



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 11:45 am BST

PDB ID : 1U5R
Title : Crystal Structure of the TAO2 Kinase Domain: Activation and Specifity of a Ste20p MAP3K
Authors : Zhou, T.; Raman, M.; Gao, Y.; Earnest, S.; Chen, Z.; Machius, M.; Cobb, M.H.; Goldsmith, E.J.
Deposited on : 2004-07-28
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 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

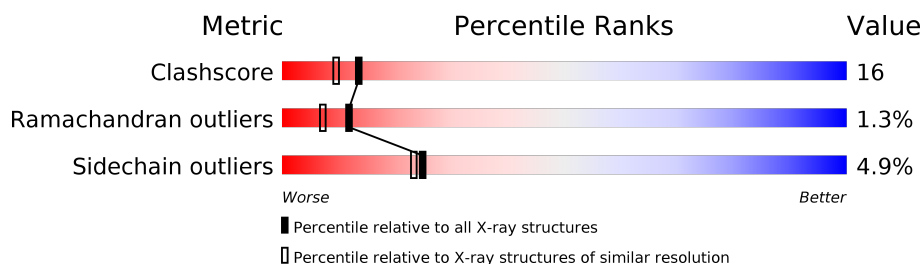
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	348	
1	B	348	

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
1	SEP	B	181	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5431 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 TAO2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	P	S	0	0	0
			2490	1586	432	457	1	14			
1	B	309	Total	C	N	O	P	S	0	0	0
			2490	1586	432	457	1	14			

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	CLONING ARTIFACT	UNP Q9JLS3
A	-26	SER	-	CLONING ARTIFACT	UNP Q9JLS3
A	-25	TYR	-	CLONING ARTIFACT	UNP Q9JLS3
A	-24	TYR	-	CLONING ARTIFACT	UNP Q9JLS3
A	-23	HIS	-	EXPRESSION TAG	UNP Q9JLS3
A	-22	HIS	-	EXPRESSION TAG	UNP Q9JLS3
A	-21	HIS	-	EXPRESSION TAG	UNP Q9JLS3
A	-20	HIS	-	EXPRESSION TAG	UNP Q9JLS3
A	-19	HIS	-	EXPRESSION TAG	UNP Q9JLS3
A	-18	HIS	-	EXPRESSION TAG	UNP Q9JLS3
A	-17	ASP	-	CLONING ARTIFACT	UNP Q9JLS3
A	-16	TYR	-	CLONING ARTIFACT	UNP Q9JLS3
A	-15	ASP	-	CLONING ARTIFACT	UNP Q9JLS3
A	-14	ILE	-	CLONING ARTIFACT	UNP Q9JLS3
A	-13	PRO	-	CLONING ARTIFACT	UNP Q9JLS3
A	-12	THR	-	CLONING ARTIFACT	UNP Q9JLS3
A	-11	THR	-	CLONING ARTIFACT	UNP Q9JLS3
A	-10	GLU	-	CLONING ARTIFACT	UNP Q9JLS3
A	-9	ASN	-	CLONING ARTIFACT	UNP Q9JLS3
A	-8	LEU	-	CLONING ARTIFACT	UNP Q9JLS3
A	-7	TYR	-	CLONING ARTIFACT	UNP Q9JLS3
A	-6	PHE	-	CLONING ARTIFACT	UNP Q9JLS3
A	-5	GLN	-	CLONING ARTIFACT	UNP Q9JLS3
A	-4	GLY	-	CLONING ARTIFACT	UNP Q9JLS3
A	-3	ALA	-	CLONING ARTIFACT	UNP Q9JLS3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	CLONING ARTIFACT	UNP Q9JLS3
A	-1	ASP	-	CLONING ARTIFACT	UNP Q9JLS3
A	0	PRO	-	CLONING ARTIFACT	UNP Q9JLS3
A	181	SEP	SER	MODIFIED RESIDUE	UNP Q9JLS3
B	-27	MET	-	CLONING ARTIFACT	UNP Q9JLS3
B	-26	SER	-	CLONING ARTIFACT	UNP Q9JLS3
B	-25	TYR	-	CLONING ARTIFACT	UNP Q9JLS3
B	-24	TYR	-	CLONING ARTIFACT	UNP Q9JLS3
B	-23	HIS	-	EXPRESSION TAG	UNP Q9JLS3
B	-22	HIS	-	EXPRESSION TAG	UNP Q9JLS3
B	-21	HIS	-	EXPRESSION TAG	UNP Q9JLS3
B	-20	HIS	-	EXPRESSION TAG	UNP Q9JLS3
B	-19	HIS	-	EXPRESSION TAG	UNP Q9JLS3
B	-18	HIS	-	EXPRESSION TAG	UNP Q9JLS3
B	-17	ASP	-	CLONING ARTIFACT	UNP Q9JLS3
B	-16	TYR	-	CLONING ARTIFACT	UNP Q9JLS3
B	-15	ASP	-	CLONING ARTIFACT	UNP Q9JLS3
B	-14	ILE	-	CLONING ARTIFACT	UNP Q9JLS3
B	-13	PRO	-	CLONING ARTIFACT	UNP Q9JLS3
B	-12	THR	-	CLONING ARTIFACT	UNP Q9JLS3
B	-11	THR	-	CLONING ARTIFACT	UNP Q9JLS3
B	-10	GLU	-	CLONING ARTIFACT	UNP Q9JLS3
B	-9	ASN	-	CLONING ARTIFACT	UNP Q9JLS3
B	-8	LEU	-	CLONING ARTIFACT	UNP Q9JLS3
B	-7	TYR	-	CLONING ARTIFACT	UNP Q9JLS3
B	-6	PHE	-	CLONING ARTIFACT	UNP Q9JLS3
B	-5	GLN	-	CLONING ARTIFACT	UNP Q9JLS3
B	-4	GLY	-	CLONING ARTIFACT	UNP Q9JLS3
B	-3	ALA	-	CLONING ARTIFACT	UNP Q9JLS3
B	-2	MET	-	CLONING ARTIFACT	UNP Q9JLS3
B	-1	ASP	-	CLONING ARTIFACT	UNP Q9JLS3
B	0	PRO	-	CLONING ARTIFACT	UNP Q9JLS3
B	181	SEP	SER	MODIFIED RESIDUE	UNP Q9JLS3

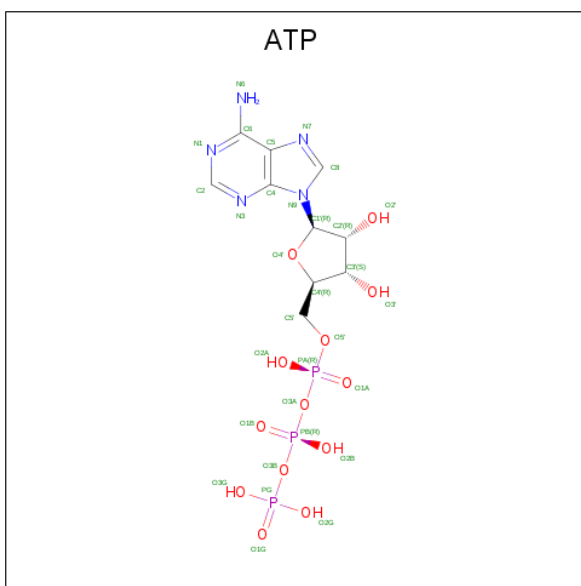
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mg 2 2	0	0
2	A	2	Total Mg 2 2	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Ca	0	0
			1	1		
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
4	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	209	Total	O	0	0
			209	209		
5	B	174	Total	O	0	0
			174	174		

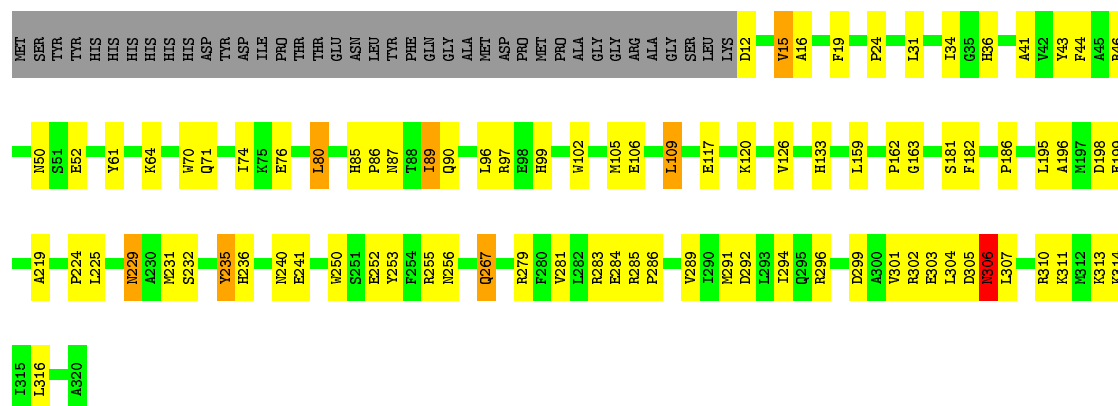
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

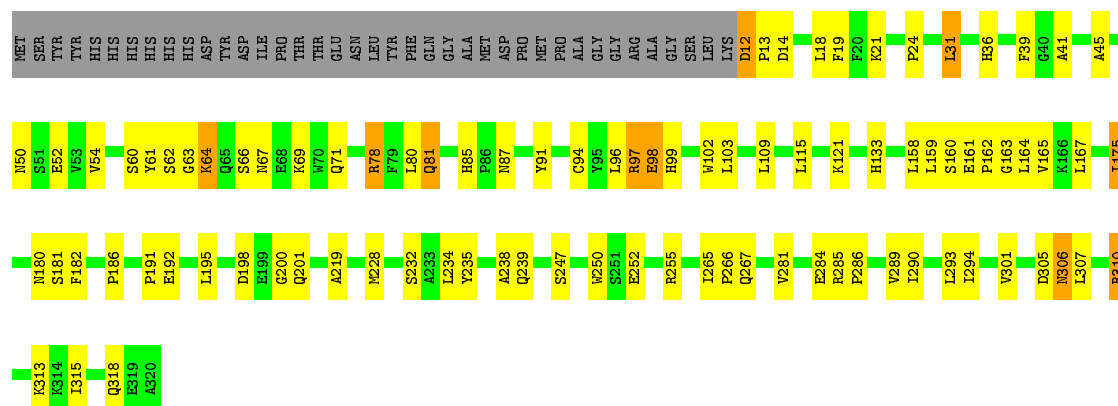
- Molecule 1: serine/threonine protein kinase TAO2

Chain A: 



- Molecule 1: serine/threonine protein kinase TAO2

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	186.47Å 186.47Å 91.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.10	Depositor
% Data completeness (in resolution range)	96.9 (50.00-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.211 , 0.244	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5431	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CA, ATP, SEP

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	0.49	0/2538	0.70	0/3428
1	B	0.46	0/2538	0.68	0/3428
All	All	0.48	0/5076	0.69	0/6856

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	2490	0	2468	75	0
1	B	2490	0	2467	85	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	31	0	10	0	0
4	B	31	0	10	0	0
5	A	209	0	0	8	0
5	B	174	0	0	9	0
All	All	5431	0	4955	159	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 16.

All (159) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:SEP:C	1:B:182:PHE:N	2.30	0.94
1:A:126:VAL:HG23	5:A:637:HOH:O	1.68	0.93
1:B:64:LYS:HA	1:B:64:LYS:NZ	1.85	0.92
1:A:256:ASN:HB2	5:A:668:HOH:O	1.77	0.84
1:A:117:GLU:HG2	5:A:704:HOH:O	1.76	0.84
1:A:85:HIS:HD2	1:A:87:ASN:H	1.28	0.82
1:A:286:PRO:O	1:A:289:VAL:HG23	1.80	0.82
1:B:50:ASN:ND2	1:B:52:GLU:HB2	1.95	0.81
1:B:307:LEU:HA	1:B:310:ARG:HB2	1.64	0.80
1:A:311:LYS:HA	1:A:311:LYS:HE2	1.64	0.79
1:B:80:LEU:HD13	1:B:103:LEU:HD21	1.63	0.79
1:B:21:LYS:O	1:B:21:LYS:HD3	1.83	0.78
1:B:61:TYR:CZ	1:B:99:HIS:HA	2.19	0.77
1:B:85:HIS:HD2	1:B:87:ASN:H	1.33	0.77
1:A:85:HIS:CD2	1:A:87:ASN:H	2.04	0.75
1:B:191:PRO:O	1:B:195:LEU:HD13	1.87	0.75
1:B:306:ASN:HD22	1:B:310:ARG:HH12	1.34	0.75
1:B:181:SEP:HA	1:B:182:PHE:N	2.02	0.73
1:A:307:LEU:HA	1:A:310:ARG:HG2	1.71	0.73
1:B:286:PRO:O	1:B:289:VAL:HG23	1.89	0.73
1:B:85:HIS:CD2	1:B:87:ASN:H	2.06	0.73
1:A:109:LEU:HD11	1:A:294:ILE:HG23	1.70	0.72
1:B:50:ASN:HD21	1:B:52:GLU:HB2	1.55	0.71
1:A:181:SEP:C	1:A:182:PHE:CA	2.68	0.70
1:B:64:LYS:HA	1:B:64:LYS:HZ2	1.56	0.68
1:A:12:ASP:HB3	1:A:15:VAL:HG13	1.75	0.67
1:B:306:ASN:O	1:B:310:ARG:HG2	1.94	0.67
1:B:306:ASN:HD22	1:B:310:ARG:NH1	1.91	0.67
1:B:181:SEP:O	1:B:182:PHE:N	2.28	0.66
1:A:299:ASP:O	1:A:303:GLU:HG2	1.96	0.66
1:B:307:LEU:O	1:B:313:LYS:HD3	1.97	0.65
1:A:267:GLN:H	1:A:267:GLN:CD	2.00	0.64
1:A:133:HIS:CD2	1:A:285:ARG:HH22	2.15	0.63
1:B:109:LEU:HD11	1:B:161:GLU:HA	1.80	0.63
1:B:307:LEU:O	1:B:307:LEU:HD23	1.98	0.63
1:A:310:ARG:HB2	1:A:313:LYS:HB3	1.81	0.63
1:B:18:LEU:HD11	1:B:78:ARG:HD2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:HIS:HD2	1:A:285:ARG:HH22	1.46	0.62
1:B:284:GLU:HG3	5:B:680:HOH:O	1.99	0.61
1:B:247:SER:O	1:B:255:ARG:NH2	2.33	0.61
1:B:97:ARG:HE	1:B:97:ARG:HA	1.64	0.61
1:B:175:ILE:H	1:B:175:ILE:HD13	1.64	0.61
1:B:121:LYS:HE2	5:B:724:HOH:O	1.99	0.60
1:B:181:SEP:CA	1:B:182:PHE:N	2.63	0.60
1:B:175:ILE:H	1:B:175:ILE:CD1	2.15	0.60
1:A:89:ILE:HD13	1:A:90:GLN:N	2.17	0.59
1:B:305:ASP:O	1:B:306:ASN:HB3	2.03	0.59
1:B:14:ASP:HB3	1:B:18:LEU:HD12	1.83	0.59
1:B:98:GLU:HG3	5:B:712:HOH:O	2.01	0.59
1:A:71:GLN:NE2	5:A:737:HOH:O	2.34	0.59
1:B:60:SER:O	1:B:69:LYS:HE2	2.03	0.59
1:B:80:LEU:CD1	1:B:103:LEU:HD21	2.32	0.59
1:B:64:LYS:HZ1	1:B:64:LYS:HA	1.69	0.58
1:B:81:GLN:HG3	1:B:91:TYR:HE2	1.69	0.58
1:A:224:PRO:O	1:A:225:LEU:HB2	2.03	0.57
1:A:231:MET:HG2	1:A:235:TYR:OH	2.05	0.57
1:A:255:ARG:CZ	1:A:255:ARG:HB2	2.35	0.56
1:B:109:LEU:HD12	1:B:109:LEU:H	1.71	0.56
1:A:241:GLU:HG2	5:A:666:HOH:O	2.06	0.56
1:A:61:TYR:CZ	1:A:99:HIS:HA	2.41	0.56
1:B:175:ILE:N	1:B:175:ILE:HD13	2.21	0.56
1:A:279:ARG:NH1	1:A:283:ARG:HB2	2.22	0.55
1:A:279:ARG:HH11	1:A:279:ARG:HG3	1.72	0.55
1:A:305:ASP:O	1:A:306:ASN:HB2	2.05	0.55
1:A:310:ARG:NE	1:A:310:ARG:HA	2.22	0.54
1:B:235:TYR:CZ	1:B:239:GLN:HG3	2.42	0.54
1:A:236:HIS:HE1	5:A:689:HOH:O	1.90	0.54
1:B:235:TYR:CE1	1:B:239:GLN:HG3	2.43	0.53
1:A:311:LYS:HE2	1:A:311:LYS:CA	2.38	0.53
1:A:229:ASN:ND2	1:A:232:SER:H	2.07	0.53
1:B:165:VAL:HG23	1:B:290:ILE:HD13	1.89	0.53
1:B:64:LYS:CE	1:B:64:LYS:HA	2.38	0.53
1:A:41:ALA:HB3	1:A:43:TYR:CZ	2.45	0.51
1:B:31:LEU:HD22	1:B:45:ALA:HB2	1.92	0.51
1:A:292:ASP:O	1:A:296:ARG:HB2	2.10	0.51
1:A:310:ARG:O	1:A:313:LYS:HG2	2.11	0.51
1:A:231:MET:HG2	1:A:235:TYR:CZ	2.45	0.51
1:B:109:LEU:HD11	1:B:161:GLU:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:HIS:HE1	5:B:653:HOH:O	1.93	0.50
1:B:14:ASP:OD1	1:B:78:ARG:NH2	2.44	0.50
1:B:228:MET:HG2	1:B:232:SER:HB2	1.92	0.50
1:A:279:ARG:HH12	1:A:283:ARG:HD3	1.76	0.50
1:A:89:ILE:CD1	1:A:105:MET:HB3	2.42	0.49
1:B:265:ILE:HG22	1:B:267:GLN:HG2	1.94	0.49
1:B:133:HIS:ND1	1:B:281:VAL:HG13	2.28	0.49
1:A:109:LEU:HD23	1:A:159:LEU:O	2.12	0.49
1:A:89:ILE:HD12	1:A:105:MET:HB3	1.95	0.49
1:B:318:GLN:HG2	5:B:760:HOH:O	2.13	0.49
1:A:85:HIS:CG	1:A:86:PRO:HD2	2.49	0.48
1:A:97:ARG:HH11	1:A:97:ARG:HG3	1.78	0.48
1:A:306:ASN:O	1:A:310:ARG:HG2	2.13	0.48
1:B:301:VAL:O	1:B:307:LEU:HD12	2.14	0.48
1:B:81:GLN:HG3	1:B:91:TYR:CE2	2.48	0.48
1:A:34:ILE:HG22	1:A:314:LYS:HB2	1.96	0.47
1:A:109:LEU:HD11	1:A:294:ILE:CG2	2.41	0.47
1:A:267:GLN:N	1:A:267:GLN:CD	2.67	0.47
1:A:133:HIS:HE1	5:A:713:HOH:O	1.96	0.47
1:B:192:GLU:CG	1:B:266:PRO:HG3	2.44	0.47
1:B:109:LEU:HD11	1:B:161:GLU:CA	2.45	0.47
1:A:120:LYS:HE3	1:B:52:GLU:OE2	2.15	0.47
1:A:181:SEP:CA	1:A:182:PHE:N	2.72	0.47
1:A:19:PHE:CE2	1:A:96:LEU:HD13	2.49	0.47
1:A:235:TYR:N	1:A:235:TYR:CD2	2.83	0.47
1:B:91:TYR:OH	1:B:94:CYS:HB2	2.15	0.46
1:B:24:PRO:HB2	1:B:102:TRP:CE3	2.49	0.46
1:B:195:LEU:HD11	1:B:238:ALA:HB1	1.97	0.46
1:A:303:GLU:OE2	1:A:303:GLU:HA	2.16	0.46
1:B:161:GLU:HB3	1:B:162:PRO:HD3	1.97	0.46
1:B:192:GLU:HG2	1:B:266:PRO:CG	2.45	0.46
1:B:67:ASN:O	1:B:71:GLN:HG2	2.15	0.46
1:B:12:ASP:HA	1:B:13:PRO:C	2.37	0.45
1:B:61:TYR:O	1:B:66:SER:HB3	2.16	0.45
1:B:19:PHE:CD2	1:B:96:LEU:HG	2.50	0.45
1:B:109:LEU:HD22	1:B:294:ILE:HG23	1.99	0.45
1:B:252:GLU:HG3	5:B:771:HOH:O	2.16	0.45
1:A:15:VAL:CG2	1:A:16:ALA:N	2.80	0.45
1:B:19:PHE:HE2	1:B:94:CYS:HG	1.64	0.45
1:A:64:LYS:HD2	1:A:64:LYS:HA	1.67	0.45
1:B:31:LEU:HD22	1:B:45:ALA:CB	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:PRO:O	1:A:291:MET:HG2	2.16	0.44
1:A:50:ASN:OD1	1:A:52:GLU:CB	2.65	0.44
1:B:180:ASN:O	1:B:198:ASP:HA	2.17	0.44
1:B:219:ALA:HB1	1:B:250:TRP:CZ2	2.52	0.44
1:B:97:ARG:HB3	5:B:675:HOH:O	2.17	0.44
1:B:14:ASP:OD1	1:B:78:ARG:CZ	2.65	0.44
1:A:46:ARG:HG2	1:A:46:ARG:HH11	1.82	0.44
1:B:63:GLY:O	1:B:64:LYS:NZ	2.51	0.44
1:A:219:ALA:HB1	1:A:250:TRP:CZ2	2.54	0.43
1:A:284:GLU:HB2	5:A:780:HOH:O	2.16	0.43
1:B:61:TYR:CE1	1:B:99:HIS:HA	2.54	0.43
1:A:196:ALA:C	1:A:198:ASP:N	2.68	0.43
1:A:89:ILE:HD13	1:A:106:GLU:HG2	2.01	0.43
1:A:76:GLU:HG2	1:A:80:LEU:CD2	2.48	0.43
1:A:252:GLU:OE2	1:A:252:GLU:HA	2.19	0.42
1:A:46:ARG:HG2	1:A:46:ARG:NH1	2.33	0.42
1:A:279:ARG:NH1	1:A:279:ARG:HG3	2.34	0.42
1:B:307:LEU:C	1:B:307:LEU:HD23	2.40	0.42
1:A:133:HIS:ND1	1:A:281:VAL:HG13	2.34	0.42
1:B:109:LEU:HD12	1:B:159:LEU:O	2.19	0.42
1:A:253:TYR:CE1	1:A:279:ARG:NH1	2.87	0.42
1:B:36:HIS:HA	1:B:41:ALA:HA	2.02	0.42
1:A:70:TRP:CE2	1:A:74:ILE:HD11	2.55	0.41
1:B:285:ARG:HD2	5:B:682:HOH:O	2.20	0.41
1:A:24:PRO:HB2	1:A:102:TRP:CE3	2.55	0.41
1:A:296:ARG:HH11	1:A:296:ARG:HG2	1.85	0.41
1:B:180:ASN:HB3	1:B:200:GLY:O	2.21	0.41
1:A:224:PRO:O	1:A:225:LEU:CB	2.66	0.41
1:A:50:ASN:OD1	1:A:52:GLU:HB2	2.20	0.41
1:B:164:LEU:HD23	5:B:641:HOH:O	2.21	0.41
1:B:182:PHE:HZ	1:B:234:LEU:HD13	1.86	0.41
1:A:225:LEU:HD21	1:A:236:HIS:CE1	2.56	0.41
1:B:315:ILE:O	1:B:315:ILE:HG22	2.20	0.40
1:A:301:VAL:HA	1:A:304:LEU:HG	2.03	0.40
1:A:307:LEU:HA	1:A:310:ARG:CG	2.46	0.40
1:B:39:PHE:CD1	1:B:39:PHE:N	2.89	0.40
1:A:240:ASN:HD22	1:A:240:ASN:N	2.20	0.40
1:B:192:GLU:HG2	1:B:266:PRO:HG2	2.03	0.40
1:A:302:ARG:NH1	1:A:316:LEU:HD22	2.36	0.40
1:B:115:LEU:HD13	1:B:293:LEU:HD21	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	306/348 (88%)	291 (95%)	12 (4%)	3 (1%)	15	11
1	B	305/348 (88%)	286 (94%)	14 (5%)	5 (2%)	9	5
All	All	611/696 (88%)	577 (94%)	26 (4%)	8 (1%)	12	7

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	306	ASN
1	B	163	GLY
1	B	98	GLU
1	B	306	ASN
1	B	62	SER
1	A	163	GLY
1	B	186	PRO
1	A	186	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	268/300 (89%)	255 (95%)	13 (5%)	25	23
1	B	268/300 (89%)	255 (95%)	13 (5%)	25	23
All	All	536/600 (89%)	510 (95%)	26 (5%)	25	23

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	31	LEU
1	A	36	HIS
1	A	44	PHE
1	A	80	LEU
1	A	89	ILE
1	A	109	LEU
1	A	195	LEU
1	A	199	GLU
1	A	229	ASN
1	A	235	TYR
1	A	267	GLN
1	A	306	ASN
1	B	12	ASP
1	B	31	LEU
1	B	54	VAL
1	B	64	LYS
1	B	78	ARG
1	B	81	GLN
1	B	97	ARG
1	B	158	LEU
1	B	160	SER
1	B	167	LEU
1	B	175	ILE
1	B	201	GLN
1	B	310	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	HIS
1	A	133	HIS
1	A	201	GLN
1	A	229	ASN
1	A	240	ASN
1	A	295	GLN
1	A	306	ASN
1	A	308	GLN
1	B	85	HIS
1	B	124	GLN
1	B	133	HIS
1	B	201	GLN
1	B	239	GLN

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Mol	Chain	Res	Type
1	B	240	ASN
1	B	246	GLN
1	B	306	ASN
1	B	308	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	SEP	B	181	1,3	8,9,10	1.07	0	8,12,14	3.51	3 (37%)
1	SEP	A	181	1,3	8,9,10	1.05	0	8,12,14	2.09	4 (50%)

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
1	SEP	B	181	1,3	-	1/5/8/10	-
1	SEP	A	181	1,3	-	0/5/8/10	-

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	181	SEP	OG-CB-CA	-7.62	100.73	108.14
1	B	181	SEP	O2P-P-OG	-4.82	93.92	106.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	181	SEP	O2P-P-OG	-3.42	97.64	106.73
1	A	181	SEP	OG-CB-CA	2.60	110.67	108.14
1	A	181	SEP	OG-P-O1P	-2.53	99.39	106.47
1	B	181	SEP	O3P-P-O2P	2.44	116.96	107.64
1	A	181	SEP	O3P-P-O2P	2.24	116.20	107.64

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	181	SEP	N-CA-CB-OG

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	181	SEP	4	0
1	A	181	SEP	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 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	$\# Z > 2$
4	ATP	B	412	2	26,33,33	2.37	11 (42%)	31,52,52	3.86	12 (38%)
4	ATP	A	411	2	26,33,33	2.35	12 (46%)	31,52,52	3.96	12 (38%)

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
4	ATP	B	412	2	-	2/18/38/38	0/3/3/3
4	ATP	A	411	2	-	2/18/38/38	0/3/3/3

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	412	ATP	O5'-C5'	-5.47	1.23	1.44
4	A	411	ATP	O5'-C5'	-5.14	1.25	1.44
4	A	411	ATP	O4'-C1'	4.69	1.47	1.41
4	A	411	ATP	C4-N3	4.54	1.41	1.35
4	B	412	ATP	C4-N3	4.46	1.41	1.35
4	B	412	ATP	O4'-C1'	4.23	1.47	1.41
4	B	412	ATP	PA-O5'	-4.13	1.42	1.59
4	A	411	ATP	PA-O5'	-3.92	1.43	1.59
4	B	412	ATP	C2'-C1'	3.47	1.59	1.53
4	A	411	ATP	C8-N7	-3.21	1.29	1.34
4	B	412	ATP	C2-N3	2.79	1.36	1.32
4	B	412	ATP	PB-O1B	-2.74	1.41	1.50
4	A	411	ATP	PB-O1B	-2.59	1.41	1.50
4	B	412	ATP	C8-N7	-2.33	1.30	1.34
4	A	411	ATP	PA-O1A	-2.31	1.42	1.50
4	A	411	ATP	C2-N3	2.21	1.35	1.32
4	B	412	ATP	PB-O2B	-2.17	1.45	1.55
4	B	412	ATP	PA-O1A	-2.14	1.43	1.50
4	A	411	ATP	C2'-C1'	2.06	1.56	1.53
4	A	411	ATP	C3'-C4'	-2.04	1.47	1.53
4	A	411	ATP	PG-O2G	-2.03	1.47	1.54
4	B	412	ATP	C3'-C4'	-2.01	1.47	1.53
4	A	411	ATP	PB-O2B	-2.01	1.45	1.55

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	411	ATP	O5'-C5'-C4'	16.46	165.64	108.99
4	B	412	ATP	O5'-C5'-C4'	15.61	162.73	108.99
4	A	411	ATP	C5'-C4'-C3'	-7.79	85.99	115.18
4	B	412	ATP	C5'-C4'-C3'	-7.60	86.70	115.18
4	B	412	ATP	O5'-PA-O1A	-7.11	81.30	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	411	ATP	O5'-PA-O1A	-6.64	83.12	109.07
4	B	412	ATP	PA-O5'-C5'	5.19	152.09	121.68
4	A	411	ATP	PA-O5'-C5'	4.69	149.19	121.68
4	A	411	ATP	C3'-C2'-C1'	4.14	107.20	100.98
4	A	411	ATP	O4'-C4'-C3'	4.09	113.21	105.11
4	B	412	ATP	C3'-C2'-C1'	3.84	106.77	100.98
4	B	412	ATP	O4'-C4'-C3'	3.78	112.60	105.11
4	B	412	ATP	O4'-C4'-C5'	-3.09	99.19	109.37
4	A	411	ATP	O2A-PA-O5'	-2.85	94.50	107.75
4	A	411	ATP	C4-C5-N7	2.85	112.37	109.40
4	A	411	ATP	O4'-C4'-C5'	-2.70	100.50	109.37
4	A	411	ATP	O2A-PA-O1A	2.64	125.27	112.24
4	B	412	ATP	O2A-PA-O1A	2.60	125.10	112.24
4	B	412	ATP	C4-C5-N7	2.53	112.04	109.40
4	B	412	ATP	O3'-C3'-C4'	2.43	118.08	111.05
4	B	412	ATP	O2A-PA-O5'	-2.41	96.57	107.75
4	A	411	ATP	O3'-C3'-C4'	2.36	117.86	111.05
4	A	411	ATP	O2B-PB-O1B	2.12	122.73	112.24
4	B	412	ATP	O2B-PB-O1B	2.11	122.66	112.24

There are no chirality outliers.

All (4) torsion outliers are listed below:

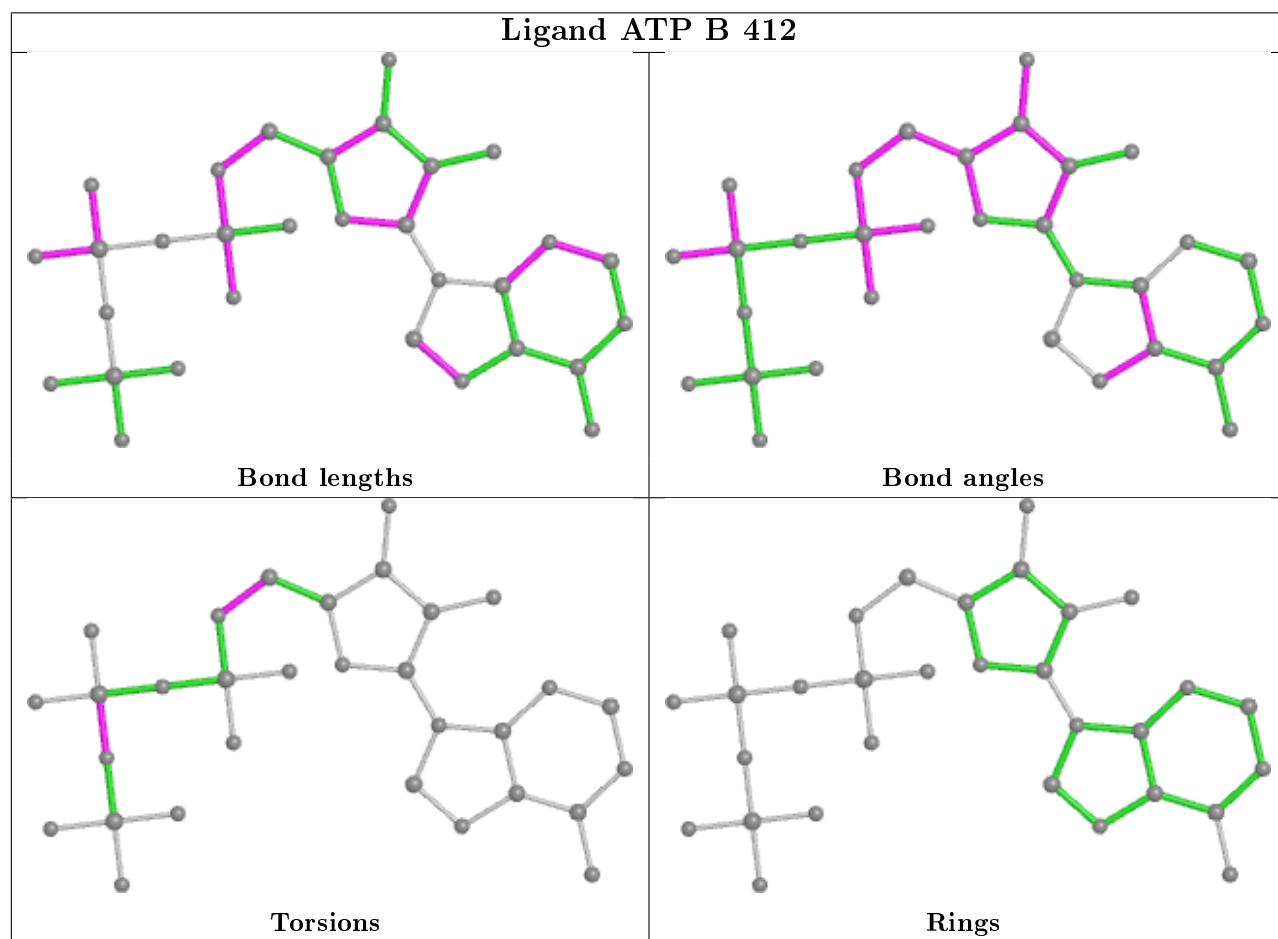
Mol	Chain	Res	Type	Atoms
4	B	412	ATP	PG-O3B-PB-O2B
4	A	411	ATP	PG-O3B-PB-O2B
4	B	412	ATP	C4'-C5'-O5'-PA
4	A	411	ATP	C4'-C5'-O5'-PA

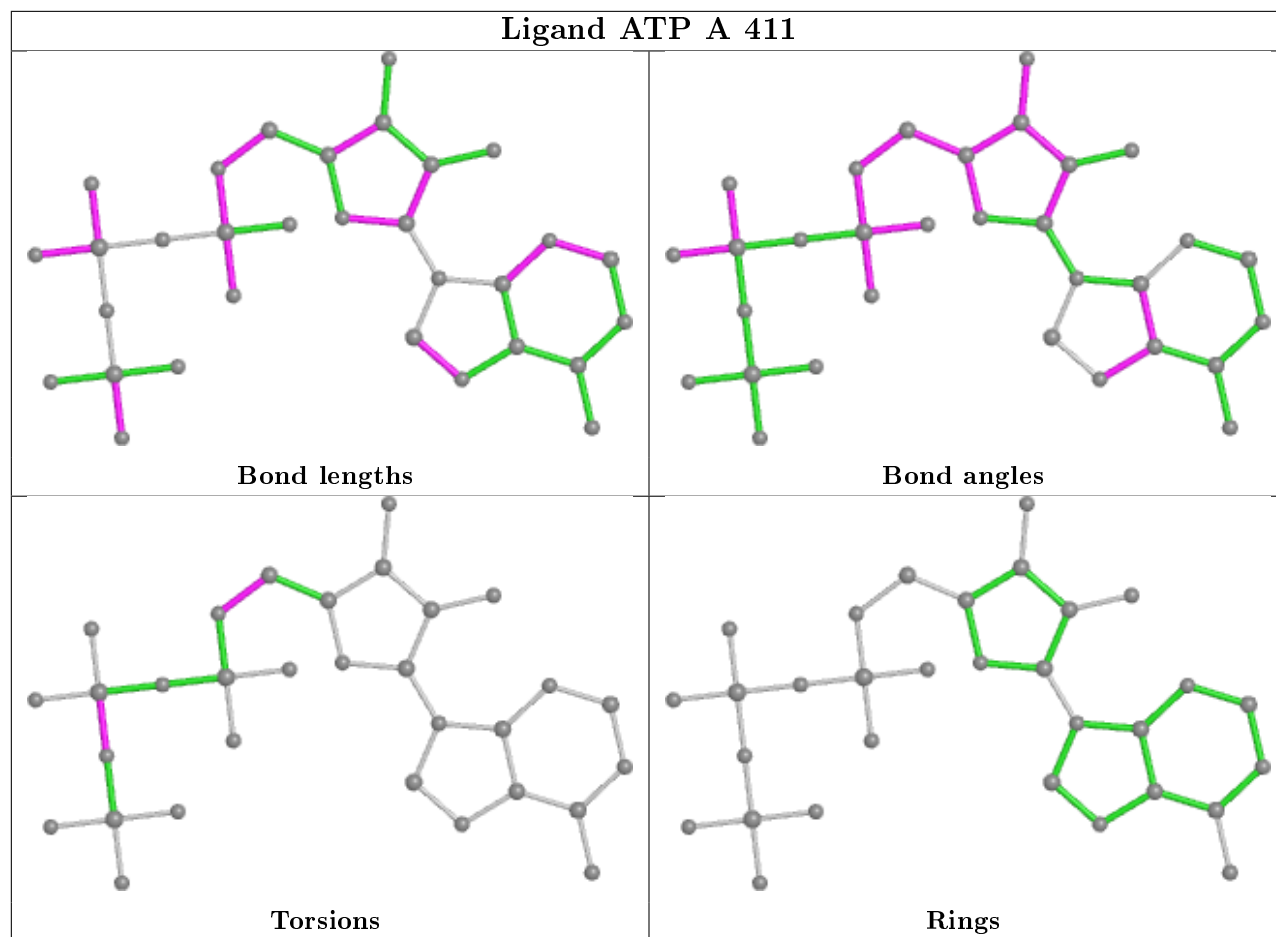
There are no ring outliers.

No monomer is involved in short contacts.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	181:SEP	C	182:PHE	N	2.30
1	A	181:SEP	C	182:PHE	N	1.85

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.