



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:54 AM UTC

PDB ID : 1V25 / pdb_00001v25
Title : Crystal structure of tt0168 from *Thermus thermophilus* HB8
Authors : Hisanaga, Y.; Ago, H.; Nakatsu, T.; Hamada, K.; Ida, K.; Kanda, H.; Yamamoto, M.; Hori, T.; Arii, Y.; Sugahara, M.; Kuramitsu, S.; Yokoyama, S.; Miyano, M.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2003-10-07
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

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

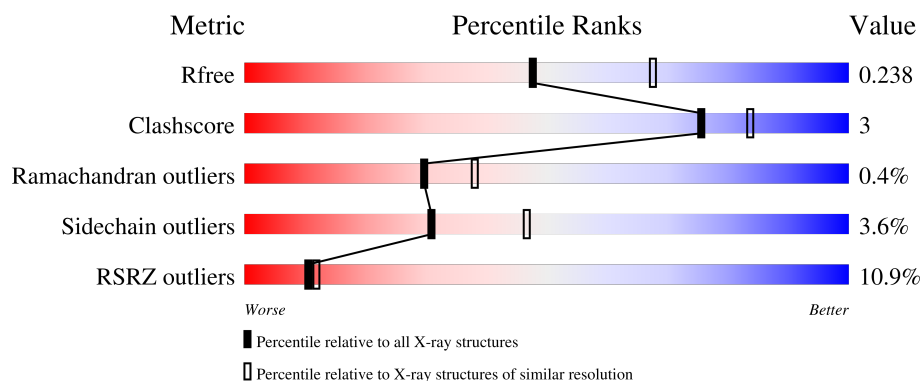
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	541	10% 81% 9% 9%
1	B	541	11% 85% 8% 6%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8236 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.

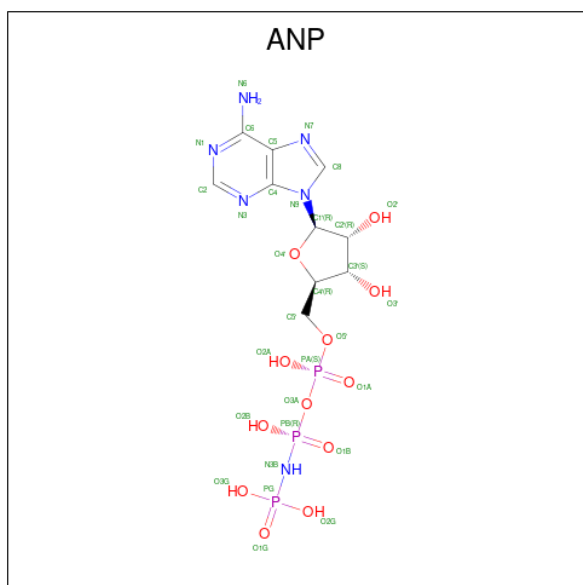
- Molecule 1 is a protein called long-chain-fatty-acid-CoA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	0	0
			3812	2441	663	698	10			
1	B	507	Total	C	N	O	S	0	0	0
			3939	2525	686	717	11			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
3	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	225	Total	O	0	0
			225	225		
4	B	196	Total	O	0	0
			196	196		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.52Å 101.15Å 176.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.60 – 2.30 48.60 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.60-2.30) 99.1 (48.60-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.204 , 0.240 0.203 , 0.238	Depositor DCC
R_{free} test set	5205 reflections (10.08%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.1	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	0.92	EDS
Total number of atoms	8236	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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: MG, ANP

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	0.42	0/3900	0.82	3/5297 (0.1%)
1	B	0.41	0/4031	0.79	1/5471 (0.0%)
All	All	0.41	0/7931	0.80	4/10768 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	473	TRP	CA-C-N	-6.15	112.56	121.98
1	A	473	TRP	C-N-CA	-6.15	112.56	121.98
1	A	330	SER	N-CA-C	6.09	123.27	109.81
1	B	330	SER	N-CA-C	5.97	123.00	109.81

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	3812	0	3822	26	0
1	B	3939	0	3950	21	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	31	0	13	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	31	0	13	2	0
4	A	225	0	0	3	0
4	B	196	0	0	0	0
All	All	8236	0	7798	47	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 (47) 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:230:HIS:HA	3:B:1666:ANP:O1G	1.86	0.76
1:A:231:VAL:HG22	3:A:666:ANP:O2G	1.86	0.73
1:A:330:SER:N	1:A:331:PRO:HA	2.08	0.69
1:B:330:SER:N	1:B:331:PRO:HA	2.08	0.69
1:B:231:VAL:HG23	3:B:1666:ANP:HNB1	1.64	0.63
1:A:42:THR:OG1	1:A:44:GLU:HG2	2.00	0.61
1:A:308:SER:O	1:A:312:ARG:HG3	2.00	0.61
1:A:296:ARG:HG2	4:A:1133:HOH:O	2.00	0.60
1:B:225:VAL:HG11	1:B:277:VAL:HG11	1.83	0.60
1:B:275:PRO:HB2	1:B:474:GLN:OE1	2.02	0.59
1:B:19:ASN:HD22	1:B:21:TRP:H	1.50	0.58
1:B:92:VAL:HB	1:B:93:PRO:HD3	1.86	0.57
1:A:474:GLN:NE2	4:A:1154:HOH:O	2.36	0.57
1:A:128:ASN:HD22	1:A:128:ASN:H	1.53	0.57
1:A:307:ARG:NH1	1:A:351:LEU:HD23	2.20	0.56
1:B:329:THR:C	1:B:331:PRO:HA	2.30	0.56
1:A:89:TYR:OH	1:A:232:ASN:HA	2.07	0.55
1:A:230:HIS:HA	3:A:666:ANP:O1G	2.07	0.55
1:A:438:ILE:HD13	1:A:477:PRO:HG3	1.87	0.54
1:A:329:THR:C	1:A:331:PRO:HA	2.33	0.54
1:A:445:ILE:HG12	1:A:506:GLN:HG2	1.90	0.53
1:A:471:PRO:HG3	1:A:540:GLY:HA2	1.91	0.53
1:A:92:VAL:HB	1:A:93:PRO:HD3	1.92	0.51
1:A:225:VAL:HG11	1:A:277:VAL:HG11	1.93	0.50
1:A:19:ASN:HD22	1:A:21:TRP:H	1.59	0.50
1:B:454:LEU:HG	1:B:497:LEU:HD21	1.93	0.49
1:A:477:PRO:HB2	1:A:508:PRO:HA	1.93	0.49
1:B:128:ASN:H	1:B:128:ASN:HD22	1.60	0.49
1:A:127:PRO:HG3	1:A:150:ASP:HB2	1.95	0.49
1:B:419:ILE:HD11	1:B:434:LEU:HG	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1222:HOH:O	1:B:341:HIS:HD2	1.97	0.47
1:B:311:ALA:HB2	1:B:351:LEU:HD21	1.97	0.46
1:B:388:LEU:HB3	1:B:393:ILE:HD13	1.97	0.45
1:A:128:ASN:H	1:A:128:ASN:ND2	2.14	0.45
1:B:474:GLN:O	1:B:475:GLU:HG3	2.18	0.43
1:B:82:HIS:HE1	1:B:126:ASP:OD1	2.01	0.43
1:B:372:GLU:HG3	1:B:374:ARG:NH1	2.34	0.43
1:B:128:ASN:H	1:B:128:ASN:ND2	2.17	0.43
1:A:528:ARG:H	1:A:528:ARG:HG2	1.65	0.43
1:B:453:ALA:O	1:B:496:HIS:HE1	2.02	0.43
1:A:419:ILE:HD11	1:A:434:LEU:HG	2.00	0.42
1:A:435:LYS:H	1:A:435:LYS:HG3	1.57	0.41
1:B:89:TYR:OH	1:B:232:ASN:HA	2.21	0.41
1:A:153:ALA:HA	1:A:154:PRO:HD3	1.94	0.41
1:A:187:THR:HG21	1:A:192:LYS:HD2	2.03	0.41
1:B:226:VAL:HA	1:B:227:PRO:HD3	1.89	0.41
1:A:339:LYS:HB2	1:A:342:LEU:HD12	2.03	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	483/541 (89%)	465 (96%)	16 (3%)	2 (0%)	30	38
1	B	499/541 (92%)	488 (98%)	9 (2%)	2 (0%)	30	38
All	All	982/1082 (91%)	953 (97%)	25 (2%)	4 (0%)	30	38

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	330	SER

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Mol	Chain	Res	Type
1	B	330	SER
1	B	539	GLY
1	A	473	TRP

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	395/437 (90%)	379 (96%)	16 (4%)	27	41
1	B	407/437 (93%)	394 (97%)	13 (3%)	34	51
All	All	802/874 (92%)	773 (96%)	29 (4%)	31	47

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	GLU
1	A	128	ASN
1	A	185	THR
1	A	231	VAL
1	A	235	CYS
1	A	242	LEU
1	A	299	VAL
1	A	336	ASN
1	A	374	ARG
1	A	406	SER
1	A	435	LYS
1	A	437	LEU
1	A	447	SER
1	A	452	ASN
1	A	474	GLN
1	A	528	ARG
1	B	11	SER
1	B	139	GLU
1	B	166	GLU
1	B	185	THR

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Mol	Chain	Res	Type
1	B	231	VAL
1	B	235	CYS
1	B	299	VAL
1	B	300	VAL
1	B	372	GLU
1	B	381	LYS
1	B	405	ARG
1	B	435	LYS
1	B	528	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	41	HIS
1	A	82	HIS
1	A	128	ASN
1	A	145	HIS
1	A	290	HIS
1	A	322	GLN
1	A	336	ASN
1	A	536	ASN
1	B	19	ASN
1	B	41	HIS
1	B	82	HIS
1	B	128	ASN
1	B	290	HIS
1	B	335	GLN
1	B	336	ASN
1	B	341	HIS
1	B	496	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are 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	$\# Z > 2$
3	ANP	A	666	2	33,33,33	1.27	5 (15%)	45,52,52	1.90	9 (20%)
3	ANP	B	1666	2	33,33,33	1.31	3 (9%)	45,52,52	1.85	9 (20%)

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
3	ANP	A	666	2	-	3/18/38/38	0/3/3/3
3	ANP	B	1666	2	-	2/18/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1666	ANP	PG-O1G	3.86	1.52	1.46
3	A	666	ANP	PG-O1G	3.66	1.51	1.46
3	B	1666	ANP	PB-O1B	3.64	1.51	1.46
3	A	666	ANP	PB-O1B	3.12	1.50	1.46
3	B	1666	ANP	C8-N7	2.14	1.35	1.31
3	A	666	ANP	C8-N7	2.11	1.35	1.31
3	A	666	ANP	C4-N9	-2.09	1.33	1.37
3	A	666	ANP	PG-O3G	-2.02	1.51	1.56

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	666	ANP	C4-N9-C8	5.12	111.11	105.74
3	B	1666	ANP	C5-C4-N3	-4.83	120.07	126.72
3	A	666	ANP	C5-C4-N3	-4.80	120.10	126.72
3	A	666	ANP	N3-C2-N1	-4.79	121.33	128.58
3	B	1666	ANP	C4-N9-C8	4.70	110.68	105.74
3	B	1666	ANP	N3-C2-N1	-4.66	121.53	128.58
3	A	666	ANP	N9-C8-N7	-4.41	107.68	113.94
3	B	1666	ANP	N9-C8-N7	-4.28	107.86	113.94
3	A	666	ANP	N3-C4-N9	3.93	133.85	127.17
3	B	1666	ANP	N3-C4-N9	3.76	133.56	127.17
3	A	666	ANP	C2-N3-C4	3.38	120.07	111.83
3	B	1666	ANP	C2-N3-C4	3.29	119.86	111.83
3	B	1666	ANP	C4-C5-N7	-2.81	107.37	110.58
3	B	1666	ANP	C5-N7-C8	2.72	107.72	103.45
3	B	1666	ANP	O2G-PG-O1G	-2.67	106.76	113.45
3	A	666	ANP	C5-N7-C8	2.63	107.58	103.45
3	A	666	ANP	C4-C5-N7	-2.63	107.58	110.58
3	A	666	ANP	O3G-PG-O1G	-2.17	108.00	113.45

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	666	ANP	PG-N3B-PB-O1B
3	A	666	ANP	PG-N3B-PB-O3A
3	B	1666	ANP	PG-N3B-PB-O1B
3	B	1666	ANP	PG-N3B-PB-O3A
3	A	666	ANP	PB-N3B-PG-O1G

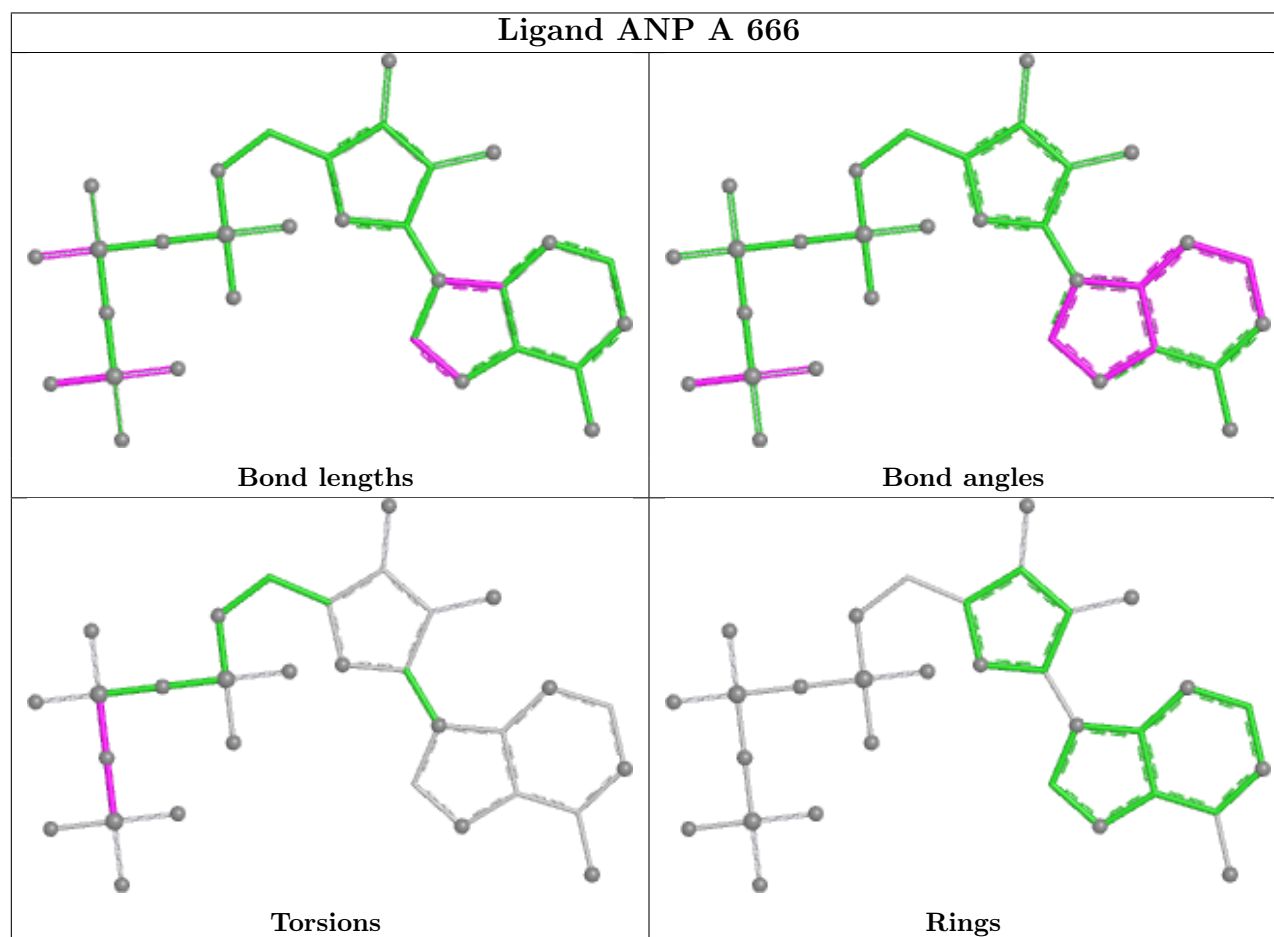
There are no ring outliers.

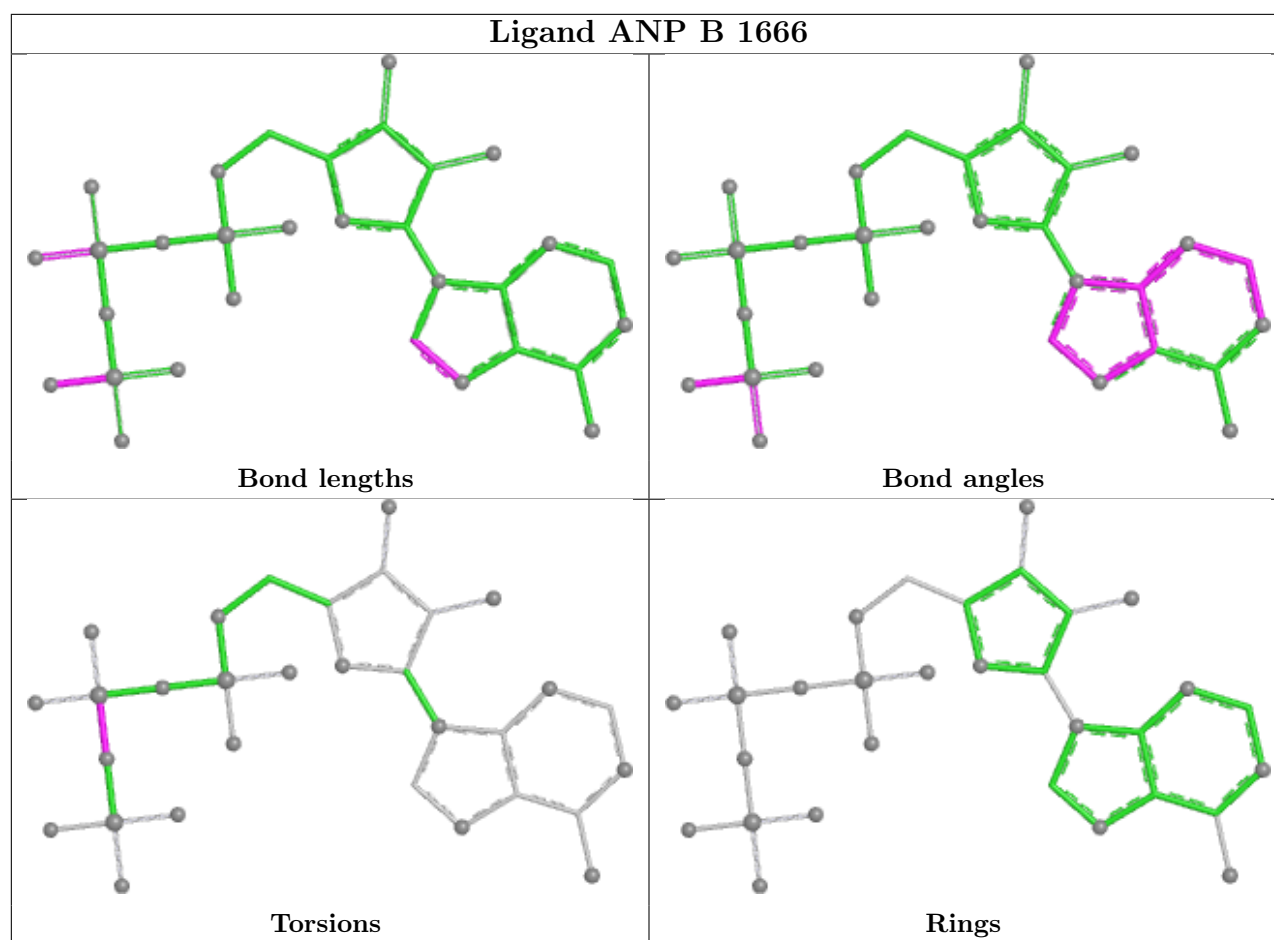
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	666	ANP	2	0
3	B	1666	ANP	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

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	491/541 (90%)	0.33	52 (10%)	11 12	7, 16, 58, 98	0
1	B	507/541 (93%)	0.36	57 (11%)	10 11	7, 16, 72, 96	0
All	All	998/1082 (92%)	0.35	109 (10%)	10 12	7, 16, 65, 98	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	526	LEU	9.4
1	A	540	GLY	7.5
1	B	539	GLY	7.3
1	A	541	ALA	7.3
1	A	501	GLY	6.0
1	B	541	ALA	5.8
1	B	501	GLY	5.6
1	A	530	LEU	5.5
1	B	500	ALA	5.4
1	B	526	LEU	5.3
1	B	525	PHE	5.2
1	B	497	LEU	5.0
1	B	513	PHE	4.9
1	B	474	GLN	4.8
1	B	498	LEU	4.7
1	A	529	ALA	4.7
1	A	534	TYR	4.7
1	A	511	TYR	4.7
1	B	531	ARG	4.6
1	B	8	ALA	4.5
1	B	523	GLY	4.5
1	A	473	TRP	4.5
1	A	528	ARG	4.5
1	B	494	ASN	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	481	VAL	4.4
1	B	540	GLY	4.3
1	B	528	ARG	4.2
1	A	537	TYR	4.2
1	A	539	GLY	4.1
1	B	535	LYS	4.1
1	B	537	TYR	4.0
1	A	532	GLU	4.0
1	B	534	TYR	4.0
1	B	502	PHE	3.9
1	A	531	ARG	3.8
1	A	538	TYR	3.8
1	B	464	ALA	3.8
1	B	454	LEU	3.8
1	B	530	LEU	3.7
1	A	453	ALA	3.7
1	B	538	TYR	3.6
1	A	507	LEU	3.6
1	B	371	GLU	3.6
1	A	527	LYS	3.5
1	A	448	VAL	3.5
1	A	374	ARG	3.5
1	B	463	ALA	3.4
1	A	535	LYS	3.4
1	B	524	LYS	3.4
1	B	456	GLY	3.4
1	B	532	GLU	3.3
1	A	480	VAL	3.3
1	B	495	GLU	3.2
1	B	536	ASN	3.1
1	A	436	ASP	3.1
1	B	457	HIS	3.1
1	A	464	ALA	3.0
1	A	502	PHE	3.0
1	A	503	ALA	3.0
1	A	474	GLN	3.0
1	B	287	SER	2.9
1	A	450	LEU	2.9
1	A	504	LYS	2.8
1	A	536	ASN	2.8
1	B	529	ALA	2.8
1	A	471	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	402	GLU	2.7
1	B	512	VAL	2.7
1	A	479	ALA	2.7
1	A	510	ALA	2.7
1	B	480	VAL	2.7
1	A	505	TRP	2.7
1	B	450	LEU	2.7
1	A	508	PRO	2.6
1	B	449	ASP	2.6
1	B	527	LYS	2.6
1	A	449	ASP	2.6
1	A	347	GLU	2.5
1	B	452	ASN	2.5
1	B	496	HIS	2.5
1	B	448	VAL	2.5
1	B	503	ALA	2.5
1	A	468	ILE	2.5
1	B	510	ALA	2.5
1	A	452	ASN	2.4
1	B	230	HIS	2.4
1	A	8	ALA	2.4
1	B	499	LYS	2.4
1	B	347	GLU	2.4
1	A	533	GLN	2.3
1	B	511	TYR	2.3
1	A	405	ARG	2.3
1	A	451	GLU	2.3
1	B	401	GLU	2.3
1	A	465	VAL	2.3
1	A	402	GLU	2.3
1	A	296	ARG	2.2
1	B	504	LYS	2.2
1	A	467	ALA	2.2
1	A	401	GLU	2.2
1	A	466	VAL	2.2
1	A	469	PRO	2.2
1	B	505	TRP	2.1
1	B	166	GLU	2.1
1	B	424	GLU	2.1
1	A	435	LYS	2.1
1	B	155	GLU	2.0
1	B	453	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	315	ARG	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](#)

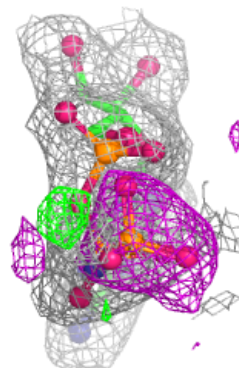
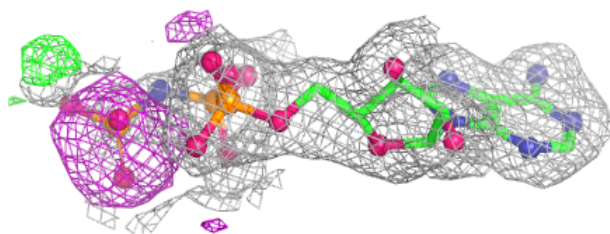
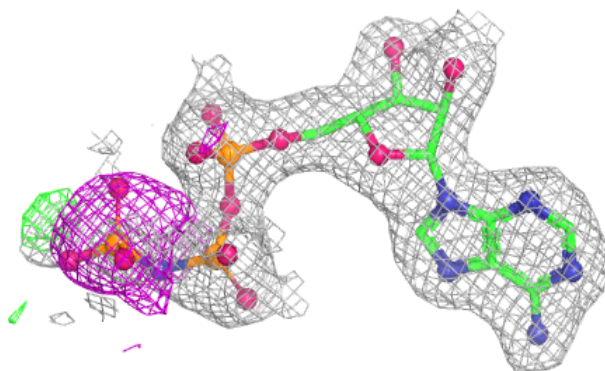
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	ANP	B	1666	31/31	0.89	0.12	15,16,41,41	0
3	ANP	A	666	31/31	0.91	0.12	10,11,40,42	0
2	MG	B	1002	1/1	0.94	0.07	17,17,17,17	0
2	MG	A	1001	1/1	0.95	0.18	23,23,23,23	0

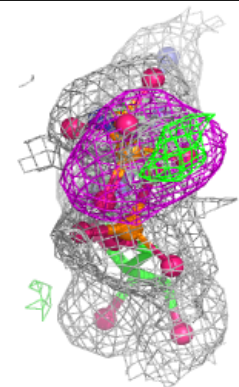
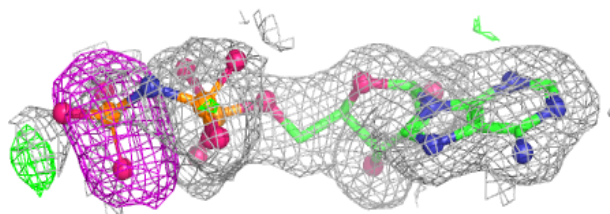
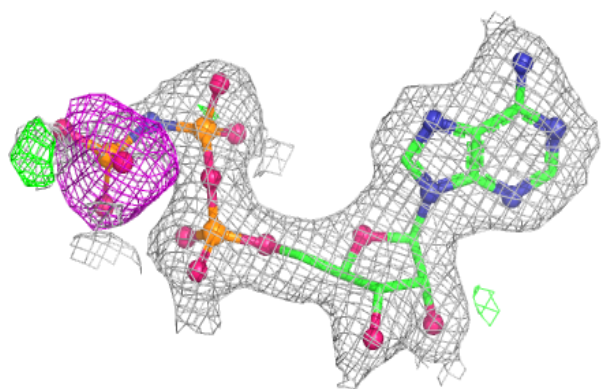
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ANP B 1666:

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

**Electron density around ANP A 666:**

$2mF_o-DF_c$ (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.