



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:33 PM UTC

PDB ID : 7P71 / pdb_00007p71
Title : The PDZ domain of MAGI1_2 complexed with the PDZ-binding motif of HPV35-E6
Authors : Gogl, G.; Cousido-Siah, A.; Trave, G.
Deposited on : 2021-07-19
Resolution : 2.60 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

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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

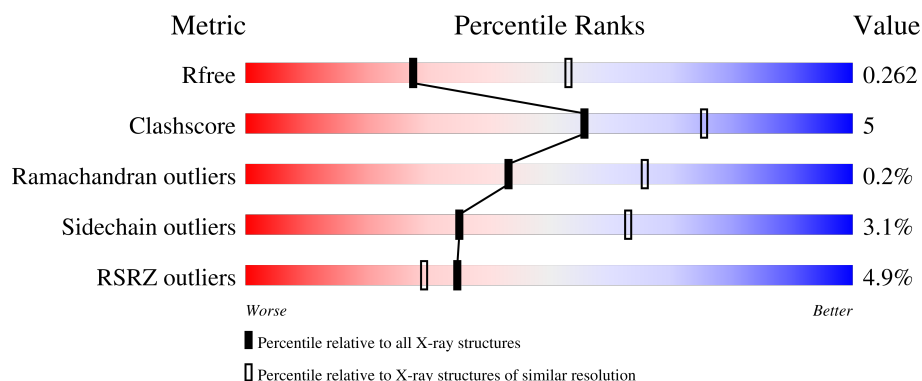
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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 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	A	427	81% 18% .
1	B	427	8% 87% 10% ..
2	C	13	8% 38% 8% 8% 46%
2	D	13	31% 69%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6701 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	423	Total	C	N	O	S	0	0	0
			3313	2084	567	648	14			
1	B	420	Total	C	N	O	S	0	0	0
			3227	2030	551	632	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 Protein E6.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			62	35	13	14			
2	D	4	Total	C	N	O	0	0	0
			33	19	4	10			

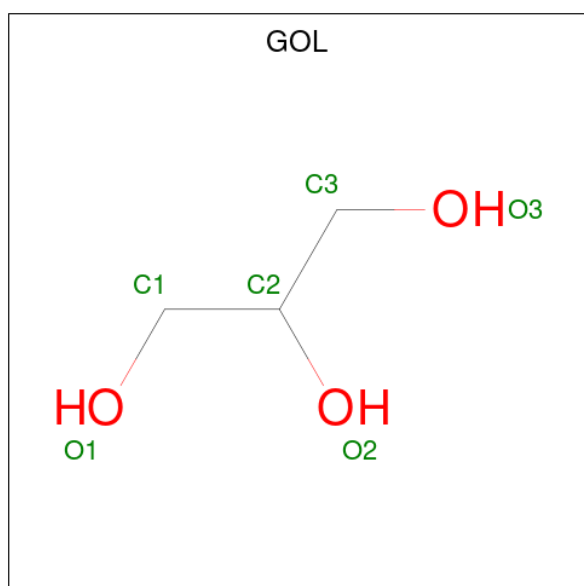
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	137	THR	-	linker	UNP P27228
C	138	ASP	-	linker	UNP P27228
C	139	ASP	-	linker	UNP P27228
C	140	SER	-	linker	UNP P27228
D	137	THR	-	linker	UNP P27228
D	138	ASP	-	linker	UNP P27228
D	139	ASP	-	linker	UNP P27228
D	140	SER	-	linker	UNP P27228

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	4	Total Ca 4 4	0	0
3	B	4	Total Ca 4 4	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



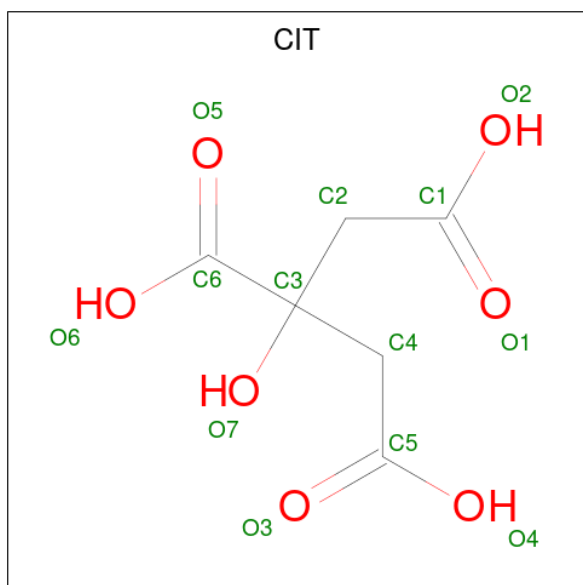
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0

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

- Molecule 5 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



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

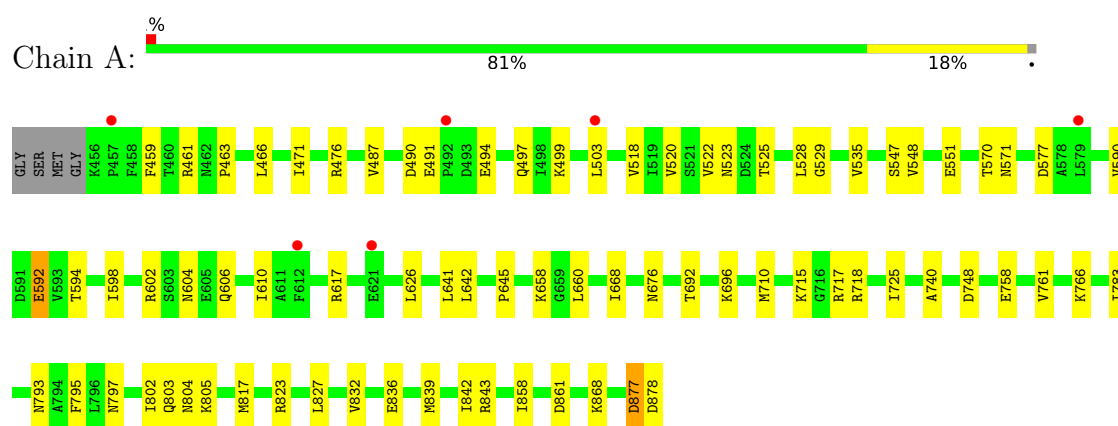
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	11	Total	O	0	0
			11	11		
6	B	4	Total	O	0	0
			4	4		

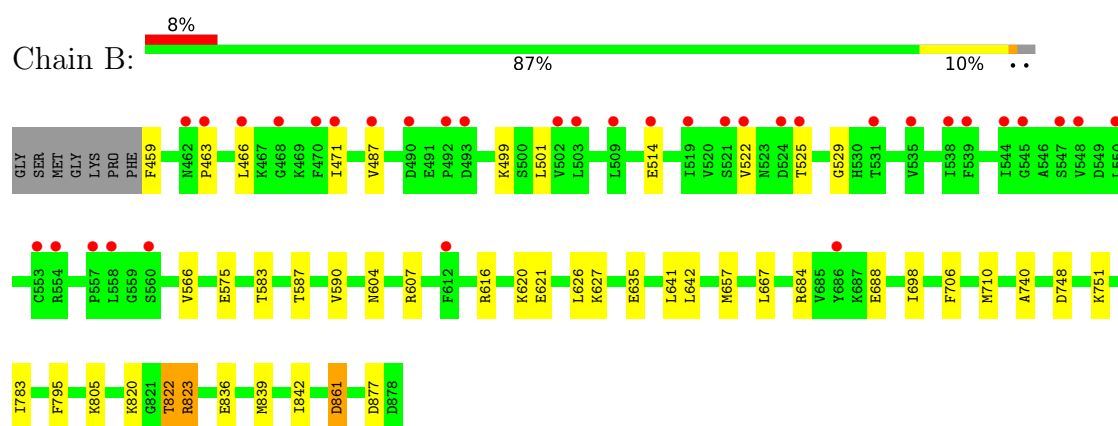
3 Residue-property plots

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.

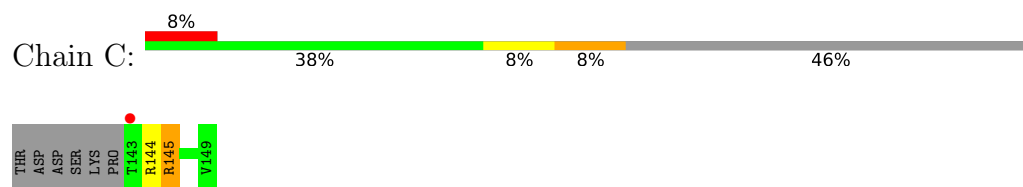
- Molecule 1: Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1, Annexin A2



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



- Molecule 2: Protein E6



- Molecule 2: Protein E6



THR	ASP	ASP	SER	LYS	PRO	THR	ARG	E146	Y149
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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	192.13Å 61.03Å 98.99Å 90.00° 97.33° 90.00°	Depositor
Resolution (Å)	47.64 – 2.60 47.64 – 2.60	Depositor EDS
% Data completeness (in resolution range)	93.6 (47.64-2.60) 93.6 (47.64-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.241 , 0.281 (Not available) , 0.262	Depositor DCC
R_{free} test set	1651 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	70.7	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6701	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.84% 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: CIT, GOL, CA

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	0.21	0/3364	0.40	0/4534
1	B	0.08	0/3274	0.23	0/4418
2	C	0.46	0/61	0.70	0/79
2	D	0.04	0/32	0.14	0/41
All	All	0.16	0/6731	0.33	0/9072

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	3313	0	3282	40	0
1	B	3227	0	3172	23	0
2	C	62	0	60	1	0
2	D	33	0	27	0	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
4	A	18	0	24	2	0
4	B	12	0	16	0	0
5	A	13	0	5	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	11	0	0	4	0
6	B	4	0	0	1	0
All	All	6701	0	6586	62	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 5.

All (62) 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:803:GLN:NE2	6:A:1001:HOH:O	2.03	0.91
1:A:817:MET:HE1	1:A:858:ILE:HA	1.70	0.73
1:B:805:LYS:NZ	6:B:1002:HOH:O	2.24	0.70
1:A:805:LYS:HD2	6:A:1004:HOH:O	1.92	0.69
1:B:783:ILE:HD13	1:B:795:PHE:HB3	1.79	0.65
1:A:805:LYS:NZ	6:A:1004:HOH:O	2.30	0.65
1:A:758:GLU:OE2	1:B:751:LYS:NZ	2.27	0.63
1:B:740:ALA:HB1	1:B:748:ASP:HB3	1.80	0.63
1:A:491:GLU:HG2	1:A:494:GLU:HB2	1.81	0.62
1:B:822:THR:HB	1:B:861:ASP:OD2	2.00	0.61
1:A:676:ASN:ND2	1:A:718:ARG:O	2.31	0.61
1:A:626:LEU:HD12	1:A:642:LEU:HD11	1.84	0.60
1:A:740:ALA:HB1	1:A:748:ASP:HB3	1.85	0.58
1:A:843:ARG:HB3	1:A:878:ASP:OD2	2.04	0.58
1:B:583:THR:O	1:B:587:THR:OG1	2.20	0.58
1:A:463:PRO:HA	1:A:466:LEU:HD13	1.85	0.57
1:A:577:ASP:HB2	1:A:610:ILE:HD12	1.87	0.56
1:A:725:ILE:HD13	1:A:766:LYS:HE2	1.86	0.56
1:A:804:ASN:O	6:A:1002:HOH:O	2.17	0.56
1:A:793:ASN:O	1:A:797:ASN:ND2	2.34	0.56
1:B:820:LYS:O	1:B:823:ARG:NH2	2.39	0.55
1:A:520:VAL:HB	1:A:551:GLU:HG2	1.88	0.54
1:A:522:VAL:O	1:A:525:THR:OG1	2.25	0.54
1:A:645:PRO:HB3	4:A:906:GOL:H12	1.89	0.53
1:A:461:ARG:HA	1:A:528:LEU:HB3	1.91	0.53
1:A:817:MET:HE2	1:A:861:ASP:HB3	1.91	0.52
1:B:566:VAL:HG23	1:B:836:GLU:HG2	1.91	0.52
1:B:463:PRO:HA	1:B:466:LEU:HD13	1.91	0.52
1:A:783:ILE:HD13	1:A:795:PHE:HB3	1.90	0.52
1:B:487:VAL:HB	1:B:499:LYS:HB2	1.92	0.51
1:A:839:MET:HE3	1:A:842:ILE:HB	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:715:LYS:HB3	1:A:717:ARG:HG3	1.93	0.51
1:A:497:GLN:HG2	1:A:518:VAL:HG22	1.94	0.50
1:A:487:VAL:HB	1:A:499:LYS:HB2	1.94	0.50
1:A:641:LEU:HD23	1:A:832:VAL:HG13	1.95	0.48
1:B:604:ASN:N	1:B:836:GLU:OE2	2.46	0.48
1:B:626:LEU:HD12	1:B:642:LEU:HD11	1.97	0.47
1:A:606:GLN:O	1:A:610:ILE:HG12	2.14	0.47
1:B:575:GLU:OE2	1:B:616:ARG:NH1	2.37	0.46
1:B:839:MET:HE3	1:B:842:ILE:HB	1.98	0.46
1:B:684:ARG:NH1	1:B:688:GLU:OE1	2.49	0.46
1:A:459:PHE:HZ	1:A:529:GLY:HA2	1.81	0.46
1:A:817:MET:HE3	1:A:827:LEU:HD22	1.97	0.45
1:B:667:LEU:HG	1:B:710:MET:HE2	1.98	0.45
1:B:459:PHE:HZ	1:B:529:GLY:HA2	1.82	0.45
1:B:522:VAL:O	1:B:525:THR:OG1	2.34	0.44
1:A:668:ILE:HA	1:A:710:MET:HE1	1.99	0.44
1:A:604:ASN:N	1:A:836:GLU:OE2	2.43	0.44
1:A:761:VAL:HG13	1:A:802:ILE:HG23	2.00	0.44
1:A:476:ARG:HA	1:A:547:SER:HA	2.00	0.44
1:B:627:LYS:HG3	1:B:635:GLU:OE2	2.18	0.44
1:A:692:THR:HG23	1:A:696:LYS:HD3	2.00	0.43
1:A:718:ARG:NH1	4:A:904:GOL:O2	2.52	0.43
1:A:592:GLU:H	1:A:592:GLU:HG2	1.29	0.42
1:A:598:ILE:O	1:A:602:ARG:HG2	2.19	0.42
1:A:523:ASN:ND2	1:A:548:VAL:HG23	2.34	0.42
1:B:607:ARG:NE	1:B:641:LEU:O	2.52	0.41
1:B:501:LEU:HD11	1:B:514:GLU:HA	2.02	0.41
1:A:877:ASP:OD2	1:A:877:ASP:N	2.53	0.41
1:A:490:ASP:HA	2:C:145:ARG:HH12	1.86	0.41
1:B:657:MET:HE1	1:B:698:ILE:HG12	2.01	0.41
1:B:706:PHE:O	1:B:710:MET: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	421/427 (99%)	410 (97%)	10 (2%)	1 (0%)	43	66
1	B	418/427 (98%)	407 (97%)	10 (2%)	1 (0%)	43	66
2	C	5/13 (38%)	4 (80%)	1 (20%)	0	100	100
2	D	2/13 (15%)	2 (100%)	0	0	100	100
All	All	846/880 (96%)	823 (97%)	21 (2%)	2 (0%)	43	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
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	357/370 (96%)	344 (96%)	13 (4%)	31	58
1	B	341/370 (92%)	334 (98%)	7 (2%)	47	73
2	C	7/13 (54%)	5 (71%)	2 (29%)	0	1
2	D	4/13 (31%)	4 (100%)	0	100	100
All	All	709/766 (93%)	687 (97%)	22 (3%)	35	63

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	ILE
1	A	503	LEU
1	A	535	VAL
1	A	570	THR
1	A	571	ASN
1	A	592	GLU

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Mol	Chain	Res	Type
1	A	594	THR
1	A	617	ARG
1	A	658	LYS
1	A	660	LEU
1	A	823	ARG
1	A	868	LYS
1	A	877	ASP
1	B	471	ILE
1	B	620	LYS
1	B	621	GLU
1	B	822	THR
1	B	823	ARG
1	B	861	ASP
1	B	877	ASP
2	C	144	ARG
2	C	145	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	532	HIS
1	B	472	HIS
1	B	633	HIS
1	B	797	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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	GOL	A	905	-	5,5,5	0.95	0	5,5,5	1.08	0
5	CIT	A	907	3	12,12,12	1.05	0	17,17,17	1.54	2 (11%)
4	GOL	B	905	-	5,5,5	0.94	0	5,5,5	1.09	0
4	GOL	A	906	-	5,5,5	0.93	0	5,5,5	1.06	0
4	GOL	B	904	-	5,5,5	0.92	0	5,5,5	1.11	0
4	GOL	A	904	-	5,5,5	0.96	0	5,5,5	1.04	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	GOL	A	905	-	-	0/4/4/4	-
5	CIT	A	907	3	-	3/16/16/16	-
4	GOL	B	905	-	-	0/4/4/4	-
4	GOL	A	906	-	-	2/4/4/4	-
4	GOL	B	904	-	-	0/4/4/4	-
4	GOL	A	904	-	-	2/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	907	CIT	O6-C6-C3	4.30	121.39	113.14
5	A	907	CIT	O2-C1-C2	2.12	121.07	114.35

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	904	GOL	C1-C2-C3-O3
4	A	906	GOL	O1-C1-C2-C3
4	A	906	GOL	O1-C1-C2-O2
5	A	907	CIT	C6-C3-C4-C5
4	A	904	GOL	O2-C2-C3-O3
5	A	907	CIT	C2-C3-C4-C5
5	A	907	CIT	C1-C2-C3-O7

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	906	GOL	1	0
4	A	904	GOL	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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	423/427 (99%)	0.55	6 (1%) 73 69	57, 95, 128, 151	0
1	B	420/427 (98%)	0.74	35 (8%) 17 13	58, 100, 180, 192	0
2	C	7/13 (53%)	0.93	1 (14%) 6 5	109, 116, 143, 155	0
2	D	4/13 (30%)	1.29	0 100 100	175, 183, 188, 206	0
All	All	854/880 (97%)	0.65	42 (4%) 35 29	57, 98, 174, 206	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	470	PHE	4.4
1	B	509	LEU	3.2
1	B	462	ASN	3.2
1	B	554	ARG	2.9
1	B	519	ILE	2.9
1	A	503	LEU	2.9
1	B	535	VAL	2.9
1	B	550	LEU	2.7
1	B	538	ILE	2.7
1	B	525	THR	2.6
1	B	557	PRO	2.6
1	B	524	ASP	2.6
1	B	493	ASP	2.5
1	B	471	ILE	2.5
1	A	579	LEU	2.5
1	B	558	LEU	2.5
1	B	545	GLY	2.5
1	B	548	VAL	2.5
1	B	539	PHE	2.5
1	B	502	VAL	2.4
1	B	521	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	553	CYS	2.3
1	B	463	PRO	2.3
1	B	560	SER	2.3
1	B	531	THR	2.2
1	B	487	VAL	2.2
1	B	503	LEU	2.2
2	C	143	THR	2.2
1	B	544	ILE	2.2
1	B	466	LEU	2.2
1	B	490	ASP	2.2
1	A	612	PHE	2.2
1	A	457	PRO	2.1
1	B	492	PRO	2.1
1	B	686	TYR	2.1
1	B	547	SER	2.1
1	B	468	GLY	2.1
1	A	621	GLU	2.1
1	B	514	GLU	2.1
1	B	612	PHE	2.1
1	A	492	PRO	2.1
1	B	522	VAL	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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($\text{\AA}^2$)	Q<0.9
3	CA	A	903	1/1	0.39	0.21	254,254,254,254	0
5	CIT	A	907	13/13	0.56	0.12	142,149,155,156	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CA	A	902	1/1	0.57	0.12	153,153,153,153	0
3	CA	A	908	1/1	0.58	0.18	164,164,164,164	0
3	CA	B	906	1/1	0.61	0.18	121,121,121,121	0
3	CA	B	902	1/1	0.61	0.12	151,151,151,151	0
3	CA	B	901	1/1	0.69	0.15	180,180,180,180	0
4	GOL	B	905	6/6	0.77	0.18	85,95,97,103	0
3	CA	B	903	1/1	0.81	0.08	152,152,152,152	0
4	GOL	A	904	6/6	0.86	0.15	62,68,76,91	0
4	GOL	B	904	6/6	0.91	0.13	68,76,80,85	0
4	GOL	A	905	6/6	0.92	0.12	70,87,94,97	0
4	GOL	A	906	6/6	0.93	0.12	86,94,97,97	0
3	CA	A	901	1/1	0.94	0.05	124,124,124,124	0

6.5 Other polymers [i](#)

There are no such residues in this entry.