



wwPDB X-ray Structure Validation Summary Report (i)

Feb 27, 2014 – 05:17 AM GMT

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 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/ValidationPDFNotes.html>

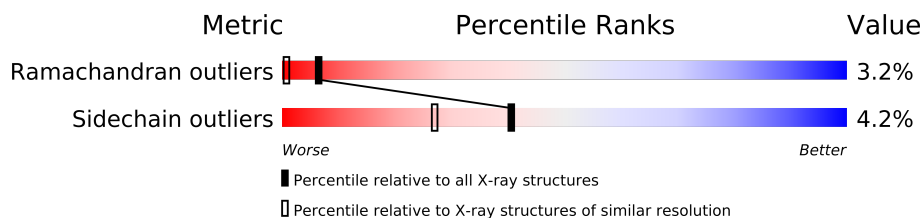
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : **FAILED**
Percentile statistics : 21963
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 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))
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 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.

Note EDS failed to run properly.

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	
1	16-A	326	
1	2-A	326	
1	3-A	326	
1	4-A	326	
1	5-A	326	
1	6-A	326	
1	7-A	326	
1	8-A	326	
1	9-A	326	

2 Entry composition

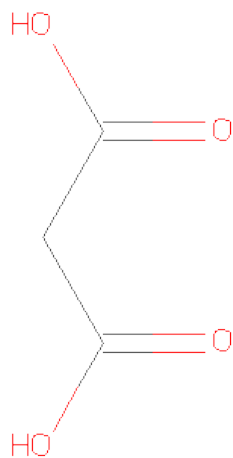
There are 3 unique types of molecules in this entry. The entry contains 40432 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Flavonol sulfotransferase-like.

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

- Molecule 2 is MALONIC ACID (three-letter code: MLA) (formula: $C_3H_4O_4$).



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

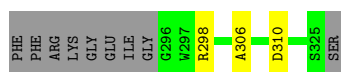
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	14-A	1	Total	C	O	0	0
			7	3	4		
2	15-A	1	Total	C	O	0	0
			7	3	4		
2	16-A	1	Total	C	O	0	0
			7	3	4		

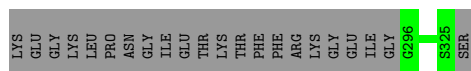
- Molecule 3 is water.

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		



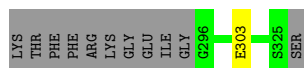
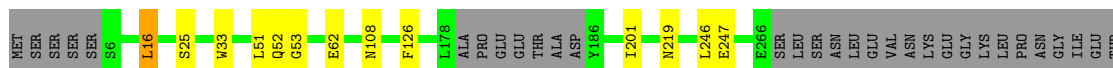
- Molecule 1: Flavonol sulfotransferase-like

Chain 5-A:



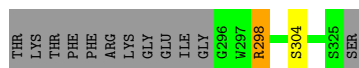
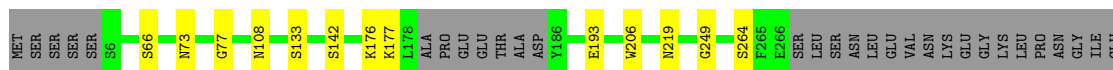
- Molecule 1: Flavonol sulfotransferase-like

Chain 6-A:



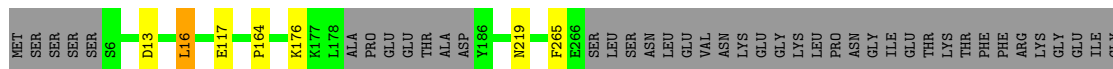
- Molecule 1: Flavonol sulfotransferase-like

Chain 7-A:



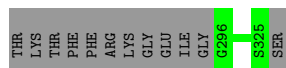
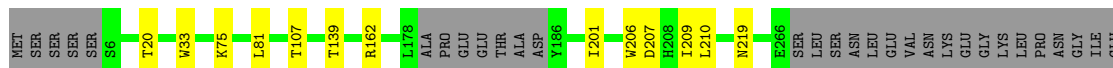
- Molecule 1: Flavonol sulfotransferase-like

Chain 8-A:



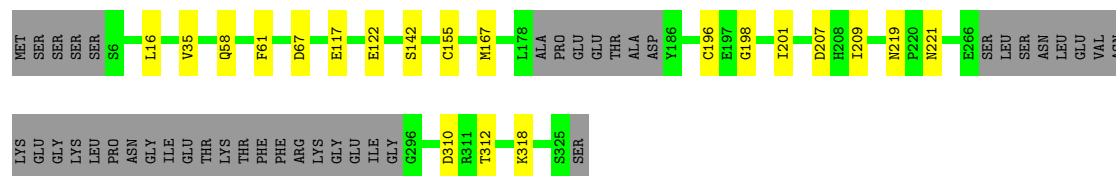
- Molecule 1: Flavonol sulfotransferase-like

Chain 9-A:



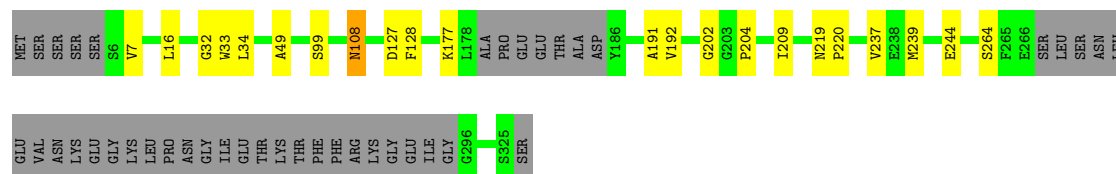
- Molecule 1: Flavonol sulfotransferase-like

Chain 10-A:



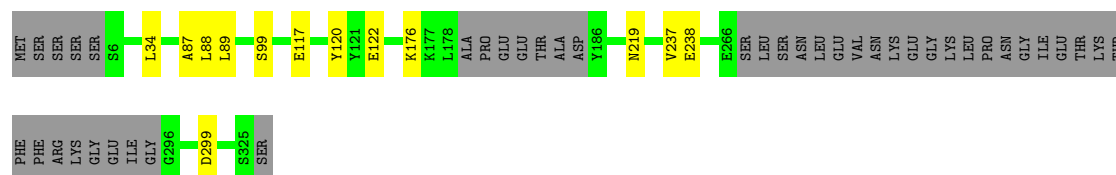
- Molecule 1: Flavonol sulfotransferase-like

Chain 11-A:



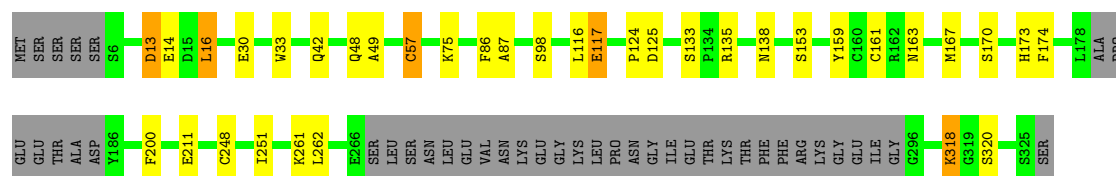
- Molecule 1: Flavonol sulfotransferase-like

Chain 12-A:



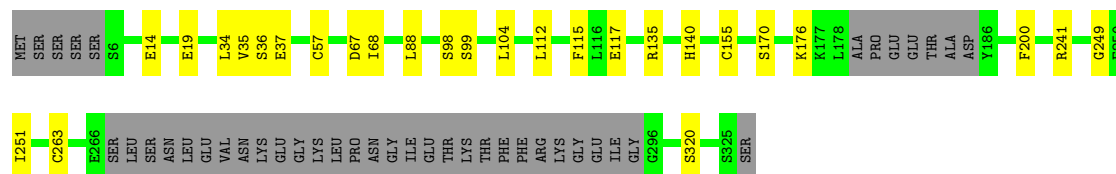
- Molecule 1: Flavonol sulfotransferase-like

Chain 13-A:



- Molecule 1: Flavonol sulfotransferase-like

Chain 14-A:



- Molecule 1: Flavonol sulfotransferase-like

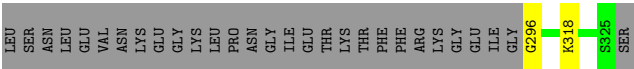
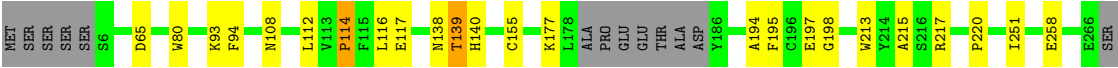
Chain 15-A:





● Molecule 1: Flavonol sulfotransferase-like

Chain 16-A:



4 Data and refinement statistics

EDS failed to run properly - this section will therefore be incomplete.

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	Depositor
% Data completeness (in resolution range)	99.3 (19.79-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.42 (at 1.90Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.157 , 0.217	Depositor
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.121	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 32629 reflections	Xtriage
Total number of atoms	40432	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage'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.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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 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	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	6-A	2306	0	2277	0	0
1	7-A	2306	0	2277	0	0
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	1
1	14-A	2306	0	2277	0	1
1	15-A	2306	0	2277	0	1
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	1
3	14-A	214	0	0	0	1
3	15-A	214	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	16-A	214	0	0	0	0
All	All	40432	0	36465	0	3

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

All (3) 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	Distance(Å)	Clash(Å)
1:A:218:GLU:OE2	3:A:1095:HOH:O[6_654]	1.97	0.23
1:A:14:GLU:OE2	3:A:1086:HOH:O[3_655]	2.04	0.16
1:A:125:ASP:OD2	3:A:980:HOH:O[3_655]	2.16	0.04

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	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%)	5	0
1	3-A	278/326 (85%)	253 (91%)	19 (7%)	6 (2%)	10	2
1	4-A	278/326 (85%)	258 (93%)	14 (5%)	6 (2%)	10	2
1	5-A	278/326 (85%)	244 (88%)	25 (9%)	9 (3%)	6	1
1	6-A	278/326 (85%)	256 (92%)	15 (5%)	7 (2%)	9	1
1	7-A	278/326 (85%)	252 (91%)	17 (6%)	9 (3%)	6	1
1	8-A	278/326 (85%)	263 (95%)	14 (5%)	1 (0%)	43	29
1	9-A	278/326 (85%)	245 (88%)	28 (10%)	5 (2%)	13	3
1	10-A	278/326 (85%)	239 (86%)	33 (12%)	6 (2%)	10	2
1	11-A	278/326 (85%)	239 (86%)	26 (9%)	13 (5%)	4	0
1	12-A	278/326 (85%)	253 (91%)	19 (7%)	6 (2%)	10	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	13-A	278/326 (85%)	238 (86%)	25 (9%)	15 (5%)	3	0
1	14-A	278/326 (85%)	240 (86%)	32 (12%)	6 (2%)	10	2
1	15-A	278/326 (85%)	236 (85%)	34 (12%)	8 (3%)	7	1
1	16-A	278/326 (85%)	240 (86%)	24 (9%)	14 (5%)	3	0
All	All	4448/5216 (85%)	3915 (88%)	390 (9%)	143 (3%)	6	1

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 ⓘ

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%)	17	6
1	2-A	258/294 (88%)	251 (97%)	7 (3%)	57	47
1	3-A	258/294 (88%)	247 (96%)	11 (4%)	40	26
1	4-A	258/294 (88%)	248 (96%)	10 (4%)	43	30
1	5-A	258/294 (88%)	246 (95%)	12 (5%)	36	22
1	6-A	258/294 (88%)	251 (97%)	7 (3%)	57	47
1	7-A	258/294 (88%)	251 (97%)	7 (3%)	57	47
1	8-A	258/294 (88%)	252 (98%)	6 (2%)	63	55
1	9-A	258/294 (88%)	251 (97%)	7 (3%)	57	47
1	10-A	258/294 (88%)	247 (96%)	11 (4%)	40	26
1	11-A	258/294 (88%)	250 (97%)	8 (3%)	52	41
1	12-A	258/294 (88%)	252 (98%)	6 (2%)	63	55
1	13-A	258/294 (88%)	241 (93%)	17 (7%)	24	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	14-A	258/294 (88%)	242 (94%)	16 (6%)	26	12
1	15-A	258/294 (88%)	243 (94%)	15 (6%)	28	15
1	16-A	258/294 (88%)	247 (96%)	11 (4%)	40	26
All	All	4128/4704 (88%)	3956 (96%)	172 (4%)	40	27

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

Mol	Chain	Res	Type
1	8-A	164	PRO
1	10-A	221	ASN
1	15-A	265	PHE
1	8-A	265	PHE
1	9-A	219	ASN

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

Mol	Chain	Res	Type
1	8-A	110	HIS
1	10-A	52	GLN
1	15-A	140	HIS
1	8-A	219	ASN
1	9-A	110	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

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	1-A	901	-	6,6,6	0.88	0	7,7,7	1.06	0
2	MLA	10-A	901	-	6,6,6	1.36	1 (16%)	7,7,7	1.18	1 (14%)
2	MLA	11-A	901	-	6,6,6	1.76	2 (33%)	7,7,7	1.30	1 (14%)
2	MLA	12-A	901	-	6,6,6	1.18	1 (16%)	7,7,7	1.03	0
2	MLA	13-A	901	-	6,6,6	1.66	1 (16%)	7,7,7	1.28	1 (14%)
2	MLA	14-A	901	-	6,6,6	1.43	1 (16%)	7,7,7	1.41	1 (14%)
2	MLA	15-A	901	-	6,6,6	0.92	0	7,7,7	0.93	0
2	MLA	16-A	901	-	6,6,6	1.97	2 (33%)	7,7,7	1.51	1 (14%)
2	MLA	2-A	901	-	6,6,6	1.12	1 (16%)	7,7,7	1.31	1 (14%)
2	MLA	3-A	901	-	6,6,6	1.38	1 (16%)	7,7,7	1.27	1 (14%)
2	MLA	4-A	901	-	6,6,6	1.65	1 (16%)	7,7,7	1.21	0
2	MLA	5-A	901	-	6,6,6	1.11	1 (16%)	7,7,7	1.23	0
2	MLA	6-A	901	-	6,6,6	0.98	0	7,7,7	1.30	1 (14%)
2	MLA	7-A	901	-	6,6,6	0.94	0	7,7,7	1.12	0
2	MLA	8-A	901	-	6,6,6	1.38	1 (16%)	7,7,7	1.27	0
2	MLA	9-A	901	-	6,6,6	0.96	0	7,7,7	1.22	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
2	MLA	1-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	10-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	11-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	12-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	13-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	14-A	901	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MLA	15-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	16-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	2-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	3-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	4-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	5-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	6-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	7-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	8-A	901	-	-	0/4/4/4	0/0/0/0
2	MLA	9-A	901	-	-	0/4/4/4	0/0/0/0

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	3.87	1.56	1.51
2	13-A	901	MLA	C2-C1	3.84	1.56	1.51
2	11-A	901	MLA	C2-C3	3.18	1.55	1.51
2	8-A	901	MLA	C2-C1	3.00	1.55	1.51
2	4-A	901	MLA	C2-C1	2.95	1.55	1.51

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	16-A	901	MLA	O1A-C1-O1B	-2.32	117.39	123.30
2	2-A	901	MLA	C3-C2-C1	2.32	119.11	112.77
2	14-A	901	MLA	O1A-C1-O1B	-2.22	117.65	123.30
2	6-A	901	MLA	O1A-C1-O1B	-2.22	117.66	123.30
2	11-A	901	MLA	O3B-C3-O3A	-2.19	117.73	123.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

EDS failed to run properly - this section will therefore be empty.

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

EDS failed to run properly - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS failed to run properly - this section will therefore be empty.

6.4 Ligands ⓘ

EDS failed to run properly - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS failed to run properly - this section will therefore be empty.