



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 03:05 am BST

PDB ID : 3HQD
Title : Human kinesin Eg5 motor domain in complex with AMPPNP and Mg2+
Authors : Parke, C.L.; Wojcik, E.J.; Kim, S.; Worthylake, D.K.
Deposited on : 2009-06-05
Resolution : 2.19 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

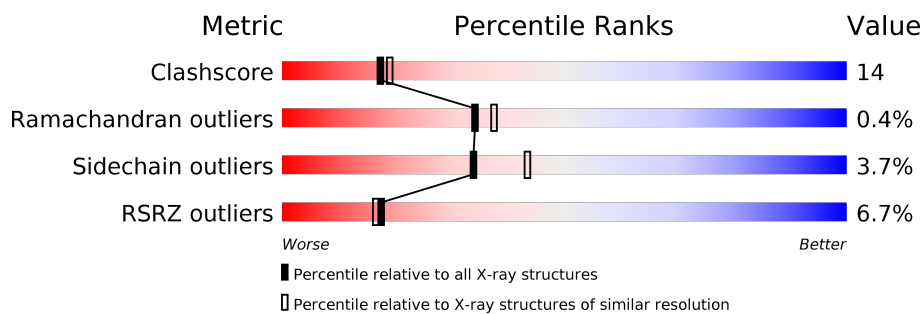
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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))
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 ≥ 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	369	<div> <div>3%</div> <div>72%</div> <div>22%</div> <div>• 5%</div> </div>
1	B	369	<div> <div>9%</div> <div>68%</div> <div>23%</div> <div>• 5%</div> </div>

2 Entry composition [i](#)

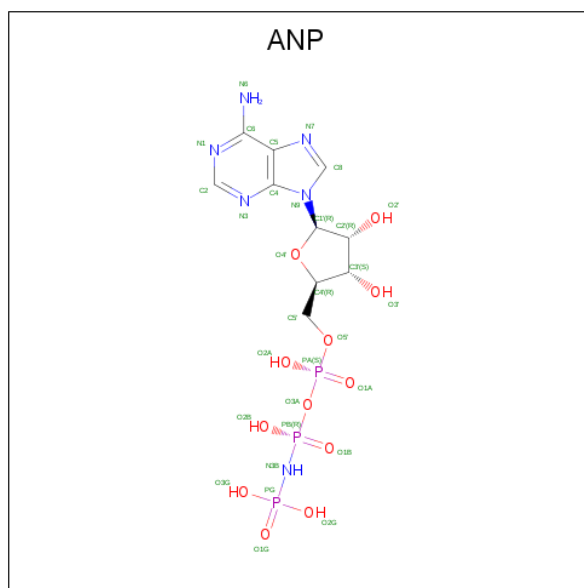
There are 5 unique types of molecules in this entry. The entry contains 5832 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Kinesin-like protein KIF11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2741	1711	484	536	10			
1	B	350	Total	C	N	O	S	0	0	0
			2741	1711	484	536	10			

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



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 PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

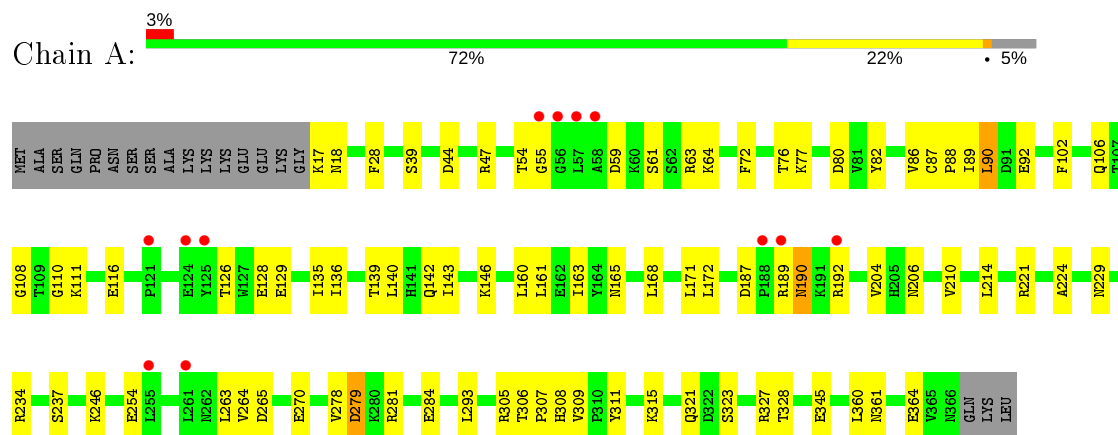
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	181	Total	O	0	0
			181	181		
5	B	100	Total	O	0	0
			100	100		

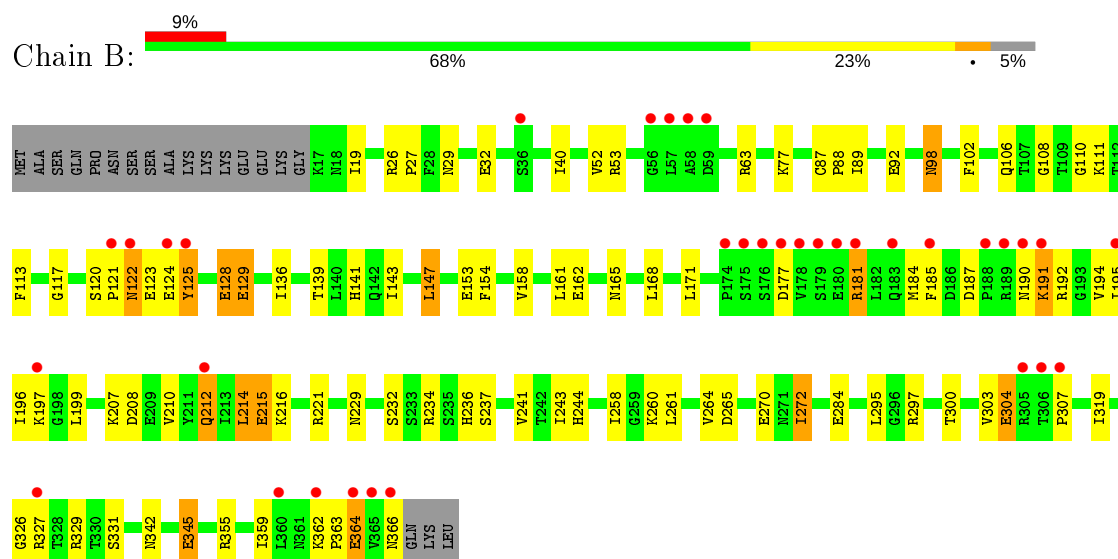
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Kinesin-like protein KIF11



- Molecule 1: Kinesin-like protein KIF11



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	60.50Å 71.44Å 94.85Å 90.00° 98.86° 90.00°	Depositor
Resolution (Å)	25.00 – 2.19 24.78 – 2.17	Depositor EDS
% Data completeness (in resolution range)	99.6 (25.00-2.19) 97.9 (24.78-2.17)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.17Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.224 , 0.262 0.219 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	21.7	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5832	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, ANP, MG

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	0/2781	0.63	0/3759
1	B	0.30	0/2781	0.58	0/3759
All	All	0.32	0/5562	0.61	0/7518

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

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	2741	0	2769	73	0
1	B	2741	0	2769	78	0
2	A	31	0	13	7	0
2	B	31	0	13	5	0
3	A	5	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	181	0	0	5	0
5	B	100	0	0	2	0
All	All	5832	0	5564	153	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 14.

All (153) 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:122:ASN:HB3	1:B:124:GLU:HG3	1.51	0.91
1:B:191:LYS:H	1:B:191:LYS:HD3	1.38	0.87
1:B:53:ARG:HD3	1:B:63:ARG:HH21	1.42	0.84
1:A:90:LEU:HD22	1:A:146:LYS:HD2	1.59	0.84
1:A:90:LEU:HD21	1:A:143:ILE:HD13	1.66	0.77
1:A:108:GLY:H	2:A:601:ANP:HNB1	1.32	0.76
1:A:192:ARG:CZ	1:A:327:ARG:HD2	2.16	0.76
1:B:110:GLY:HA2	2:B:602:ANP:O2A	1.86	0.76
1:B:272:ILE:HD13	1:B:272:ILE:H	1.52	0.74
1:B:158:VAL:HG12	1:B:241:VAL:HG12	1.72	0.71
1:A:17:LYS:HB3	1:A:360:LEU:HD11	1.73	0.70
1:A:192:ARG:HA	5:A:497:HOH:O	1.92	0.70
1:B:106:GLN:NE2	1:B:345:GLU:HG3	2.05	0.70
1:A:206:ASN:O	1:A:210:VAL:HG23	1.92	0.69
1:A:165:ASN:HD21	1:A:284:GLU:HA	1.58	0.69
1:A:110:GLY:HA2	2:A:601:ANP:O2A	1.94	0.68
1:B:125:TYR:HB3	1:B:129:GLU:HB3	1.76	0.68
1:B:108:GLY:H	2:B:602:ANP:HNB1	1.45	0.64
1:A:315:LYS:HE3	5:A:456:HOH:O	1.98	0.64
1:B:229:ASN:HD22	2:B:602:ANP:HNB1	1.47	0.61
1:B:191:LYS:CD	1:B:191:LYS:H	2.13	0.60
1:B:272:ILE:N	1:B:272:ILE:HD13	2.16	0.60
1:A:192:ARG:NE	1:A:327:ARG:HD2	2.18	0.59
1:B:258:ILE:H	1:B:366:ASN:HB3	1.68	0.59
1:A:116:GLU:HG2	5:A:503:HOH:O	2.03	0.58
1:A:55:GLY:CA	1:A:59:ASP:HB3	2.33	0.58
1:A:55:GLY:HA3	1:A:59:ASP:HB3	1.86	0.58
1:B:272:ILE:CD1	1:B:272:ILE:H	2.17	0.58
1:A:140:LEU:HD12	1:A:214:LEU:HD22	1.86	0.57
1:B:165:ASN:HD21	1:B:284:GLU:HA	1.68	0.57
1:B:207:LYS:O	1:B:210:VAL:HG12	2.04	0.57
1:B:181:ARG:H	1:B:181:ARG:HD3	1.68	0.57
1:B:98:ASN:ND2	1:B:260:LYS:HB3	2.20	0.56
1:A:54:THR:HG21	1:A:64:LYS:HD3	1.87	0.55
1:A:224:ALA:HB1	1:A:281:ARG:HE	1.71	0.55
1:A:17:LYS:HB3	1:A:360:LEU:CD1	2.36	0.55
1:B:147:LEU:HD23	1:B:154:PHE:CD1	2.41	0.55
1:B:161:LEU:HD12	1:B:161:LEU:C	2.27	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:ARG:HD3	1:B:284:GLU:OE1	2.05	0.55
1:B:92:GLU:OE2	1:B:329:ARG:HD3	2.07	0.54
1:A:102:PHE:HB3	1:A:264:VAL:HB	1.90	0.54
1:B:168:LEU:HD12	1:B:168:LEU:N	2.22	0.54
1:A:163:ILE:HG12	1:A:168:LEU:CD2	2.39	0.53
1:A:140:LEU:HD13	1:A:210:VAL:CG1	2.39	0.53
1:B:194:VAL:HG11	1:B:319:ILE:HD13	1.89	0.53
1:B:153:GLU:HB2	5:B:463:HOH:O	2.08	0.53
1:A:246:LYS:HE2	1:A:254:GLU:CD	2.28	0.52
1:A:111:LYS:NZ	2:A:601:ANP:O1G	2.40	0.52
1:B:194:VAL:HG22	1:B:195:ILE:N	2.24	0.52
1:A:305:ARG:NH1	1:A:305:ARG:HG3	2.24	0.52
1:A:306:THR:HG23	1:A:307:PRO:HD2	1.92	0.52
1:B:102:PHE:HB3	1:B:264:VAL:HB	1.92	0.52
1:B:89:ILE:HA	1:B:92:GLU:OE2	2.10	0.51
1:A:311:TYR:CG	1:A:321:GLN:HG3	2.45	0.51
1:A:82:TYR:OH	1:A:142:GLN:HG2	2.11	0.51
1:B:345:GLU:CD	1:B:345:GLU:H	2.09	0.51
1:A:305:ARG:HH11	1:A:305:ARG:HG3	1.76	0.51
1:B:40:ILE:O	1:B:52:VAL:HA	2.10	0.51
1:A:72:PHE:HB3	1:A:76:THR:OG1	2.11	0.51
1:A:140:LEU:HD13	1:A:210:VAL:HG12	1.93	0.50
1:A:192:ARG:NH1	5:A:541:HOH:O	2.39	0.50
1:A:161:LEU:HD12	1:A:161:LEU:C	2.32	0.50
1:B:212:GLN:HE21	1:B:212:GLN:C	2.15	0.50
1:A:311:TYR:CD1	1:A:321:GLN:HG3	2.47	0.49
1:B:122:ASN:HD22	1:B:124:GLU:CD	2.15	0.49
1:B:181:ARG:N	1:B:181:ARG:HD3	2.28	0.49
1:A:90:LEU:CD2	1:A:143:ILE:HD13	2.38	0.49
1:A:327:ARG:HG2	1:A:327:ARG:HH11	1.77	0.49
1:B:196:ILE:N	1:B:196:ILE:HD12	2.27	0.49
1:B:143:ILE:HD13	1:B:243:ILE:HD11	1.95	0.49
1:A:102:PHE:CB	1:A:264:VAL:HB	2.43	0.49
1:A:28:PHE:HZ	1:A:39:SER:HB2	1.76	0.49
1:B:329:ARG:HG3	1:B:363:PRO:HG3	1.94	0.49
1:A:86:VAL:HG21	1:A:135:ILE:HG23	1.95	0.48
1:B:102:PHE:CB	1:B:264:VAL:HB	2.43	0.48
1:A:136:ILE:HG12	1:A:263:LEU:HD13	1.96	0.48
1:B:207:LYS:HG3	1:B:208:ASP:N	2.28	0.48
1:B:162:GLU:HG2	1:B:171:LEU:HD21	1.95	0.48
1:A:229:ASN:HD22	2:A:601:ANP:HNB1	1.60	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:SER:O	1:A:63:ARG:HG3	2.14	0.48
1:A:140:LEU:CD1	1:A:214:LEU:HD22	2.42	0.48
1:A:108:GLY:N	2:A:601:ANP:HNB1	2.05	0.48
1:A:160:LEU:HG	1:A:171:LEU:HD12	1.96	0.47
1:A:278:VAL:HG12	1:A:279:ASP:N	2.29	0.47
1:A:234:ARG:CD	1:A:284:GLU:OE1	2.63	0.47
1:A:237:SER:HB3	1:A:265:ASP:HB3	1.95	0.47
1:A:246:LYS:HE2	1:A:254:GLU:OE1	2.14	0.47
1:B:229:ASN:HB3	1:B:232:SER:HB2	1.97	0.47
1:B:303:VAL:HG11	1:B:355:ARG:O	2.14	0.47
1:B:327:ARG:HG3	1:B:327:ARG:HH11	1.79	0.47
1:A:327:ARG:HD3	1:A:364:GLU:CD	2.35	0.47
1:B:87:CYS:N	1:B:88:PRO:HD2	2.30	0.46
1:A:234:ARG:HD3	1:A:284:GLU:OE1	2.15	0.46
1:B:329:ARG:HH11	1:B:329:ARG:HG2	1.80	0.46
1:A:306:THR:HG22	1:A:308:HIS:H	1.81	0.45
1:B:128:GLU:HG2	1:B:141:HIS:CD2	2.51	0.45
1:B:185:PHE:O	1:B:194:VAL:HG23	2.16	0.45
1:B:53:ARG:HD3	1:B:63:ARG:NH2	2.20	0.45
1:B:136:ILE:HG22	1:B:214:LEU:HD11	1.99	0.45
1:B:162:GLU:HA	1:B:236:HIS:O	2.17	0.45
1:A:87:CYS:HB2	1:A:88:PRO:HD3	1.99	0.45
2:B:602:ANP:H8	2:B:602:ANP:O2A	2.17	0.44
1:A:106:GLN:NE2	1:A:345:GLU:HG2	2.33	0.44
1:A:234:ARG:NH2	1:A:270:GLU:OE1	2.45	0.44
1:A:44:ASP:OD2	1:A:47:ARG:HD3	2.17	0.44
2:A:601:ANP:H8	2:A:601:ANP:O2A	2.18	0.44
1:B:147:LEU:HB3	1:B:154:PHE:CE2	2.53	0.44
1:B:327:ARG:HA	1:B:362:LYS:O	2.17	0.44
1:B:342:ASN:HB3	1:B:345:GLU:HG2	1.99	0.44
1:A:323:SER:HA	1:A:328:THR:HB	1.98	0.44
1:B:111:LYS:NZ	2:B:602:ANP:O1G	2.44	0.44
1:A:28:PHE:CZ	1:A:39:SER:HB2	2.53	0.43
1:B:234:ARG:CD	1:B:284:GLU:OE1	2.66	0.43
1:A:306:THR:CG2	5:A:423:HOH:O	2.67	0.43
1:B:196:ILE:HG22	1:B:199:LEU:HB2	2.01	0.43
1:A:246:LYS:NZ	1:A:254:GLU:HG3	2.33	0.43
1:A:77:LYS:HB2	1:A:80:ASP:OD2	2.19	0.43
1:A:293:LEU:C	1:A:293:LEU:HD23	2.39	0.43
1:B:139:THR:O	1:B:143:ILE:HG13	2.18	0.43
1:A:204:VAL:HB	1:A:210:VAL:HG22	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:237:SER:OG	1:B:265:ASP:HB3	2.19	0.43
1:B:244:HIS:CD2	5:B:448:HOH:O	2.72	0.42
1:A:140:LEU:HD22	1:A:210:VAL:HG11	2.01	0.42
1:B:184:MET:SD	1:B:194:VAL:HG21	2.59	0.42
1:B:234:ARG:NH2	1:B:270:GLU:OE2	2.40	0.42
1:A:224:ALA:HB1	1:A:281:ARG:NE	2.34	0.42
1:B:120:SER:HA	1:B:121:PRO:HD3	1.88	0.42
1:A:309:VAL:HG11	1:A:311:TYR:CZ	2.54	0.42
1:B:212:GLN:HE22	1:B:216:LYS:HD2	1.85	0.42
1:B:297:ARG:HG2	1:B:297:ARG:HH11	1.85	0.42
1:B:300:THR:O	1:B:304:GLU:HB2	2.19	0.42
1:B:192:ARG:NH1	1:B:326:GLY:HA2	2.35	0.42
1:B:241:VAL:CG2	1:B:261:LEU:HB3	2.49	0.42
1:B:19:ILE:HD12	1:B:359:ILE:HB	2.00	0.42
1:B:102:PHE:HA	1:B:264:VAL:O	2.20	0.41
1:B:123:GLU:HG2	1:B:123:GLU:O	2.21	0.41
1:B:77:LYS:HD3	1:B:77:LYS:HA	1.86	0.41
1:A:139:THR:O	1:A:143:ILE:HG12	2.21	0.41
1:B:327:ARG:HB3	1:B:364:GLU:HG3	2.03	0.41
1:A:126:THR:OG1	1:A:129:GLU:HG2	2.20	0.41
1:A:187:ASP:HB3	1:A:190:ASN:O	2.21	0.41
1:A:17:LYS:HA	1:A:361:ASN:O	2.21	0.41
1:B:215:GLU:HA	1:B:215:GLU:OE1	2.20	0.41
1:A:110:GLY:CA	2:A:601:ANP:O2A	2.67	0.41
1:A:160:LEU:HB3	1:A:172:LEU:HG	2.01	0.40
1:B:26:ARG:HB2	1:B:27:PRO:HD2	2.02	0.40
1:A:187:ASP:OD1	1:A:189:ARG:HG2	2.21	0.40
1:A:89:ILE:HA	1:A:92:GLU:OE2	2.21	0.40
1:B:329:ARG:HG2	1:B:329:ARG:NH1	2.36	0.40
1:B:113:PHE:O	1:B:117:GLY:HA2	2.21	0.40
1:B:29:ASN:OD1	1:B:32:GLU:HG3	2.22	0.40
1:B:89:ILE:HD11	1:B:331:SER:OG	2.21	0.40
1:B:187:ASP:HB3	1:B:190:ASN:HB2	2.04	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	348/369 (94%)	337 (97%)	9 (3%)	2 (1%)	25	26
1	B	348/369 (94%)	333 (96%)	14 (4%)	1 (0%)	41	46
All	All	696/738 (94%)	670 (96%)	23 (3%)	3 (0%)	34	37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	279	ASP
1	A	190	ASN
1	B	307	PRO

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	307/323 (95%)	303 (99%)	4 (1%)	69	81
1	B	307/323 (95%)	288 (94%)	19 (6%)	18	21
All	All	614/646 (95%)	591 (96%)	23 (4%)	34	43

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

Mol	Chain	Res	Type
1	A	18	ASN
1	A	90	LEU
1	A	128	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	221	ARG
1	B	98	ASN
1	B	122	ASN
1	B	125	TYR
1	B	128	GLU
1	B	129	GLU
1	B	147	LEU
1	B	177	ASP
1	B	181	ARG
1	B	191	LYS
1	B	197	LYS
1	B	212	GLN
1	B	214	LEU
1	B	215	GLU
1	B	221	ARG
1	B	272	ILE
1	B	295	LEU
1	B	304	GLU
1	B	345	GLU
1	B	364	GLU

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

Mol	Chain	Res	Type
1	A	18	ASN
1	A	20	GLN
1	A	38	HIS
1	A	165	ASN
1	A	190	ASN
1	A	262	ASN
1	B	20	GLN
1	B	98	ASN
1	B	122	ASN
1	B	141	HIS
1	B	142	GLN
1	B	165	ASN
1	B	190	ASN
1	B	212	GLN
1	B	229	ASN
1	B	244	HIS
1	B	262	ASN
1	B	321	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	PO4	A	562	-	4,4,4	1.89	1 (25%)	6,6,6	0.43	0
2	ANP	B	602	-	29,33,33	1.82	7 (24%)	31,52,52	2.94	15 (48%)
2	ANP	A	601	-	29,33,33	1.82	7 (24%)	31,52,52	3.20	17 (54%)

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	B	602	-	-	3/14/38/38	0/3/3/3
2	ANP	A	601	-	-	3/14/38/38	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	ANP	PG-O1G	4.64	1.53	1.46
2	B	602	ANP	O4'-C1'	4.46	1.47	1.41
2	A	601	ANP	O4'-C1'	4.01	1.46	1.41
2	A	601	ANP	PA-O5'	3.82	1.74	1.59
2	B	602	ANP	PG-O1G	3.80	1.52	1.46
2	B	602	ANP	PA-O5'	3.48	1.73	1.59
3	A	562	PO4	P-O1	3.17	1.58	1.50
2	A	601	ANP	O5'-C5'	-3.14	1.32	1.44
2	B	602	ANP	PB-N3B	3.04	1.71	1.63
2	B	602	ANP	O5'-C5'	-2.73	1.34	1.44
2	A	601	ANP	PB-N3B	2.45	1.69	1.63
2	A	601	ANP	PG-O3G	-2.36	1.50	1.56
2	B	602	ANP	C2-N3	2.17	1.35	1.32
2	B	602	ANP	PG-O3G	-2.06	1.51	1.56
2	A	601	ANP	PG-O2G	-2.01	1.51	1.56

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	ANP	C5'-C4'-C3'	-7.24	88.06	115.18
2	A	601	ANP	PA-O3A-PB	-6.42	110.02	132.62
2	B	602	ANP	C5'-C4'-C3'	-6.40	91.19	115.18
2	B	602	ANP	PA-O3A-PB	-6.13	111.02	132.62
2	A	601	ANP	O5'-C5'-C4'	5.95	129.48	108.99
2	A	601	ANP	O3A-PB-N3B	-5.25	92.03	106.59
2	B	602	ANP	N3-C2-N1	-5.10	120.71	128.68
2	A	601	ANP	N3-C2-N1	-4.97	120.91	128.68
2	A	601	ANP	O5'-PA-O1A	-4.77	90.42	109.07
2	B	602	ANP	O5'-C5'-C4'	4.76	125.38	108.99
2	A	601	ANP	O2A-PA-O5'	-4.76	85.66	107.75
2	B	602	ANP	O2A-PA-O5'	-4.66	86.10	107.75
2	B	602	ANP	O5'-PA-O1A	-4.57	91.22	109.07
2	B	602	ANP	O3A-PB-N3B	-4.41	94.36	106.59
2	B	602	ANP	C2'-C3'-C4'	3.45	109.35	102.64
2	A	601	ANP	O2B-PB-O3A	3.42	116.06	104.64
2	B	602	ANP	PA-O5'-C5'	-3.24	102.66	121.68
2	A	601	ANP	PA-O5'-C5'	-3.10	103.48	121.68
2	B	602	ANP	O2B-PB-O3A	3.01	114.69	104.64
2	A	601	ANP	O1G-PG-N3B	2.63	115.65	111.77
2	A	601	ANP	O4'-C4'-C5'	-2.61	100.77	109.37
2	A	601	ANP	O2A-PA-O1A	2.60	125.11	112.24
2	A	601	ANP	C2'-C3'-C4'	2.56	107.62	102.64
2	B	602	ANP	O4'-C4'-C5'	-2.52	101.08	109.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	ANP	O4'-C1'-C2'	2.51	110.60	106.93
2	B	602	ANP	C3'-C2'-C1'	2.50	104.75	100.98
2	A	601	ANP	O2G-PG-O1G	-2.37	107.49	113.45
2	B	602	ANP	C1'-N9-C4	-2.33	122.54	126.64
2	A	601	ANP	C1'-N9-C4	-2.32	122.56	126.64
2	B	602	ANP	O2A-PA-O1A	2.14	122.81	112.24
2	B	602	ANP	O2G-PG-O1G	-2.10	108.18	113.45
2	A	601	ANP	O4'-C4'-C3'	2.05	109.17	105.11

There are no chirality outliers.

All (6) torsion outliers are listed below:

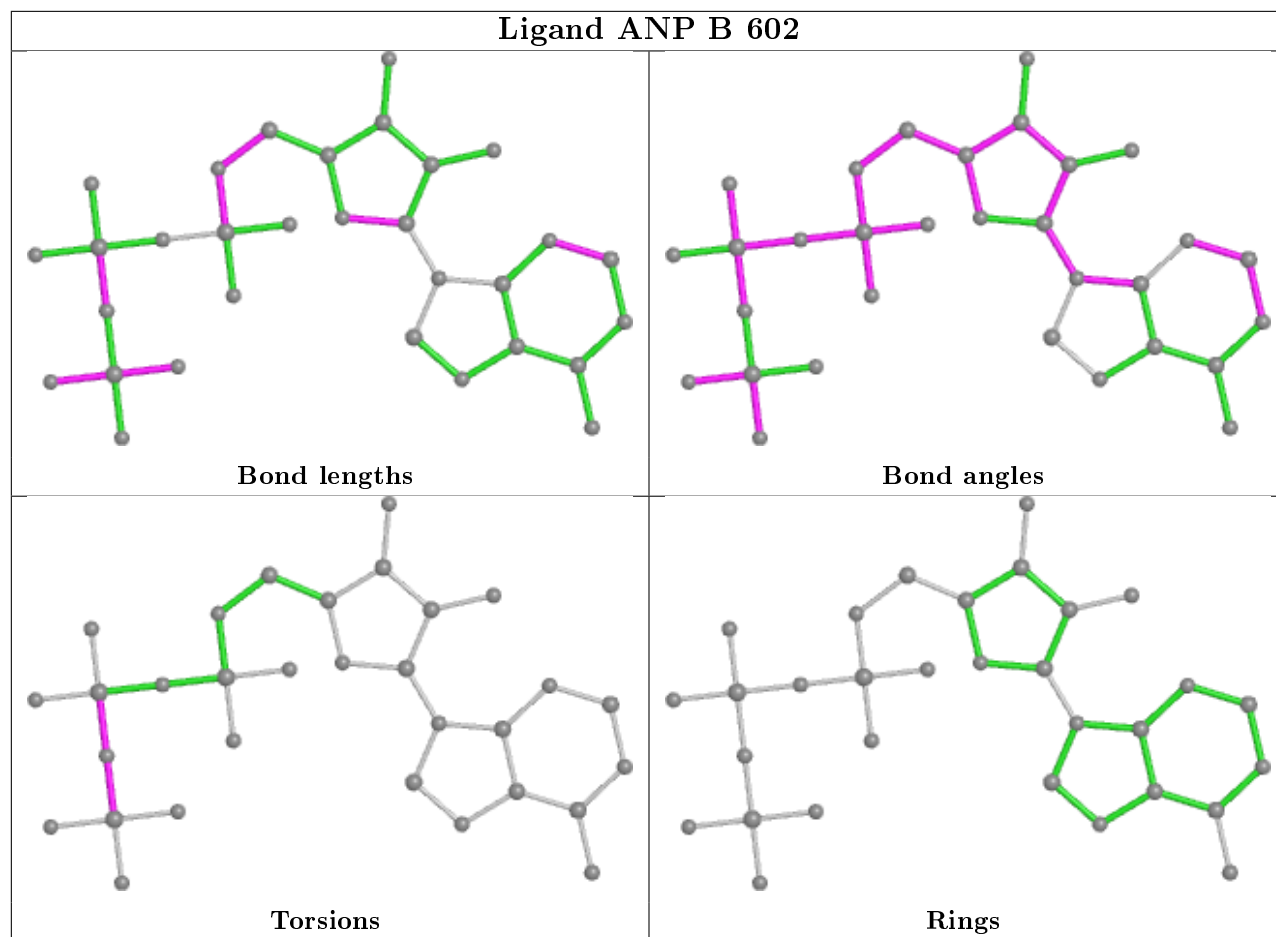
Mol	Chain	Res	Type	Atoms
2	B	602	ANP	PB-N3B-PG-O1G
2	B	602	ANP	PG-N3B-PB-O1B
2	B	602	ANP	PG-N3B-PB-O3A
2	A	601	ANP	PB-N3B-PG-O1G
2	A	601	ANP	PG-N3B-PB-O1B
2	A	601	ANP	PG-N3B-PB-O3A

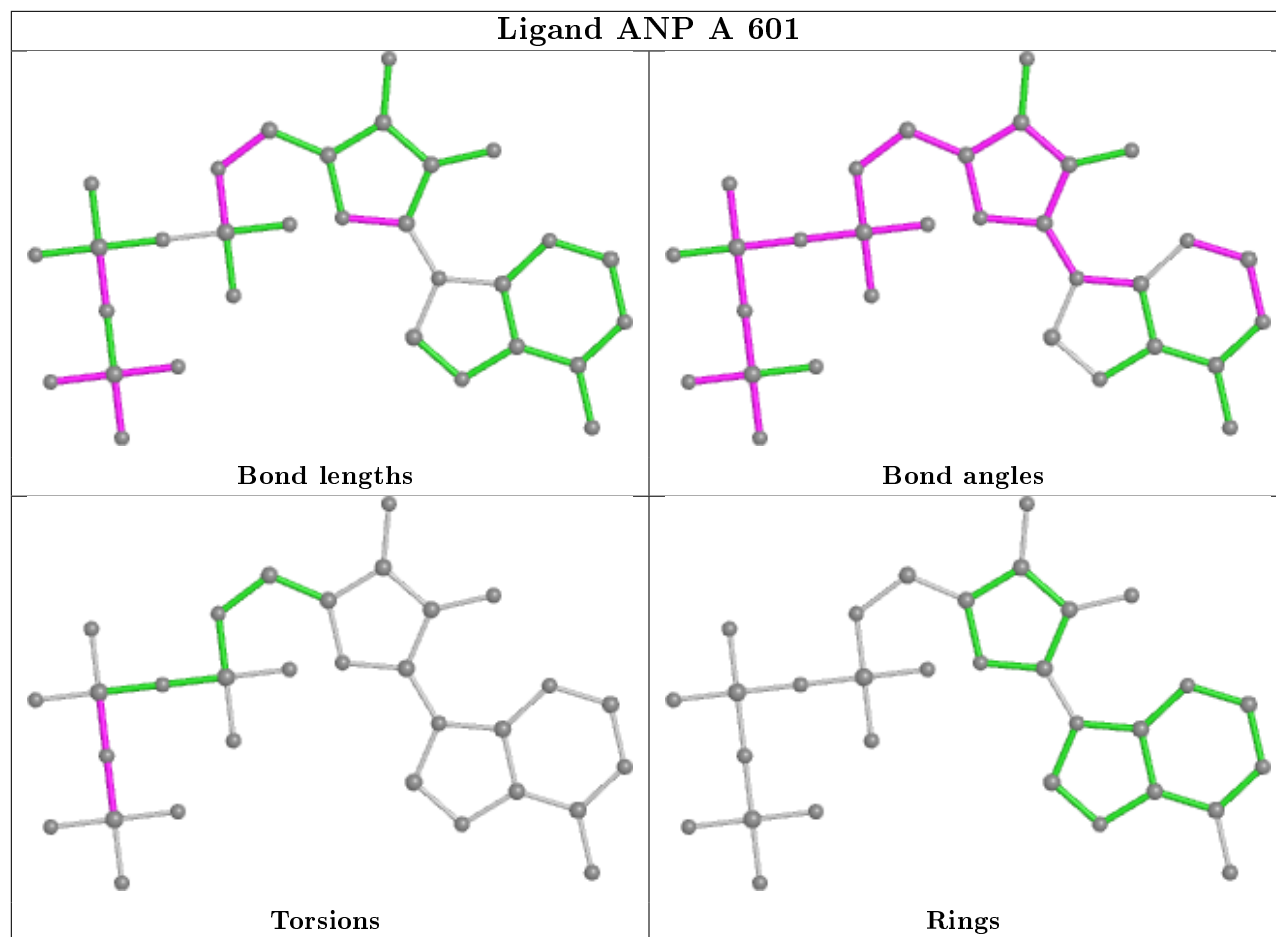
There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	602	ANP	5	0
2	A	601	ANP	7	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	350/369 (94%)	0.33	12 (3%) 45 43	8, 22, 43, 60	0
1	B	350/369 (94%)	0.73	35 (10%) 7 6	9, 29, 64, 90	0
All	All	700/738 (94%)	0.53	47 (6%) 17 16	8, 26, 54, 90	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	178	VAL	16.1
1	B	179	SER	15.0
1	B	57	LEU	6.2
1	B	121	PRO	5.9
1	A	57	LEU	5.6
1	B	124	GLU	5.3
1	A	58	ALA	5.2
1	B	185	PHE	5.2
1	B	175	SER	5.1
1	B	58	ALA	4.7
1	B	189	ARG	4.6
1	A	188	PRO	4.6
1	B	366	ASN	4.5
1	B	177	ASP	4.3
1	B	365	VAL	4.1
1	A	189	ARG	3.7
1	B	56	GLY	3.7
1	B	125	TYR	3.6
1	B	364	GLU	3.6
1	B	183	GLN	3.5
1	B	188	PRO	3.3
1	B	181	ARG	3.3
1	B	122	ASN	3.3
1	B	190	ASN	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	176	SER	3.1
1	A	192	ARG	3.0
1	B	360	LEU	3.0
1	B	327	ARG	2.8
1	A	255	LEU	2.8
1	B	305	ARG	2.7
1	B	180	GLU	2.7
1	B	212	GLN	2.6
1	B	59	ASP	2.5
1	B	307	PRO	2.4
1	B	197	LYS	2.4
1	A	125	TYR	2.4
1	A	124	GLU	2.3
1	A	121	PRO	2.3
1	A	56	GLY	2.2
1	B	191	LYS	2.2
1	B	195	ILE	2.2
1	A	55	GLY	2.2
1	B	362	LYS	2.2
1	B	36	SER	2.0
1	B	306	THR	2.0
1	A	261	LEU	2.0
1	B	174	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 carbohydrates in this entry.

6.4 Ligands [i](#)

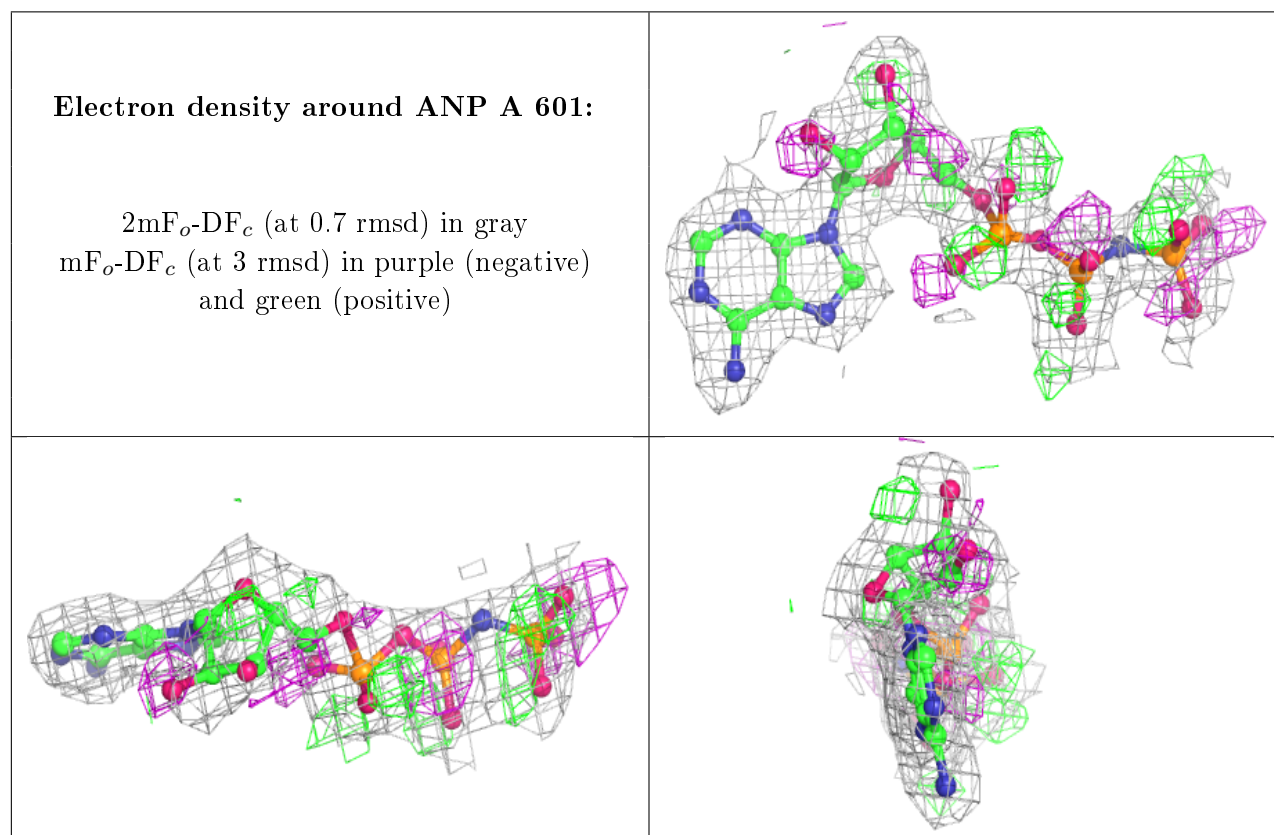
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

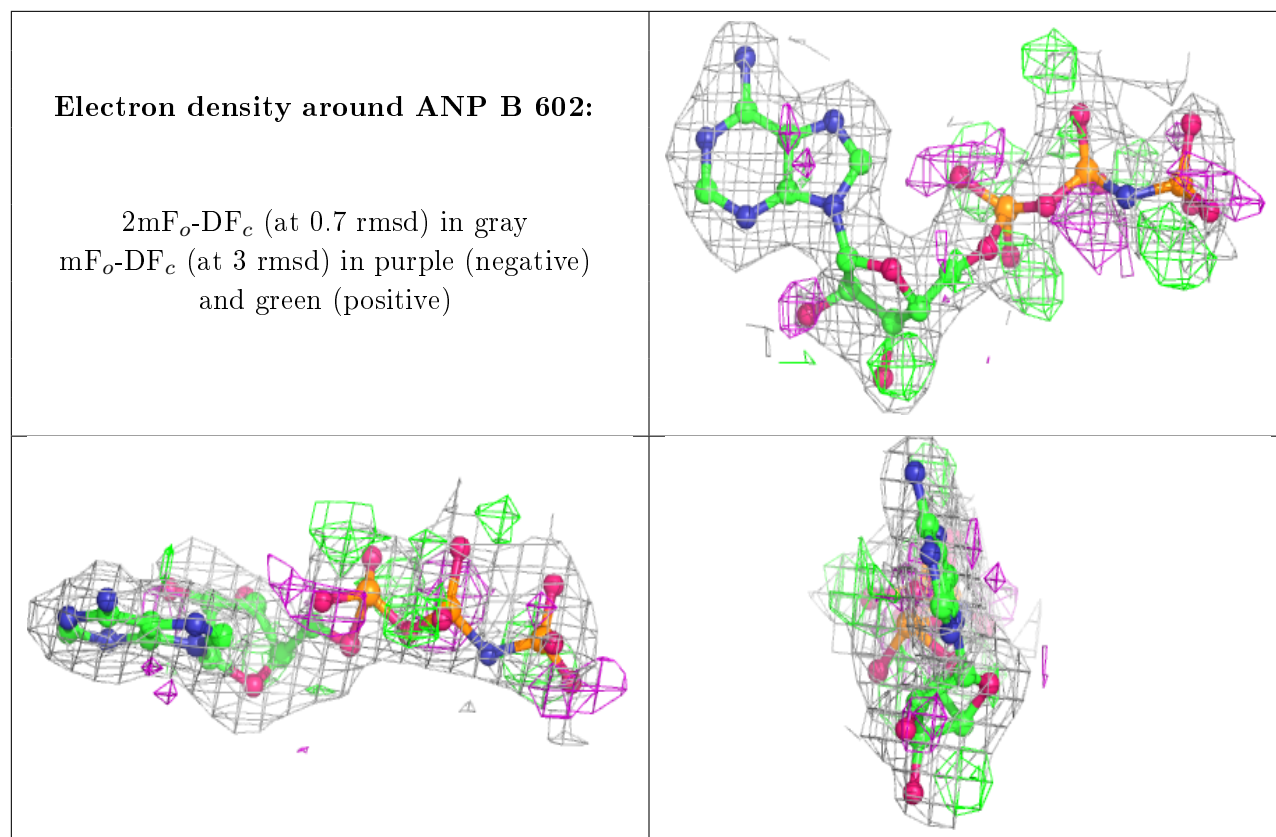
Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MG	B	502	1/1	0.83	0.25	31,31,31,31	0
3	PO4	A	562	5/5	0.90	0.17	38,39,42,43	0
2	ANP	A	601	31/31	0.91	0.18	11,17,27,31	0
2	ANP	B	602	31/31	0.91	0.19	14,21,31,35	0
4	MG	A	501	1/1	0.94	0.11	14,14,14,14	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.