



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 05:12 AM UTC

PDB ID : 6ZWB / pdb_00006zwb
Title : Z-SBTub3 photoswitch bound to tubulin-DARPin D1 complex
Authors : Wranik, M.; Weinert, T.; Olieric, N.; Gao, L.; Kraus, Y.C.M.; Bingham, R.;
Ntoulou, E.; Ahlfeld, J.; Thorn-Seshold, O.; Steinmetz, M.O.; Standfuss, J.
Deposited on : 2020-07-28
Resolution : 1.75 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

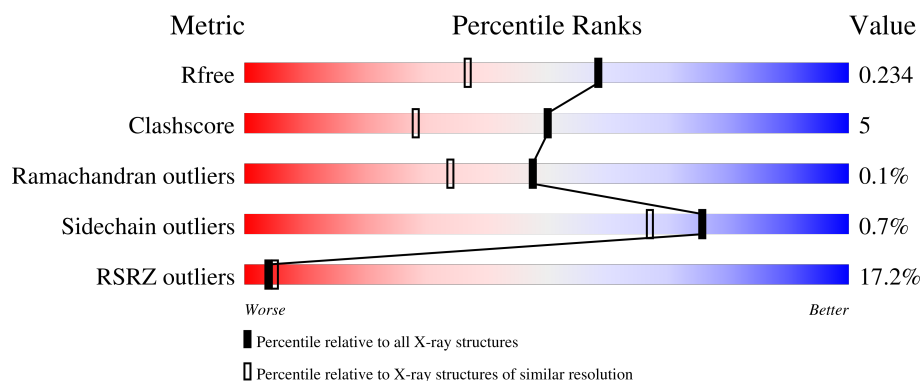
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	16% 88% 8% .
2	B	445	22% 85% 11% .
3	F	169	5% 84% 8% 8%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 16412 atoms, of which 7729 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-1B chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	437	Total	C	H	N	O	S	1	8	0
			6748	2169	3324	581	650	24			

- Molecule 2 is a protein called Tubulin beta-2B chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	431	Total	C	H	N	O	S	0	3	0
			6569	2110	3215	569	647	28			

- Molecule 3 is a protein called Designed Ankyrin Repeat Protein (DARPIN) D1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	F	155	Total	C	H	N	O	S	0	2	0
			2317	731	1158	196	229	3			

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

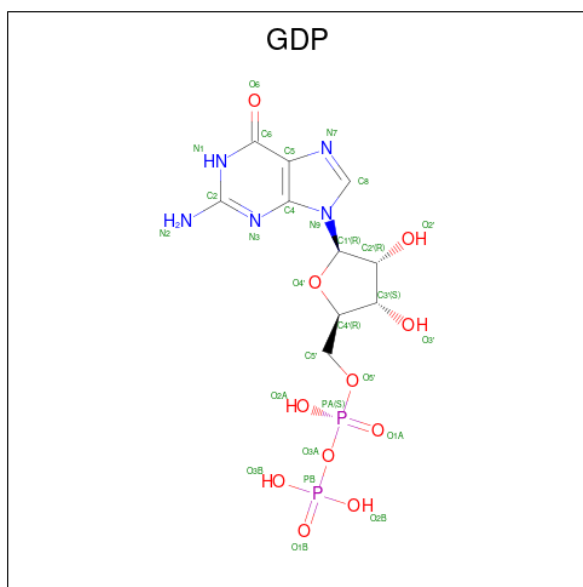


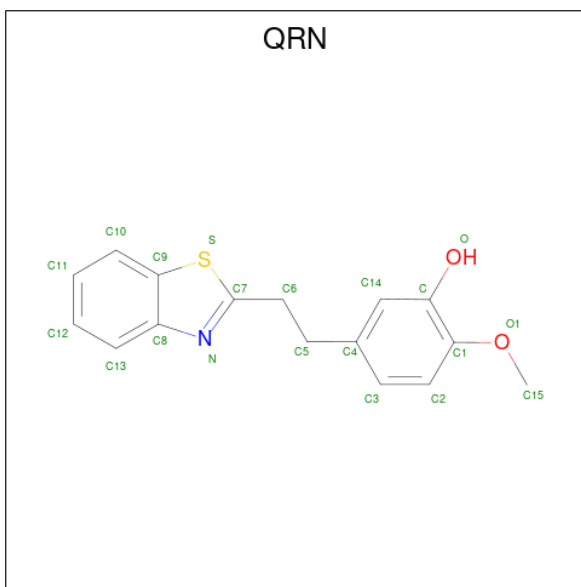
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	P	0	0
			41	10	9	5	14	3		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	H	N	O	S	
			33	16	13	1	2	1	
								0	0

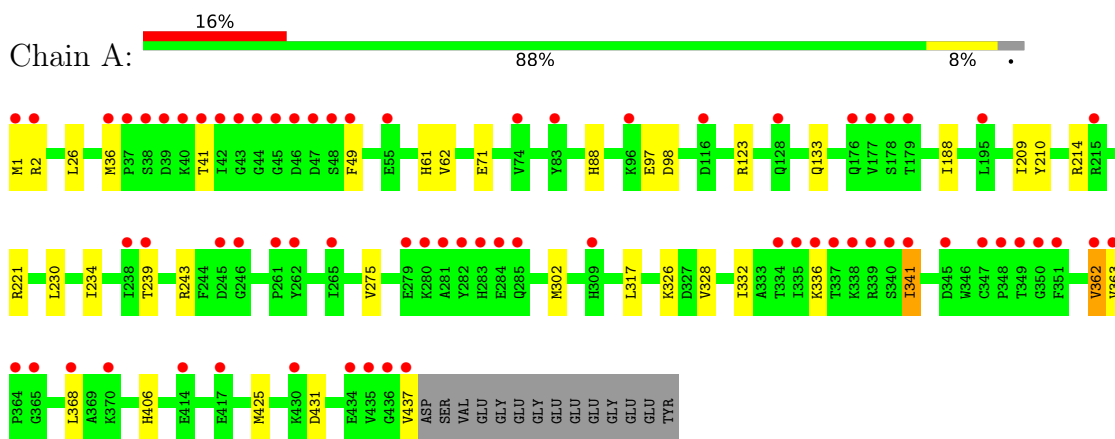
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	310	Total	O		
			310	310	0	0
8	B	219	Total	O		
			219	219	0	0
8	F	136	Total	O		
			136	136	0	0

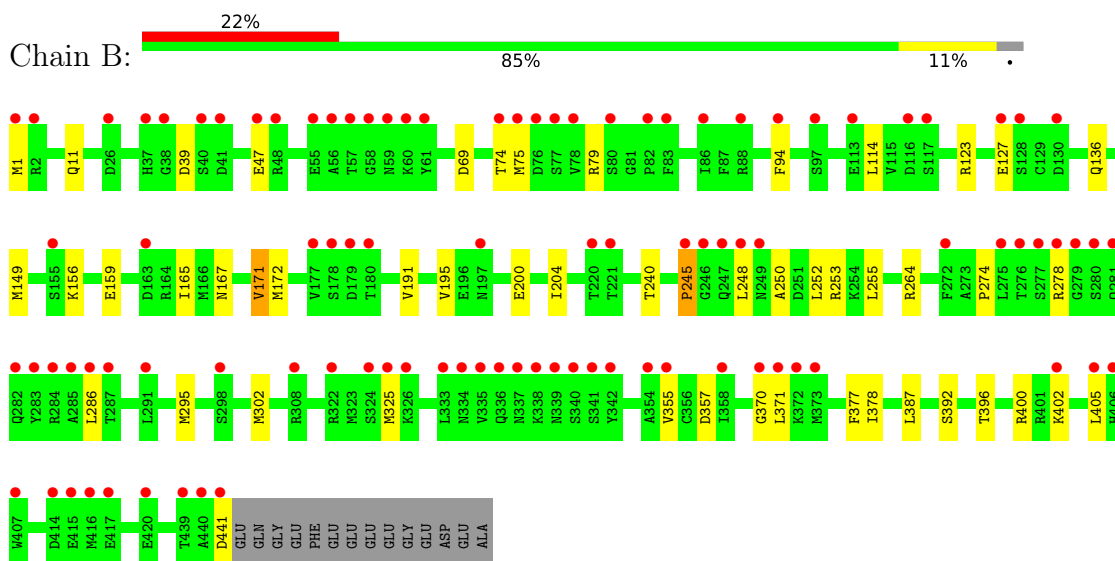
3 Residue-property plots

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.

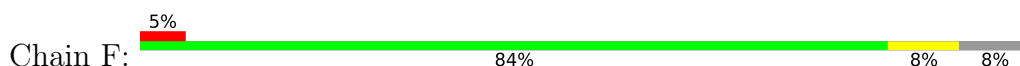
- Molecule 1: Tubulin alpha-1B chain



- Molecule 2: Tubulin beta-2B chain



- Molecule 3: Designed Ankyrin Repeat Protein (DARPIN) D1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.87Å 91.72Å 83.01Å 90.00° 97.06° 90.00°	Depositor
Resolution (Å)	45.04 – 1.75 45.04 – 1.75	Depositor EDS
% Data completeness (in resolution range)	61.2 (45.04-1.75) 61.3 (45.04-1.75)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.18	Depositor
R, R_{free}	0.185 , 0.234 0.186 , 0.234	Depositor DCC
R_{free} test set	2000 reflections (1.80%)	wwPDB-VP
Wilson B-factor (Å ²)	23.2	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16412	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.59% 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: GDP, QRN, MG, GTP

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	0.15	0/3529	0.34	0/4793
2	B	0.17	0/3440	0.33	0/4663
3	F	0.12	0/1181	0.29	0/1606
All	All	0.16	0/8150	0.33	0/11062

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	3424	3324	3309	29	0
2	B	3354	3215	3215	43	0
3	F	1159	1158	1157	14	0
4	A	32	9	12	0	0
5	A	1	0	0	0	0
6	B	28	10	12	0	0
7	B	20	13	0	2	0
8	A	310	0	0	13	0
8	B	219	0	0	16	0
8	F	136	0	0	8	0
All	All	8683	7729	7705	84	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 (84) 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)
2:B:325:MET:SD	2:B:355:VAL:HG11	2.07	0.94
2:B:264:ARG:NH1	8:B:601:HOH:O	2.05	0.90
2:B:75:MET:HE2	2:B:79:ARG:HH22	1.49	0.78
1:A:221:ARG:NE	8:A:604:HOH:O	2.15	0.78
3:F:94:GLU:OE1	8:F:201:HOH:O	2.03	0.76
2:B:248:LEU:HD23	2:B:250:ALA:HB2	1.68	0.75
2:B:200:GLU:OE1	8:B:602:HOH:O	2.06	0.72
1:A:437:VAL:HG12	8:A:652:HOH:O	1.91	0.70
2:B:255:LEU:HD21	8:B:758:HOH:O	1.91	0.70
1:A:36:MET:HE1	1:A:49:PHE:CZ	2.27	0.69
2:B:278:ARG:NH2	8:B:604:HOH:O	2.24	0.69
2:B:392:SER:OG	8:B:603:HOH:O	2.13	0.66
3:F:144:LYS:NZ	8:F:205:HOH:O	2.27	0.66
1:A:431:ASP:OD1	8:A:603:HOH:O	2.14	0.66
1:A:239:THR:OG1	8:A:602:HOH:O	2.13	0.66
1:A:332:ILE:HG22	1:A:336:LYS:HE2	1.78	0.66
1:A:243:ARG:NE	8:A:602:HOH:O	2.27	0.65
2:B:252:LEU:HD22	8:B:602:HOH:O	1.97	0.65
3:F:156[B]:ASN:ND2	8:F:206:HOH:O	2.29	0.65
3:F:36:ASN:O	8:F:202:HOH:O	2.14	0.65
1:A:214:ARG:NH2	8:A:611:HOH:O	2.34	0.61
1:A:234:ILE:HD13	1:A:302:MET:SD	2.41	0.61
1:A:362:VAL:HG23	8:A:835:HOH:O	1.99	0.60
3:F:121:ALA:HB1	3:F:161:LEU:HD21	1.82	0.60
2:B:171:VAL:HA	2:B:204:ILE:O	2.03	0.59
1:A:326:LYS:NZ	8:A:601:HOH:O	2.11	0.58
2:B:295:MET:HG2	2:B:377:PHE:HB2	1.85	0.58
1:A:1:MET:HE3	8:A:873:HOH:O	2.05	0.57
3:F:166:GLN:NE2	8:F:209:HOH:O	2.36	0.57
3:F:156[A]:ASN:ND2	8:F:207:HOH:O	2.32	0.56
1:A:209:ILE:HG23	1:A:230:LEU:HD23	1.88	0.56
3:F:64[A]:GLU:OE2	8:F:203:HOH:O	2.18	0.55
2:B:255:LEU:HD11	8:B:758:HOH:O	2.06	0.55
3:F:160:ASP:OD2	8:F:204:HOH:O	2.18	0.55
3:F:130:GLU:O	3:F:134:LYS:HG2	2.09	0.53
8:A:604:HOH:O	2:B:325:MET:HE3	2.08	0.53
2:B:75:MET:HG3	2:B:94:PHE:CD2	2.44	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:191:VAL:O	2:B:195:VAL:HG13	2.10	0.51
2:B:11:GLN:HA	2:B:74:THR:HG21	1.93	0.51
2:B:278:ARG:NH1	8:B:610:HOH:O	2.41	0.50
2:B:114:LEU:HD23	2:B:149:MET:HE1	1.94	0.49
3:F:144:LYS:HD2	3:F:144:LYS:H	1.76	0.49
2:B:165:ILE:HG21	2:B:252:LEU:HB3	1.93	0.49
1:A:275:VAL:HG13	1:A:368:LEU:HD21	1.95	0.49
3:F:112:TRP:O	3:F:144:LYS:HD2	2.12	0.49
2:B:302:MET:HE3	8:B:661:HOH:O	2.11	0.49
1:A:97:GLU:HG3	2:B:1:MET:HG3	1.96	0.47
2:B:396:THR:O	2:B:400:ARG:HG3	2.14	0.47
1:A:341:ILE:HD12	1:A:341:ILE:O	2.15	0.46
1:A:123[B]:ARG:NH1	8:A:631:HOH:O	2.49	0.45
1:A:188:ILE:HG23	1:A:425:MET:HG3	1.98	0.45
2:B:69:ASP:HB3	2:B:94:PHE:CD2	2.51	0.45
2:B:240:THR:HG23	8:B:609:HOH:O	2.17	0.44
1:A:210:TYR:CZ	1:A:214:ARG:HD3	2.53	0.44
1:A:36:MET:HE2	1:A:61:HIS:CE1	2.53	0.44
2:B:248:LEU:HD12	8:B:641:HOH:O	2.18	0.44
2:B:172:MET:HG3	2:B:387:LEU:HD21	1.99	0.43
2:B:402:LYS:HG3	2:B:405:LEU:HD22	1.99	0.43
2:B:195:VAL:HB	8:B:601:HOH:O	2.17	0.43
2:B:255:LEU:HD13	7:B:502:QRN:C8	2.48	0.43
2:B:39:ASP:OD2	2:B:39:ASP:N	2.51	0.43
2:B:370:GLY:C	2:B:371:LEU:HD12	2.43	0.43
1:A:2:ARG:O	1:A:133:GLN:NE2	2.48	0.43
2:B:123:ARG:O	2:B:127:GLU:HG2	2.19	0.43
2:B:248:LEU:HD21	7:B:502:QRN:S	2.58	0.43
1:A:328:VAL:O	1:A:332:ILE:HG12	2.19	0.43
2:B:47:GLU:HB3	8:B:759:HOH:O	2.19	0.42
2:B:195:VAL:CG2	8:B:601:HOH:O	2.67	0.42
1:A:26:LEU:HD12	1:A:363:VAL:HG22	2.01	0.42
1:A:1:MET:HG3	1:A:2:ARG:H	1.83	0.42
2:B:75:MET:HE2	2:B:79:ARG:NH2	2.26	0.42
1:A:62:VAL:HG11	1:A:88:HIS:CE1	2.55	0.42
2:B:378:ILE:HG21	8:B:758:HOH:O	2.20	0.42
2:B:274:PRO:HB3	2:B:286:LEU:CD2	2.50	0.41
2:B:136:GLN:HA	2:B:167:ASN:O	2.21	0.41
2:B:400:ARG:HD2	3:F:112:TRP:NE1	2.35	0.41
1:A:71:GLU:HG2	1:A:98:ASP:HB3	2.03	0.41
2:B:245:PRO:HB3	8:B:759:HOH:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:144:LYS:HD3	3:F:145:PHE:HD1	1.87	0.40
1:A:406:HIS:HD2	8:A:887:HOH:O	2.04	0.40
2:B:156:LYS:O	2:B:159:GLU:HG2	2.21	0.40
1:A:317:LEU:HD13	1:A:332:ILE:HD11	2.04	0.40
1:A:341:ILE:HB	8:A:614:HOH:O	2.20	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	443/451 (98%)	431 (97%)	12 (3%)	0	100	100
2	B	432/445 (97%)	416 (96%)	15 (4%)	1 (0%)	43	29
3	F	155/169 (92%)	154 (99%)	1 (1%)	0	100	100
All	All	1030/1065 (97%)	1001 (97%)	28 (3%)	1 (0%)	48	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	245	PRO

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	368/379 (97%)	365 (99%)	3 (1%)	73	64
2	B	364/383 (95%)	361 (99%)	3 (1%)	73	64
3	F	121/132 (92%)	121 (100%)	0	100	100
All	All	853/894 (95%)	847 (99%)	6 (1%)	76	67

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

Mol	Chain	Res	Type
1	A	41	THR
1	A	341	ILE
1	A	362	VAL
2	B	171	VAL
2	B	357	ASP
2	B	441	ASP

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	11	GLN
1	A	35	GLN
1	A	85	GLN
1	A	88	HIS
1	A	256	GLN
1	A	393	HIS
2	B	385	GLN
2	B	433	GLN
2	B	436	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 1 is 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$
6	GDP	B	501	-	29,30,30	1.16	4 (13%)	45,47,47	1.55	5 (11%)
7	QRN	B	502	-	22,22,22	1.00	1 (4%)	28,30,30	1.08	1 (3%)
4	GTP	A	501	5	33,34,34	0.91	1 (3%)	50,54,54	1.52	8 (16%)

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
6	GDP	B	501	-	-	5/16/32/32	0/3/3/3
7	QRN	B	502	-	-	3/7/7/7	0/3/3/3
4	GTP	A	501	5	-	6/22/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	502	QRN	C5-C6	-3.98	1.33	1.52
6	B	501	GDP	C5-C4	3.07	1.47	1.38
6	B	501	GDP	C6-N1	-2.57	1.34	1.38
4	A	501	GTP	PA-O3A	2.22	1.61	1.59
6	B	501	GDP	C5-N7	-2.15	1.34	1.39
6	B	501	GDP	C4-N9	-2.09	1.32	1.38

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	501	GDP	C5-C4-N3	-5.03	120.39	128.39
7	B	502	QRN	C6-C5-C4	4.90	129.93	112.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	GTP	C2-N3-C4	4.49	120.04	112.30
4	A	501	GTP	C5-C4-N3	-4.42	121.36	128.39
6	B	501	GDP	C2-N3-C4	4.26	119.64	112.30
6	B	501	GDP	N9-C4-N3	4.04	134.03	125.95
6	B	501	GDP	C6-C5-N7	3.40	136.48	130.29
4	A	501	GTP	N9-C8-N7	-2.93	107.96	113.40
4	A	501	GTP	C2-N1-C6	-2.77	120.08	125.11
4	A	501	GTP	N9-C4-N3	2.69	131.32	125.95
4	A	501	GTP	C5-C6-N1	2.54	119.72	113.25
4	A	501	GTP	C8-N7-C5	2.53	108.77	104.26
4	A	501	GTP	O6-C6-C5	-2.30	120.47	126.53
6	B	501	GDP	C4-C5-N7	-2.22	107.15	110.67

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	GTP	C5'-O5'-PA-O3A
4	A	501	GTP	C5'-O5'-PA-O1A
4	A	501	GTP	C5'-O5'-PA-O2A
6	B	501	GDP	C5'-O5'-PA-O3A
6	B	501	GDP	C5'-O5'-PA-O1A
6	B	501	GDP	C5'-O5'-PA-O2A
4	A	501	GTP	PB-O3A-PA-O1A
4	A	501	GTP	PB-O3B-PG-O1G
7	B	502	QRN	C3-C4-C5-C6
7	B	502	QRN	C14-C4-C5-C6
7	B	502	QRN	C4-C5-C6-C7
4	A	501	GTP	PB-O3B-PG-O3G
6	B	501	GDP	PB-O3A-PA-O1A
6	B	501	GDP	PB-O3A-PA-O2A

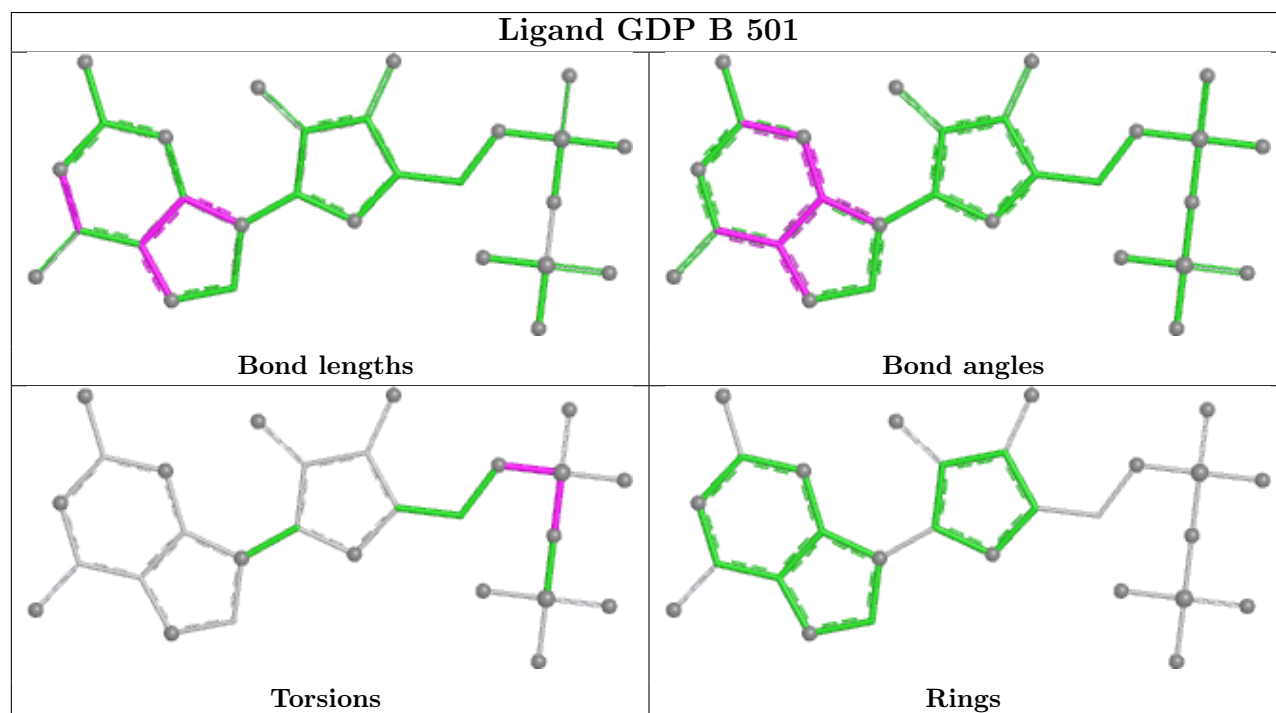
There are no ring outliers.

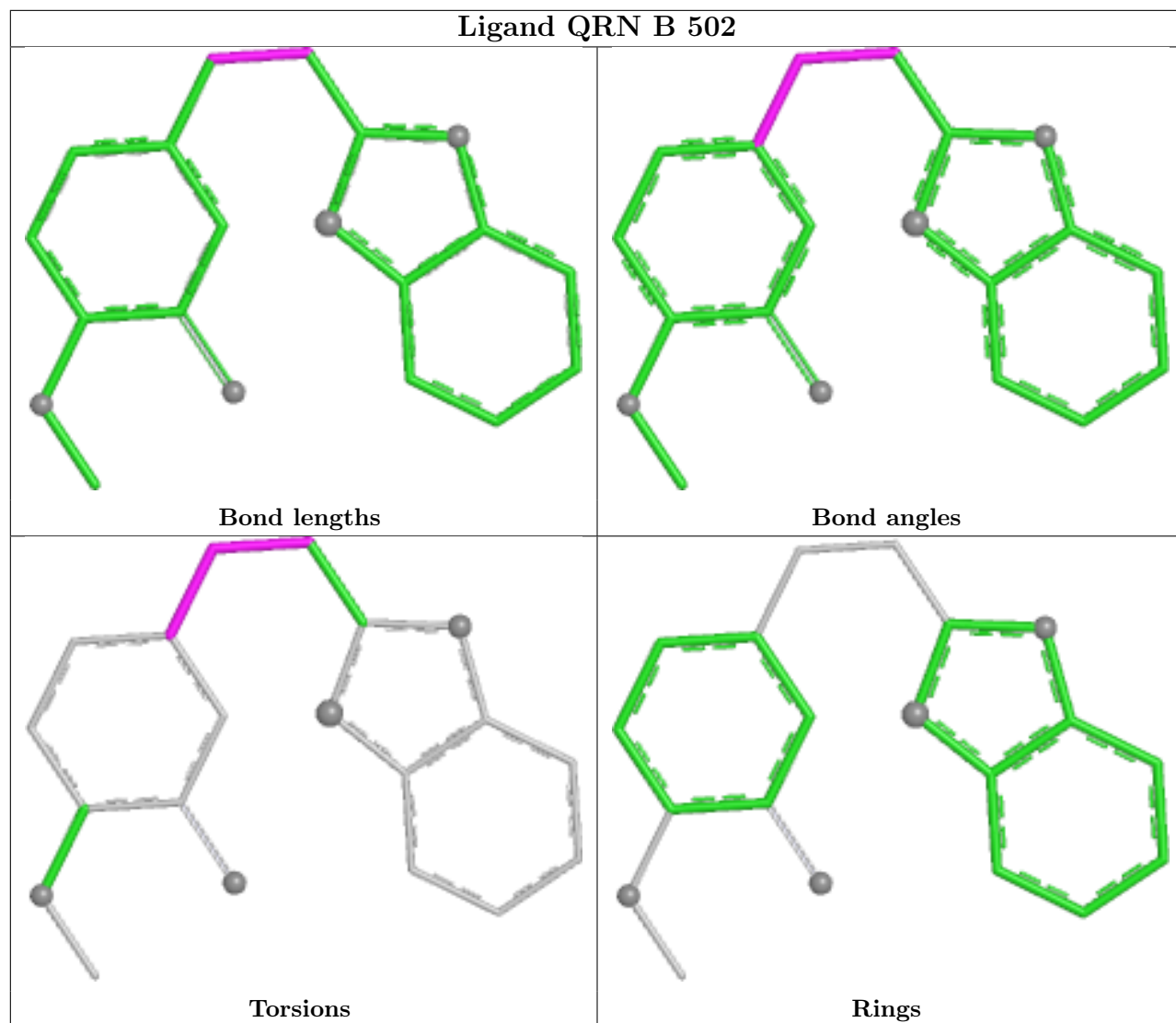
1 monomer is involved in 2 short contacts:

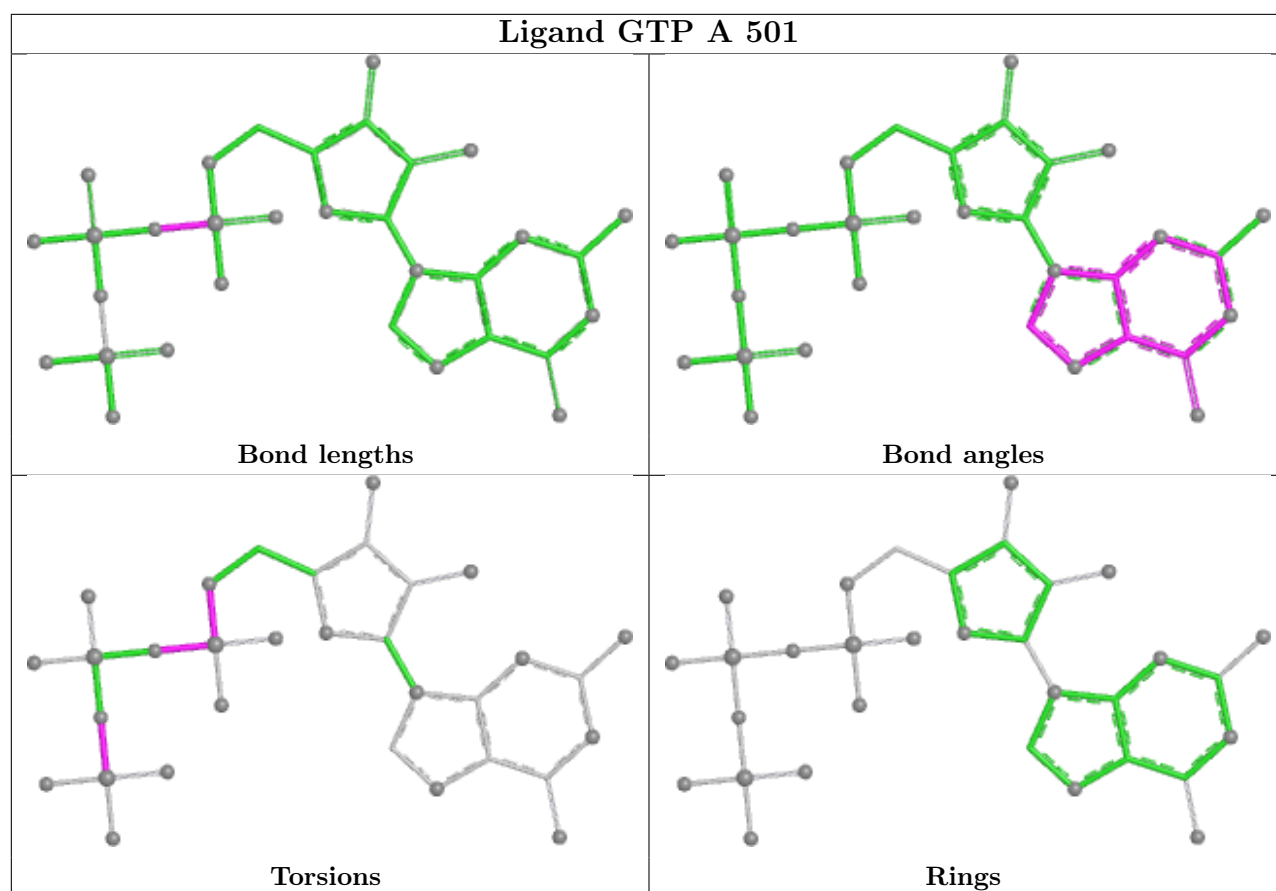
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	502	QRN	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	437/451 (96%)	0.58	70 (16%) 5 6	14, 30, 103, 165	8 (1%)
2	B	431/445 (96%)	0.96	98 (22%) 2 2	17, 42, 108, 172	3 (0%)
3	F	155/169 (91%)	-0.06	8 (5%) 33 40	16, 26, 67, 123	2 (1%)
All	All	1023/1065 (96%)	0.64	176 (17%) 4 5	14, 34, 103, 172	13 (1%)

All (176) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	239	THR	10.2
2	B	283	TYR	9.3
1	A	44	GLY	8.2
1	A	177	VAL	7.7
1	A	42	ILE	7.5
1	A	437	VAL	6.9
1	A	43	GLY	6.8
2	B	333	LEU	6.5
2	B	285	ALA	6.4
2	B	94	PHE	6.1
1	A	341	ILE	5.8
1	A	435	VAL	5.8
1	A	347	CYS	5.8
1	A	39	ASP	5.8
1	A	436	GLY	5.7
2	B	286	LEU	5.6
1	A	339	ARG	5.5
2	B	284	ARG	5.4
1	A	41	THR	5.4
2	B	1	MET	5.3
2	B	355	VAL	5.3
2	B	75	MET	5.2
2	B	281	GLN	5.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	364	PRO	5.1
1	A	48	SER	5.0
1	A	335	ILE	5.0
2	B	179	ASP	4.9
1	A	337	THR	4.9
2	B	59	ASN	4.9
2	B	56	ALA	4.8
1	A	363	VAL	4.8
2	B	282	GLN	4.8
2	B	272	PHE	4.8
2	B	371	LEU	4.8
2	B	358	ILE	4.7
1	A	1	MET	4.6
2	B	279	GLY	4.6
2	B	57	THR	4.5
2	B	275	LEU	4.5
2	B	277	SER	4.4
2	B	406	HIS	4.4
3	F	167	LYS	4.4
2	B	416	MET	4.3
2	B	247	GLN	4.2
1	A	49	PHE	4.2
2	B	128	SER	4.2
2	B	278	ARG	4.1
2	B	58	GLY	4.0
1	A	368	LEU	4.0
2	B	440	ALA	4.0
1	A	45	GLY	4.0
2	B	26	ASP	4.0
1	A	40	LYS	3.9
1	A	365	GLY	3.9
1	A	362	VAL	3.9
1	A	349	THR	3.9
1	A	282	TYR	3.9
1	A	262	TYR	3.8
1	A	281	ALA	3.7
1	A	351	PHE	3.7
2	B	246	GLY	3.7
2	B	60	LYS	3.7
2	B	325	MET	3.7
1	A	38	SER	3.7
2	B	248	LEU	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	340	SER	3.6
1	A	37	PRO	3.6
2	B	82	PRO	3.6
1	A	279	GLU	3.6
2	B	74	THR	3.5
2	B	77	SER	3.4
1	A	348	PRO	3.4
2	B	339	ASN	3.4
2	B	37	HIS	3.4
2	B	276	THR	3.4
2	B	441	ASP	3.4
1	A	2	ARG	3.3
1	A	176	GLN	3.3
1	A	36	MET	3.2
1	A	47	ASP	3.2
1	A	238	ILE	3.2
2	B	249	ASN	3.2
1	A	246	GLY	3.2
1	A	280	LYS	3.2
1	A	285	GLN	3.1
1	A	245	ASP	3.1
2	B	338	LYS	3.1
2	B	76	ASP	3.1
1	A	178	SER	3.1
2	B	341	SER	3.1
1	A	83	TYR	3.1
2	B	372	LYS	3.1
1	A	434	GLU	3.0
2	B	407	TRP	3.0
2	B	47	GLU	3.0
1	A	350	GLY	3.0
1	A	417	GLU	3.0
2	B	334	ASN	3.0
1	A	309	HIS	3.0
1	A	46	ASP	2.9
2	B	40	SER	2.9
2	B	127	GLU	2.9
2	B	280	SER	2.9
1	A	265	ILE	2.8
2	B	439	THR	2.8
2	B	245	PRO	2.8
2	B	337	ASN	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	338	LYS	2.8
2	B	2	ARG	2.8
2	B	322	ARG	2.8
2	B	415	GLU	2.8
1	A	179	THR	2.8
1	A	261	PRO	2.7
2	B	291	LEU	2.7
2	B	220	THR	2.7
2	B	370	GLY	2.7
2	B	420	GLU	2.6
1	A	128	GLN	2.6
2	B	342	TYR	2.6
2	B	113	GLU	2.6
1	A	336	LYS	2.6
2	B	405	LEU	2.6
2	B	61	TYR	2.6
2	B	197	ASN	2.6
2	B	221	THR	2.5
2	B	340	SER	2.5
2	B	402	LYS	2.5
1	A	195	LEU	2.5
2	B	336	GLN	2.5
2	B	414	ASP	2.5
3	F	78	ILE	2.5
1	A	430	LYS	2.5
2	B	97	SER	2.5
1	A	116	ASP	2.4
2	B	373	MET	2.4
2	B	155	SER	2.4
2	B	298	SER	2.4
3	F	32	ILE	2.4
1	A	96	LYS	2.4
1	A	55	GLU	2.4
1	A	215	ARG	2.3
1	A	345	ASP	2.3
2	B	78	VAL	2.3
2	B	38	GLY	2.3
2	B	130	ASP	2.3
3	F	13	ASP	2.3
2	B	354	ALA	2.3
2	B	326	LYS	2.3
2	B	287	THR	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	414	GLU	2.2
2	B	55	GLU	2.2
1	A	284	GLU	2.2
1	A	370	LYS	2.2
2	B	117	SER	2.2
3	F	26	GLN	2.2
2	B	48	ARG	2.2
2	B	308	ARG	2.2
3	F	144	LYS	2.2
2	B	41	ASP	2.1
2	B	80	SER	2.1
1	A	334	THR	2.1
2	B	88	ARG	2.1
2	B	335	VAL	2.1
2	B	324	SER	2.1
2	B	417	GLU	2.1
3	F	139	VAL	2.1
2	B	83	PHE	2.1
2	B	116	ASP	2.0
2	B	163[A]	ASP	2.0
2	B	177	VAL	2.0
2	B	178	SER	2.0
2	B	180	THR	2.0
2	B	86	ILE	2.0
3	F	145	PHE	2.0
1	A	74	VAL	2.0
1	A	283	HIS	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.

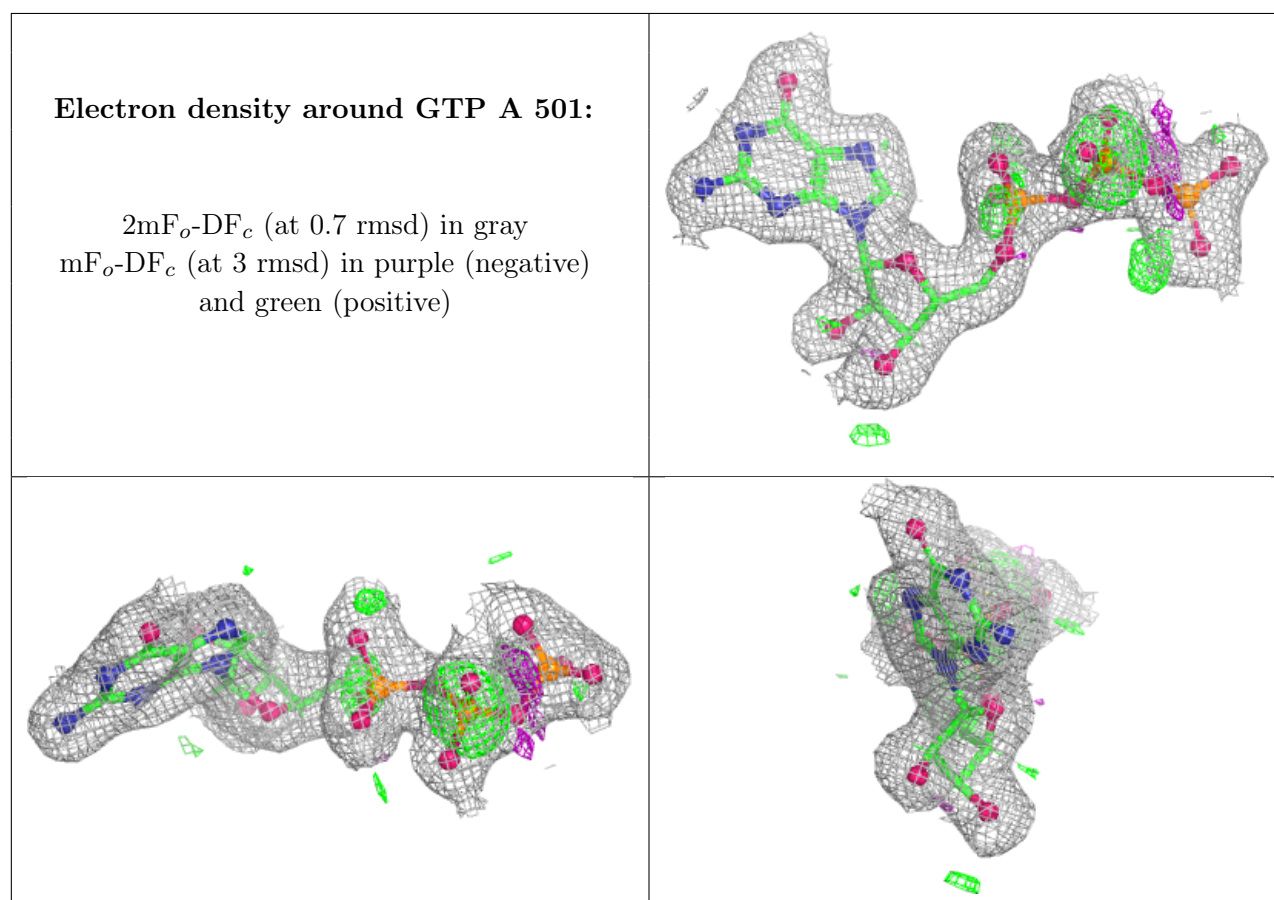
6.4 Ligands [i](#)

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.

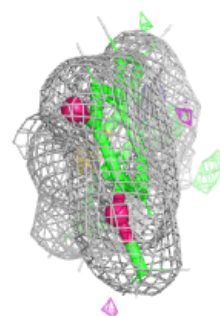
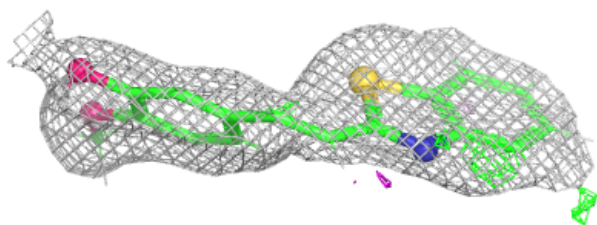
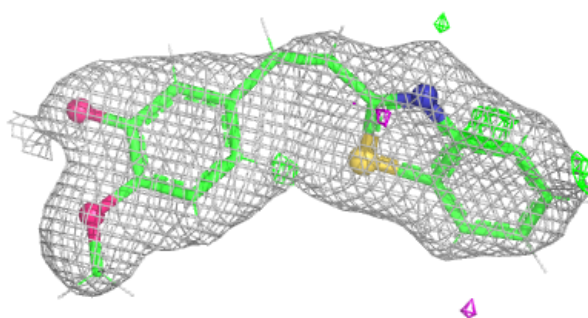
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GTP	A	501	32/32	0.91	0.08	10,16,30,69	0
7	QRN	B	502	20/20	0.91	0.14	21,49,71,85	0
6	GDP	B	501	28/28	0.97	0.06	15,23,29,30	0
5	MG	A	502	1/1	0.97	0.03	28,28,28,28	0

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.



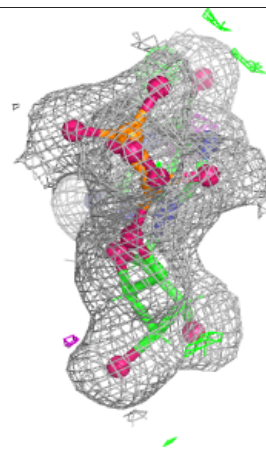
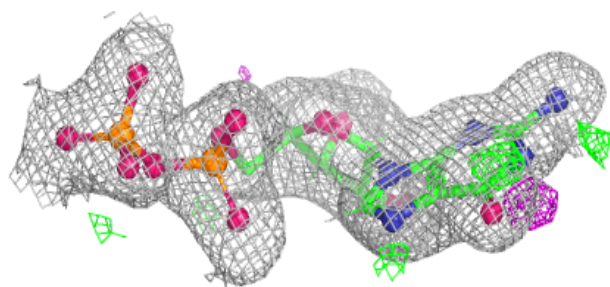
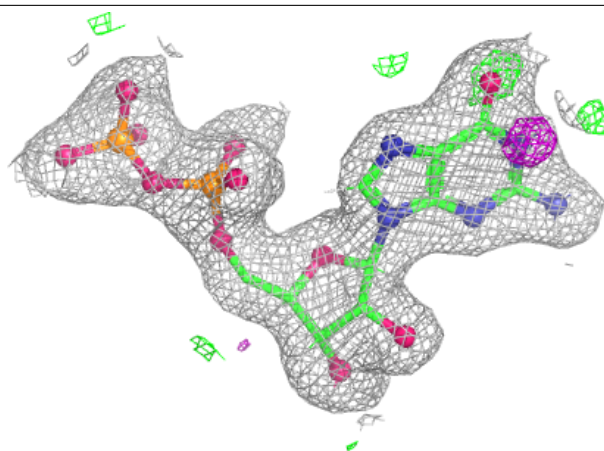
Electron density around QRN B 502:

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



Electron density around 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.