



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 08:01 PM GMT

PDB ID : 4J2T  
Title : Inhibitor-bound Ca<sup>2+</sup> ATPase  
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Deposited on : 2013-02-05  
Resolution : 3.20 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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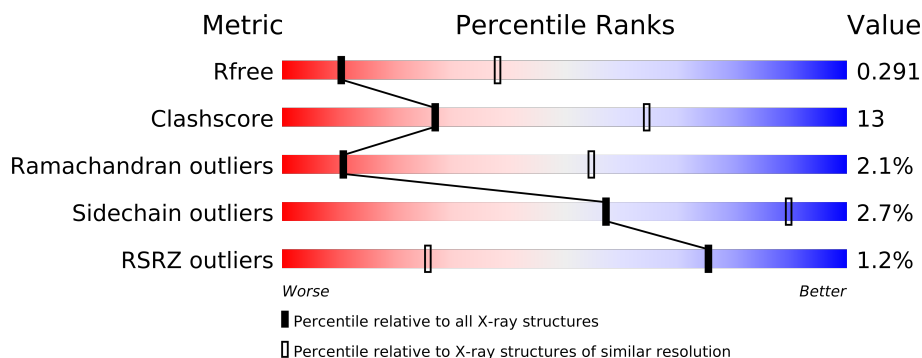
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.20 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))
$R_{free}$	66092	1824 (3.30-3.10)
Clashscore	79885	1078 (3.26-3.14)
Ramachandran outliers	78287	1059 (3.26-3.14)
Sidechain outliers	78261	1058 (3.26-3.14)
RSRZ outliers	66119	1825 (3.30-3.10)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	994	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	PTY	A	1002	-	X

## 2 Entry composition i

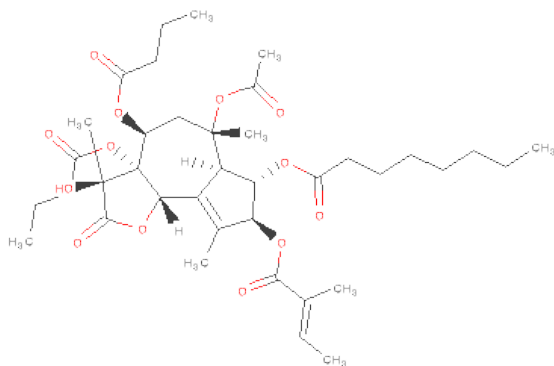
There are 5 unique types of molecules in this entry. The entry contains 7748 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called SERCA1a.

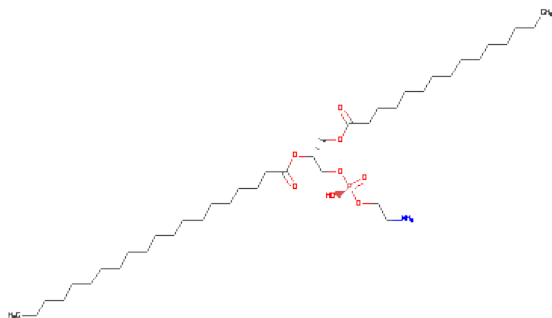
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	994	7671	4876	1287	1451	57	0	0	0

- Molecule 2 is (3S,3AR,4S,6S,6AR,7S,8S,9BS)-6-(ACETYLOXY)-3A,4-BIS(BUTANOYLOXY)-3-HYDROXY-3,6,9-TRIMETHYL-8-{[(2E)-2-METHYLBUT-2-ENOYL]OXY}-2-OXO-2,3,3A,4,5,6,6A,7,8,9B-DECAHYDROAZULENO[4,5-B]FURAN-7-YLOCTANOATE (three-letter code: 1HT) (formula: C<sub>38</sub>H<sub>56</sub>O<sub>13</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	51	38	13	0	0

- Molecule 3 is PHOSPHATIDYLETHANOLAMINE (three-letter code: PTY) (formula: C<sub>40</sub>H<sub>80</sub>NO<sub>8</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			24	14	1	8	1		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	K	0	0
			1	1		

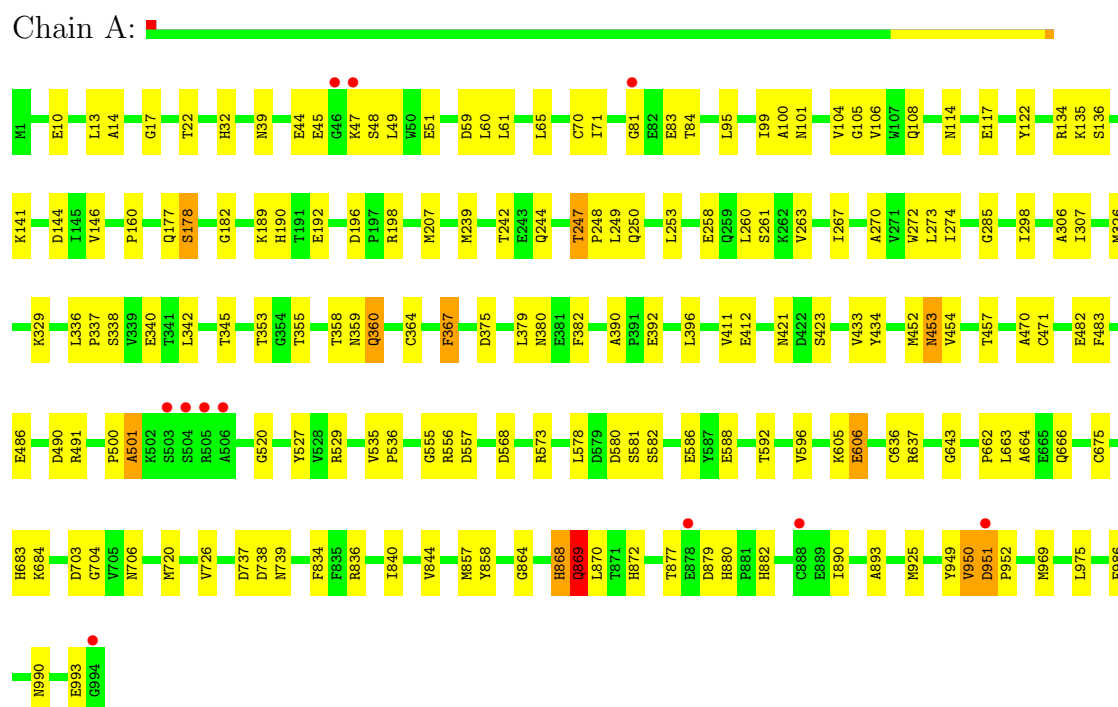
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	O	0	0
			1	1		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: SERCA1a



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.90Å 70.90Å 587.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.71 – 3.20 28.71 – 3.01	Depositor EDS
% Data completeness (in resolution range)	99.7 (28.71-3.20) 99.6 (28.71-3.01)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.88 (at 3.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.260 , 0.286 0.270 , 0.291	Depositor DCC
$R_{free}$ test set	2001 reflections (6.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	73.5	Xtriage
Anisotropy	0.212	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 48.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.35$ , $\langle L^2 \rangle = 0.18$	Xtriage
Outliers	0 of 31414 reflections	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	7748	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, PTY, 1HT

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	0.46	1/7812 (0.0%)	0.69	1/10592 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	39	ASN	C-N	-5.05	1.22	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	870	LEU	N-CA-C	-5.64	95.78	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7671	0	724	111	0
2	A	51	0	55	4	0
3	A	24	0	21	2	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	1	0	0	2	0
All	All	7748	0	800	111	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

All (111) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:527:TYR:CB	1:A:592:THR:CG2	2.30	1.09
1:A:247:THR:HG22	1:A:250:GLN:H	1.24	0.98
1:A:483:PHE:CE1	1:A:578:LEU:CD2	2.48	0.97
1:A:248:PRO:HG2	1:A:340:GLU:OE2	1.73	0.89
1:A:834:PHE:CE2	2:A:1001:1HT:OAM	2.31	0.83
1:A:47:LYS:HA	1:A:51:GLU:OE1	1.81	0.80
1:A:986:PHE:CZ	1:A:990:ASN:OD1	2.34	0.80
1:A:986:PHE:CE1	1:A:990:ASN:OD1	2.36	0.79
1:A:267:ILE:HD11	2:A:1001:1HT:H2	1.65	0.77
1:A:239:MET:O	1:A:242:THR:HG22	1.85	0.76
1:A:342:LEU:O	1:A:345:THR:HG23	1.86	0.74
1:A:247:THR:HG22	1:A:250:GLN:N	2.01	0.74
1:A:106:VAL:C	1:A:108:GLN:N	2.41	0.72
1:A:105:GLY:O	1:A:108:GLN:HB3	1.96	0.65
1:A:247:THR:HG23	1:A:340:GLU:OE1	1.96	0.65
1:A:527:TYR:CD2	1:A:592:THR:CG2	2.80	0.64
1:A:44:GLU:H	1:A:44:GLU:CD	1.99	0.64
1:A:192:GLU:OE1	1:A:580:ASP:CB	2.47	0.63
1:A:244:GLN:HB3	5:A:1101:HOH:O	1.98	0.62
1:A:869:GLN:CB	1:A:872:HIS:ND1	2.62	0.62
1:A:483:PHE:CD1	1:A:578:LEU:CD2	2.82	0.62
1:A:263:VAL:HG11	2:A:1001:1HT:OAN	2.00	0.62
1:A:358:THR:HG22	1:A:360:GLN:HG3	1.82	0.61
1:A:45:GLU:OE2	1:A:47:LYS:HG3	2.00	0.61
1:A:326:MET:O	1:A:329:LYS:N	2.37	0.57
1:A:10:GLU:N	1:A:10:GLU:OE1	2.38	0.56
1:A:527:TYR:CG	1:A:592:THR:CG2	2.88	0.56
1:A:61:LEU:CD2	1:A:260:LEU:HD23	2.36	0.56
1:A:104:VAL:O	1:A:108:GLN:HB2	2.06	0.56
1:A:177:GLN:O	1:A:178:SER:C	2.44	0.56
1:A:247:THR:CG2	1:A:250:GLN:HG3	2.36	0.55
1:A:247:THR:HB	1:A:250:GLN:HG3	1.88	0.55
1:A:122:TYR:HE2	1:A:726:VAL:CG2	2.19	0.54
1:A:95:LEU:O	1:A:99:ILE:N	2.40	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:857:MET:O	1:A:858:TYR:CB	2.55	0.54
1:A:358:THR:O	1:A:359:ASN:HB3	2.08	0.54
1:A:247:THR:HG23	1:A:249:LEU:H	1.73	0.54
1:A:421:ASN:OD1	1:A:423:SER:N	2.43	0.52
1:A:272:TRP:CZ3	1:A:273:LEU:HD23	2.45	0.52
1:A:114:ASN:HB3	1:A:117:GLU:HG2	1.92	0.52
1:A:65:LEU:CG	1:A:307:ILE:CD1	2.88	0.52
1:A:482:GLU:OE1	1:A:573:ARG:NH1	2.43	0.51
1:A:244:GLN:CB	5:A:1101:HOH:O	2.58	0.51
1:A:270:ALA:O	1:A:274:ILE:CG1	2.60	0.50
1:A:529:ARG:NH2	1:A:568:ASP:OD1	2.44	0.50
1:A:338:SER:C	1:A:340:GLU:N	2.65	0.50
1:A:580:ASP:O	1:A:582:SER:N	2.45	0.50
1:A:367:PHE:CD1	1:A:367:PHE:C	2.84	0.49
1:A:70:CYS:O	1:A:71:ILE:C	2.51	0.49
1:A:267:ILE:CD1	2:A:1001:1HT:H2	2.38	0.48
1:A:412:GLU:OE2	1:A:529:ARG:NE	2.46	0.48
1:A:100:ALA:CB	3:A:1002:PTY:H311	2.43	0.48
1:A:491:ARG:NE	1:A:588:GLU:OE1	2.46	0.48
1:A:59:ASP:OD1	1:A:60:LEU:N	2.45	0.47
1:A:48:SER:N	1:A:51:GLU:OE1	2.44	0.47
1:A:662:PRO:O	1:A:664:ALA:N	2.48	0.47
1:A:134:ARG:NH2	1:A:136:SER:OG	2.47	0.47
1:A:453:ASN:CB	1:A:471:CYS:SG	3.03	0.46
1:A:949:TYR:O	1:A:951:ASP:N	2.48	0.46
1:A:380:ASN:O	1:A:382:PHE:CE1	2.69	0.46
1:A:483:PHE:CZ	1:A:578:LEU:CD2	2.99	0.45
1:A:44:GLU:HG3	1:A:117:GLU:OE2	2.16	0.45
1:A:190:HIS:NE2	1:A:486:GLU:OE2	2.50	0.45
1:A:706:ASN:N	1:A:706:ASN:OD1	2.49	0.45
1:A:338:SER:O	1:A:340:GLU:N	2.50	0.45
1:A:535:VAL:CG1	1:A:536:PRO:CD	2.95	0.45
1:A:358:THR:CG2	1:A:360:GLN:HG3	2.47	0.45
1:A:44:GLU:N	1:A:44:GLU:CD	2.70	0.44
1:A:247:THR:CB	1:A:250:GLN:HG3	2.48	0.44
1:A:586:GLU:N	1:A:586:GLU:OE1	2.50	0.44
1:A:178:SER:O	1:A:182:GLY:N	2.51	0.44
1:A:949:TYR:O	1:A:950:VAL:C	2.56	0.44
1:A:390:ALA:O	1:A:392:GLU:N	2.50	0.44
1:A:14:ALA:O	1:A:17:GLY:N	2.51	0.44
1:A:868:HIS:C	1:A:868:HIS:ND1	2.72	0.44
1:A:877:THR:O	1:A:880:HIS:ND1	2.51	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:247:THR:CG2	1:A:340:GLU:OE1	2.65	0.43
1:A:555:GLY:O	1:A:557:ASP:N	2.51	0.43
1:A:258:GLU:O	1:A:261:SER:HB3	2.18	0.43
1:A:737:ASP:C	1:A:739:ASN:N	2.72	0.43
1:A:737:ASP:O	1:A:739:ASN:N	2.51	0.43
1:A:500:PRO:O	1:A:501:ALA:CB	2.66	0.43
1:A:890:ILE:O	1:A:893:ALA:CB	2.67	0.42
1:A:355:THR:CG2	1:A:720:MET:SD	3.07	0.42
1:A:879:ASP:OD1	1:A:882:HIS:CB	2.67	0.42
1:A:951:ASP:O	1:A:952:PRO:C	2.58	0.42
1:A:336:LEU:HB2	1:A:337:PRO:HD3	2.01	0.42
1:A:192:GLU:CD	1:A:580:ASP:CB	2.87	0.42
1:A:836:ARG:O	1:A:840:ILE:N	2.53	0.42
1:A:196:ASP:OD1	1:A:198:ARG:N	2.53	0.42
1:A:59:ASP:OD1	1:A:61:LEU:N	2.53	0.41
1:A:10:GLU:O	1:A:13:LEU:N	2.53	0.41
1:A:636:CYS:SG	1:A:675:CYS:SG	3.19	0.41
1:A:253:LEU:HD23	1:A:253:LEU:C	2.40	0.41
1:A:177:GLN:OE1	1:A:189:LYS:NZ	2.53	0.41
1:A:452:MET:O	1:A:454:VAL:N	2.53	0.41
1:A:834:PHE:C	1:A:834:PHE:CD1	2.94	0.41
1:A:32:HIS:CB	1:A:146:VAL:CG1	2.98	0.41
1:A:338:SER:C	1:A:340:GLU:H	2.23	0.41
1:A:260:LEU:HD11	1:A:306:ALA:CB	2.51	0.41
1:A:433:VAL:CG1	1:A:434:TYR:N	2.83	0.41
1:A:105:GLY:CA	3:A:1002:PTY:HC21	2.51	0.41
1:A:367:PHE:CE1	1:A:379:LEU:CD2	3.05	0.40
1:A:141:LYS:O	1:A:144:ASP:N	2.54	0.40
1:A:637:ARG:NH1	1:A:643:GLY:O	2.54	0.40
1:A:247:THR:HG22	1:A:250:GLN:HG3	2.02	0.40
1:A:580:ASP:C	1:A:582:SER:N	2.73	0.40
1:A:683:HIS:O	1:A:684:LYS:C	2.57	0.40
1:A:192:GLU:OE2	1:A:580:ASP:CA	2.70	0.40
1:A:83:GLU:O	1:A:84:THR:OG1	2.39	0.40
1:A:703:ASP:OD1	1:A:704:GLY:N	2.55	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	992/994 (100%)	865 (87%)	106 (11%)	21 (2%)	11	55

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	353	THR
1	A	950	VAL
1	A	453	ASN
1	A	501	ALA
1	A	581	SER
1	A	606	GLU
1	A	663	LEU
1	A	869	GLN
1	A	285	GLY
1	A	457	THR
1	A	556	ARG
1	A	178	SER
1	A	520	GLY
1	A	738	ASP
1	A	951	ASP
1	A	81	GLY
1	A	160	PRO
1	A	470	ALA
1	A	605	LYS
1	A	864	GLY
1	A	975	LEU

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	840/840 (100%)	817 (97%)	23 (3%)	57 90

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	THR
1	A	49	LEU
1	A	101	ASN
1	A	135	LYS
1	A	207	MET
1	A	247	THR
1	A	298	ILE
1	A	360	GLN
1	A	364	CYS
1	A	367	PHE
1	A	375	ASP
1	A	396	LEU
1	A	411	VAL
1	A	490	ASP
1	A	596	VAL
1	A	606	GLU
1	A	666	GLN
1	A	844	VAL
1	A	868	HIS
1	A	869	GLN
1	A	925	MET
1	A	969	MET
1	A	993	GLU

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 chains in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is 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	$\# Z  > 2$
2	1HT	A	1001	-	53,53,53	3.31	24 (45%)	78,78,78	3.42	36 (46%)
3	PTY	A	1002	-	23,23,49	2.16	4 (17%)	27,28,54	2.07	4 (14%)

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	1HT	A	1001	-	-	0/41/107/107	0/0/3/3
3	PTY	A	1002	-	-	0/27/27/53	0/0/0/0

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	1HT	CBN-CBQ	11.66	1.54	1.33
3	A	1002	PTY	O30-C30	7.02	1.43	1.22
2	A	1001	1HT	OAO-CBP	6.60	1.36	1.20
2	A	1001	1HT	OBG-CBX	-6.52	1.36	1.48
2	A	1001	1HT	OBD-CBT	-6.40	1.34	1.44
2	A	1001	1HT	CBU-CBQ	6.24	1.57	1.50
2	A	1001	1HT	OBF-CBU	-5.49	1.37	1.46
2	A	1001	1HT	OBC-CBR	-5.38	1.36	1.46
2	A	1001	1HT	OBE-CBS	-5.26	1.34	1.44
2	A	1001	1HT	OBF-CBP	4.42	1.42	1.35
2	A	1001	1HT	CAQ-CBJ	4.30	1.60	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	1HT	CBY-CBU	-4.29	1.47	1.52
3	A	1002	PTY	C35-C34	-4.25	1.53	1.55
3	A	1002	PTY	C12-C11	-4.24	1.53	1.55
2	A	1001	1HT	CAG-CBN	-4.14	1.43	1.50
2	A	1001	1HT	CBW-CBY	-3.69	1.46	1.55
2	A	1001	1HT	OBE-CBO	3.69	1.43	1.34
2	A	1001	1HT	CBS-CBN	3.40	1.55	1.50
3	A	1002	PTY	O4-C30	3.36	1.43	1.33
2	A	1001	1HT	CAF-CBJ	3.33	1.59	1.50
2	A	1001	1HT	CBO-CBJ	3.09	1.62	1.50
2	A	1001	1HT	OBH-CBY	-2.91	1.40	1.45
2	A	1001	1HT	CBX-CBV	2.82	1.62	1.54
2	A	1001	1HT	OBC-CBK	2.42	1.41	1.34
2	A	1001	1HT	CBW-CBP	-2.35	1.49	1.53
2	A	1001	1HT	OAP-CBW	-2.28	1.38	1.42
2	A	1001	1HT	CBV-CBT	-2.26	1.51	1.54
2	A	1001	1HT	OBH-CBM	2.25	1.41	1.33

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	1HT	OAO-CBP-CBW	-14.19	119.08	128.26
2	A	1001	1HT	OBF-CBP-OAO	-11.52	104.43	121.67
2	A	1001	1HT	CAG-CBN-CBQ	-9.79	103.88	129.63
2	A	1001	1HT	OBF-CBP-CBW	-6.93	103.85	110.10
3	A	1002	PTY	O7-C8-C11	6.86	119.75	110.64
2	A	1001	1HT	CBU-OBF-CBP	-5.84	102.10	110.79
2	A	1001	1HT	OBF-CBU-CBY	-5.84	100.44	104.24
2	A	1001	1HT	CBY-CBU-CBQ	5.83	129.00	115.31
3	A	1002	PTY	O4-C30-O30	-5.48	108.45	123.43
2	A	1001	1HT	CBU-CBQ-CBN	-4.76	115.36	123.41
2	A	1001	1HT	CBT-CBS-CBN	4.74	109.13	103.06
2	A	1001	1HT	OBH-CBM-OAM	-4.42	115.81	125.01
2	A	1001	1HT	CBY-OBH-CBM	4.29	131.51	121.27
2	A	1001	1HT	CAI-CBX-CBB	4.01	118.42	110.42
3	A	1002	PTY	O30-C30-C31	-3.80	108.09	123.78
2	A	1001	1HT	OBE-CBO-CBJ	3.60	121.16	111.61
2	A	1001	1HT	CBW-CBY-CBU	-3.48	96.09	102.91
2	A	1001	1HT	CBB-CBR-CBY	3.46	122.70	115.79
2	A	1001	1HT	CBS-CBN-CBQ	-3.35	96.98	107.76
2	A	1001	1HT	OBG-CBX-CBV	-3.09	91.83	103.50
2	A	1001	1HT	CAF-CBJ-CAQ	-2.81	110.55	123.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	1HT	CBX-OBG-CBI	2.71	129.08	122.10
2	A	1001	1HT	OAP-CBW-CAH	-2.70	104.88	109.57
2	A	1001	1HT	OBH-CBM-CAZ	2.67	116.08	110.64
2	A	1001	1HT	OBF-CBU-CBQ	2.67	115.73	111.42
2	A	1001	1HT	OAM-CBM-CAZ	-2.63	112.93	123.78
2	A	1001	1HT	OBC-CBR-CBY	-2.62	102.04	108.72
2	A	1001	1HT	OBC-CBK-OAK	-2.57	116.75	123.65
3	A	1002	PTY	C6-O7-C8	-2.56	111.60	117.92
2	A	1001	1HT	OBE-CBO-OAN	-2.54	118.32	123.23
2	A	1001	1HT	OBG-CBI-OAJ	-2.41	118.53	123.58
2	A	1001	1HT	CAG-CBN-CBS	-2.41	116.10	120.78
2	A	1001	1HT	OBE-CBS-CBN	2.41	116.00	108.64
2	A	1001	1HT	OAN-CBO-CBJ	-2.29	117.66	125.20
2	A	1001	1HT	OBG-CBI-CAE	2.27	115.41	110.73
2	A	1001	1HT	OBD-CBL-CBA	2.26	116.51	111.56
2	A	1001	1HT	OBH-CBY-CBR	-2.16	103.63	108.07
2	A	1001	1HT	OBE-CBS-CBT	-2.12	107.34	112.92
2	A	1001	1HT	OAJ-CBI-CAE	-2.06	117.44	124.96
2	A	1001	1HT	CBX-CBV-CBT	2.06	120.02	114.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	994/994 (100%)	-0.07	11 (1%) 77 27	30, 91, 164, 257	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	46	GLY	3.6
1	A	81	GLY	3.1
1	A	47	LYS	3.1
1	A	878	GLU	3.0
1	A	503	SER	2.5
1	A	504	SER	2.5
1	A	888	CYS	2.4
1	A	951	ASP	2.3
1	A	506	ALA	2.3
1	A	505	ARG	2.2
1	A	994	GLY	2.1

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.



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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	PTY	A	1002	24/50	0.52	6.57	114,124,132,133	0
2	1HT	A	1001	51/51	0.36	1.89	152,152,152,152	0
4	K	A	1003	1/1	0.14	-1.62	78,78,78,78	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.