



wwPDB X-ray Structure Validation Summary Report

Jan 31, 2016 – 10:50 PM GMT

PDB ID : 1VBO
Title : Crystal structure of artocarpin-mannotriose complex
Authors : Jeyaprakash, A.A.; Srivastav, A.; Surolia, A.; Vijayan, M.
Deposited on : 2004-02-28
Resolution : 2.35 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

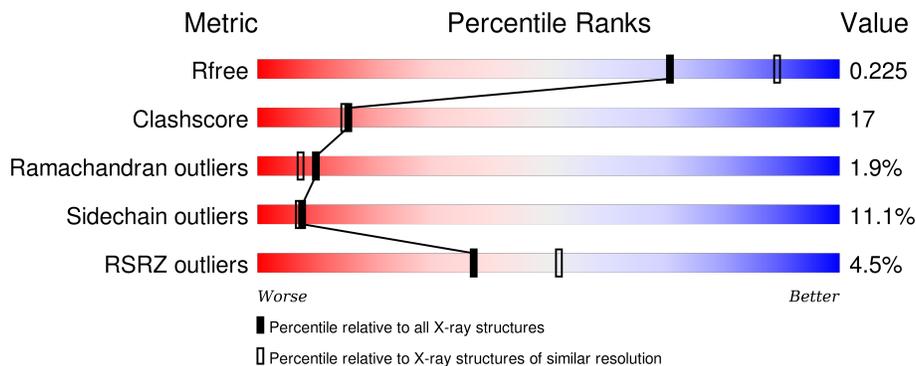
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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}	91344	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	149	 4% 67% 28% 5% •
1	B	149	 9% 70% 24% • •
1	C	149	 3% 74% 20% 5% •
1	D	149	 3% 68% 22% 5% •
1	E	149	 6% 62% 31% 5% •

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Mol	Chain	Length	Quality of chain
1	F	149	
1	G	149	
1	H	149	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	AYA	A	1	X	-	-	-
1	AYA	C	1	X	-	-	-
1	AYA	D	1	X	-	-	-
1	AYA	E	1	X	-	-	-
1	AYA	F	1	X	-	-	-
1	AYA	G	1	X	-	-	-
1	AYA	H	1	X	-	-	-
2	MAN	A	406	X	-	-	-
2	MAN	B	406	X	-	-	-
2	MAN	C	406	X	-	-	-
3	MAN	F	2405	X	-	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9846 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.

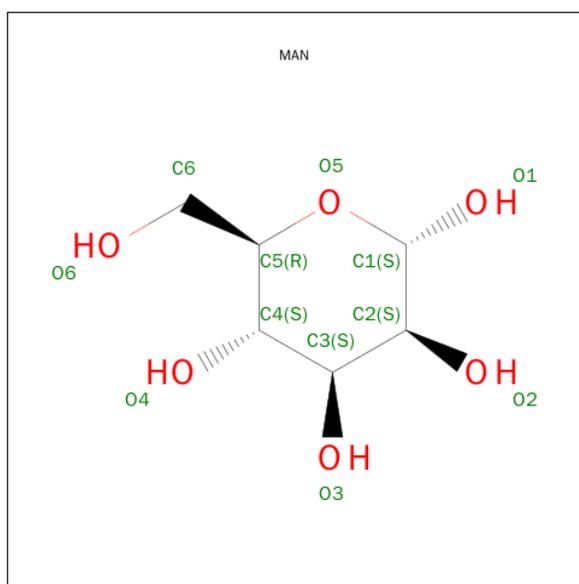
- Molecule 1 is a protein called artocarpin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	149	1141	734	184	222	1	0	0	0
1	B	149	1141	734	184	222	1	0	0	0
1	C	149	1141	734	184	222	1	0	0	0
1	D	149	1141	734	184	222	1	0	0	0
1	E	149	1141	734	184	222	1	0	0	0
1	F	149	1141	734	184	222	1	0	0	0
1	G	149	1141	734	184	222	1	0	0	0
1	H	149	1141	734	184	222	1	0	0	0

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	3	34	18	16	0	0
2	B	3	34	18	16	0	0
2	C	3	34	18	16	0	0
2	E	3	34	18	16	0	0
2	G	3	34	18	16	0	0
2	H	3	34	18	16	0	0

- Molecule 3 is SUGAR (ALPHA-D-MANNOSE) (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total C O 12 6 6	0	0
3	F	1	Total C O 12 6 6	0	0

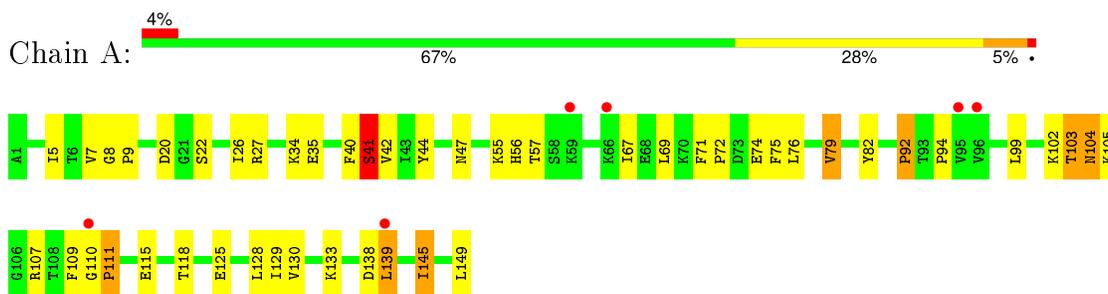
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	59	Total O 59 59	0	0
4	B	60	Total O 60 60	0	0
4	C	75	Total O 75 75	0	0
4	D	74	Total O 74 74	0	0
4	E	36	Total O 36 36	0	0
4	F	51	Total O 51 51	0	0
4	G	73	Total O 73 73	0	0
4	H	62	Total O 62 62	0	0

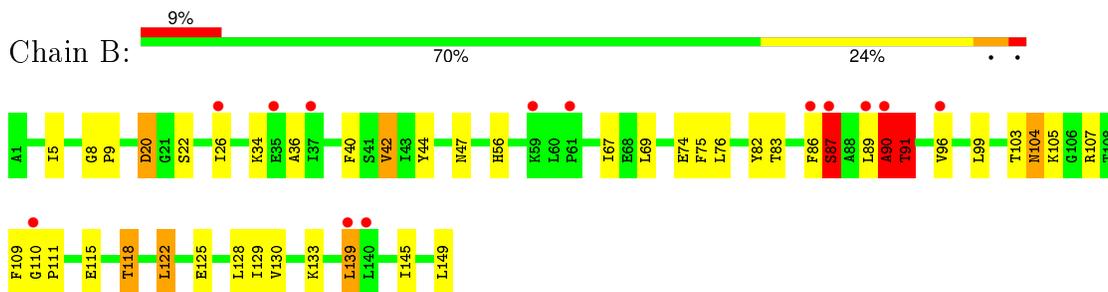
3 Residue-property plots [i](#)

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.

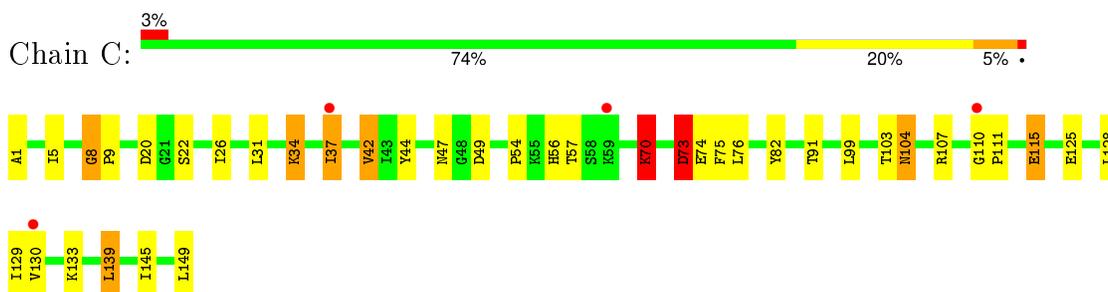
- Molecule 1: artocarpin



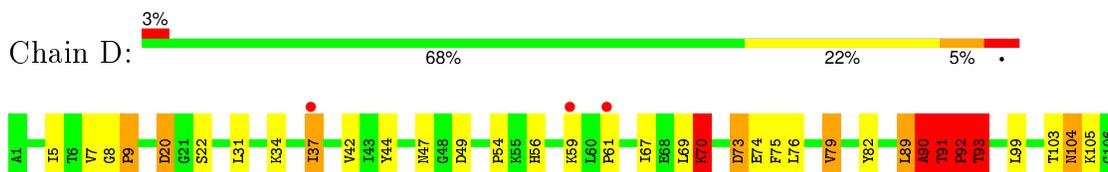
- Molecule 1: artocarpin

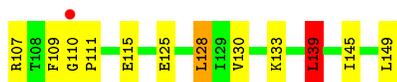


- Molecule 1: artocarpin



- Molecule 1: artocarpin





● Molecule 1: artocarpin



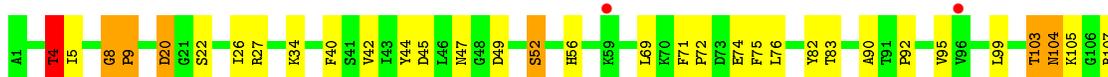
● Molecule 1: artocarpin



● Molecule 1: artocarpin



● Molecule 1: artocarpin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	138.22Å 72.30Å 59.37Å 90.00° 94.48° 90.00°	Depositor
Resolution (Å)	19.85 – 2.35 19.85 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.85-2.35) 99.4 (19.85-2.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.35Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.209 , 0.226 0.221 , 0.225	Depositor DCC
R_{free} test set	2456 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	38.1	Xtrriage
Anisotropy	0.232	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 39.7	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Outliers	3 of 48504 reflections (0.006%)	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9846	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.94 % 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 1.6374e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: AYA, MAN

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	0.68	2/1165 (0.2%)	1.17	8/1580 (0.5%)
1	B	1.09	6/1165 (0.5%)	1.49	21/1580 (1.3%)
1	C	0.71	3/1165 (0.3%)	1.29	16/1580 (1.0%)
1	D	1.12	6/1165 (0.5%)	1.82	29/1580 (1.8%)
1	E	0.87	6/1165 (0.5%)	1.47	25/1580 (1.6%)
1	F	1.03	5/1165 (0.4%)	1.36	20/1580 (1.3%)
1	G	0.70	2/1165 (0.2%)	1.34	14/1580 (0.9%)
1	H	0.76	2/1165 (0.2%)	1.14	10/1580 (0.6%)
All	All	0.89	32/9320 (0.3%)	1.40	143/12640 (1.1%)

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	2	1
1	B	1	3
1	C	1	3
1	D	3	4
1	E	1	5
1	F	1	0
1	G	1	2
1	H	1	0
2	A	1	0
2	B	1	0
2	C	1	0
All	All	14	18

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	91	THR	N-CA	-21.68	1.03	1.46
1	F	8	GLY	C-N	20.97	1.74	1.34
1	D	91	THR	N-CA	-20.40	1.05	1.46
1	H	8	GLY	C-N	17.68	1.67	1.34
1	B	8	GLY	C-N	16.29	1.65	1.34

The worst 5 of 143 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	8	GLY	O-C-N	-26.88	70.02	121.10
1	D	70	LYS	CD-CE-NZ	22.34	163.09	111.70
1	C	110	GLY	C-N-CD	-21.31	73.72	120.60
1	B	110	GLY	C-N-CD	-21.18	74.00	120.60
1	F	110	GLY	C-N-CD	-21.07	74.25	120.60

5 of 14 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	1	AYA	CA
1	A	139	LEU	CA
2	A	406	MAN	C1
1	B	91	THR	CA
2	B	406	MAN	C1

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	27	ARG	Sidechain
1	B	90	ALA	Mainchain,Peptide
1	B	91	THR	Mainchain
1	C	1	AYA	Mainchain
1	C	8	GLY	Mainchain

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	1141	0	1107	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1141	0	1107	51	0
1	C	1141	0	1107	28	0
1	D	1141	0	1105	52	0
1	E	1141	0	1107	50	0
1	F	1141	0	1106	46	0
1	G	1141	0	1107	44	0
1	H	1141	0	1107	40	0
2	A	34	0	30	1	0
2	B	34	0	30	4	0
2	C	34	0	30	0	0
2	E	34	0	30	2	0
2	G	34	0	30	4	0
2	H	34	0	30	3	0
3	D	12	0	12	0	0
3	F	12	0	12	1	0
4	A	59	0	0	6	0
4	B	60	0	0	0	0
4	C	75	0	0	7	0
4	D	74	0	0	5	0
4	E	36	0	0	9	0
4	F	51	0	0	6	0
4	G	73	0	0	4	0
4	H	62	0	0	2	0
All	All	9846	0	9057	317	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 17.

The worst 5 of 317 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:B:91:THR:CA	1:B:91:THR:CB	1.80	1.57
1:D:90:ALA:N	1:D:90:ALA:CA	1.71	1.52
1:B:90:ALA:C	1:B:90:ALA:CA	1.80	1.47
1:H:8:GLY:C	1:H:9:PRO:N	1.67	1.44
1:F:8:GLY:C	1:F:9:PRO:N	1.74	1.39

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	147/149 (99%)	140 (95%)	5 (3%)	2 (1%)	14	12
1	B	147/149 (99%)	139 (95%)	4 (3%)	4 (3%)	6	3
1	C	147/149 (99%)	140 (95%)	5 (3%)	2 (1%)	14	12
1	D	147/149 (99%)	136 (92%)	7 (5%)	4 (3%)	6	3
1	E	147/149 (99%)	137 (93%)	6 (4%)	4 (3%)	6	3
1	F	147/149 (99%)	140 (95%)	5 (3%)	2 (1%)	14	12
1	G	147/149 (99%)	140 (95%)	5 (3%)	2 (1%)	14	12
1	H	147/149 (99%)	140 (95%)	5 (3%)	2 (1%)	14	12
All	All	1176/1192 (99%)	1112 (95%)	42 (4%)	22 (2%)	10	7

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	111	PRO
1	B	87	SER
1	B	111	PRO
1	C	111	PRO
1	D	90	ALA

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	122/122 (100%)	107 (88%)	15 (12%)	6	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	122/122 (100%)	108 (88%)	14 (12%)	7	6
1	C	122/122 (100%)	111 (91%)	11 (9%)	12	12
1	D	122/122 (100%)	108 (88%)	14 (12%)	7	6
1	E	122/122 (100%)	108 (88%)	14 (12%)	7	6
1	F	122/122 (100%)	109 (89%)	13 (11%)	8	8
1	G	122/122 (100%)	110 (90%)	12 (10%)	10	9
1	H	122/122 (100%)	107 (88%)	15 (12%)	6	5
All	All	976/976 (100%)	868 (89%)	108 (11%)	8	7

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	104	ASN
1	E	93	THR
1	H	99	LEU
1	D	130	VAL
1	E	42	VAL

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	D	56	HIS
1	E	47	ASN
1	H	56	HIS
1	D	104	ASN
1	E	56	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](#)

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	6,7,8	0.68	0	7,8,10	6.62	1 (14%)
1	AYA	B	1	1	6,7,8	1.35	1 (16%)	7,8,10	6.54	2 (28%)
1	AYA	C	1	1	6,7,8	0.74	0	7,8,10	7.36	1 (14%)
1	AYA	D	1	1	6,7,8	0.92	0	7,8,10	5.15	1 (14%)
1	AYA	E	1	1	6,7,8	0.83	0	7,8,10	5.93	1 (14%)
1	AYA	F	1	1	6,7,8	0.79	0	7,8,10	6.18	2 (28%)
1	AYA	G	1	1	6,7,8	0.85	0	7,8,10	4.84	1 (14%)
1	AYA	H	1	1	6,7,8	0.62	0	7,8,10	7.59	2 (28%)

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	-	0/4/6/8	0/0/0/0
1	AYA	C	1	1	1/1/2/4	0/4/6/8	0/0/0/0
1	AYA	D	1	1	1/1/2/4	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	1/1/2/4	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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1	AYA	CB-CA	2.48	1.62	1.51

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1	AYA	CB-CA-N	-5.69	102.99	109.61
1	F	1	AYA	CB-CA-N	-2.39	106.83	109.61
1	H	1	AYA	CB-CA-N	-2.07	107.20	109.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	1	AYA	C-CA-N	12.55	137.00	110.64
1	D	1	AYA	C-CA-N	13.35	138.70	110.64

5 of 7 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	H	1	AYA	CA
1	C	1	AYA	CA
1	G	1	AYA	CA
1	A	1	AYA	CA
1	D	1	AYA	CA

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

18 carbohydrates 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
2	MAN	A	405	2	11,11,12	0.56	0	14,15,17	0.59	0
2	MAN	A	406	2	12,12,12	0.66	1 (8%)	17,17,17	1.69	3 (17%)
2	MAN	A	407	2	11,11,12	0.83	0	14,15,17	1.26	1 (7%)
2	MAN	B	405	2	11,11,12	0.55	0	14,15,17	0.59	0
2	MAN	B	406	2	12,12,12	0.39	0	17,17,17	2.15	4 (23%)
2	MAN	B	407	2	11,11,12	0.56	0	14,15,17	3.36	1 (7%)
2	MAN	C	405	2	11,11,12	0.61	0	14,15,17	0.51	0
2	MAN	C	406	2	12,12,12	0.39	0	17,17,17	1.23	2 (11%)
2	MAN	C	407	2	11,11,12	0.58	0	14,15,17	1.88	1 (7%)
2	MAN	E	405	2	11,11,12	0.41	0	14,15,17	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	E	406	2	12,12,12	0.50	0	17,17,17	1.56	3 (17%)
2	MAN	E	407	2	11,11,12	0.41	0	14,15,17	0.75	0
2	MAN	G	405	2	11,11,12	0.55	0	14,15,17	0.68	0
2	MAN	G	406	2	12,12,12	0.55	0	17,17,17	1.28	2 (11%)
2	MAN	G	407	2	11,11,12	0.95	1 (9%)	14,15,17	1.25	2 (14%)
2	MAN	H	405	2	11,11,12	0.59	0	14,15,17	0.69	0
2	MAN	H	406	2	12,12,12	0.52	0	17,17,17	1.48	2 (11%)
2	MAN	H	407	2	11,11,12	1.12	1 (9%)	14,15,17	3.73	3 (21%)

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
2	MAN	A	405	2	-	0/2/19/22	0/1/1/1
2	MAN	A	406	2	1/1/5/5	0/2/22/22	0/1/1/1
2	MAN	A	407	2	-	0/2/19/22	0/1/1/1
2	MAN	B	405	2	-	0/2/19/22	0/1/1/1
2	MAN	B	406	2	1/1/5/5	0/2/22/22	0/1/1/1
2	MAN	B	407	2	-	0/2/19/22	0/1/1/1
2	MAN	C	405	2	-	0/2/19/22	0/1/1/1
2	MAN	C	406	2	1/1/5/5	0/2/22/22	0/1/1/1
2	MAN	C	407	2	-	0/2/19/22	0/1/1/1
2	MAN	E	405	2	-	0/2/19/22	0/1/1/1
2	MAN	E	406	2	-	0/2/22/22	0/1/1/1
2	MAN	E	407	2	-	0/2/19/22	0/1/1/1
2	MAN	G	405	2	-	0/2/19/22	0/1/1/1
2	MAN	G	406	2	-	0/2/22/22	0/1/1/1
2	MAN	G	407	2	-	0/2/19/22	0/1/1/1
2	MAN	H	405	2	-	0/2/19/22	0/1/1/1
2	MAN	H	406	2	-	0/2/22/22	0/1/1/1
2	MAN	H	407	2	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	407	MAN	C6-C5	-2.62	1.42	1.51
2	A	406	MAN	C6-C5	-2.03	1.44	1.51
2	H	407	MAN	C4-C5	2.81	1.59	1.53

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	407	MAN	O5-C5-C6	-7.89	90.27	107.35
2	B	406	MAN	O1-C1-O5	-4.52	97.87	110.25
2	H	407	MAN	C6-C5-C4	-4.52	101.87	113.02
2	A	406	MAN	O1-C1-O5	-4.49	97.97	110.25
2	A	407	MAN	C6-C5-C4	-4.21	102.62	113.02

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	406	MAN	C1
2	C	406	MAN	C1
2	A	406	MAN	C1

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	406	MAN	1	0
2	B	405	MAN	1	0
2	B	406	MAN	3	0
2	E	405	MAN	2	0
2	G	405	MAN	1	0
2	G	406	MAN	1	0
2	G	407	MAN	2	0
2	H	405	MAN	1	0
2	H	406	MAN	2	0
2	H	407	MAN	1	0

5.6 Ligand geometry

2 ligands 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
3	MAN	D	1405	-	12,12,12	0.34	0	17,17,17	0.31	0
3	MAN	F	2405	-	12,12,12	0.38	0	17,17,17	0.34	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	MAN	D	1405	-	-	0/2/22/22	0/1/1/1
3	MAN	F	2405	-	1/1/5/5	0/2/22/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	F	2405	MAN	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	2405	MAN	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, 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	148/149 (99%)	0.22	6 (4%) 41 55	23, 37, 57, 63	0
1	B	148/149 (99%)	0.62	13 (8%) 12 20	21, 45, 77, 88	0
1	C	148/149 (99%)	0.02	4 (2%) 58 70	20, 30, 47, 55	0
1	D	148/149 (99%)	0.06	4 (2%) 58 70	17, 32, 49, 56	0
1	E	148/149 (99%)	0.43	9 (6%) 25 37	26, 44, 63, 68	0
1	F	148/149 (99%)	0.53	10 (6%) 20 31	25, 46, 71, 79	0
1	G	148/149 (99%)	0.14	4 (2%) 58 70	22, 33, 52, 57	0
1	H	148/149 (99%)	-0.02	3 (2%) 68 79	20, 32, 46, 58	0
All	All	1184/1192 (99%)	0.25	53 (4%) 37 52	17, 36, 62, 88	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	59	LYS	4.5
1	F	89	LEU	4.2
1	F	90	ALA	4.1
1	H	59	LYS	4.0
1	A	59	LYS	4.0

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. 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, 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	LLDF	B-factors(\AA^2)	Q<0.9
1	AYA	H	1	8/9	0.95	0.15	-	30,33,35,39	0
1	AYA	C	1	8/9	0.94	0.12	-	29,31,32,34	0
1	AYA	G	1	8/9	0.88	0.17	-	34,36,37,38	0
1	AYA	A	1	8/9	0.92	0.16	-	27,29,33,34	0
1	AYA	B	1	8/9	0.95	0.13	-	27,29,32,32	0
1	AYA	D	1	8/9	0.92	0.17	-	34,34,34,35	0
1	AYA	E	1	8/9	0.94	0.12	-	32,34,34,35	0
1	AYA	F	1	8/9	0.90	0.18	-	33,34,34,34	0

6.3 Carbohydrates [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. 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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	MAN	A	406	12/12	0.82	0.16	0.14	52,58,66,73	0
2	MAN	H	406	12/12	0.88	0.14	0.03	39,42,44,48	0
2	MAN	H	405	11/12	0.93	0.12	-0.10	25,33,35,36	0
2	MAN	E	406	12/12	0.83	0.19	-0.19	63,68,72,75	0
2	MAN	A	405	11/12	0.90	0.13	-0.39	41,44,46,48	0
2	MAN	G	406	12/12	0.86	0.15	-0.48	54,61,69,75	0
2	MAN	G	405	11/12	0.92	0.12	-0.48	39,44,46,48	0
2	MAN	B	405	11/12	0.83	0.19	-0.48	72,75,78,78	0
2	MAN	E	405	11/12	0.88	0.14	-0.74	50,55,59,59	0
2	MAN	C	406	12/12	0.93	0.10	-0.75	36,38,44,47	0
2	MAN	C	405	11/12	0.96	0.09	-0.89	22,28,32,32	0
2	MAN	B	406	12/12	0.78	0.20	-1.12	81,86,91,95	0
2	MAN	H	407	11/12	0.84	0.19	-	49,50,51,51	0
2	MAN	E	407	11/12	0.83	0.33	-	77,78,79,81	0
2	MAN	B	407	11/12	0.65	0.53	-	97,99,100,100	0
2	MAN	G	407	11/12	0.74	0.36	-	80,83,84,84	0
2	MAN	C	407	11/12	0.88	0.26	-	51,53,56,56	0
2	MAN	A	407	11/12	0.78	0.39	-	77,79,83,83	0

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. 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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	MAN	F	2405	12/12	0.78	0.32	1.52	100,100,101,101	0
3	MAN	D	1405	12/12	0.87	0.17	0.45	46,48,49,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.