



# Full wwPDB X-ray Structure Validation Report ⓘ

May 20, 2026 – 08:08 PM EDT

PDB ID : 9YAR / pdb\_00009yar  
Title : Rana catesbeiana saxiphilin:STX-C13-OBz (co-crystal)  
Authors : Chen, Z.; Zakrzewska, S.; Minor, D.L.  
Deposited on : 2025-09-16  
Resolution : 2.40 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
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

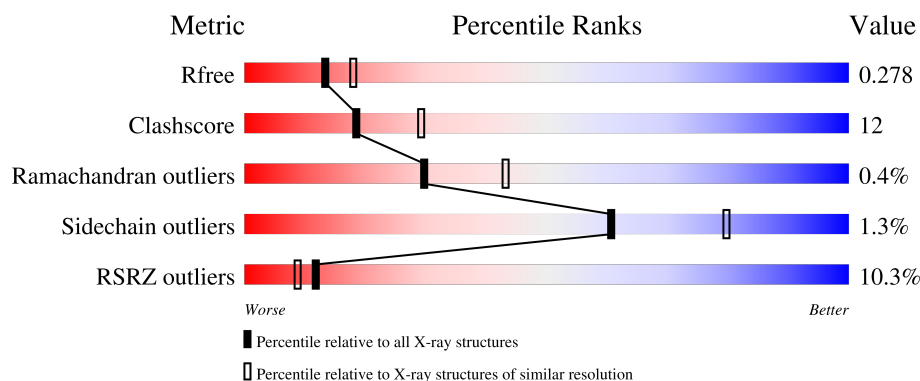
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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  $\geq 3$ , 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	853	<div> <div>11%</div> <div>74%</div> <div>22%</div> <div>.</div> </div>
1	B	853	<div> <div>9%</div> <div>72%</div> <div>23%</div> <div>..</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13011 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.

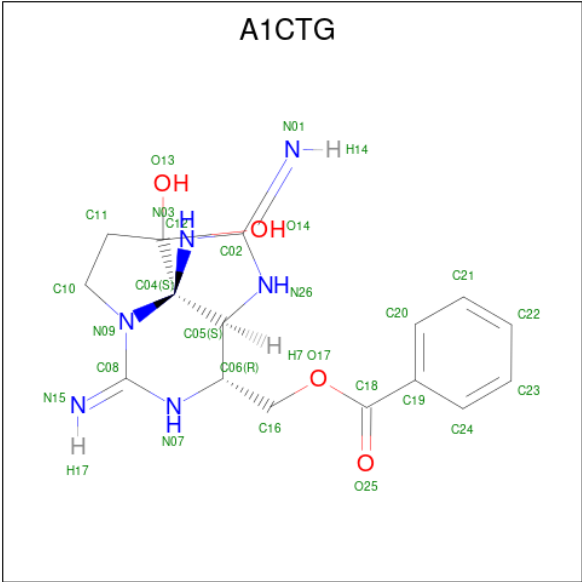
- Molecule 1 is a protein called Saxiphilin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	818	Total	C	N	O	S	0	0	0
			6315	3945	1090	1221	59			
1	B	818	Total	C	N	O	S	0	0	0
			6315	3945	1090	1221	59			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	826	SER	-	expression tag	UNP P31226
A	827	ASN	-	expression tag	UNP P31226
A	828	SER	-	expression tag	UNP P31226
A	829	LEU	-	expression tag	UNP P31226
A	830	GLU	-	expression tag	UNP P31226
A	831	VAL	-	expression tag	UNP P31226
A	832	LEU	-	expression tag	UNP P31226
A	833	PHE	-	expression tag	UNP P31226
A	834	GLN	-	expression tag	UNP P31226
B	826	SER	-	expression tag	UNP P31226
B	827	ASN	-	expression tag	UNP P31226
B	828	SER	-	expression tag	UNP P31226
B	829	LEU	-	expression tag	UNP P31226
B	830	GLU	-	expression tag	UNP P31226
B	831	VAL	-	expression tag	UNP P31226
B	832	LEU	-	expression tag	UNP P31226
B	833	PHE	-	expression tag	UNP P31226
B	834	GLN	-	expression tag	UNP P31226

- Molecule 2 is [(2Z,3aS,4R,6Z,7R,10aS)-10,10-dihydroxy-2,6-diiminooctahydro-1H,8H-pyrrolo[1,2-c]purin-4-yl]methyl benzoate (CCD ID: A1CTG) (formula: C<sub>16</sub>H<sub>20</sub>N<sub>6</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	16	6	4		
2	B	1	Total	C	N	O	0	0
			26	16	6	4		

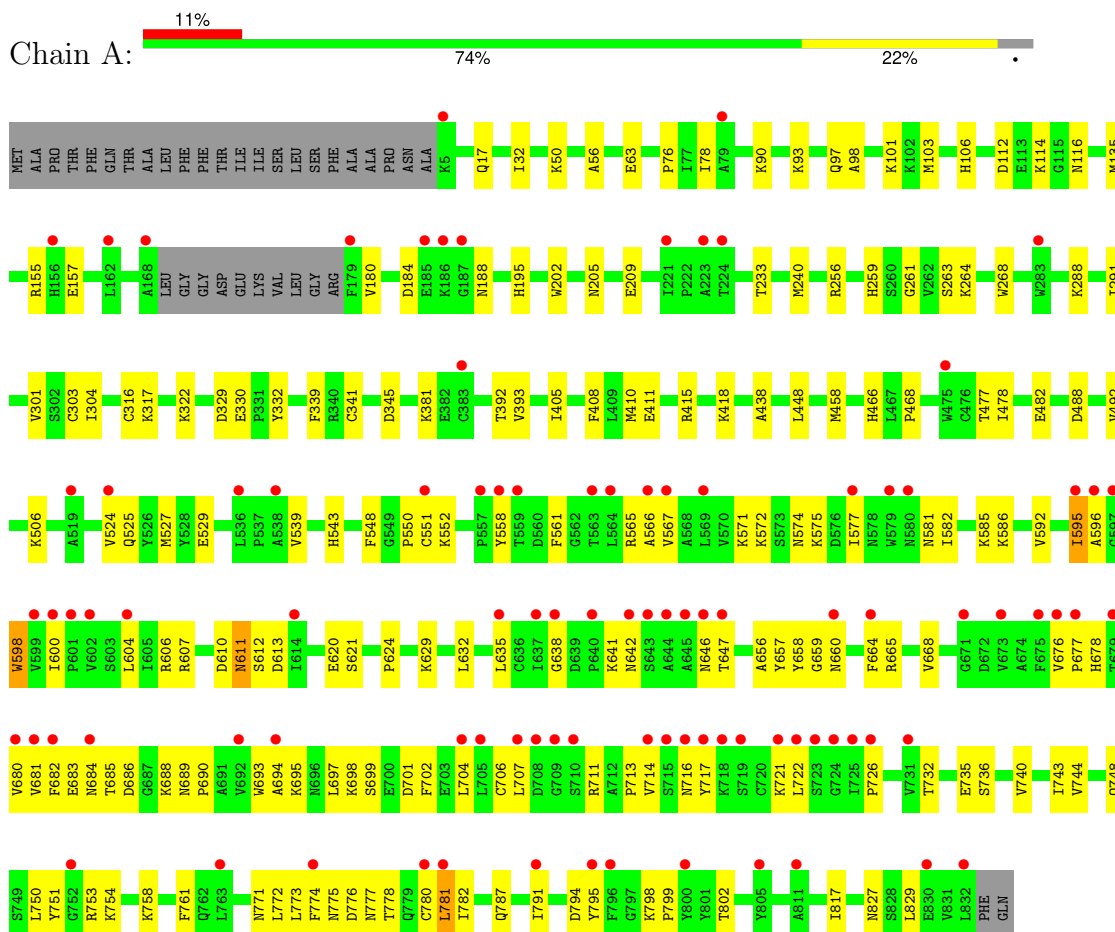
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	192	Total	O	0	0
			192	192		
3	B	137	Total	O	0	0
			137	137		

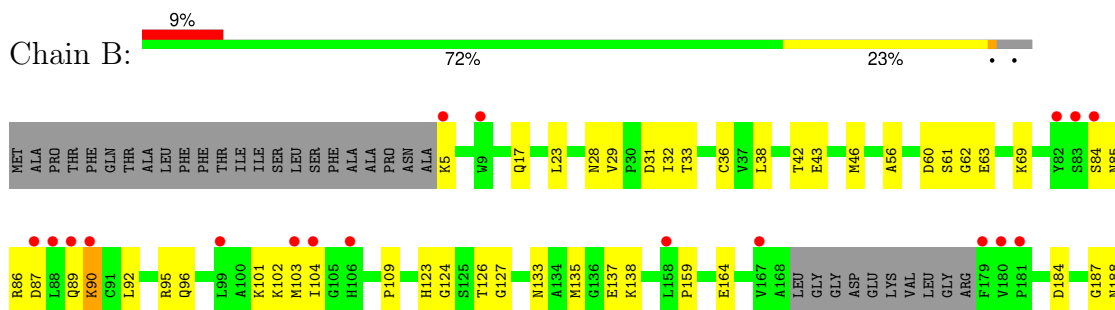
### 3 Residue-property plots [i](#)

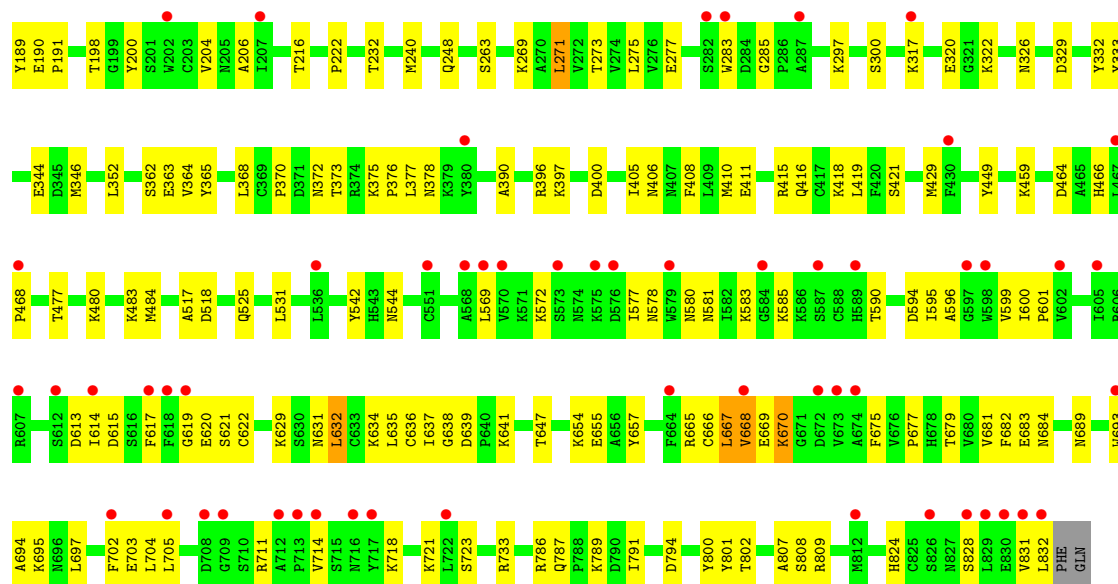
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Saxiphilin



#### • Molecule 1: Saxiphilin





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.98Å 105.69Å 253.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.77 – 2.40 48.77 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.77-2.40) 99.9 (48.77-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.28 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.21.1_5286: ???)	Depositor
R, $R_{free}$	0.249 , 0.278 0.249 , 0.278	Depositor DCC
$R_{free}$ test set	4973 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	64.5	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 56.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13011	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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: A1CTG

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	0.16	0/6441	0.34	0/8693
1	B	0.18	0/6441	0.34	0/8693
All	All	0.17	0/12882	0.34	0/17386

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	6315	0	6181	155	1
1	B	6315	0	6181	145	0
2	A	26	0	0	3	0
2	B	26	0	0	1	0
3	A	192	0	0	9	0
3	B	137	0	0	10	0
All	All	13011	0	12362	300	1

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 12.

All (300) 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:703:GLU:OE1	1:B:711:ARG:NH1	2.04	0.91
1:B:86:ARG:HB2	1:B:89:GLN:HE21	1.42	0.85
1:A:525:GLN:HE21	1:A:595:ILE:HD11	1.42	0.82
1:A:316:CYS:SG	3:A:1048:HOH:O	2.36	0.82
1:B:668:VAL:HB	1:B:693:TRP:CZ2	2.15	0.81
1:B:620:GLU:HB3	1:B:635:LEU:HD21	1.63	0.81
1:B:362:SER:HA	1:B:377:LEU:HD23	1.64	0.80
1:A:660:ASN:OD1	1:A:677:PRO:HD2	1.83	0.78
1:B:86:ARG:HB2	1:B:89:GLN:NE2	1.99	0.78
1:B:164:GLU:OE2	1:B:189:TYR:OH	2.01	0.77
1:B:517:ALA:O	3:B:1001:HOH:O	2.00	0.77
1:A:621:SER:HB2	1:A:632:LEU:HA	1.68	0.76
1:B:733:ARG:NH1	3:B:1001:HOH:O	2.15	0.76
1:A:565:ARG:HB3	1:A:721:LYS:HG2	1.69	0.75
1:B:138:LYS:NZ	3:B:1002:HOH:O	2.20	0.75
1:A:750:LEU:HB3	1:A:751:TYR:CD1	2.22	0.75
1:B:322:LYS:HD3	1:B:329:ASP:HB3	1.67	0.73
1:B:123:HIS:HD2	1:B:126:THR:HG23	1.53	0.73
1:B:5:LYS:NZ	3:B:1003:HOH:O	2.20	0.73
1:A:240:MET:HE1	1:A:339:PHE:CD1	2.24	0.72
1:A:240:MET:HE1	1:A:339:PHE:HD1	1.55	0.72
1:A:572:LYS:HD2	1:A:701:ASP:HB3	1.70	0.72
1:A:693:TRP:CD1	1:A:694:ALA:H	2.08	0.71
1:B:620:GLU:CB	1:B:635:LEU:HD21	2.20	0.71
1:A:565:ARG:HB2	1:A:721:LYS:HZ1	1.54	0.71
1:A:303:CYS:SG	3:A:1048:HOH:O	2.48	0.71
1:B:600:ILE:HD12	1:B:723:SER:HB3	1.71	0.70
1:A:600:ILE:HD12	1:A:600:ILE:H	1.56	0.70
1:A:524:VAL:HG11	1:A:726:PRO:HD2	1.71	0.70
1:B:92:LEU:O	1:B:96:GLN:HG3	1.93	0.69
1:A:664:PHE:CZ	1:A:702:PHE:HE2	2.12	0.68
1:B:56:ALA:HB2	1:B:405:ILE:HD13	1.74	0.68
1:A:539:VAL:HG23	1:A:781:LEU:HD12	1.75	0.68
1:A:606:ARG:HD2	1:A:612:SER:HA	1.77	0.67
1:A:771:ASN:N	1:A:776:ASP:OD2	2.19	0.67
1:A:791:ILE:HD12	1:A:791:ILE:H	1.58	0.67
1:A:748:GLN:HE22	1:A:781:LEU:H	1.41	0.66
1:B:135:MET:HE3	1:B:232:THR:HG23	1.78	0.66
1:A:114:LYS:HD2	1:A:116:ASN:OD1	1.95	0.66
1:B:665:ARG:HH11	1:B:693:TRP:HB2	1.62	0.65
1:A:660:ASN:OD1	1:A:680:VAL:HG21	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:ARG:O	1:B:90:LYS:NZ	2.26	0.64
1:B:665:ARG:NH1	1:B:693:TRP:HB2	2.13	0.64
1:A:751:TYR:CD2	1:A:761:PHE:HB3	2.32	0.64
1:B:601:PRO:HB3	1:B:675:PHE:CD1	2.32	0.64
1:A:571:LYS:HE3	1:A:668:VAL:HA	1.78	0.64
1:B:657:TYR:CE1	1:B:666:CYS:HA	2.32	0.64
1:B:668:VAL:HB	1:B:693:TRP:HZ2	1.63	0.63
1:B:578:ASN:HD21	1:B:580:ASN:HB2	1.62	0.63
1:A:740:VAL:O	1:A:744:VAL:HG23	1.99	0.63
1:B:572:LYS:HB2	1:B:703:GLU:HG3	1.81	0.63
1:A:751:TYR:HD2	1:A:761:PHE:HB3	1.64	0.62
1:A:114:LYS:NZ	3:A:1004:HOH:O	2.31	0.62
1:A:410:MET:HE1	1:A:438:ALA:HA	1.82	0.62
1:A:690:PRO:HA	1:A:695:LYS:HE2	1.81	0.62
1:A:646:ASN:O	1:A:646:ASN:ND2	2.34	0.61
1:B:531:LEU:HD22	1:B:791:ILE:HG13	1.82	0.61
1:A:794:ASP:OD1	2:A:901:A1CTG:N01	2.34	0.61
1:A:330:GLU:HB2	3:A:1002:HOH:O	1.99	0.60
1:A:17:GLN:OE1	3:A:1001:HOH:O	2.16	0.60
1:B:29:VAL:HG23	1:B:411:GLU:HG2	1.82	0.60
1:A:268:TRP:HZ2	1:A:291:ILE:HG23	1.66	0.60
1:A:638:GLY:HA2	1:A:656:ALA:H	1.67	0.60
1:B:636:CYS:HB3	1:B:655:GLU:OE2	2.02	0.59
1:B:787:GLN:HB2	1:B:789:LYS:HE3	1.84	0.59
1:A:641:LYS:HG2	1:A:642:ASN:H	1.66	0.59
1:B:619:GLY:O	1:B:631:ASN:ND2	2.35	0.59
1:A:686:ASP:HA	1:A:698:LYS:HD3	1.85	0.59
1:A:488:ASP:O	1:A:492:VAL:HG22	2.03	0.58
1:A:288:LYS:HE2	1:A:288:LYS:HA	1.84	0.58
1:A:586:LYS:HD2	1:A:635:LEU:HD11	1.85	0.58
1:B:647:THR:HG23	1:B:654:LYS:HB3	1.85	0.58
1:B:620:GLU:HB3	1:B:635:LEU:CD2	2.32	0.58
1:B:704:LEU:HD13	1:B:714:VAL:HA	1.84	0.58
1:B:62:GLY:O	1:B:269:LYS:NZ	2.35	0.58
1:A:697:LEU:C	1:A:697:LEU:HD13	2.29	0.58
1:A:697:LEU:HD11	1:A:702:PHE:CG	2.38	0.58
1:A:732:THR:HG21	1:A:740:VAL:HG21	1.87	0.57
1:B:363:GLU:OE2	1:B:363:GLU:N	2.21	0.57
1:B:694:ALA:HA	1:B:697:LEU:HG	1.86	0.57
1:A:543:HIS:ND1	1:A:777:ASN:OD1	2.36	0.57
1:B:639:ASP:OD2	1:B:641:LYS:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:657:TYR:OH	1:B:670:LYS:NZ	2.39	0.56
1:A:794:ASP:O	2:A:901:A1CTG:N03	2.38	0.56
1:B:32:ILE:HG21	1:B:408:PHE:HB2	1.87	0.56
1:A:492:VAL:O	1:A:751:TYR:OH	2.10	0.56
1:A:56:ALA:HB2	1:A:405:ILE:HD13	1.88	0.56
1:A:381:LYS:HE3	1:A:827:ASN:OD1	2.05	0.56
1:B:297:LYS:NZ	3:B:1007:HOH:O	2.32	0.56
1:B:363:GLU:H	1:B:363:GLU:CD	2.12	0.56
1:A:750:LEU:HB3	1:A:751:TYR:HD1	1.70	0.56
1:A:683:GLU:O	1:A:689:ASN:ND2	2.39	0.56
1:A:114:LYS:HD3	1:A:114:LYS:O	2.06	0.56
1:B:621:SER:HB2	1:B:632:LEU:HA	1.88	0.56
1:B:518:ASP:HA	3:B:1001:HOH:O	2.04	0.55
1:B:786:ARG:NH1	1:B:794:ASP:OD2	2.40	0.55
1:A:195:HIS:HB2	1:A:202:TRP:CH2	2.42	0.55
1:B:17:GLN:OE1	1:B:36:CYS:HB3	2.05	0.55
1:B:362:SER:HA	1:B:377:LEU:CD2	2.35	0.55
1:A:771:ASN:H	1:A:776:ASP:CG	2.11	0.55
1:A:322:LYS:HD2	1:A:329:ASP:HB3	1.89	0.55
1:A:641:LYS:HG2	1:A:642:ASN:N	2.21	0.54
1:B:5:LYS:HB2	1:B:31:ASP:O	2.08	0.54
1:B:583:LYS:HG3	1:B:617:PHE:HA	1.88	0.54
1:A:660:ASN:HD21	1:A:676:VAL:CG1	2.20	0.54
1:B:17:GLN:OE1	1:B:17:GLN:HA	2.08	0.54
1:B:87:ASP:H	1:B:89:GLN:HE22	1.56	0.54
1:B:377:LEU:HD22	1:B:377:LEU:H	1.73	0.54
1:B:480:LYS:O	1:B:484:MET:HG3	2.08	0.53
1:A:418:LYS:NZ	3:A:1007:HOH:O	2.36	0.53
1:B:283:TRP:CD1	1:B:285:GLY:H	2.27	0.53
1:A:135:MET:HG3	1:A:829:LEU:HD23	1.89	0.53
1:A:527:MET:HG3	1:A:795:TYR:CZ	2.43	0.53
1:B:668:VAL:HB	1:B:693:TRP:CH2	2.44	0.53
1:B:789:LYS:NZ	3:B:1005:HOH:O	2.41	0.53
1:A:638:GLY:O	1:A:647:THR:OG1	2.25	0.53
1:B:29:VAL:HG11	1:B:408:PHE:CD1	2.44	0.53
1:A:684:ASN:OD1	1:A:689:ASN:ND2	2.42	0.52
1:B:635:LEU:N	1:B:635:LEU:HD22	2.24	0.52
1:B:364:VAL:HG23	1:B:365:TYR:CD2	2.44	0.52
1:B:60:ASP:OD1	1:B:62:GLY:N	2.32	0.52
1:A:155:ARG:HH11	1:A:157:GLU:CD	2.18	0.52
1:A:577:ILE:HA	1:A:581:ASN:HD21	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:607:ARG:HH12	1:A:802:THR:HG22	1.74	0.52
1:A:664:PHE:CZ	1:A:702:PHE:CE2	2.96	0.52
1:A:76:PRO:HB3	1:A:392:THR:HG21	1.92	0.52
1:B:569:LEU:HD11	1:B:702:PHE:HB3	1.92	0.52
1:B:577:ILE:HD13	1:B:585:LYS:HZ2	1.74	0.52
1:A:572:LYS:HB3	1:A:701:ASP:O	2.10	0.52
1:B:378:ASN:N	1:B:378:ASN:OD1	2.37	0.52
1:A:592:VAL:HG23	1:A:598:TRP:CE2	2.45	0.51
1:A:701:ASP:O	1:A:702:PHE:CD1	2.63	0.51
1:B:133:ASN:HD21	1:B:137:GLU:HB2	1.74	0.51
1:A:548:PHE:CD2	1:A:551:CYS:HB3	2.44	0.51
1:A:736:SER:O	1:A:740:VAL:HG23	2.10	0.51
1:A:772:LEU:O	1:A:774:PHE:N	2.41	0.51
1:A:90:LYS:HE3	1:A:135:MET:O	2.11	0.51
1:A:561:PHE:N	3:A:1012:HOH:O	2.43	0.51
1:A:610:ASP:CG	1:A:610:ASP:O	2.53	0.51
1:B:542:TYR:CZ	1:B:544:ASN:HB3	2.45	0.51
1:B:684:ASN:OD1	1:B:689:ASN:ND2	2.43	0.51
1:A:565:ARG:HD2	1:A:717:TYR:HE1	1.74	0.51
1:A:681:VAL:O	1:A:685:THR:HG22	2.11	0.51
1:B:43:GLU:HA	1:B:46:MET:HE2	1.93	0.51
1:A:686:ASP:HB2	1:A:688:LYS:HZ2	1.76	0.50
1:A:548:PHE:HD2	1:A:548:PHE:O	1.94	0.50
1:B:127:GLY:N	3:B:1008:HOH:O	2.35	0.50
1:A:676:VAL:HG23	1:A:677:PRO:O	2.11	0.50
1:B:684:ASN:HA	1:B:689:ASN:HB2	1.94	0.50
1:A:611:ASN:ND2	1:A:613:ASP:O	2.43	0.50
1:A:754:LYS:O	1:A:754:LYS:HG2	2.11	0.50
1:B:679:THR:O	1:B:683:GLU:HG3	2.12	0.50
1:A:506:LYS:NZ	1:A:529:GLU:OE2	2.44	0.50
1:B:95:ARG:HA	1:B:109:PRO:HD2	1.94	0.50
1:B:87:ASP:H	1:B:89:GLN:NE2	2.10	0.50
1:A:550:PRO:HG3	1:A:558:TYR:HB3	1.93	0.50
1:A:753:ARG:O	1:A:758:LYS:NZ	2.25	0.50
1:B:17:GLN:HB2	1:B:38:LEU:HD13	1.93	0.50
1:A:750:LEU:HB3	1:A:751:TYR:CE1	2.47	0.49
1:A:529:GLU:HG2	1:A:817:ILE:HD11	1.94	0.49
1:B:28:ASN:O	1:B:415:ARG:NH1	2.45	0.49
1:A:565:ARG:HB2	1:A:721:LYS:NZ	2.26	0.49
1:A:566:ALA:O	1:A:721:LYS:HD2	2.13	0.49
1:A:750:LEU:HD23	1:A:751:TYR:HE1	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:HIS:HB2	1:A:202:TRP:HH2	1.77	0.49
1:A:256:ARG:HG2	1:A:301:VAL:HG23	1.95	0.49
1:A:506:LYS:NZ	1:A:529:GLU:OE1	2.46	0.48
1:B:23:LEU:HD13	1:B:419:LEU:HD23	1.94	0.48
1:A:681:VAL:HG11	1:A:714:VAL:HG21	1.95	0.48
1:A:93:LYS:O	1:A:97:GLN:HG3	2.13	0.48
1:B:786:ARG:NH1	1:B:787:GLN:O	2.47	0.48
1:B:667:LEU:HD12	1:B:667:LEU:HA	1.63	0.48
1:A:567:VAL:HG11	1:A:704:LEU:HD13	1.96	0.47
1:B:240:MET:HE2	1:B:352:LEU:HD21	1.96	0.47
1:A:775:ASN:O	1:A:778:THR:OG1	2.15	0.47
1:B:525:GLN:OE1	1:B:525:GLN:N	2.37	0.47
1:B:802:THR:HG22	1:B:807:ALA:HB2	1.95	0.47
1:A:112:ASP:OD1	1:A:116:ASN:N	2.48	0.47
1:B:406:ASN:O	1:B:410:MET:HG2	2.14	0.47
1:B:525:GLN:H	1:B:525:GLN:CD	2.21	0.47
1:B:317:LYS:HD2	1:B:317:LYS:HA	1.59	0.47
1:A:50:LYS:HB3	1:A:50:LYS:HE3	1.76	0.47
1:A:706:CYS:SG	1:A:707:LEU:N	2.88	0.47
1:B:590:THR:OG1	1:B:594:ASP:OD2	2.25	0.46
1:A:657:TYR:HE1	1:A:665:ARG:HD3	1.79	0.46
1:A:548:PHE:CE2	1:A:551:CYS:HB3	2.50	0.46
1:A:261:GLY:HA3	1:A:264:LYS:HD2	1.98	0.46
1:A:704:LEU:HD11	1:A:714:VAL:HG23	1.97	0.46
1:B:248:GLN:HA	1:B:368:LEU:HD21	1.96	0.45
1:B:418:LYS:HD2	1:B:421:SER:OG	2.16	0.45
1:B:620:GLU:C	1:B:635:LEU:HD21	2.40	0.45
1:B:326:ASN:HD22	1:B:333:TYR:HE2	1.64	0.45
1:A:620:GLU:N	1:A:620:GLU:OE1	2.49	0.45
1:A:566:ALA:O	1:A:722:LEU:HD12	2.16	0.45
1:A:63:GLU:HG2	1:A:263:SER:HB2	1.99	0.45
1:B:69:LYS:NZ	1:B:464:ASP:OD2	2.46	0.45
1:B:273:THR:O	1:B:277:GLU:HG3	2.16	0.45
1:A:686:ASP:HB2	1:A:688:LYS:NZ	2.31	0.45
1:A:798:LYS:N	1:A:799:PRO:HD2	2.32	0.45
1:B:63:GLU:HG2	1:B:263:SER:HB3	1.98	0.45
1:B:459:LYS:HE3	1:B:459:LYS:HB2	1.80	0.45
1:A:458:MET:HE2	1:A:458:MET:HA	1.99	0.44
1:A:572:LYS:HB3	1:A:701:ASP:C	2.42	0.44
1:B:363:GLU:OE1	1:B:364:VAL:HG22	2.17	0.44
1:B:622:CYS:SG	1:B:657:TYR:HB2	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:HIS:CD2	1:A:304:ILE:HG12	2.53	0.44
1:A:713:PRO:HG2	1:A:716:ASN:OD1	2.17	0.44
1:B:373:THR:OG1	1:B:375:LYS:NZ	2.51	0.44
1:A:714:VAL:HG11	3:A:1143:HOH:O	2.16	0.44
1:B:477:THR:HG21	1:B:483:LYS:HA	2.00	0.44
1:A:681:VAL:HG13	1:A:682:PHE:HD1	1.82	0.44
1:B:397:LYS:HB2	1:B:397:LYS:HE3	1.62	0.44
1:A:575:LYS:H	1:A:575:LYS:HG2	1.66	0.44
1:A:721:LYS:HA	1:A:721:LYS:HD3	1.81	0.44
1:B:594:ASP:O	1:B:599:VAL:HG23	2.18	0.44
1:A:317:LYS:HD3	1:A:317:LYS:HA	1.75	0.43
1:B:621:SER:HB2	1:B:632:LEU:HD12	2.00	0.43
1:A:98:ALA:HA	1:A:101:LYS:HD3	2.00	0.43
1:B:638:GLY:HA3	1:B:647:THR:O	2.18	0.43
1:B:665:ARG:HH11	1:B:693:TRP:CB	2.30	0.43
1:B:669:GLU:HB3	1:B:670:LYS:HG2	2.00	0.43
1:A:268:TRP:CZ2	1:A:291:ILE:HG23	2.51	0.43
1:B:718:LYS:O	1:B:721:LYS:NZ	2.49	0.43
1:A:735:GLU:OE2	1:A:735:GLU:N	2.27	0.43
1:A:184:ASP:OD1	1:A:188:ASN:N	2.52	0.43
1:A:32:ILE:HG21	1:A:408:PHE:HB2	2.01	0.43
1:B:578:ASN:OD1	1:B:581:ASN:N	2.52	0.43
1:B:637:ILE:HG13	1:B:670:LYS:HZ1	1.83	0.43
1:B:665:ARG:HH11	1:B:693:TRP:CG	2.37	0.43
1:A:466:HIS:CE1	1:A:468:PRO:HA	2.53	0.43
1:A:685:THR:HG23	1:A:686:ASP:OD1	2.18	0.43
1:B:733:ARG:NH2	3:B:1001:HOH:O	2.52	0.43
1:B:271:LEU:HD22	1:B:275:LEU:HG	2.00	0.43
1:B:466:HIS:O	1:B:468:PRO:HD3	2.19	0.43
1:B:828:SER:HB3	1:B:831:VAL:HG21	2.01	0.43
1:B:198:THR:HG23	1:B:200:TYR:H	1.83	0.43
1:B:390:ALA:O	1:B:449:TYR:OH	2.26	0.43
1:A:291:ILE:N	3:A:1021:HOH:O	2.52	0.43
1:B:190:GLU:OE2	1:B:808:SER:OG	2.27	0.43
1:A:624:PRO:HG2	1:A:658:TYR:HA	2.01	0.42
1:B:657:TYR:N	1:B:657:TYR:CD2	2.87	0.42
1:B:206:ALA:HB3	1:B:824:HIS:HE1	1.84	0.42
1:A:78:ILE:HB	1:A:393:VAL:HB	2.01	0.42
1:A:477:THR:HG22	1:A:773:LEU:HD21	2.01	0.42
1:A:658:TYR:CG	1:A:659:GLY:N	2.88	0.42
1:B:84:SER:OG	1:B:85:ASN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:TYR:OH	1:B:344:GLU:OE1	2.28	0.42
1:B:681:VAL:HG13	1:B:682:PHE:H	1.85	0.42
1:A:572:LYS:HE3	1:A:572:LYS:HB2	1.87	0.42
1:A:787:GLN:HG2	2:A:901:A1CTG:N01	2.34	0.42
1:B:101:LYS:HB3	1:B:103:MET:SD	2.60	0.42
1:A:681:VAL:O	1:A:685:THR:N	2.52	0.42
1:A:693:TRP:CD1	1:A:694:ALA:N	2.82	0.42
1:B:801:TYR:CE2	1:B:807:ALA:HA	2.54	0.42
1:A:586:LYS:HA	1:A:620:GLU:O	2.20	0.41
1:A:735:GLU:H	1:A:735:GLU:CD	2.17	0.41
1:B:124:GLY:N	3:B:1008:HOH:O	2.53	0.41
1:B:578:ASN:HA	1:B:705:LEU:HD11	2.01	0.41
1:B:42:THR:O	1:B:46:MET:HG3	2.20	0.41
1:B:216:THR:HG21	1:B:222:PRO:HA	2.01	0.41
1:B:595:ILE:HD12	1:B:800:TYR:OH	2.19	0.41
1:B:615:ASP:OD1	1:B:631:ASN:ND2	2.54	0.41
1:B:794:ASP:O	2:B:901:A1CTG:N03	2.52	0.41
1:A:604:LEU:HA	1:A:604:LEU:HD23	1.78	0.41
1:A:575:LYS:HG3	1:A:577:ILE:HG12	2.03	0.41
1:B:614:ILE:HB	1:B:632:LEU:HD22	2.02	0.41
1:A:205:ASN:HD21	1:A:209:GLU:HB2	1.84	0.41
1:B:102:LYS:NZ	1:B:416:GLN:OE1	2.27	0.41
1:A:681:VAL:HG13	1:A:682:PHE:N	2.35	0.41
1:A:574:ASN:HA	1:A:711:ARG:NH1	2.36	0.41
1:A:582:ILE:C	1:A:585:LYS:HG2	2.45	0.41
1:A:678:HIS:ND1	1:A:678:HIS:C	2.79	0.41
1:B:370:PRO:C	1:B:372:ASN:H	2.29	0.41
1:B:569:LEU:CD1	1:B:702:PHE:HB3	2.51	0.41
1:B:684:ASN:HB3	1:B:689:ASN:HD22	1.86	0.41
1:A:506:LYS:NZ	1:A:529:GLU:CD	2.78	0.41
1:A:686:ASP:OD1	1:A:699:SER:N	2.51	0.41
1:B:317:LYS:HE2	1:B:346:MET:HE2	2.02	0.41
1:B:320:GLU:H	1:B:320:GLU:HG2	1.60	0.41
1:A:660:ASN:HD21	1:A:676:VAL:HG12	1.85	0.41
1:A:697:LEU:HD13	1:A:698:LYS:N	2.36	0.41
1:B:159:PRO:HG2	1:B:187:GLY:HA3	2.03	0.41
1:A:332:TYR:CG	1:A:341:CYS:HB2	2.56	0.41
1:B:191:PRO:HD2	1:B:809:ARG:HG3	2.03	0.41
1:A:103:MET:HG3	1:A:106:HIS:ND1	2.36	0.40
1:A:205:ASN:ND2	1:A:209:GLU:HB2	2.35	0.40
1:A:758:LYS:HB3	1:A:758:LYS:HE2	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:LYS:HB2	1:B:69:LYS:HE3	1.82	0.40
1:B:396:ARG:HH21	1:B:400:ASP:CG	2.29	0.40
1:B:418:LYS:HD3	1:B:418:LYS:HA	1.70	0.40
1:B:60:ASP:OD1	1:B:61:SER:N	2.54	0.40
1:B:596:ALA:HB3	1:B:677:PRO:HD3	2.02	0.40
1:B:376:PRO:HB2	1:B:378:ASN:OD1	2.21	0.40
1:B:694:ALA:CA	1:B:697:LEU:HG	2.51	0.40
1:A:697:LEU:HD22	1:A:697:LEU:HA	1.83	0.40
1:B:184:ASP:OD1	1:B:188:ASN:N	2.54	0.40
1:B:629:LYS:HE3	1:B:629:LYS:HB3	1.91	0.40
1:A:180:VAL:HG23	1:A:180:VAL:O	2.22	0.40
1:A:411:GLU:OE1	1:A:415:ARG:NH1	2.54	0.40
1:A:478:ILE:HG12	1:A:482:GLU:OE1	2.22	0.40

All (1) 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)
1:A:345:ASP:OD2	1:A:629:LYS:NZ[4_455]	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	814/853 (95%)	766 (94%)	45 (6%)	3 (0%)	30	43
1	B	814/853 (95%)	775 (95%)	35 (4%)	4 (0%)	24	37
All	All	1628/1706 (95%)	1541 (95%)	80 (5%)	7 (0%)	30	43

All (7) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	B	300	SER
1	A	552	LYS
1	A	596	ALA
1	B	429	MET
1	B	90	LYS
1	A	598	TRP
1	B	613	ASP

### 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	704/731 (96%)	696 (99%)	8 (1%)	65	82
1	B	704/731 (96%)	693 (98%)	11 (2%)	55	76
All	All	1408/1462 (96%)	1389 (99%)	19 (1%)	61	80

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	233	THR
1	A	448	LEU
1	A	595	ILE
1	A	611	ASN
1	A	743	ILE
1	A	780	CYS
1	A	781	LEU
1	A	782	ILE
1	B	33	THR
1	B	104	ILE
1	B	204	VAL
1	B	271	LEU
1	B	632	LEU
1	B	634	LYS
1	B	667	LEU
1	B	668	VAL
1	B	670	LYS

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Mol	Chain	Res	Type
1	B	695	LYS
1	B	832	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	156	HIS
1	A	248	GLN
1	A	335	ASN
1	A	378	ASN
1	A	525	GLN
1	A	578	ASN
1	A	581	ASN
1	A	660	ASN
1	A	746	ASN
1	A	748	GLN
1	B	28	ASN
1	B	89	GLN
1	B	123	HIS
1	B	143	ASN
1	B	309	GLN
1	B	315	GLN
1	B	323	ASN
1	B	326	ASN
1	B	335	ASN
1	B	406	ASN
1	B	511	GLN
1	B	689	ASN
1	B	824	HIS

### 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

2 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	A1CTG	B	901	-	23,29,29	0.52	0	22,45,45	1.04	1 (4%)
2	A1CTG	A	901	-	23,29,29	0.45	0	22,45,45	1.20	4 (18%)

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	A1CTG	B	901	-	-	1/9/57/57	0/4/4/4
2	A1CTG	A	901	-	-	2/9/57/57	0/4/4/4

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	A1CTG	C16-C06-N07	3.13	115.28	109.64
2	B	901	A1CTG	N03-C04-N09	-2.94	107.36	112.45
2	A	901	A1CTG	C05-C06-N07	2.43	111.54	108.86
2	A	901	A1CTG	N03-C04-N09	-2.14	108.75	112.45
2	A	901	A1CTG	N03-C02-N26	2.01	111.25	109.21

There are no chirality outliers.

All (3) torsion outliers are listed below:

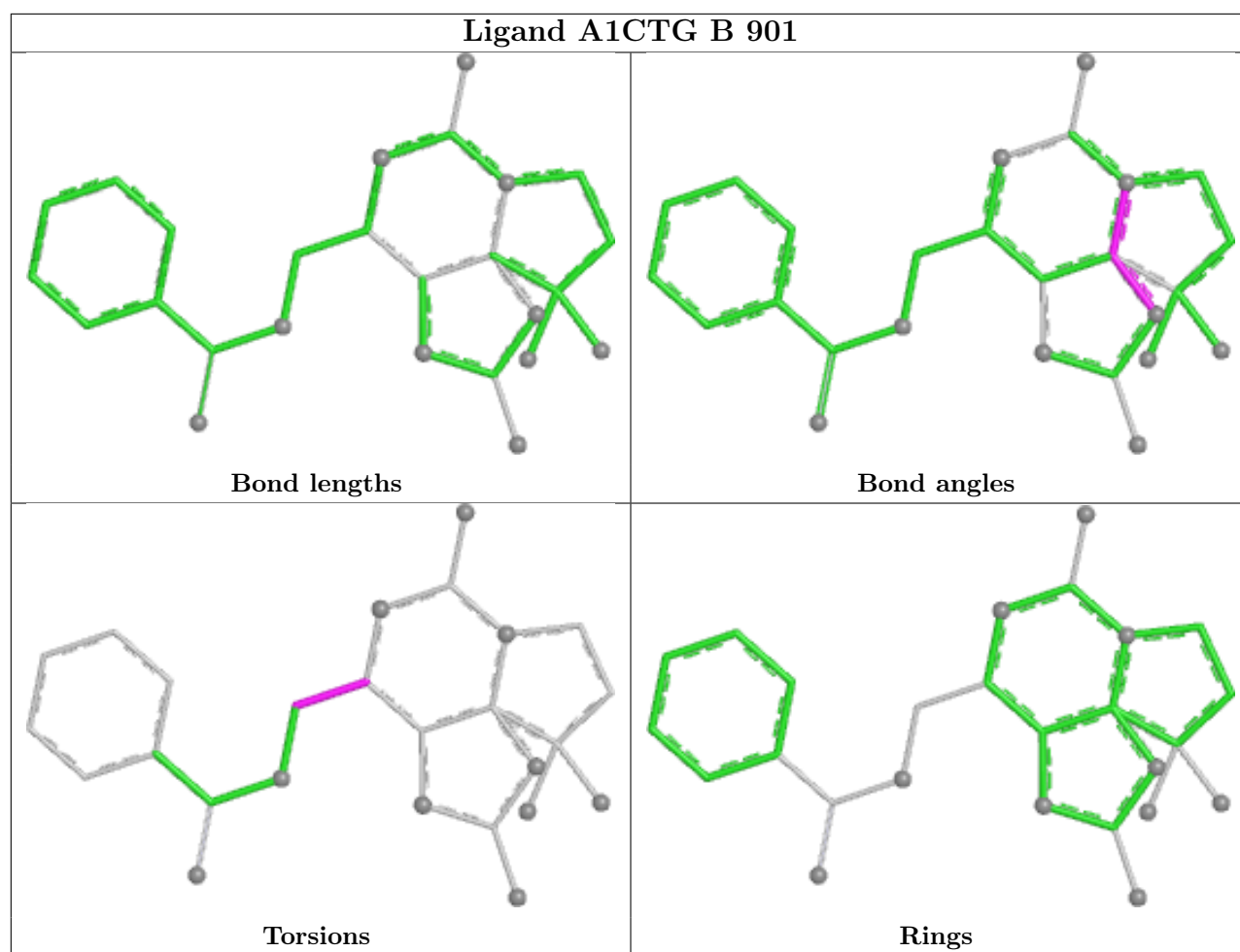
Mol	Chain	Res	Type	Atoms
2	A	901	A1CTG	C05-C06-C16-O17
2	B	901	A1CTG	C05-C06-C16-O17
2	A	901	A1CTG	N07-C06-C16-O17

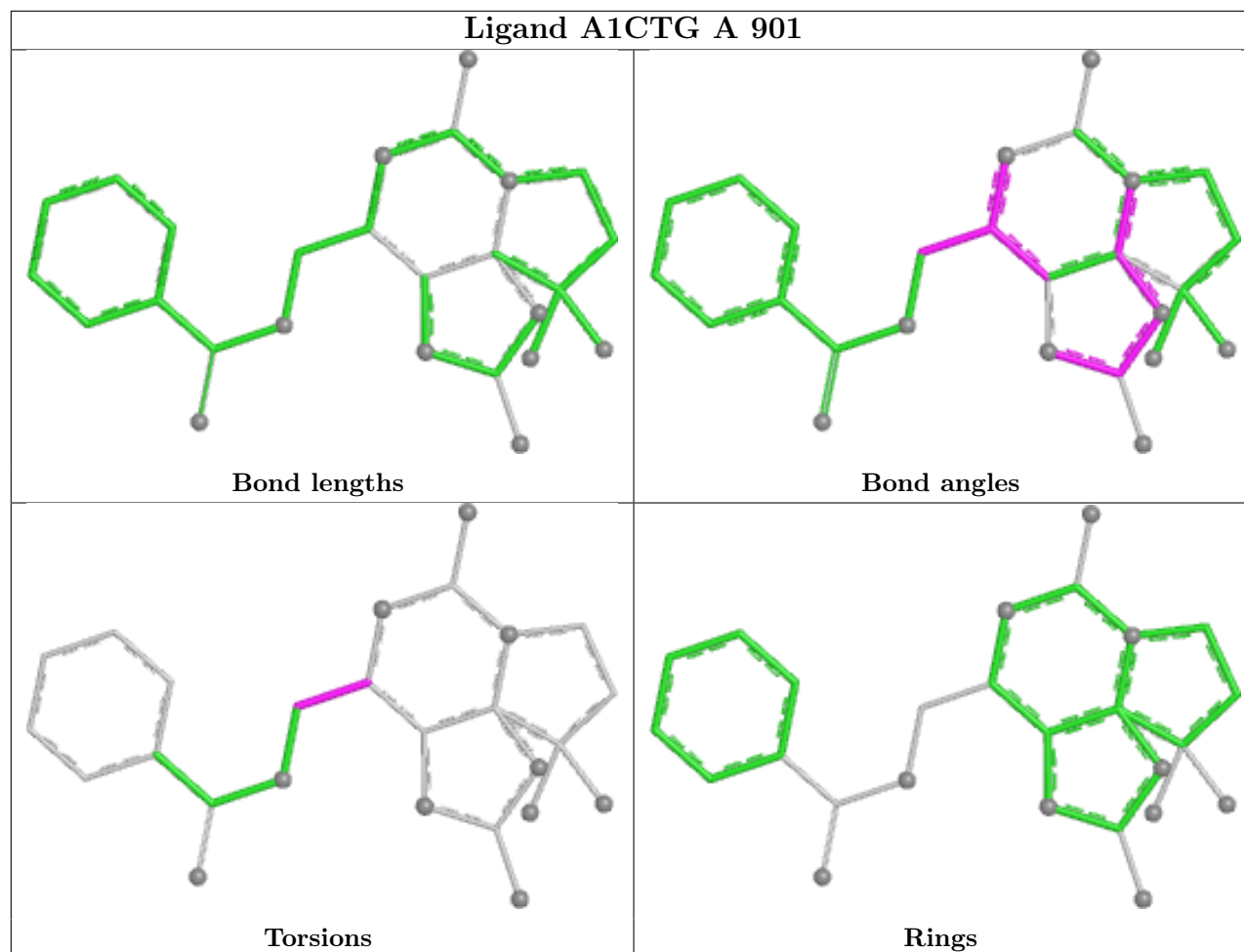
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	A1CTG	1	0
2	A	901	A1CTG	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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	818/853 (95%)	0.71	96 (11%) <b>9</b> <b>7</b>	46, 82, 174, 218	0
1	B	818/853 (95%)	0.74	73 (8%) <b>15</b> <b>12</b>	51, 85, 159, 224	0
All	All	1636/1706 (95%)	0.73	169 (10%) <b>12</b> <b>9</b>	46, 84, 172, 224	0

All (169) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	832	LEU	9.6
1	A	595	ILE	8.8
1	B	618	PHE	6.9
1	A	645	ALA	5.8
1	B	88	LEU	5.4
1	B	831	VAL	5.1
1	A	596	ALA	4.8
1	B	83	SER	4.8
1	A	168	ALA	4.6
1	B	674	ALA	4.6
1	B	614	ILE	4.2
1	A	724	GLY	4.1
1	A	579	TRP	4.1
1	B	829	LEU	4.1
1	A	644	ALA	4.0
1	A	564	LEU	3.9
1	A	162	LEU	3.8
1	A	707	LEU	3.8
1	A	725	ILE	3.7
1	B	179	PHE	3.7
1	A	780	CYS	3.7
1	A	637	ILE	3.5
1	A	186	LYS	3.5
1	B	717	TYR	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	723	SER	3.5
1	B	708	ASP	3.4
1	A	614	ILE	3.4
1	B	87	ASP	3.3
1	A	676	VAL	3.3
1	A	795	TYR	3.3
1	A	640	PRO	3.3
1	B	693	TRP	3.3
1	B	570	VAL	3.2
1	A	566	ALA	3.2
1	A	722	LEU	3.2
1	A	675	PHE	3.2
1	A	682	PHE	3.2
1	B	82	TYR	3.2
1	A	635	LEU	3.2
1	A	721	LYS	3.2
1	B	602	VAL	3.2
1	B	207	ILE	3.2
1	A	643	SER	3.1
1	A	577	ILE	3.1
1	B	569	LEU	3.1
1	B	167	VAL	3.1
1	B	607	ARG	3.1
1	A	680	VAL	3.1
1	A	551	CYS	3.1
1	B	589	HIS	3.0
1	B	99	LEU	3.0
1	B	617	PHE	3.0
1	B	551	CYS	3.0
1	A	692	VAL	2.9
1	B	605	ILE	2.9
1	B	712	ALA	2.9
1	A	600	ILE	2.9
1	A	726	PRO	2.9
1	A	774	PHE	2.9
1	A	642	ASN	2.9
1	B	612	SER	2.9
1	B	287	ALA	2.9
1	A	283	TRP	2.9
1	B	9	TRP	2.9
1	A	601	PRO	2.8
1	B	668	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	568	ALA	2.8
1	B	664	PHE	2.8
1	A	717	TYR	2.8
1	A	805	TYR	2.8
1	A	673	VAL	2.8
1	A	221	ILE	2.7
1	B	90	LYS	2.7
1	A	185	GLU	2.7
1	B	468	PRO	2.7
1	A	731	VAL	2.7
1	B	5	LYS	2.7
1	A	781	LEU	2.7
1	B	579	TRP	2.7
1	A	679	THR	2.7
1	B	587	SER	2.7
1	A	677	PRO	2.6
1	A	569	LEU	2.6
1	B	673	VAL	2.6
1	B	830	GLU	2.6
1	B	709	GLY	2.6
1	B	722	LEU	2.6
1	A	156	HIS	2.6
1	A	638	GLY	2.6
1	A	599	VAL	2.6
1	A	647	THR	2.6
1	B	103	MET	2.5
1	A	791	ILE	2.5
1	B	104	ILE	2.5
1	A	664	PHE	2.5
1	A	796	PHE	2.5
1	A	830	GLU	2.5
1	A	684	ASN	2.5
1	B	89	GLN	2.5
1	B	826	SER	2.5
1	A	567	VAL	2.5
1	B	714	VAL	2.5
1	B	573	SER	2.5
1	A	705	LEU	2.4
1	A	557	PRO	2.4
1	A	5	LYS	2.4
1	A	681	VAL	2.4
1	A	714	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	763	LEU	2.4
1	A	811	ALA	2.4
1	A	719	SER	2.4
1	A	536	LEU	2.4
1	A	604	LEU	2.4
1	A	179	PHE	2.4
1	A	538	ALA	2.4
1	A	694	ALA	2.4
1	B	158	LEU	2.3
1	B	467	LEU	2.3
1	A	646	ASN	2.3
1	B	716	ASN	2.3
1	A	563	THR	2.3
1	A	475	TRP	2.3
1	B	84	SER	2.3
1	B	828	SER	2.3
1	B	812	MET	2.3
1	A	800	TYR	2.3
1	A	832	LEU	2.2
1	B	705	LEU	2.2
1	A	580	ASN	2.2
1	A	558	TYR	2.2
1	B	380	TYR	2.2
1	B	282	SER	2.2
1	A	708	ASP	2.2
1	B	702	PHE	2.2
1	A	79	ALA	2.2
1	A	718	LYS	2.2
1	A	224	THR	2.2
1	A	602	VAL	2.2
1	A	187	GLY	2.2
1	A	383	CYS	2.2
1	A	709	GLY	2.2
1	B	181	PRO	2.2
1	A	519	ALA	2.1
1	A	660	ASN	2.1
1	A	704	LEU	2.1
1	A	752	GLY	2.1
1	B	597	GLY	2.1
1	A	524	VAL	2.1
1	B	180	VAL	2.1
1	A	716	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	576	ASP	2.1
1	B	106	HIS	2.1
1	B	430	PHE	2.1
1	A	559	THR	2.1
1	A	597	GLY	2.1
1	A	715	SER	2.1
1	A	223	ALA	2.1
1	B	584	GLY	2.1
1	B	317	LYS	2.1
1	B	575	LYS	2.1
1	A	710	SER	2.1
1	B	283	TRP	2.0
1	B	598	TRP	2.0
1	B	619	GLY	2.0
1	B	536	LEU	2.0
1	A	671	GLY	2.0
1	B	202	TRP	2.0
1	B	672	ASP	2.0
1	B	713	PRO	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 oligosaccharides 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.

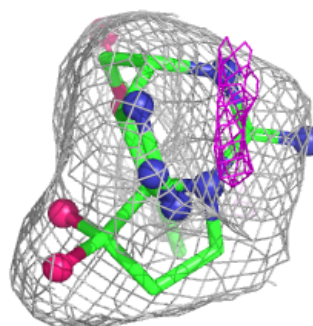
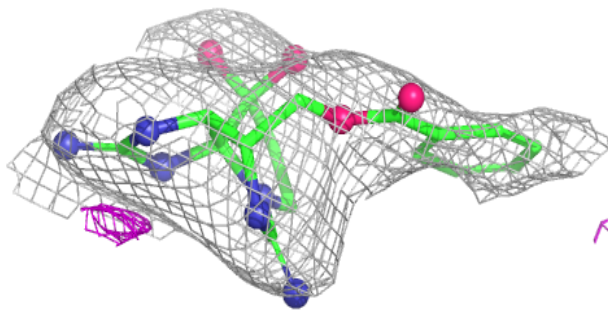
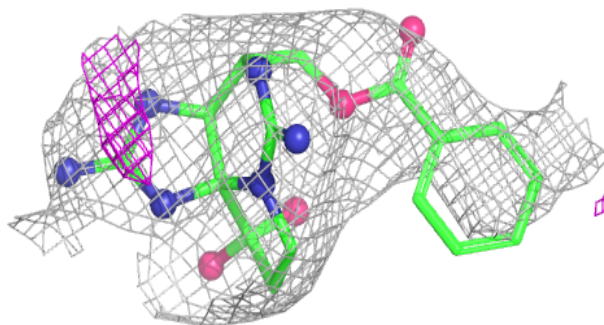
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	A1CTG	A	901	26/26	0.85	0.12	116,125,133,149	0
2	A1CTG	B	901	26/26	0.94	0.12	73,89,101,112	0

The following is a graphical depiction of the model fit to experimental electron density of all

instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

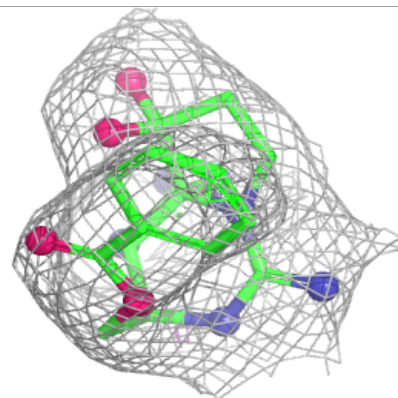
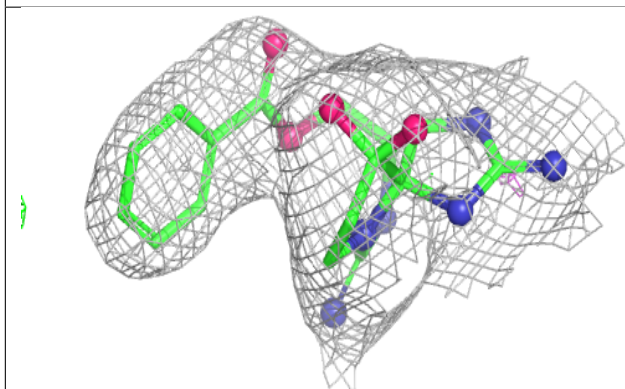
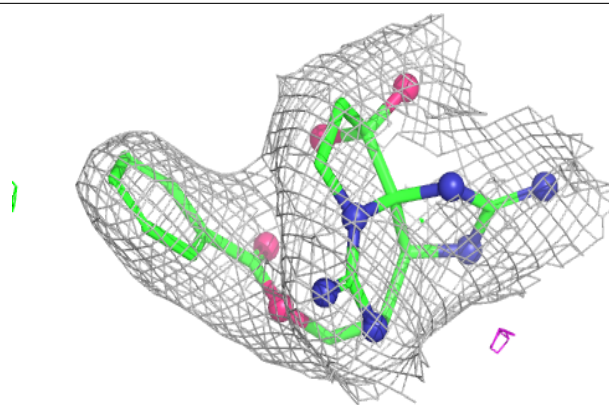
**Electron density around A1CTG A 901:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around A1CTG B 901:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.