



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 10:16 am BST

PDB ID : 4YZG  
Title : Structure of the Arabidopsis TAP38/PPH1, a state-transition phosphatase responsible for dephosphorylation of LHCII  
Authors : Wei, X.P.; Guo, J.T.; Li, M.; Liu, Z.F.  
Deposited on : 2015-03-25  
Resolution : 1.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

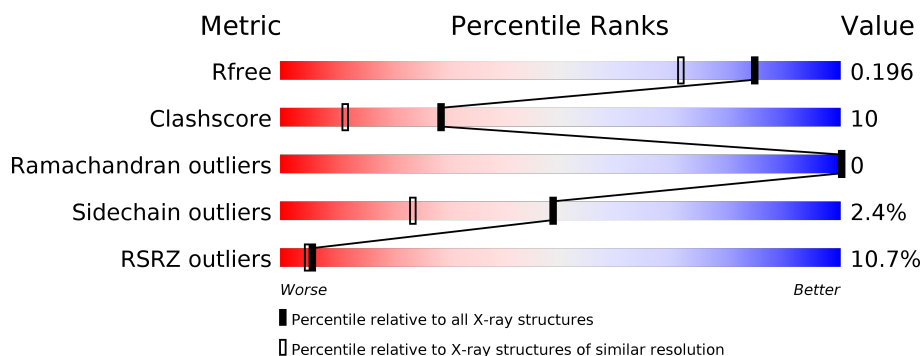
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	302	<div> <div>10%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>..</div> </div> </div>
1	B	302	<div> <div>11%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5177 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 Protein phosphatase 2C 57.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	1	0
			2294	1435	400	448	11			
1	B	294	Total	C	N	O	S	0	1	0
			2295	1436	400	449	10			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	58	MET	-	expression tag	UNP P49599
A	352	LEU	-	expression tag	UNP P49599
A	353	GLU	-	expression tag	UNP P49599
A	354	HIS	-	expression tag	UNP P49599
A	355	HIS	-	expression tag	UNP P49599
A	356	HIS	-	expression tag	UNP P49599
A	357	HIS	-	expression tag	UNP P49599
A	358	HIS	-	expression tag	UNP P49599
A	359	HIS	-	expression tag	UNP P49599
B	58	MET	-	expression tag	UNP P49599
B	352	LEU	-	expression tag	UNP P49599
B	353	GLU	-	expression tag	UNP P49599
B	354	HIS	-	expression tag	UNP P49599
B	355	HIS	-	expression tag	UNP P49599
B	356	HIS	-	expression tag	UNP P49599
B	357	HIS	-	expression tag	UNP P49599
B	358	HIS	-	expression tag	UNP P49599
B	359	HIS	-	expression tag	UNP P49599

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Mn	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

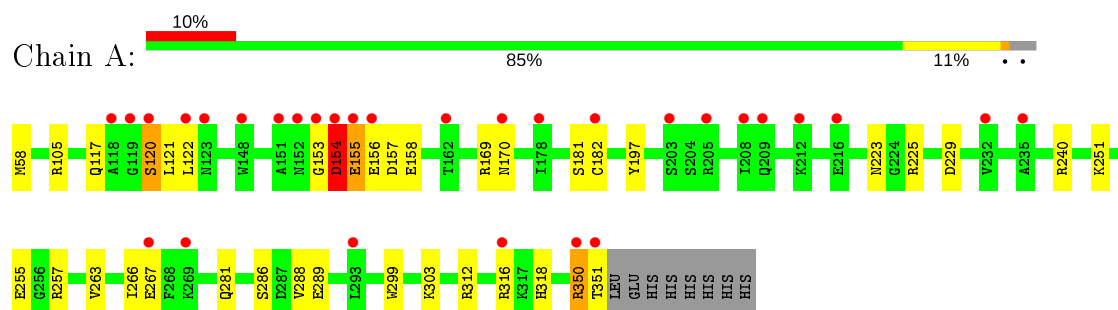
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	313	Total	O	0	0
			313	313		
4	B	261	Total	O	0	0
			261	261		

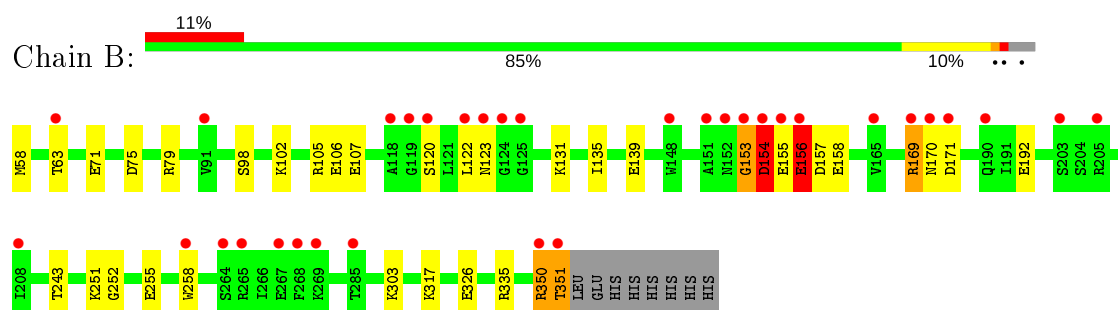
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Protein phosphatase 2C 57



- Molecule 1: Protein phosphatase 2C 57



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.40 Å 73.88 Å 82.00 Å 90.00° 109.15° 90.00°	Depositor
Resolution (Å)	26.73 – 1.60 26.73 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.3 (26.73-1.60) 98.3 (26.73-1.60)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.73 (at 1.60 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.180 , 0.203 0.174 , 0.196	Depositor DCC
$R_{free}$ test set	4063 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.4	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 53.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.049 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5177	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, SO4

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	0.72	0/2333	0.82	3/3142 (0.1%)
1	B	0.65	0/2334	0.72	4/3144 (0.1%)
All	All	0.68	0/4667	0.77	7/6286 (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	A	0	2
1	B	0	3
All	All	0	5

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	155	GLU	N-CA-CB	17.37	141.87	110.60
1	B	350	ARG	CB-CA-C	-8.99	92.41	110.40
1	B	79	ARG	O-C-N	-8.48	109.13	122.70
1	B	153	GLY	N-CA-C	7.88	132.79	113.10
1	A	154	ASP	N-CA-C	6.99	129.88	111.00
1	B	79	ARG	CA-C-N	5.91	130.21	117.20
1	A	155	GLU	N-CA-C	-5.81	95.32	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	153	GLY	Peptide
1	A	154	ASP	Peptide
1	B	154	ASP	Peptide
1	B	156	GLU	Peptide
1	B	169	ARG	Peptide

## 5.2 Too-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 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	2294	0	2253	47	0
1	B	2295	0	2255	40	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	313	0	0	16	4
4	B	261	0	0	14	2
All	All	5177	0	4508	88	4

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 10.

All (88) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:GLU:CG	1:A:156:GLU:HA	1.50	1.38
1:B:350:ARG:O	1:B:351:THR:CG2	1.75	1.35
1:B:156:GLU:HB3	1:B:158:GLU:HG3	1.26	1.18
1:A:156:GLU:O	1:A:156:GLU:HG3	1.55	1.06
1:A:155:GLU:HG3	1:A:156:GLU:CA	1.87	1.05
1:B:350:ARG:O	1:B:351:THR:HG23	0.87	1.04
1:B:156:GLU:HB3	1:B:158:GLU:CG	1.86	1.04
1:B:106:GLU:HG2	1:B:107:GLU:N	1.74	1.00
1:B:350:ARG:C	1:B:351:THR:HG23	1.83	0.99
1:A:105:ARG:NH2	4:A:501:HOH:O	1.96	0.98
1:A:182[B]:CYS:SG	1:A:197:TYR:CE1	2.56	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:GLU:CG	1:A:156:GLU:CA	2.40	0.97
1:A:155:GLU:HG3	1:A:156:GLU:HA	0.94	0.92
1:B:156:GLU:CB	1:B:158:GLU:HG3	2.01	0.90
1:A:281:GLN:NE2	4:A:503:HOH:O	2.03	0.89
1:A:105:ARG:NH2	4:A:504:HOH:O	2.07	0.87
1:B:335:ARG:NH2	4:B:502:HOH:O	2.07	0.86
1:A:182[A]:CYS:SG	4:A:783:HOH:O	1.97	0.85
1:A:181:SER:C	4:A:502:HOH:O	2.16	0.83
1:A:182[A]:CYS:SG	4:A:763:HOH:O	2.38	0.81
1:B:131:LYS:HD2	4:B:506:HOH:O	1.79	0.81
1:A:156:GLU:O	1:A:156:GLU:CG	2.29	0.79
1:A:251:LYS:NZ	1:A:255:GLU:OE2	2.13	0.79
1:B:131:LYS:CD	4:B:506:HOH:O	2.30	0.78
1:B:75:ASP:OD2	1:B:105:ARG:NH1	2.17	0.78
1:B:139:GLU:OE2	4:B:501:HOH:O	2.03	0.76
1:B:131:LYS:NZ	4:B:506:HOH:O	2.18	0.76
1:B:106:GLU:HG2	1:B:107:GLU:H	1.53	0.73
1:B:123:ASN:OD1	4:B:503:HOH:O	2.10	0.69
1:A:155:GLU:HG2	1:A:156:GLU:HA	1.67	0.67
1:A:154:ASP:OD1	1:A:154:ASP:C	2.34	0.65
1:B:106:GLU:OE2	4:B:505:HOH:O	2.13	0.65
1:B:350:ARG:O	4:B:504:HOH:O	2.13	0.65
1:B:350:ARG:C	1:B:351:THR:CG2	2.49	0.64
1:B:303:LYS:HG3	4:B:716:HOH:O	1.97	0.64
1:B:154:ASP:OD1	1:B:154:ASP:N	2.30	0.63
1:B:123:ASN:ND2	1:B:169:ARG:HH21	1.98	0.62
1:B:156:GLU:HB3	1:B:158:GLU:HG2	1.81	0.61
1:A:181:SER:CB	4:A:502:HOH:O	2.47	0.61
1:A:289:GLU:HA	1:A:350:ARG:HG3	1.82	0.61
1:A:182[B]:CYS:SG	1:A:197:TYR:CZ	2.95	0.60
1:A:182[B]:CYS:SG	1:A:197:TYR:HE1	2.20	0.59
1:B:106:GLU:CG	1:B:107:GLU:N	2.60	0.58
1:A:155:GLU:HG2	1:A:156:GLU:CA	2.29	0.57
1:B:170:ASN:N	4:B:511:HOH:O	2.39	0.56
1:A:117:GLN:HG3	4:A:673:HOH:O	2.06	0.56
1:A:316:ARG:HD2	4:A:512:HOH:O	2.05	0.55
1:A:318:HIS:O	4:A:505:HOH:O	2.18	0.54
1:B:98:SER:O	1:B:102:LYS:HG3	2.08	0.53
1:B:155:GLU:HA	1:B:157:ASP:H	1.73	0.53
1:B:192:GLU:OE2	4:B:507:HOH:O	2.19	0.52
1:A:182[B]:CYS:HB2	1:A:299:TRP:NE1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:ARG:HG3	1:A:105:ARG:HH11	1.73	0.51
1:A:154:ASP:OD1	1:A:155:GLU:HA	2.10	0.51
1:B:155:GLU:HA	1:B:157:ASP:N	2.26	0.51
1:A:225:ARG:NH1	4:A:506:HOH:O	2.20	0.50
1:A:286:SER:O	1:A:350:ARG:HD3	2.11	0.49
1:A:154:ASP:OD1	1:A:154:ASP:O	2.30	0.49
1:A:288:VAL:O	1:A:350:ARG:HD2	2.11	0.49
1:A:117:GLN:NE2	4:A:515:HOH:O	2.45	0.49
1:B:171:ASP:N	1:B:171:ASP:OD1	2.29	0.49
1:A:223:ASN:HD22	1:A:223:ASN:N	2.11	0.48
1:B:123:ASN:N	1:B:123:ASN:OD1	2.46	0.48
1:A:225:ARG:NH1	1:A:229:ASP:O	2.47	0.47
1:A:121:LEU:HA	1:A:121:LEU:HD23	1.56	0.47
1:A:105:ARG:NH1	1:A:105:ARG:HG3	2.30	0.46
1:B:139:GLU:CD	4:B:501:HOH:O	2.50	0.46
1:A:154:ASP:O	1:A:157:ASP:N	2.48	0.46
1:A:154:ASP:O	1:A:157:ASP:HB2	2.16	0.46
1:A:303:LYS:HB3	1:A:303:LYS:HE3	1.62	0.45
1:B:135:ILE:O	1:B:139:GLU:HG3	2.16	0.45
1:A:312:ARG:HG3	4:A:637:HOH:O	2.15	0.45
1:A:263:VAL:HA	1:A:266:ILE:HD12	1.99	0.44
1:B:63[B]:THR:HG21	1:B:326:GLU:HA	2.00	0.44
1:A:267:GLU:O	1:A:267:GLU:HG3	2.18	0.43
1:A:182[B]:CYS:HB2	1:A:299:TRP:CE2	2.52	0.43
1:A:158:GLU:HB3	1:A:240:ARG:NH1	2.34	0.42
1:B:153:GLY:O	1:B:154:ASP:C	2.57	0.42
1:A:257:ARG:HD3	4:A:508:HOH:O	2.19	0.42
1:B:122:LEU:HA	1:B:122:LEU:HD23	1.62	0.42
1:B:252:GLY:HA3	1:B:258:TRP:CE3	2.54	0.42
1:B:170:ASN:HB2	4:B:511:HOH:O	2.20	0.42
1:B:243:THR:HG22	4:B:649:HOH:O	2.19	0.41
1:A:225:ARG:NH2	4:A:506:HOH:O	2.53	0.41
1:A:120:SER:C	1:A:122:LEU:N	2.69	0.41
1:B:251:LYS:NZ	1:B:255:GLU:OE2	2.37	0.41
1:B:317:LYS:HE3	1:B:317:LYS:HB2	1.84	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:651:HOH:O	4:B:520:HOH:O[1_454]	1.84	0.36

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:545:HOH:O	4:B:516:HOH:O[1_454]	1.95	0.25
4:A:667:HOH:O	4:A:787:HOH:O[2_858]	1.99	0.21
4:A:527:HOH:O	4:A:699:HOH:O[2_848]	2.14	0.06

## 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	293/302 (97%)	287 (98%)	6 (2%)	0	100	100
1	B	293/302 (97%)	287 (98%)	6 (2%)	0	100	100
All	All	586/604 (97%)	574 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	246/253 (97%)	240 (98%)	6 (2%)	49	24
1	B	246/253 (97%)	240 (98%)	6 (2%)	49	24
All	All	492/506 (97%)	480 (98%)	12 (2%)	49	24

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	MET
1	A	120	SER
1	A	169	ARG
1	A	170	ASN
1	A	350	ARG
1	A	351	THR
1	B	58	MET
1	B	71	GLU
1	B	120	SER
1	B	154	ASP
1	B	156	GLU
1	B	351	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	223	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	SO4	B	403	-	4,4,4	0.17	0	6,6,6	0.14	0
3	SO4	A	403	-	4,4,4	0.19	0	6,6,6	0.20	0

There are no bond length outliers.

There are no bond angle outliers.

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 ⓘ

### 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	294/302 (97%)	0.48	30 (10%)	6 5	11, 24, 64, 146	1 (0%)
1	B	294/302 (97%)	0.61	33 (11%)	5 4	13, 30, 59, 128	1 (0%)
All	All	588/604 (97%)	0.54	63 (10%)	6 5	11, 27, 63, 146	2 (0%)

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	351	THR	10.4
1	A	208	ILE	6.2
1	A	182[A]	CYS	6.0
1	A	156	GLU	5.7
1	B	123	ASN	5.6
1	B	124	GLY	5.4
1	B	156	GLU	5.3
1	B	119	GLY	5.2
1	B	120	SER	5.1
1	A	154	ASP	5.0
1	B	350	ARG	5.0
1	A	120	SER	4.7
1	A	153	GLY	4.6
1	B	118	ALA	4.6
1	B	154	ASP	4.4
1	A	119	GLY	4.2
1	B	153	GLY	4.1
1	A	351	THR	4.0
1	A	155	GLU	3.8
1	B	170	ASN	3.8
1	B	171	ASP	3.5
1	B	264	SER	3.5
1	B	285	THR	3.4
1	B	63[A]	THR	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	155	GLU	3.4
1	B	267	GLU	3.4
1	A	123	ASN	3.3
1	B	125	GLY	2.9
1	A	316	ARG	2.9
1	B	152	ASN	2.9
1	A	148	TRP	2.9
1	B	203	SER	2.9
1	A	232	VAL	2.9
1	B	258	TRP	2.8
1	A	216	GLU	2.8
1	B	190	GLN	2.8
1	A	152	ASN	2.8
1	B	205	ARG	2.8
1	B	169	ARG	2.7
1	A	205	ARG	2.6
1	A	170	ASN	2.6
1	B	151	ALA	2.6
1	B	122	LEU	2.6
1	A	350	ARG	2.6
1	B	265	ARG	2.5
1	A	293	LEU	2.4
1	B	268	PHE	2.3
1	B	91	VAL	2.3
1	A	269	LYS	2.2
1	A	212	LYS	2.2
1	B	148	TRP	2.1
1	A	267	GLU	2.1
1	A	118	ALA	2.1
1	A	151	ALA	2.1
1	A	162	THR	2.1
1	B	165	VAL	2.1
1	A	209	GLN	2.1
1	A	178	ILE	2.1
1	A	235	ALA	2.0
1	A	122	LEU	2.0
1	B	208	ILE	2.0
1	A	203	SER	2.0
1	B	269	LYS	2.0



## 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 carbohydrates 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, 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	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	B	403	5/5	0.94	0.08	38,46,63,64	0
3	SO4	A	403	5/5	0.94	0.10	29,35,49,54	0
2	MN	A	401	1/1	1.00	0.06	16,16,16,16	0
2	MN	A	402	1/1	1.00	0.07	13,13,13,13	0
2	MN	B	401	1/1	1.00	0.06	14,14,14,14	0
2	MN	B	402	1/1	1.00	0.03	17,17,17,17	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.