



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:13 PM UTC

PDB ID : 5CNO / pdb_00005cno
Title : Crystal structure of the EGFR kinase domain mutant V924R
Authors : Kovacs, E.; Das, R.; Mirza, A.; Jura, N.; Barros, T.; Kuriyan, J.
Deposited on : 2015-07-17
Resolution : 1.55 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

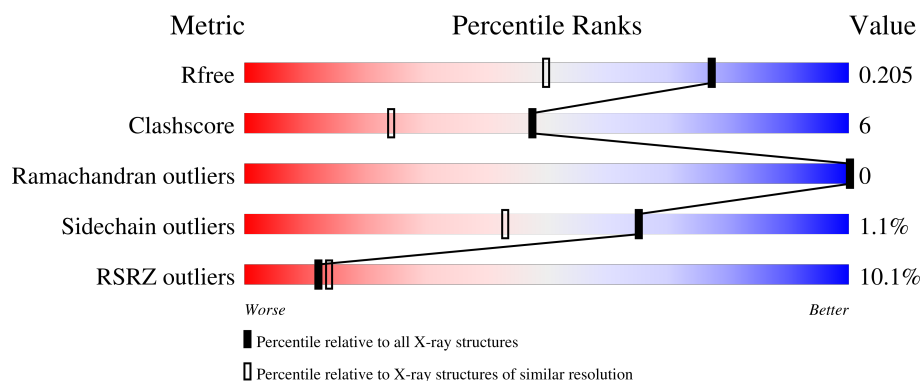
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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	330	
1	B	330	
1	X	330	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5579 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.

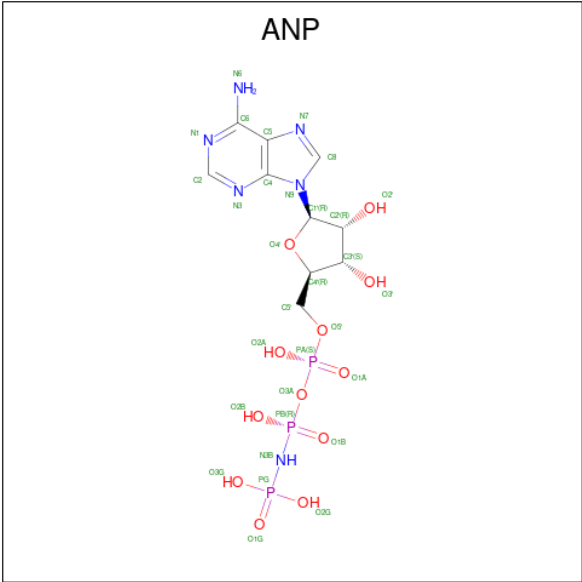
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	300	Total	C	N	O	S	0	3	0
			2434	1563	411	440	20			
1	B	302	Total	C	N	O	S	0	5	0
			2461	1583	414	442	22			
1	X	10	Total	C	N	O		0	0	0
			79	50	12	17				

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	669	GLY	-	expression tag	UNP P00533
A	670	ALA	-	expression tag	UNP P00533
A	671	MET	-	expression tag	UNP P00533
A	924	ARG	VAL	engineered mutation	UNP P00533
B	669	GLY	-	expression tag	UNP P00533
B	670	ALA	-	expression tag	UNP P00533
B	671	MET	-	expression tag	UNP P00533
B	924	ARG	VAL	engineered mutation	UNP P00533
X	669	GLY	-	expression tag	UNP P00533
X	670	ALA	-	expression tag	UNP P00533
X	671	MET	-	expression tag	UNP P00533
X	924	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	268	Total	O	0	0
			268	268		
4	B	268	Total	O	0	0
			268	268		
4	X	5	Total	O	0	0
			5	5		

- Molecule 1: Epidermal growth factor receptor



THR	ASP	ASN	PHE	TYR	ARG	ALA	LEU	MET	ASP	GLU	GLU	ASP	MET	ASP	ASP	VAL	VAL	ASP	A989	D990	E991	Y992	L993	I994	P995	Q996	Q997	G998																													
LEU	PRO	GLN	PRO	PRO	ILE	CYS	THR	ILE	ASP	VAL	TYR	MET	ILE	MET	ARG	LYS	TRP	MET	ILE	ASP	ALA	ASP	ARG	PRO	LYS	PHE	ARG	GLU	LEU	ILE	ILE	GLU	PHE	SER	LYS	MET	ALA	ARG	ASP	PRO	GLN	ARG	TYR	LEU	VAL	ILE	GLN	GLY	ASP	GLU	ARG	MET	HIS	LEU	PRO	SER	PRO

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	155.40Å 71.84Å 76.40Å 90.00° 113.27° 90.00°	Depositor
Resolution (Å)	38.56 – 1.55 38.56 – 1.55	Depositor EDS
% Data completeness (in resolution range)	99.1 (38.56-1.55) 93.2 (38.56-1.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 1.55Å)	Xtriage
Refinement program	PHENIX dev_1839	Depositor
R, R_{free}	0.175 , 0.203 0.177 , 0.205	Depositor DCC
R_{free} test set	5573 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.519	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5579	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 53.18 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.3719e-05.*

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

5.1 Standard geometry

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	0.95	0/2493	1.04	6/3367 (0.2%)
1	B	0.97	0/2527	1.02	1/3412 (0.0%)
1	X	0.81	0/80	1.01	1/108 (0.9%)
All	All	0.96	0/5100	1.03	8/6887 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	965	LEU	CA-C-N	-6.06	114.03	120.03
1	A	965	LEU	C-N-CA	-6.06	114.03	120.03
1	A	823	THR	CA-C-N	-5.67	113.78	119.56
1	A	823	THR	C-N-CA	-5.67	113.78	119.56
1	B	990	ASP	N-CA-C	5.48	116.93	111.07
1	X	990	ASP	N-CA-C	5.46	115.77	108.23
1	A	784	ASN	CA-C-N	-5.38	116.13	123.12
1	A	784	ASN	C-N-CA	-5.38	116.13	123.12

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	2434	0	2484	24	0
1	B	2461	0	2524	33	0
1	X	79	0	71	4	0
2	A	31	0	13	0	0
2	B	31	0	13	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	268	0	0	6	2
4	B	268	0	0	15	2
4	X	5	0	0	0	0
All	All	5579	0	5105	57	2

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 6.

All (57) 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:740:TYR:OH	4:B:1101:HOH:O	1.82	0.96
1:B:836:LYS:NZ	4:B:1102:HOH:O	1.97	0.95
1:B:784:ASN:N	4:B:1109:HOH:O	2.20	0.73
1:A:747:ASN:HD21	1:X:989:ALA:HB1	1.53	0.73
1:B:851:LYS:NZ	4:B:1110:HOH:O	2.21	0.73
1:B:780:GLU:OE1	4:B:1103:HOH:O	2.06	0.73
1:A:748:PRO:HD2	1:X:989:ALA:HA	1.70	0.72
1:B:943:GLU:OE1	4:B:1105:HOH:O	2.08	0.71
1:B:776:ASP:OD1	4:B:1104:HOH:O	2.08	0.71
1:B:675:PRO:HG2	4:B:1184:HOH:O	1.93	0.69
1:B:687:GLU:OE1	4:B:1106:HOH:O	2.10	0.68
1:B:692:LYS:HE2	1:X:990:ASP:HA	1.75	0.68
1:B:851:LYS:O	4:B:1107:HOH:O	2.11	0.67
1:B:925[B]:LYS:HG2	1:B:935:PRO:HD3	1.75	0.67
1:A:723:LEU:HD13	1:A:838:LEU:HD11	1.78	0.65
1:B:880:VAL:HG12	1:B:923[B]:MET:HE2	1.79	0.64
1:A:700:GLY:HA2	1:A:724:ARG:HG3	1.80	0.64
1:B:812:ARG:NH1	4:B:1108:HOH:O	2.12	0.62
1:A:946[A]:LYS:NZ	4:A:1105:HOH:O	2.31	0.62
1:A:902:ILE:HG23	1:A:907:GLU:HB2	1.81	0.61
1:B:779:ARG:HD3	1:B:887:GLY:O	2.03	0.59
1:A:720:ILE:HG12	1:A:765:ILE:CD1	2.33	0.58
1:B:989:ALA:HB1	1:B:991:GLU:HB2	1.87	0.56
1:B:949:ARG:NH2	4:B:1117:HOH:O	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:676:ASN:HD21	1:A:678:ALA:HB3	1.70	0.56
1:A:949:ARG:NH1	4:A:1101:HOH:O	2.22	0.53
1:B:781:HIS:HB2	1:B:785:ILE:HD11	1.90	0.52
1:A:676:ASN:ND2	1:A:678:ALA:HB3	2.24	0.52
1:A:946[B]:LYS:HG3	4:A:1186:HOH:O	2.10	0.50
1:A:689:LYS:HE3	1:A:691:ILE:HD11	1.93	0.50
1:B:812:ARG:NE	4:B:1114:HOH:O	2.36	0.49
1:B:858:ALA:HA	1:B:874:TRP:CD2	2.48	0.49
1:A:748:PRO:CD	1:X:989:ALA:HA	2.40	0.48
1:B:786:GLY:HA2	1:B:963:MET:HE3	1.96	0.48
1:B:902:ILE:HG23	1:B:907:GLU:HB2	1.96	0.47
1:A:858:ALA:HA	1:A:874:TRP:CD2	2.49	0.47
1:A:720:ILE:HG12	1:A:765:ILE:HD13	1.96	0.46
1:B:674:ALA:N	4:B:1121:HOH:O	2.47	0.46
1:B:779:ARG:HG2	1:B:887:GLY:HA3	1.97	0.46
1:B:963:MET:C	4:B:1112:HOH:O	2.58	0.46
1:B:745:VAL:HG11	1:B:832:PHE:CZ	2.51	0.46
1:A:825:GLN:NE2	4:A:1113:HOH:O	2.48	0.46
1:A:938:ARG:NH1	4:A:1102:HOH:O	2.24	0.45
1:A:946[B]:LYS:HG2	1:A:949:ARG:NH2	2.32	0.44
1:B:989:ALA:CB	1:B:991:GLU:HB2	2.47	0.44
1:B:730:LYS:NZ	1:B:836:LYS:O	2.48	0.43
1:A:699:PHE:CZ	1:A:835:ALA:HA	2.54	0.43
1:B:674:ALA:HA	1:B:675:PRO:HD3	1.89	0.42
1:B:779:ARG:HG2	1:B:886:PHE:O	2.20	0.42
1:A:769:MET:HE1	1:A:822:LYS:HB2	2.02	0.42
1:B:947[A]:MET:HG2	1:B:954:TYR:CG	2.55	0.42
1:A:683:LEU:CD1	1:A:765:ILE:HG13	2.50	0.41
1:A:912:PRO:HA	1:A:913:PRO:HD3	1.98	0.41
1:A:851:LYS:NZ	4:A:1118:HOH:O	2.53	0.41
1:B:960:ASP:HA	1:B:963:MET:HE2	2.02	0.41
1:A:852:VAL:HG12	1:A:857:MET:SD	2.61	0.40
1:B:917:ILE:HD11	1:B:921[A]:MET:HE3	2.04	0.40

All (2) 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)
4:A:1290:HOH:O	4:B:1337:HOH:O[4_456]	1.69	0.51
4:A:1201:HOH:O	4:B:1272:HOH:O[4_456]	2.15	0.05

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	297/330 (90%)	291 (98%)	6 (2%)	0	100	100
1	B	301/330 (91%)	292 (97%)	9 (3%)	0	100	100
1	X	8/330 (2%)	6 (75%)	2 (25%)	0	100	100
All	All	606/990 (61%)	589 (97%)	17 (3%)	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	271/288 (94%)	267 (98%)	4 (2%)	57	31
1	B	275/288 (96%)	275 (100%)	0	100	100
1	X	8/288 (3%)	6 (75%)	2 (25%)	0	0
All	All	554/864 (64%)	548 (99%)	6 (1%)	65	43

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	708	ILE
1	A	725	GLU
1	A	852	VAL
1	A	991	GLU
1	X	990	ASP

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Mol	Chain	Res	Type
1	X	997	GLN

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	747	ASN
1	A	825	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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	$\# Z > 2$
2	ANP	A	1001	3	33,33,33	2.27	6 (18%)	45,52,52	0.80	3 (6%)
2	ANP	B	1001	3	33,33,33	1.40	5 (15%)	45,52,52	1.04	3 (6%)

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	ANP	A	1001	3	-	3/18/38/38	0/3/3/3
2	ANP	B	1001	3	-	2/18/38/38	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	ANP	PG-O1G	11.19	1.63	1.46
2	B	1001	ANP	PG-O1G	4.09	1.52	1.46
2	B	1001	ANP	PB-O1B	4.08	1.52	1.46
2	B	1001	ANP	PB-O2B	-3.41	1.47	1.56
2	A	1001	ANP	PG-O3G	-3.01	1.48	1.56
2	A	1001	ANP	PB-O1B	2.91	1.50	1.46
2	B	1001	ANP	PG-N3B	2.80	1.70	1.63
2	A	1001	ANP	PB-O3A	-2.25	1.56	1.59
2	A	1001	ANP	PG-N3B	2.12	1.68	1.63
2	A	1001	ANP	PA-O3A	2.07	1.61	1.59
2	B	1001	ANP	PB-N3B	2.00	1.68	1.63

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	ANP	O2B-PB-O1B	3.19	116.70	109.87
2	A	1001	ANP	O3G-PG-O1G	-2.86	106.28	113.45
2	B	1001	ANP	O1G-PG-N3B	2.72	115.78	111.77
2	A	1001	ANP	O1G-PG-N3B	-2.45	108.17	111.77
2	A	1001	ANP	O2G-PG-O3G	2.16	113.39	107.59
2	B	1001	ANP	O3'-C3'-C4'	2.14	117.23	111.08

There are no chirality outliers.

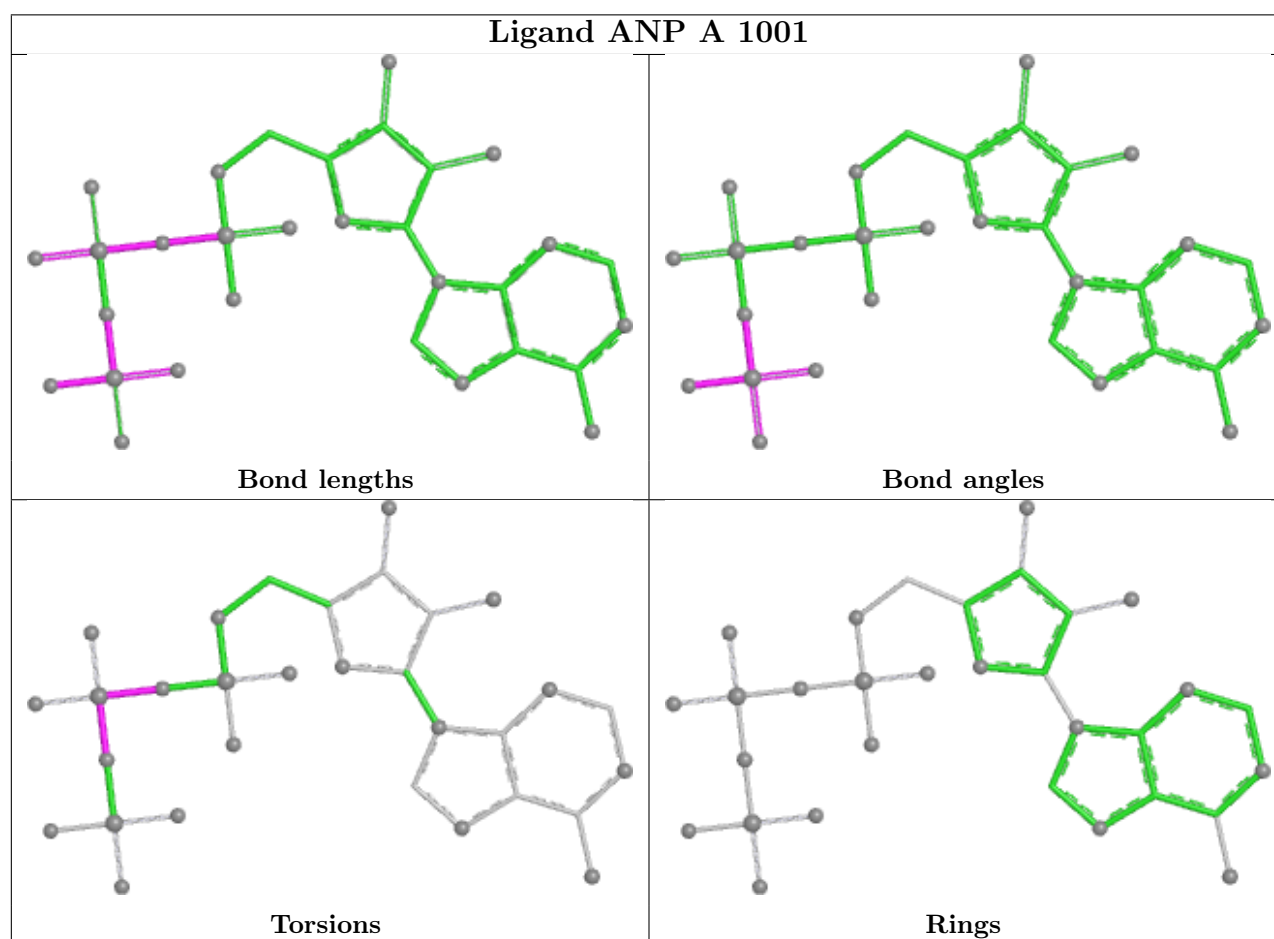
All (5) torsion outliers are listed below:

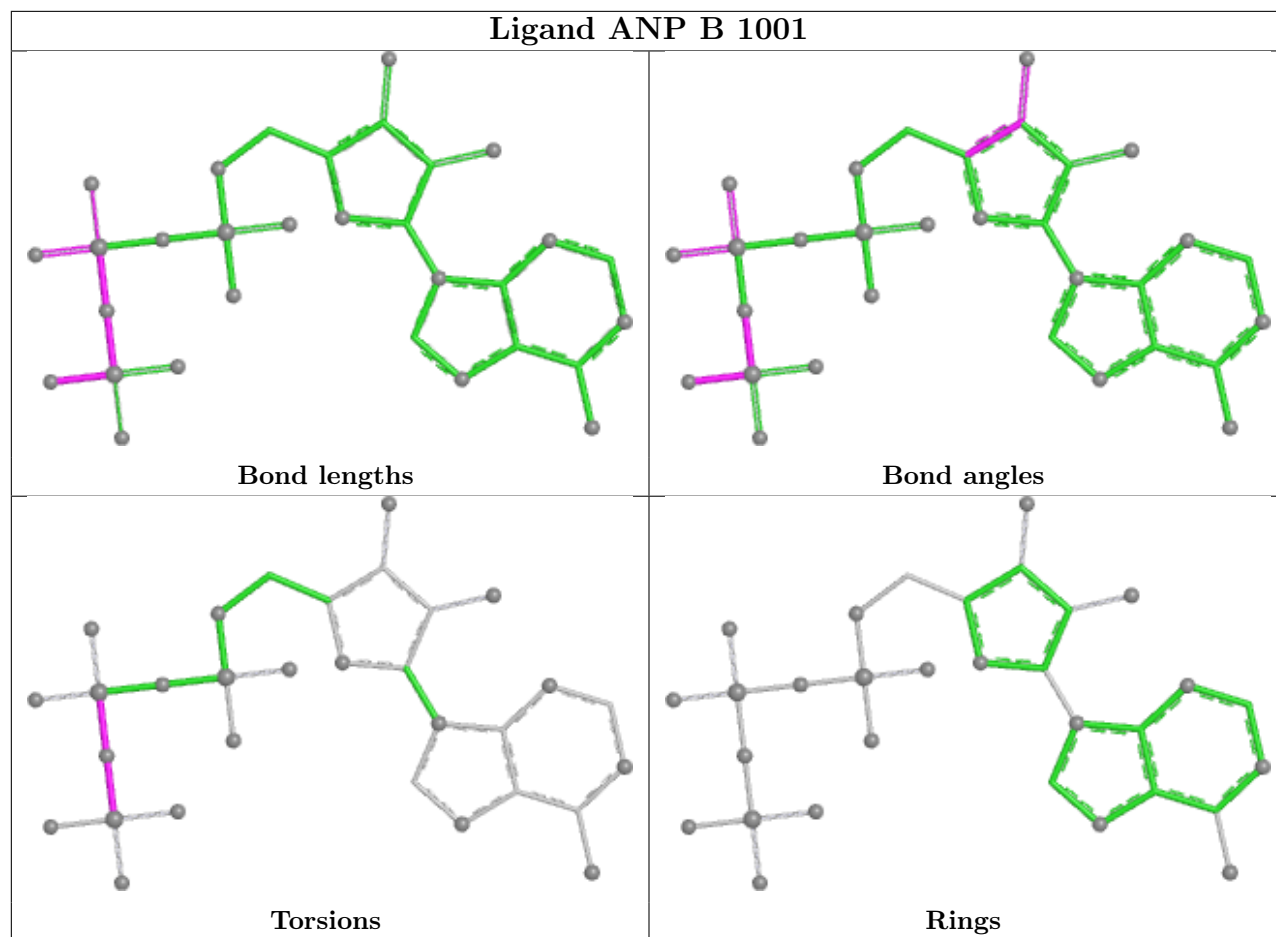
Mol	Chain	Res	Type	Atoms
2	A	1001	ANP	PG-N3B-PB-O1B
2	A	1001	ANP	PA-O3A-PB-O2B
2	B	1001	ANP	PG-N3B-PB-O1B
2	A	1001	ANP	PA-O3A-PB-O1B
2	B	1001	ANP	PB-N3B-PG-O1G

There are no ring outliers.

No monomer is involved in short contacts.

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	300/330 (90%)	0.46	24 (8%)	18 21	13, 24, 51, 87	3 (1%)
1	B	302/330 (91%)	0.41	30 (9%)	13 14	12, 23, 55, 78	5 (1%)
1	X	10/330 (3%)	3.37	8 (80%)	0 0	37, 49, 53, 66	0
All	All	612/990 (61%)	0.48	62 (10%)	12 14	12, 24, 54, 87	8 (1%)

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	989	ALA	5.7
1	B	837	LEU	5.6
1	B	838	LEU	5.4
1	X	993	LEU	5.0
1	B	675	PRO	4.3
1	A	839	GLY	4.3
1	A	837	LEU	4.1
1	A	731	ALA	4.1
1	X	995	PRO	4.1
1	B	674	ALA	4.1
1	A	691	ILE	4.0
1	A	676	ASN	3.8
1	A	699	PHE	3.7
1	X	997	GLN	3.7
1	B	964	HIS	3.6
1	X	998	GLY	3.5
1	A	838	LEU	3.5
1	X	994	ILE	3.5
1	X	992	TYR	3.4
1	B	986	VAL	3.3
1	A	693	VAL	3.2
1	B	730	LYS	3.2
1	A	991	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	731	ALA	3.1
1	A	852	VAL	3.1
1	B	725	GLU	3.1
1	B	851	LYS	3.0
1	A	698	ALA	2.9
1	B	678	ALA	2.9
1	B	991	GLU	2.9
1	B	990	ASP	2.9
1	B	989	ALA	2.8
1	A	851	LYS	2.7
1	B	783	ASP	2.7
1	B	852	VAL	2.7
1	B	708	ILE	2.6
1	B	758	LEU	2.6
1	B	711	GLY	2.5
1	A	677	GLN	2.5
1	A	678	ALA	2.5
1	A	894	ILE	2.5
1	B	740	TYR	2.4
1	A	725	GLU	2.4
1	A	893	GLY	2.4
1	B	965	LEU	2.4
1	A	835	ALA	2.4
1	A	982	ASP	2.4
1	B	938	ARG	2.3
1	B	836	LYS	2.3
1	B	963	MET	2.3
1	B	676	ASN	2.3
1	A	724	ARG	2.3
1	B	833	GLY	2.3
1	A	989	ALA	2.2
1	A	708	ILE	2.2
1	B	738	GLU	2.2
1	A	964	HIS	2.2
1	A	783	ASP	2.1
1	B	677	GLN	2.1
1	B	832	PHE	2.1
1	X	990	ASP	2.1
1	B	988	ASP	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](#)

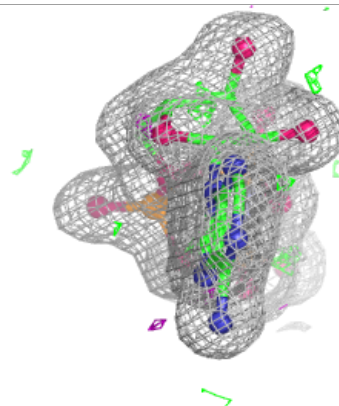
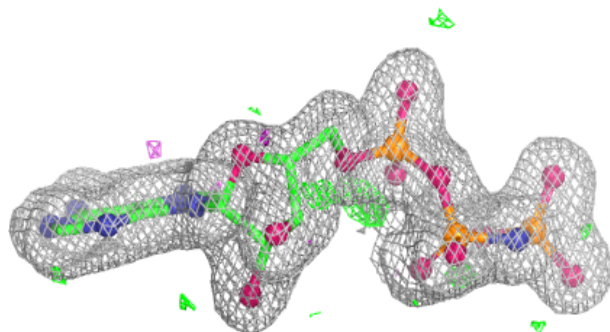
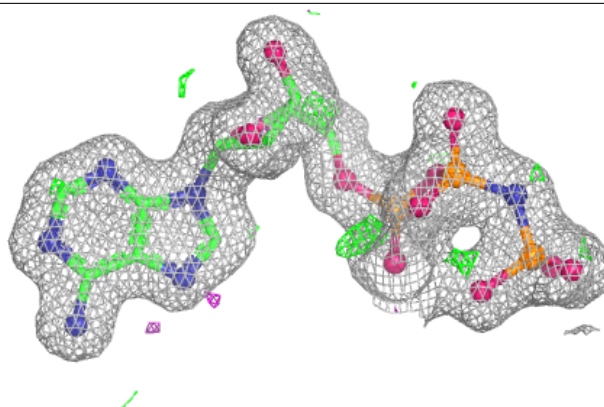
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	ANP	A	1001	31/31	0.98	0.05	18,22,26,29	0
2	ANP	B	1001	31/31	0.99	0.04	13,17,20,22	0
3	MG	A	1002	1/1	0.99	0.03	20,20,20,20	0
3	MG	B	1002	1/1	0.99	0.02	15,15,15,15	0

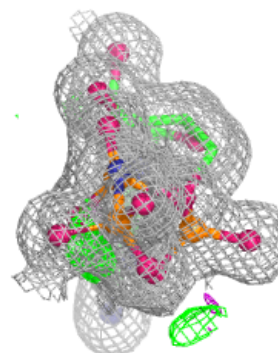
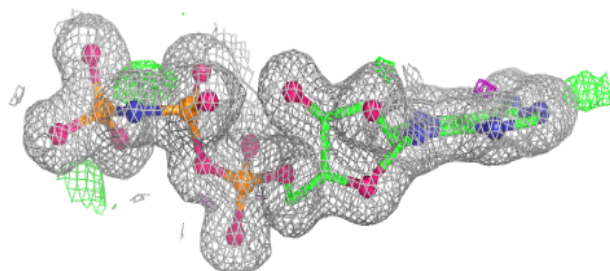
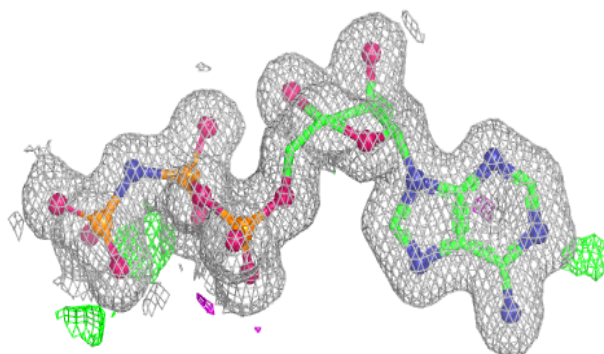
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ANP A 1001:

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

**Electron density around ANP B 1001:**

$2mF_o-DF_c$ (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.