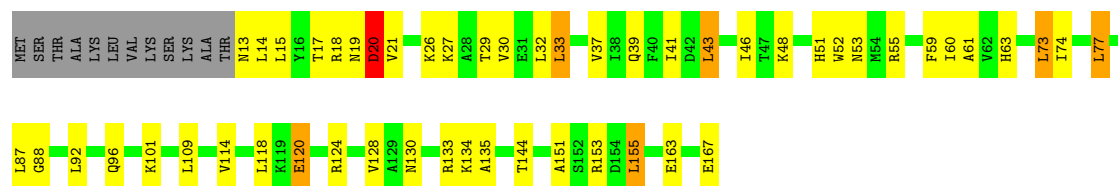
Chain I: % 62% 27% 7%



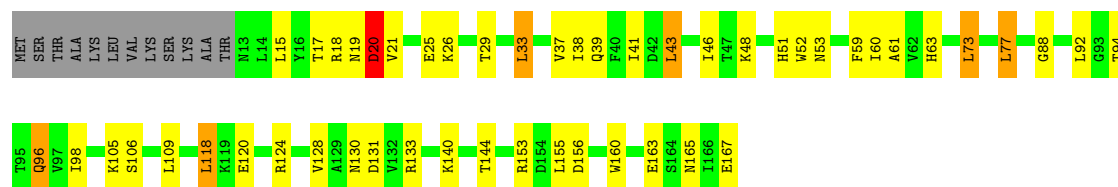
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN



• 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, α , β , γ	90.58Å 90.58Å 226.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.92 – 2.65 45.92 – 2.65	Depositor EDS
% Data completeness (in resolution range)	97.1 (45.92-2.65) 97.1 (45.92-2.65)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.05 (at 2.61Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.229 , 0.264 0.225 , 0.258	Depositor DCC
R_{free} test set	3074 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	60.5	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 68.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.008 for -h,-k,l 0.042 for h,-h-k,-l 0.025 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15083	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, CD

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	0.56	0/1254	1.00	7/1698 (0.4%)
1	B	0.54	0/1254	0.90	4/1698 (0.2%)
1	C	0.48	0/1242	0.94	4/1681 (0.2%)
1	D	0.47	0/1254	0.90	2/1698 (0.1%)
1	E	0.45	0/1249	0.92	5/1691 (0.3%)
1	F	0.44	0/1249	0.89	2/1691 (0.1%)
1	G	0.57	0/1242	0.90	3/1681 (0.2%)
1	H	0.49	0/1254	0.90	2/1698 (0.1%)
1	I	0.45	0/1249	0.88	2/1691 (0.1%)
1	J	0.47	0/1242	0.91	4/1681 (0.2%)
1	K	0.50	0/1242	0.88	3/1681 (0.2%)
1	L	0.49	0/1242	0.88	2/1681 (0.1%)
All	All	0.49	0/14973	0.91	40/20270 (0.2%)

There are no bond length outliers.

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	13	ASN	N-CA-C	-7.92	103.19	113.17
1	C	70	ARG	NE-CZ-NH2	7.74	126.17	119.20
1	A	70	ARG	NE-CZ-NH2	7.58	126.02	119.20
1	C	53	ASN	N-CA-C	7.46	121.29	112.93
1	E	53	ASN	N-CA-C	7.41	120.94	112.57

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	1236	0	1239	51	0
1	B	1236	0	1239	46	0
1	C	1224	0	1227	44	0
1	D	1236	0	1239	46	0
1	E	1231	0	1234	41	0
1	F	1231	0	1234	44	0
1	G	1224	0	1227	42	0
1	H	1236	0	1239	46	0
1	I	1231	0	1234	42	0
1	J	1224	0	1227	45	0
1	K	1224	0	1227	42	0
1	L	1224	0	1227	40	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	1	0	0	0	0
2	F	1	0	0	0	0
2	G	2	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	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	16	0	24	4	0
3	B	16	0	24	6	0
3	C	16	0	24	4	0
3	D	24	0	36	5	0
3	E	8	0	12	0	0
3	H	8	0	12	0	0
3	K	8	0	12	0	0
4	A	32	0	0	7	0
4	B	23	0	0	2	0
4	C	16	0	0	0	0
4	D	9	0	0	1	0
4	E	20	0	0	0	0
4	F	11	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	31	0	0	3	0
4	H	20	0	0	1	0
4	I	15	0	0	0	0
4	J	11	0	0	0	0
4	K	15	0	0	1	0
4	L	14	0	0	0	0
All	All	15083	0	14937	477	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 477 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)
4:A:550:HOH:O	1:B:95:THR:HB	1.68	0.94
1:B:98:ILE:O	1:B:102:THR:HG22	1.73	0.89
1:A:21:VAL:O	1:A:26:LYS:HE3	1.76	0.85
1:L:21:VAL:O	1:L:26:LYS:HE3	1.78	0.82
1:K:21:VAL:O	1:K:26:LYS:HE3	1.78	0.82

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	155/167 (93%)	149 (96%)	6 (4%)	0	100	100
1	B	155/167 (93%)	150 (97%)	5 (3%)	0	100	100
1	C	153/167 (92%)	148 (97%)	4 (3%)	1 (1%)	18	30
1	D	155/167 (93%)	147 (95%)	7 (4%)	1 (1%)	21	34
1	E	154/167 (92%)	148 (96%)	5 (3%)	1 (1%)	21	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	154/167 (92%)	147 (96%)	7 (4%)	0	100	100
1	G	153/167 (92%)	144 (94%)	8 (5%)	1 (1%)	18	30
1	H	155/167 (93%)	149 (96%)	5 (3%)	1 (1%)	21	34
1	I	154/167 (92%)	150 (97%)	4 (3%)	0	100	100
1	J	153/167 (92%)	147 (96%)	6 (4%)	0	100	100
1	K	153/167 (92%)	148 (97%)	5 (3%)	0	100	100
1	L	153/167 (92%)	147 (96%)	6 (4%)	0	100	100
All	All	1847/2004 (92%)	1774 (96%)	68 (4%)	5 (0%)	36	52

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	13	ASN
1	E	13	ASN
1	G	14	LEU
1	H	12	THR
1	C	14	LEU

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%)	124 (93%)	9 (7%)	14	25
1	B	133/142 (94%)	121 (91%)	12 (9%)	9	14
1	C	132/142 (93%)	121 (92%)	11 (8%)	10	18
1	D	133/142 (94%)	123 (92%)	10 (8%)	12	21
1	E	133/142 (94%)	124 (93%)	9 (7%)	14	25
1	F	133/142 (94%)	123 (92%)	10 (8%)	12	21
1	G	132/142 (93%)	123 (93%)	9 (7%)	14	25
1	H	133/142 (94%)	123 (92%)	10 (8%)	12	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	133/142 (94%)	123 (92%)	10 (8%)	12	21
1	J	132/142 (93%)	121 (92%)	11 (8%)	10	18
1	K	132/142 (93%)	121 (92%)	11 (8%)	10	18
1	L	132/142 (93%)	123 (93%)	9 (7%)	14	25
All	All	1591/1704 (93%)	1470 (92%)	121 (8%)	12	21

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	96	GLN
1	K	153	ARG
1	H	20	ASP
1	K	120	GLU
1	L	118	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	99	ASN
1	I	96	GLN
1	L	96	GLN
1	G	112	HIS
1	H	96	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 25 ligands modelled in this entry, 13 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	D	310	-	7,7,7	0.29	0	9,9,9	1.15	0
3	TRS	C	303	-	7,7,7	0.44	0	9,9,9	1.06	0
3	TRS	D	305	-	7,7,7	0.62	0	9,9,9	0.99	0
3	TRS	B	312	-	7,7,7	0.19	0	9,9,9	1.14	1 (11%)
3	TRS	A	301	-	7,7,7	0.36	0	9,9,9	1.08	0
3	TRS	B	304	-	7,7,7	0.16	0	9,9,9	1.14	0
3	TRS	H	308	-	7,7,7	0.68	0	9,9,9	1.04	0
3	TRS	A	309	-	7,7,7	0.30	0	9,9,9	1.09	0
3	TRS	K	302	-	7,7,7	0.62	0	9,9,9	1.03	0
3	TRS	E	311	-	7,7,7	0.43	0	9,9,9	1.11	1 (11%)
3	TRS	D	306	-	7,7,7	0.43	0	9,9,9	1.09	1 (11%)
3	TRS	C	307	-	7,7,7	0.30	0	9,9,9	1.16	1 (11%)

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	D	310	-	-	0/9/9/9	-
3	TRS	C	303	-	-	0/9/9/9	-
3	TRS	D	305	-	-	1/9/9/9	-
3	TRS	B	312	-	-	0/9/9/9	-
3	TRS	A	301	-	-	0/9/9/9	-
3	TRS	B	304	-	-	0/9/9/9	-
3	TRS	H	308	-	-	1/9/9/9	-
3	TRS	A	309	-	-	0/9/9/9	-
3	TRS	K	302	-	-	1/9/9/9	-
3	TRS	E	311	-	-	2/9/9/9	-
3	TRS	D	306	-	-	0/9/9/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TRS	C	307	-	-	0/9/9/9	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	307	TRS	C3-C-N	2.04	113.37	108.17
3	D	306	TRS	C1-C-N	-2.03	102.98	108.17
3	E	311	TRS	C1-C-N	-2.02	103.03	108.17
3	B	312	TRS	C1-C-N	-2.01	103.05	108.17

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	311	TRS	N-C-C2-O2
3	E	311	TRS	C3-C-C2-O2
3	D	305	TRS	N-C-C2-O2
3	H	308	TRS	N-C-C2-O2
3	K	302	TRS	N-C-C2-O2

There are no ring outliers.

6 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	310	TRS	2	0
3	C	303	TRS	4	0
3	B	312	TRS	5	0
3	B	304	TRS	1	0
3	A	309	TRS	4	0
3	D	306	TRS	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	157/167 (94%)	-0.09	1 (0%) 85 83	36, 54, 70, 97	0
1	B	157/167 (94%)	-0.08	0 100 100	36, 54, 77, 105	0
1	C	155/167 (92%)	0.27	1 (0%) 85 83	45, 68, 89, 98	0
1	D	157/167 (94%)	0.41	2 (1%) 75 71	48, 70, 84, 99	0
1	E	156/167 (93%)	0.12	0 100 100	42, 62, 89, 102	0
1	F	156/167 (93%)	0.61	2 (1%) 75 71	45, 74, 89, 104	0
1	G	155/167 (92%)	0.05	1 (0%) 85 83	34, 54, 83, 95	0
1	H	157/167 (94%)	0.01	0 100 100	42, 58, 79, 100	0
1	I	156/167 (93%)	0.42	1 (0%) 85 83	49, 71, 87, 100	0
1	J	155/167 (92%)	0.45	1 (0%) 85 83	48, 70, 87, 92	0
1	K	155/167 (92%)	-0.05	0 100 100	42, 60, 78, 84	0
1	L	155/167 (92%)	0.19	0 100 100	44, 64, 83, 91	0
All	All	1871/2004 (93%)	0.19	9 (0%) 87 85	34, 64, 85, 105	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	136	ILE	2.9
1	A	12	THR	2.5
1	C	38	ILE	2.4
1	F	14	LEU	2.2
1	F	121	LEU	2.2

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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	TRS	E	311	8/8	0.66	0.17	86,87,88,91	0
3	TRS	H	308	8/8	0.66	0.15	81,85,86,87	0
3	TRS	D	305	8/8	0.68	0.13	81,84,84,84	0
3	TRS	K	302	8/8	0.75	0.14	81,84,85,85	0
3	TRS	D	306	8/8	0.83	0.10	72,75,75,76	0
3	TRS	C	307	8/8	0.85	0.12	63,65,66,66	0
3	TRS	C	303	8/8	0.86	0.12	79,80,81,82	0
3	TRS	D	310	8/8	0.87	0.13	50,52,53,55	0
3	TRS	A	309	8/8	0.87	0.10	52,54,57,58	0
3	TRS	A	301	8/8	0.88	0.14	70,71,73,73	0
3	TRS	B	304	8/8	0.89	0.16	73,74,75,76	0
3	TRS	B	312	8/8	0.93	0.07	44,46,48,52	0
2	CD	C	201	1/1	0.98	0.05	90,90,90,90	0
2	CD	G	201	1/1	0.99	0.02	67,67,67,67	0
2	CD	I	201	1/1	0.99	0.04	72,72,72,72	0
2	CD	J	201	1/1	0.99	0.03	75,75,75,75	0
2	CD	K	201	1/1	0.99	0.03	67,67,67,67	0
2	CD	D	201	1/1	0.99	0.05	71,71,71,71	0
2	CD	E	201	1/1	0.99	0.03	73,73,73,73	0
2	CD	F	201	1/1	0.99	0.02	65,65,65,65	0
2	CD	G	202	1/1	0.99	0.03	87,87,87,87	0
2	CD	A	201	1/1	1.00	0.03	61,61,61,61	0
2	CD	B	201	1/1	1.00	0.01	61,61,61,61	0
2	CD	H	201	1/1	1.00	0.02	57,57,57,57	0
2	CD	L	201	1/1	1.00	0.05	74,74,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.