



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 9, 2023 – 11:07 PM EDT

PDB ID : 4HNA
Title : Kinesin motor domain in the ADP-MG-ALFX state in complex with tubulin and a DARPIN
Authors : Gigant, B.; Knossow, M.
Deposited on : 2012-10-19
Resolution : 3.19 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 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

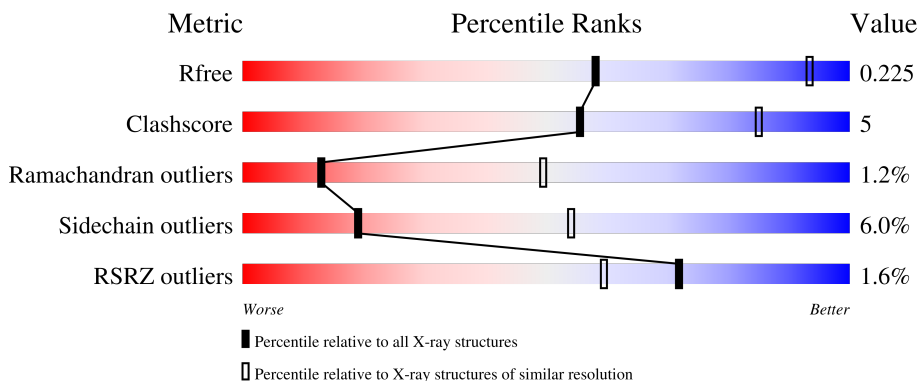
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

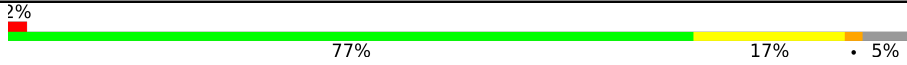



The reported resolution of this entry is 3.19 Å.

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))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 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	451	 2% 77% 17% • 5%
2	B	445	 86% 10% • •
3	D	169	 2% 84% 10% 6%
4	K	349	 2% 72% 21% • 5%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 10607 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 Tubulin alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	430	3349	2123	571	633	22	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	SER	GLY	SEE REMARK 999	UNP D0VWZ0
A	340	SER	THR	SEE REMARK 999	UNP D0VWZ0

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	431	3378	2118	579	655	26	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	318	ILE	VAL	SEE REMARK 999	UNP D0VWY9

- Molecule 3 is a protein called DESIGNED ANKYRIN REPEAT PROTEIN (DARPIN) D2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	159	1185	743	202	238	2	0	0	0

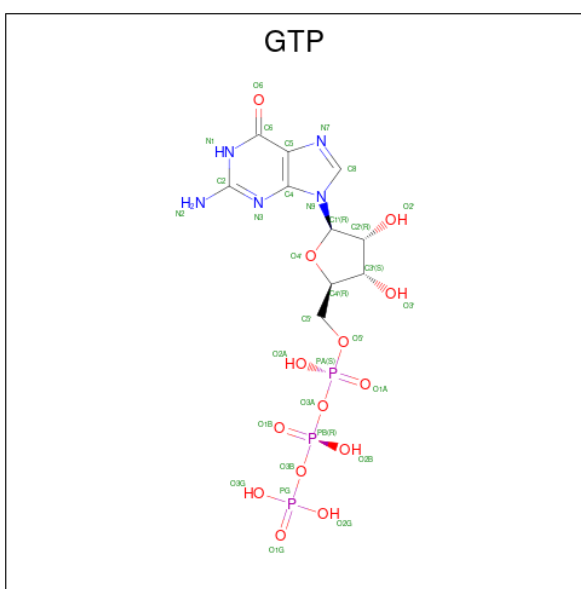
- Molecule 4 is a protein called Kinesin-1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	K	333	2593	1616	447	520	10	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	7	SER	CYS	SEE REMARK 999	UNP P33176
K	65	ALA	CYS	SEE REMARK 999	UNP P33176
K	168	ALA	CYS	SEE REMARK 999	UNP P33176
K	174	SER	CYS	SEE REMARK 999	UNP P33176
K	294	ALA	CYS	SEE REMARK 999	UNP P33176
K	330	SER	CYS	SEE REMARK 999	UNP P33176

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
5	A	1	32	10	5	14	3	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

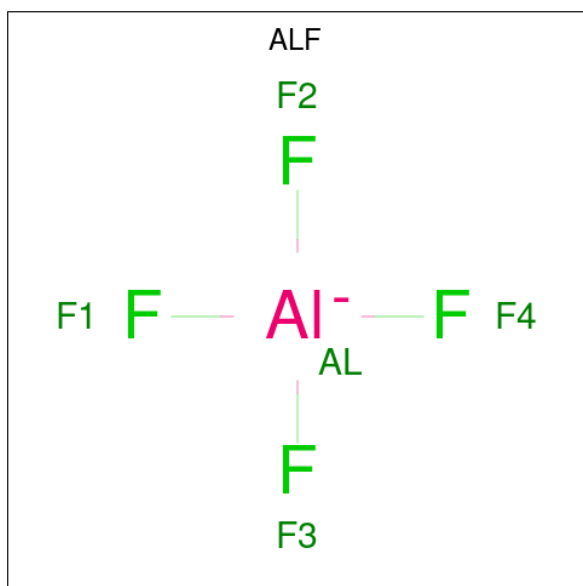
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	A	1	1	1	0	0
6	B	1	1	1	0	0
6	K	1	1	1	0	0

- Molecule 7 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
7	B	1	28	10	5	11	2	0	0

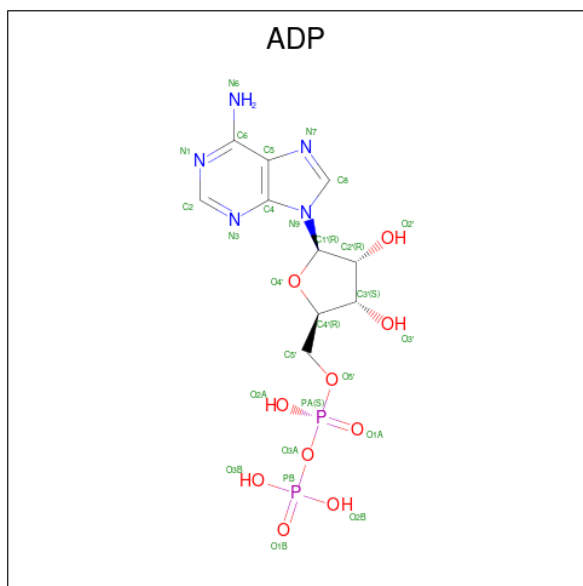
- Molecule 8 is TETRAFLUOROALUMINATE ION (three-letter code: ALF) (formula: AlF_4^-).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Al	F		
8	B	1	5	1	4	0	0
8	K	1	5	1	4	0	0

- Molecule 9 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:

C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
9	K	1	27	10	5	10	2	0	0

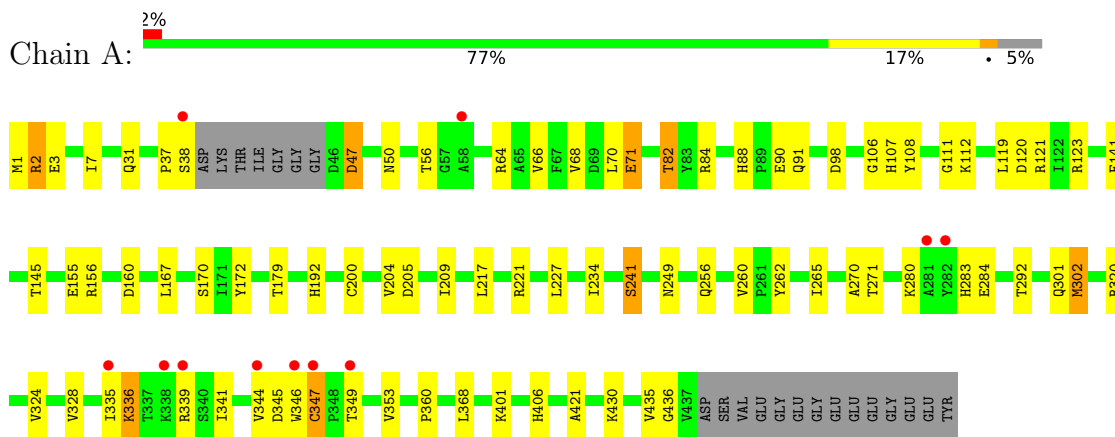
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	K	2	2	2	0	0

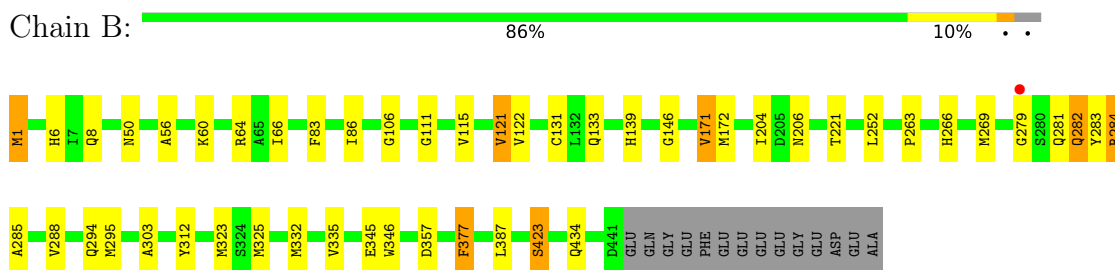
3 Residue-property plots [i](#)

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.

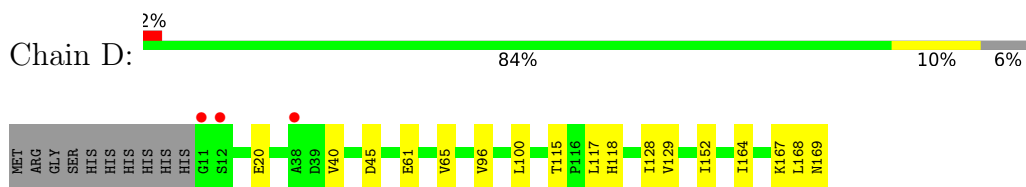
- Molecule 1: Tubulin alpha chain



- Molecule 2: Tubulin beta chain

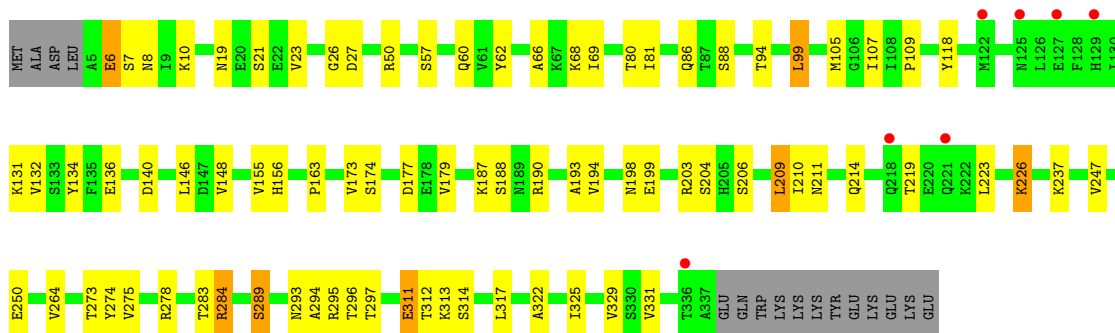


- Molecule 3: DESIGNED ANKYRIN REPEAT PROTEIN (DARPIN) D2



- Molecule 4: Kinesin-1 heavy chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	77.05Å 160.54Å 174.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.14 – 3.19 59.14 – 3.19	Depositor EDS
% Data completeness (in resolution range)	80.2 (59.14-3.19) 80.4 (59.14-3.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.08 (at 3.19Å)	Xtrriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.177 , 0.211 0.203 , 0.225	Depositor DCC
R_{free} test set	1519 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	62.5	Xtrriage
Anisotropy	0.080	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 60.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	10607	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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: GDP, ALF, GTP, ADP, 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	0.50	0/3424	0.74	1/4649 (0.0%)
2	B	0.47	0/3452	0.71	0/4676
3	D	0.49	0/1200	0.72	0/1626
4	K	0.53	0/2632	0.79	0/3551
All	All	0.49	0/10708	0.74	1/14502 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	THR	N-CA-C	-5.80	95.33	111.00

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	3349	0	3264	43	0
2	B	3378	0	3253	34	0
3	D	1185	0	1171	5	0
4	K	2593	0	2563	31	0
5	A	32	0	12	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	1	0	0	0	0
6	K	1	0	0	0	0
7	B	28	0	12	1	0
8	B	5	0	0	0	0
8	K	5	0	0	0	0
9	K	27	0	12	0	0
10	K	2	0	0	0	0
All	All	10607	0	10287	106	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 5.

All (106) 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)
4:K:88:SER:HB3	4:K:198:ASN:HB2	1.61	0.83
1:A:221:ARG:HG2	2:B:325:MET:HB3	1.64	0.80
1:A:71:GLU:HB3	1:A:98:ASP:HB3	1.70	0.74
4:K:194:VAL:HG13	4:K:199:GLU:HA	1.71	0.72
2:B:281:GLN:HA	2:B:282:GLN:CB	2.20	0.71
1:A:88:HIS:HB3	1:A:91:GLN:HE21	1.56	0.71
1:A:262:TYR:HB2	1:A:265:ILE:HD12	1.72	0.71
2:B:1:MET:HB3	2:B:131:CYS:SG	2.31	0.70
1:A:265:ILE:HD13	1:A:435:VAL:HG21	1.73	0.70
2:B:66:ILE:HG12	2:B:121:VAL:HG13	1.75	0.69
1:A:70:LEU:HD13	1:A:145:THR:HG23	1.74	0.68
2:B:6:HIS:HE1	2:B:8:GLN:HG3	1.62	0.64
1:A:108:TYR:HD2	1:A:112:LYS:HZ1	1.45	0.62
2:B:263:PRO:O	2:B:266:HIS:HD2	1.83	0.61
2:B:1:MET:HG2	2:B:133:GLN:HG2	1.81	0.61
2:B:206:ASN:HD21	7:B:501:GDP:HN22	1.49	0.61
2:B:50:ASN:O	2:B:64:ARG:NH2	2.33	0.61
4:K:94:THR:HG22	4:K:107:ILE:HD11	1.82	0.61
1:A:344:VAL:HG23	1:A:347:CYS:HB2	1.82	0.60
1:A:70:LEU:HD13	1:A:145:THR:CG2	2.32	0.60
4:K:105:MET:HB2	4:K:109:PRO:HG2	1.84	0.59
1:A:50:ASN:O	1:A:64:ARG:NH1	2.36	0.59
2:B:1:MET:CB	2:B:131:CYS:SG	2.90	0.59
2:B:6:HIS:CE1	2:B:8:GLN:HG3	2.39	0.58
2:B:133:GLN:NE2	2:B:252:LEU:H	2.03	0.57
1:A:292:THR:HG22	1:A:335:ILE:HD12	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:ILE:HG21	1:A:302:MET:SD	2.45	0.57
4:K:322:ALA:HA	4:K:325:ILE:HD12	1.87	0.57
2:B:6:HIS:HE1	2:B:8:GLN:HE21	1.52	0.56
1:A:7:ILE:HG23	1:A:66:VAL:HG13	1.87	0.56
2:B:288:VAL:HG22	2:B:323:MET:HE3	1.88	0.56
2:B:312:TYR:CE2	2:B:377:PHE:HZ	2.24	0.56
4:K:284:ARG:HH11	4:K:284:ARG:HG2	1.71	0.56
4:K:19:ASN:O	4:K:23:VAL:HG23	2.06	0.55
4:K:289:SER:HA	4:K:294:ALA:HB3	1.87	0.55
2:B:172:MET:HG3	2:B:387:LEU:HD11	1.88	0.55
1:A:256:GLN:O	1:A:260:VAL:HG22	2.08	0.53
1:A:292:THR:HG22	1:A:335:ILE:CD1	2.39	0.53
1:A:270:ALA:HB3	1:A:302:MET:HG3	1.91	0.52
2:B:139:HIS:HD2	2:B:146:GLY:O	1.91	0.52
1:A:265:ILE:CD1	1:A:435:VAL:HG21	2.39	0.52
1:A:167:LEU:HG	1:A:200:CYS:HB3	1.92	0.52
2:B:106:GLY:O	2:B:111:GLY:HA3	2.10	0.52
2:B:295:MET:CG	2:B:377:PHE:HB2	2.40	0.51
2:B:434:GLN:NE2	4:K:274:TYR:HB3	2.26	0.51
1:A:88:HIS:HD2	1:A:90:GLU:H	1.57	0.51
4:K:295:ARG:HG2	4:K:329:VAL:HG21	1.93	0.51
4:K:131:LYS:HG3	4:K:211:ASN:HB3	1.93	0.50
1:A:271:THR:CG2	1:A:301:GLN:HG2	2.41	0.50
4:K:156:HIS:O	4:K:163:PRO:HA	2.11	0.49
4:K:193:ALA:HB3	4:K:203:ARG:HD2	1.93	0.49
1:A:241:SER:HB2	1:A:249:ASN:O	2.13	0.49
1:A:401:LYS:HG3	2:B:346:TRP:CE3	2.48	0.49
1:A:119:LEU:HD11	1:A:156:ARG:HB3	1.94	0.49
2:B:6:HIS:CE1	2:B:8:GLN:HE21	2.29	0.48
3:D:118:HIS:HD2	3:D:152:ILE:HD11	1.78	0.48
4:K:247:VAL:HA	4:K:250:GLU:OE1	2.14	0.47
1:A:217:LEU:HD21	1:A:368:LEU:HD23	1.96	0.47
4:K:311:GLU:H	4:K:311:GLU:HG2	1.36	0.47
1:A:346:TRP:HZ2	1:A:435:VAL:HG13	1.79	0.47
1:A:2:ARG:HH11	1:A:2:ARG:HA	1.80	0.47
2:B:434:GLN:NE2	4:K:274:TYR:CB	2.78	0.47
2:B:269:MET:HG3	2:B:303:ALA:HB3	1.97	0.47
4:K:136:GLU:HB2	4:K:204:SER:HB2	1.97	0.47
1:A:107:HIS:HE1	1:A:155:GLU:OE2	1.98	0.46
3:D:61:GLU:O	3:D:65:VAL:HG23	2.16	0.46
1:A:344:VAL:HG12	1:A:436:GLY:HA3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:194:VAL:HG22	4:K:199:GLU:O	2.15	0.46
4:K:264:VAL:HG21	4:K:283:THR:HB	1.97	0.46
1:A:209:ILE:HD11	1:A:302:MET:HE2	1.96	0.46
2:B:171:VAL:HA	2:B:204:ILE:O	2.15	0.46
4:K:80:THR:HB	4:K:296:THR:HG23	1.98	0.46
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.98	0.45
3:D:117:LEU:HD11	3:D:129:VAL:HG13	1.97	0.45
4:K:284:ARG:HG2	4:K:284:ARG:NH1	2.32	0.45
2:B:56:ALA:HB3	2:B:60:LYS:HG3	1.99	0.44
1:A:336:LYS:HA	1:A:341:ILE:HD11	1.99	0.44
1:A:141:PHE:CE2	1:A:170:SER:HB3	2.53	0.44
2:B:133:GLN:HE22	2:B:252:LEU:H	1.64	0.44
2:B:332:MET:O	2:B:335:VAL:HG12	2.18	0.44
1:A:280:LYS:HE3	1:A:283:HIS:CB	2.48	0.44
4:K:62:TYR:HD1	4:K:107:ILE:HG23	1.82	0.44
1:A:106:GLY:O	1:A:111:GLY:HA3	2.18	0.43
1:A:406:HIS:CG	2:B:263:PRO:HD3	2.53	0.43
2:B:83:PHE:O	2:B:86:ILE:HG22	2.18	0.43
1:A:123:ARG:HH21	1:A:160:ASP:HB3	1.83	0.43
1:A:328:VAL:HG11	1:A:353:VAL:HG11	1.99	0.43
1:A:1:MET:N	1:A:3:GLU:OE2	2.49	0.43
4:K:66:ALA:C	4:K:68:LYS:H	2.21	0.43
1:A:204:VAL:HG13	1:A:302:MET:HE2	2.01	0.43
4:K:173:VAL:HG21	4:K:179:VAL:HG22	1.99	0.43
2:B:423:SER:HB3	4:K:278:ARG:HH22	1.83	0.42
2:B:295:MET:HG3	2:B:377:PHE:HB2	2.00	0.42
4:K:99:LEU:HD11	4:K:187:LYS:HD2	2.01	0.42
4:K:214:GLN:HG3	4:K:223:LEU:HB2	2.01	0.42
2:B:345:GLU:H	2:B:345:GLU:HG2	1.61	0.42
1:A:192:HIS:CG	1:A:421:ALA:HA	2.55	0.41
1:A:209:ILE:HG22	1:A:227:LEU:HD22	2.01	0.41
2:B:221:THR:HG21	3:D:20:GLU:CD	2.40	0.41
1:A:320:ARG:HG3	1:A:360:PRO:HD3	2.03	0.41
3:D:96:VAL:HG11	3:D:128:ILE:HG23	2.02	0.41
4:K:209:LEU:HD11	4:K:226:LYS:HG2	2.02	0.41
1:A:2:ARG:HA	1:A:2:ARG:NH1	2.36	0.41
4:K:10:LYS:O	4:K:297:THR:HA	2.21	0.40
4:K:69:ILE:HG13	4:K:81:ILE:HD11	2.02	0.40
4:K:132:VAL:HG12	4:K:210:ILE:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	426/451 (94%)	406 (95%)	18 (4%)	2 (0%)	29	67
2	B	429/445 (96%)	416 (97%)	8 (2%)	5 (1%)	13	49
3	D	157/169 (93%)	155 (99%)	2 (1%)	0	100	100
4	K	331/349 (95%)	299 (90%)	23 (7%)	9 (3%)	5	30
All	All	1343/1414 (95%)	1276 (95%)	51 (4%)	16 (1%)	13	49

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	284	GLU
2	B	282	GLN
2	B	285	ALA
4	K	7	SER
4	K	27	ASP
1	A	47	ASP
2	B	283	TYR
2	B	284	ARG
4	K	6	GLU
4	K	99	LEU
4	K	273	THR
4	K	26	GLY
4	K	293	ASN
2	B	279	GLY
4	K	188	SER
4	K	275	VAL

5.3.2 Protein sidechains [i](#)

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	359/379 (95%)	337 (94%)	22 (6%)	18	54
2	B	370/383 (97%)	360 (97%)	10 (3%)	44	75
3	D	121/131 (92%)	113 (93%)	8 (7%)	16	51
4	K	291/309 (94%)	262 (90%)	29 (10%)	7	30
All	All	1141/1202 (95%)	1072 (94%)	69 (6%)	19	54

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	31	GLN
1	A	37	PRO
1	A	38	SER
1	A	47	ASP
1	A	56	THR
1	A	68	VAL
1	A	71	GLU
1	A	82	THR
1	A	84	ARG
1	A	120	ASP
1	A	121	ARG
1	A	179	THR
1	A	241	SER
1	A	302	MET
1	A	324	VAL
1	A	336	LYS
1	A	339	ARG
1	A	345	ASP
1	A	347	CYS
1	A	349	THR
1	A	430	LYS
2	B	1	MET
2	B	115	VAL
2	B	121	VAL
2	B	122	VAL
2	B	171	VAL
2	B	284	ARG
2	B	294	GLN
2	B	357	ASP

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Mol	Chain	Res	Type
2	B	377	PHE
2	B	423	SER
3	D	40	VAL
3	D	45	ASP
3	D	100	LEU
3	D	115	THR
3	D	164	ILE
3	D	167	LYS
3	D	168	LEU
3	D	169	ASN
4	K	6	GLU
4	K	8	ASN
4	K	21	SER
4	K	50	ARG
4	K	57	SER
4	K	60	GLN
4	K	86	GLN
4	K	118	TYR
4	K	134	TYR
4	K	140	ASP
4	K	146	LEU
4	K	148	VAL
4	K	155	VAL
4	K	174	SER
4	K	177	ASP
4	K	190	ARG
4	K	206	SER
4	K	209	LEU
4	K	219	THR
4	K	226	LYS
4	K	237	LYS
4	K	284	ARG
4	K	289	SER
4	K	311	GLU
4	K	312	THR
4	K	313	LYS
4	K	314	SER
4	K	317	LEU
4	K	331	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	15	GLN
1	A	88	HIS
1	A	91	GLN
1	A	139	HIS
1	A	197	HIS
1	A	301	GLN
1	A	329	ASN
1	A	342	GLN
2	B	6	HIS
2	B	8	GLN
2	B	14	ASN
2	B	133	GLN
2	B	136	GLN
2	B	139	HIS
2	B	206	ASN
2	B	266	HIS
2	B	294	GLN
2	B	385	GLN
2	B	433	GLN
2	B	434	GLN
2	B	436	GLN
4	K	24	ASN
4	K	34	GLN
4	K	78	ASN
4	K	93	HIS
4	K	191	HIS
4	K	218	GLN
4	K	287	GLN
4	K	332	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 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
8	ALF	K	403	9,6	0,4,4	-	-	-		
5	GTP	A	600	6	26,34,34	0.78	2 (7%)	32,54,54	0.50	0
8	ALF	B	503	7,6	0,4,4	-	-	-		
9	ADP	K	401	8,6	24,29,29	0.65	0	29,45,45	0.87	1 (3%)
7	GDP	B	501	8,6	24,30,30	0.68	0	30,47,47	0.80	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
5	GTP	A	600	6	-	6/18/38/38	0/3/3/3
9	ADP	K	401	8,6	-	0/12/32/32	0/3/3/3
7	GDP	B	501	8,6	-	3/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	600	GTP	C8-N7	-2.15	1.31	1.35
5	A	600	GTP	C5-C4	-2.08	1.37	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	K	401	ADP	C5-C6-N6	2.22	123.72	120.35

There are no chirality outliers.

All (9) torsion outliers are listed below:

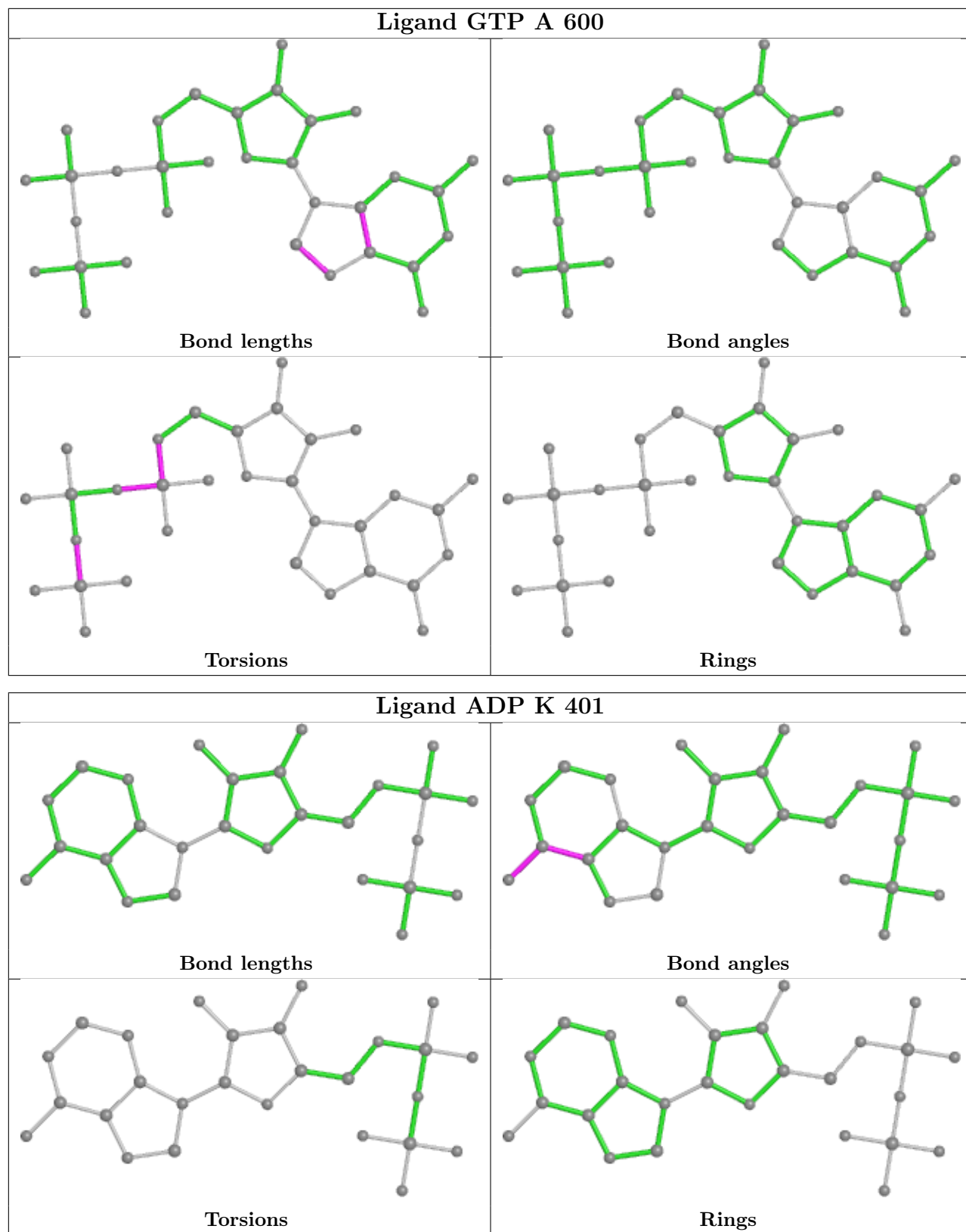
Mol	Chain	Res	Type	Atoms
5	A	600	GTP	C5'-O5'-PA-O1A
5	A	600	GTP	C5'-O5'-PA-O2A
7	B	501	GDP	C5'-O5'-PA-O1A
7	B	501	GDP	C5'-O5'-PA-O2A
5	A	600	GTP	PB-O3B-PG-O3G
5	A	600	GTP	PB-O3A-PA-O2A
5	A	600	GTP	PB-O3B-PG-O1G
5	A	600	GTP	C5'-O5'-PA-O3A
7	B	501	GDP	C5'-O5'-PA-O3A

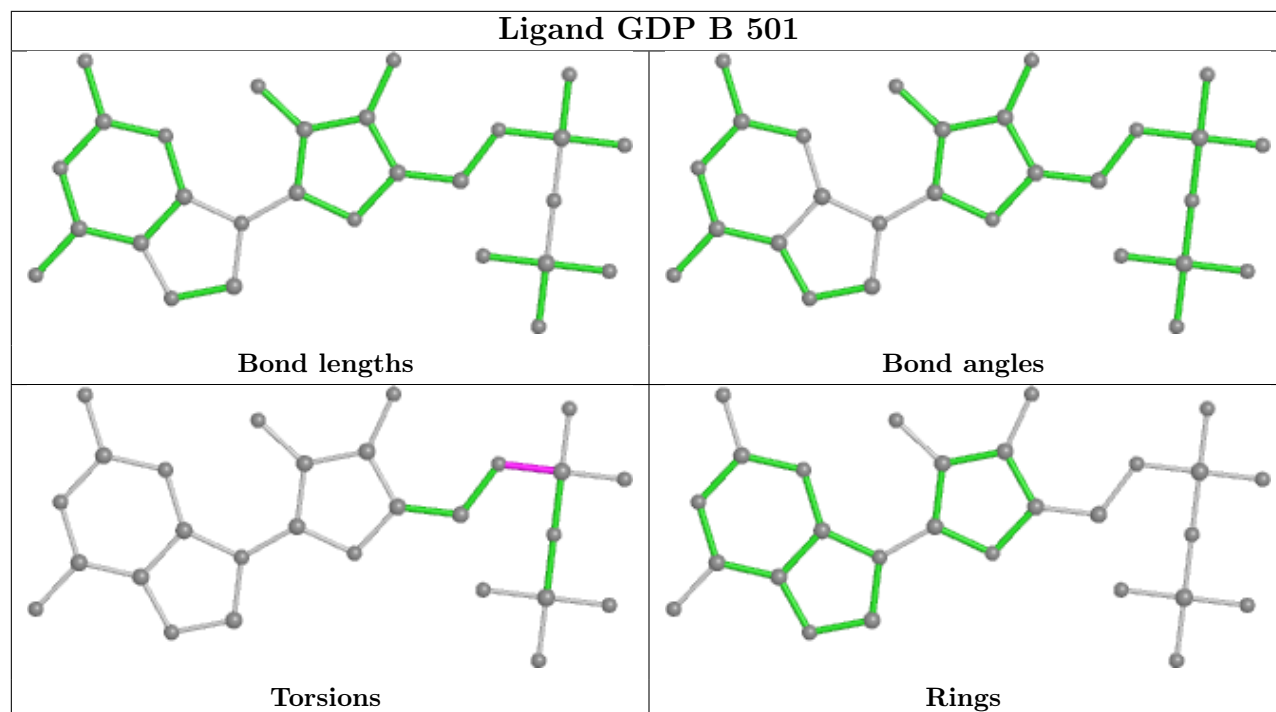
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	501	GDP	1	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	430/451 (95%)	0.03	11 (2%) 56 40	45, 87, 139, 161	0
2	B	431/445 (96%)	-0.03	1 (0%) 95 94	42, 71, 117, 154	0
3	D	159/169 (94%)	0.08	3 (1%) 66 53	45, 75, 114, 158	0
4	K	333/349 (95%)	-0.04	7 (2%) 63 49	44, 70, 118, 144	0
All	All	1353/1414 (95%)	-0.00	22 (1%) 72 59	42, 75, 127, 161	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	11	GLY	7.0
1	A	346	TRP	4.0
1	A	281	ALA	3.9
3	D	12	SER	3.4
2	B	279	GLY	2.9
1	A	282	TYR	2.9
4	K	221	GLN	2.8
1	A	347	CYS	2.8
4	K	127	GLU	2.7
1	A	349	THR	2.6
1	A	38	SER	2.6
4	K	129	HIS	2.6
4	K	122	MET	2.4
1	A	338	LYS	2.4
1	A	339	ARG	2.4
1	A	335	ILE	2.3
3	D	38	ALA	2.3
4	K	336	THR	2.2
1	A	58	ALA	2.1
4	K	125	ASN	2.1
4	K	218	GLN	2.0
1	A	344	VAL	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](#)

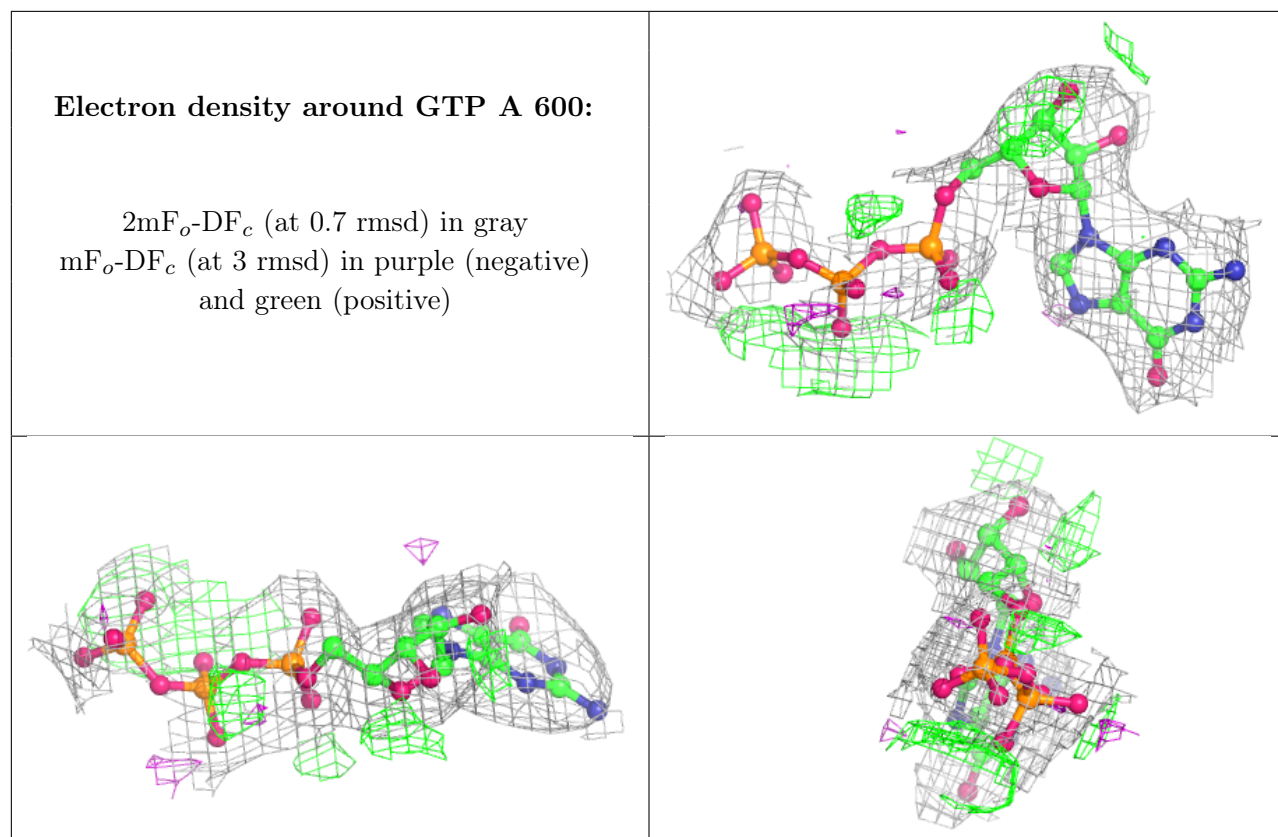
There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

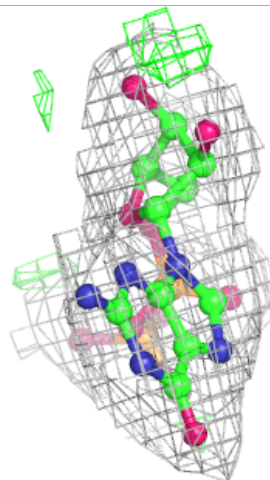
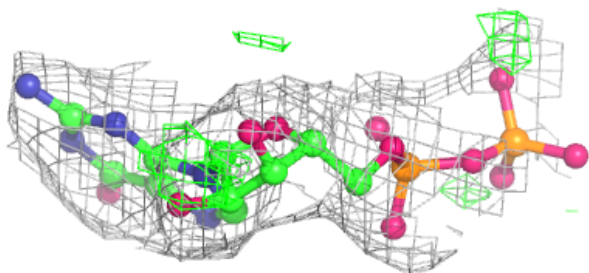
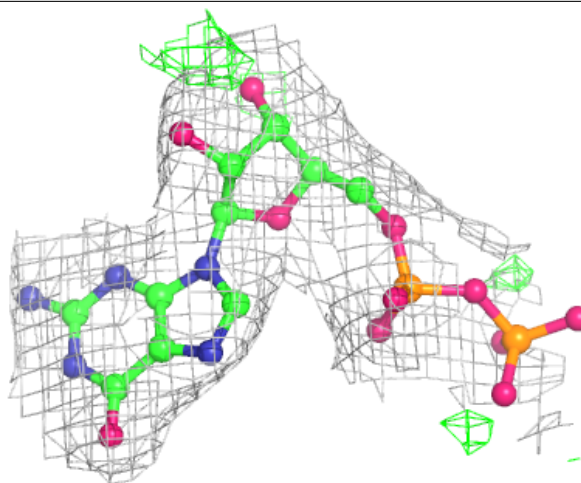
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	MG	A	601	1/1	0.91	0.27	28,28,28,28	0
5	GTP	A	600	32/32	0.96	0.20	51,63,70,74	0
6	MG	B	502	1/1	0.96	0.09	55,55,55,55	0
7	GDP	B	501	28/28	0.96	0.17	64,71,79,85	0
8	ALF	B	503	5/5	0.96	0.11	86,93,98,99	0
9	ADP	K	401	27/27	0.97	0.20	55,60,65,69	0
6	MG	K	402	1/1	0.98	0.13	27,27,27,27	0
8	ALF	K	403	5/5	0.99	0.21	50,51,54,55	0

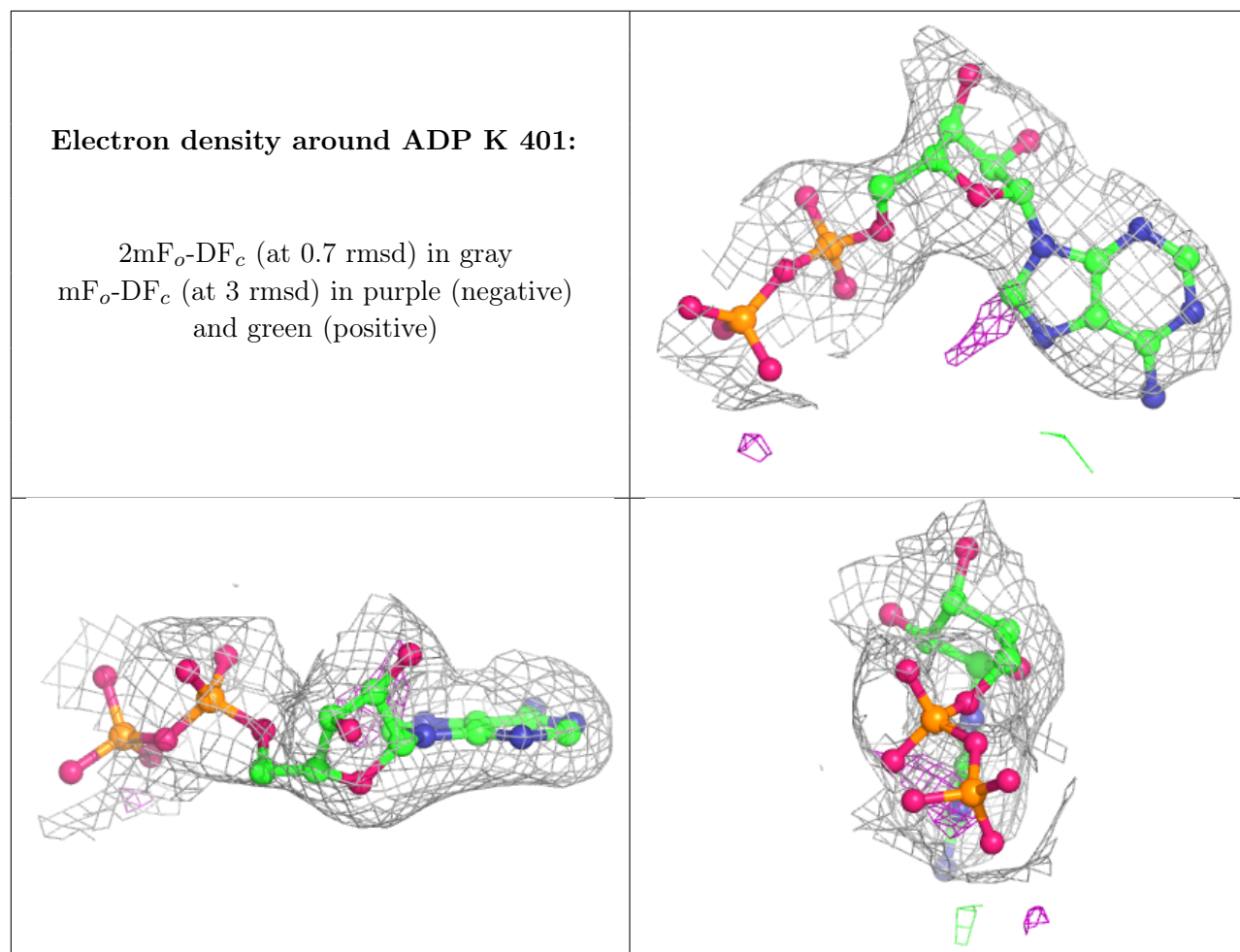
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



Electron density around GDP B 501:

$2mF_o-DF_c$ (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.