



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 12:02 AM BST

PDB ID : 6TWX  
Title : MAGI1\_2 complexed with a phosphorylated 16E6 peptide  
Authors : Gogl, G.; Cousido-Siah, A.; Trave, G.  
Deposited on : 2020-01-13  
Resolution : 2.30 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 : 2.13.1  
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) : 2.13.1

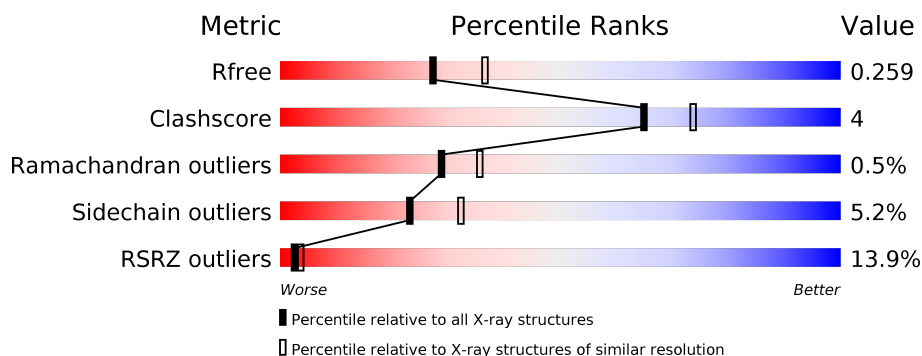
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	427	<div> <div>20%</div> <div>85%</div> <div>12%</div> <div>..</div> </div>
1	B	427	<div> <div>7%</div> <div>83%</div> <div>15%</div> <div>..</div> </div>
2	C	10	<div> <div>30%</div> <div>10%</div> <div>60%</div> </div>
2	D	10	<div> <div>20%</div> <div>20%</div> <div>10%</div> <div>70%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	TPO	D	156	-	-	-	X
4	CIT	B	903	-	-	-	X
5	CA	A	903	-	-	-	X
5	CA	B	907	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6920 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 Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1,Annexin A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	1	0
			3319	2088	568	649	14			
1	B	421	Total	C	N	O	S	0	1	0
			3326	2091	571	650	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	452	GLY	-	expression tag	UNP Q96QZ7
A	453	SER	-	expression tag	UNP Q96QZ7
A	454	MET	-	expression tag	UNP Q96QZ7
A	559	GLY	-	linker	UNP Q96QZ7
A	560	SER	-	linker	UNP Q96QZ7
A	605	GLU	ALA	conflict	UNP P07355
B	452	GLY	-	expression tag	UNP Q96QZ7
B	453	SER	-	expression tag	UNP Q96QZ7
B	454	MET	-	expression tag	UNP Q96QZ7
B	559	GLY	-	linker	UNP Q96QZ7
B	560	SER	-	linker	UNP Q96QZ7
B	605	GLU	ALA	conflict	UNP P07355

- Molecule 2 is a protein called 16E6 peptide.

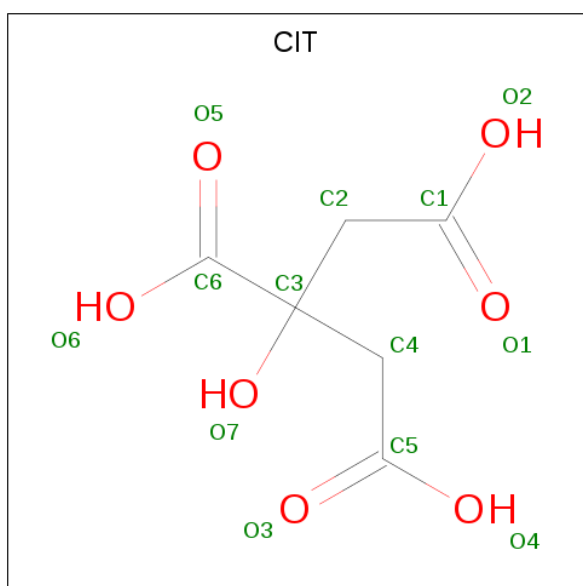
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	P	0	0	0
			38	20	5	12	1			
2	D	3	Total	C	N	O	P	0	0	0
			29	15	4	9	1			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula:  $C_6H_8O_7$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	6	7		
4	B	1	Total	C	O	0	0
			13	6	7		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	6	Total	Ca	0	0
			6	6		
5	A	5	Total	Ca	0	0
			5	5		

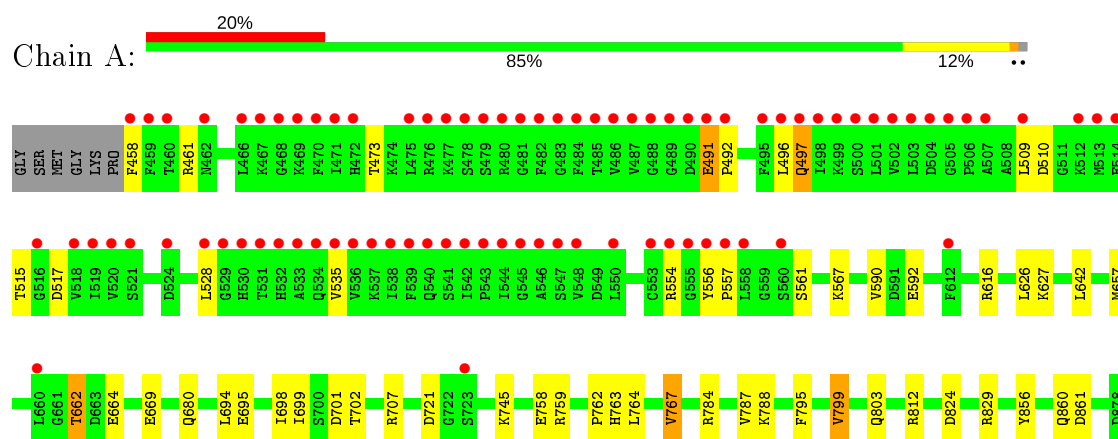
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	68	Total	O	0	0
			68	68		
6	B	78	Total	O	0	0
			78	78		

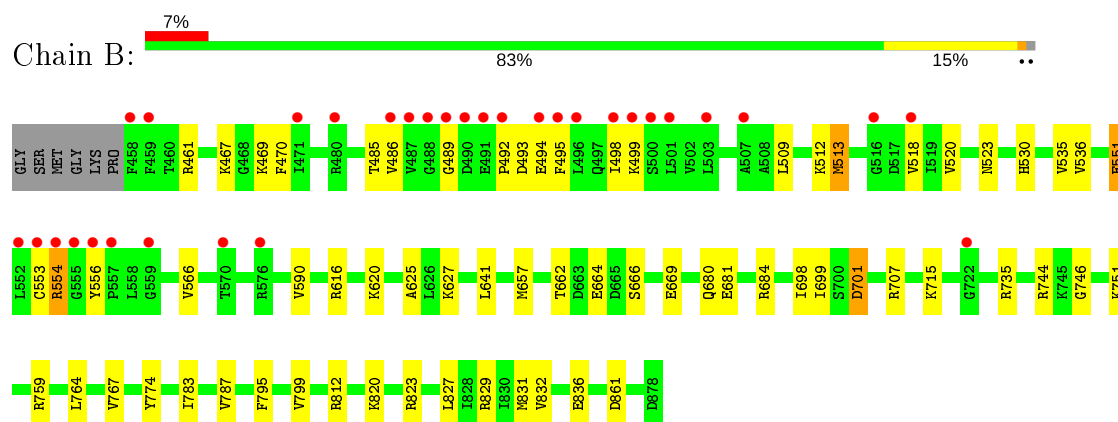
### 3 Residue-property plots

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.

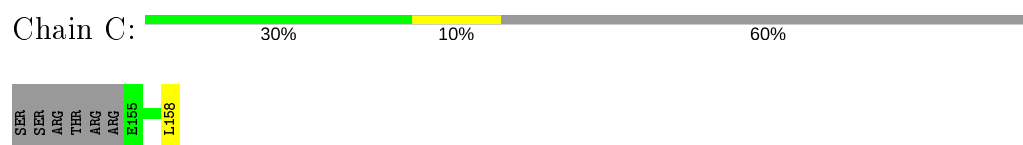
- Molecule 1: Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1,Annexin A2



- Molecule 1: Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1,Annexin A2



- Molecule 2: 16E6 peptide



- Molecule 2: 16E6 peptide



SER	SER	ARG	THR	ARG	ARG	GLU	TI156	Q157	L158



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.47Å 96.55Å 198.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.91 – 2.30 46.91 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.91-2.30) 98.8 (46.91-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.14_3260, PHENIX 1.14_3260	Depositor
R, $R_{free}$	0.209 , 0.259 0.209 , 0.259	Depositor DCC
$R_{free}$ test set	2560 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.9	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 51.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6920	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.63% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, GOL, CA, CIT

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	0.29	0/3369	0.45	0/4534
1	B	0.31	0/3376	0.46	0/4542
2	C	0.20	0/25	0.34	0/29
2	D	0.19	0/17	0.33	0/20
All	All	0.30	0/6787	0.45	0/9125

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	3319	0	3309	26	0
1	B	3326	0	3323	29	0
2	C	38	0	30	1	0
2	D	29	0	26	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
4	A	13	0	5	1	0
4	B	26	0	10	1	0
5	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	6	0	0	0	0
6	A	68	0	0	1	0
6	B	78	0	0	3	0
All	All	6920	0	6719	55	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 4.

All (55) 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:520:VAL:HB	1:B:551:GLU:HG2	1.68	0.76
1:A:657:MET:HE1	1:A:698:ILE:HA	1.68	0.76
1:B:795:PHE:O	1:B:799:VAL:HG12	1.93	0.68
1:B:518:VAL:HB	1:B:553:CYS:HB3	1.74	0.68
1:A:561:SER:O	1:A:567:LYS:NZ	2.24	0.67
1:B:662:THR:HG21	1:B:701:ASP:HB3	1.76	0.67
1:B:512:LYS:O	1:B:554:ARG:NH1	2.28	0.64
1:B:812:ARG:NH2	6:B:1005:HOH:O	2.29	0.64
1:B:681:GLU:OE2	1:B:684:ARG:NH2	2.27	0.63
1:B:566:VAL:HG23	1:B:836:GLU:HG3	1.80	0.63
1:B:669:GLU:OE2	1:B:812:ARG:NH1	2.32	0.63
1:B:783:ILE:HD13	1:B:795:PHE:HB3	1.82	0.62
1:A:824:ASP:OD2	4:A:902:CIT:O7	2.22	0.58
4:B:903:CIT:O2	4:B:903:CIT:O7	2.23	0.57
1:B:536:VAL:HG22	2:C:158:LEU:HD21	1.88	0.56
1:B:735:ARG:HG3	1:B:774:TYR:CE1	2.43	0.54
1:A:626:LEU:HD12	1:A:642:LEU:HD11	1.90	0.54
1:A:662:THR:HG21	1:A:701:ASP:HB3	1.90	0.53
1:B:657:MET:HE1	1:B:698:ILE:HA	1.89	0.53
1:A:491:GLU:HG3	1:A:492:PRO:HD2	1.90	0.53
1:B:620:LYS:HE3	1:B:625:ALA:HB2	1.89	0.52
1:A:473:THR:OG1	1:A:510:ASP:OD2	2.23	0.52
1:A:461:ARG:HA	1:A:528:LEU:HB3	1.91	0.52
1:B:489:GLY:H	1:B:494:GLU:HG3	1.75	0.52
1:A:657:MET:HE3	1:A:698:ILE:HG12	1.91	0.52
1:A:803:GLN:NE2	6:A:1005:HOH:O	2.43	0.50
1:A:795:PHE:O	1:A:799:VAL:HG13	2.11	0.49
1:A:758:GLU:OE1	1:B:751:LYS:NZ	2.44	0.49
1:B:827:LEU:O	1:B:831:MET:HG2	2.14	0.48
1:A:694:LEU:O	1:A:698:ILE:HG13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:695:GLU:O	1:A:699:ILE:HG12	2.15	0.46
1:B:823:ARG:NH1	6:B:1018:HOH:O	2.49	0.46
1:A:497:GLN:HA	1:A:517:ASP:O	2.17	0.45
1:B:469:LYS:O	1:B:553:CYS:HA	2.17	0.45
1:B:498:ILE:HG13	1:B:513:MET:SD	2.56	0.45
1:A:763:HIS:O	1:A:767:VAL:HG13	2.18	0.43
1:B:744:ARG:HH21	1:B:746:GLY:HA3	1.82	0.43
1:A:721:ASP:CG	1:A:762:PRO:HG2	2.38	0.43
1:A:759:ARG:HB2	1:A:764:LEU:HG	2.01	0.43
1:B:666:SER:OG	1:B:829:ARG:NH2	2.51	0.43
1:A:787:VAL:O	1:A:788:LYS:NZ	2.43	0.43
1:B:820:LYS:O	1:B:823:ARG:NH2	2.42	0.42
1:B:715:LYS:NZ	6:B:1019:HOH:O	2.51	0.42
1:B:469:LYS:N	1:B:554:ARG:O	2.30	0.42
1:B:759:ARG:HB2	1:B:764:LEU:HG	2.01	0.42
1:B:470:PHE:HE1	1:B:520:VAL:HG21	1.85	0.42
1:A:702:THR:OG1	1:A:707:ARG:HG3	2.20	0.42
1:B:641:LEU:HD23	1:B:832:VAL:HG13	2.00	0.42
1:A:458:PHE:HD2	1:A:556:TYR:HE1	1.66	0.42
1:A:496:LEU:HD13	1:A:535:VAL:HG21	2.02	0.41
1:A:784:ARG:O	1:A:788:LYS:NZ	2.50	0.41
1:A:517:ASP:OD1	1:A:554:ARG:HB3	2.21	0.41
1:A:669:GLU:OE1	1:A:829:ARG:HD2	2.20	0.40
1:B:699:ILE:O	1:B:707:ARG:NH1	2.54	0.40
1:A:856:TYR:O	1:A:860:GLN:HG2	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	420/427 (98%)	409 (97%)	9 (2%)	2 (0%)	29	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	420/427 (98%)	409 (97%)	9 (2%)	2 (0%)	29	35
2	C	1/10 (10%)	1 (100%)	0	0	100	100
2	D	1/10 (10%)	1 (100%)	0	0	100	100
All	All	842/874 (96%)	820 (97%)	18 (2%)	4 (0%)	29	35

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	557	PRO
1	B	492	PRO
1	A	590	VAL
1	B	590	VAL

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	360/370 (97%)	345 (96%)	15 (4%)	30	42
1	B	362/370 (98%)	339 (94%)	23 (6%)	17	23
2	C	3/9 (33%)	3 (100%)	0	100	100
2	D	2/9 (22%)	2 (100%)	0	100	100
All	All	727/758 (96%)	689 (95%)	38 (5%)	23	32

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	491	GLU
1	A	497	GLN
1	A	509	LEU
1	A	515	THR
1	A	592	GLU
1	A	616	ARG
1	A	627	LYS

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Mol	Chain	Res	Type
1	A	662	THR
1	A	664	GLU
1	A	680	GLN
1	A	745	LYS
1	A	767	VAL
1	A	799	VAL
1	A	812	ARG
1	A	861	ASP
1	B	461	ARG
1	B	467	LYS
1	B	485	THR
1	B	486	VAL
1	B	493	ASP
1	B	495	PHE
1	B	499	LYS
1	B	509	LEU
1	B	513	MET
1	B	523	ASN
1	B	530	HIS
1	B	535	VAL
1	B	551	GLU
1	B	554	ARG
1	B	556	TYR
1	B	616	ARG
1	B	627	LYS
1	B	664	GLU
1	B	680	GLN
1	B	701	ASP
1	B	767	VAL
1	B	787	VAL
1	B	861	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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
2	TPO	C	156	2	8,10,11	1.23	0	10,14,16	1.16	0
2	TPO	D	156	2	8,10,11	1.24	0	10,14,16	1.24	1 (10%)

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	TPO	C	156	2	-	2/9/11/13	-
2	TPO	D	156	2	-	6/9/11/13	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	156	TPO	P-OG1-CB	-2.41	115.93	123.21

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	156	TPO	CG2-CB-OG1-P
2	D	156	TPO	N-CA-CB-CG2
2	D	156	TPO	N-CA-CB-OG1
2	D	156	TPO	C-CA-CB-CG2
2	D	156	TPO	CG2-CB-OG1-P
2	D	156	TPO	CB-OG1-P-O1P
2	C	156	TPO	CB-OG1-P-O2P
2	D	156	TPO	CB-OG1-P-O2P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 11 are monoatomic - leaving 5 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	$\# Z  > 2$
4	CIT	B	903	-	3,12,12	1.21	0	3,17,17	1.26	1 (33%)
3	GOL	B	902	-	5,5,5	0.97	0	5,5,5	1.14	0
3	GOL	A	901	-	5,5,5	0.82	0	5,5,5	1.14	1 (20%)
4	CIT	B	901	-	3,12,12	1.46	0	3,17,17	2.47	2 (66%)
4	CIT	A	902	-	3,12,12	1.11	0	3,17,17	1.02	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
4	CIT	B	903	-	-	3/6/16/16	-
3	GOL	B	902	-	-	3/4/4/4	-
3	GOL	A	901	-	-	2/4/4/4	-
4	CIT	B	901	-	-	3/6/16/16	-
4	CIT	A	902	-	-	0/6/16/16	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	901	CIT	C3-C2-C1	-3.18	109.89	114.98
4	B	901	CIT	C3-C4-C5	-2.79	110.51	114.98
4	B	903	CIT	C3-C4-C5	-2.07	111.66	114.98
3	A	901	GOL	C3-C2-C1	-2.02	103.87	111.70

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	903	CIT	C1-C2-C3-O7
4	B	903	CIT	C1-C2-C3-C4
4	B	903	CIT	C1-C2-C3-C6
4	B	901	CIT	C2-C3-C4-C5
4	B	901	CIT	O7-C3-C4-C5
3	A	901	GOL	C1-C2-C3-O3
3	B	902	GOL	O1-C1-C2-C3
3	B	902	GOL	O1-C1-C2-O2
3	A	901	GOL	O2-C2-C3-O3
3	B	902	GOL	O2-C2-C3-O3
4	B	901	CIT	C6-C3-C4-C5

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	903	CIT	1	0
4	A	902	CIT	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 ⓘ

### 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	421/427 (98%)	1.00	84 (19%) 1 1	41, 69, 153, 209	0
1	B	421/427 (98%)	0.56	32 (7%) 13 18	41, 74, 121, 167	0
2	C	3/10 (30%)	1.12	0 100 100	115, 115, 123, 130	0
2	D	2/10 (20%)	7.87	2 (100%) 0 0	142, 142, 142, 162	0
All	All	847/874 (96%)	0.80	118 (13%) 2 4	41, 72, 144, 209	0

All (118) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	158	LEU	9.7
1	A	501	LEU	9.3
1	A	533	ALA	8.5
1	A	535	VAL	7.6
1	A	539	PHE	7.4
1	B	487	VAL	7.2
1	B	500	SER	7.1
1	A	491	GLU	6.6
1	A	528	LEU	6.2
1	B	486	VAL	6.1
2	D	157	GLN	6.1
1	A	503	LEU	6.1
1	A	485	THR	5.8
1	A	542	ILE	5.6
1	A	484	PHE	5.5
1	A	557	PRO	5.5
1	A	482	PHE	5.5
1	A	467	LYS	5.5
1	A	504	ASP	5.5
1	B	491	GLU	5.4
1	A	553	CYS	5.4

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Mol	Chain	Res	Type	RSRZ
1	A	537	LYS	5.3
1	A	532	HIS	5.2
1	A	538	ILE	5.1
1	A	550	LEU	5.1
1	A	513	MET	5.0
1	A	499	LYS	5.0
1	A	487	VAL	5.0
1	A	502	VAL	4.6
1	A	496	LEU	4.6
1	A	540	GLN	4.6
1	B	559	GLY	4.6
1	A	483	GLY	4.5
1	A	478	SER	4.5
1	A	458	PHE	4.4
1	A	534	GLN	4.4
1	A	479	SER	4.3
1	A	472	HIS	4.3
1	A	486	VAL	4.3
1	B	518	VAL	4.3
1	A	460	THR	4.3
1	B	503	LEU	4.3
1	A	536	VAL	4.2
1	B	490	ASP	4.2
1	A	459	PHE	4.1
1	A	481	GLY	4.1
1	A	469	LYS	4.0
1	A	490	ASP	4.0
1	A	468	GLY	4.0
1	A	498	ILE	4.0
1	B	458	PHE	4.0
1	A	543	PRO	3.9
1	A	507	ALA	3.9
1	A	505	GLY	3.9
1	A	660	LEU	3.8
1	A	509	LEU	3.8
1	A	544	ILE	3.7
1	A	470	PHE	3.7
1	A	488	GLY	3.7
1	B	498	ILE	3.6
1	A	475	LEU	3.6
1	A	521	SER	3.6
1	B	576	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	554	ARG	3.5
1	A	516	GLY	3.4
1	B	489	GLY	3.4
1	B	471	ILE	3.4
1	A	512	LYS	3.4
1	B	459	PHE	3.4
1	A	518	VAL	3.4
1	A	546	ALA	3.3
1	B	496	LEU	3.2
1	B	495	PHE	3.2
1	B	557	PRO	3.2
1	A	545	GLY	3.1
1	A	531	THR	3.1
1	B	556	TYR	3.0
1	A	466	LEU	3.0
1	A	554	ARG	3.0
1	A	524	ASP	3.0
1	A	555	GLY	2.9
1	B	492	PRO	2.9
1	A	556	TYR	2.9
1	A	495	PHE	2.9
1	B	555	GLY	2.9
1	B	722	GLY	2.9
1	A	477	LYS	2.9
1	A	500	SER	2.8
1	B	553	CYS	2.8
1	B	516	GLY	2.8
1	A	547	SER	2.7
1	B	494	GLU	2.7
1	A	462	ASN	2.7
1	A	723	SER	2.7
1	A	529	GLY	2.7
1	A	492	PRO	2.6
1	B	552	LEU	2.6
1	A	506	PRO	2.6
1	A	514	GLU	2.5
1	A	489	GLY	2.5
1	B	570	THR	2.5
1	B	499	LYS	2.5
1	B	480	ARG	2.4
1	A	548	VAL	2.4
1	A	497	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	541	SER	2.3
1	B	507	ALA	2.2
1	A	558	LEU	2.2
1	B	488	GLY	2.2
1	B	501	LEU	2.2
1	A	612	PHE	2.2
1	A	476	ARG	2.2
1	A	471	ILE	2.2
1	A	520	VAL	2.1
1	A	530	HIS	2.1
1	A	560	SER	2.1
1	A	480	ARG	2.1
1	A	519	ILE	2.0

## 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. 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(Å <sup>2</sup> )	Q<0.9
2	TPO	D	156	11/12	0.76	0.41	102,134,154,158	0
2	TPO	C	156	11/12	0.80	0.25	126,142,147,147	0

## 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, 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(Å <sup>2</sup> )	Q<0.9
5	CA	B	907	1/1	0.33	0.42	160,160,160,160	0
5	CA	A	903	1/1	0.43	0.41	135,135,135,135	0
4	CIT	B	903	13/13	0.44	0.41	116,122,133,135	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	CA	A	906	1/1	0.45	0.17	108,108,108,108	0
5	CA	A	904	1/1	0.66	0.14	128,128,128,128	0
5	CA	B	906	1/1	0.68	0.21	140,140,140,140	0
4	CIT	A	902	13/13	0.74	0.23	102,129,135,136	0
5	CA	B	905	1/1	0.75	0.15	122,122,122,122	0
4	CIT	B	901	13/13	0.84	0.28	75,116,131,132	0
5	CA	A	905	1/1	0.84	0.09	133,133,133,133	0
5	CA	B	908	1/1	0.88	0.08	112,112,112,112	0
5	CA	B	904	1/1	0.88	0.29	85,85,85,85	0
5	CA	B	909	1/1	0.91	0.05	87,87,87,87	0
3	GOL	A	901	6/6	0.93	0.23	52,55,96,120	0
5	CA	A	907	1/1	0.95	0.13	73,73,73,73	0
3	GOL	B	902	6/6	0.95	0.17	45,59,61,63	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.