



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:55 AM UTC

PDB ID : 6FDM / pdb_00006fdm
Title : Human Rio2 kinase structure
Authors : Fribourg, S.
Deposited on : 2017-12-26
Resolution : 2.10 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

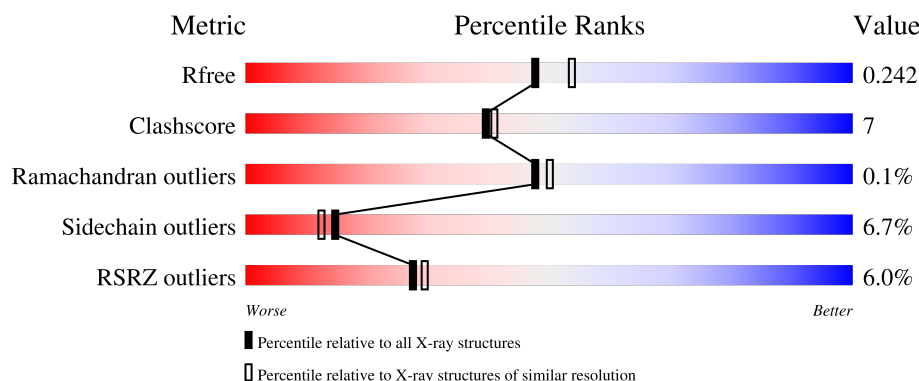
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	313	7% 74% 15% • 9%
1	B	313	5% 72% 16% •• 11%
1	C	313	5% 75% 16% 9%
1	D	313	4% 75% 13% •• 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ANP	A	401	-	-	X	X
2	ANP	C	401	-	-	-	X

2 Entry composition [i](#)

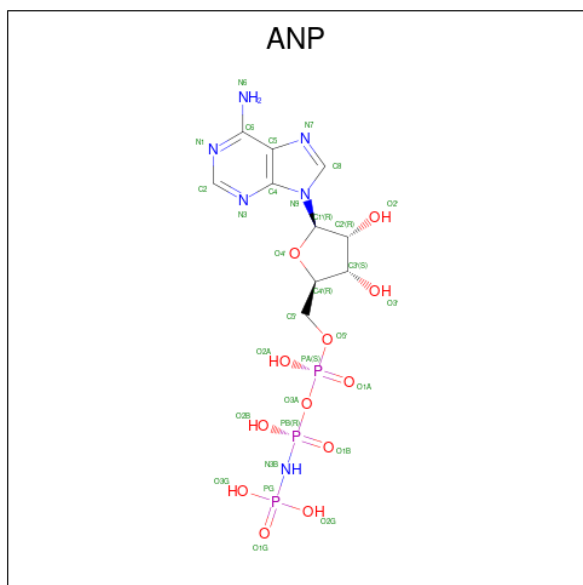
There are 4 unique types of molecules in this entry. The entry contains 9863 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	1	0
			2325	1483	399	428	15			
1	B	280	Total	C	N	O	S	0	0	0
			2262	1441	386	420	15			
1	C	285	Total	C	N	O	S	0	0	0
			2313	1476	398	424	15			
1	D	283	Total	C	N	O	S	7	2	0
			2303	1469	396	423	15			

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: 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	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

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

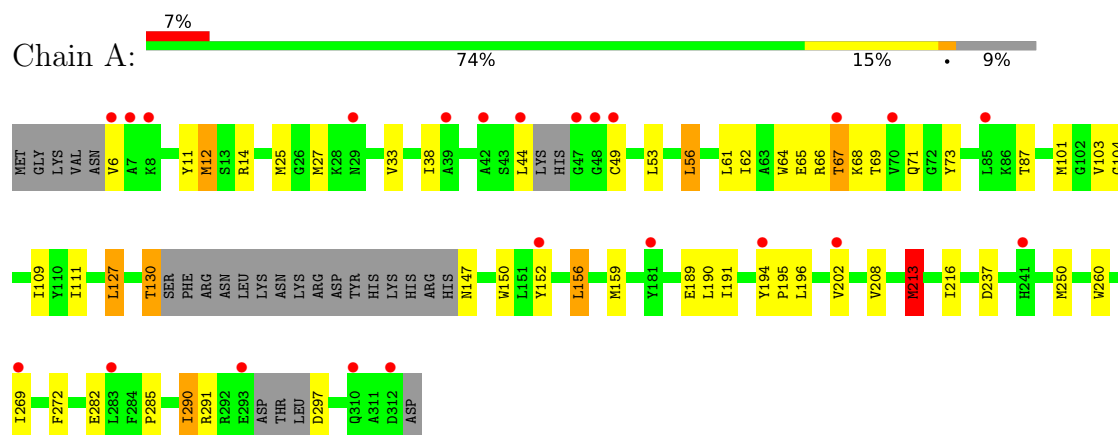
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	159	Total	O	0	0
			159	159		
4	B	128	Total	O	0	0
			128	128		
4	C	156	Total	O	0	0
			156	156		
4	D	153	Total	O	0	0
			153	153		

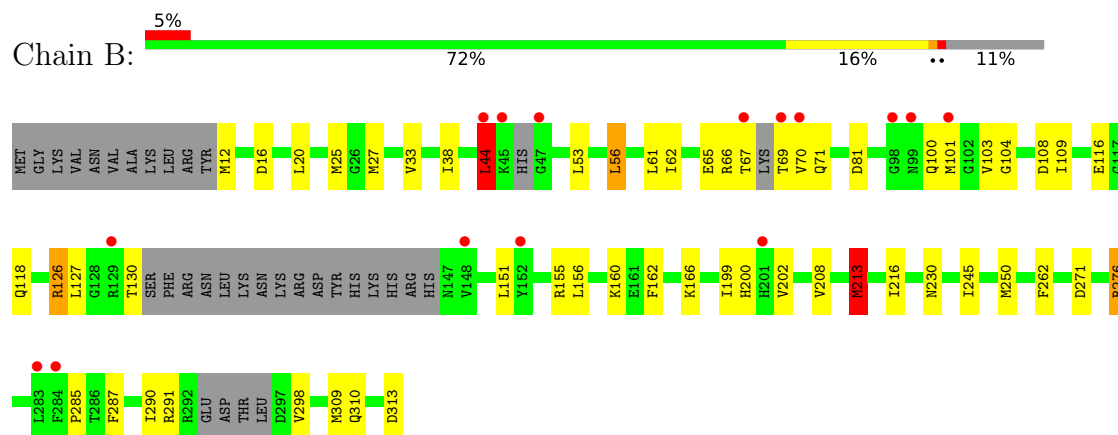
3 Residue-property plots [i](#)

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.

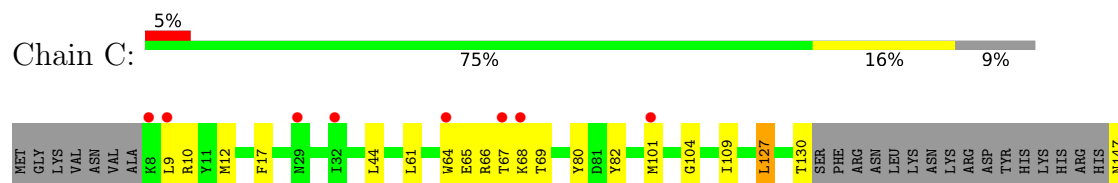
- Molecule 1: Serine/threonine-protein kinase RIO2

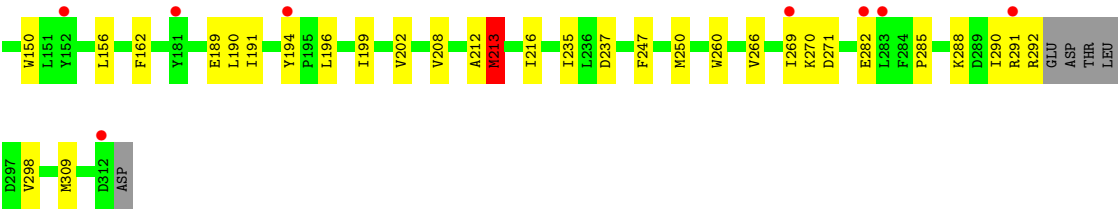


- Molecule 1: Serine/threonine-protein kinase RIO2

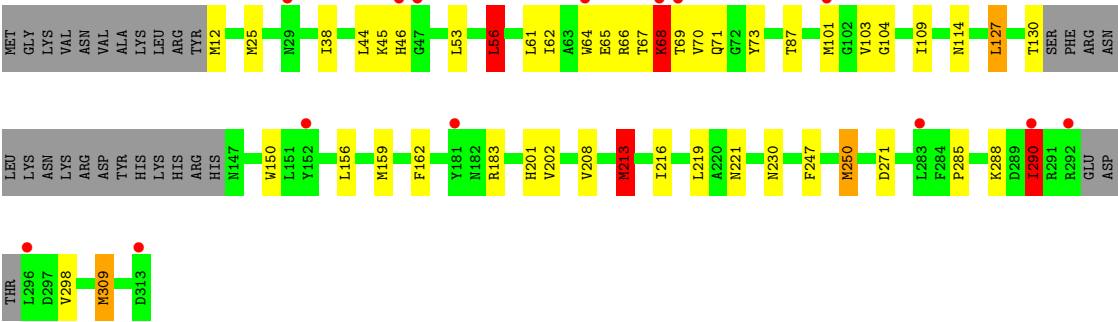


- Molecule 1: Serine/threonine-protein kinase RIO2





● Molecule 1: Serine/threonine-protein kinase RIO2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.92Å 98.33Å 117.07Å 90.00° 95.22° 90.00°	Depositor
Resolution (Å)	66.64 – 2.10 66.64 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.6 (66.64-2.10) 98.6 (66.64-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.10Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.202 , 0.237 0.205 , 0.242	Depositor DCC
R_{free} test set	4370 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtriage
Anisotropy	0.453	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 66.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9863	wwPDB-VP
Average B, all atoms (Å ²)	56.0	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 38.55 % 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 3.6269e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: ANP, NA

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	1.02	3/2375 (0.1%)	1.33	10/3201 (0.3%)
1	B	0.95	4/2309 (0.2%)	1.40	9/3111 (0.3%)
1	C	1.01	3/2364 (0.1%)	1.33	7/3186 (0.2%)
1	D	0.90	3/2361 (0.1%)	1.40	9/3184 (0.3%)
All	All	0.97	13/9409 (0.1%)	1.36	35/12682 (0.3%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	130	THR	C-N	26.45	1.69	1.33
1	C	130	THR	C-N	22.89	1.66	1.33
1	D	213	MET	SD-CE	-12.84	1.47	1.79
1	B	309	MET	SD-CE	-12.08	1.49	1.79
1	C	213	MET	SD-CE	-11.48	1.50	1.79
1	B	213	MET	SD-CE	-10.41	1.53	1.79
1	D	250	MET	SD-CE	-10.15	1.54	1.79
1	A	213	MET	SD-CE	-9.66	1.55	1.79
1	B	130	THR	C-N	9.62	1.46	1.33
1	C	250	MET	SD-CE	-8.70	1.57	1.79
1	A	250	MET	SD-CE	-8.61	1.58	1.79
1	B	250	MET	SD-CE	-8.11	1.59	1.79
1	D	309	MET	SD-CE	-5.44	1.66	1.79

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	130	THR	O-C-N	-24.54	93.05	123.24
1	C	130	THR	O-C-N	-21.86	91.77	122.81
1	B	130	THR	O-C-N	-20.83	96.07	123.15
1	A	130	THR	O-C-N	-19.56	96.90	123.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	130	THR	CA-C-N	18.71	150.95	121.19
1	D	130	THR	C-N-CA	18.71	150.95	121.19
1	B	130	THR	CA-C-N	17.22	142.83	120.44
1	B	130	THR	C-N-CA	17.22	142.83	120.44
1	A	130	THR	CA-C-N	10.46	135.14	120.29
1	A	130	THR	C-N-CA	10.46	135.14	120.29
1	C	130	THR	CA-C-N	8.24	134.68	120.58
1	C	130	THR	C-N-CA	8.24	134.68	120.58
1	B	44	LEU	N-CA-C	8.21	121.03	111.02
1	C	290	ILE	N-CA-C	7.54	117.61	110.30
1	B	276	ARG	CB-CG-CD	7.39	128.29	111.30
1	D	290	ILE	N-CA-CB	7.19	119.16	110.31
1	A	49	CYS	N-CA-C	6.87	119.40	111.02
1	C	147	ASN	N-CA-C	-6.10	104.19	111.69
1	D	68	LYS	N-CA-C	5.92	123.42	110.80
1	A	33	VAL	N-CA-C	5.84	112.88	107.56
1	B	104	GLY	N-CA-C	-5.68	103.61	112.58
1	B	33	VAL	N-CA-C	5.51	113.33	107.76
1	A	237	ASP	CA-CB-CG	5.47	118.07	112.60
1	C	237	ASP	CA-CB-CG	5.46	118.06	112.60
1	B	245	ILE	N-CA-C	5.43	118.36	113.10
1	A	290	ILE	N-CA-CB	5.34	117.58	110.26
1	A	104	GLY	N-CA-C	-5.16	104.43	112.58
1	B	100	GLN	N-CA-C	5.13	117.11	109.25
1	D	104	GLY	N-CA-C	-5.06	103.83	112.64
1	D	114	ASN	CA-CB-CG	5.05	117.66	112.60
1	A	297	ASP	CA-C-N	5.00	127.06	120.60
1	A	297	ASP	C-N-CA	5.00	127.06	120.60
1	C	104	GLY	N-CA-C	-5.00	104.67	112.58
1	D	56	LEU	CA-C-N	5.00	126.86	120.56
1	D	56	LEU	C-N-CA	5.00	126.86	120.56

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	2325	0	2297	38	0
1	B	2262	0	2228	30	0
1	C	2313	0	2292	35	0
1	D	2303	0	2275	22	0
2	A	31	0	13	13	0
2	C	31	0	13	6	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	159	0	0	1	0
4	B	128	0	0	1	0
4	C	156	0	0	1	0
4	D	153	0	0	1	0
All	All	9863	0	9118	123	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 7.

All (123) 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:130:THR:C	1:A:147:ASN:N	1.69	1.47
1:C:266:VAL:O	1:C:269:ILE:HG22	1.32	1.25
1:C:266:VAL:O	1:C:269:ILE:CG2	2.18	0.91
1:D:213:MET:HA	1:D:213:MET:HE3	1.58	0.85
1:B:199:ILE:O	1:B:276:ARG:HD2	1.79	0.83
1:C:212:ALA:HB3	1:C:269:ILE:HD11	1.60	0.83
1:C:213:MET:HE3	1:C:213:MET:HA	1.61	0.82
1:A:213:MET:HE3	1:A:213:MET:HA	1.60	0.81
1:B:213:MET:HE3	1:B:213:MET:HA	1.60	0.80
1:C:190:LEU:HD21	2:C:401:ANP:O1G	1.82	0.78
1:B:199:ILE:O	1:B:276:ARG:CD	2.34	0.75
1:A:130:THR:O	1:A:147:ASN:N	2.20	0.74
1:B:56:LEU:HB3	1:B:62:ILE:HG12	1.69	0.73
1:C:191:ILE:H	2:C:401:ANP:HN61	1.38	0.71
1:A:191:ILE:O	2:A:401:ANP:O2'	2.05	0.69
1:A:111:ILE:HD11	2:A:401:ANP:H5'1	1.75	0.68
1:A:101:MET:O	2:A:401:ANP:O1B	2.11	0.68
1:C:213:MET:SD	1:C:269:ILE:HG21	2.36	0.66
1:C:269:ILE:HG23	1:C:270:LYS:N	2.11	0.65
1:A:6:VAL:HG12	1:A:6:VAL:O	1.96	0.64
1:A:195:PRO:CD	2:A:401:ANP:O1G	2.47	0.63
1:C:212:ALA:CB	1:C:269:ILE:HD11	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:PHE:CE2	1:B:166:LYS:HD2	2.36	0.61
1:A:195:PRO:HD2	2:A:401:ANP:O1G	2.00	0.61
1:B:155:ARG:HD3	1:B:313:ASP:OD2	2.01	0.60
1:A:101:MET:HB2	2:A:401:ANP:O3A	2.01	0.59
1:A:67:THR:HG22	1:A:69:THR:H	1.68	0.59
1:C:202:VAL:HG21	1:C:208:VAL:HG21	1.84	0.58
1:A:202:VAL:HG21	1:A:208:VAL:HG21	1.85	0.57
1:D:64:TRP:HD1	1:D:73:TYR:CE2	2.22	0.57
1:D:202:VAL:HG21	1:D:208:VAL:HG21	1.85	0.57
1:A:56:LEU:HB3	1:A:62:ILE:HG12	1.86	0.56
1:A:194:TYR:HA	2:A:401:ANP:PG	2.46	0.55
1:C:288:LYS:HG2	4:C:532:HOH:O	2.05	0.55
1:B:202:VAL:HG21	1:B:208:VAL:HG21	1.87	0.55
1:A:11:TYR:O	1:A:14:ARG:HG2	2.05	0.55
1:D:56:LEU:HB3	1:D:62:ILE:HG12	1.89	0.55
1:D:213:MET:HE2	1:D:285:PRO:CD	2.37	0.55
1:B:67:THR:HG1	1:B:69:THR:N	2.04	0.55
1:A:194:TYR:HA	2:A:401:ANP:O1G	2.07	0.54
1:B:213:MET:HE2	1:B:285:PRO:CD	2.37	0.54
1:C:213:MET:SD	1:C:269:ILE:HD13	2.48	0.54
1:C:12:MET:HE1	1:C:82:TYR:CD2	2.43	0.53
1:C:269:ILE:CG2	1:C:270:LYS:N	2.71	0.53
1:B:38:ILE:HG21	1:B:53:LEU:HD21	1.90	0.52
1:D:213:MET:HE2	1:D:285:PRO:HD2	1.91	0.52
1:B:213:MET:HE2	1:B:285:PRO:HD2	1.93	0.51
1:A:260:TRP:CZ2	1:B:230:ASN:HB3	2.45	0.51
1:D:64:TRP:CH2	1:D:66:ARG:HD2	2.46	0.51
1:A:189:GLU:O	2:A:401:ANP:H2	2.10	0.51
1:D:38:ILE:HG21	1:D:53:LEU:HD21	1.93	0.51
1:B:213:MET:HE3	1:B:216:ILE:HD12	1.93	0.51
1:B:262:PHE:CE1	1:B:290:ILE:HD11	2.46	0.51
1:C:12:MET:HE1	1:C:82:TYR:HD2	1.76	0.50
1:C:213:MET:HE3	1:C:216:ILE:HD12	1.94	0.50
1:C:191:ILE:N	2:C:401:ANP:HN61	2.07	0.50
1:C:213:MET:HE2	1:C:285:PRO:CD	2.42	0.50
1:B:81:ASP:OD1	1:B:126:ARG:NH2	2.43	0.50
1:A:213:MET:HE2	1:A:285:PRO:CD	2.42	0.50
1:A:213:MET:HE3	1:A:216:ILE:HD12	1.93	0.50
1:D:70:VAL:HG12	1:D:71:GLN:N	2.25	0.50
1:B:66:ARG:HG3	1:B:71:GLN:HB3	1.95	0.49
1:D:64:TRP:CZ3	1:D:66:ARG:HD2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:199:ILE:O	1:B:276:ARG:HD3	2.11	0.49
1:A:195:PRO:HD3	2:A:401:ANP:O1G	2.12	0.48
1:D:67:THR:O	1:D:67:THR:OG1	2.23	0.48
1:A:213:MET:HE2	1:A:285:PRO:HD2	1.94	0.48
1:C:213:MET:HE2	1:C:285:PRO:HD2	1.96	0.48
1:A:6:VAL:O	1:A:6:VAL:CG1	2.60	0.48
1:B:287:PHE:HA	1:B:290:ILE:HD12	1.94	0.48
1:A:12:MET:HE1	1:A:87:THR:HA	1.96	0.47
1:C:212:ALA:CB	1:C:269:ILE:CD1	2.91	0.47
1:D:87:THR:OG1	1:D:183:ARG:NH2	2.47	0.47
1:C:12:MET:HB3	1:C:17:PHE:CE2	2.49	0.47
1:B:101:MET:HE3	1:B:109:ILE:HG22	1.96	0.47
1:B:310:GLN:NE2	4:B:401:HOH:O	2.48	0.47
1:C:189:GLU:O	2:C:401:ANP:N6	2.48	0.47
1:B:44:LEU:HD12	1:B:44:LEU:HA	1.73	0.47
1:A:27:MET:CE	1:A:147:ASN:HB3	2.45	0.46
1:A:190:LEU:HD11	2:A:401:ANP:O4'	2.15	0.46
1:A:27:MET:HE3	1:A:147:ASN:HB3	1.98	0.46
1:B:12:MET:HG2	1:B:16:ASP:HB2	1.98	0.46
1:B:27:MET:HB3	1:B:151:LEU:HD22	1.98	0.45
1:D:127:LEU:O	1:D:150:TRP:HA	2.16	0.45
1:C:260:TRP:CZ2	1:D:230:ASN:HB3	2.51	0.45
1:A:101:MET:HE3	1:A:109:ILE:HG22	1.99	0.45
1:D:159:MET:HG3	1:D:309:MET:HE2	1.99	0.45
1:D:213:MET:HE3	1:D:216:ILE:HD12	1.98	0.45
1:C:213:MET:HA	1:C:213:MET:CE	2.41	0.45
1:B:200:HIS:CE1	1:B:276:ARG:NH1	2.85	0.44
1:D:101:MET:HE3	1:D:109:ILE:HG22	1.98	0.44
1:A:127:LEU:O	1:A:150:TRP:HA	2.17	0.44
1:A:195:PRO:HD3	2:A:401:ANP:PG	2.57	0.44
1:C:67:THR:HG22	1:C:69:THR:H	1.83	0.44
1:A:66:ARG:HD3	1:A:71:GLN:HG2	1.99	0.44
1:D:70:VAL:CG1	1:D:71:GLN:N	2.81	0.44
1:C:213:MET:CE	1:C:216:ILE:HD12	2.49	0.43
1:C:9:LEU:HA	1:C:12:MET:HE3	2.00	0.43
4:A:531:HOH:O	1:B:160:LYS:HE3	2.19	0.43
1:C:194:TYR:HE1	2:C:401:ANP:O1A	2.02	0.43
1:B:12:MET:HE1	1:B:20:LEU:HD22	2.01	0.42
1:C:101:MET:HE3	1:C:109:ILE:HG22	2.01	0.42
1:D:219:LEU:HD22	1:D:250:MET:HE1	2.02	0.42
1:C:127:LEU:O	1:C:150:TRP:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:ASP:OD2	1:B:126:ARG:NH1	2.52	0.42
1:C:266:VAL:C	1:C:269:ILE:HG22	2.28	0.42
1:D:162:PHE:HB3	1:D:309:MET:HE1	2.02	0.42
1:A:196:LEU:HG	1:A:272:PHE:CE2	2.54	0.42
1:D:288:LYS:HG2	4:D:404:HOH:O	2.19	0.42
1:B:213:MET:CE	1:B:216:ILE:HD12	2.50	0.42
1:C:235:ILE:HD12	2:C:401:ANP:H1'	2.03	0.41
1:C:64:TRP:CZ3	1:C:66:ARG:HB2	2.55	0.41
1:A:213:MET:CE	1:A:216:ILE:HD12	2.50	0.41
1:A:152:TYR:CE2	1:A:156:LEU:HD22	2.56	0.41
1:A:213:MET:HA	1:A:213:MET:CE	2.41	0.41
1:B:213:MET:HA	1:B:213:MET:CE	2.41	0.41
1:C:196:LEU:HA	1:C:199:ILE:HD12	2.02	0.41
1:A:194:TYR:HD1	2:A:401:ANP:O1G	2.04	0.41
1:A:38:ILE:HG21	1:A:53:LEU:HD21	2.04	0.40
1:B:81:ASP:OD2	1:B:126:ARG:NH2	2.55	0.40
1:A:64:TRP:HD1	1:A:73:TYR:CZ	2.40	0.40
1:C:162:PHE:HB3	1:C:309:MET:HE1	2.04	0.40
1:D:221:ASN:HD22	1:D:290:ILE:HG12	1.85	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	281/313 (90%)	280 (100%)	1 (0%)	0	100	100
1	B	272/313 (87%)	269 (99%)	3 (1%)	0	100	100
1	C	281/313 (90%)	279 (99%)	2 (1%)	0	100	100
1	D	281/313 (90%)	276 (98%)	4 (1%)	1 (0%)	30	28
All	All	1115/1252 (89%)	1104 (99%)	10 (1%)	1 (0%)	48	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	68	LYS

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	253/278 (91%)	236 (93%)	17 (7%)	15	12
1	B	247/278 (89%)	231 (94%)	16 (6%)	15	13
1	C	252/278 (91%)	237 (94%)	15 (6%)	17	15
1	D	252/278 (91%)	232 (92%)	20 (8%)	11	9
All	All	1004/1112 (90%)	936 (93%)	68 (7%)	15	12

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	MET
1	A	25	MET
1	A	44	LEU
1	A	56	LEU
1	A	61	LEU
1	A	65	GLU
1	A	67	THR
1	A	68	LYS
1	A	103	VAL
1	A	127	LEU
1	A	156	LEU
1	A	159	MET
1	A	213	MET
1	A	269	ILE
1	A	282	GLU
1	A	290	ILE
1	A	291	ARG
1	B	25	MET
1	B	44	LEU

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Mol	Chain	Res	Type
1	B	56	LEU
1	B	61	LEU
1	B	65	GLU
1	B	70	VAL
1	B	103	VAL
1	B	116	GLU
1	B	118	GLN
1	B	126	ARG
1	B	127	LEU
1	B	156	LEU
1	B	213	MET
1	B	271	ASP
1	B	291	ARG
1	B	298	VAL
1	C	10	ARG
1	C	44	LEU
1	C	61	LEU
1	C	65	GLU
1	C	68	LYS
1	C	80	TYR
1	C	127	LEU
1	C	156	LEU
1	C	213	MET
1	C	247	PHE
1	C	271	ASP
1	C	282	GLU
1	C	291	ARG
1	C	292	ARG
1	C	298	VAL
1	D	12	MET
1	D	25	MET
1	D	44	LEU
1	D	45	LYS
1	D	46[A]	HIS
1	D	46[B]	HIS
1	D	56	LEU
1	D	61	LEU
1	D	65	GLU
1	D	68	LYS
1	D	69	THR
1	D	103	VAL
1	D	127	LEU

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Mol	Chain	Res	Type
1	D	156	LEU
1	D	201	HIS
1	D	213	MET
1	D	247	PHE
1	D	271	ASP
1	D	290	ILE
1	D	298	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	201	HIS
1	B	29	ASN
1	B	200	HIS
1	C	29	ASN
1	C	241	HIS
1	D	29	ASN
1	D	118	GLN
1	D	192	ASN
1	D	257	ASN

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	401	-	33,33,33	1.57	4 (12%)	45,52,52	1.05	4 (8%)
2	ANP	C	401	-	33,33,33	0.77	2 (6%)	45,52,52	0.74	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	ANP	A	401	-	-	5/18/38/38	0/3/3/3
2	ANP	C	401	-	-	4/18/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	ANP	PB-O1B	6.88	1.56	1.46
2	A	401	ANP	PB-O2B	-3.37	1.47	1.56
2	A	401	ANP	PG-O3G	-2.78	1.49	1.56
2	C	401	ANP	PG-O3G	-2.55	1.50	1.56
2	C	401	ANP	PG-O2G	-2.54	1.50	1.56
2	A	401	ANP	PG-O2G	-2.47	1.50	1.56

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	ANP	O1G-PG-N3B	-3.84	106.12	111.77
2	A	401	ANP	O1B-PB-N3B	-2.68	107.82	111.77
2	A	401	ANP	O2'-C2'-C3'	2.32	119.27	111.82
2	A	401	ANP	O3G-PG-O1G	-2.29	107.70	113.45

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	ANP	PG-N3B-PB-O1B

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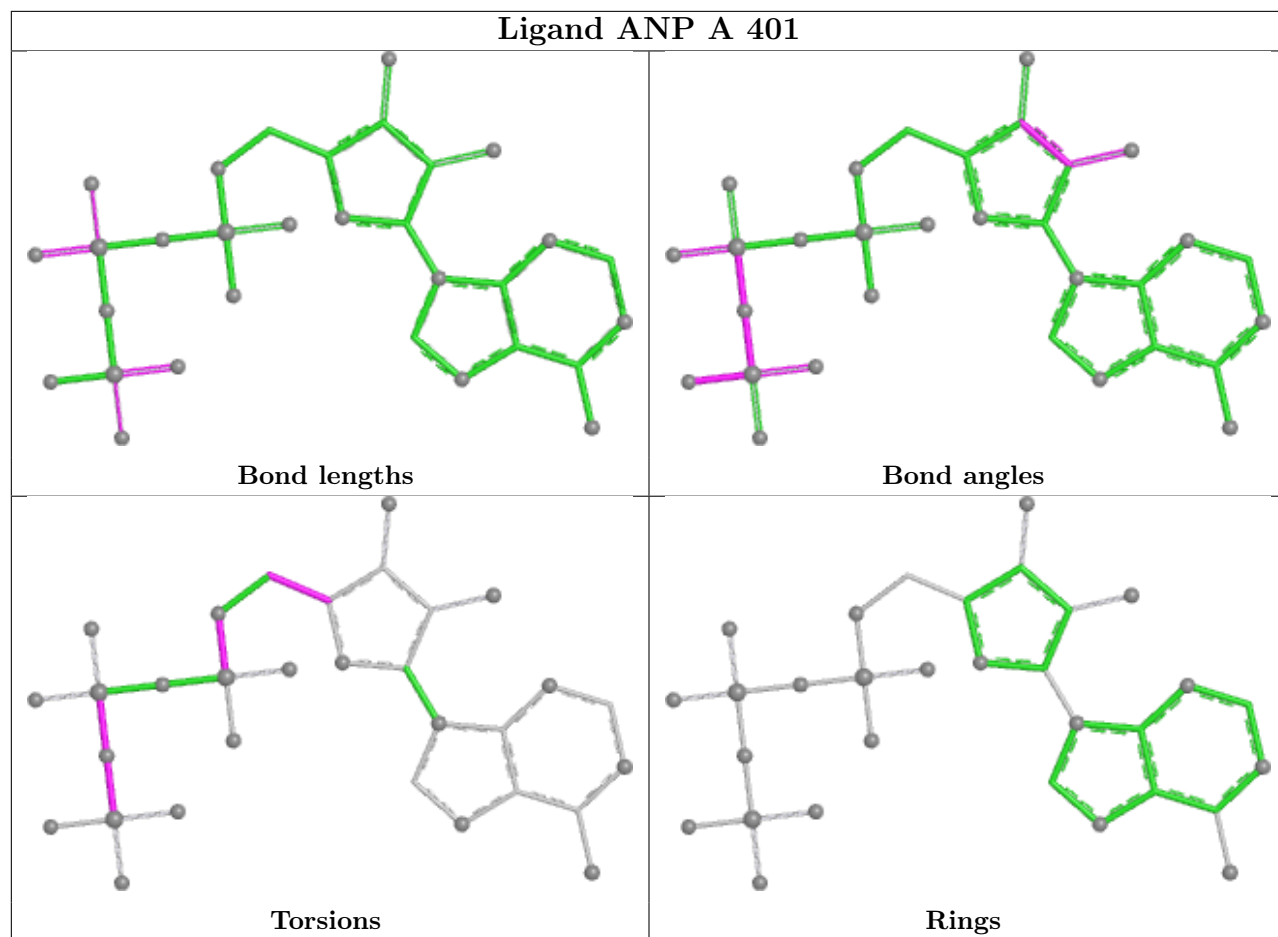
Mol	Chain	Res	Type	Atoms
2	C	401	ANP	PG-N3B-PB-O1B
2	A	401	ANP	O4'-C4'-C5'-O5'
2	A	401	ANP	C3'-C4'-C5'-O5'
2	C	401	ANP	C2'-C1'-N9-C4
2	C	401	ANP	C2'-C1'-N9-C8
2	A	401	ANP	C5'-O5'-PA-O1A
2	C	401	ANP	C3'-C4'-C5'-O5'
2	A	401	ANP	PB-N3B-PG-O1G

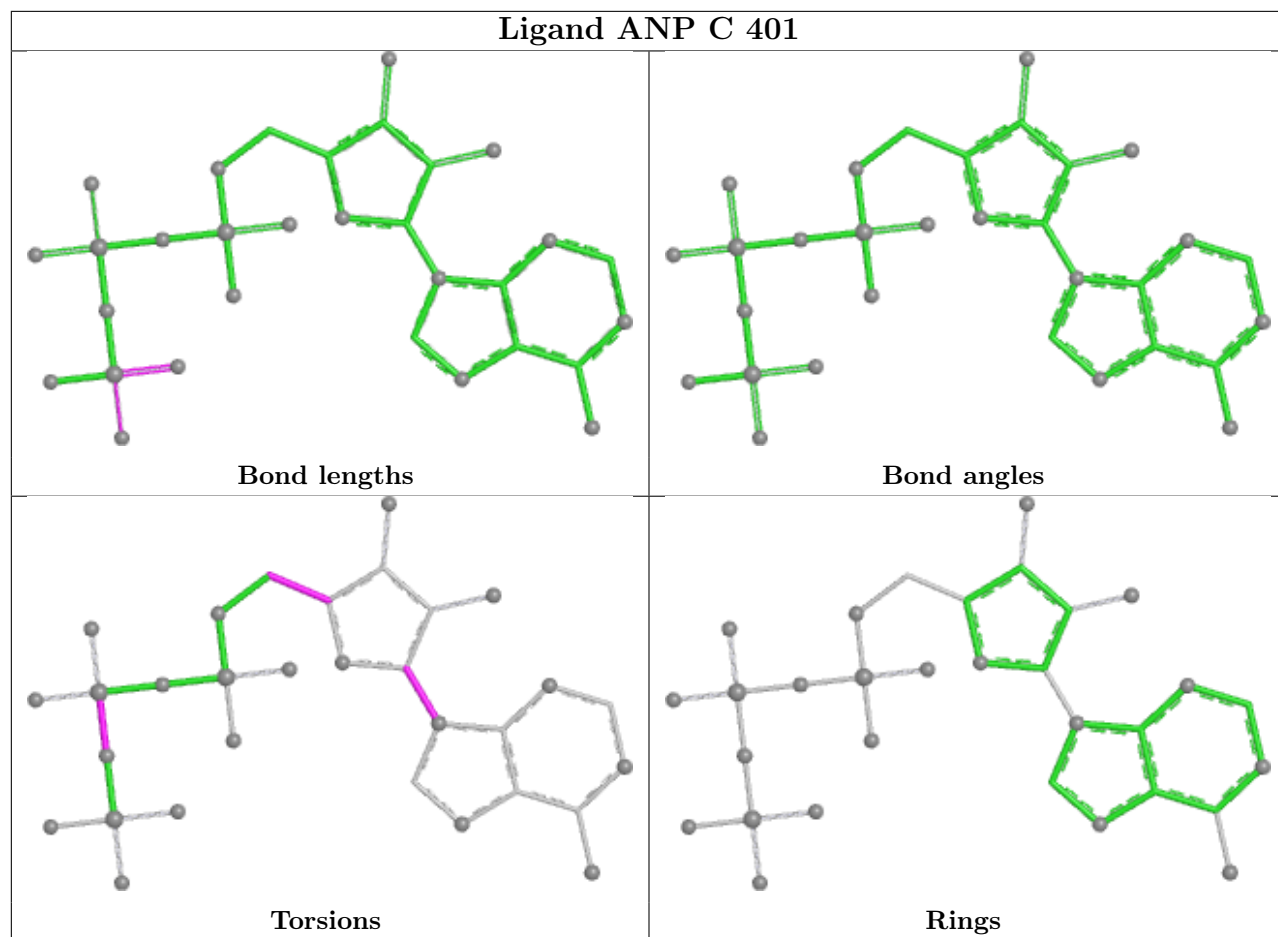
There are no ring outliers.

2 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	ANP	13	0
2	C	401	ANP	6	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	286/313 (91%)	0.51	23 (8%)	18 19	27, 53, 87, 117	1 (0%)
1	B	280/313 (89%)	0.48	15 (5%)	31 33	30, 52, 93, 130	0
1	C	285/313 (91%)	0.42	16 (5%)	30 32	33, 50, 85, 114	0
1	D	283/313 (90%)	0.44	14 (4%)	35 37	19, 50, 84, 106	2 (0%)
All	All	1134/1252 (90%)	0.46	68 (5%)	27 29	19, 51, 88, 130	3 (0%)

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	6	VAL	6.6
1	B	99	ASN	5.4
1	D	46[A]	HIS	5.2
1	C	269	ILE	4.8
1	C	194	TYR	4.6
1	A	47	GLY	4.1
1	A	8	LYS	3.8
1	D	47	GLY	3.5
1	A	39	ALA	3.4
1	A	152	TYR	3.4
1	A	293	GLU	3.4
1	D	64	TRP	3.2
1	A	44	LEU	3.1
1	D	290	ILE	3.1
1	C	152	TYR	3.1
1	D	152	TYR	3.1
1	B	67	THR	3.1
1	C	312	ASP	3.0
1	B	283	LEU	3.0
1	C	8	LYS	3.0
1	A	48	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	241[A]	HIS	3.0
1	B	148	VAL	2.9
1	D	313	ASP	2.9
1	C	181	TYR	2.9
1	D	296	LEU	2.8
1	B	45	LYS	2.8
1	A	42	ALA	2.8
1	C	29	ASN	2.8
1	B	47	GLY	2.7
1	B	101	MET	2.7
1	A	70	VAL	2.7
1	C	283	LEU	2.6
1	A	202	VAL	2.6
1	A	181	TYR	2.6
1	C	67	THR	2.5
1	C	32	ILE	2.5
1	B	201	HIS	2.5
1	A	49	CYS	2.5
1	C	282	GLU	2.5
1	A	85	LEU	2.5
1	D	69	THR	2.4
1	A	312	ASP	2.4
1	C	64	TRP	2.4
1	B	98	GLY	2.4
1	A	310	GLN	2.4
1	B	69	THR	2.4
1	D	292	ARG	2.4
1	D	181	TYR	2.4
1	A	269	ILE	2.3
1	B	152	TYR	2.3
1	D	101	MET	2.3
1	B	70	VAL	2.3
1	A	67	THR	2.3
1	A	283	LEU	2.3
1	D	283	LEU	2.2
1	B	129	ARG	2.2
1	B	284	PHE	2.1
1	C	9	LEU	2.1
1	D	29	ASN	2.1
1	A	7	ALA	2.1
1	A	29	ASN	2.1
1	C	291	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	68	LYS	2.1
1	B	44	LEU	2.1
1	A	194	TYR	2.1
1	C	68	LYS	2.0
1	C	101	MET	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](#)

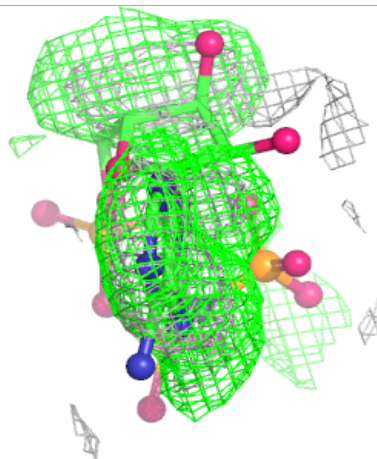
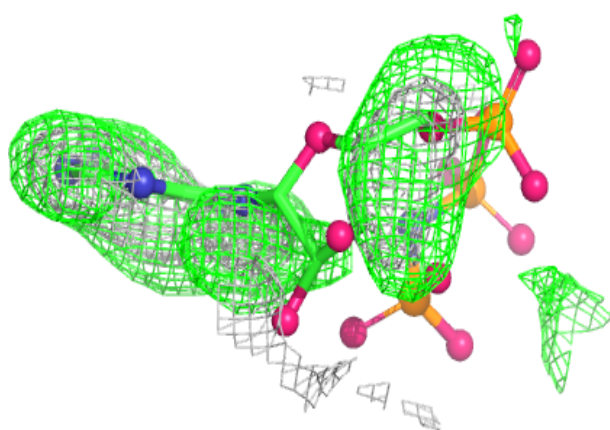
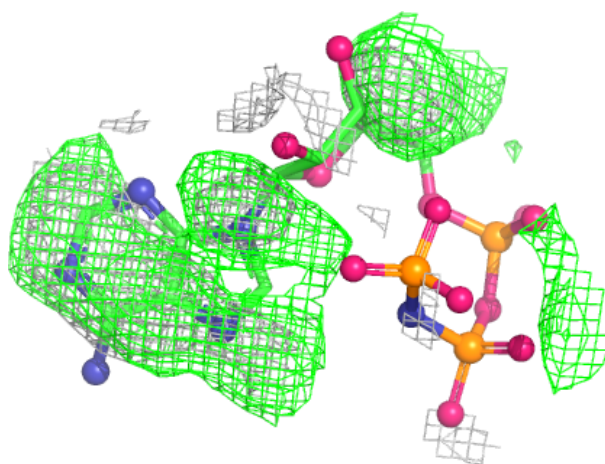
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	401	31/31	0.63	0.74	30,58,81,82	31
2	ANP	C	401	31/31	0.77	0.59	22,56,74,75	31
3	NA	A	402	1/1	0.87	0.13	73,73,73,73	0
3	NA	C	402	1/1	0.90	0.14	82,82,82,82	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.

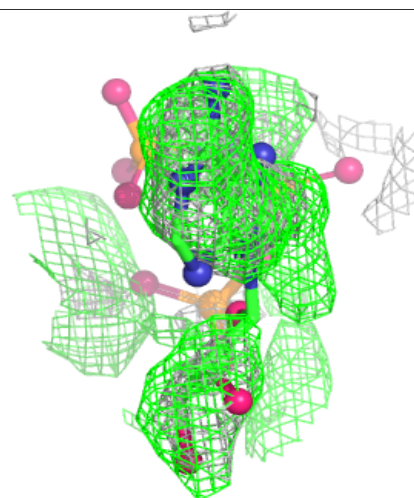
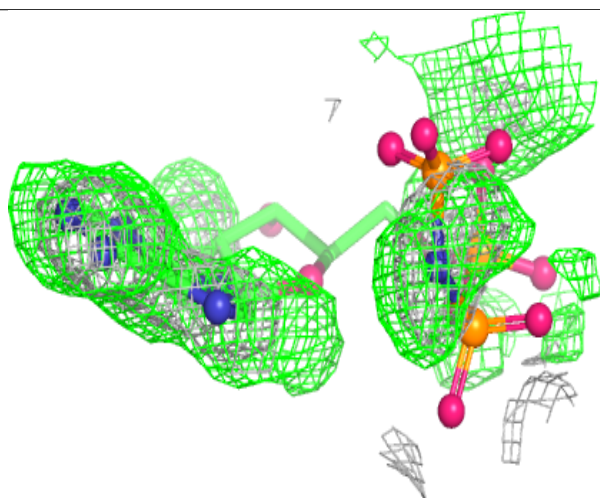
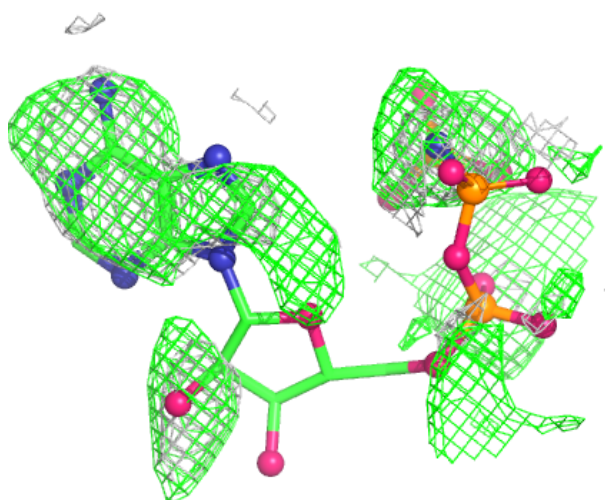
Electron density around ANP A 401:

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



Electron density around ANP C 401:

$2mF_o-DF_c$ (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.