



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 21, 2023 – 08:38 PM EDT

PDB ID : 2Q3M
Title : Ensemble refinement of the protein crystal structure of an Arabidopsis thaliana putative steroid sulphotransferase
Authors : Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on : 2007-05-30
Resolution : 1.90 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

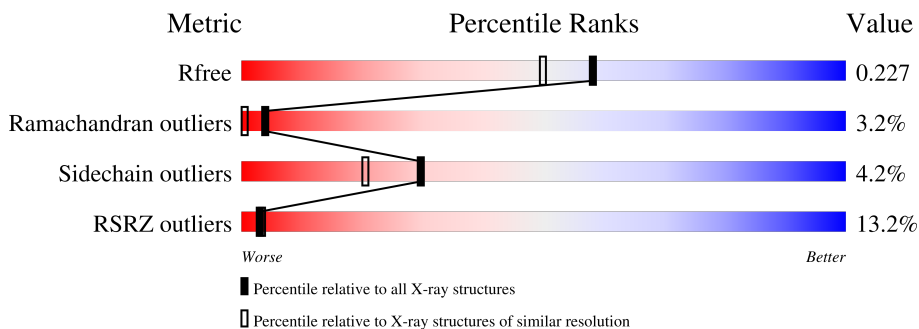
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	1-A	326	
1	10-A	326	
1	11-A	326	
1	12-A	326	
1	13-A	326	
1	14-A	326	
1	15-A	326	

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Mol	Chain	Length	Quality of chain
1	16-A	326	<p>11% 79% 7% 13%</p>
1	2-A	326	<p>11% 81% 6% 13%</p>
1	3-A	326	<p>11% 83% 2% 13%</p>
1	4-A	326	<p>11% 83% 1% 13%</p>
1	5-A	326	<p>11% 81% 6% 13%</p>
1	6-A	326	<p>11% 83% 1% 13%</p>
1	7-A	326	<p>11% 83% 1% 13%</p>
1	8-A	326	<p>11% 85% 1% 13%</p>
1	9-A	326	<p>11% 83% 1% 13%</p>

2 Entry composition

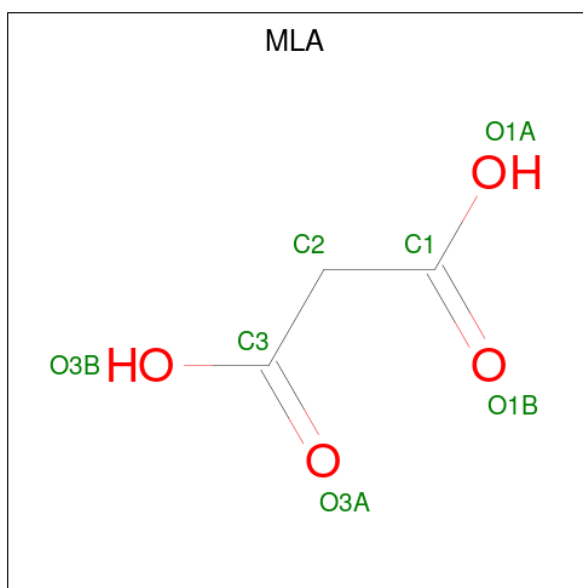
There are 3 unique types of molecules in this entry. The entry contains 40432 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Flavonol sulfotransferase-like.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1-A	284	2306	1496	373	427	10	0	0	0
1	2-A	284	2306	1496	373	427	10	0	0	0
1	3-A	284	2306	1496	373	427	10	0	0	0
1	4-A	284	2306	1496	373	427	10	0	0	0
1	5-A	284	2306	1496	373	427	10	0	0	0
1	6-A	284	2306	1496	373	427	10	0	0	0
1	7-A	284	2306	1496	373	427	10	0	0	0
1	8-A	284	2306	1496	373	427	10	0	0	0
1	9-A	284	2306	1496	373	427	10	0	0	0
1	10-A	284	2306	1496	373	427	10	0	0	0
1	11-A	284	2306	1496	373	427	10	0	0	0
1	12-A	284	2306	1496	373	427	10	0	0	0
1	13-A	284	2306	1496	373	427	10	0	0	0
1	14-A	284	2306	1496	373	427	10	0	0	0
1	15-A	284	2306	1496	373	427	10	0	0	0
1	16-A	284	2306	1496	373	427	10	0	0	0

- Molecule 2 is MALONIC ACID (three-letter code: MLA) (formula: C₃H₄O₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1-A	1	Total C O 7 3 4	0	0
2	2-A	1	Total C O 7 3 4	0	0
2	3-A	1	Total C O 7 3 4	0	0
2	4-A	1	Total C O 7 3 4	0	0
2	5-A	1	Total C O 7 3 4	0	0
2	6-A	1	Total C O 7 3 4	0	0
2	7-A	1	Total C O 7 3 4	0	0
2	8-A	1	Total C O 7 3 4	0	0
2	9-A	1	Total C O 7 3 4	0	0
2	10-A	1	Total C O 7 3 4	0	0
2	11-A	1	Total C O 7 3 4	0	0
2	12-A	1	Total C O 7 3 4	0	0
2	13-A	1	Total C O 7 3 4	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	14-A	1	Total	C	O	0	0
			7	3	4		
2	15-A	1	Total	C	O	0	0
			7	3	4		
2	16-A	1	Total	C	O	0	0
			7	3	4		

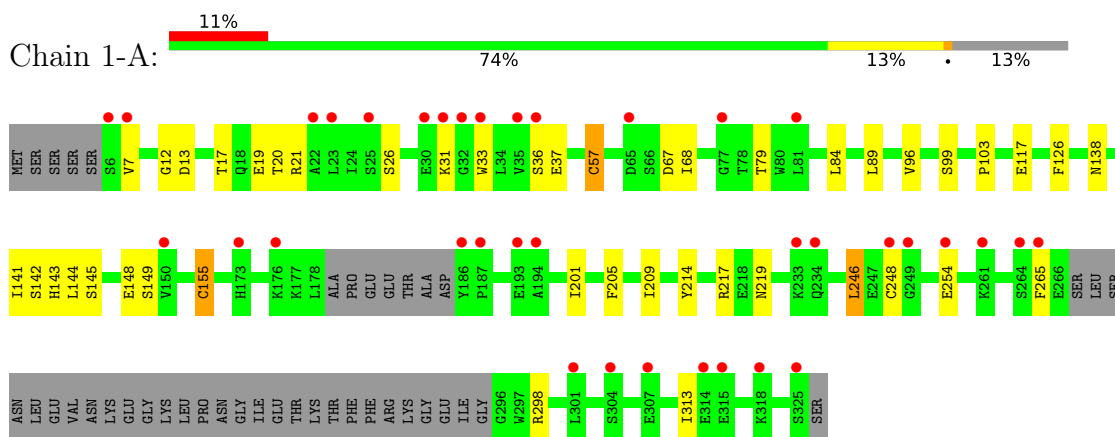
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	1-A	214	Total	O	0	0
			214	214		
3	2-A	214	Total	O	0	0
			214	214		
3	3-A	214	Total	O	0	0
			214	214		
3	4-A	214	Total	O	0	0
			214	214		
3	5-A	214	Total	O	0	0
			214	214		
3	6-A	214	Total	O	0	0
			214	214		
3	7-A	214	Total	O	0	0
			214	214		
3	8-A	214	Total	O	0	0
			214	214		
3	9-A	214	Total	O	0	0
			214	214		
3	10-A	214	Total	O	0	0
			214	214		
3	11-A	214	Total	O	0	0
			214	214		
3	12-A	214	Total	O	0	0
			214	214		
3	13-A	214	Total	O	0	0
			214	214		
3	14-A	214	Total	O	0	0
			214	214		
3	15-A	214	Total	O	0	0
			214	214		
3	16-A	214	Total	O	0	0
			214	214		

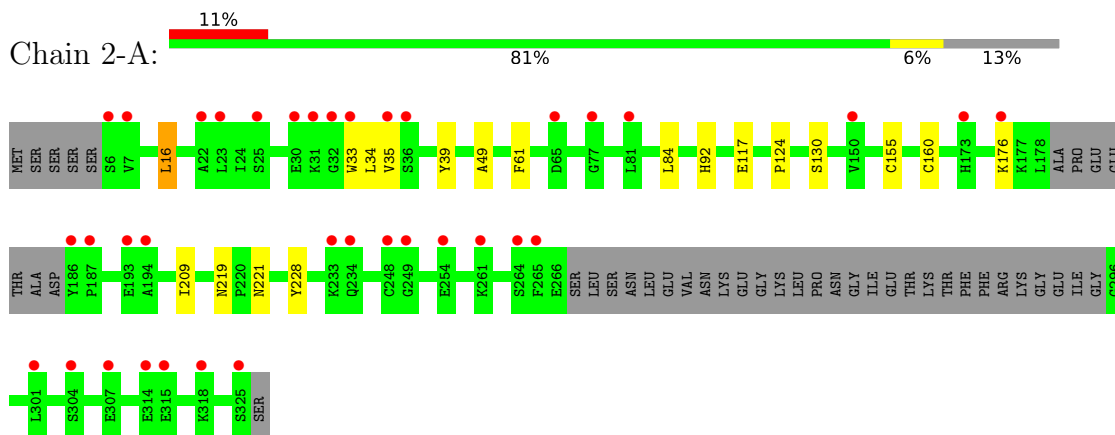
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

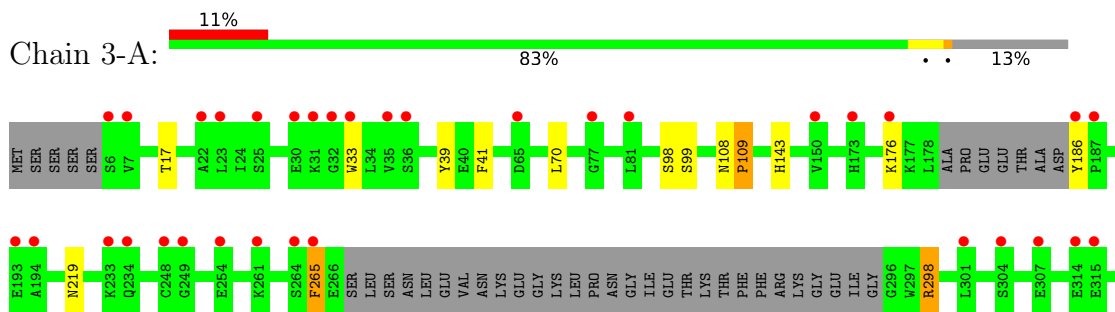
- Molecule 1: Flavonol sulfotransferase-like



- Molecule 1: Flavonol sulfotransferase-like

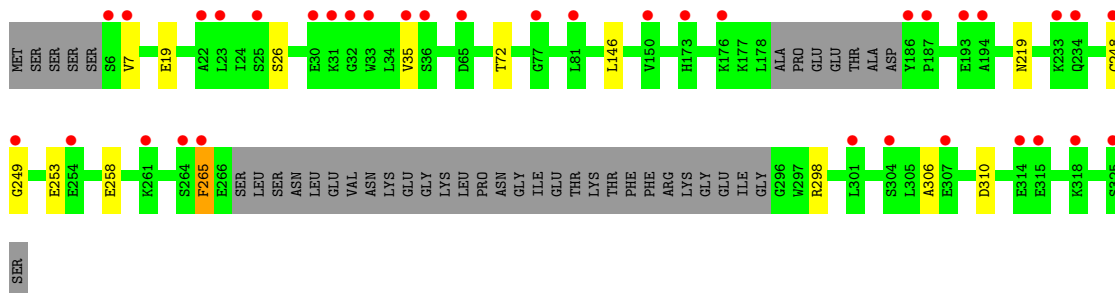
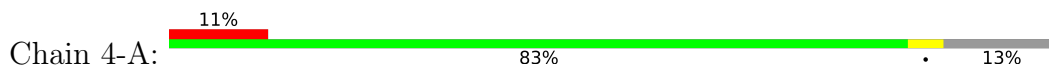


- Molecule 1: Flavonol sulfotransferase-like

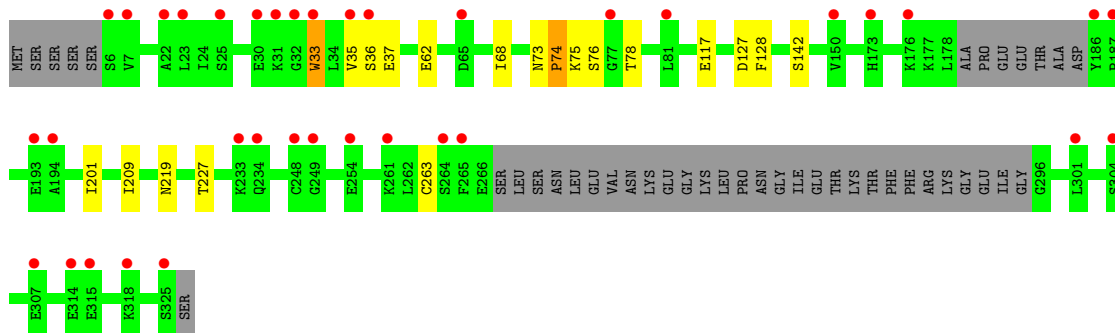
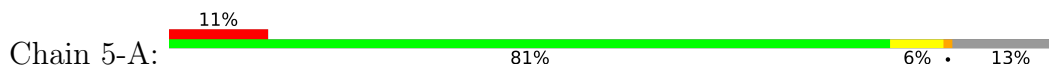




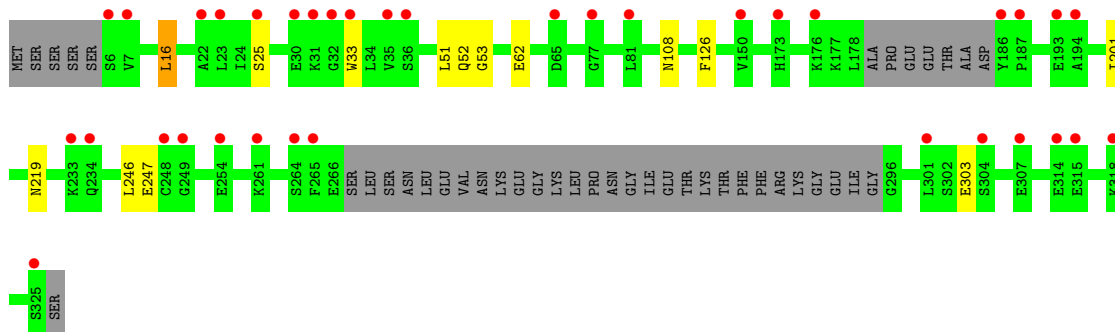
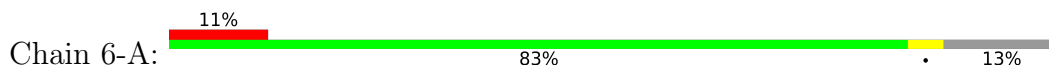
- Molecule 1: Flavonol sulfotransferase-like



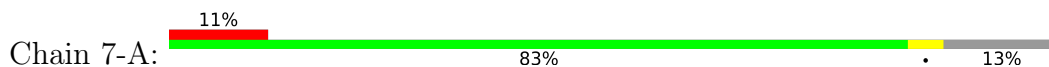
- Molecule 1: Flavonol sulfotransferase-like

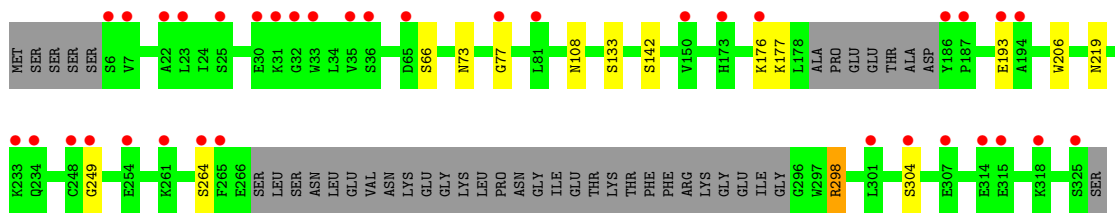


- Molecule 1: Flavonol sulfotransferase-like

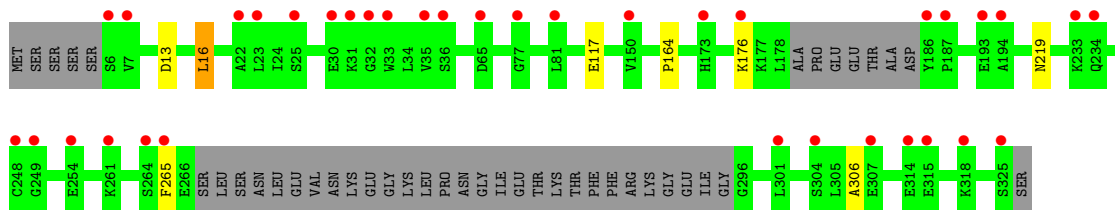
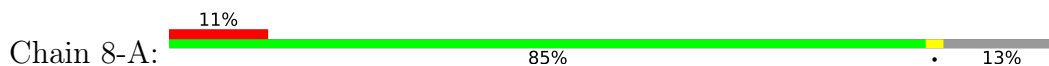


- Molecule 1: Flavonol sulfotransferase-like

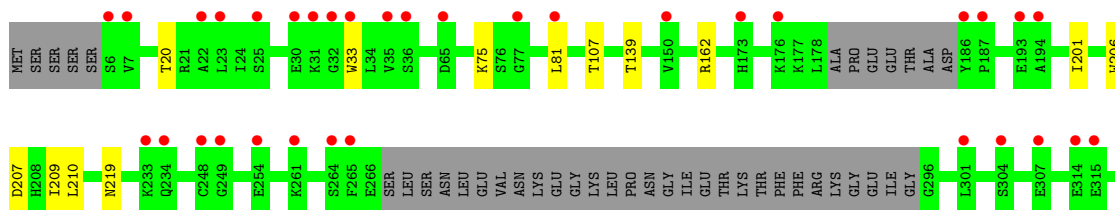
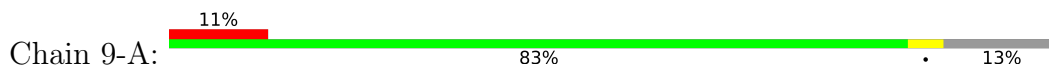




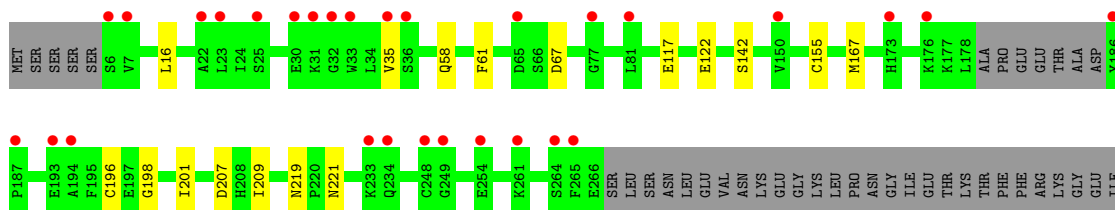
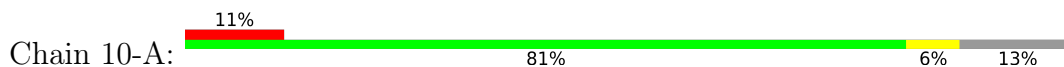
- Molecule 1: Flavonol sulfotransferase-like



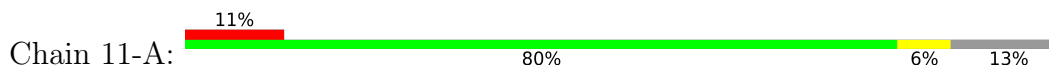
- Molecule 1: Flavonol sulfotransferase-like

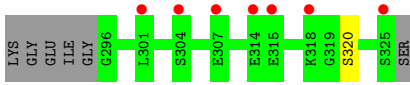


- Molecule 1: Flavonol sulfotransferase-like

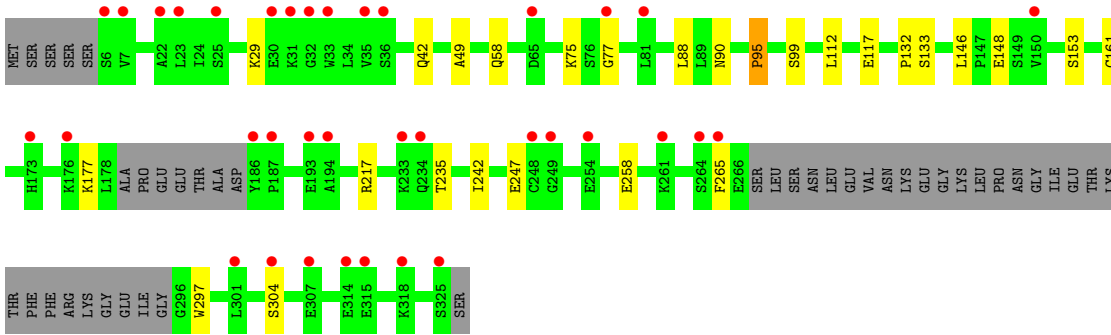
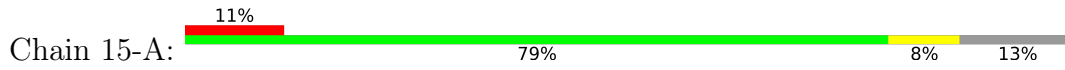


- Molecule 1: Flavonol sulfotransferase-like

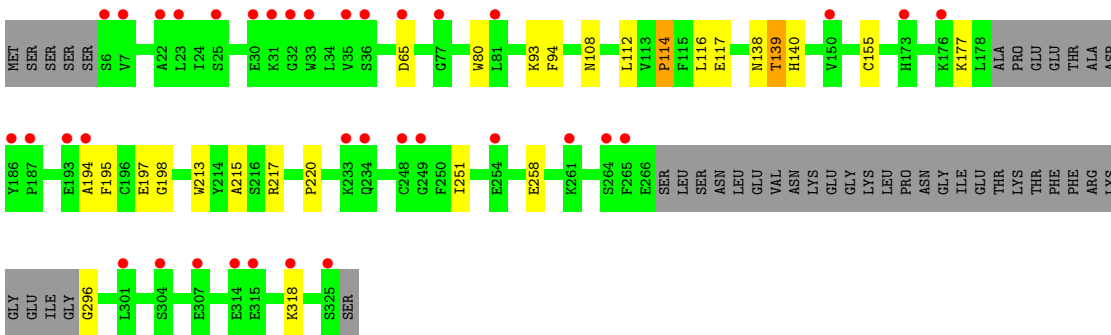
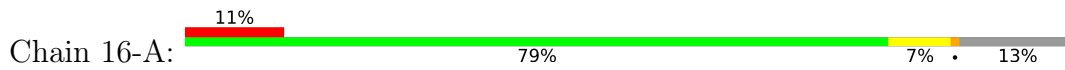




● Molecule 1: Flavonol sulfotransferase-like



● Molecule 1: Flavonol sulfotransferase-like



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	91.48Å 120.90Å 74.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.79 – 1.90 19.79 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.3 (19.79-1.90) 99.3 (19.79-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.42 (at 1.90Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.157 , 0.217 0.169 , 0.227	Depositor DCC
R_{free} test set	1654 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtrriage
Anisotropy	0.121	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 77.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	40432	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.70% 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: MLA

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	1-A	0.80	2/2367 (0.1%)	0.85	2/3201 (0.1%)
1	2-A	0.75	1/2367 (0.0%)	0.79	1/3201 (0.0%)
1	3-A	0.75	0/2367	0.79	0/3201
1	4-A	0.76	0/2367	0.78	0/3201
1	5-A	0.75	0/2367	0.78	1/3201 (0.0%)
1	6-A	0.76	0/2367	0.79	1/3201 (0.0%)
1	7-A	0.72	0/2367	0.76	0/3201
1	8-A	0.74	1/2367 (0.0%)	0.80	1/3201 (0.0%)
1	9-A	0.73	0/2367	0.79	1/3201 (0.0%)
1	10-A	0.77	0/2367	0.84	3/3201 (0.1%)
1	11-A	0.76	0/2367	0.80	2/3201 (0.1%)
1	12-A	0.74	0/2367	0.77	0/3201
1	13-A	0.91	2/2367 (0.1%)	0.97	5/3201 (0.2%)
1	14-A	0.90	0/2367	0.97	4/3201 (0.1%)
1	15-A	0.94	2/2367 (0.1%)	0.96	3/3201 (0.1%)
1	16-A	0.91	1/2367 (0.0%)	0.92	3/3201 (0.1%)
All	All	0.80	9/37872 (0.0%)	0.84	27/51216 (0.1%)

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	1-A	0	1
1	2-A	0	1
1	3-A	0	1
1	12-A	0	1
1	13-A	0	1
All	All	0	5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	15-A	117	GLU	CB-CG	-9.26	1.34	1.52
1	15-A	58	GLN	CG-CD	6.42	1.65	1.51
1	1-A	248	CYS	CB-SG	5.88	1.92	1.82
1	1-A	57	CYS	CB-SG	5.76	1.92	1.82
1	16-A	65	ASP	CB-CG	5.72	1.63	1.51

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	11-A	16	LEU	CA-CB-CG	-7.15	98.86	115.30
1	13-A	16	LEU	CA-CB-CG	-7.13	98.90	115.30
1	16-A	65	ASP	CB-CG-OD1	7.01	124.61	118.30
1	8-A	16	LEU	CA-CB-CG	-6.77	99.74	115.30
1	16-A	94	PHE	N-CA-C	-6.75	92.77	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-A	214	TYR	Sidechain
1	12-A	120	TYR	Sidechain
1	13-A	159	TYR	Sidechain
1	2-A	39	TYR	Sidechain
1	3-A	39	TYR	Sidechain

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	1-A	2306	0	2277	0	0
1	2-A	2306	0	2277	0	0
1	3-A	2306	0	2277	0	0
1	4-A	2306	0	2277	0	0
1	5-A	2306	0	2277	0	0
1	6-A	2306	0	2277	0	0
1	7-A	2306	0	2277	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	8-A	2306	0	2277	0	0
1	9-A	2306	0	2277	0	0
1	10-A	2306	0	2277	0	0
1	11-A	2306	0	2277	0	0
1	12-A	2306	0	2277	0	0
1	13-A	2306	0	2277	0	0
1	14-A	2306	0	2277	0	0
1	15-A	2306	0	2277	0	0
1	16-A	2306	0	2277	0	0
2	1-A	7	0	2	0	0
2	2-A	7	0	2	0	0
2	3-A	7	0	2	0	0
2	4-A	7	0	2	0	0
2	5-A	7	0	2	0	0
2	6-A	7	0	2	0	0
2	7-A	7	0	2	0	0
2	8-A	7	0	2	0	0
2	9-A	7	0	2	0	0
2	10-A	7	0	2	0	0
2	11-A	7	0	3	0	0
2	12-A	7	0	2	0	0
2	13-A	7	0	2	0	0
2	14-A	7	0	2	0	0
2	15-A	7	0	2	0	0
2	16-A	7	0	2	0	0
3	1-A	214	0	0	0	0
3	2-A	214	0	0	0	0
3	3-A	214	0	0	0	0
3	4-A	214	0	0	0	0
3	5-A	214	0	0	0	0
3	6-A	214	0	0	0	0
3	7-A	214	0	0	0	0
3	8-A	214	0	0	0	0
3	9-A	214	0	0	0	0
3	10-A	214	0	0	0	0
3	11-A	214	0	0	0	0
3	12-A	214	0	0	0	0
3	13-A	214	0	0	0	0
3	14-A	214	0	0	0	0
3	15-A	214	0	0	0	0
3	16-A	214	0	0	0	0
All	All	40432	0	36465	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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	1-A	278/326 (85%)	217 (78%)	39 (14%)	22 (8%)	1	0
1	2-A	278/326 (85%)	242 (87%)	26 (9%)	10 (4%)	3	0
1	3-A	278/326 (85%)	253 (91%)	19 (7%)	6 (2%)	6	1
1	4-A	278/326 (85%)	258 (93%)	14 (5%)	6 (2%)	6	1
1	5-A	278/326 (85%)	244 (88%)	25 (9%)	9 (3%)	4	0
1	6-A	278/326 (85%)	256 (92%)	15 (5%)	7 (2%)	5	1
1	7-A	278/326 (85%)	252 (91%)	17 (6%)	9 (3%)	4	0
1	8-A	278/326 (85%)	263 (95%)	14 (5%)	1 (0%)	34	24
1	9-A	278/326 (85%)	245 (88%)	28 (10%)	5 (2%)	8	2
1	10-A	278/326 (85%)	239 (86%)	33 (12%)	6 (2%)	6	1
1	11-A	278/326 (85%)	239 (86%)	26 (9%)	13 (5%)	2	0
1	12-A	278/326 (85%)	253 (91%)	19 (7%)	6 (2%)	6	1
1	13-A	278/326 (85%)	238 (86%)	25 (9%)	15 (5%)	2	0
1	14-A	278/326 (85%)	240 (86%)	32 (12%)	6 (2%)	6	1
1	15-A	278/326 (85%)	236 (85%)	34 (12%)	8 (3%)	4	1
1	16-A	278/326 (85%)	240 (86%)	24 (9%)	14 (5%)	2	0
All	All	4448/5216 (85%)	3915 (88%)	390 (9%)	143 (3%)	4	0

5 of 143 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	13	ASP
1	1-A	33	TRP
1	1-A	67	ASP
1	1-A	79	THR
1	1-A	84	LEU

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	1-A	258/294 (88%)	237 (92%)	21 (8%)	11	4
1	2-A	258/294 (88%)	251 (97%)	7 (3%)	44	38
1	3-A	258/294 (88%)	247 (96%)	11 (4%)	29	19
1	4-A	258/294 (88%)	248 (96%)	10 (4%)	32	23
1	5-A	258/294 (88%)	246 (95%)	12 (5%)	26	16
1	6-A	258/294 (88%)	251 (97%)	7 (3%)	44	38
1	7-A	258/294 (88%)	251 (97%)	7 (3%)	44	38
1	8-A	258/294 (88%)	252 (98%)	6 (2%)	50	45
1	9-A	258/294 (88%)	251 (97%)	7 (3%)	44	38
1	10-A	258/294 (88%)	247 (96%)	11 (4%)	29	19
1	11-A	258/294 (88%)	250 (97%)	8 (3%)	40	32
1	12-A	258/294 (88%)	252 (98%)	6 (2%)	50	45
1	13-A	258/294 (88%)	241 (93%)	17 (7%)	16	8
1	14-A	258/294 (88%)	242 (94%)	16 (6%)	18	9
1	15-A	258/294 (88%)	243 (94%)	15 (6%)	20	10
1	16-A	258/294 (88%)	247 (96%)	11 (4%)	29	19
All	All	4128/4704 (88%)	3956 (96%)	172 (4%)	30	20

5 of 172 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	13-A	30	GLU

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Mol	Chain	Res	Type
1	14-A	200	PHE
1	13-A	117	GLU
1	14-A	19	GLU
1	15-A	112	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
1	9-A	221	ASN
1	11-A	138	ASN
1	15-A	234	GLN
1	10-A	52	GLN
1	10-A	143	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

16 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
2	MLA	16-A	901	-	6,6,6	1.92	2 (33%)	7,7,7	1.52	1 (14%)
2	MLA	10-A	901	-	6,6,6	1.33	1 (16%)	7,7,7	1.23	1 (14%)
2	MLA	6-A	901	-	6,6,6	0.94	0	7,7,7	1.35	1 (14%)
2	MLA	9-A	901	-	6,6,6	0.93	0	7,7,7	1.22	1 (14%)
2	MLA	8-A	901	-	6,6,6	1.33	1 (16%)	7,7,7	1.29	1 (14%)
2	MLA	15-A	901	-	6,6,6	0.90	0	7,7,7	1.01	0
2	MLA	12-A	901	-	6,6,6	1.18	1 (16%)	7,7,7	1.02	0
2	MLA	1-A	901	-	6,6,6	0.84	0	7,7,7	1.15	0
2	MLA	5-A	901	-	6,6,6	1.07	1 (16%)	7,7,7	1.22	0
2	MLA	4-A	901	-	6,6,6	1.66	1 (16%)	7,7,7	1.32	1 (14%)
2	MLA	3-A	901	-	6,6,6	1.33	1 (16%)	7,7,7	1.32	1 (14%)
2	MLA	13-A	901	-	6,6,6	1.60	1 (16%)	7,7,7	1.29	1 (14%)
2	MLA	11-A	901	-	6,6,6	1.77	2 (33%)	7,7,7	1.42	1 (14%)
2	MLA	7-A	901	-	6,6,6	0.91	0	7,7,7	1.09	0
2	MLA	2-A	901	-	6,6,6	1.08	1 (16%)	7,7,7	1.23	0
2	MLA	14-A	901	-	6,6,6	1.39	1 (16%)	7,7,7	1.52	1 (14%)

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	MLA	16-A	901	-	-	0/4/4/4	-
2	MLA	10-A	901	-	-	0/4/4/4	-
2	MLA	6-A	901	-	-	0/4/4/4	-
2	MLA	9-A	901	-	-	0/4/4/4	-
2	MLA	8-A	901	-	-	0/4/4/4	-
2	MLA	15-A	901	-	-	0/4/4/4	-
2	MLA	12-A	901	-	-	0/4/4/4	-
2	MLA	1-A	901	-	-	0/4/4/4	-
2	MLA	5-A	901	-	-	0/4/4/4	-
2	MLA	4-A	901	-	-	0/4/4/4	-
2	MLA	3-A	901	-	-	0/4/4/4	-
2	MLA	13-A	901	-	-	0/4/4/4	-
2	MLA	11-A	901	-	-	0/4/4/4	-
2	MLA	7-A	901	-	-	0/4/4/4	-
2	MLA	2-A	901	-	-	0/4/4/4	-
2	MLA	14-A	901	-	-	0/4/4/4	-

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	16-A	901	MLA	C2-C3	3.74	1.56	1.51
2	13-A	901	MLA	C2-C1	3.70	1.56	1.51
2	11-A	901	MLA	C2-C3	3.06	1.55	1.51
2	8-A	901	MLA	C2-C1	2.89	1.55	1.51
2	4-A	901	MLA	C2-C1	2.84	1.55	1.51

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	16-A	901	MLA	O1A-C1-O1B	-2.37	117.39	123.30
2	14-A	901	MLA	O1A-C1-O1B	-2.27	117.65	123.30
2	6-A	901	MLA	O1A-C1-O1B	-2.26	117.66	123.30
2	11-A	901	MLA	O3B-C3-O3A	-2.24	117.73	123.30
2	13-A	901	MLA	O1A-C1-O1B	-2.20	117.81	123.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	1-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	2-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	3-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	4-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	5-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	6-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	7-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	8-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	9-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	10-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	11-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	12-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	13-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	14-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	15-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
1	16-A	284/326 (87%)	0.74	36 (12%) 3 4	12, 25, 50, 67	284 (100%)
All	All	4544/5216 (87%)	0.74	576 (12%) 3 4	12, 25, 50, 67	4544 (100%)

The worst 5 of 576 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-A	33	TRP	14.9
1	2-A	33	TRP	14.9
1	3-A	33	TRP	14.9
1	4-A	33	TRP	14.9
1	5-A	33	TRP	14.9

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
2	MLA	1-A	901	7/7	0.95	0.14	0,10,27,29	7
2	MLA	2-A	901	7/7	0.95	0.14	15,20,25,27	7
2	MLA	3-A	901	7/7	0.95	0.14	15,21,27,30	7
2	MLA	4-A	901	7/7	0.95	0.14	17,20,25,28	7
2	MLA	5-A	901	7/7	0.95	0.14	22,25,25,28	7
2	MLA	6-A	901	7/7	0.95	0.14	19,24,24,28	7
2	MLA	7-A	901	7/7	0.95	0.14	20,23,25,26	7
2	MLA	8-A	901	7/7	0.95	0.14	22,24,25,27	7
2	MLA	9-A	901	7/7	0.95	0.14	23,26,27,28	7
2	MLA	10-A	901	7/7	0.95	0.14	0,11,25,28	7
2	MLA	11-A	901	7/7	0.95	0.14	2,10,19,22	7
2	MLA	12-A	901	7/7	0.95	0.14	0,11,29,31	7
2	MLA	13-A	901	7/7	0.95	0.14	17,21,22,24	7
2	MLA	14-A	901	7/7	0.95	0.14	8,15,24,27	7
2	MLA	15-A	901	7/7	0.95	0.14	20,21,25,25	7
2	MLA	16-A	901	7/7	0.95	0.14	12,18,24,26	7

6.5 Other polymers [i](#)

There are no such residues in this entry.