



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:32 PM UTC

PDB ID : 5T3O / pdb_00005t3o
Title : Crystal structure of the Phosphorybosylpyrophosphate synthetase II from *Thermus thermophilus*
Authors : Timofeev, V.I.; Sinitsyna, E.V.; Abramchik, Y.A.; Kostromina, M.A.; Esipov, R.S.; Kuranova, I.P.
Deposited on : 2016-08-26
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

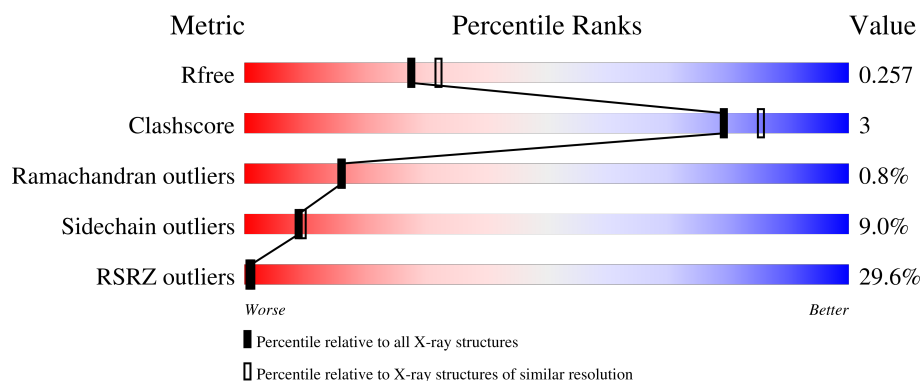
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	307	52% 86% 13% .
1	B	307	15% 87% 11% .
1	C	307	22% 87% 10% .

2 Entry composition [i](#)

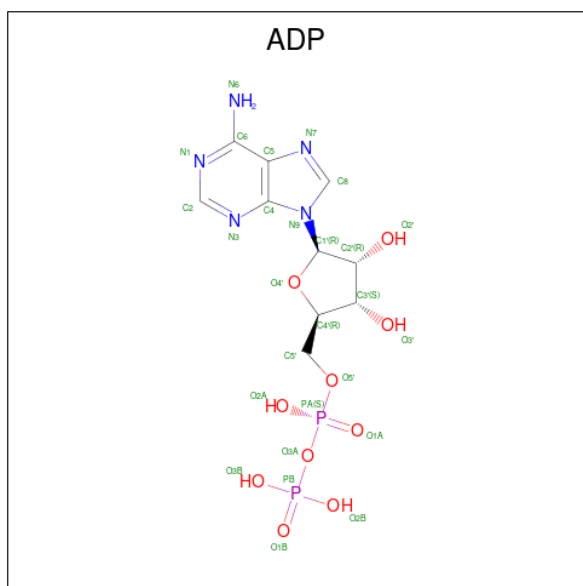
There are 4 unique types of molecules in this entry. The entry contains 7294 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ribose-phosphate pyrophosphokinase.

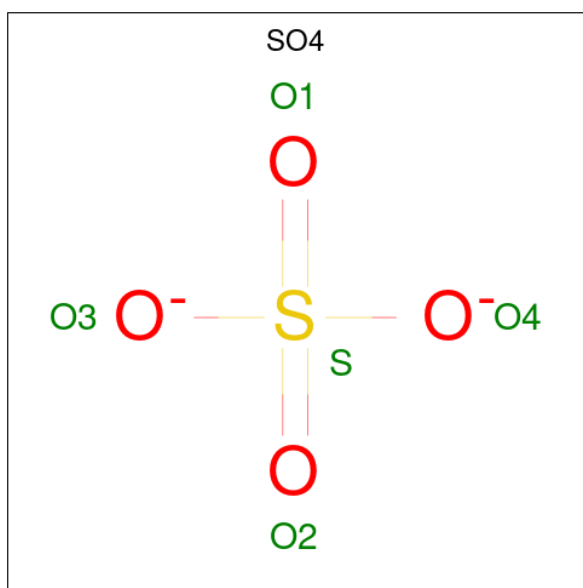
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2331	1483	405	436	7			
1	B	307	Total	C	N	O	S	0	0	0
			2331	1483	405	436	7			
1	C	307	Total	C	N	O	S	0	0	0
			2331	1483	405	436	7			

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

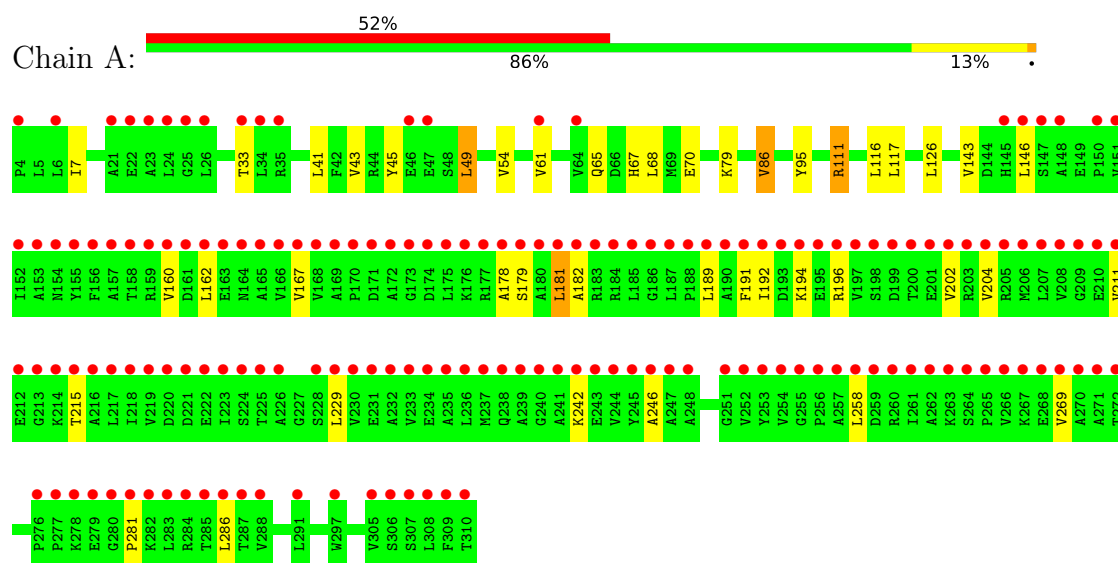
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	29	Total	O	0	0
			29	29		
4	B	102	Total	O	0	0
			102	102		
4	C	59	Total	O	0	0
			59	59		

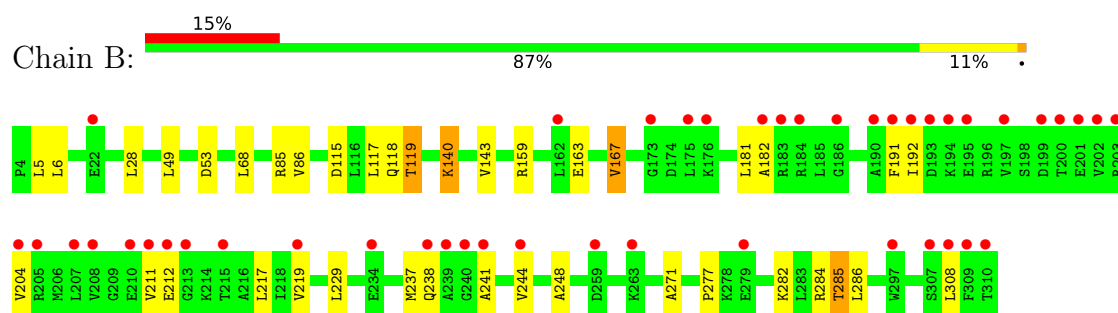
3 Residue-property plots

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.

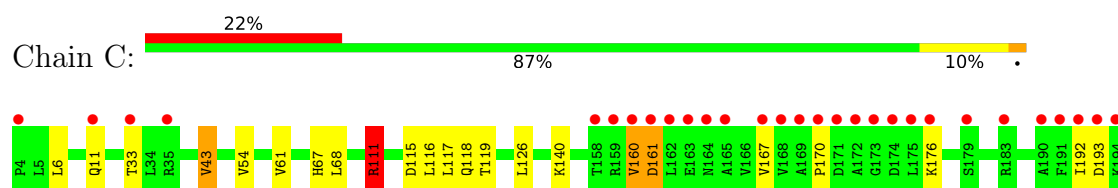
• Molecule 1: Ribose-phosphate pyrophosphokinase

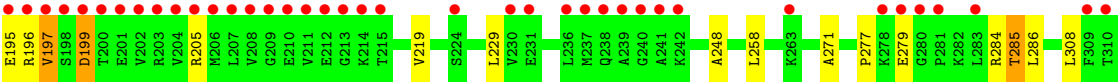


• Molecule 1: Ribose-phosphate pyrophosphokinase



• Molecule 1: Ribose-phosphate pyrophosphokinase





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	115.97Å 115.97Å 207.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	64.39 – 2.20 64.39 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (64.39-2.20) 99.9 (64.39-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.16 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.227 , 0.254 0.232 , 0.257	Depositor DCC
R_{free} test set	3548 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7294	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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: ADP, SO4

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	0.68	0/2374	0.91	3/3227 (0.1%)
1	B	0.65	0/2374	0.87	1/3227 (0.0%)
1	C	0.65	0/2374	0.85	3/3227 (0.1%)
All	All	0.66	0/7122	0.88	7/9681 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	181	LEU	N-CA-C	9.25	121.13	111.14
1	C	111	ARG	NE-CZ-NH2	6.28	124.85	119.20
1	C	160	VAL	N-CA-C	5.94	116.92	111.81
1	A	191	PHE	N-CA-C	5.47	117.16	108.79
1	C	111	ARG	NE-CZ-NH1	-5.46	116.04	121.50
1	A	111	ARG	NE-CZ-NH2	5.16	123.84	119.20
1	B	191	PHE	N-CA-C	5.11	116.61	108.79

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	2331	0	2387	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2331	0	2387	16	0
1	C	2331	0	2387	11	0
2	A	27	0	12	0	0
2	B	27	0	12	0	0
2	C	27	0	12	0	0
3	A	10	0	0	0	0
3	B	10	0	0	0	0
3	C	10	0	0	0	0
4	A	29	0	0	0	0
4	B	102	0	0	0	0
4	C	59	0	0	0	0
All	All	7294	0	7197	39	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 3.

All (39) 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:167:VAL:HG11	1:A:182:ALA:HB2	1.76	0.67
1:B:181:LEU:HD22	1:B:219:VAL:HG11	1.79	0.63
1:B:237:MET:HE3	1:B:244:VAL:HG23	1.82	0.61
1:A:65:GLN:NE2	1:A:95:TYR:OH	2.33	0.60
1:A:181:LEU:HB3	1:A:182:ALA:HB3	1.87	0.57
1:B:192:ILE:HG23	1:B:204:VAL:HG23	1.88	0.56
1:C:33:THR:HG22	1:C:43:VAL:HG22	1.86	0.56
1:B:237:MET:HA	1:B:237:MET:HE2	1.88	0.55
1:B:181:LEU:CD2	1:B:219:VAL:HG11	2.37	0.54
1:B:277:PRO:HB3	1:B:285:THR:HG21	1.90	0.53
1:B:53:ASP:OD1	1:B:85:ARG:HD2	2.11	0.51
1:A:33:THR:HG21	1:A:70:GLU:OE2	2.11	0.49
1:A:246:ALA:HB3	1:A:269:VAL:HG12	1.93	0.48
1:C:111:ARG:HD2	1:C:115:ASP:OD2	2.14	0.48
1:A:160:VAL:HG12	1:A:162:LEU:HD13	1.96	0.48
1:C:160:VAL:O	1:C:161:ASP:HB3	2.15	0.47
1:B:115:ASP:O	1:B:119:THR:HG23	2.13	0.47
1:A:33:THR:HG22	1:A:43:VAL:HG22	1.97	0.47
1:C:118:GLN:HE22	1:C:140:LYS:H	1.63	0.47
1:A:179:SER:C	1:A:182:ALA:O	2.59	0.46
1:C:61:VAL:O	1:C:67:HIS:HD2	1.99	0.46
1:C:196:ARG:O	1:C:197:VAL:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:GLN:HE22	1:B:140:LYS:H	1.64	0.45
1:A:79:LYS:HE3	1:A:86:VAL:HG13	1.99	0.44
1:C:11:GLN:NE2	1:C:33:THR:OG1	2.49	0.44
1:A:178:ALA:O	1:A:182:ALA:HB1	2.18	0.44
1:B:237:MET:HE3	1:B:244:VAL:CG2	2.49	0.43
1:B:167:VAL:HG13	1:B:182:ALA:HB2	2.00	0.43
1:A:61:VAL:O	1:A:67:HIS:HD2	2.02	0.43
1:C:277:PRO:CB	1:C:285:THR:HG21	2.49	0.42
1:B:277:PRO:CB	1:B:285:THR:HG21	2.49	0.42
1:C:193:ASP:O	1:C:205:ARG:NE	2.53	0.42
1:B:271:ALA:O	1:B:285:THR:HA	2.21	0.41
1:B:167:VAL:CG1	1:B:182:ALA:HB2	2.51	0.41
1:B:248:ALA:O	1:B:271:ALA:HA	2.20	0.41
1:C:248:ALA:O	1:C:271:ALA:HA	2.21	0.41
1:B:237:MET:HE2	1:B:241:ALA:HB3	2.03	0.41
1:C:160:VAL:O	1:C:161:ASP:CB	2.68	0.40
1:A:45:TYR:CG	1:A:49:LEU:HD11	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	305/307 (99%)	277 (91%)	26 (8%)	2 (1%)	18	19
1	B	305/307 (99%)	293 (96%)	11 (4%)	1 (0%)	36	42
1	C	305/307 (99%)	289 (95%)	12 (4%)	4 (1%)	9	8
All	All	915/921 (99%)	859 (94%)	49 (5%)	7 (1%)	16	16

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	204	VAL
1	C	197	VAL
1	B	212	GLU
1	C	199	ASP
1	C	161	ASP
1	A	281	PRO
1	C	170	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	247/247 (100%)	224 (91%)	23 (9%)	8	9
1	B	247/247 (100%)	225 (91%)	22 (9%)	9	10
1	C	247/247 (100%)	225 (91%)	22 (9%)	9	10
All	All	741/741 (100%)	674 (91%)	67 (9%)	9	9

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ILE
1	A	41	LEU
1	A	49	LEU
1	A	54	VAL
1	A	68	LEU
1	A	86	VAL
1	A	111	ARG
1	A	116	LEU
1	A	117	LEU
1	A	126	LEU
1	A	143	VAL
1	A	146	LEU
1	A	189	LEU
1	A	192	ILE
1	A	194	LYS
1	A	196	ARG

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Mol	Chain	Res	Type
1	A	202	VAL
1	A	211	VAL
1	A	215	THR
1	A	229	LEU
1	A	242	LYS
1	A	258	LEU
1	A	286	LEU
1	B	5	LEU
1	B	6	LEU
1	B	28	LEU
1	B	49	LEU
1	B	68	LEU
1	B	86	VAL
1	B	117	LEU
1	B	119	THR
1	B	140	LYS
1	B	143	VAL
1	B	159	ARG
1	B	163	GLU
1	B	167	VAL
1	B	211	VAL
1	B	217	LEU
1	B	229	LEU
1	B	238	GLN
1	B	282	LYS
1	B	284	ARG
1	B	285	THR
1	B	286	LEU
1	B	308	LEU
1	C	6	LEU
1	C	43	VAL
1	C	54	VAL
1	C	68	LEU
1	C	111	ARG
1	C	116	LEU
1	C	117	LEU
1	C	119	THR
1	C	126	LEU
1	C	167	VAL
1	C	176	LYS
1	C	192	ILE
1	C	195	GLU

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Mol	Chain	Res	Type
1	C	199	ASP
1	C	219	VAL
1	C	229	LEU
1	C	258	LEU
1	C	279	GLU
1	C	284	ARG
1	C	285	THR
1	C	286	LEU
1	C	308	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	65	GLN
1	A	164	ASN
1	B	118	GLN
1	B	136	HIS
1	B	238	GLN
1	B	300	HIS
1	C	11	GLN
1	C	67	HIS
1	C	118	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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	$\# Z > 2$
3	SO4	A	403	-	4,4,4	0.43	0	6,6,6	0.29	0
3	SO4	B	403	-	4,4,4	0.44	0	6,6,6	0.27	0
3	SO4	C	403	-	4,4,4	0.44	0	6,6,6	0.28	0
3	SO4	C	402	-	4,4,4	0.36	0	6,6,6	0.53	0
2	ADP	A	401	-	28,29,29	1.38	4 (14%)	43,45,45	1.85	9 (20%)
2	ADP	B	401	-	28,29,29	1.41	5 (17%)	43,45,45	1.87	9 (20%)
3	SO4	B	402	-	4,4,4	0.40	0	6,6,6	0.27	0
3	SO4	A	402	-	4,4,4	0.40	0	6,6,6	0.62	0
2	ADP	C	401	-	28,29,29	1.43	5 (17%)	43,45,45	1.89	8 (18%)

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	ADP	A	401	-	-	5/16/32/32	0/3/3/3
2	ADP	B	401	-	-	7/16/32/32	0/3/3/3
2	ADP	C	401	-	-	5/16/32/32	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	ADP	C5-C4	4.63	1.47	1.39
2	C	401	ADP	C5-C4	4.49	1.47	1.39
2	B	401	ADP	C5-C4	4.37	1.46	1.39
2	B	401	ADP	C5-C6	2.73	1.48	1.41
2	C	401	ADP	C5-N7	-2.71	1.34	1.39
2	C	401	ADP	C5-C6	2.60	1.48	1.41
2	C	401	ADP	PA-O3A	2.57	1.62	1.59
2	A	401	ADP	C5-C6	2.55	1.48	1.41
2	B	401	ADP	C5-N7	-2.31	1.34	1.39
2	A	401	ADP	C5-N7	-2.28	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	ADP	PA-O3A	2.26	1.61	1.59
2	B	401	ADP	C8-N7	2.09	1.35	1.31
2	A	401	ADP	C8-N7	2.08	1.35	1.31
2	C	401	ADP	C8-N7	2.04	1.35	1.31

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	ADP	C5-C4-N3	-6.13	118.27	126.72
2	A	401	ADP	C5-C4-N3	-6.02	118.43	126.72
2	B	401	ADP	C5-C4-N3	-6.01	118.44	126.72
2	B	401	ADP	N3-C4-N9	5.21	136.02	127.17
2	C	401	ADP	N3-C4-N9	5.02	135.71	127.17
2	A	401	ADP	N3-C4-N9	4.92	135.54	127.17
2	A	401	ADP	C2-N3-C4	4.14	121.94	111.83
2	B	401	ADP	C2-N3-C4	4.12	121.90	111.83
2	C	401	ADP	C2-N3-C4	4.06	121.74	111.83
2	A	401	ADP	N3-C2-N1	-3.86	122.75	128.58
2	C	401	ADP	N3-C2-N1	-3.72	122.95	128.58
2	B	401	ADP	N3-C2-N1	-3.71	122.97	128.58
2	C	401	ADP	C4-C5-N7	-3.03	107.11	110.58
2	B	401	ADP	C4-N9-C8	2.97	108.86	105.74
2	A	401	ADP	C4-C5-N7	-2.96	107.19	110.58
2	C	401	ADP	C5-N7-C8	2.64	107.61	103.45
2	B	401	ADP	C4-C5-N7	-2.57	107.64	110.58
2	A	401	ADP	C5-N7-C8	2.53	107.43	103.45
2	A	401	ADP	C4-N9-C8	2.53	108.39	105.74
2	C	401	ADP	C4-N9-C8	2.52	108.38	105.74
2	B	401	ADP	C5-N7-C8	2.45	107.30	103.45
2	B	401	ADP	N9-C8-N7	-2.30	110.68	113.94
2	C	401	ADP	N9-C8-N7	-2.16	110.87	113.94
2	B	401	ADP	C5-C6-N6	-2.16	117.95	123.29
2	A	401	ADP	N9-C8-N7	-2.10	110.95	113.94
2	A	401	ADP	C6-C5-N7	2.03	136.01	132.09

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	ADP	C5'-O5'-PA-O2A
2	B	401	ADP	PA-O3A-PB-O2B
2	B	401	ADP	C5'-O5'-PA-O2A

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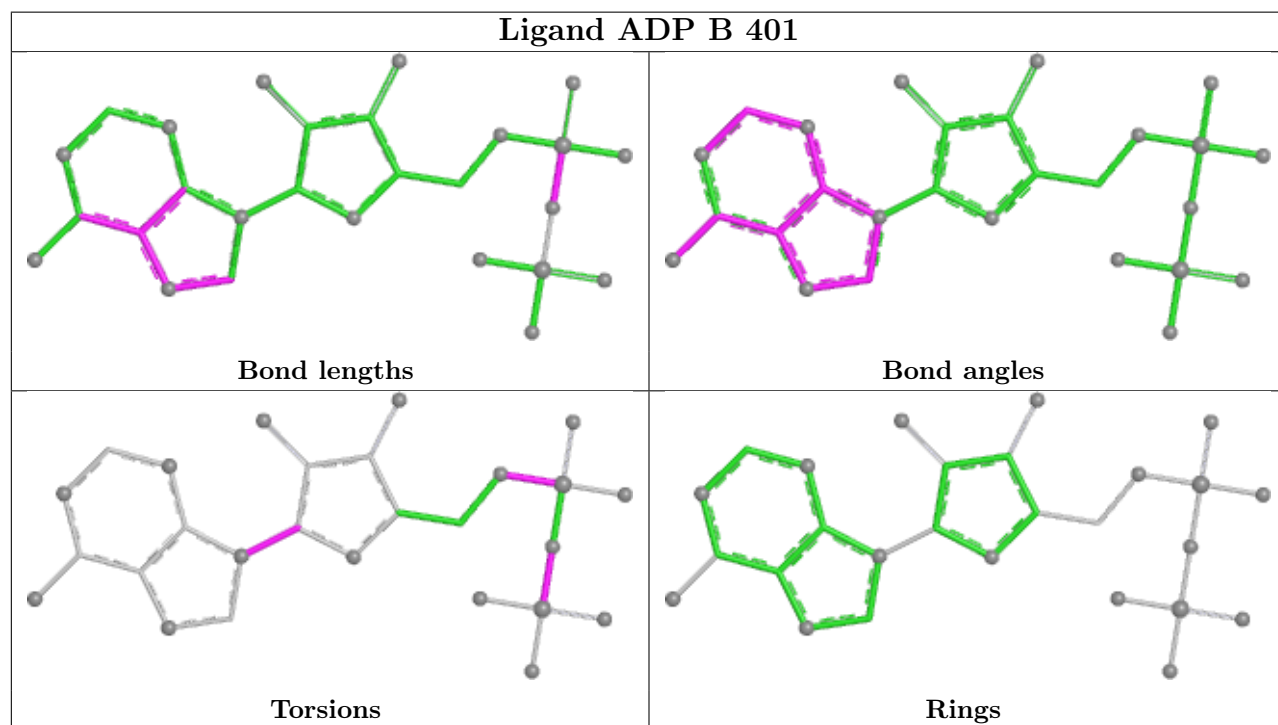
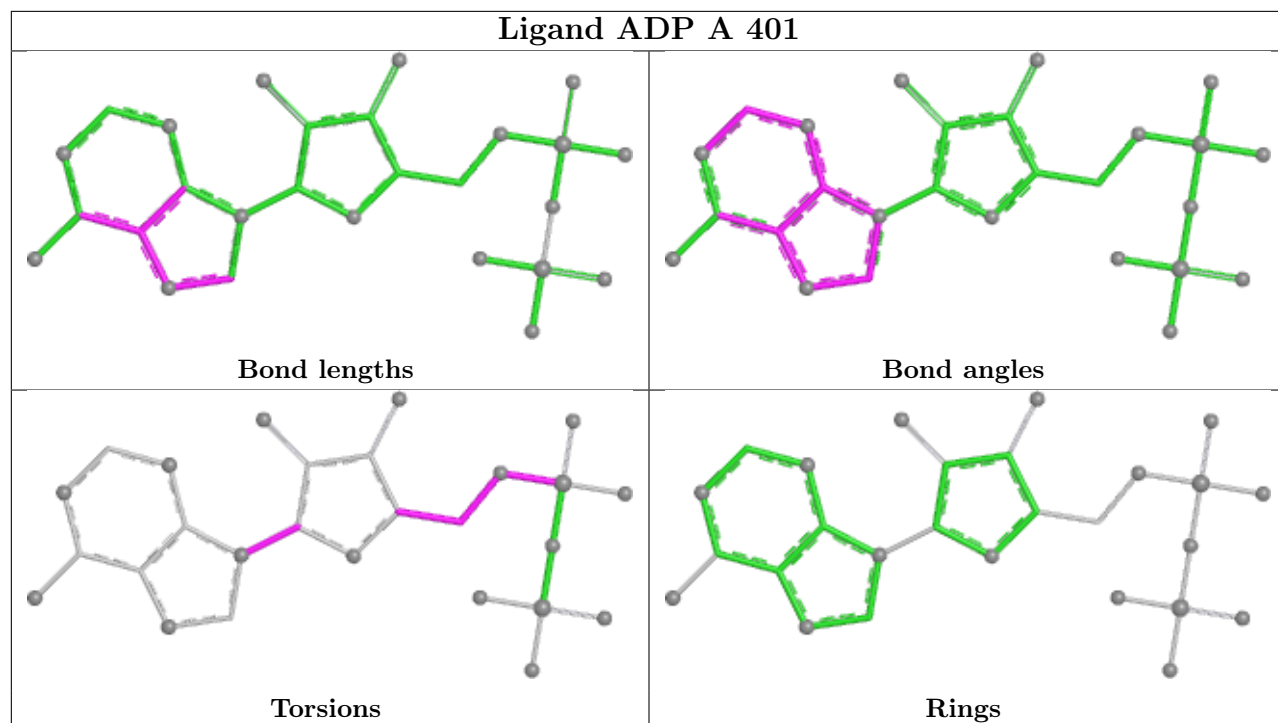
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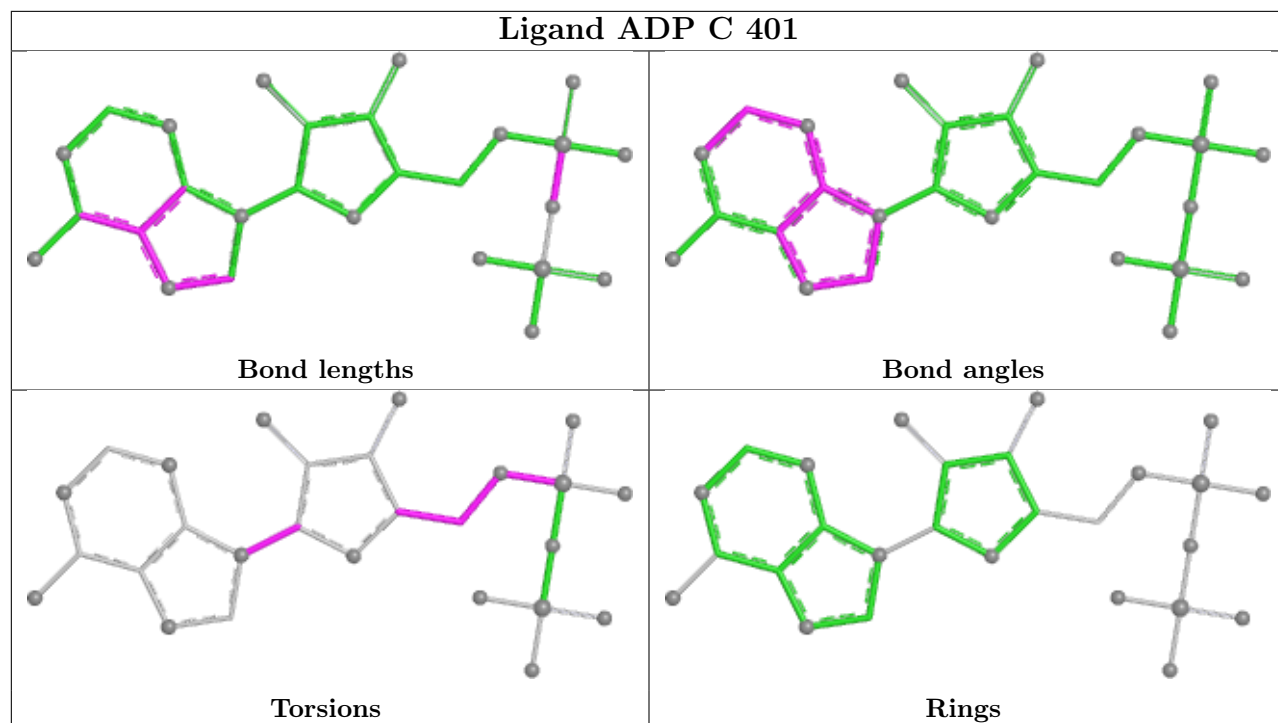
Mol	Chain	Res	Type	Atoms
2	B	401	ADP	PA-O3A-PB-O3B
2	A	401	ADP	C2'-C1'-N9-C8
2	B	401	ADP	C2'-C1'-N9-C8
2	C	401	ADP	C2'-C1'-N9-C8
2	A	401	ADP	C3'-C4'-C5'-O5'
2	B	401	ADP	C5'-O5'-PA-O3A
2	C	401	ADP	C5'-O5'-PA-O1A
2	C	401	ADP	C4'-C5'-O5'-PA
2	C	401	ADP	C3'-C4'-C5'-O5'
2	A	401	ADP	C4'-C5'-O5'-PA
2	A	401	ADP	O4'-C1'-N9-C8
2	B	401	ADP	PA-O3A-PB-O1B
2	B	401	ADP	O4'-C1'-N9-C8
2	C	401	ADP	O4'-C1'-N9-C8

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](#)

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	307/307 (100%)	2.44	160 (52%) 0 0	22, 52, 139, 170	0
1	B	307/307 (100%)	0.57	45 (14%) 6 4	12, 29, 65, 93	0
1	C	307/307 (100%)	1.06	68 (22%) 2 1	15, 33, 97, 167	0
All	All	921/921 (100%)	1.36	273 (29%) 1 1	12, 37, 113, 170	0

All (273) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	VAL	11.9
1	C	204	VAL	10.5
1	A	204	VAL	9.7
1	A	309	PHE	9.5
1	C	202	VAL	9.0
1	A	4	PRO	8.2
1	A	193	ASP	7.6
1	A	202	VAL	7.6
1	A	207	LEU	7.5
1	A	191	PHE	7.2
1	A	283	LEU	7.0
1	A	258	LEU	6.9
1	A	239	ALA	6.8
1	A	310	THR	6.8
1	A	198	SER	6.7
1	A	189	LEU	6.6
1	C	194	LYS	6.4
1	A	215	THR	6.2
1	A	308	LEU	6.2
1	A	216	ALA	5.9
1	C	197	VAL	5.9
1	A	172	ALA	5.9
1	C	195	GLU	5.9

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Mol	Chain	Res	Type	RSRZ
1	A	206	MET	5.8
1	A	173	GLY	5.7
1	C	278	LYS	5.7
1	A	281	PRO	5.7
1	A	208	VAL	5.6
1	A	162	LEU	5.6
1	B	310	THR	5.4
1	C	206	MET	5.4
1	A	181	LEU	5.3
1	C	171	ASP	5.3
1	A	236	LEU	5.3
1	A	168	VAL	5.2
1	A	190	ALA	5.2
1	A	200	THR	5.2
1	A	245	TYR	5.2
1	C	200	THR	5.1
1	C	170	PRO	5.1
1	A	160	VAL	5.1
1	A	165	ALA	5.0
1	A	244	VAL	4.9
1	A	176	LYS	4.9
1	A	278	LYS	4.9
1	C	310	THR	4.9
1	A	182	ALA	4.9
1	C	207	LEU	4.8
1	A	196	ARG	4.8
1	C	210	GLU	4.8
1	A	188	PRO	4.7
1	A	171	ASP	4.7
1	A	170	PRO	4.7
1	C	199	ASP	4.7
1	A	263	LYS	4.6
1	A	266	VAL	4.6
1	A	282	LYS	4.6
1	C	205	ARG	4.6
1	C	198	SER	4.6
1	A	262	ALA	4.5
1	A	155	TYR	4.5
1	A	211	VAL	4.5
1	A	183	ARG	4.5
1	A	307	SER	4.5
1	C	158	THR	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	192	ILE	4.4
1	A	230	VAL	4.4
1	A	213	GLY	4.4
1	A	157	ALA	4.4
1	B	200	THR	4.4
1	A	199	ASP	4.4
1	B	309	PHE	4.3
1	A	166	VAL	4.3
1	C	172	ALA	4.3
1	A	261	ILE	4.3
1	A	195	GLU	4.2
1	A	218	ILE	4.2
1	A	178	ALA	4.2
1	A	187	LEU	4.2
1	A	269	VAL	4.1
1	B	211	VAL	4.1
1	C	211	VAL	4.1
1	C	169	ALA	4.0
1	C	192	ILE	4.0
1	A	219	VAL	4.0
1	A	175	LEU	4.0
1	A	246	ALA	4.0
1	A	223	ILE	4.0
1	B	308	LEU	4.0
1	C	213	GLY	4.0
1	C	196	ARG	3.9
1	C	203	ARG	3.9
1	A	229	LEU	3.9
1	C	208	VAL	3.9
1	A	163	GLU	3.9
1	A	167	VAL	3.9
1	A	201	GLU	3.9
1	A	33	THR	3.9
1	B	201	GLU	3.9
1	A	284	ARG	3.9
1	C	193	ASP	3.8
1	C	160	VAL	3.8
1	A	247	ALA	3.8
1	A	179	SER	3.8
1	C	159	ARG	3.8
1	A	240	GLY	3.8
1	A	217	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	213	GLY	3.8
1	A	161	ASP	3.7
1	A	232	ALA	3.7
1	C	279	GLU	3.7
1	A	156	PHE	3.7
1	A	257	ALA	3.7
1	A	242	LYS	3.7
1	C	168	VAL	3.7
1	A	164	ASN	3.7
1	A	177	ARG	3.7
1	A	264	SER	3.7
1	A	169	ALA	3.7
1	A	209	GLY	3.6
1	A	185	LEU	3.6
1	A	297	TRP	3.6
1	A	237	MET	3.6
1	A	238	GLN	3.6
1	A	253	TYR	3.5
1	A	152	ILE	3.5
1	A	214	LYS	3.5
1	B	279	GLU	3.5
1	C	174	ASP	3.5
1	A	241	ALA	3.5
1	A	174	ASP	3.5
1	A	150	PRO	3.5
1	A	158	THR	3.5
1	A	205	ARG	3.5
1	C	191	PHE	3.4
1	A	147	SER	3.4
1	B	212	GLU	3.4
1	C	176	LYS	3.4
1	A	279	GLU	3.4
1	A	194	LYS	3.4
1	A	277	PRO	3.3
1	C	309	PHE	3.3
1	A	233	VAL	3.3
1	C	240	GLY	3.3
1	B	210	GLU	3.3
1	B	190	ALA	3.3
1	B	204	VAL	3.3
1	A	146	LEU	3.3
1	B	234	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	209	GLY	3.2
1	C	230	VAL	3.2
1	A	267	LYS	3.2
1	A	280	GLY	3.2
1	A	234	GLU	3.1
1	A	151	VAL	3.1
1	A	265	PRO	3.1
1	B	238	GLN	3.1
1	A	286	LEU	3.1
1	C	161	ASP	3.1
1	A	64	VAL	3.1
1	B	202	VAL	3.1
1	A	148	ALA	3.1
1	A	235	ALA	3.1
1	A	270	ALA	3.1
1	A	61	VAL	3.1
1	C	212	GLU	3.0
1	A	285	THR	3.0
1	A	203	ARG	3.0
1	A	271	ALA	3.0
1	C	164	ASN	3.0
1	A	254	VAL	3.0
1	A	184	ARG	3.0
1	C	4	PRO	3.0
1	A	180	ALA	2.9
1	C	163	GLU	2.9
1	C	231	GLU	2.9
1	A	210	GLU	2.9
1	A	212	GLU	2.9
1	C	162	LEU	2.9
1	B	173	GLY	2.8
1	B	162	LEU	2.8
1	A	260	ARG	2.8
1	A	24	LEU	2.8
1	C	283	LEU	2.8
1	A	231	GLU	2.8
1	A	153	ALA	2.8
1	A	225	THR	2.8
1	B	197	VAL	2.8
1	A	256	PRO	2.7
1	B	215	THR	2.7
1	B	263	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	167	VAL	2.7
1	A	228	SER	2.7
1	C	175	LEU	2.7
1	B	199	ASP	2.7
1	A	47	GLU	2.7
1	B	297	TRP	2.7
1	A	46	GLU	2.6
1	A	268	GLU	2.6
1	A	34	LEU	2.6
1	B	191	PHE	2.6
1	B	186	GLY	2.6
1	B	219	VAL	2.6
1	C	237	MET	2.6
1	B	192	ILE	2.6
1	A	259	ASP	2.6
1	A	186	GLY	2.6
1	A	224	SER	2.6
1	C	201	GLU	2.5
1	C	239	ALA	2.5
1	C	35	ARG	2.5
1	A	226	ALA	2.5
1	B	205	ARG	2.5
1	C	183	ARG	2.5
1	A	26	LEU	2.5
1	A	21	ALA	2.5
1	B	203	ARG	2.5
1	A	23	ALA	2.5
1	C	280	GLY	2.5
1	C	33	THR	2.4
1	A	145	HIS	2.4
1	A	22	GLU	2.4
1	B	22	GLU	2.4
1	B	175	LEU	2.4
1	A	276	PRO	2.4
1	A	248	ALA	2.4
1	B	208	VAL	2.4
1	C	238	GLN	2.4
1	A	272	THR	2.3
1	A	287	THR	2.3
1	B	183	ARG	2.3
1	A	6	LEU	2.3
1	A	243	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	239	ALA	2.3
1	A	252	VAL	2.3
1	B	207	LEU	2.3
1	C	236	LEU	2.3
1	A	220	ASP	2.3
1	A	25	GLY	2.3
1	C	173	GLY	2.3
1	B	307	SER	2.3
1	A	291	LEU	2.2
1	A	305	VAL	2.3
1	C	281	PRO	2.2
1	B	240	GLY	2.2
1	A	306	SER	2.2
1	B	244	VAL	2.2
1	C	241	ALA	2.2
1	C	242	LYS	2.2
1	C	224	SER	2.2
1	A	154	ASN	2.2
1	B	176	LYS	2.2
1	B	241	ALA	2.2
1	A	288	VAL	2.2
1	B	195	GLU	2.2
1	C	165	ALA	2.2
1	C	179	SER	2.2
1	A	222	GLU	2.1
1	A	35	ARG	2.1
1	C	263	LYS	2.1
1	B	193	ASP	2.1
1	B	259	ASP	2.1
1	C	11	GLN	2.1
1	A	255	GLY	2.1
1	B	184	ARG	2.1
1	A	221	ASP	2.1
1	C	215	THR	2.1
1	A	251	GLY	2.1
1	A	159	ARG	2.1
1	B	182	ALA	2.0
1	C	190	ALA	2.0
1	B	194	LYS	2.0
1	C	214	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

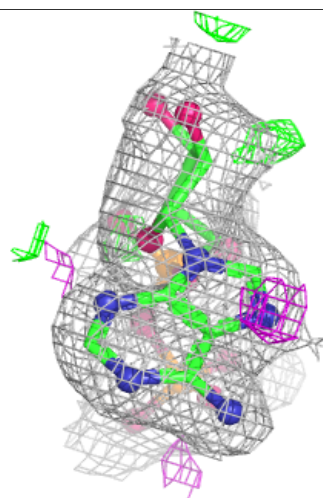
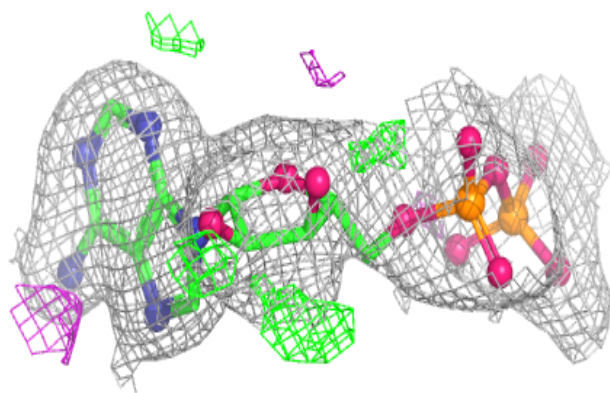
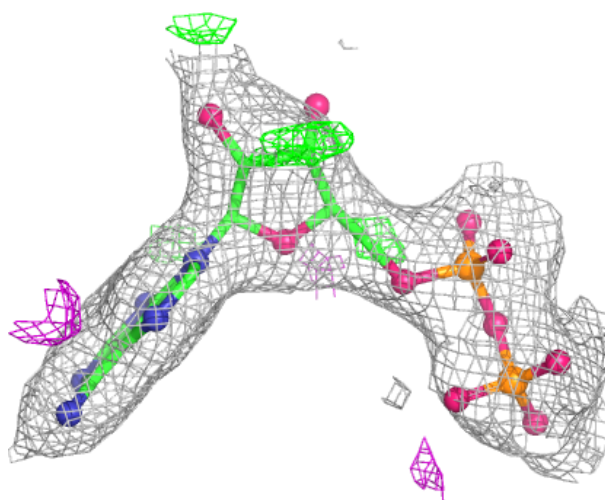
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	A	403	5/5	0.82	0.16	58,58,60,65	0
2	ADP	C	401	27/27	0.86	0.13	36,53,79,81	0
2	ADP	A	401	27/27	0.87	0.13	40,54,88,89	0
2	ADP	B	401	27/27	0.89	0.11	24,35,72,75	0
3	SO4	A	402	5/5	0.94	0.10	32,33,36,40	0
3	SO4	C	403	5/5	0.94	0.10	39,39,41,41	0
3	SO4	B	403	5/5	0.97	0.07	31,31,34,35	0
3	SO4	B	402	5/5	0.97	0.07	37,38,39,39	0
3	SO4	C	402	5/5	0.99	0.04	21,21,22,22	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.

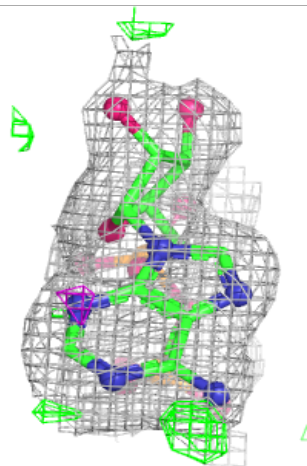
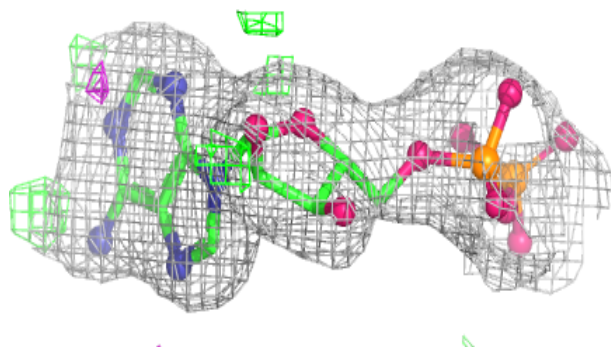
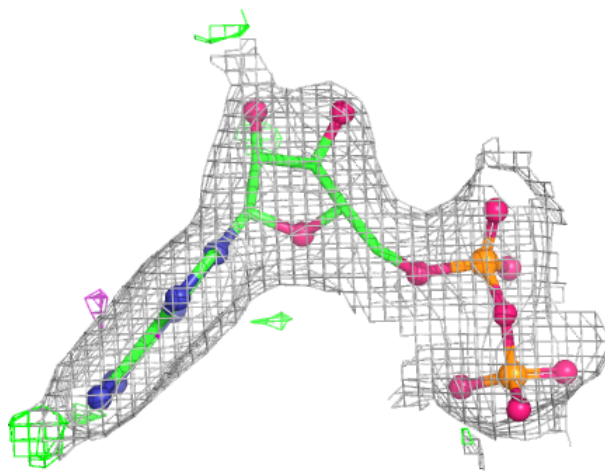
Electron density around ADP C 401:

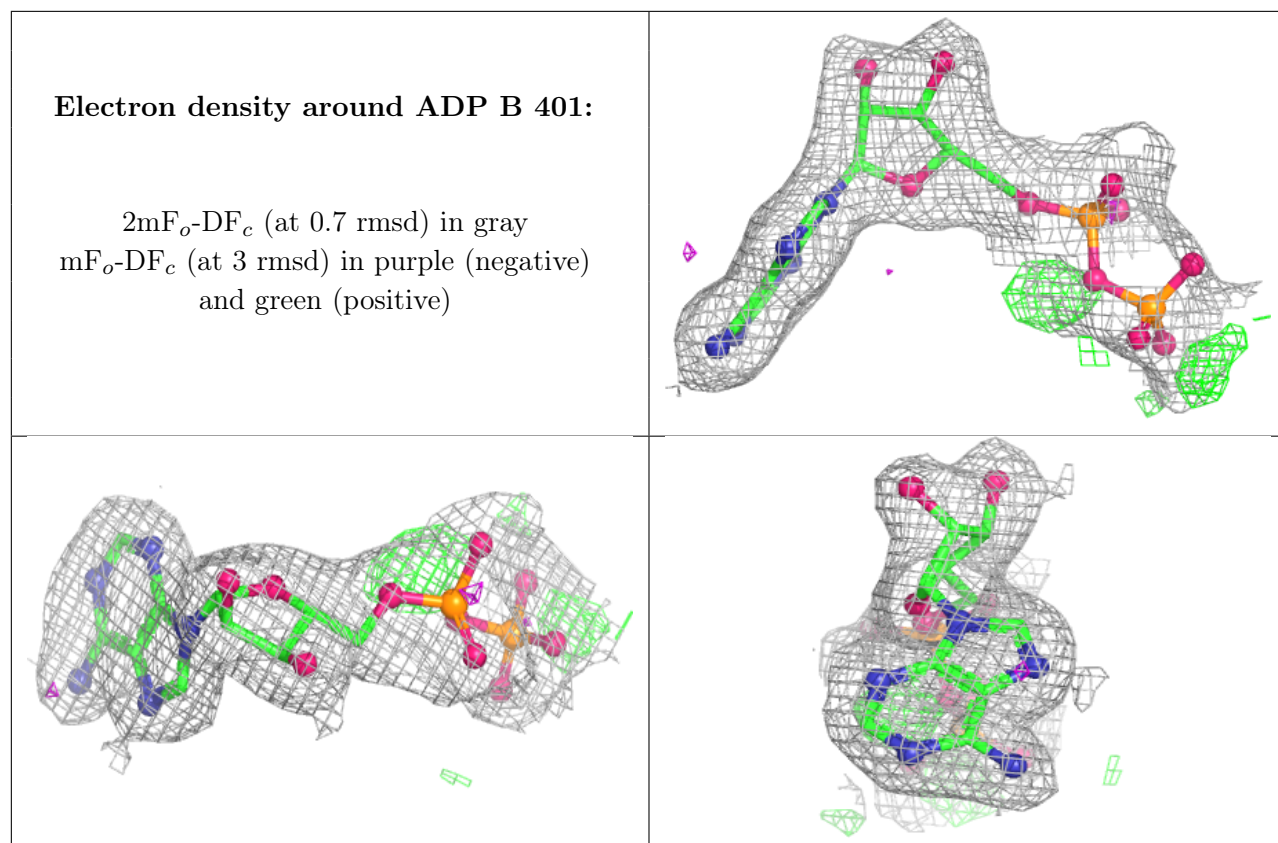
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ADP A 401:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.