



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 12:28 pm BST

PDB ID : 4A0K
Title : STRUCTURE OF DDB1-DDB2-CUL4A-RBX1 BOUND TO A 12 BP ABA-SIC SITE CONTAINING DNA-DUPLEX
Authors : Fischer, E.S.; Scrima, A.; Gut, H.; Thoma, N.H.
Deposited on : 2011-09-09
Resolution : 5.93 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

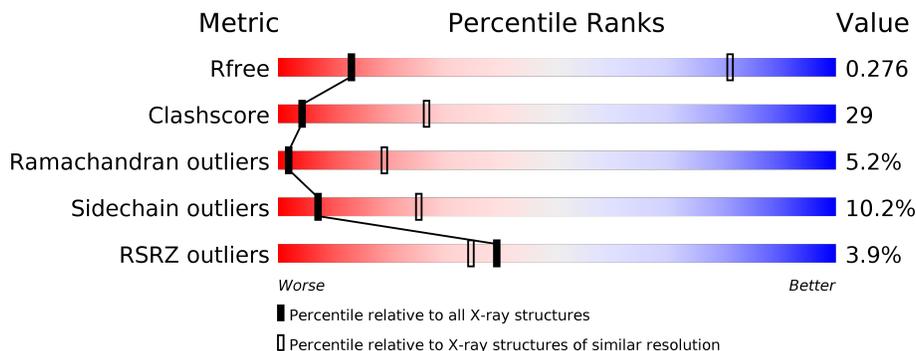
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

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 5.93 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	1000 (8.00-3.88)
Clashscore	141614	1043 (7.94-3.90)
Ramachandran outliers	138981	1016 (8.00-3.86)
Sidechain outliers	138945	1017 (8.00-3.82)
RSRZ outliers	127900	1014 (8.00-3.78)

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 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	742	
2	B	117	
3	C	1159	
4	D	382	
5	E	12	
6	F	12	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17885 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 CULLIN-4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	719	5809	3692	1007	1076	34	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	MET	-	expression tag	UNP Q13619
A	19	HIS	-	expression tag	UNP Q13619
A	20	HIS	-	expression tag	UNP Q13619
A	21	HIS	-	expression tag	UNP Q13619
A	22	HIS	-	expression tag	UNP Q13619
A	23	HIS	-	expression tag	UNP Q13619
A	24	HIS	-	expression tag	UNP Q13619
A	25	VAL	-	expression tag	UNP Q13619
A	26	ASP	-	expression tag	UNP Q13619
A	27	GLU	-	expression tag	UNP Q13619
A	28	GLU	-	expression tag	UNP Q13619
A	29	ASN	-	expression tag	UNP Q13619
A	30	LEU	-	expression tag	UNP Q13619
A	31	TYR	-	expression tag	UNP Q13619
A	32	PHE	-	expression tag	UNP Q13619
A	33	GLN	-	expression tag	UNP Q13619
A	34	GLY	-	expression tag	UNP Q13619
A	35	GLY	-	expression tag	UNP Q13619
A	36	GLY	-	expression tag	UNP Q13619
A	37	ARG	-	expression tag	UNP Q13619

- Molecule 2 is a protein called E3 UBIQUITIN-PROTEIN LIGASE RBX1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	21	184	126	32	26	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	MET	-	expression tag	UNP P62877
B	-7	HIS	-	expression tag	UNP P62877
B	-6	HIS	-	expression tag	UNP P62877
B	-5	HIS	-	expression tag	UNP P62877
B	-4	HIS	-	expression tag	UNP P62877
B	-3	HIS	-	expression tag	UNP P62877
B	-2	HIS	-	expression tag	UNP P62877
B	-1	VAL	-	expression tag	UNP P62877
B	0	ASP	-	expression tag	UNP P62877
B	1	GLU	-	expression tag	UNP P62877
B	2	GLU	-	expression tag	UNP P62877
B	3	ASN	-	expression tag	UNP P62877
B	4	LEU	-	expression tag	UNP P62877
B	5	TYR	-	expression tag	UNP P62877
B	6	PHE	-	expression tag	UNP P62877
B	7	GLN	-	expression tag	UNP P62877
B	8	GLY	-	expression tag	UNP P62877
B	9	GLY	-	expression tag	UNP P62877
B	10	GLY	-	expression tag	UNP P62877
B	11	ARG	-	expression tag	UNP P62877

- Molecule 3 is a protein called DNA DAMAGE-BINDING PROTEIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	1105	8605	5460	1442	1657	46	0	0	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	MET	-	expression tag	UNP Q16531
C	-17	HIS	-	expression tag	UNP Q16531
C	-16	HIS	-	expression tag	UNP Q16531
C	-15	HIS	-	expression tag	UNP Q16531
C	-14	HIS	-	expression tag	UNP Q16531
C	-13	HIS	-	expression tag	UNP Q16531
C	-12	HIS	-	expression tag	UNP Q16531
C	-11	VAL	-	expression tag	UNP Q16531
C	-10	ASP	-	expression tag	UNP Q16531
C	-9	GLU	-	expression tag	UNP Q16531
C	-8	ASN	-	expression tag	UNP Q16531

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	LEU	-	expression tag	UNP Q16531
C	-6	TYR	-	expression tag	UNP Q16531
C	-5	PHE	-	expression tag	UNP Q16531
C	-4	GLN	-	expression tag	UNP Q16531
C	-3	GLY	-	expression tag	UNP Q16531
C	-2	GLY	-	expression tag	UNP Q16531
C	-1	GLY	-	expression tag	UNP Q16531
C	0	ARG	-	expression tag	UNP Q16531

- Molecule 4 is a protein called DNA DAMAGE-BINDING PROTEIN 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	355	2804	1781	491	521	11	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	76	MET	-	expression tag	UNP Q2YDS1
D	77	HIS	-	expression tag	UNP Q2YDS1
D	78	HIS	-	expression tag	UNP Q2YDS1
D	79	HIS	-	expression tag	UNP Q2YDS1
D	80	HIS	-	expression tag	UNP Q2YDS1
D	81	HIS	-	expression tag	UNP Q2YDS1
D	82	HIS	-	expression tag	UNP Q2YDS1
D	83	ARG	-	expression tag	UNP Q2YDS1
D	84	ARG	-	expression tag	UNP Q2YDS1
D	85	LEU	-	expression tag	UNP Q2YDS1
D	86	VAL	-	expression tag	UNP Q2YDS1
D	87	PRO	-	expression tag	UNP Q2YDS1
D	88	ARG	-	expression tag	UNP Q2YDS1
D	89	GLY	-	expression tag	UNP Q2YDS1
D	90	SER	-	expression tag	UNP Q2YDS1
D	91	GLY	-	expression tag	UNP Q2YDS1
D	92	GLY	-	expression tag	UNP Q2YDS1
D	93	ARG	-	expression tag	UNP Q2YDS1
D	180	GLN	LEU	variant	UNP Q2YDS1
D	214	ARG	TRP	variant	UNP Q2YDS1

- Molecule 5 is a DNA chain called 12 BP THF CONTAINING DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
5	E	12	234	111	41	70	12	0	0	0

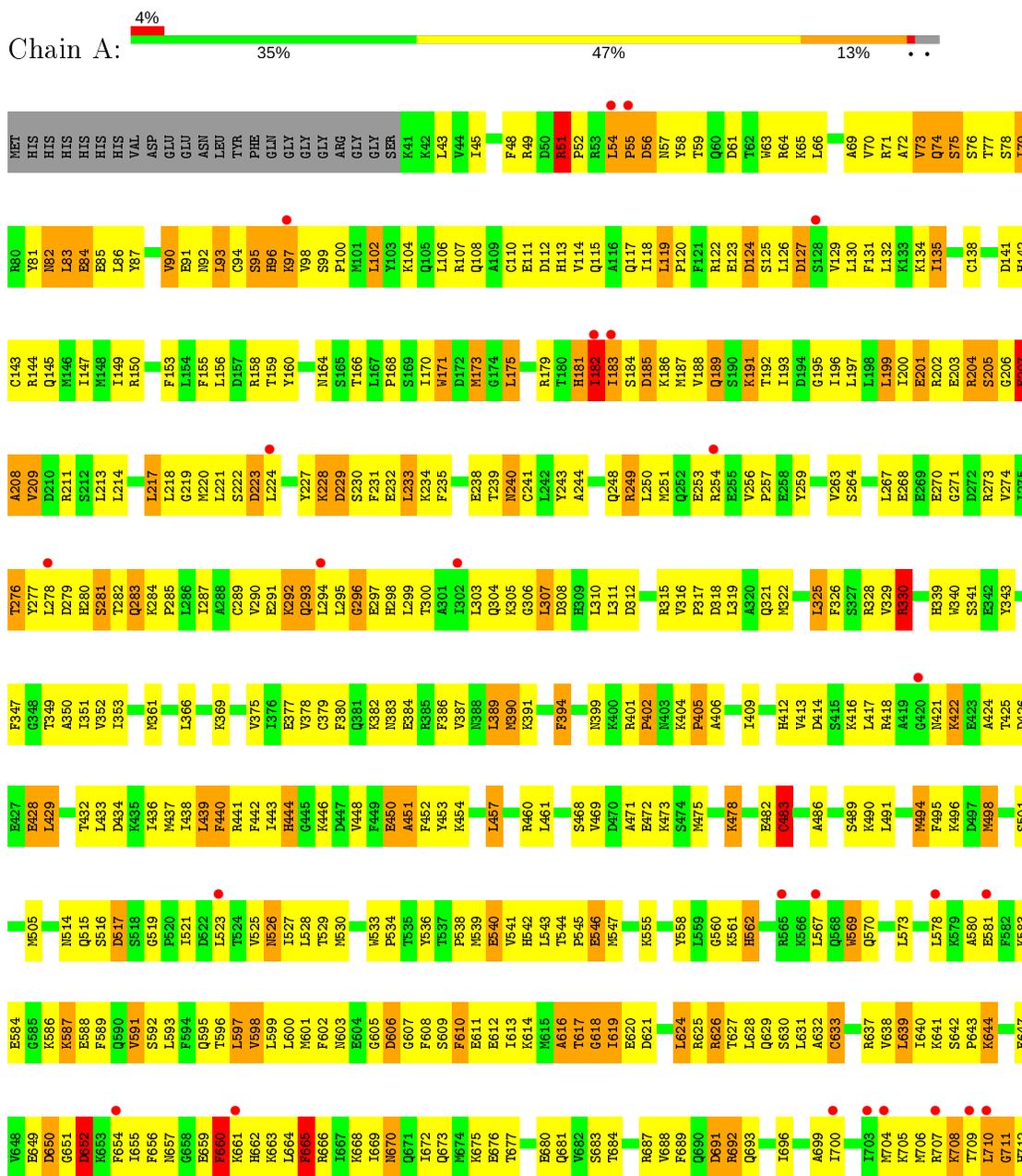
- Molecule 6 is a DNA chain called 12 BP DNA.

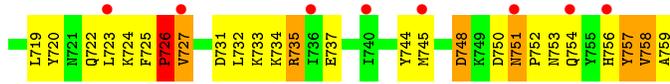
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
6	F	12	249	118	47	72	12	0	0	0

3 Residue-property plots

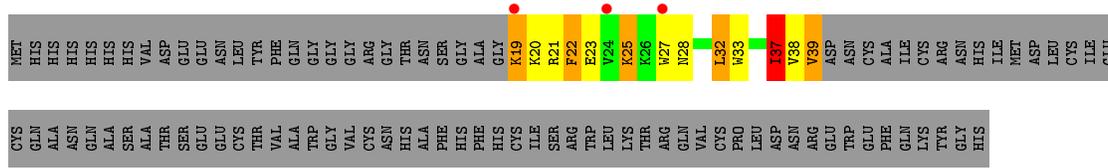
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: CULLIN-4A

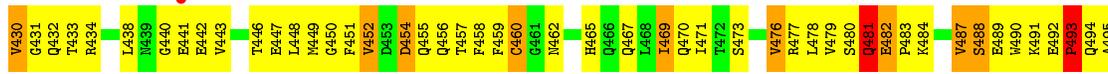
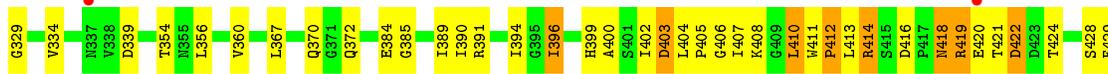


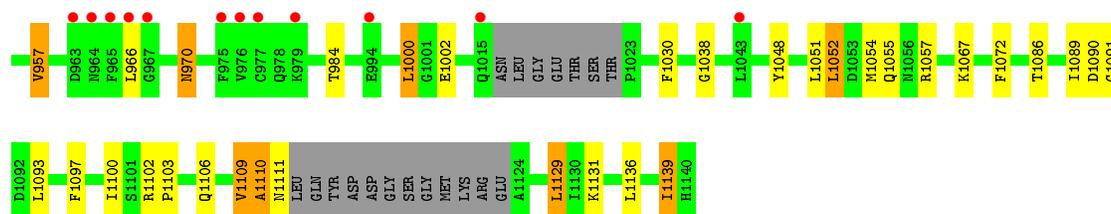


• Molecule 2: E3 UBIQUITIN-PROTEIN LIGASE RBX1

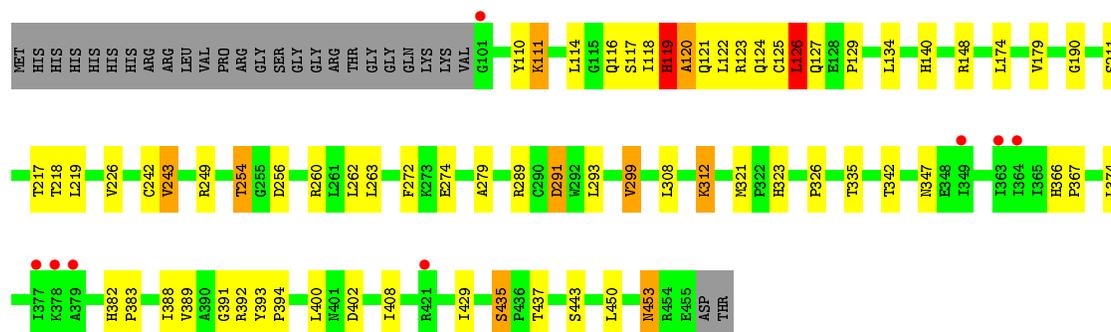
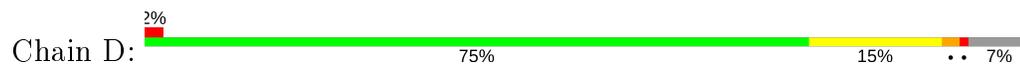


• Molecule 3: DNA DAMAGE-BINDING PROTEIN 1

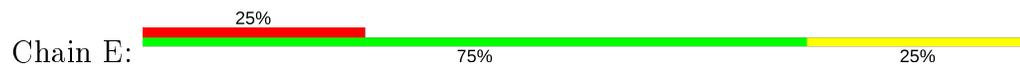




- Molecule 4: DNA DAMAGE-BINDING PROTEIN 2



- Molecule 5: 12 BP THF CONTAINING DNA



- Molecule 6: 12 BP DNA



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	210.65Å 78.02Å 276.62Å 90.00° 108.50° 90.00°	Depositor
Resolution (Å)	19.98 – 5.93 47.64 – 5.93	Depositor EDS
% Data completeness (in resolution range)	99.3 (19.98-5.93) 98.9 (47.64-5.93)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 6.15Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.269 , 0.270 0.281 , 0.276	Depositor DCC
R_{free} test set	565 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	261.2	Xtrriage
Anisotropy	0.597	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 330.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	17885	wwPDB-VP
Average B, all atoms (Å ²)	326.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 3DR

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	0.44	0/5915	0.74	11/7954 (0.1%)
2	B	0.40	0/190	0.48	0/257
3	C	0.46	5/8762 (0.1%)	0.67	9/11875 (0.1%)
4	D	0.37	0/2877	0.58	0/3912
5	E	0.93	1/248 (0.4%)	1.12	0/377
6	F	0.89	0/279	1.36	1/429 (0.2%)
All	All	0.46	6/18271 (0.0%)	0.70	21/24804 (0.1%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	354	THR	C-N	-11.77	1.06	1.34
3	C	582	LEU	C-N	6.64	1.45	1.33
3	C	13	THR	C-N	6.59	1.49	1.34
3	C	706	GLU	C-N	-5.68	1.21	1.34
5	E	9	DC	C1'-N1	5.59	1.56	1.49

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	298	HIS	CB-CA-C	-10.74	88.92	110.40
1	A	182	ILE	N-CA-C	9.33	136.18	111.00
1	A	181	HIS	CB-CA-C	7.11	124.62	110.40
3	C	624	SER	N-CA-C	7.02	129.96	111.00
1	A	48	PHE	N-CA-C	-6.88	92.43	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5809	0	5796	617	0
2	B	184	0	192	29	0
3	C	8605	0	8542	369	1
4	D	2804	0	2720	45	0
5	E	234	0	132	3	0
6	F	249	0	136	7	0
All	All	17885	0	17518	1034	1

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 29.

The worst 5 of 1034 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:131:PHE:CZ	1:A:188:VAL:HA	1.63	1.33
1:A:696:ILE:CD1	1:A:723:LEU:HG	1.57	1.33
1:A:118:ILE:CD1	1:A:181:HIS:HB3	1.60	1.29
1:A:135:ILE:HD11	1:A:188:VAL:CG1	1.63	1.26
1:A:696:ILE:HD13	1:A:723:LEU:CD1	1.69	1.21

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:103:ARG:NH1	3:C:769:LYS:NZ[1_565]	2.04	0.16

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	717/742 (97%)	512 (71%)	132 (18%)	73 (10%)	0	8
2	B	19/117 (16%)	14 (74%)	4 (21%)	1 (5%)	2	19
3	C	1095/1159 (94%)	963 (88%)	97 (9%)	35 (3%)	4	26
4	D	353/382 (92%)	326 (92%)	22 (6%)	5 (1%)	11	46
All	All	2184/2400 (91%)	1815 (83%)	255 (12%)	114 (5%)	2	19

5 of 114 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	56	ASP
1	A	58	TYR
1	A	76	SER
1	A	83	LEU
1	A	84	GLU

5.3.2 Protein sidechains [i](#)

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	631/674 (94%)	562 (89%)	69 (11%)	6	23
2	B	18/99 (18%)	11 (61%)	7 (39%)	0	0
3	C	957/1015 (94%)	865 (90%)	92 (10%)	8	27
4	D	304/335 (91%)	278 (91%)	26 (9%)	10	33
All	All	1910/2123 (90%)	1716 (90%)	194 (10%)	7	25

5 of 194 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	334	VAL
3	C	518	TYR
4	D	254	THR

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Mol	Chain	Res	Type
3	C	370	GLN
3	C	452	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	30	ASN
3	C	374	GLN
3	C	1034	ASN
3	C	85	ASN
3	C	186	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](#)

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
5	3DR	E	7	5	8,11,12	0.41	0	9,14,17	1.08	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
5	3DR	E	7	5	-	1/3/15/16	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	7	3DR	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	354:THR	C	355:ASN	N	1.07

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	719/742 (96%)	0.36	33 (4%) 32 30	288, 322, 371, 414	0
2	B	21/117 (17%)	1.04	3 (14%) 2 5	312, 322, 356, 365	0
3	C	1105/1159 (95%)	0.33	39 (3%) 44 39	185, 326, 367, 403	0
4	D	355/382 (92%)	0.27	8 (2%) 60 53	275, 310, 352, 367	0
5	E	11/12 (91%)	1.74	3 (27%) 0 2	342, 359, 437, 441	0
6	F	12/12 (100%)	0.60	1 (8%) 11 13	363, 379, 420, 442	0
All	All	2223/2424 (91%)	0.34	87 (3%) 39 34	185, 322, 367, 442	0

The worst 5 of 87 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	1	DG	6.0
4	D	377	ILE	5.0
1	A	709	THR	4.6
3	C	1015	GLN	4.4
5	E	12	DA	4.4

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
5	3DR	E	7	11/12	0.82	0.24	357,362,366,367	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.