



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:26 AM UTC

PDB ID : 4ZZJ / pdb_00004zzj
Title : SIRT1/Activator/Substrate Complex
Authors : Dai, H.
Deposited on : 2015-05-22
Resolution : 2.74 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
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

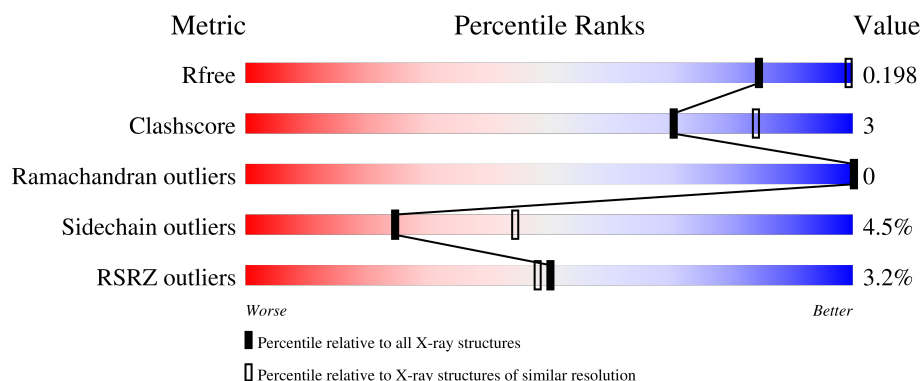
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.74 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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	356	3% 86% 10% ..
2	B	7	57% 29% 14%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 2961 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 NAD-dependent protein deacetylase sirtuin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	344	2755	1774	463	500	18	0	2	0

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	633	GLY	-	expression tag	UNP Q96EB6
A	634	GLY	-	expression tag	UNP Q96EB6
A	635	GLY	-	expression tag	UNP Q96EB6
A	636	SER	-	expression tag	UNP Q96EB6
A	637	GLY	-	expression tag	UNP Q96EB6
A	638	GLY	-	expression tag	UNP Q96EB6
A	639	GLY	-	expression tag	UNP Q96EB6
A	640	SER	-	expression tag	UNP Q96EB6
A	641	GLN	-	expression tag	UNP Q96EB6
A	642	TYR	-	expression tag	UNP Q96EB6
A	643	LEU	-	expression tag	UNP Q96EB6
A	644	PHE	-	expression tag	UNP Q96EB6
A	645	LEU	-	expression tag	UNP Q96EB6
A	646	PRO	-	expression tag	UNP Q96EB6
A	647	PRO	-	expression tag	UNP Q96EB6
A	648	ASN	-	expression tag	UNP Q96EB6
A	649	ARG	-	expression tag	UNP Q96EB6
A	650	TYR	-	expression tag	UNP Q96EB6
A	651	ILE	-	expression tag	UNP Q96EB6
A	652	PHE	-	expression tag	UNP Q96EB6
A	653	HIS	-	expression tag	UNP Q96EB6
A	654	GLY	-	expression tag	UNP Q96EB6
A	655	ALA	-	expression tag	UNP Q96EB6
A	656	GLU	-	expression tag	UNP Q96EB6
A	657	VAL	-	expression tag	UNP Q96EB6
A	658	TYR	-	expression tag	UNP Q96EB6
A	659	SER	-	expression tag	UNP Q96EB6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	660	ASP	-	expression tag	UNP Q96EB6
A	661	SER	-	expression tag	UNP Q96EB6
A	662	GLU	-	expression tag	UNP Q96EB6
A	663	ASP	-	expression tag	UNP Q96EB6
A	664	ASP	-	expression tag	UNP Q96EB6
A	665	VAL	-	expression tag	UNP Q96EB6

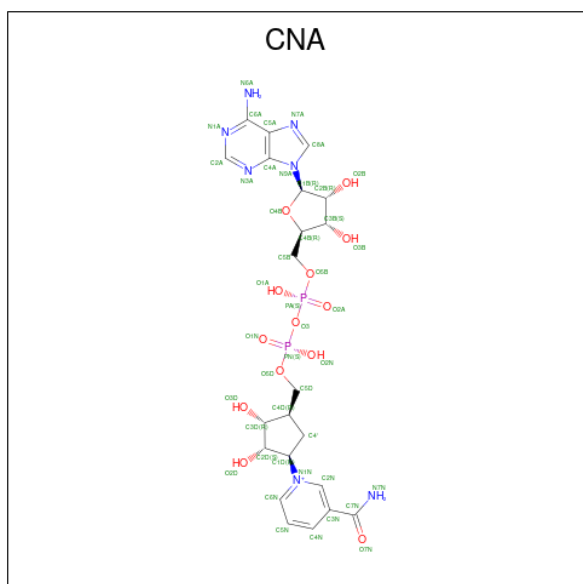
- Molecule 2 is a protein called Ac-p53.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	7	Total	C	N	O	0	0	0
			69	47	14	8			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

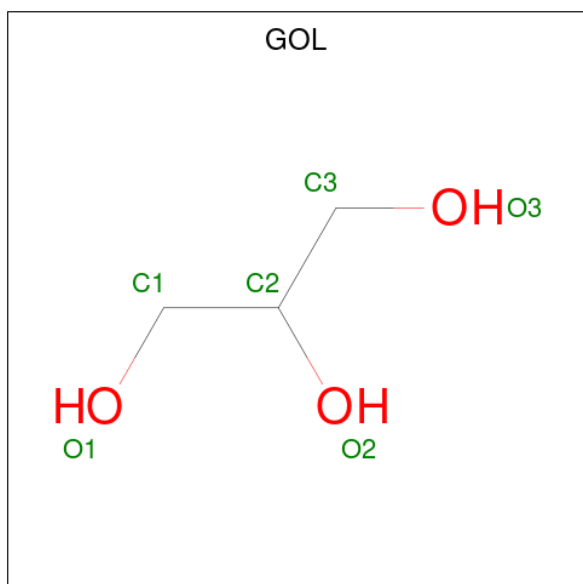
- Molecule 4 is CARBA-NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: CNA) (formula: C₂₂H₃₀N₇O₁₃P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			44	22	7	13	2		

- # 4TQ

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



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

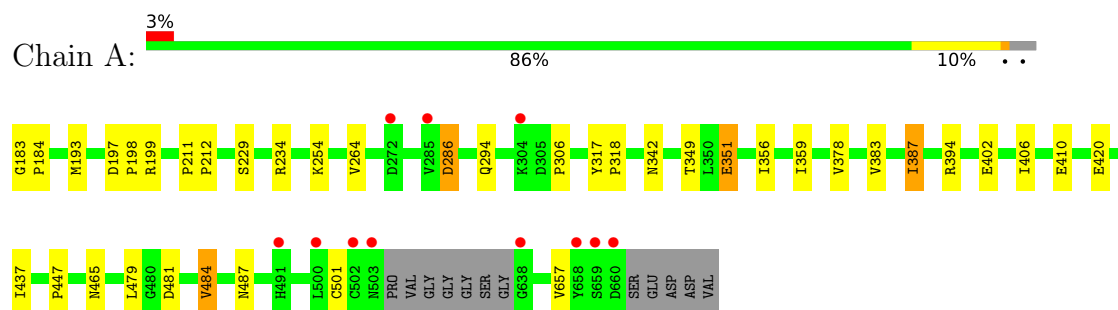
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	41	Total	O	0	0
			41	41		
7	B	3	Total	O	0	0
			3	3		

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: NAD-dependent protein deacetylase sirtuin-1



- Molecule 2: Ac-p53



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	94.51Å 94.51Å 356.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.68 – 2.74 45.68 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.4 (45.68-2.74) 99.4 (45.68-2.74)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.73Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.182 , 0.221 (Not available) , 0.198	Depositor DCC
R_{free} test set	1116 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	64.5	Xtriage
Anisotropy	0.635	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2961	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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: GOL, CNA, 4TQ, ALY, ZN, NLE

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	0.34	0/2829	0.80	4/3838 (0.1%)
2	B	0.22	0/48	0.43	0/58
All	All	0.33	0/2877	0.79	4/3896 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	PRO	CA-C-N	5.44	125.78	119.47
1	A	212	PRO	C-N-CA	5.44	125.78	119.47
1	A	183	GLY	CA-C-N	5.41	125.06	119.05
1	A	183	GLY	C-N-CA	5.41	125.06	119.05

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	2755	0	2770	17	0
2	B	69	0	79	3	0
3	A	1	0	0	0	0
4	A	44	0	29	0	0
5	A	36	0	18	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	12	0	16	0	0
7	A	41	0	0	2	0
7	B	3	0	0	0	0
All	All	2961	0	2912	20	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 3.

All (20) 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:394:ARG:NH1	1:A:402:GLU:O	2.27	0.67
1:A:481:ASP:HB2	1:A:484:VAL:HG13	1.80	0.60
1:A:294:GLN:HG2	2:B:6:NLE:HG2	1.87	0.56
1:A:487:ASN:OD1	1:A:501:CYS:HB2	2.08	0.54
5:A:703:4TQ:NAW	5:A:703:4TQ:NAL	2.47	0.54
2:B:1:ARG:HD3	2:B:2:HIS:H	1.74	0.53
1:A:410[A]:GLU:HG2	7:A:808:HOH:O	2.08	0.52
1:A:447:PRO:HB3	2:B:2:HIS:HB3	1.91	0.52
1:A:184:PRO:HG2	1:A:229:SER:HB3	1.93	0.50
1:A:286:ASP:OD1	1:A:286:ASP:N	2.44	0.50
1:A:306:PRO:HG3	1:A:406:ILE:HD13	1.94	0.48
1:A:351:GLU:HG2	7:A:833:HOH:O	2.14	0.47
1:A:342:ASN:O	1:A:359:ILE:HD12	2.16	0.45
1:A:351:GLU:HB3	1:A:356:ILE:HD12	1.98	0.45
5:A:703:4TQ:OAN	5:A:703:4TQ:H17	2.18	0.43
1:A:197:ASP:HA	1:A:198:PRO:HD2	1.93	0.42
1:A:199:ARG:NH1	1:A:211:PRO:HG2	2.34	0.42
1:A:317:TYR:HA	1:A:318:PRO:HD3	1.93	0.41
1:A:383:VAL:O	1:A:387:ILE:HG13	2.21	0.41
1:A:465:ASN:O	1:A:479:LEU:HA	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	342/356 (96%)	334 (98%)	8 (2%)	0	100	100
2	B	3/7 (43%)	3 (100%)	0	0	100	100
All	All	345/363 (95%)	337 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	310/316 (98%)	297 (96%)	13 (4%)	26	47
2	B	5/5 (100%)	4 (80%)	1 (20%)	1	1
All	All	315/321 (98%)	301 (96%)	14 (4%)	24	45

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	193	MET
1	A	234	ARG
1	A	254	LYS
1	A	264	VAL
1	A	286	ASP
1	A	349	THR
1	A	351	GLU
1	A	378	VAL
1	A	387	ILE
1	A	420	GLU
1	A	437	ILE
1	A	484	VAL
1	A	657	VAL
2	B	1	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	342	ASN
1	A	457	HIS

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	ALY	B	4	2	10,11,12	0.67	0	7,12,14	0.83	0
2	NLE	B	6	2	6,7,8	0.47	0	2,7,9	0.41	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
2	ALY	B	4	2	-	0/9/10/12	-
2	NLE	B	6	2	-	2/5/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	6	NLE	N-CA-CB-CG
2	B	6	NLE	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	6	NLE	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	CNA	A	702	-	47,48,48	1.98	12 (25%)	65,73,73	1.72	12 (18%)
6	GOL	A	705	-	5,5,5	0.34	0	5,5,5	0.38	0
6	GOL	A	704	-	5,5,5	0.41	0	5,5,5	0.28	0
5	4TQ	A	703	-	40,40,40	2.06	9 (22%)	51,59,59	3.39	12 (23%)

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	CNA	A	702	-	-	6/28/62/62	0/5/5/5
6	GOL	A	705	-	-	2/4/4/4	-
6	GOL	A	704	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	4TQ	A	703	-	-	0/22/38/38	0/4/5/5

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	702	CNA	C3N-C7N	-6.91	1.40	1.50
5	A	703	4TQ	CAF-CAD	-6.17	1.34	1.48
5	A	703	4TQ	CBA-CAX	-5.90	1.39	1.49
4	A	702	CNA	C2N-N1N	5.60	1.41	1.35
5	A	703	4TQ	CBG-CBE	-4.69	1.40	1.49
4	A	702	CNA	C2A-N1A	3.61	1.40	1.33
4	A	702	CNA	C2A-N3A	3.58	1.40	1.33
5	A	703	4TQ	CAP-NAO	-3.57	1.36	1.39
5	A	703	4TQ	CAQ-NAR	-3.54	1.32	1.38
4	A	702	CNA	PN-O1N	3.18	1.61	1.50
4	A	702	CNA	PA-O3	3.04	1.62	1.59
5	A	703	4TQ	CAH-NAL	-2.99	1.35	1.41
5	A	703	4TQ	CAV-NAR	-2.96	1.43	1.46
4	A	702	CNA	C5A-N7A	-2.94	1.33	1.39
4	A	702	CNA	C5A-C4A	-2.80	1.34	1.39
4	A	702	CNA	C6N-N1N	2.55	1.41	1.35
4	A	702	CNA	C5A-C6A	-2.53	1.34	1.41
5	A	703	4TQ	CAM-NAO	-2.30	1.35	1.39
4	A	702	CNA	C8A-N9A	-2.29	1.33	1.37
4	A	702	CNA	PN-O3	2.10	1.61	1.59
5	A	703	4TQ	CAC-NAB	-2.01	1.34	1.37

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	703	4TQ	CAU-CAV-NAR	-18.64	89.54	110.89
5	A	703	4TQ	CAF-CAD-CAC	-7.57	126.10	135.21
4	A	702	CNA	N3A-C2A-N1A	-6.90	118.14	128.58
5	A	703	4TQ	CAS-NAR-CAV	-6.55	103.69	114.99
5	A	703	4TQ	CAS-NAR-CAQ	5.43	128.01	119.29
4	A	702	CNA	N9A-C8A-N7A	-4.32	107.80	113.94
4	A	702	CNA	C5A-C4A-N3A	-4.16	120.98	126.72
5	A	703	4TQ	CAZ-CAQ-CAP	4.03	121.94	117.55
5	A	703	4TQ	CBA-CAX-NAW	3.61	121.25	116.04
5	A	703	4TQ	OAE-CAA-NAB	-3.21	107.47	114.64
4	A	702	CNA	C2A-N3A-C4A	3.16	119.56	111.83
4	A	702	CNA	C5A-N7A-C8A	3.10	108.33	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	702	CNA	O2N-PN-O3	2.97	115.29	107.27
4	A	702	CNA	C6N-N1N-C2N	-2.95	119.36	121.88
4	A	702	CNA	C5A-C6A-N6A	-2.74	116.49	123.29
4	A	702	CNA	C6A-C5A-C4A	2.53	120.63	117.18
4	A	702	CNA	C4A-C5A-N7A	-2.52	107.70	110.58
5	A	703	4TQ	CAQ-CAP-NAW	-2.45	119.43	123.32
5	A	703	4TQ	CAZ-CAQ-NAR	2.43	125.11	122.03
5	A	703	4TQ	CAC-NAB-CAA	2.38	109.39	104.05
4	A	702	CNA	C4A-N9A-C8A	2.36	108.22	105.74
4	A	702	CNA	N3A-C4A-N9A	2.29	131.07	127.17
5	A	703	4TQ	CAT-CAU-CAV	-2.27	99.84	110.66
5	A	703	4TQ	CAY-CAX-CBA	-2.24	117.83	121.97

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	702	CNA	C5D-O5D-PN-O1N
4	A	702	CNA	C2D-C1D-N1N-C2N
4	A	702	CNA	C2D-C1D-N1N-C6N
6	A	704	GOL	C1-C2-C3-O3
6	A	705	GOL	O1-C1-C2-C3
6	A	705	GOL	O1-C1-C2-O2
4	A	702	CNA	C4D-C5D-O5D-PN
4	A	702	CNA	C5D-O5D-PN-O2N
4	A	702	CNA	C2B-C1B-N9A-C8A
6	A	704	GOL	O2-C2-C3-O3

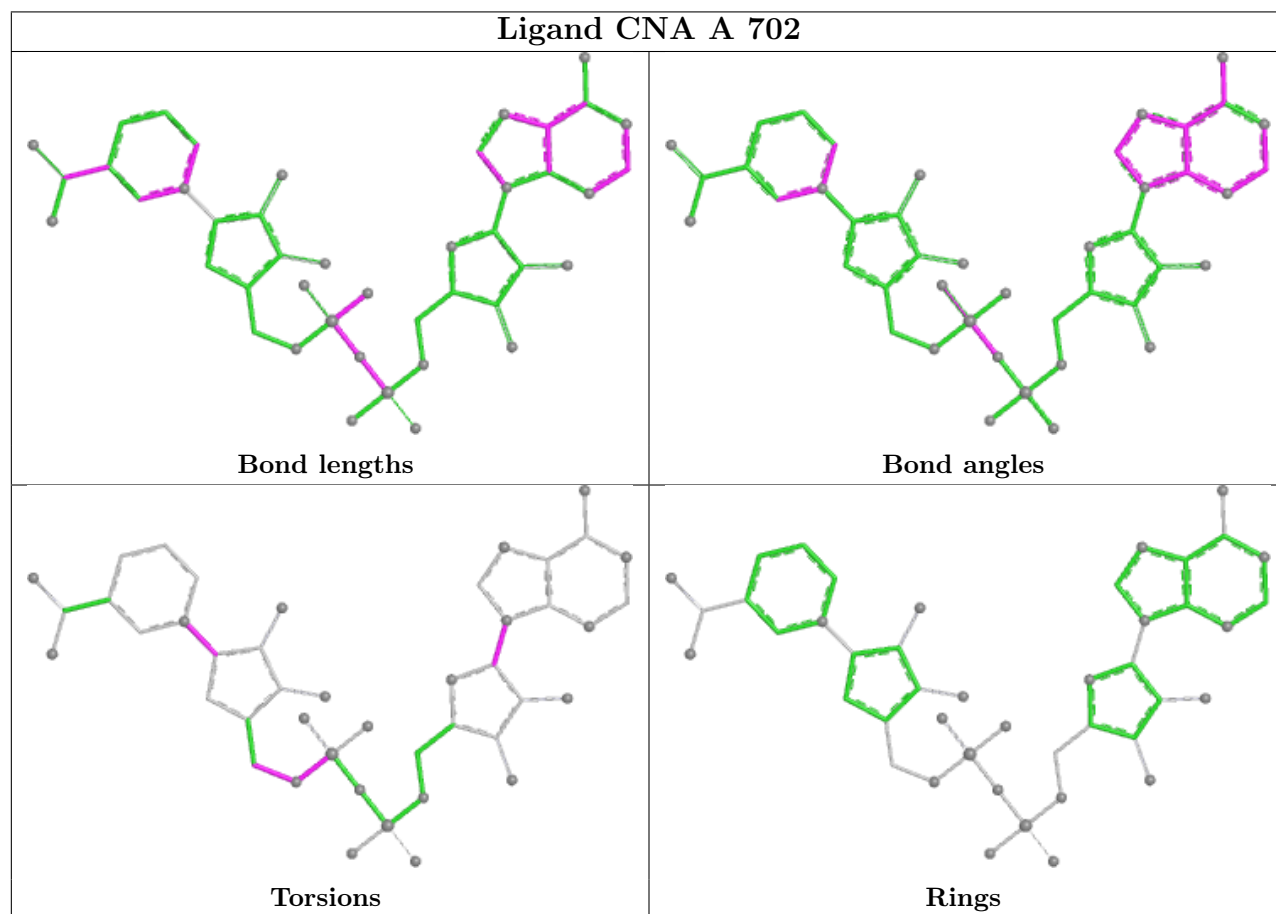
There are no ring outliers.

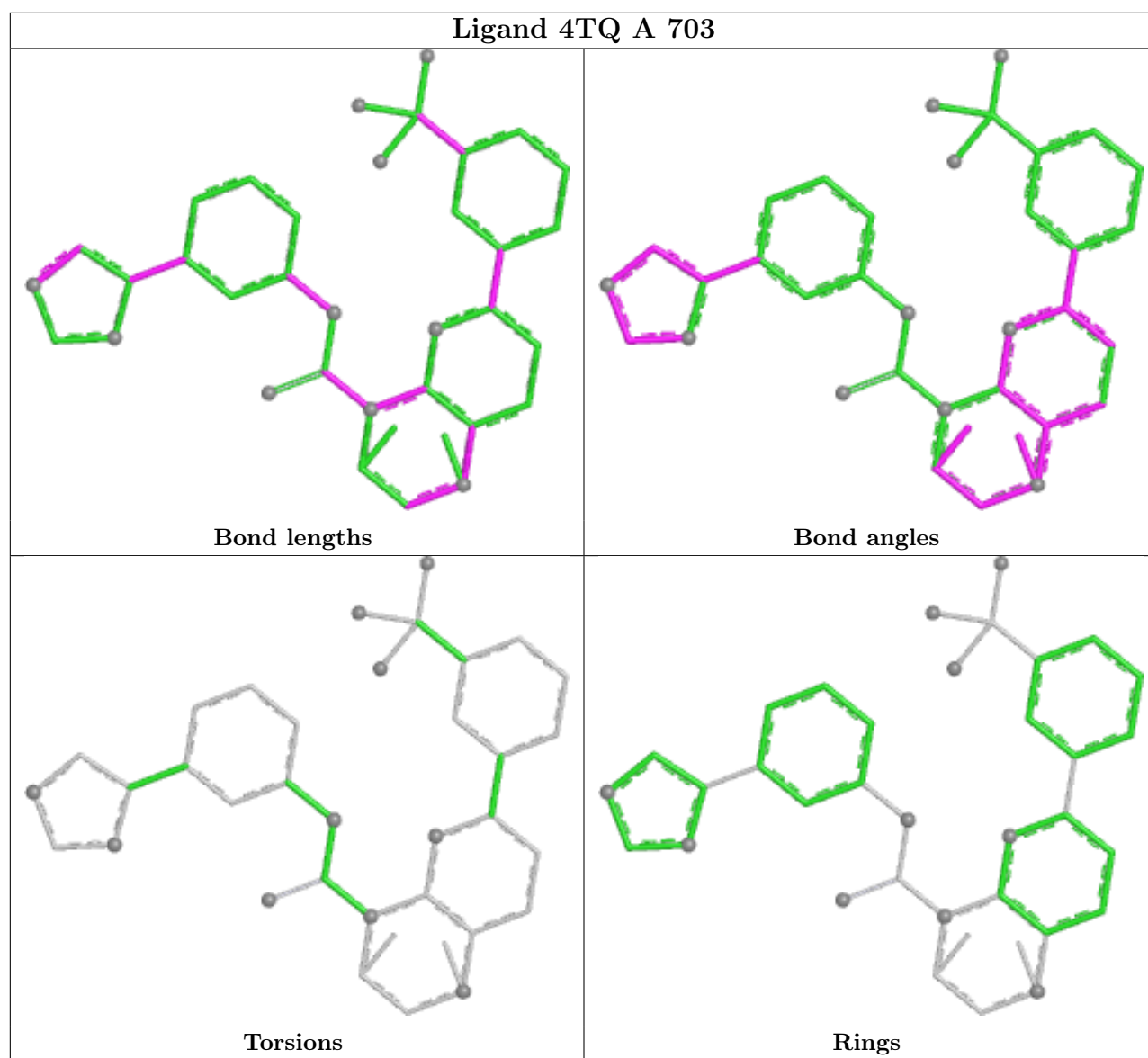
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	703	4TQ	2	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	344/356 (96%)	-0.07	11 (3%)	50	48	34, 66, 109, 149	2 (0%)
2	B	5/7 (71%)	0.73	0	100	100	65, 71, 116, 122	0
All	All	349/363 (96%)	-0.06	11 (3%)	50	48	34, 66, 111, 149	2 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	638	GLY	6.1
1	A	503	ASN	5.0
1	A	502	CYS	3.0
1	A	660	ASP	2.9
1	A	285	VAL	2.9
1	A	272	ASP	2.6
1	A	659	SER	2.4
1	A	491	HIS	2.4
1	A	304	LYS	2.3
1	A	500	LEU	2.3
1	A	658	TYR	2.1

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, 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(Å ²)	Q<0.9
2	NLE	B	6	8/9	0.94	0.14	59,60,70,74	0
2	ALY	B	4	12/13	0.98	0.09	49,56,66,73	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

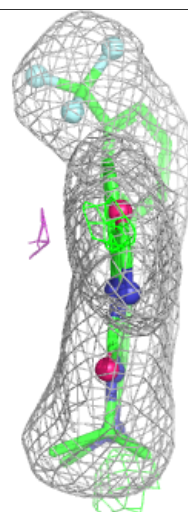
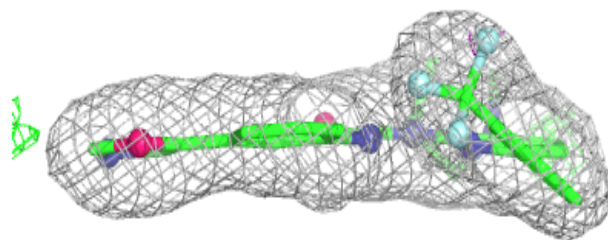
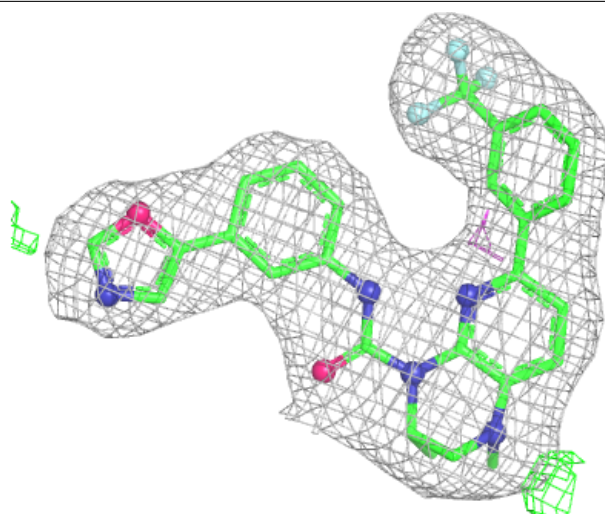
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	GOL	A	705	6/6	0.90	0.24	106,114,115,115	0
6	GOL	A	704	6/6	0.96	0.17	61,62,67,73	0
5	4TQ	A	703	36/36	0.96	0.08	49,64,77,88	0
4	CNA	A	702	44/44	0.97	0.07	51,63,69,70	0
3	ZN	A	701	1/1	1.00	0.02	68,68,68,68	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.

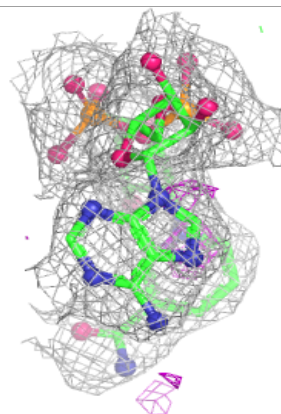
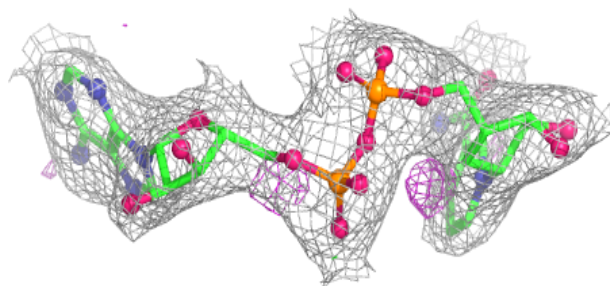
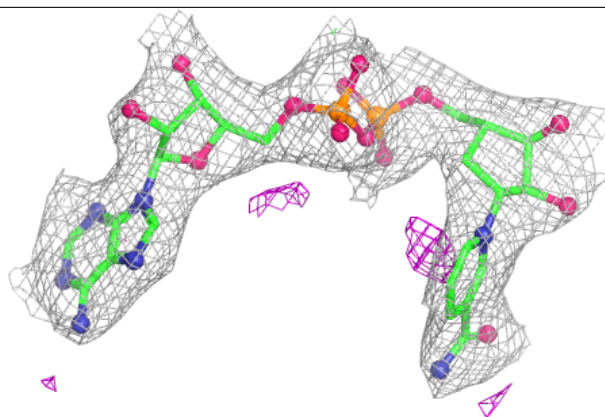
Electron density around 4TQ A 703:

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



Electron density around CNA A 702:

$2mF_o-DF_c$ (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.