



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:02 PM UTC

PDB ID : 1G41 / pdb_00001g41
Title : CRYSTAL STRUCTURE OF HSLU HAEMOPHILUS INFLUENZAE
Authors : Trame, C.B.; McKay, D.B.
Deposited on : 2000-10-25
Resolution : 2.30 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

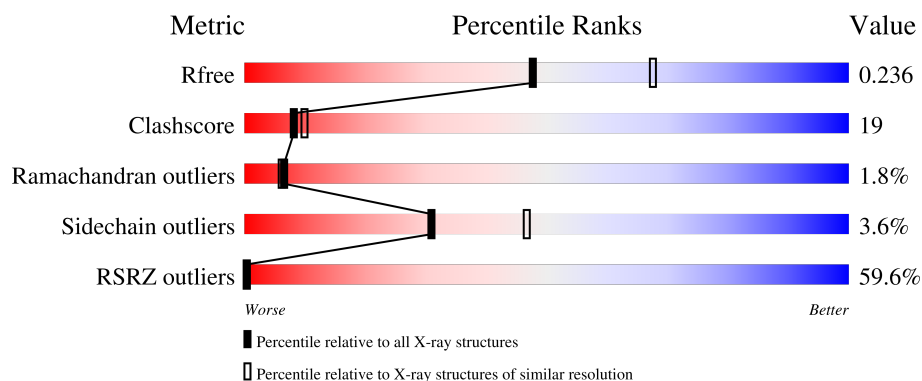
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	444	45% 48%23%•25%

2 Entry composition [i](#)

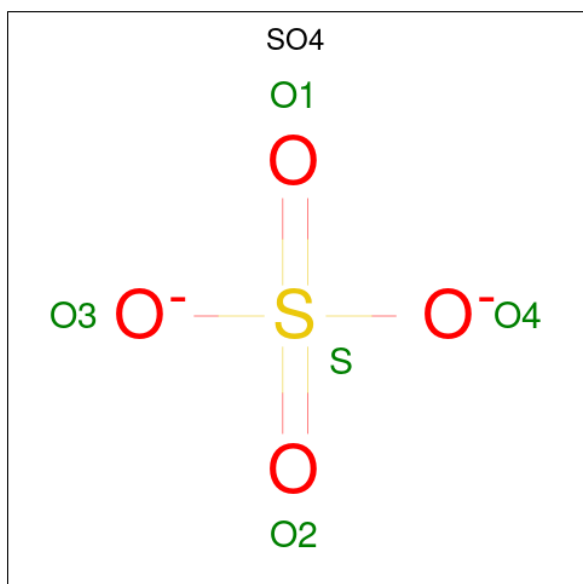
There are 4 unique types of molecules in this entry. The entry contains 2726 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HEAT SHOCK PROTEIN HSLU.

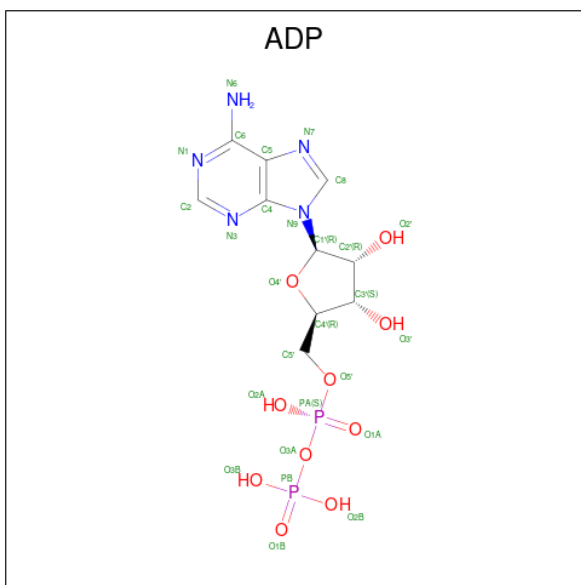
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	334	2598	1626	463	499	10	0	0	0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	96	Total O 96 96	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 6 2 2	Depositor
Cell constants a, b, c, α , β , γ	110.62Å 110.62Å 335.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.40 – 2.30 35.40 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.9 (35.40-2.30) 89.9 (35.40-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	5.80	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.67 (at 2.29Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.264 , 0.276 0.208 , 0.236	Depositor DCC
R_{free} test set	1026 reflections (2.06%)	wwPDB-VP
Wilson B-factor (Å ²)	29.4	Xtriage
Anisotropy	0.966	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.9	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	0.89	EDS
Total number of atoms	2726	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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: 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	0.43	0/2627	0.92	7/3541 (0.2%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	271	ALA	N-CA-C	-7.02	105.34	114.04
1	A	327	LEU	CA-C-N	6.67	126.45	119.05
1	A	327	LEU	C-N-CA	6.67	126.45	119.05
1	A	273	VAL	N-CA-C	-6.38	106.33	111.81
1	A	433	VAL	N-CA-C	6.33	117.01	110.36
1	A	301	ASP	N-CA-C	5.75	118.29	111.33
1	A	443	ILE	N-CA-C	5.33	116.80	111.00

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	2598	0	2666	103	0
2	A	5	0	0	0	0
3	A	27	0	12	4	0
4	A	96	0	0	9	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2726	0	2678	103	1

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 (103) 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:112:ARG:HH11	1:A:112:ARG:HB3	1.27	1.00
1:A:236:ASN:HB3	1:A:239:GLU:HB2	1.50	0.92
1:A:415:ASN:HD22	1:A:416:GLY:N	1.77	0.82
1:A:64:THR:HB	3:A:450:ADP:O2A	1.82	0.79
1:A:108:MET:HE2	1:A:244:ALA:HB2	1.65	0.79
1:A:54:LEU:HD21	4:A:536:HOH:O	1.82	0.78
1:A:279:GLN:HE22	1:A:320:ILE:H	1.28	0.78
1:A:116:ILE:HD12	1:A:117:ALA:N	1.99	0.77
1:A:112:ARG:HB3	1:A:112:ARG:NH1	2.02	0.74
1:A:38:MET:HA	1:A:38:MET:HE2	1.69	0.74
1:A:108:MET:HE1	1:A:240:LEU:HB3	1.68	0.74
1:A:269:SER:H	1:A:272:ASP:HB2	1.54	0.72
1:A:316:PRO:HG3	4:A:536:HOH:O	1.88	0.72
1:A:63:LYS:HG3	4:A:518:HOH:O	1.89	0.72
1:A:436:ASN:C	1:A:436:ASN:HD22	1.98	0.71
1:A:111:VAL:O	1:A:115:GLU:HG2	1.91	0.70
1:A:232:ALA:HA	1:A:235:ILE:HD13	1.75	0.68
1:A:415:ASN:HD22	1:A:415:ASN:C	2.02	0.67
1:A:279:GLN:NE2	1:A:320:ILE:H	1.94	0.66
1:A:118:LYS:O	1:A:119:ASN:HB2	1.96	0.64
1:A:34:ARG:O	1:A:38:MET:HG2	1.98	0.64
1:A:436:ASN:HD21	1:A:438:ASP:HB2	1.63	0.63
1:A:37:ARG:NH1	1:A:38:MET:HE3	2.12	0.63
1:A:16:HIS:HB2	1:A:17:ILE:HD12	1.80	0.62
1:A:290:THR:HG22	1:A:297:MET:HE3	1.81	0.62
1:A:233:LYS:HD2	1:A:233:LYS:N	2.14	0.62
1:A:268:TYR:HA	1:A:272:ASP:OD2	2.00	0.62
1:A:82:GLU:O	1:A:85:LYS:HB3	2.01	0.61
1:A:59:THR:HG23	4:A:520:HOH:O	1.99	0.61
1:A:313:VAL:HG23	1:A:314:ALA:N	2.16	0.61
1:A:235:ILE:N	1:A:235:ILE:HD12	2.17	0.60
1:A:107:ALA:O	1:A:111:VAL:HG23	2.02	0.60
1:A:241:LYS:O	1:A:245:ILE:HG12	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:MET:O	1:A:112:ARG:HG3	2.04	0.57
1:A:236:ASN:HB3	1:A:239:GLU:CB	2.30	0.57
1:A:283:LEU:HB2	1:A:284:PRO:HD3	1.86	0.57
1:A:63:LYS:HD2	1:A:308:SER:OG	2.05	0.56
1:A:329:ILE:HD12	4:A:548:HOH:O	2.04	0.56
1:A:241:LYS:HD2	1:A:295:HIS:HA	1.86	0.56
1:A:112:ARG:HH11	1:A:112:ARG:CB	2.11	0.56
1:A:376:LYS:HG2	4:A:543:HOH:O	2.06	0.56
1:A:322:GLU:H	1:A:322:GLU:CD	2.14	0.55
1:A:357:LYS:HD2	4:A:500:HOH:O	2.05	0.55
1:A:430:LEU:O	1:A:433:VAL:HG23	2.05	0.55
1:A:118:LYS:HE3	1:A:118:LYS:C	2.33	0.54
1:A:257:ASP:C	1:A:258:GLU:HG2	2.33	0.54
1:A:313:VAL:HG23	1:A:314:ALA:H	1.71	0.54
1:A:436:ASN:C	1:A:436:ASN:ND2	2.65	0.53
1:A:271:ALA:O	1:A:275:ARG:HG3	2.09	0.53
1:A:27:VAL:HB	1:A:70:LEU:HD22	1.91	0.52
1:A:104:THR:HA	1:A:248:VAL:HG21	1.90	0.52
1:A:237:PRO:O	1:A:241:LYS:HG3	2.09	0.52
1:A:62:GLY:O	1:A:66:ILE:HG13	2.10	0.52
1:A:87:THR:HG22	1:A:278:VAL:HG21	1.92	0.52
1:A:65:GLU:HB2	3:A:450:ADP:O1A	2.12	0.50
1:A:279:GLN:HE22	1:A:320:ILE:N	2.04	0.49
1:A:394:ARG:NH1	3:A:450:ADP:O1B	2.46	0.49
1:A:436:ASN:ND2	1:A:438:ASP:H	2.11	0.49
1:A:82:GLU:N	1:A:82:GLU:OE1	2.46	0.48
1:A:17:ILE:HD12	1:A:17:ILE:N	2.29	0.47
1:A:436:ASN:ND2	1:A:438:ASP:HB2	2.30	0.46
1:A:345:LEU:HD13	1:A:396:LEU:HD13	1.97	0.46
1:A:110:LEU:O	1:A:114:GLN:HG3	2.15	0.46
1:A:239:GLU:O	1:A:243:LYS:HG3	2.16	0.46
1:A:105:ASP:OD1	1:A:294:LYS:HE2	2.15	0.45
1:A:340:ASP:O	1:A:344:ILE:HG13	2.16	0.45
1:A:363:GLU:HG3	1:A:412:SER:HA	1.99	0.45
1:A:245:ILE:HD12	1:A:298:VAL:HG22	1.99	0.45
1:A:230:GLU:O	1:A:230:GLU:HG2	2.15	0.45
1:A:118:LYS:O	1:A:118:LYS:HG3	2.17	0.44
1:A:227:ILE:HG12	1:A:227:ILE:O	2.18	0.44
1:A:294:LYS:HE3	1:A:295:HIS:NE2	2.33	0.44
1:A:52:ASN:HB2	1:A:326:ARG:O	2.17	0.44
1:A:37:ARG:NH1	1:A:38:MET:CE	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:LYS:HB3	1:A:266:GLY:H	1.47	0.43
1:A:387:LYS:NZ	1:A:435:GLU:O	2.51	0.43
1:A:5:THR:OG1	1:A:8:GLU:HG3	2.18	0.43
1:A:290:THR:CG2	1:A:297:MET:HE3	2.48	0.43
1:A:271:ALA:C	1:A:273:VAL:H	2.26	0.43
1:A:60:GLY:N	3:A:450:ADP:O3B	2.52	0.43
1:A:268:TYR:O	1:A:269:SER:HB3	2.19	0.43
1:A:56:ILE:HG12	4:A:536:HOH:O	2.18	0.42
1:A:300:THR:HA	1:A:303:ILE:HD12	2.01	0.42
1:A:284:PRO:O	1:A:289:SER:OG	2.35	0.42
1:A:80:LYS:HZ3	1:A:257:ASP:HB2	1.85	0.42
1:A:267:GLU:O	1:A:268:TYR:O	2.38	0.42
1:A:264:LYS:O	1:A:264:LYS:HG3	2.20	0.42
1:A:415:ASN:C	1:A:415:ASN:ND2	2.71	0.41
1:A:330:ARG:HH11	1:A:330:ARG:HG3	1.85	0.41
1:A:118:LYS:HE3	1:A:118:LYS:CA	2.50	0.41
1:A:327:LEU:N	1:A:328:PRO:CD	2.83	0.41
1:A:233:LYS:N	1:A:233:LYS:CD	2.83	0.41
1:A:271:ALA:C	1:A:273:VAL:N	2.77	0.41
1:A:236:ASN:O	1:A:239:GLU:N	2.54	0.41
1:A:116:ILE:HD12	1:A:116:ILE:C	2.45	0.41
1:A:30:ALA:HB2	4:A:548:HOH:O	2.20	0.41
1:A:356:TYR:O	1:A:360:MET:HG2	2.20	0.41
1:A:37:ARG:NH2	1:A:302:HIS:NE2	2.68	0.40
1:A:258:GLU:HB2	1:A:261:LYS:HD2	2.03	0.40
1:A:42:GLU:OE2	1:A:42:GLU:HA	2.22	0.40
1:A:79:ILE:CG2	1:A:254:VAL:HG22	2.51	0.40
1:A:81:VAL:HG11	1:A:86:PHE:CE1	2.57	0.40
1:A:268:TYR:O	1:A:269:SER:CB	2.69	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:458:HOH:O	4:A:458:HOH:O[4_665]	2.05	0.15

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	328/444 (74%)	312 (95%)	10 (3%)	6 (2%)	6 6

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	119	ASN
1	A	232	ALA
1	A	268	TYR
1	A	234	LEU
1	A	265	LYS
1	A	269	SER

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	280/373 (75%)	270 (96%)	10 (4%)	31 47

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	MET
1	A	69	ARG
1	A	101	ARG
1	A	108	MET
1	A	112	ARG

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Mol	Chain	Res	Type
1	A	118	LYS
1	A	345	LEU
1	A	359	LEU
1	A	386	GLU
1	A	436	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	16	HIS
1	A	114	GLN
1	A	236	ASN
1	A	279	GLN
1	A	415	ASN
1	A	420	ASN
1	A	436	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	ADP	A	450	-	28,29,29	1.52	5 (17%)	43,45,45	1.06	2 (4%)
2	SO4	A	600	-	4,4,4	0.43	0	6,6,6	0.09	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	A	450	-	-	2/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	450	ADP	PA-O3A	4.10	1.63	1.59
3	A	450	ADP	C1'-N9	3.31	1.55	1.46
3	A	450	ADP	C8-N9	-2.34	1.33	1.37
3	A	450	ADP	C8-N7	-2.19	1.27	1.31
3	A	450	ADP	C2'-C3'	2.16	1.59	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	450	ADP	C4'-O4'-C1'	2.19	114.31	109.47
3	A	450	ADP	C2'-C3'-C4'	2.03	106.54	102.61

There are no chirality outliers.

All (2) torsion outliers are listed below:

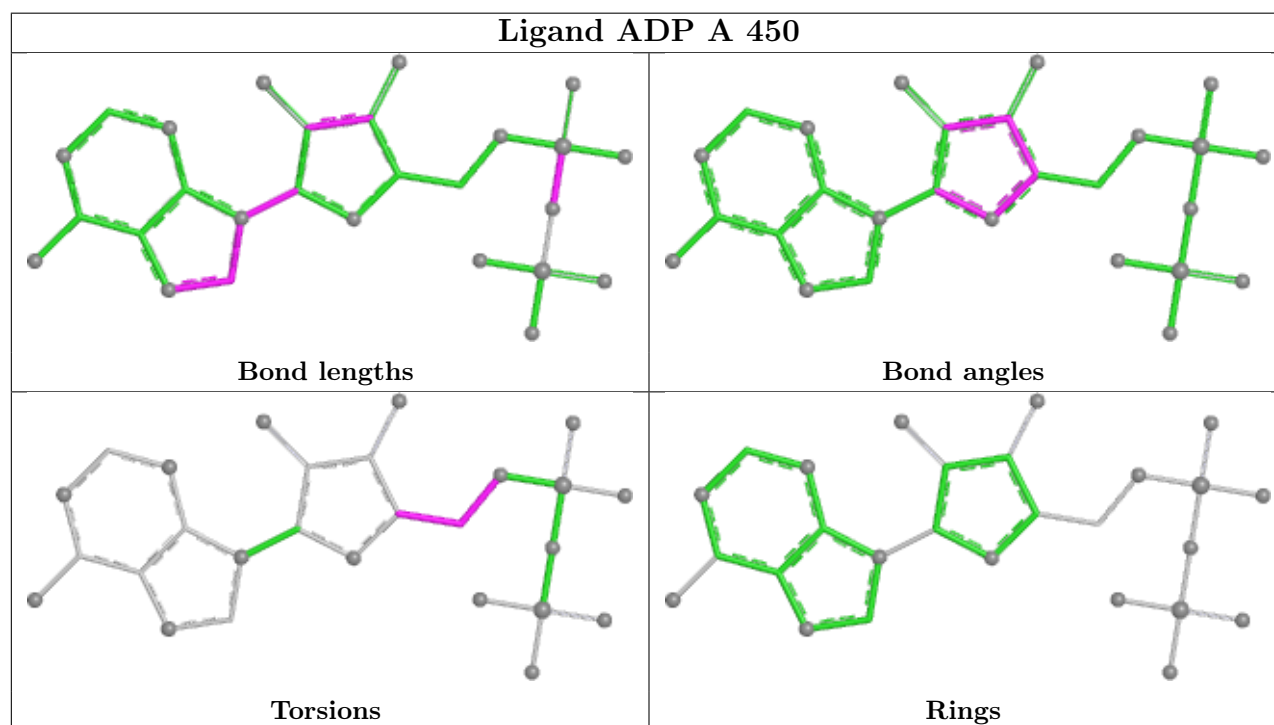
Mol	Chain	Res	Type	Atoms
3	A	450	ADP	O4'-C4'-C5'-O5'
3	A	450	ADP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	450	ADP	4	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	334/444 (75%)	2.67	199 (59%) 0 0	13, 32, 124, 183	0

All (199) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	LEU	11.0
1	A	93	GLY	9.2
1	A	268	TYR	8.9
1	A	240	LEU	8.1
1	A	227	ILE	8.1
1	A	226	LEU	8.1
1	A	92	VAL	7.4
1	A	272	ASP	7.2
1	A	270	GLY	7.2
1	A	273	VAL	7.2
1	A	120	ARG	6.9
1	A	271	ALA	6.9
1	A	274	SER	6.7
1	A	228	ASP	6.4
1	A	113	GLN	6.4
1	A	231	ALA	6.1
1	A	269	SER	5.9
1	A	232	ALA	5.9
1	A	118	LYS	5.7
1	A	349	HIS	5.7
1	A	233	LYS	5.6
1	A	258	GLU	5.4
1	A	46	HIS	5.4
1	A	265	LYS	5.4
1	A	313	VAL	5.4
1	A	229	ASP	5.2
1	A	112	ARG	5.2

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Mol	Chain	Res	Type	RSRZ
1	A	267	GLU	5.2
1	A	87	THR	5.2
1	A	114	GLN	5.1
1	A	115	GLU	5.1
1	A	299	LYS	5.1
1	A	292	SER	5.1
1	A	312	GLN	4.9
1	A	82	GLU	4.8
1	A	235	ILE	4.7
1	A	116	ILE	4.7
1	A	72	LYS	4.7
1	A	96	VAL	4.6
1	A	354	GLU	4.5
1	A	356	TYR	4.5
1	A	2	SER	4.4
1	A	237	PRO	4.4
1	A	266	GLY	4.3
1	A	94	LYS	4.3
1	A	238	GLU	4.2
1	A	83	ALA	4.2
1	A	109	LYS	4.1
1	A	95	GLU	4.0
1	A	80	LYS	4.0
1	A	45	ARG	3.9
1	A	250	GLN	3.9
1	A	405	ASP	3.8
1	A	314	ALA	3.8
1	A	81	VAL	3.8
1	A	230	GLU	3.7
1	A	315	ARG	3.7
1	A	44	LEU	3.7
1	A	41	GLN	3.6
1	A	108	MET	3.6
1	A	298	VAL	3.6
1	A	341	PHE	3.6
1	A	283	LEU	3.6
1	A	43	PRO	3.6
1	A	119	ASN	3.6
1	A	275	ARG	3.5
1	A	61	VAL	3.5
1	A	245	ILE	3.5
1	A	246	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	241	LYS	3.4
1	A	278	VAL	3.4
1	A	29	ILE	3.4
1	A	117	ALA	3.4
1	A	424	ALA	3.4
1	A	379	GLU	3.4
1	A	276	GLU	3.3
1	A	85	LYS	3.3
1	A	111	VAL	3.3
1	A	346	THR	3.3
1	A	288	GLY	3.2
1	A	30	ALA	3.2
1	A	408	SER	3.2
1	A	286	VAL	3.2
1	A	110	LEU	3.2
1	A	372	ASP	3.1
1	A	259	ILE	3.1
1	A	239	GLU	3.1
1	A	106	SER	3.1
1	A	79	ILE	3.1
1	A	289	SER	3.1
1	A	382	PHE	3.1
1	A	243	LYS	3.1
1	A	437	GLU	3.0
1	A	60	GLY	3.0
1	A	97	ASP	3.0
1	A	236	ASN	3.0
1	A	244	ALA	3.0
1	A	344	ILE	3.0
1	A	407	ILE	3.0
1	A	69	ARG	3.0
1	A	378	ALA	2.9
1	A	326	ARG	2.9
1	A	294	LYS	2.9
1	A	426	VAL	2.9
1	A	329	ILE	2.9
1	A	68	ARG	2.9
1	A	323	LEU	2.9
1	A	42	GLU	2.9
1	A	242	GLN	2.8
1	A	320	ILE	2.8
1	A	302	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	357	LYS	2.8
1	A	290	THR	2.8
1	A	421	ILE	2.8
1	A	374	VAL	2.8
1	A	280	ARG	2.8
1	A	397	HIS	2.7
1	A	368	ALA	2.7
1	A	37	ARG	2.7
1	A	75	ASN	2.7
1	A	253	ILE	2.7
1	A	310	ALA	2.7
1	A	107	ALA	2.6
1	A	355	GLN	2.6
1	A	247	ALA	2.6
1	A	47	GLU	2.6
1	A	415	ASN	2.6
1	A	101	ARG	2.6
1	A	443	ILE	2.6
1	A	393	ALA	2.6
1	A	411	ALA	2.6
1	A	376	LYS	2.6
1	A	285	LEU	2.6
1	A	296	GLY	2.6
1	A	371	THR	2.6
1	A	15	GLN	2.5
1	A	23	ALA	2.5
1	A	282	LEU	2.5
1	A	338	ALA	2.5
1	A	429	ALA	2.5
1	A	48	VAL	2.5
1	A	261	LYS	2.5
1	A	33	ASN	2.5
1	A	381	ALA	2.5
1	A	432	GLU	2.4
1	A	11	SER	2.4
1	A	9	ILE	2.4
1	A	373	ALA	2.4
1	A	337	SER	2.4
1	A	351	SER	2.4
1	A	367	ILE	2.4
1	A	65	GLU	2.4
1	A	325	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	295	HIS	2.4
1	A	398	THR	2.3
1	A	394	ARG	2.3
1	A	308	SER	2.3
1	A	433	VAL	2.3
1	A	321	PRO	2.3
1	A	38	MET	2.3
1	A	84	THR	2.3
1	A	262	ILE	2.3
1	A	427	ALA	2.3
1	A	370	THR	2.3
1	A	396	LEU	2.2
1	A	102	ASP	2.2
1	A	76	ALA	2.2
1	A	49	THR	2.2
1	A	359	LEU	2.2
1	A	399	VAL	2.2
1	A	301	ASP	2.2
1	A	28	ALA	2.2
1	A	31	LEU	2.2
1	A	40	LEU	2.2
1	A	73	LEU	2.2
1	A	322	GLU	2.2
1	A	26	ALA	2.2
1	A	425	TYR	2.2
1	A	363	GLU	2.2
1	A	248	VAL	2.1
1	A	78	PHE	2.1
1	A	21	ALA	2.1
1	A	104	THR	2.1
1	A	353	THR	2.1
1	A	441	ARG	2.1
1	A	86	PHE	2.1
1	A	387	LYS	2.1
1	A	256	ILE	2.1
1	A	306	ILE	2.1
1	A	366	ASN	2.1
1	A	39	GLN	2.1
1	A	62	GLY	2.1
1	A	352	LEU	2.1
1	A	305	PHE	2.1
1	A	264	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	297	MET	2.0
1	A	53	ILE	2.0
1	A	3	GLU	2.0
1	A	18	ILE	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](#)

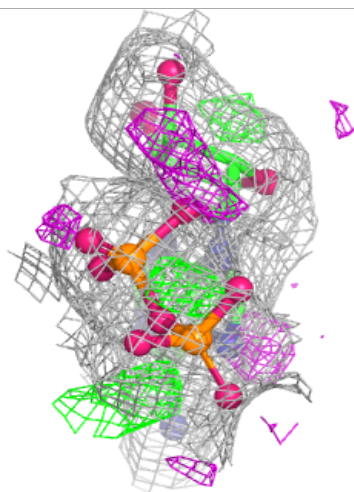
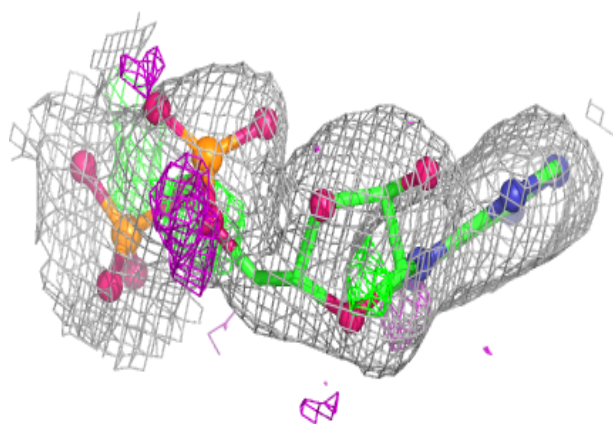
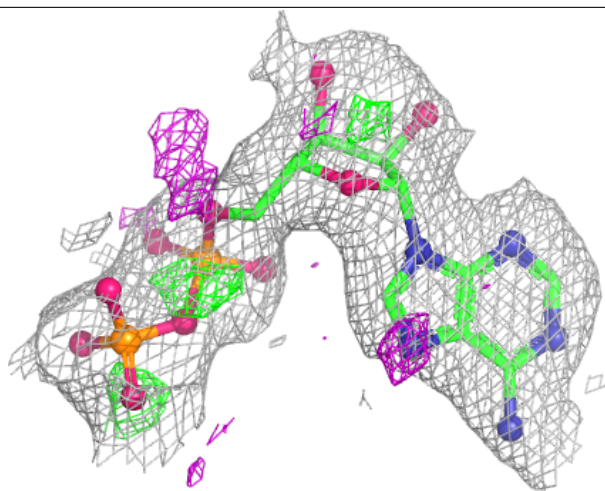
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	ADP	A	450	27/27	0.84	0.17	30,32,51,63	0
2	SO4	A	600	5/5	0.92	0.12	27,27,27,27	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 A 450:

$2mF_o-DF_c$ (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.