



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 02:07 PM GMT

PDB ID : 1J4T  
Title : Structure of Artocarpin: a Lectin with Mannose Specificity (Form 2)  
Authors : Pratap, J.V.; Jeyaprakash, A.A.; Rani, P.G.; Sekar, K.; Surolia, A.; Vijayan, M.  
Deposited on : 2001-10-30  
Resolution : 2.40 Å(reported)

This is a wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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

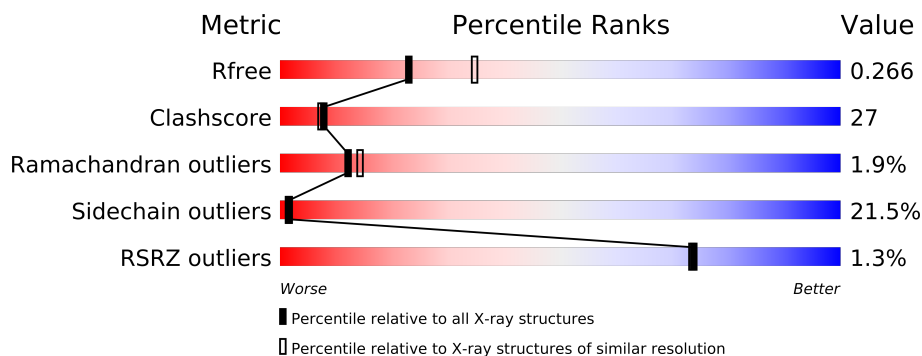
MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683



# 1 Overall quality at a glance

The reported resolution of this entry is 2.40 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))
$R_{free}$	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	149	
1	B	149	
1	C	149	
1	D	149	
1	E	149	
1	F	149	
1	G	149	
1	H	149	



## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9922 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Artocarpin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	149	Total	C	N	O	S	0	0	0
			1132	727	182	222	1			
1	B	149	Total	C	N	O	S	0	0	0
			1132	727	182	222	1			
1	C	149	Total	C	N	O	S	0	0	0
			1132	727	182	222	1			
1	D	149	Total	C	N	O	S	0	0	0
			1132	727	182	222	1			
1	E	149	Total	C	N	O	S	0	0	0
			1128	724	181	222	1			
1	F	149	Total	C	N	O	S	0	0	0
			1128	724	181	222	1			
1	G	149	Total	C	N	O	S	0	0	0
			1132	727	182	222	1			
1	H	149	Total	C	N	O	S	0	0	0
			1132	727	182	222	1			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	AYA	ALA	MODIFIED RESIDUE	UNP Q7M1T4
A	9	SER	PRO	CONFLICT	UNP Q7M1T4
A	20	GLU	ASP	CONFLICT	UNP Q7M1T4
A	49	ASP	GLU	CONFLICT	UNP Q7M1T4
A	70	LYS	ARG	CONFLICT	UNP Q7M1T4
A	84	GLY	ALA	CONFLICT	UNP Q7M1T4
A	145	ILE	VAL	CONFLICT	UNP Q7M1T4
A	148	SER	ALA	CONFLICT	UNP Q7M1T4
B	1	AYA	ALA	MODIFIED RESIDUE	UNP Q7M1T4
B	9	SER	PRO	CONFLICT	UNP Q7M1T4
B	20	GLU	ASP	CONFLICT	UNP Q7M1T4
B	49	ASP	GLU	CONFLICT	UNP Q7M1T4
B	70	LYS	ARG	CONFLICT	UNP Q7M1T4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	84	GLY	ALA	CONFLICT	UNP Q7M1T4
B	145	ILE	VAL	CONFLICT	UNP Q7M1T4
B	148	SER	ALA	CONFLICT	UNP Q7M1T4
C	1	AYA	ALA	MODIFIED RESIDUE	UNP Q7M1T4
C	9	SER	PRO	CONFLICT	UNP Q7M1T4
C	20	GLU	ASP	CONFLICT	UNP Q7M1T4
C	49	ASP	GLU	CONFLICT	UNP Q7M1T4
C	70	LYS	ARG	CONFLICT	UNP Q7M1T4
C	84	GLY	ALA	CONFLICT	UNP Q7M1T4
C	145	ILE	VAL	CONFLICT	UNP Q7M1T4
C	148	SER	ALA	CONFLICT	UNP Q7M1T4
D	1	AYA	ALA	MODIFIED RESIDUE	UNP Q7M1T4
D	9	SER	PRO	CONFLICT	UNP Q7M1T4
D	20	GLU	ASP	CONFLICT	UNP Q7M1T4
D	49	ASP	GLU	CONFLICT	UNP Q7M1T4
D	70	LYS	ARG	CONFLICT	UNP Q7M1T4
D	84	GLY	ALA	CONFLICT	UNP Q7M1T4
D	145	ILE	VAL	CONFLICT	UNP Q7M1T4
D	148	SER	ALA	CONFLICT	UNP Q7M1T4
E	1	AYA	ALA	MODIFIED RESIDUE	UNP Q7M1T4
E	9	SER	PRO	CONFLICT	UNP Q7M1T4
E	20	GLU	ASP	CONFLICT	UNP Q7M1T4
E	49	ASP	GLU	CONFLICT	UNP Q7M1T4
E	70	LYS	ARG	CONFLICT	UNP Q7M1T4
E	84	GLY	ALA	CONFLICT	UNP Q7M1T4
E	145	ILE	VAL	CONFLICT	UNP Q7M1T4
E	148	SER	ALA	CONFLICT	UNP Q7M1T4
F	1	AYA	ALA	MODIFIED RESIDUE	UNP Q7M1T4
F	9	SER	PRO	CONFLICT	UNP Q7M1T4
F	20	GLU	ASP	CONFLICT	UNP Q7M1T4
F	49	ASP	GLU	CONFLICT	UNP Q7M1T4
F	70	LYS	ARG	CONFLICT	UNP Q7M1T4
F	84	GLY	ALA	CONFLICT	UNP Q7M1T4
F	145	ILE	VAL	CONFLICT	UNP Q7M1T4
F	148	SER	ALA	CONFLICT	UNP Q7M1T4
G	1	AYA	ALA	MODIFIED RESIDUE	UNP Q7M1T4
G	9	SER	PRO	CONFLICT	UNP Q7M1T4
G	20	GLU	ASP	CONFLICT	UNP Q7M1T4
G	49	ASP	GLU	CONFLICT	UNP Q7M1T4
G	70	LYS	ARG	CONFLICT	UNP Q7M1T4
G	84	GLY	ALA	CONFLICT	UNP Q7M1T4
G	145	ILE	VAL	CONFLICT	UNP Q7M1T4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	148	SER	ALA	CONFLICT	UNP Q7M1T4
H	1	AYA	ALA	MODIFIED RESIDUE	UNP Q7M1T4
H	9	SER	PRO	CONFLICT	UNP Q7M1T4
H	20	GLU	ASP	CONFLICT	UNP Q7M1T4
H	49	ASP	GLU	CONFLICT	UNP Q7M1T4
H	70	LYS	ARG	CONFLICT	UNP Q7M1T4
H	84	GLY	ALA	CONFLICT	UNP Q7M1T4
H	145	ILE	VAL	CONFLICT	UNP Q7M1T4
H	148	SER	ALA	CONFLICT	UNP Q7M1T4

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	118	Total O 118 118	0	0
2	B	123	Total O 123 123	0	0
2	C	121	Total O 121 121	0	0
2	D	121	Total O 121 121	0	0
2	E	93	Total O 93 93	0	0
2	F	115	Total O 115 115	0	0
2	G	102	Total O 102 102	0	0
2	H	81	Total O 81 81	0	0

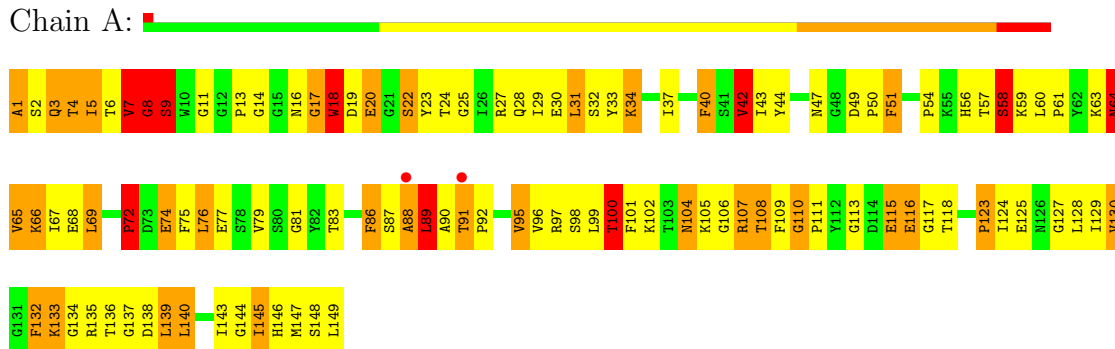


### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

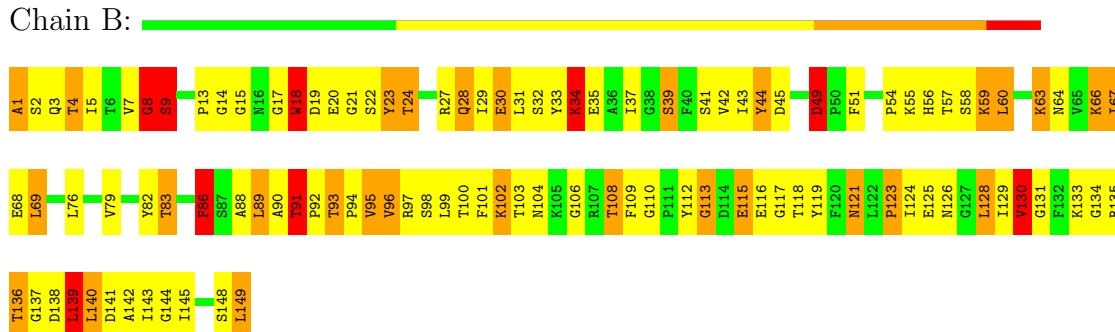
#### • Molecule 1: Artocarpin

Chain A:



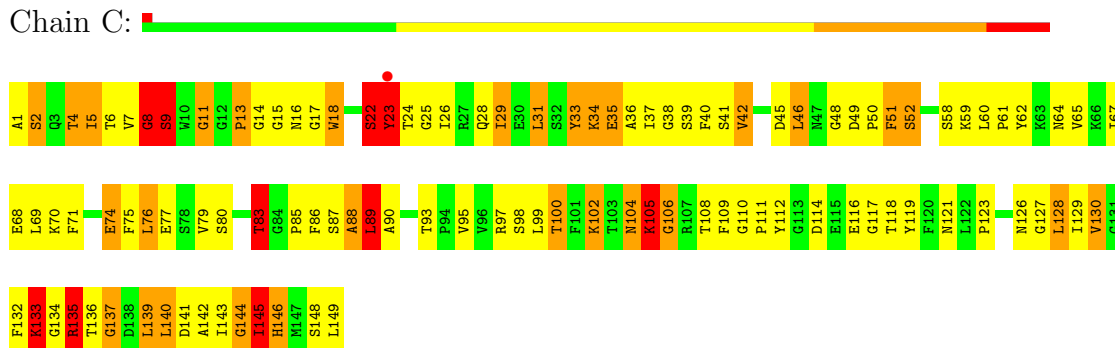
#### • Molecule 1: Artocarpin

Chain B:



#### • Molecule 1: Artocarpin

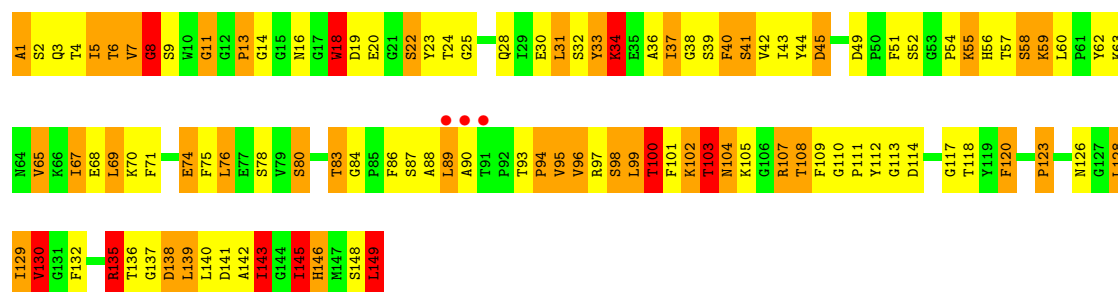
Chain C:



#### • Molecule 1: Artocarpin

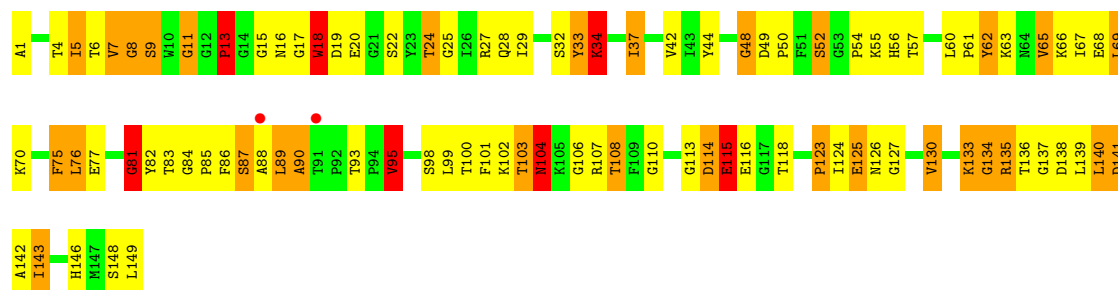


Chain D: 



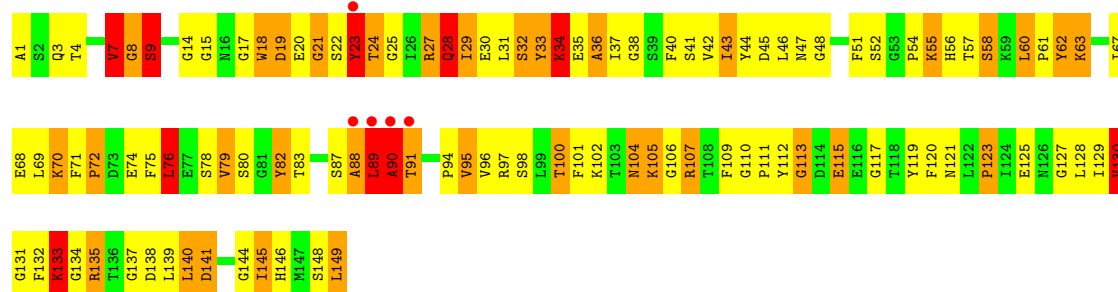
• Molecule 1: Artocarpin

Chain E: 



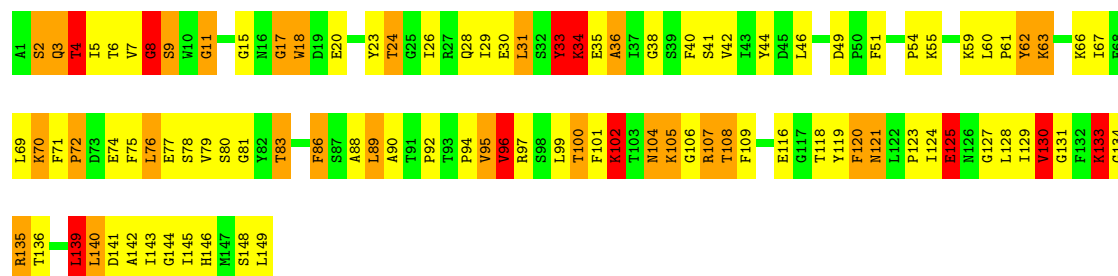
• Molecule 1: Artocarpin

Chain F: 



• Molecule 1: Artocarpin

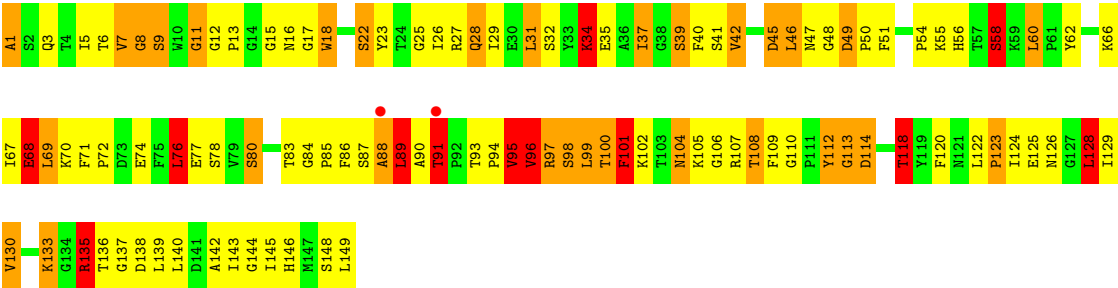
Chain G: 



• Molecule 1: Artocarpin

Chain H: 







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.69Å 72.19Å 92.63Å 90.00° 101.15° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 10.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.40) 83.5 (10.00-2.40)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.91 (at 2.41Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.191 , 0.258 0.207 , 0.266	Depositor DCC
$R_{free}$ test set	1536 reflections (4.18%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.7	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 46.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	0 of 36759 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9922	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	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 64.61 % 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 8.0588e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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



## 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: AYA

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	1.08	4/1155 (0.3%)	2.09	74/1569 (4.7%)
1	B	1.03	6/1155 (0.5%)	2.09	66/1569 (4.2%)
1	C	1.06	5/1155 (0.4%)	2.21	79/1569 (5.0%)
1	D	0.97	5/1155 (0.4%)	2.31	82/1569 (5.2%)
1	E	0.99	3/1151 (0.3%)	2.40	77/1565 (4.9%)
1	F	1.50	6/1151 (0.5%)	2.31	70/1565 (4.5%)
1	G	1.52	3/1155 (0.3%)	2.20	68/1569 (4.3%)
1	H	0.96	1/1155 (0.1%)	2.31	73/1569 (4.7%)
All	All	1.16	33/9232 (0.4%)	2.24	589/12544 (4.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	8
1	B	1	4
1	C	1	8
1	D	0	5
1	E	1	5
1	F	0	7
1	G	1	5
1	H	1	4
All	All	6	46

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	70	LYS	CD-CE	39.71	2.50	1.51
1	F	70	LYS	CD-CE	37.27	2.44	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	33	TYR	C-N	11.14	1.59	1.34
1	A	34	LYS	C-N	10.43	1.58	1.34
1	C	33	TYR	C-N	9.15	1.55	1.34

The worst 5 of 589 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	34	LYS	O-C-N	-36.39	64.47	122.70
1	G	70	LYS	CD-CE-NZ	-35.79	29.38	111.70
1	F	70	LYS	CD-CE-NZ	-35.17	30.80	111.70
1	D	34	LYS	O-C-N	-28.27	77.46	122.70
1	H	9	SER	O-C-N	-27.94	77.99	122.70

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1	AYA	CA
1	B	1	AYA	CA
1	C	1	AYA	CA
1	E	1	AYA	CA
1	G	1	AYA	CA

5 of 46 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	AYA	Mainchain
1	A	34	LYS	Mainchain
1	A	42	VAL	Mainchain
1	A	8	GLY	Mainchain,Peptide
1	A	9	SER	Mainchain

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1132	0	1084	69	0
1	B	1132	0	1083	59	0
1	C	1132	0	1084	58	0
1	D	1132	0	1080	86	0
1	E	1128	0	1071	48	0
1	F	1128	0	1067	69	0
1	G	1132	0	1081	55	0
1	H	1132	0	1082	72	0
2	A	118	0	0	7	0
2	B	123	0	0	9	0
2	C	121	0	0	4	0
2	D	121	0	0	7	0
2	E	93	0	0	4	0
2	F	115	0	0	6	0
2	G	102	0	0	6	0
2	H	81	0	0	6	0
All	All	9922	0	8632	481	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 27.

The worst 5 of 481 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:8:GLY:HA2	1:D:123:PRO:HG2	1.22	1.18
1:D:18:TRP:HZ3	1:D:136:THR:HG23	0.98	1.10
1:D:18:TRP:CZ3	1:D:136:THR:HG23	1.89	1.07
1:A:61:PRO:HD2	2:A:181:HOH:O	1.57	1.04
1:E:60:LEU:HD11	1:E:89:LEU:HD11	1.47	0.97

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	147/149 (99%)	133 (90%)	12 (8%)	2 (1%)	16 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	147/149 (99%)	136 (92%)	8 (5%)	3 (2%)	11	13
1	C	147/149 (99%)	131 (89%)	11 (8%)	5 (3%)	6	4
1	D	147/149 (99%)	132 (90%)	12 (8%)	3 (2%)	11	13
1	E	147/149 (99%)	131 (89%)	12 (8%)	4 (3%)	8	7
1	F	147/149 (99%)	135 (92%)	11 (8%)	1 (1%)	30	43
1	G	147/149 (99%)	139 (95%)	6 (4%)	2 (1%)	16	22
1	H	147/149 (99%)	128 (87%)	17 (12%)	2 (1%)	16	22
All	All	1176/1192 (99%)	1065 (91%)	89 (8%)	22 (2%)	12	14

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	SER
1	A	110	GLY
1	B	9	SER
1	B	110	GLY
1	C	9	SER

### 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	120/122 (98%)	95 (79%)	25 (21%)	2	2
1	B	120/122 (98%)	93 (78%)	27 (22%)	1	1
1	C	120/122 (98%)	95 (79%)	25 (21%)	2	2
1	D	120/122 (98%)	93 (78%)	27 (22%)	1	1
1	E	119/122 (98%)	95 (80%)	24 (20%)	2	2
1	F	119/122 (98%)	95 (80%)	24 (20%)	2	2
1	G	120/122 (98%)	96 (80%)	24 (20%)	2	2
1	H	120/122 (98%)	90 (75%)	30 (25%)	1	1
All	All	958/976 (98%)	752 (78%)	206 (22%)	1	1



5 of 206 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	104	ASN
1	E	95	VAL
1	H	80	SER
1	D	118	THR
1	E	5	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	104	ASN
1	D	104	ASN
1	H	104	ASN
1	D	28	GLN
1	E	47	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

8 non-standard protein/DNA/RNA residues are 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$
1	AYA	A	1	1	7,7,8	7.77	2 (28%)	6,8,10	28.34	5 (83%)
1	AYA	B	1	1	7,7,8	7.23	3 (42%)	6,8,10	29.98	6 (100%)
1	AYA	C	1	1	7,7,8	6.57	3 (42%)	6,8,10	30.21	5 (83%)
1	AYA	D	1	1	7,7,8	6.49	3 (42%)	6,8,10	29.16	3 (50%)
1	AYA	E	1	1	7,7,8	6.88	2 (28%)	6,8,10	31.34	3 (50%)
1	AYA	F	1	1	7,7,8	6.10	3 (42%)	6,8,10	30.99	6 (100%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	AYA	G	1	1	7,7,8	8.35	3 (42%)	6,8,10	29.30	3 (50%)
1	AYA	H	1	1	7,7,8	7.79	3 (42%)	6,8,10	34.31	5 (83%)

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
1	AYA	A	1	1	1/1/2/4	0/4/6/8	0/0/0/0
1	AYA	B	1	1	1/1/2/4	0/4/6/8	0/0/0/0
1	AYA	C	1	1	1/1/2/4	1/4/6/8	0/0/0/0
1	AYA	D	1	1	-	0/4/6/8	0/0/0/0
1	AYA	E	1	1	1/1/2/4	0/4/6/8	0/0/0/0
1	AYA	F	1	1	-	0/4/6/8	0/0/0/0
1	AYA	G	1	1	1/1/2/4	0/4/6/8	0/0/0/0
1	AYA	H	1	1	1/1/2/4	0/4/6/8	0/0/0/0

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	1	AYA	O-C	21.47	1.26	1.11
1	A	1	AYA	O-C	20.28	1.25	1.11
1	H	1	AYA	O-C	19.90	1.25	1.11
1	B	1	AYA	O-C	18.73	1.24	1.11
1	E	1	AYA	O-C	17.65	1.23	1.11

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	1	AYA	CB-CA-C	82.08	145.07	108.46
1	E	1	AYA	CB-CA-C	74.66	141.76	108.46
1	F	1	AYA	CB-CA-C	73.69	141.33	108.46
1	C	1	AYA	CB-CA-C	71.46	140.34	108.46
1	B	1	AYA	CB-CA-C	71.18	140.21	108.46

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	G	1	AYA	CA
1	A	1	AYA	CA

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Mol	Chain	Res	Type	Atom
1	C	1	AYA	CA
1	H	1	AYA	CA
1	B	1	AYA	CA

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	1	AYA	OT-CT-N-CA

There are no ring outliers.

## 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, 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	149/149 (100%)	-0.64	2 (1%) 74 73	7, 20, 37, 60	0
1	B	149/149 (100%)	-0.54	0 100 100	11, 24, 37, 46	0
1	C	149/149 (100%)	-0.65	1 (0%) 84 84	7, 22, 34, 57	0
1	D	149/149 (100%)	-0.33	3 (2%) 62 59	11, 26, 44, 66	0
1	E	149/149 (100%)	-0.53	2 (1%) 74 73	8, 23, 47, 61	0
1	F	149/149 (100%)	-0.38	5 (3%) 43 41	9, 26, 44, 63	0
1	G	149/149 (100%)	-0.71	0 100 100	10, 21, 33, 52	0
1	H	149/149 (100%)	-0.42	2 (1%) 74 73	11, 26, 40, 60	0
All	All	1192/1192 (100%)	-0.52	15 (1%) 74 73	7, 24, 43, 66	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	91	THR	6.7
1	A	88	ALA	4.4
1	F	91	THR	4.3
1	D	91	THR	4.0
1	F	89	LEU	3.9

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	AYA	A	1	8/9	0.13	1.14	24,26,31,35	0
1	AYA	C	1	8/9	0.12	0.92	18,23,29,34	0
1	AYA	E	1	8/9	0.11	0.32	12,20,22,22	0
1	AYA	G	1	8/9	0.10	0.19	22,26,31,31	0
1	AYA	B	1	8/9	0.12	0.16	30,33,37,38	0
1	AYA	F	1	8/9	0.10	-0.28	17,23,32,32	0
1	AYA	D	1	8/9	0.11	-0.32	22,28,32,34	0
1	AYA	H	1	8/9	0.08	-0.88	23,25,30,32	0

### 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.