



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 07:08 am BST

PDB ID : 3X0C
Title : Crystal structure of PIP4KIIBETA I368A complex with GMP
Authors : Takeuchi, K.; Lo, Y.H.; Sumita, K.; Senda, M.; Terakawa, J.; Dimitoris, A.; Locasale, J.W.; Sasaki, M.; Yoshino, H.; Zhang, Y.; Kahoud, E.R.; Takano, T.; Yokota, T.; Emerling, B.; Asara, J.A.; Ishida, T.; Shimada, I.; Daikoku, T.; Cantley, L.C.; Senda, T.; Sasaki, A.T.
Deposited on : 2014-10-09
Resolution : 2.55 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

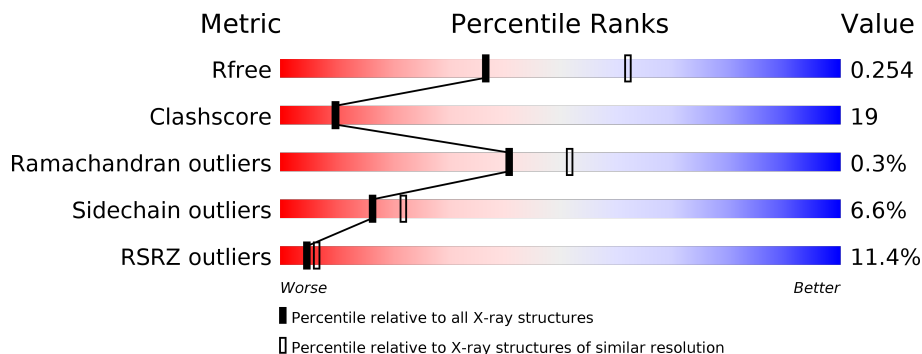
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	393	 7% 55% 22% 19%
1	B	393	 11% 48% 27% 22%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5311 atoms, of which 46 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.

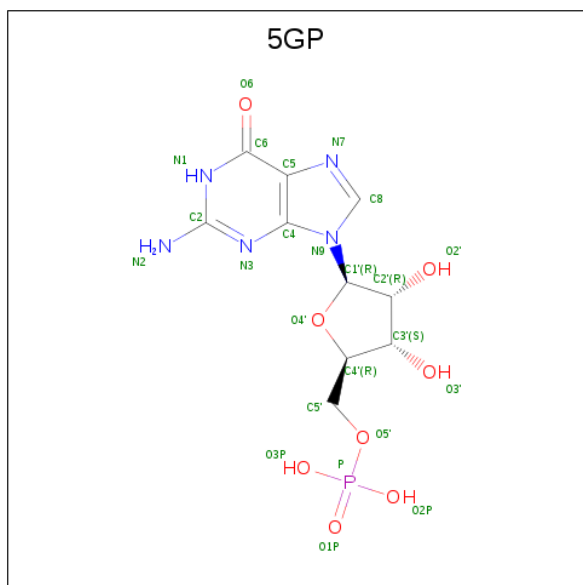
- Molecule 1 is a protein called Phosphatidylinositol 5-phosphate 4-kinase type-2 beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	319	2620	1666	447	493	14	0	0	0
1	B	305	2507	1603	428	463	13	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	EXPRESSION TAG	UNP P78356
A	25	PRO	-	EXPRESSION TAG	UNP P78356
A	26	ASN	-	EXPRESSION TAG	UNP P78356
A	27	CYS	-	EXPRESSION TAG	UNP P78356
A	28	ALA	-	EXPRESSION TAG	UNP P78356
A	29	PRO	-	EXPRESSION TAG	UNP P78356
A	30	GLY	-	EXPRESSION TAG	UNP P78356
A	368	ALA	ILE	ENGINEERED MUTATION	UNP P78356
B	24	GLY	-	EXPRESSION TAG	UNP P78356
B	25	PRO	-	EXPRESSION TAG	UNP P78356
B	26	ASN	-	EXPRESSION TAG	UNP P78356
B	27	CYS	-	EXPRESSION TAG	UNP P78356
B	28	ALA	-	EXPRESSION TAG	UNP P78356
B	29	PRO	-	EXPRESSION TAG	UNP P78356
B	30	GLY	-	EXPRESSION TAG	UNP P78356
B	368	ALA	ILE	ENGINEERED MUTATION	UNP P78356

- Molecule 2 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: 5GP) (formula: C₁₀H₁₄N₅O₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
2	A	1	Total	C	H	N	O	P	0	0
			36	10	12	5	8	1		
2	A	1	Total	C	H	N	O	P	0	0
			35	10	11	5	8	1		
2	A	1	Total	C	H	N	O	P	0	0
			35	10	11	5	8	1		
2	B	1	Total	C	H	N	O	P	0	0
			36	10	12	5	8	1		

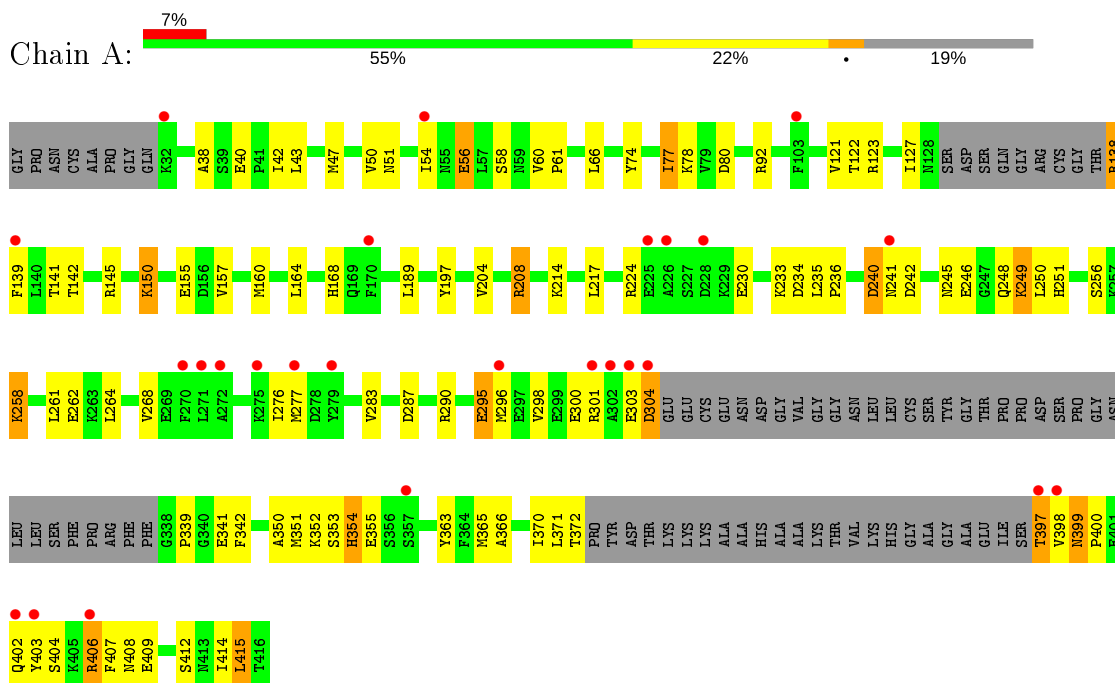
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	22	Total	O	0	0
			22	22		
3	B	20	Total	O	0	0
			20	20		

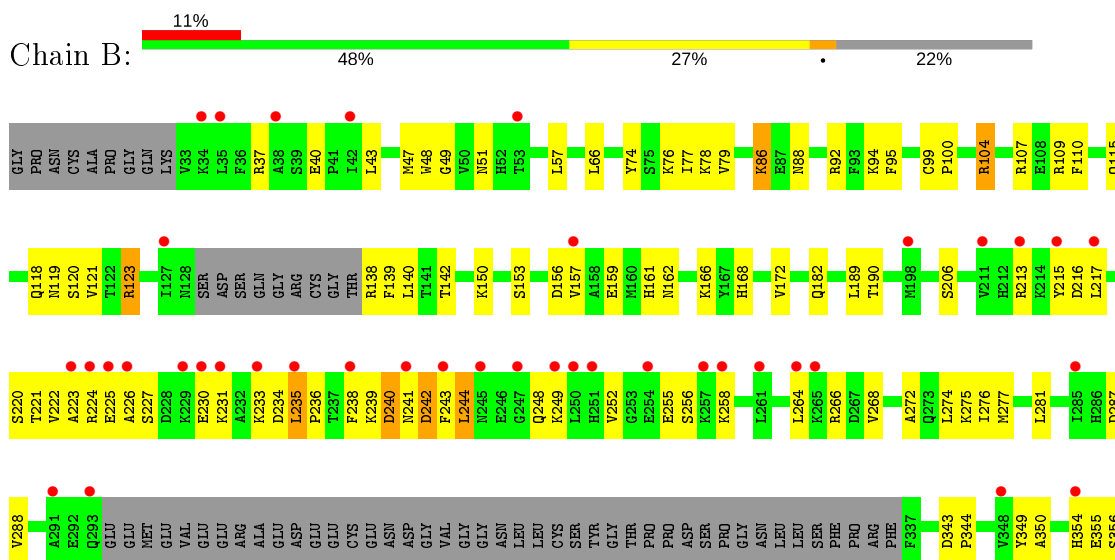
3 Residue-property plots i

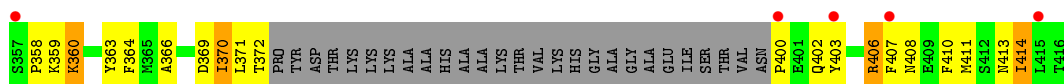
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Phosphatidylinositol 5-phosphate 4-kinase type-2 beta



- Molecule 1: Phosphatidylinositol 5-phosphate 4-kinase type-2 beta





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	109.10Å 183.39Å 106.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.55 – 2.55 93.76 – 2.55	Depositor EDS
% Data completeness (in resolution range)	98.3 (54.55-2.55) 98.3 (93.76-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.55Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.3_928)	Depositor
R, R_{free}	0.223 , 0.268 0.210 , 0.254	Depositor DCC
R_{free} test set	1731 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	65.8	Xtrriage
Anisotropy	0.226	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 64.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.007 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.016 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5311	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 3.45% 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: 5GP

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	0.45	0/2673	0.58	0/3596
1	B	0.46	1/2561 (0.0%)	0.55	0/3445
All	All	0.46	1/5234 (0.0%)	0.56	0/7041

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	369	ASP	C-N	-5.13	1.22	1.34

There are no bond angle outliers.

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	2620	0	2590	107	0
1	B	2507	0	2489	99	0
2	A	72	34	36	6	0
2	B	24	12	12	0	0
3	A	22	0	0	0	0
3	B	20	0	0	3	0
All	All	5265	46	5127	199	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 19.

All (199) 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:256:SER:HB3	1:A:351:MET:CE	1.91	1.01
1:A:77:ILE:CG1	1:B:77:ILE:HD11	1.95	0.96
1:A:139:PHE:HD2	1:A:150:LYS:HE3	1.31	0.95
1:A:139:PHE:CD2	1:A:150:LYS:HE3	2.00	0.95
1:A:141:THR:HG22	1:A:142:THR:O	1.67	0.94
1:B:236:PRO:HB2	1:B:238:PHE:CE1	2.04	0.92
1:B:235:LEU:H	1:B:235:LEU:HD12	1.33	0.90
1:A:77:ILE:HG12	1:B:77:ILE:HD11	1.54	0.90
1:A:397:THR:HG23	1:A:398:VAL:N	1.84	0.89
1:A:399:ASN:HD22	1:A:400:PRO:HD2	1.39	0.87
1:B:371:LEU:O	1:B:372:THR:HG23	1.76	0.86
1:A:341:GLU:OE2	1:A:352:LYS:HD2	1.78	0.84
1:B:110:PHE:CE1	1:B:182:GLN:HG2	2.14	0.82
1:A:77:ILE:CD1	1:B:77:ILE:HD11	2.10	0.82
1:A:258:LYS:HE3	1:A:262:GLU:OE2	1.81	0.81
1:A:256:SER:HB3	1:A:351:MET:HE2	1.62	0.81
1:A:160:MET:HG2	1:A:371:LEU:HD11	1.65	0.79
1:A:298:VAL:HA	1:A:301:ARG:NH2	1.98	0.79
1:B:161:HIS:HE1	3:B:609:HOH:O	1.64	0.78
1:A:397:THR:O	1:A:398:VAL:HG13	1.83	0.78
1:A:230:GLU:O	1:A:233:LYS:HG3	1.85	0.76
1:A:77:ILE:HD11	1:B:77:ILE:HD11	1.67	0.76
1:B:109:ARG:CZ	1:B:172:VAL:HG22	2.17	0.75
1:B:234:ASP:O	1:B:236:PRO:HD3	1.88	0.73
1:A:298:VAL:HA	1:A:301:ARG:HH21	1.53	0.71
1:A:234:ASP:O	1:A:236:PRO:HD3	1.89	0.71
1:B:166:LYS:HD3	1:B:274:LEU:HD21	1.73	0.71
1:A:160:MET:CE	1:A:164:LEU:HD13	2.21	0.70
1:B:243:PHE:CE1	1:B:248:GLN:HG2	2.25	0.70
1:B:288:VAL:HG21	1:B:360:LYS:HE2	1.73	0.70
1:A:141:THR:CG2	1:A:145:ARG:HA	2.22	0.69
1:B:243:PHE:CE2	1:B:414:ILE:CG2	2.75	0.69
1:A:56:GLU:OE2	1:B:48:TRP:NE1	2.22	0.69
1:A:398:VAL:HA	1:A:402:GLN:OE1	1.93	0.68
1:B:94:LYS:HB2	1:B:190:THR:HB	1.75	0.68
1:B:242:ASP:N	1:B:242:ASP:OD1	2.18	0.68
1:A:155:GLU:N	1:A:155:GLU:OE1	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:PHE:CE2	1:B:414:ILE:HG21	2.31	0.66
1:B:79:VAL:O	1:B:92:ARG:HA	1.94	0.66
1:A:160:MET:HE1	1:A:164:LEU:HD13	1.77	0.65
1:B:225:GLU:HA	1:B:242:ASP:OD1	1.97	0.65
1:B:213:ARG:HD3	1:B:215:TYR:OH	1.96	0.65
1:A:256:SER:HB3	1:A:351:MET:HE1	1.76	0.65
1:A:248:GLN:O	1:A:249:LYS:HD2	1.98	0.64
1:A:264:LEU:HD11	1:A:407:PHE:HE1	1.63	0.64
1:A:141:THR:HG23	1:A:145:ARG:HA	1.80	0.64
1:A:157:VAL:HG21	1:A:197:TYR:CD1	2.33	0.64
1:A:242:ASP:O	1:A:246:GLU:HG3	1.98	0.64
1:B:243:PHE:HE2	1:B:414:ILE:CG2	2.11	0.63
1:A:300:GLU:O	1:A:304:ASP:HB2	1.99	0.63
1:B:272:ALA:O	1:B:275:LYS:N	2.28	0.62
1:B:161:HIS:CE1	3:B:609:HOH:O	2.45	0.62
1:A:415:LEU:CD2	1:A:415:LEU:N	2.63	0.61
1:B:244:LEU:HD12	1:B:410:PHE:HE2	1.65	0.61
1:A:160:MET:O	1:A:164:LEU:HB2	2.00	0.61
1:A:77:ILE:HD11	1:B:77:ILE:CD1	2.31	0.61
1:B:153:SER:O	1:B:156:ASP:HB2	2.01	0.60
1:A:399:ASN:ND2	1:A:400:PRO:HD2	2.15	0.60
1:A:139:PHE:HD2	1:A:150:LYS:CE	2.11	0.60
1:B:43:LEU:HD21	1:B:140:LEU:HD11	1.83	0.60
1:B:243:PHE:CZ	1:B:414:ILE:HG21	2.37	0.60
1:A:51:ASN:HB2	1:A:122:THR:HG21	1.84	0.59
1:A:303:GLU:O	1:A:304:ASP:C	2.40	0.58
1:A:397:THR:O	1:A:398:VAL:CG1	2.50	0.58
1:B:227:SER:OG	1:B:230:GLU:HB2	2.03	0.58
1:A:298:VAL:CG2	1:A:301:ARG:HH21	2.17	0.58
1:A:298:VAL:HG22	1:A:301:ARG:HH21	1.69	0.58
1:A:264:LEU:O	1:A:268:VAL:HG13	2.04	0.57
1:B:411:MET:HA	1:B:414:ILE:HD11	1.86	0.57
1:B:110:PHE:CZ	1:B:182:GLN:HG2	2.40	0.57
1:B:49:GLY:HA3	1:B:95:PHE:CE2	2.39	0.57
1:A:217:LEU:CD1	1:A:414:ILE:HD11	2.34	0.57
1:B:255:GLU:O	1:B:258:LYS:HB3	2.04	0.57
1:A:40:GLU:OE2	1:A:138:ARG:NH2	2.37	0.57
1:A:139:PHE:CE2	1:A:150:LYS:HE3	2.40	0.57
1:B:224:ARG:HB3	1:B:239:LYS:HD3	1.87	0.57
1:B:371:LEU:O	1:B:372:THR:CG2	2.53	0.56
1:A:77:ILE:HD12	1:B:79:VAL:HG22	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:LEU:N	1:A:189:LEU:HD12	2.21	0.55
1:B:243:PHE:HE2	1:B:414:ILE:HG23	1.71	0.55
1:B:235:LEU:N	1:B:235:LEU:HD12	2.13	0.55
1:B:57:LEU:O	1:B:104:ARG:NH2	2.41	0.54
1:A:150:LYS:HE2	2:A:501:5GP:O3P	2.06	0.54
1:A:139:PHE:CD2	1:A:150:LYS:CE	2.84	0.54
1:B:189:LEU:HD12	1:B:189:LEU:N	2.22	0.54
1:B:287:ASP:OD2	1:B:359:LYS:HD3	2.08	0.54
1:B:244:LEU:HD12	1:B:410:PHE:CE2	2.42	0.54
1:B:216:ASP:C	1:B:217:LEU:HD23	2.29	0.53
1:A:214:LYS:HE2	1:A:235:LEU:HD23	1.91	0.53
1:B:222:VAL:HG23	1:B:223:ALA:N	2.23	0.52
1:B:349:TYR:CD1	1:B:366:ALA:HB2	2.43	0.52
1:B:215:TYR:HB3	1:B:217:LEU:HD21	1.90	0.52
1:A:241:ASN:O	1:A:245:ASN:HB2	2.10	0.52
1:A:208:ARG:HH12	1:A:342:PHE:HA	1.75	0.52
1:A:276:ILE:HD13	1:A:370:ILE:O	2.09	0.52
1:B:243:PHE:CZ	1:B:414:ILE:CG2	2.93	0.52
1:A:264:LEU:HD11	1:A:407:PHE:CE1	2.45	0.52
1:A:150:LYS:CE	2:A:501:5GP:O3P	2.58	0.52
1:A:283:VAL:HG22	1:A:365:MET:HG2	1.92	0.51
1:A:404:SER:O	1:A:408:ASN:HB2	2.10	0.51
1:B:281:LEU:HD12	1:B:366:ALA:O	2.10	0.51
1:A:250:LEU:HD12	1:A:414:ILE:CG2	2.41	0.51
1:A:43:LEU:O	1:A:47:MET:HG3	2.10	0.51
1:B:370:ILE:CG1	1:B:370:ILE:O	2.59	0.51
1:B:233:LYS:CG	1:B:234:ASP:H	2.24	0.51
1:A:415:LEU:H	1:A:415:LEU:CD2	2.23	0.50
1:A:277:MET:HG2	1:A:400:PRO:HA	1.92	0.50
1:A:204:VAL:HG13	1:A:366:ALA:HB2	1.93	0.50
1:B:350:ALA:HB2	1:B:364:PHE:CE2	2.47	0.50
1:B:226:ALA:HB3	1:B:231:LYS:HD3	1.94	0.50
1:A:80:ASP:OD1	1:A:92:ARG:NH1	2.45	0.49
1:A:399:ASN:N	1:A:402:GLN:OE1	2.45	0.49
1:B:240:ASP:N	1:B:240:ASP:OD1	2.45	0.49
1:B:215:TYR:CD2	1:B:238:PHE:HB2	2.48	0.49
1:B:264:LEU:O	1:B:268:VAL:HG22	2.12	0.49
1:A:251:HIS:O	1:A:353:SER:HA	2.13	0.48
1:A:415:LEU:HD22	1:A:415:LEU:N	2.28	0.48
1:A:258:LYS:CE	1:A:262:GLU:OE2	2.59	0.48
1:B:109:ARG:NH1	1:B:172:VAL:HG22	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:LEU:HD13	1:A:414:ILE:HD11	1.94	0.48
1:A:224:ARG:NH1	1:A:240:ASP:OD1	2.43	0.48
1:A:268:VAL:HG23	1:A:404:SER:HB2	1.93	0.48
1:B:40:GLU:OE1	1:B:138:ARG:NH2	2.44	0.48
1:B:159:GLU:HA	1:B:159:GLU:OE2	2.13	0.48
1:A:77:ILE:CG1	1:B:77:ILE:CD1	2.83	0.47
1:B:225:GLU:HG2	1:B:241:ASN:HB2	1.95	0.47
2:A:502:5GP:O2'	2:A:503:5GP:N3	2.30	0.47
1:B:216:ASP:O	1:B:217:LEU:HD23	2.14	0.47
1:B:213:ARG:NH1	1:B:238:PHE:CZ	2.83	0.47
1:A:250:LEU:HD22	1:A:363:TYR:CD1	2.50	0.47
1:A:204:VAL:HG13	1:A:366:ALA:CB	2.45	0.47
1:A:250:LEU:HD12	1:A:414:ILE:HG22	1.96	0.47
1:A:415:LEU:H	1:A:415:LEU:HD23	1.79	0.47
1:B:206:SER:HB2	1:B:364:PHE:CE2	2.50	0.47
1:A:234:ASP:C	1:A:236:PRO:HD3	2.36	0.47
1:B:119:ASN:O	1:B:123:ARG:HB2	2.16	0.46
1:A:217:LEU:CD1	1:A:414:ILE:CD1	2.93	0.46
1:B:74:TYR:CE1	1:B:76:LYS:HD3	2.50	0.46
1:B:51:ASN:HA	1:B:118:GLN:HE21	1.81	0.46
1:B:402:GLN:CG	1:B:403:TYR:N	2.79	0.46
1:A:261:LEU:HD21	1:A:412:SER:HA	1.98	0.45
1:A:217:LEU:HD12	1:A:414:ILE:CD1	2.45	0.45
1:B:354:HIS:CG	1:B:355:GLU:N	2.84	0.45
1:A:217:LEU:HD12	1:A:414:ILE:HD11	1.98	0.45
1:B:233:LYS:CG	1:B:234:ASP:N	2.80	0.45
1:A:350:ALA:HA	1:A:363:TYR:O	2.17	0.45
1:A:354:HIS:ND1	1:A:355:GLU:N	2.64	0.45
1:A:38:ALA:HB1	1:A:43:LEU:HB2	1.99	0.45
1:B:220:SER:HA	1:B:406:ARG:CZ	2.47	0.45
1:A:398:VAL:CA	1:A:402:GLN:OE1	2.61	0.45
1:A:403:TYR:O	1:A:407:PHE:N	2.46	0.45
2:A:502:5GP:H2'	2:A:503:5GP:N2	2.31	0.45
1:A:141:THR:CG2	1:A:142:THR:O	2.54	0.44
1:B:233:LYS:HG2	1:B:234:ASP:H	1.81	0.44
1:B:277:MET:SD	1:B:400:PRO:N	2.90	0.44
1:B:224:ARG:NH2	1:B:239:LYS:HE3	2.32	0.44
1:A:50:VAL:O	1:A:54:ILE:HG12	2.18	0.44
1:B:233:LYS:HG2	1:B:234:ASP:N	2.33	0.44
1:B:236:PRO:HB2	1:B:238:PHE:HE1	1.71	0.44
1:A:397:THR:C	1:A:398:VAL:HG13	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:LEU:HD12	1:B:168:HIS:CE1	2.52	0.43
1:B:276:ILE:HG22	1:B:277:MET:N	2.32	0.43
1:B:252:VAL:HG23	1:B:256:SER:HB2	2.00	0.43
1:A:399:ASN:O	1:A:402:GLN:HG2	2.19	0.43
1:B:343:ASP:HA	1:B:344:PRO:HD2	1.89	0.43
1:B:249:LYS:NZ	1:B:413:ASN:O	2.48	0.43
1:A:197:TYR:OH	2:A:502:5GP:O1P	2.25	0.42
1:B:402:GLN:HG2	1:B:403:TYR:H	1.84	0.42
1:B:139:PHE:O	1:B:139:PHE:CD1	2.73	0.42
1:B:157:VAL:O	1:B:161:HIS:HD2	2.03	0.42
1:A:295:GLU:O	1:A:298:VAL:HB	2.19	0.42
1:B:107:ARG:NH2	3:B:610:HOH:O	2.29	0.42
1:B:264:LEU:HD11	1:B:407:PHE:HE1	1.84	0.42
1:A:298:VAL:CA	1:A:301:ARG:NH2	2.78	0.42
1:A:402:GLN:O	1:A:406:ARG:HG3	2.19	0.42
1:A:399:ASN:O	1:A:402:GLN:CG	2.68	0.42
1:A:141:THR:CG2	1:A:142:THR:N	2.82	0.42
1:A:141:THR:HG21	1:A:145:ARG:HA	2.02	0.42
1:A:150:LYS:NZ	2:A:501:5GP:O3P	2.52	0.42
1:B:86:LYS:HB3	1:B:86:LYS:HE2	1.72	0.41
1:A:277:MET:HG3	1:A:400:PRO:HG3	2.02	0.41
1:A:60:VAL:HA	1:A:61:PRO:HD2	1.89	0.41
1:A:296:MET:HG2	1:A:296:MET:O	2.16	0.41
1:B:120:SER:O	1:B:142:THR:HB	2.21	0.41
1:A:287:ASP:HB3	1:A:290:ARG:HB3	2.03	0.41
1:B:221:THR:HG23	1:B:406:ARG:HH21	1.86	0.41
1:B:349:TYR:CE1	1:B:366:ALA:HB2	2.56	0.41
1:B:99:CYS:N	1:B:100:PRO:CD	2.83	0.41
1:A:50:VAL:HG21	1:A:121:VAL:HG11	2.03	0.41
1:A:66:LEU:HD12	1:A:168:HIS:CE1	2.55	0.40
1:A:74:TYR:C	1:A:74:TYR:CD1	2.93	0.40
1:B:37:ARG:HG3	1:B:88:ASN:OD1	2.21	0.40
1:B:226:ALA:HB3	1:B:231:LYS:CD	2.51	0.40
1:A:139:PHE:CD2	1:A:150:LYS:HD2	2.57	0.40
1:B:47:MET:HG2	1:B:121:VAL:O	2.21	0.40
1:A:78:LYS:HB3	1:B:78:LYS:HB3	2.04	0.40
1:B:243:PHE:HE1	1:B:248:GLN:HG2	1.82	0.40
1:B:276:ILE:CG2	1:B:277:MET:N	2.84	0.40
1:B:350:ALA:HA	1:B:363:TYR:O	2.22	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	311/393 (79%)	291 (94%)	19 (6%)	1 (0%)	41	51
1	B	297/393 (76%)	287 (97%)	9 (3%)	1 (0%)	41	51
All	All	608/786 (77%)	578 (95%)	28 (5%)	2 (0%)	41	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	339	PRO
1	B	358	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	295/351 (84%)	274 (93%)	21 (7%)	14	19
1	B	282/351 (80%)	265 (94%)	17 (6%)	19	25
All	All	577/702 (82%)	539 (93%)	38 (7%)	16	22

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	ILE
1	A	56	GLU
1	A	58	SER
1	A	77	ILE

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Mol	Chain	Res	Type
1	A	123	ARG
1	A	127	ILE
1	A	138	ARG
1	A	150	LYS
1	A	208	ARG
1	A	240	ASP
1	A	249	LYS
1	A	258	LYS
1	A	295	GLU
1	A	304	ASP
1	A	354	HIS
1	A	372	THR
1	A	397	THR
1	A	399	ASN
1	A	406	ARG
1	A	409	GLU
1	A	415	LEU
1	B	86	LYS
1	B	104	ARG
1	B	115	GLN
1	B	123	ARG
1	B	150	LYS
1	B	162	ASN
1	B	235	LEU
1	B	240	ASP
1	B	242	ASP
1	B	244	LEU
1	B	266	ARG
1	B	356	SER
1	B	360	LYS
1	B	370	ILE
1	B	406	ARG
1	B	408	ASN
1	B	414	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	399	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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	5GP	A	501	-	22,26,26	0.57	0	27,40,40	1.98	6 (22%)
2	5GP	A	502	-	22,26,26	1.78	7 (31%)	27,40,40	1.96	8 (29%)
2	5GP	A	503	-	22,26,26	1.21	3 (13%)	27,40,40	1.95	9 (33%)
2	5GP	B	501	-	22,26,26	0.67	0	27,40,40	1.91	8 (29%)

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	5GP	A	501	-	-	5/6/26/26	0/3/3/3
2	5GP	A	502	-	-	3/6/26/26	0/3/3/3
2	5GP	A	503	-	-	2/6/26/26	0/3/3/3
2	5GP	B	501	-	-	3/6/26/26	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	502	5GP	C4-N3	-3.26	1.30	1.35
2	A	502	5GP	C6-N1	-2.94	1.27	1.33
2	A	502	5GP	C2'-C1'	-2.76	1.49	1.53
2	A	502	5GP	P-O2P	-2.68	1.44	1.54
2	A	502	5GP	P-O3P	-2.65	1.44	1.54
2	A	502	5GP	C2-N1	-2.62	1.30	1.35
2	A	503	5GP	C2-N1	-2.29	1.31	1.35
2	A	502	5GP	C3'-C4'	-2.08	1.47	1.53
2	A	503	5GP	C4-N3	-2.05	1.32	1.35
2	A	503	5GP	C6-C5	2.02	1.44	1.41

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	5GP	N3-C2-N1	-5.12	120.39	127.22
2	B	501	5GP	N3-C2-N1	-4.56	121.14	127.22
2	B	501	5GP	C2-N3-C4	4.30	120.27	115.36
2	A	502	5GP	O4'-C1'-C2'	-4.30	100.64	106.93
2	A	502	5GP	C2-N3-C4	4.11	120.05	115.36
2	A	501	5GP	C2-N3-C4	4.07	120.00	115.36
2	A	503	5GP	C5-C6-N1	-4.04	117.90	123.43
2	A	503	5GP	C3'-C2'-C1'	4.02	107.03	100.98
2	A	501	5GP	C6-N1-C2	3.97	122.24	115.93
2	A	502	5GP	C5-C6-N1	-3.74	118.31	123.43
2	A	501	5GP	C5-C6-N1	-3.56	118.56	123.43
2	A	503	5GP	C6-N1-C2	3.44	121.40	115.93
2	A	503	5GP	C6-C5-C4	-3.27	117.68	120.80
2	A	502	5GP	C4-C5-N7	-3.22	106.04	109.40
2	B	501	5GP	C5-C6-N1	-3.21	119.04	123.43
2	B	501	5GP	O3P-P-O5'	-3.11	98.46	106.73
2	A	502	5GP	O3P-P-O1P	3.08	122.75	110.68
2	B	501	5GP	C6-N1-C2	3.08	120.83	115.93
2	A	503	5GP	C2-N3-C4	2.97	118.75	115.36
2	B	501	5GP	C4-C5-N7	-2.84	106.43	109.40
2	A	503	5GP	O2'-C2'-C3'	-2.69	103.11	111.82
2	A	501	5GP	O3P-P-O5'	-2.63	99.73	106.73
2	A	503	5GP	C4-C5-N7	-2.54	106.75	109.40
2	A	502	5GP	C6-N1-C2	2.48	119.87	115.93
2	B	501	5GP	N2-C2-N1	2.30	120.83	117.25
2	A	503	5GP	P-O5'-C5'	2.25	124.49	118.30
2	A	501	5GP	C3'-C2'-C1'	2.24	104.35	100.98
2	A	502	5GP	C3'-C2'-C1'	2.24	104.35	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	502	5GP	O3P-P-O5'	-2.23	100.79	106.73
2	A	503	5GP	O3P-P-O2P	2.04	115.43	107.64
2	B	501	5GP	O2P-P-O1P	2.01	118.55	110.68

There are no chirality outliers.

All (13) torsion outliers are listed below:

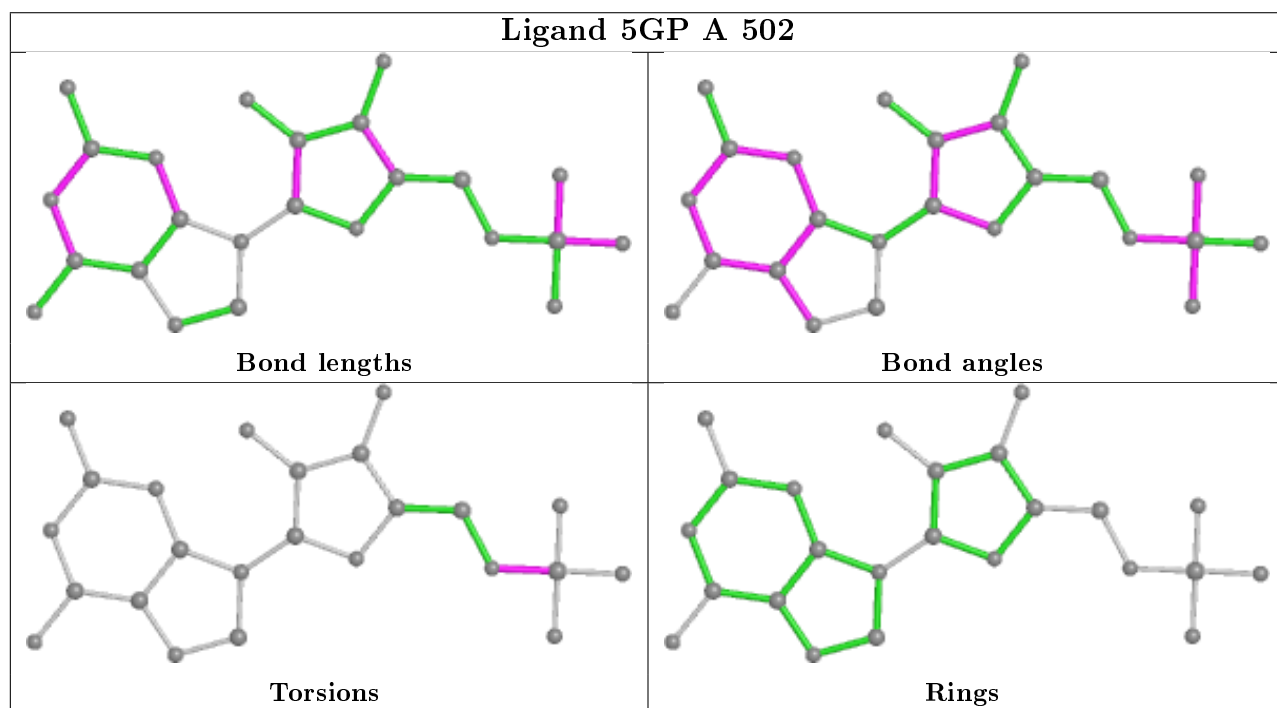
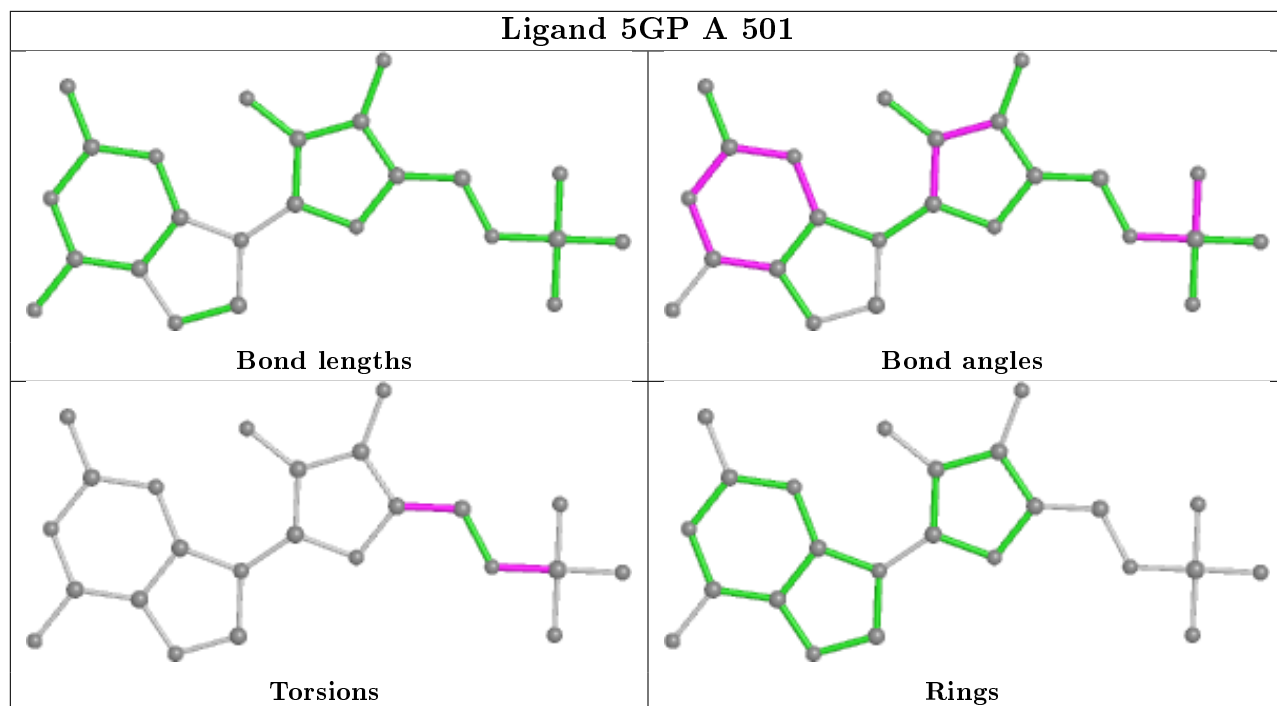
Mol	Chain	Res	Type	Atoms
2	A	501	5GP	C5'-O5'-P-O2P
2	A	501	5GP	C5'-O5'-P-O3P
2	A	502	5GP	C5'-O5'-P-O1P
2	A	502	5GP	C5'-O5'-P-O2P
2	A	502	5GP	C5'-O5'-P-O3P
2	A	503	5GP	C3'-C4'-C5'-O5'
2	B	501	5GP	C5'-O5'-P-O1P
2	B	501	5GP	C5'-O5'-P-O2P
2	B	501	5GP	C5'-O5'-P-O3P
2	A	501	5GP	O4'-C4'-C5'-O5'
2	A	501	5GP	C3'-C4'-C5'-O5'
2	A	503	5GP	O4'-C4'-C5'-O5'
2	A	501	5GP	C5'-O5'-P-O1P

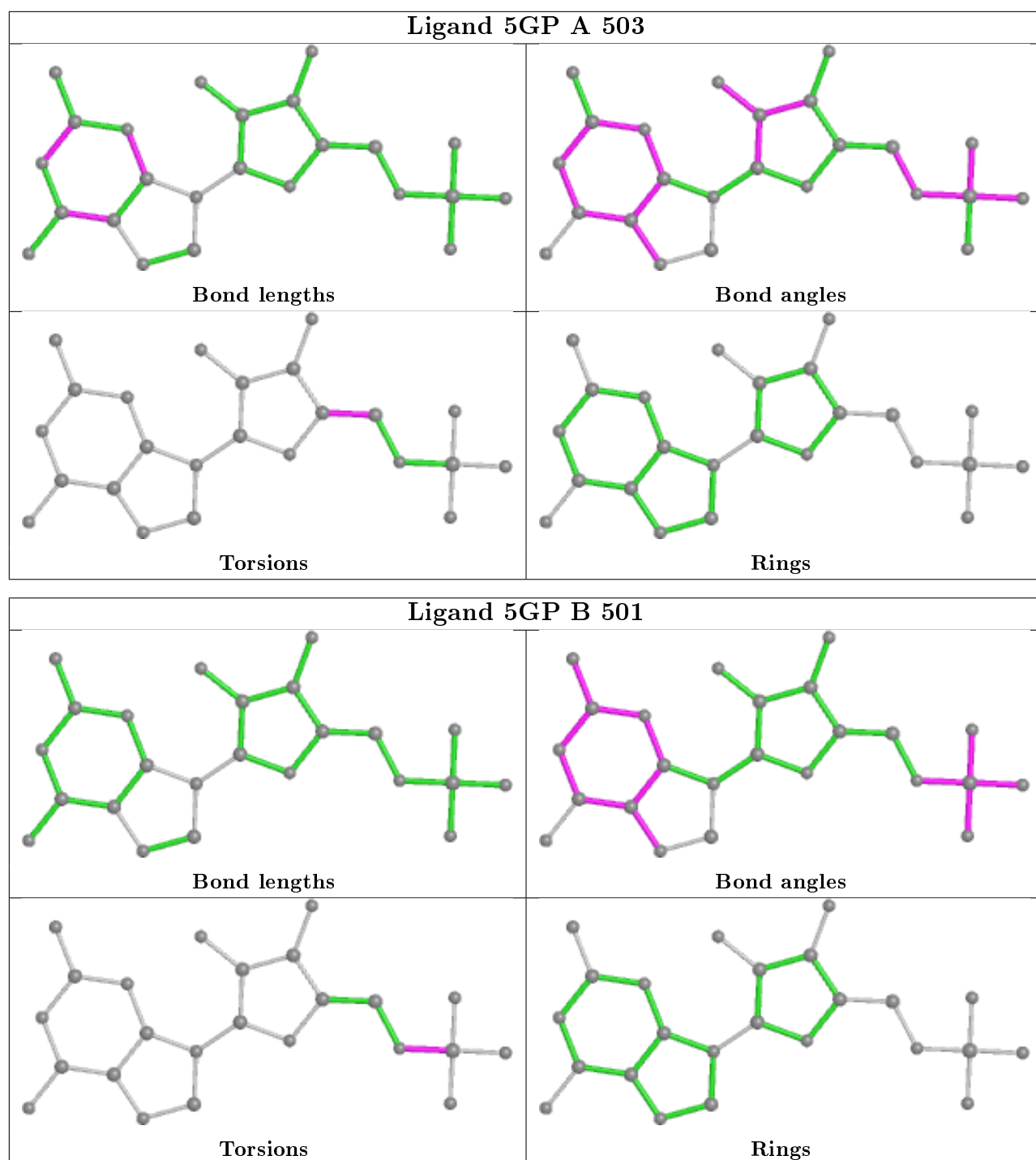
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	5GP	3	0
2	A	502	5GP	3	0
2	A	503	5GP	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	319/393 (81%)	1.07	26 (8%) 11 14	38, 70, 124, 149	0
1	B	305/393 (77%)	1.26	45 (14%) 2 2	38, 77, 139, 166	0
All	All	624/786 (79%)	1.16	71 (11%) 5 6	38, 74, 135, 166	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	398	VAL	5.7
1	B	251	HIS	5.5
1	B	241	ASN	5.5
1	B	235	LEU	4.7
1	A	32	LYS	4.7
1	A	303	GLU	4.7
1	B	238	PHE	4.5
1	B	223	ALA	4.5
1	B	250	LEU	4.4
1	A	275	LYS	4.3
1	B	231	LYS	4.2
1	A	301	ARG	4.2
1	B	224	ARG	4.1
1	A	302	ALA	4.0
1	A	304	ASP	4.0
1	B	215	TYR	4.0
1	B	254	GLU	3.9
1	B	258	LYS	3.7
1	B	233	LYS	3.6
1	A	397	THR	3.4
1	B	407	PHE	3.3
1	A	241	ASN	3.1
1	B	249	LYS	3.1
1	A	403	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	285	ILE	3.0
1	A	402	GLN	2.9
1	B	415	LEU	2.8
1	A	357	SER	2.8
1	A	225	GLU	2.8
1	A	277	MET	2.8
1	B	230	GLU	2.6
1	B	226	ALA	2.6
1	B	211	VAL	2.6
1	B	354	HIS	2.6
1	A	228	ASP	2.5
1	B	38	ALA	2.5
1	A	272	ALA	2.4
1	B	261	LEU	2.4
1	B	127	ILE	2.4
1	B	291	ALA	2.4
1	A	296	MET	2.4
1	B	357	SER	2.4
1	B	229	LYS	2.4
1	B	213	ARG	2.3
1	B	257	LYS	2.3
1	B	225	GLU	2.3
1	B	35	LEU	2.3
1	A	406	ARG	2.2
1	B	34	LYS	2.2
1	A	103	PHE	2.2
1	A	226	ALA	2.2
1	A	271	LEU	2.2
1	A	54	ILE	2.2
1	B	348	VAL	2.2
1	B	217	LEU	2.2
1	B	243	PHE	2.2
1	B	157	VAL	2.1
1	B	245	ASN	2.1
1	B	42	ILE	2.1
1	B	265	LYS	2.1
1	A	139	PHE	2.1
1	B	264	LEU	2.1
1	B	293	GLN	2.1
1	B	400	PRO	2.1
1	A	279	TYR	2.1
1	B	403	TYR	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	270	PHE	2.0
1	B	247	GLY	2.0
1	B	53	THR	2.0
1	A	170	PHE	2.0
1	B	198	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 carbohydrates in this entry.

6.4 Ligands [i](#)

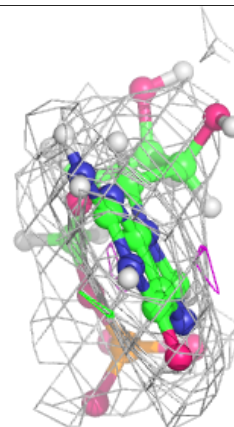
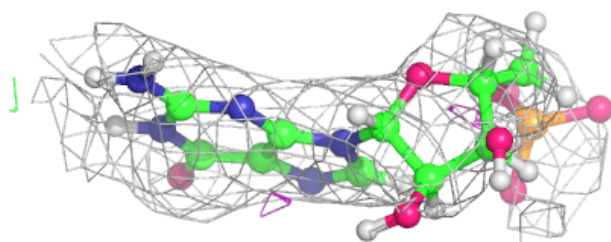
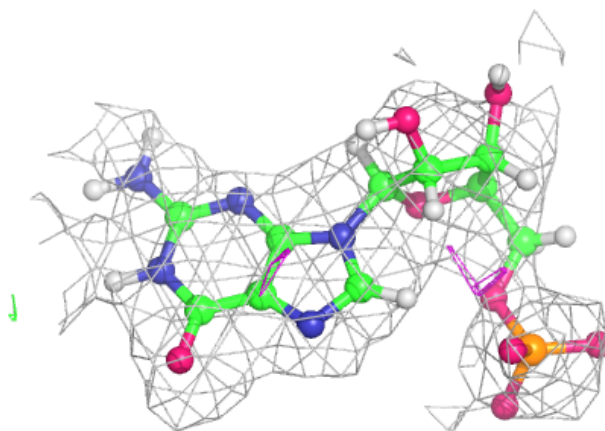
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	5GP	A	501	24/24	0.85	0.23	52,138,191,194	0
2	5GP	A	503	24/24	0.85	0.32	68,144,204,210	0
2	5GP	A	502	24/24	0.92	0.22	50,72,96,108	0
2	5GP	B	501	24/24	0.95	0.20	46,59,74,76	0

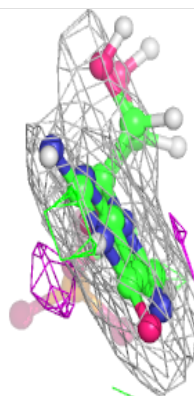
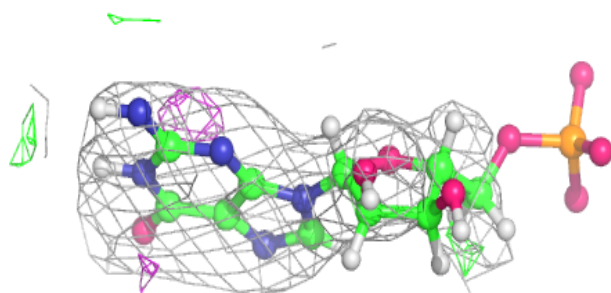
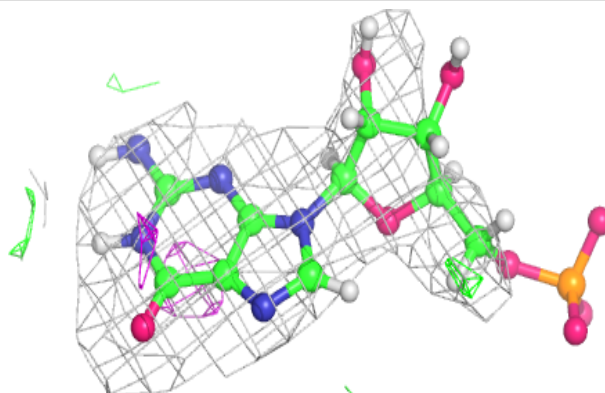
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 5GP A 501:

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

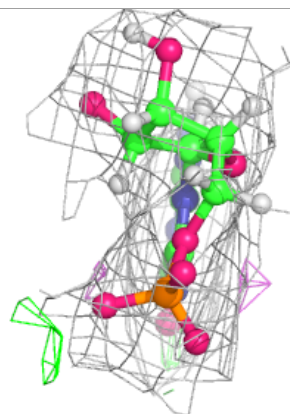
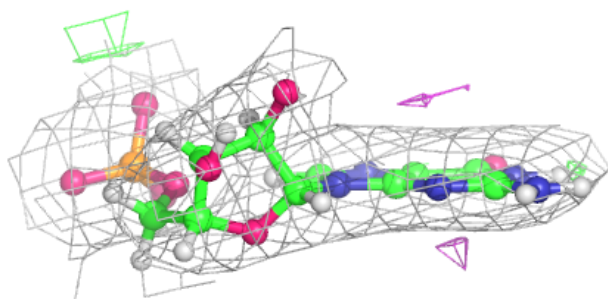
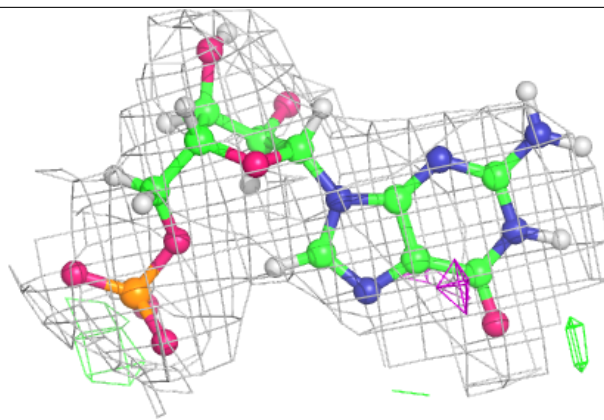
**Electron density around 5GP A 503:**

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

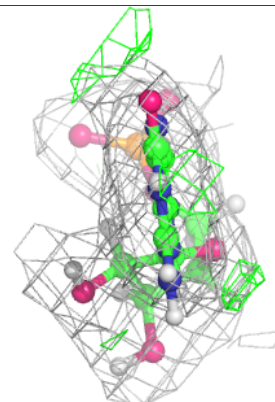
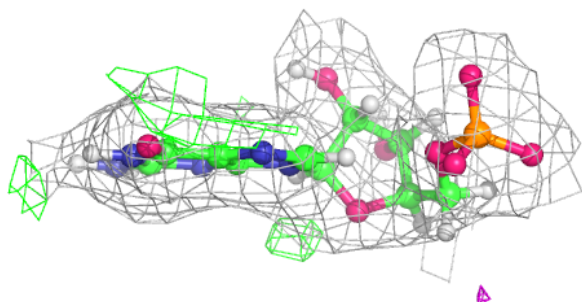
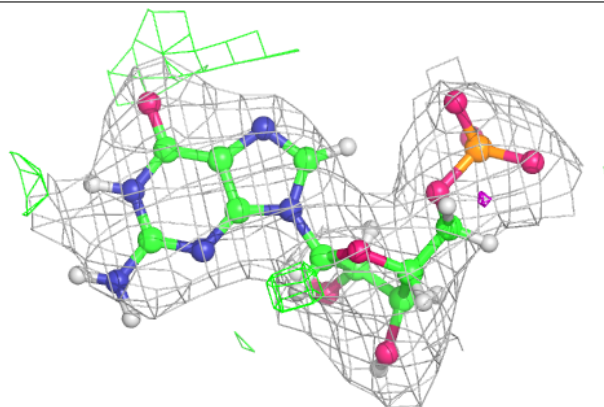


Electron density around 5GP A 502:

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

**Electron density around 5GP 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

There are no such residues in this entry.