



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 01:23 PM EDT

PDB ID : 6H77 / pdb_00006h77
Title : E1 enzyme for ubiquitin like protein activation in complex with UBL
Authors : Soudah, N.; Padala, P.; Hassouna, F.; Mashahreh, B.; Lebedev, A.A.; Isupov, M.N.; Cohen-Kfir, E.; Wiener, R.
Deposited on : 2018-07-30
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 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

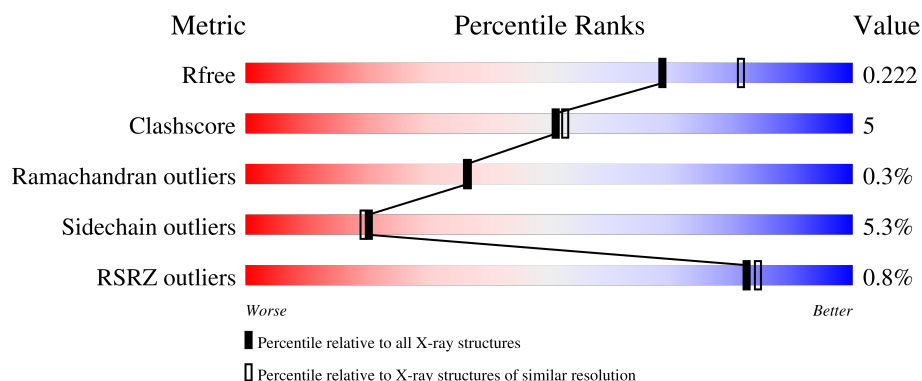
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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 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	311	82% 13% ..
1	B	311	82% 13% ..
1	C	311	81% 14% ..
1	D	311	85% 12% .
2	Q	78	88% 10% .

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Mol	Chain	Length	Quality of chain
2	R	78	 85% 13%
2	S	78	 87% 13%
2	T	78	 88% 12%

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
6	EDO	A	413	-	-	-	X
7	PEG	D	415	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12866 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.

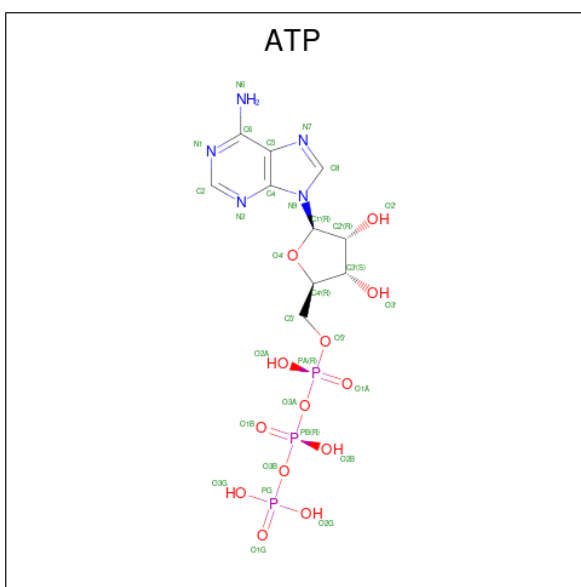
- Molecule 1 is a protein called Ubiquitin-like modifier-activating enzyme 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O	S	0	18	0
			2429	1540	409	459	21			
1	B	302	Total	C	N	O	S	0	15	0
			2421	1536	409	455	21			
1	C	301	Total	C	N	O	S	0	12	0
			2401	1520	411	450	20			
1	D	301	Total	C	N	O	S	0	11	0
			2400	1521	411	448	20			

- Molecule 2 is a protein called Ubiquitin-fold modifier 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Q	78	Total	C	N	O	S	0	2	0
			602	390	100	111	1			
2	R	78	Total	C	N	O	S	0	2	0
			602	390	100	111	1			
2	S	78	Total	C	N	O	S	0	2	0
			602	390	100	111	1			
2	T	78	Total	C	N	O	S	0	1	0
			597	387	99	110	1			

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

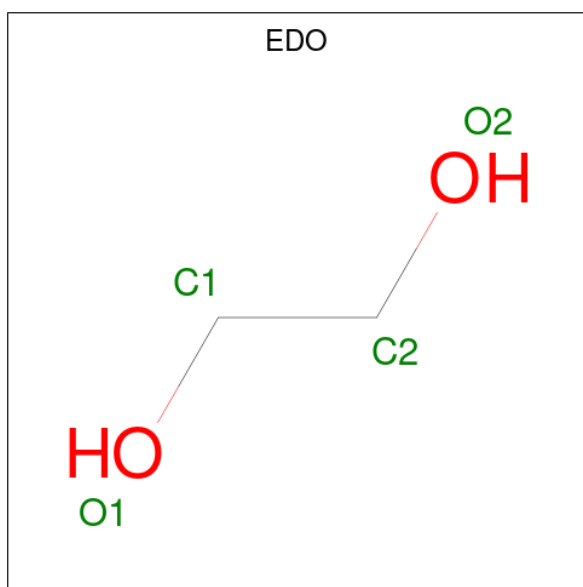
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Zn	0	0
			1	1		
5	C	1	Total	Zn	0	0
			1	1		
5	D	1	Total	Zn	0	0
			1	1		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		

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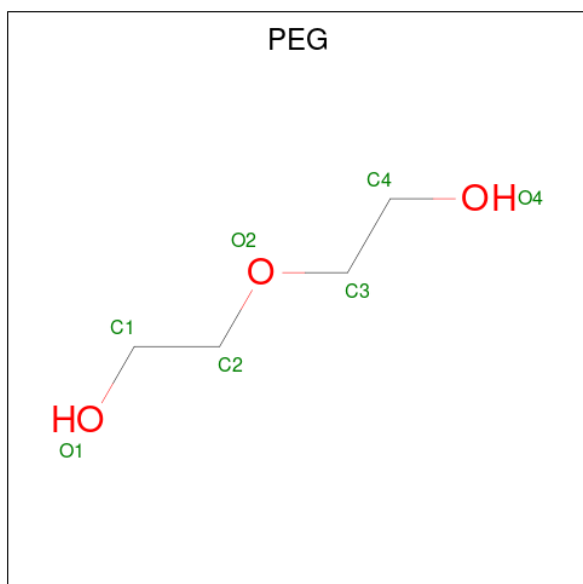
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	B	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0	0
6	D	1	Total 4	C 2	O 2	0	0
6	D	1	Total 4	C 2	O 2	0	0
6	D	1	Total 4	C 2	O 2	0	0
6	D	1	Total 4	C 2	O 2	0	0
6	D	1	Total 4	C 2	O 2	0	0
6	D	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		
6	R	1	Total	C	O	0	0
			4	2	2		
6	T	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			7	4	3		
7	D	1	Total	C	O	0	0
			7	4	3		
7	D	1	Total	C	O	0	0
			7	4	3		

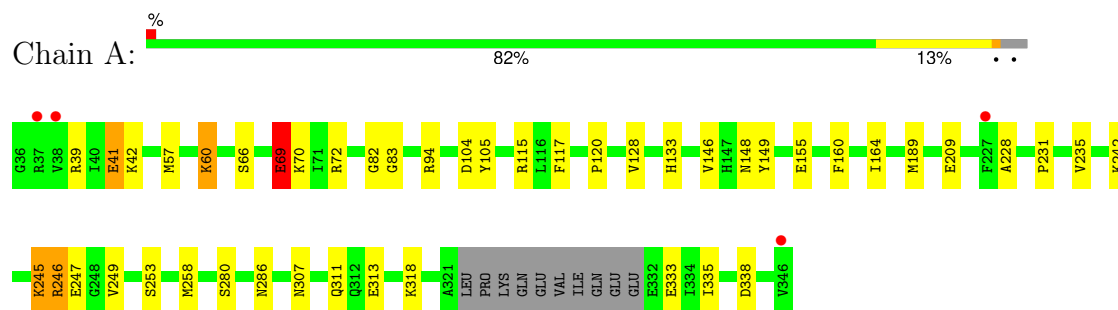
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	128	Total 128	O 128	0	0
8	B	102	Total 102	O 102	0	0
8	C	96	Total 96	O 96	0	0
8	D	118	Total 118	O 118	0	0
8	Q	17	Total 17	O 17	0	0
8	R	18	Total 18	O 18	0	0
8	S	14	Total 14	O 14	0	0
8	T	22	Total 22	O 22	0	0

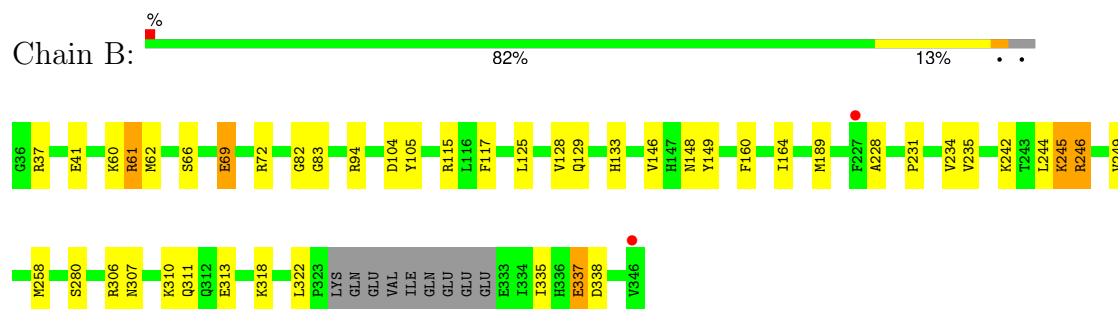
3 Residue-property plots [i](#)

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.

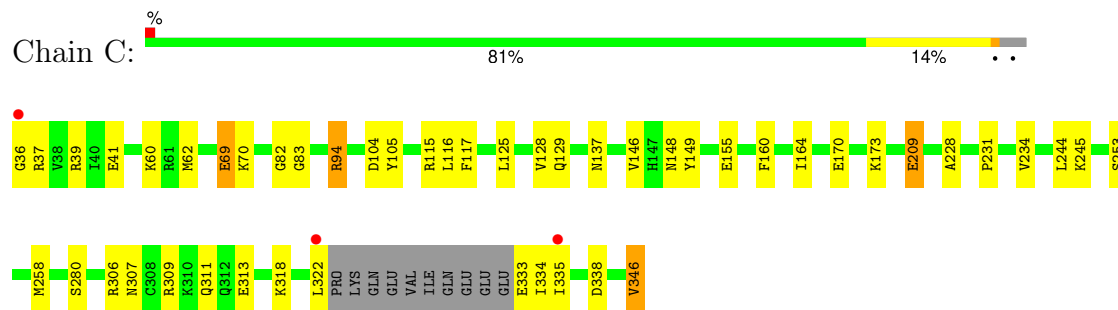
- Molecule 1: Ubiquitin-like modifier-activating enzyme 5



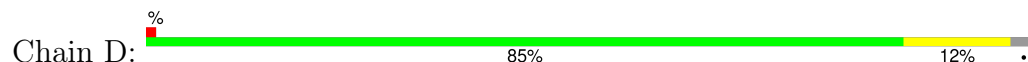
- Molecule 1: Ubiquitin-like modifier-activating enzyme 5

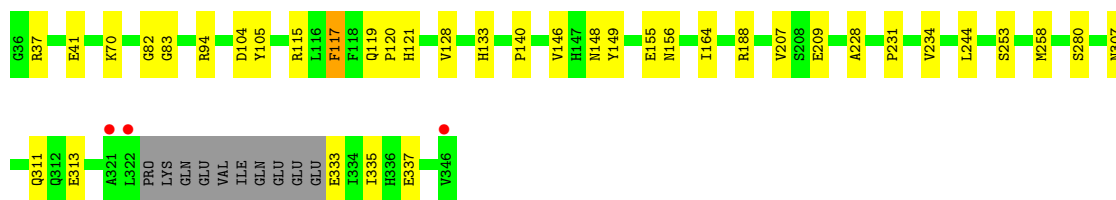


- Molecule 1: Ubiquitin-like modifier-activating enzyme 5



- Molecule 1: Ubiquitin-like modifier-activating enzyme 5





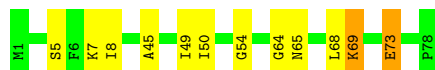
- Molecule 2: Ubiquitin-fold modifier 1

Chain Q: 88% 10% .



- Molecule 2: Ubiquitin-fold modifier 1

Chain R: 85% 13% .



- Molecule 2: Ubiquitin-fold modifier 1

Chain S: 87% 13%



- Molecule 2: Ubiquitin-fold modifier 1

Chain T: 88% 12%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.11Å 105.52Å 93.88Å 90.00° 102.29° 90.00°	Depositor
Resolution (Å)	52.76 – 2.10 52.76 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (52.76-2.10) 98.0 (52.76-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.184 , 0.221 0.184 , 0.222	Depositor DCC
R_{free} test set	2380 reflections (2.46%)	wwPDB-VP
Wilson B-factor (Å ²)	35.9	Xtrriage
Anisotropy	0.833	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.37$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12866	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.20 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.0820e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: EDO, ZN, PEG, MG, ATP

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	0.54	0/2524	0.97	2/3410 (0.1%)
1	B	0.54	0/2508	0.95	1/3390 (0.0%)
1	C	0.54	0/2478	0.96	1/3349 (0.0%)
1	D	0.56	0/2474	0.95	0/3342
2	Q	0.57	0/621	0.94	0/843
2	R	0.60	0/621	0.99	0/843
2	S	0.57	0/621	0.98	0/843
2	T	0.60	0/613	1.01	1/832 (0.1%)
All	All	0.55	0/12460	0.96	5/16852 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
1	C	0	1
1	D	0	1
All	All	0	5

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	69	GLU	CB-CG-CD	6.66	123.91	112.60
1	B	337	GLU	CB-CG-CD	6.00	122.79	112.60
1	A	42	LYS	N-CA-C	5.45	117.52	108.20
2	T	61	GLN	CB-CG-CD	-5.38	103.45	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	335	ILE	CB-CA-C	-5.21	103.85	110.98

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	94	ARG	Sidechain
1	B	61	ARG	Sidechain
1	B	94	ARG	Sidechain
1	C	94	ARG	Sidechain
1	D	94	ARG	Sidechain

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	2429	0	2450	31	0
1	B	2421	0	2441	30	0
1	C	2401	0	2414	35	0
1	D	2400	0	2420	26	0
2	Q	602	0	635	4	0
2	R	602	0	635	8	0
2	S	602	0	635	5	0
2	T	597	0	629	2	0
3	A	31	0	12	1	0
3	B	31	0	12	1	0
3	C	31	0	12	2	0
3	D	31	0	12	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	40	0	60	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	28	0	42	4	0
6	C	24	0	36	3	0
6	D	40	0	60	3	0
6	R	4	0	6	0	0
6	T	4	0	6	0	0
7	C	7	0	10	2	0
7	D	14	0	20	7	0
8	A	128	0	0	0	0
8	B	102	0	0	4	0
8	C	96	0	0	1	0
8	D	118	0	0	0	0
8	Q	17	0	0	1	0
8	R	18	0	0	0	0
8	S	14	0	0	0	0
8	T	22	0	0	0	0
All	All	12866	0	12547	129	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (129) 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:D:207:VAL:H	7:D:416:PEG:H41	1.22	1.03
1:B:189[B]:MET:HE3	1:B:235:VAL:HG11	1.40	1.00
1:A:189[B]:MET:HE3	1:A:235:VAL:HG11	1.52	0.90
6:B:405:EDO:H12	8:Q:109:HOH:O	1.73	0.88
1:B:72:ARG:HD3	8:B:579:HOH:O	1.77	0.84
1:A:41[A]:GLU:HB3	1:A:72:ARG:NH2	1.93	0.84
1:D:313:GLU:HG2	6:D:409:EDO:H21	1.60	0.82
1:B:246[A]:ARG:HG3	1:B:249:VAL:CG2	2.09	0.82
1:D:82:GLY:HA3	3:D:401:ATP:H5'2	1.64	0.79
1:A:82:GLY:HA3	3:A:401:ATP:H5'2	1.65	0.79
1:C:209:GLU:HG3	7:C:411:PEG:O1	1.86	0.75
1:A:246[A]:ARG:HG2	1:A:249:VAL:CG2	2.17	0.74
1:B:246[A]:ARG:HG3	1:B:249:VAL:HG21	1.69	0.73
1:C:82:GLY:HA3	3:C:401:ATP:H5'2	1.70	0.71
1:C:60:LYS:HE2	1:C:69:GLU:OE1	1.92	0.70
1:D:234:VAL:HG11	1:D:244:LEU:HD11	1.74	0.69
1:B:246[A]:ARG:HG3	1:B:249:VAL:HG22	1.76	0.66
6:B:406:EDO:C2	8:B:502:HOH:O	2.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41[B]:GLU:HB3	1:A:72:ARG:NH2	2.10	0.66
1:A:41[A]:GLU:HB3	1:A:72:ARG:HH22	1.62	0.65
1:B:234:VAL:HG11	1:B:244:LEU:HD11	1.79	0.65
1:A:60:LYS:HE2	1:A:69:GLU:OE1	1.97	0.65
6:B:406:EDO:H21	8:B:502:HOH:O	1.97	0.64
1:D:121:HIS:HB2	7:D:415:PEG:H11	1.80	0.63
1:A:246[A]:ARG:HG2	1:A:249:VAL:HG22	1.80	0.62
1:D:37[B]:ARG:HD2	1:D:140:PRO:HD2	1.82	0.62
1:B:160:PHE:CZ	1:B:164[A]:ILE:HD11	2.35	0.61
1:A:160:PHE:CZ	1:A:164[B]:ILE:HD11	2.35	0.61
1:D:117:PHE:O	6:D:405:EDO:H21	2.01	0.60
1:D:115:ARG:HD3	1:D:258:MET:HE3	1.83	0.60
1:A:242:LYS:O	1:A:245:LYS:HG2	2.01	0.60
1:C:115[A]:ARG:HD3	1:C:258:MET:HE3	1.82	0.60
1:D:207:VAL:N	7:D:416:PEG:H41	2.06	0.60
1:B:115:ARG:HD3	1:B:258:MET:HE3	1.84	0.60
1:C:234:VAL:HG13	2:R:45:ALA:HB1	1.84	0.59
1:A:57:MET:O	1:A:60:LYS:HG2	2.03	0.59
1:A:115:ARG:HD3	1:A:258:MET:HE3	1.85	0.59
1:C:160:PHE:CZ	1:C:164[B]:ILE:HD11	2.38	0.58
1:D:188:ARG:NH1	7:D:416:PEG:H42	2.18	0.58
1:B:82:GLY:HA3	3:B:401:ATP:H5'2	1.86	0.58
2:R:50:ILE:HD12	2:R:54:GLY:HA2	1.87	0.56
1:A:41[B]:GLU:HB3	1:A:72:ARG:HH22	1.71	0.55
1:C:209:GLU:HG3	7:C:411:PEG:HO1	1.71	0.55
2:Q:50:ILE:HD12	2:Q:54:GLY:HA2	1.88	0.55
1:C:234:VAL:HG11	1:C:244:LEU:HD11	1.88	0.55
1:B:234:VAL:HG13	2:Q:45:ALA:HB1	1.88	0.54
1:C:36:GLY:N	7:D:415:PEG:H32	2.20	0.54
1:B:146:VAL:HG22	6:B:407:EDO:H22	1.90	0.54
1:A:60:LYS:CE	1:A:69:GLU:OE1	2.56	0.53
2:S:50:ILE:HD12	2:S:54:GLY:HA2	1.90	0.53
2:R:65:ASN:O	2:R:69:LYS:CG	2.57	0.53
2:T:50:ILE:HD12	2:T:54:GLY:HA2	1.91	0.52
1:C:334:ILE:CD1	2:S:41:LYS:HE2	2.39	0.52
1:B:306:ARG:NH2	1:B:310:LYS:HE3	2.26	0.51
1:C:137[B]:ASN:HD22	1:D:119:GLN:HE21	1.59	0.51
1:D:234:VAL:HG13	2:S:45:ALA:HB1	1.93	0.51
1:B:242:LYS:O	1:B:245:LYS:HG2	2.12	0.50
2:R:64:GLY:O	2:R:68:LEU:HD13	2.11	0.50
2:R:65:ASN:O	2:R:69:LYS:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115[A]:ARG:HD3	1:C:258:MET:CE	2.42	0.50
1:C:170:GLU:OE1	1:C:173:LYS:HE2	2.12	0.49
1:C:334:ILE:HG13	2:S:39:GLU:HA	1.95	0.49
1:B:133:HIS:HA	7:D:415:PEG:H12	1.94	0.49
1:A:115:ARG:HD3	1:A:258:MET:CE	2.43	0.48
1:A:133:HIS:CD2	1:C:125:LEU:HD21	2.48	0.48
1:C:346:VAL:HG22	2:S:20:VAL:HB	1.94	0.48
1:C:37:ARG:HG3	1:D:120:PRO:HB3	1.96	0.47
1:D:115:ARG:HD3	1:D:258:MET:CE	2.44	0.47
1:C:307:ASN:O	1:C:311:GLN:HG2	2.15	0.47
1:B:115:ARG:HD3	1:B:258:MET:CE	2.45	0.47
1:C:228:ALA:O	1:C:231:PRO:HD3	2.15	0.47
1:C:125:LEU:HD22	1:C:129[A]:GLN:HE22	1.80	0.47
1:B:228:ALA:O	1:B:231:PRO:HD3	2.15	0.47
1:A:286[A]:ASN:HD21	6:A:407:EDO:H12	1.80	0.47
1:B:307:ASN:O	1:B:311:GLN:HG2	2.15	0.46
1:C:115[B]:ARG:HH22	3:C:401:ATP:PG	2.39	0.46
1:A:105:TYR:HB3	1:A:149:TYR:C	2.41	0.46
1:D:105:TYR:HB3	1:D:149:TYR:C	2.41	0.46
1:B:125:LEU:HD22	1:B:129[B]:GLN:HE22	1.79	0.46
1:D:121:HIS:CB	7:D:415:PEG:H11	2.44	0.46
1:D:128:VAL:HB	1:D:146:VAL:HB	1.98	0.46
2:R:65:ASN:O	2:R:69:LYS:HG2	2.16	0.45
1:A:128:VAL:HB	1:A:146:VAL:HB	1.97	0.45
1:B:105:TYR:HB3	1:B:149:TYR:C	2.41	0.45
1:D:156:ASN:OD1	6:D:407:EDO:H12	2.16	0.45
2:T:1:MET:HB3	2:T:2:SER:H	1.64	0.45
1:C:105:TYR:HB3	1:C:149:TYR:C	2.41	0.45
1:D:307:ASN:O	1:D:311:GLN:HG2	2.15	0.45
1:D:228:ALA:O	1:D:231:PRO:HD3	2.17	0.45
1:A:228:ALA:O	1:A:231:PRO:HD3	2.16	0.45
1:B:128:VAL:HB	1:B:146:VAL:HB	1.98	0.45
1:A:246[A]:ARG:HG2	1:A:249:VAL:HG21	1.96	0.44
1:C:128:VAL:HB	1:C:146:VAL:HB	2.00	0.44
1:C:83:GLY:HA3	1:C:258:MET:HE3	2.00	0.44
1:A:83:GLY:HA3	1:A:258:MET:HE3	1.99	0.44
1:B:37:ARG:HD3	8:B:509:HOH:O	2.18	0.44
1:B:104:ASP:O	1:B:148:ASN:HA	2.18	0.44
1:A:246[A]:ARG:CG	1:A:249:VAL:CG2	2.94	0.43
1:C:234:VAL:CG1	2:R:45:ALA:HB1	2.46	0.43
1:A:120:PRO:HB3	1:B:37:ARG:HG3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:ASN:O	1:A:311:GLN:HG2	2.19	0.43
1:A:82:GLY:HA2	6:A:411:EDO:H12	2.00	0.43
1:C:69:GLU:H	1:C:69:GLU:CD	2.26	0.43
1:D:104:ASP:O	1:D:148:ASN:HA	2.18	0.43
1:B:60:LYS:HD2	1:B:66:SER:O	2.19	0.43
1:C:115[A]:ARG:HD2	6:C:408:EDO:H12	2.01	0.43
1:A:249:VAL:HG12	1:B:61:ARG:HH11	1.83	0.42
1:D:83:GLY:HA3	1:D:258:MET:HE3	2.01	0.42
1:C:253:SER:HB2	1:C:258:MET:HE2	2.02	0.42
1:A:60:LYS:HD2	1:A:66:SER:O	2.19	0.42
1:C:116:LEU:HB3	6:C:405:EDO:H22	2.01	0.42
1:B:234:VAL:CG1	2:Q:45:ALA:HB1	2.49	0.42
1:C:94:ARG:HD3	1:D:115:ARG:O	2.19	0.42
1:B:125:LEU:HD21	1:D:133:HIS:CD2	2.55	0.41
1:C:306:ARG:HD2	1:C:309:ARG:NH1	2.35	0.41
2:R:7:LYS:HD3	2:R:73:GLU:OE2	2.20	0.41
1:D:164[B]:ILE:HD13	1:D:164[B]:ILE:HG21	1.86	0.41
1:B:69:GLU:H	1:B:69:GLU:CD	2.29	0.41
1:C:104:ASP:O	1:C:148:ASN:HA	2.20	0.41
1:B:83:GLY:HA3	1:B:258:MET:HE3	2.02	0.41
1:A:104:ASP:O	1:A:148:ASN:HA	2.21	0.41
2:Q:7:LYS:HD3	2:Q:73:GLU:OE2	2.20	0.41
1:B:246[A]:ARG:H	1:B:246[A]:ARG:HG2	1.53	0.41
1:C:37:ARG:CD	8:C:541:HOH:O	2.69	0.40
1:A:246[A]:ARG:CG	1:A:249:VAL:HG21	2.51	0.40
1:C:82:GLY:HA2	6:C:408:EDO:H21	2.02	0.40
1:C:160:PHE:CE2	1:C:164[B]:ILE:HD11	2.56	0.40
1:A:253:SER:HB2	1:A:258:MET:HE2	2.02	0.40
1:D:253:SER:HB2	1:D:258:MET:HE2	2.04	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	315/311 (101%)	304 (96%)	10 (3%)	1 (0%)	36	36
1	B	313/311 (101%)	303 (97%)	9 (3%)	1 (0%)	36	36
1	C	309/311 (99%)	298 (96%)	10 (3%)	1 (0%)	36	36
1	D	308/311 (99%)	300 (97%)	7 (2%)	1 (0%)	36	36
2	Q	78/78 (100%)	78 (100%)	0	0	100	100
2	R	78/78 (100%)	78 (100%)	0	0	100	100
2	S	78/78 (100%)	78 (100%)	0	0	100	100
2	T	77/78 (99%)	77 (100%)	0	0	100	100
All	All	1556/1556 (100%)	1516 (97%)	36 (2%)	4 (0%)	36	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	PHE
1	B	117	PHE
1	D	117	PHE
1	C	117	PHE

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	275/267 (103%)	253 (92%)	22 (8%)	11	8
1	B	273/267 (102%)	259 (95%)	14 (5%)	21	21
1	C	269/267 (101%)	254 (94%)	15 (6%)	19	18
1	D	268/267 (100%)	260 (97%)	8 (3%)	36	41
2	Q	68/66 (103%)	63 (93%)	5 (7%)	13	10
2	R	68/66 (103%)	63 (93%)	5 (7%)	13	10
2	S	68/66 (103%)	63 (93%)	5 (7%)	13	10
2	T	67/66 (102%)	63 (94%)	4 (6%)	17	15
All	All	1356/1332 (102%)	1278 (94%)	78 (6%)	20	16

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ARG
1	A	41[A]	GLU
1	A	41[B]	GLU
1	A	60	LYS
1	A	69	GLU
1	A	70	LYS
1	A	155[A]	GLU
1	A	155[B]	GLU
1	A	209[A]	GLU
1	A	209[B]	GLU
1	A	245	LYS
1	A	246[A]	ARG
1	A	246[B]	ARG
1	A	247[A]	GLU
1	A	247[B]	GLU
1	A	280[A]	SER
1	A	280[B]	SER
1	A	313	GLU
1	A	318	LYS
1	A	333	GLU
1	A	335	ILE
1	A	338	ASP
1	B	41	GLU
1	B	62	MET
1	B	69	GLU
1	B	245	LYS
1	B	246[A]	ARG
1	B	246[B]	ARG
1	B	280[A]	SER
1	B	280[B]	SER
1	B	313	GLU
1	B	318	LYS
1	B	322	LEU
1	B	335	ILE
1	B	337	GLU
1	B	338	ASP
1	C	39	ARG
1	C	41	GLU
1	C	62	MET
1	C	69	GLU
1	C	70	LYS
1	C	155	GLU

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Mol	Chain	Res	Type
1	C	209	GLU
1	C	245	LYS
1	C	280	SER
1	C	313	GLU
1	C	318	LYS
1	C	322	LEU
1	C	333	GLU
1	C	338	ASP
1	C	346	VAL
1	D	41	GLU
1	D	70	LYS
1	D	155	GLU
1	D	209	GLU
1	D	280	SER
1	D	333	GLU
1	D	335	ILE
1	D	337	GLU
2	Q	1	MET
2	Q	5	SER
2	Q	8	ILE
2	Q	49	ILE
2	Q	73	GLU
2	R	5	SER
2	R	8	ILE
2	R	49	ILE
2	R	69	LYS
2	R	73	GLU
2	S	5	SER
2	S	8	ILE
2	S	49	ILE
2	S	52[A]	ASN
2	S	52[B]	ASN
2	T	5	SER
2	T	8	ILE
2	T	49	ILE
2	T	73	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	GLN
1	A	133	HIS

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Mol	Chain	Res	Type
1	A	200	GLN
1	A	302	GLN
1	A	307	ASN
1	B	119	GLN
1	B	133	HIS
1	B	158	GLN
1	B	200	GLN
1	B	302	GLN
1	B	307	ASN
1	C	119	GLN
1	C	133	HIS
1	C	158	GLN
1	C	200	GLN
1	D	121	HIS
1	D	133	HIS
1	D	200	GLN
1	D	302	GLN
2	Q	65	ASN
2	Q	70	HIS
2	R	61	GLN
2	R	65	ASN
2	R	70	HIS
2	S	65	ASN
2	S	70	HIS
2	T	52	ASN
2	T	65	ASN
2	T	70	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 54 ligands modelled in this entry, 12 are monoatomic - leaving 42 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	A	405	-	3,3,3	0.28	0	2,2,2	1.34	0
6	EDO	B	407	-	3,3,3	0.46	0	2,2,2	0.43	0
6	EDO	A	411	-	3,3,3	0.49	0	2,2,2	0.58	0
6	EDO	D	411	-	3,3,3	0.48	0	2,2,2	0.48	0
3	ATP	D	401	4	32,33,33	1.49	6 (18%)	48,52,52	1.95	14 (29%)
7	PEG	D	416	-	6,6,6	0.39	0	5,5,5	0.64	0
3	ATP	C	401	4	32,33,33	1.52	6 (18%)	48,52,52	2.12	15 (31%)
6	EDO	C	406	-	3,3,3	0.42	0	2,2,2	0.65	0
6	EDO	C	409	-	3,3,3	0.20	0	2,2,2	0.69	0
6	EDO	R	101	-	3,3,3	0.55	0	2,2,2	0.56	0
6	EDO	B	408	-	3,3,3	0.28	0	2,2,2	1.15	0
6	EDO	C	405	-	3,3,3	0.47	0	2,2,2	0.67	0
6	EDO	B	411	-	3,3,3	0.48	0	2,2,2	0.64	0
6	EDO	C	410	-	3,3,3	0.34	0	2,2,2	0.72	0
6	EDO	D	405	-	3,3,3	0.58	0	2,2,2	0.25	0
7	PEG	C	411	-	6,6,6	0.55	0	5,5,5	0.54	0
6	EDO	A	406	-	3,3,3	0.41	0	2,2,2	0.94	0
6	EDO	A	409	-	3,3,3	0.37	0	2,2,2	0.65	0
3	ATP	A	401	4	32,33,33	1.55	5 (15%)	48,52,52	2.05	18 (37%)
6	EDO	D	413	-	3,3,3	0.51	0	2,2,2	0.24	0
6	EDO	A	410	-	3,3,3	0.28	0	2,2,2	0.78	0
6	EDO	B	405	-	3,3,3	0.58	0	2,2,2	0.08	0
6	EDO	A	414	-	3,3,3	0.38	0	2,2,2	0.68	0
7	PEG	D	415	-	6,6,6	0.67	0	5,5,5	0.18	0
6	EDO	D	406	-	3,3,3	0.48	0	2,2,2	0.33	0
6	EDO	A	413	-	3,3,3	0.39	0	2,2,2	0.65	0
6	EDO	D	412	-	3,3,3	0.43	0	2,2,2	0.47	0
6	EDO	A	407	-	3,3,3	0.35	0	2,2,2	0.68	0
6	EDO	C	407	-	3,3,3	0.34	0	2,2,2	1.26	0
6	EDO	D	409	-	3,3,3	0.44	0	2,2,2	0.42	0
6	EDO	T	101	-	3,3,3	0.69	0	2,2,2	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	B	406	-	3,3,3	0.60	0	2,2,2	0.35	0
6	EDO	A	412	-	3,3,3	0.49	0	2,2,2	0.52	0
6	EDO	D	407	-	3,3,3	0.38	0	2,2,2	0.83	0
6	EDO	C	408	-	3,3,3	0.32	0	2,2,2	0.97	0
3	ATP	B	401	4	32,33,33	1.66	4 (12%)	48,52,52	2.34	13 (27%)
6	EDO	B	409	-	3,3,3	0.55	0	2,2,2	0.43	0
6	EDO	D	410	-	3,3,3	0.35	0	2,2,2	0.91	0
6	EDO	D	414	-	3,3,3	0.38	0	2,2,2	0.99	0
6	EDO	B	410	-	3,3,3	0.48	0	2,2,2	0.40	0
6	EDO	D	408	-	3,3,3	0.42	0	2,2,2	0.79	0
6	EDO	A	408	-	3,3,3	0.59	0	2,2,2	0.12	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
6	EDO	A	405	-	-	1/1/1/1	-
6	EDO	B	407	-	-	1/1/1/1	-
6	EDO	A	411	-	-	1/1/1/1	-
6	EDO	D	411	-	-	0/1/1/1	-
3	ATP	D	401	4	-	4/22/38/38	0/3/3/3
7	PEG	D	416	-	-	2/4/4/4	-
3	ATP	C	401	4	-	3/22/38/38	0/3/3/3
6	EDO	C	406	-	-	0/1/1/1	-
6	EDO	C	409	-	-	0/1/1/1	-
6	EDO	R	101	-	-	1/1/1/1	-
6	EDO	B	408	-	-	1/1/1/1	-
6	EDO	C	405	-	-	1/1/1/1	-
6	EDO	B	411	-	-	1/1/1/1	-
6	EDO	C	410	-	-	1/1/1/1	-
6	EDO	D	405	-	-	1/1/1/1	-
7	PEG	C	411	-	-	4/4/4/4	-
6	EDO	A	406	-	-	0/1/1/1	-
6	EDO	A	409	-	-	0/1/1/1	-
3	ATP	A	401	4	-	4/22/38/38	0/3/3/3
6	EDO	D	413	-	-	1/1/1/1	-
6	EDO	A	410	-	-	1/1/1/1	-
6	EDO	B	405	-	-	1/1/1/1	-
6	EDO	A	414	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	PEG	D	415	-	-	3/4/4/4	-
6	EDO	D	406	-	-	1/1/1/1	-
6	EDO	A	413	-	-	0/1/1/1	-
6	EDO	D	412	-	-	0/1/1/1	-
6	EDO	A	407	-	-	1/1/1/1	-
6	EDO	C	407	-	-	0/1/1/1	-
6	EDO	D	409	-	-	1/1/1/1	-
6	EDO	T	101	-	-	1/1/1/1	-
6	EDO	B	406	-	-	1/1/1/1	-
6	EDO	A	412	-	-	1/1/1/1	-
6	EDO	D	407	-	-	1/1/1/1	-
6	EDO	C	408	-	-	1/1/1/1	-
3	ATP	B	401	4	-	3/22/38/38	0/3/3/3
6	EDO	B	409	-	-	1/1/1/1	-
6	EDO	D	410	-	-	1/1/1/1	-
6	EDO	D	414	-	-	1/1/1/1	-
6	EDO	B	410	-	-	1/1/1/1	-
6	EDO	D	408	-	-	0/1/1/1	-
6	EDO	A	408	-	-	1/1/1/1	-

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	ATP	C5-C4	5.12	1.48	1.39
3	A	401	ATP	C5-C4	4.33	1.46	1.39
3	C	401	ATP	C5-C4	4.20	1.46	1.39
3	B	401	ATP	PA-O3A	4.02	1.63	1.59
3	D	401	ATP	C5-C4	3.64	1.45	1.39
3	C	401	ATP	PA-O3A	3.46	1.63	1.59
3	D	401	ATP	PB-O3A	2.95	1.62	1.59
3	B	401	ATP	C5-C6	2.87	1.49	1.41
3	A	401	ATP	C4-N9	-2.87	1.31	1.37
3	C	401	ATP	PB-O3B	-2.75	1.56	1.59
3	A	401	ATP	C5-N7	-2.73	1.34	1.39
3	D	401	ATP	C5-C6	2.61	1.48	1.41
3	C	401	ATP	C5-N7	-2.50	1.34	1.39
3	A	401	ATP	PA-O3A	2.48	1.62	1.59
3	D	401	ATP	PB-O3B	-2.45	1.56	1.59
3	C	401	ATP	C4-N9	-2.40	1.32	1.37
3	A	401	ATP	C5-C6	2.31	1.47	1.41
3	D	401	ATP	C5-N7	-2.31	1.34	1.39
3	B	401	ATP	C5-N7	-2.16	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	401	ATP	C4-N9	-2.15	1.33	1.37
3	C	401	ATP	C8-N7	2.09	1.35	1.31

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	ATP	C5-C4-N3	-7.39	116.54	126.72
3	B	401	ATP	O4'-C1'-N9	5.76	119.14	108.09
3	B	401	ATP	N3-C4-N9	5.72	136.89	127.17
3	C	401	ATP	C5-C4-N3	-5.67	118.91	126.72
3	D	401	ATP	C5-C4-N3	-5.28	119.45	126.72
3	C	401	ATP	N3-C4-N9	4.76	135.27	127.17
3	A	401	ATP	C5-C4-N3	-4.62	120.35	126.72
3	B	401	ATP	C4-C5-N7	-4.52	105.41	110.58
3	A	401	ATP	O4'-C1'-N9	4.29	116.32	108.09
3	D	401	ATP	N3-C4-N9	4.23	134.35	127.17
3	C	401	ATP	O4'-C1'-N9	4.04	115.84	108.09
3	B	401	ATP	C2-N3-C4	3.96	121.51	111.83
3	A	401	ATP	N3-C4-N9	3.84	133.70	127.17
3	A	401	ATP	N3-C2-N1	-3.80	122.83	128.58
3	C	401	ATP	N3-C2-N1	-3.78	122.86	128.58
3	C	401	ATP	C2-N3-C4	3.72	120.93	111.83
3	B	401	ATP	C5-N7-C8	3.69	109.25	103.45
3	B	401	ATP	O4'-C1'-C2'	-3.63	98.84	106.62
3	D	401	ATP	O4'-C1'-N9	3.54	114.89	108.09
3	D	401	ATP	O5'-PA-O1A	3.47	122.70	108.94
3	A	401	ATP	O3'-C3'-C4'	-3.44	101.19	111.08
3	B	401	ATP	O5'-PA-O1A	3.43	122.52	108.94
3	C	401	ATP	O5'-PA-O1A	-3.42	95.39	108.94
3	A	401	ATP	C2'-C1'-N9	-3.37	104.94	113.30
3	D	401	ATP	O3'-C3'-C4'	-3.35	101.46	111.08
3	A	401	ATP	C4-C5-N7	-3.26	106.86	110.58
3	C	401	ATP	C2'-C1'-N9	-3.22	105.31	113.30
3	D	401	ATP	C4-C5-N7	-3.20	106.92	110.58
3	D	401	ATP	O4'-C1'-C2'	-3.20	99.78	106.62
3	A	401	ATP	C2-N3-C4	3.19	119.63	111.83
3	A	401	ATP	O4'-C1'-C2'	-3.13	99.92	106.62
3	C	401	ATP	O3A-PB-O1B	-3.08	101.43	110.70
3	D	401	ATP	C2-N3-C4	3.01	119.19	111.83
3	C	401	ATP	O3'-C3'-C4'	-3.01	102.44	111.08
3	C	401	ATP	O2A-PA-O5'	3.00	121.18	107.57
3	A	401	ATP	C4-N9-C8	2.92	108.81	105.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	401	ATP	O4'-C4'-C5'	2.81	118.35	109.33
3	B	401	ATP	C2'-C1'-N9	-2.74	106.49	113.30
3	A	401	ATP	O2A-PA-O5'	2.73	119.94	107.57
3	B	401	ATP	N3-C2-N1	-2.71	124.48	128.58
3	C	401	ATP	C4'-O4'-C1'	-2.60	103.73	109.47
3	A	401	ATP	C2-N1-C6	2.51	122.85	118.73
3	A	401	ATP	O2B-PB-O3B	2.40	113.77	107.27
3	D	401	ATP	C2'-C1'-N9	-2.39	107.36	113.30
3	C	401	ATP	O4'-C4'-C5'	2.39	116.99	109.33
3	C	401	ATP	C4-N9-C8	2.32	108.17	105.74
3	A	401	ATP	C5-N7-C8	2.31	107.09	103.45
3	A	401	ATP	C6-C5-N7	2.27	136.47	132.09
3	D	401	ATP	C4-N9-C8	2.25	108.10	105.74
3	D	401	ATP	N3-C2-N1	-2.24	125.19	128.58
3	D	401	ATP	C5-N7-C8	2.21	106.92	103.45
3	B	401	ATP	C4'-O4'-C1'	-2.11	104.81	109.47
3	B	401	ATP	N9-C8-N7	-2.11	110.95	113.94
3	D	401	ATP	O2A-PA-O5'	-2.09	98.08	107.57
3	A	401	ATP	O5'-C5'-C4'	2.09	116.12	108.99
3	B	401	ATP	O3'-C3'-C4'	-2.07	105.13	111.08
3	A	401	ATP	O5'-PA-O1A	-2.06	100.77	108.94
3	A	401	ATP	O2B-PB-O3A	-2.05	101.73	107.27
3	C	401	ATP	O4'-C1'-C2'	-2.04	102.26	106.62
3	C	401	ATP	C2-N1-C6	2.02	122.04	118.73

There are no chirality outliers.

All (49) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	411	PEG	C4-C3-O2-C2
7	C	411	PEG	O2-C3-C4-O4
7	D	415	PEG	O1-C1-C2-O2
7	D	415	PEG	O2-C3-C4-O4
7	D	416	PEG	O1-C1-C2-O2
6	A	412	EDO	O1-C1-C2-O2
6	C	405	EDO	O1-C1-C2-O2
3	B	401	ATP	O4'-C4'-C5'-O5'
3	C	401	ATP	O4'-C4'-C5'-O5'
7	D	416	PEG	O2-C3-C4-O4
3	D	401	ATP	O4'-C4'-C5'-O5'
6	A	410	EDO	O1-C1-C2-O2
6	A	411	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
6	B	405	EDO	O1-C1-C2-O2
6	B	407	EDO	O1-C1-C2-O2
6	C	408	EDO	O1-C1-C2-O2
6	D	407	EDO	O1-C1-C2-O2
6	D	414	EDO	O1-C1-C2-O2
6	B	410	EDO	O1-C1-C2-O2
7	D	415	PEG	C1-C2-O2-C3
6	B	411	EDO	O1-C1-C2-O2
6	D	406	EDO	O1-C1-C2-O2
7	C	411	PEG	C1-C2-O2-C3
3	A	401	ATP	O4'-C4'-C5'-O5'
3	B	401	ATP	PB-O3A-PA-O2A
6	A	405	EDO	O1-C1-C2-O2
6	A	407	EDO	O1-C1-C2-O2
6	B	406	EDO	O1-C1-C2-O2
7	C	411	PEG	O1-C1-C2-O2
3	D	401	ATP	PB-O3A-PA-O2A
6	B	408	EDO	O1-C1-C2-O2
6	T	101	EDO	O1-C1-C2-O2
3	D	401	ATP	C4'-C5'-O5'-PA
6	D	409	EDO	O1-C1-C2-O2
3	C	401	ATP	C4'-C5'-O5'-PA
3	A	401	ATP	PB-O3A-PA-O1A
6	A	408	EDO	O1-C1-C2-O2
6	D	410	EDO	O1-C1-C2-O2
3	A	401	ATP	C4'-C5'-O5'-PA
6	A	414	EDO	O1-C1-C2-O2
6	B	409	EDO	O1-C1-C2-O2
6	D	405	EDO	O1-C1-C2-O2
6	D	413	EDO	O1-C1-C2-O2
3	B	401	ATP	PB-O3A-PA-O1A
3	C	401	ATP	PB-O3A-PA-O2A
3	D	401	ATP	PB-O3A-PA-O1A
6	R	101	EDO	O1-C1-C2-O2
6	C	410	EDO	O1-C1-C2-O2
3	A	401	ATP	PB-O3A-PA-O2A

There are no ring outliers.

17 monomers are involved in 26 short contacts:

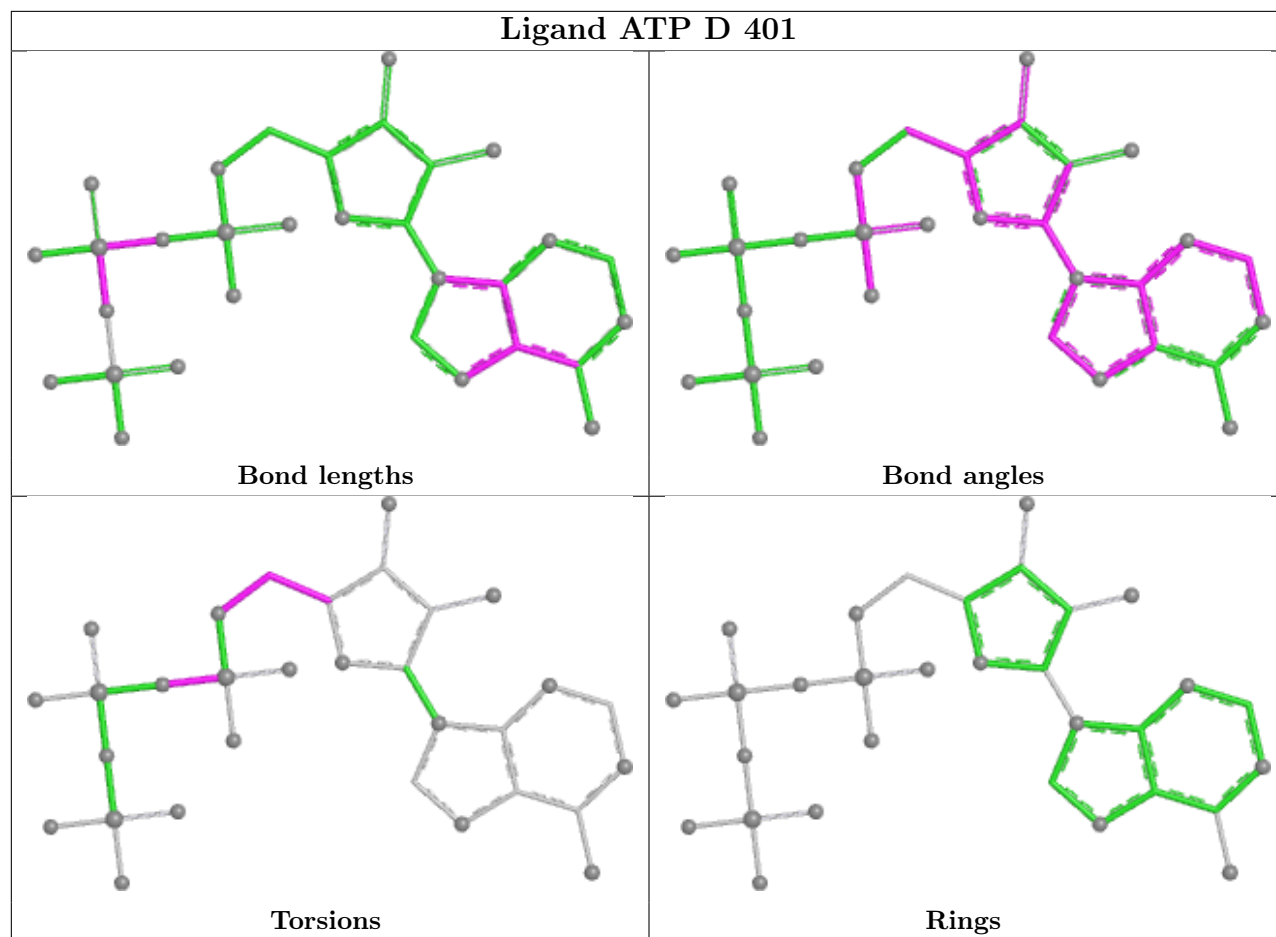
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	407	EDO	1	0

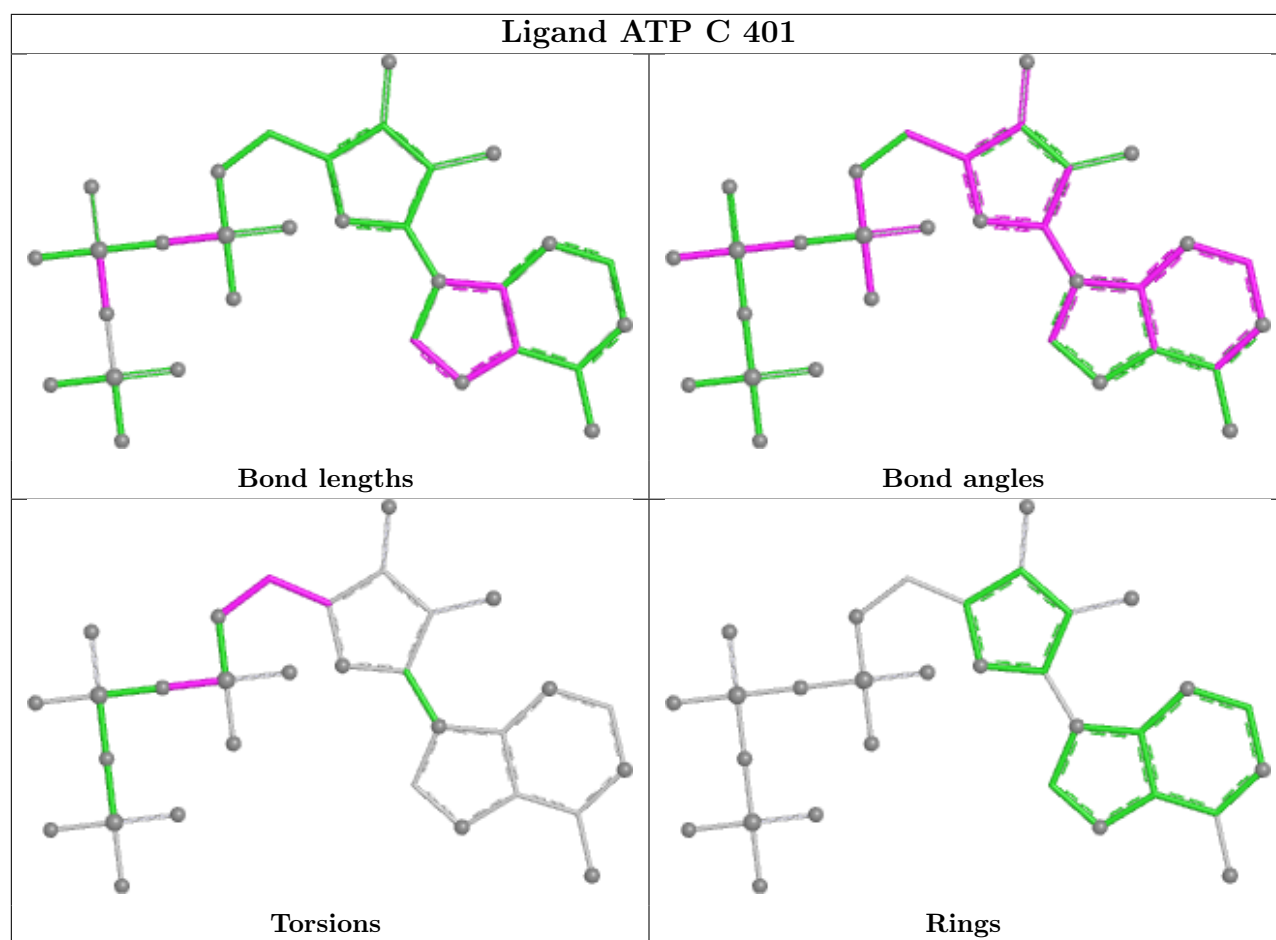
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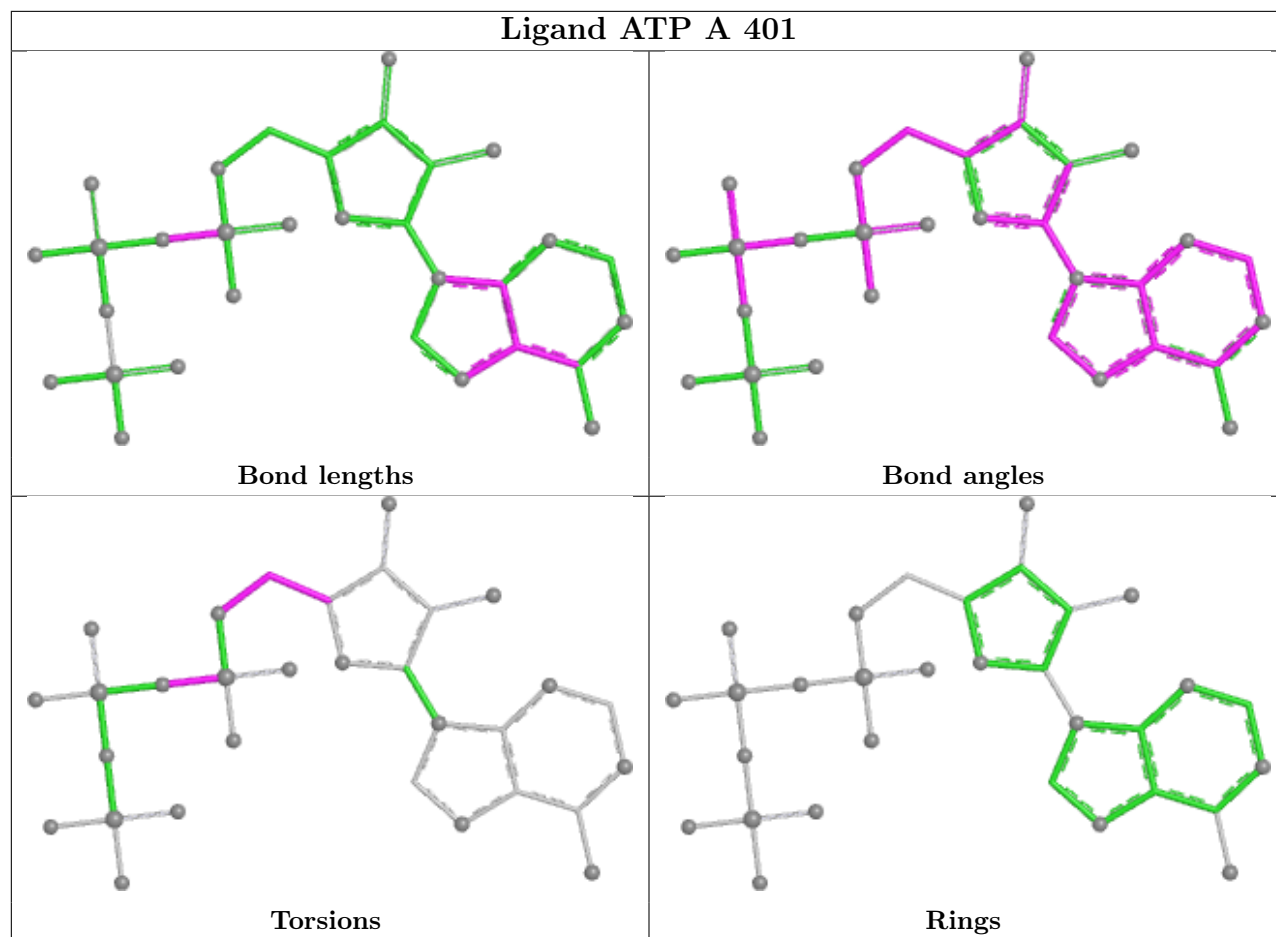
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	411	EDO	1	0
3	D	401	ATP	1	0
7	D	416	PEG	3	0
3	C	401	ATP	2	0
6	C	405	EDO	1	0
6	D	405	EDO	1	0
7	C	411	PEG	2	0
3	A	401	ATP	1	0
6	B	405	EDO	1	0
7	D	415	PEG	4	0
6	A	407	EDO	1	0
6	D	409	EDO	1	0
6	B	406	EDO	2	0
6	D	407	EDO	1	0
6	C	408	EDO	2	0
3	B	401	ATP	1	0

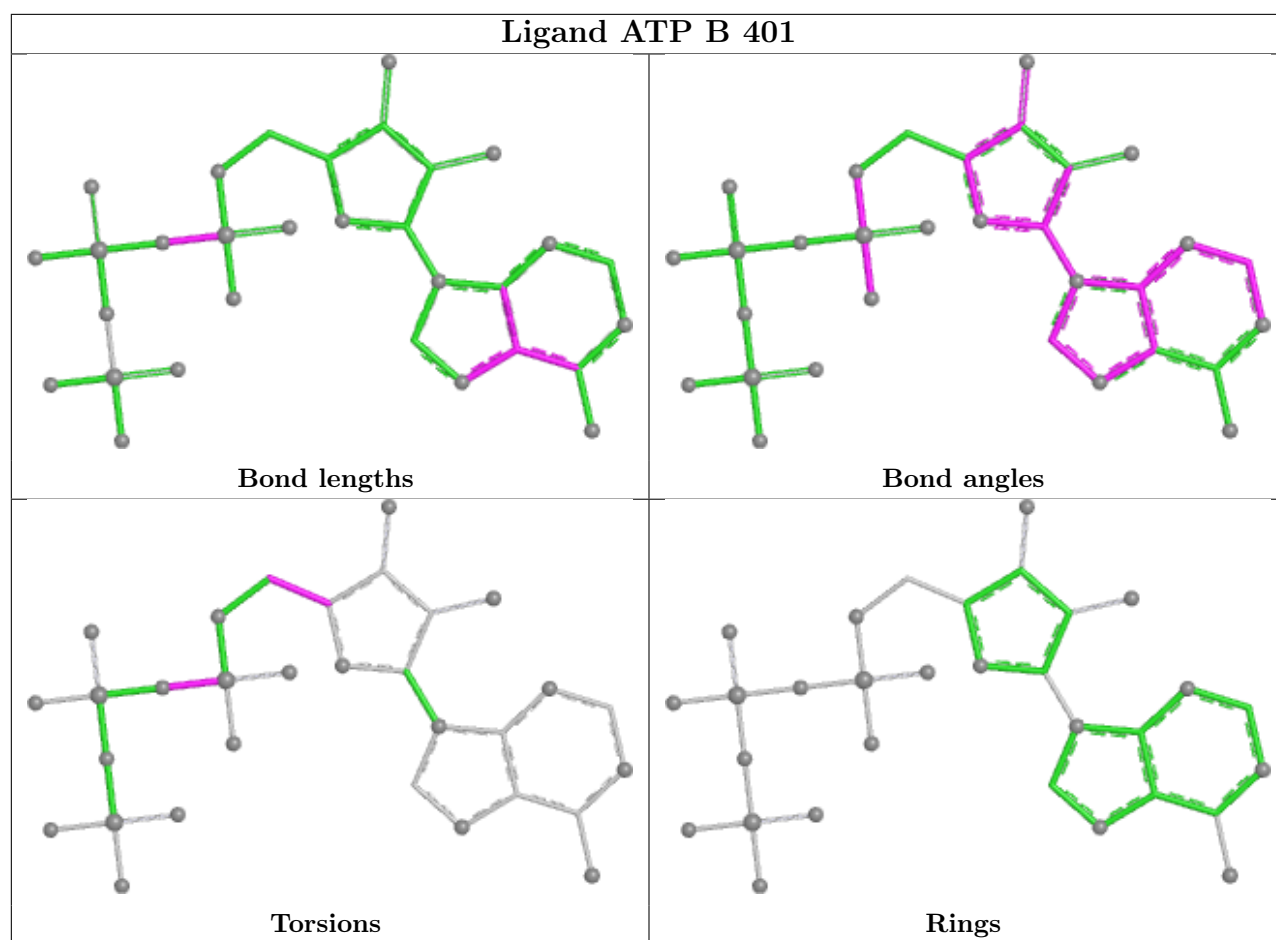
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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





Ligand ATP A 401





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	301/311 (96%)	-0.17	4 (1%) 75 77	22, 43, 104, 163	18 (5%)
1	B	302/311 (97%)	-0.17	2 (0%) 84 86	23, 44, 103, 139	15 (4%)
1	C	301/311 (96%)	-0.02	3 (0%) 79 81	22, 47, 108, 144	12 (3%)
1	D	301/311 (96%)	-0.21	3 (0%) 79 81	22, 42, 92, 124	11 (3%)
2	Q	78/78 (100%)	0.10	0 100 100	27, 53, 79, 127	2 (2%)
2	R	78/78 (100%)	0.14	0 100 100	27, 51, 79, 124	2 (2%)
2	S	78/78 (100%)	0.03	0 100 100	35, 52, 80, 121	2 (2%)
2	T	78/78 (100%)	-0.15	0 100 100	35, 50, 71, 120	1 (1%)
All	All	1517/1556 (97%)	-0.11	12 (0%) 82 84	22, 46, 100, 163	63 (4%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	322	LEU	3.9
1	C	322	LEU	3.2
1	A	38	VAL	3.0
1	C	36	GLY	2.8
1	A	227[A]	PHE	2.7
1	A	346	VAL	2.5
1	D	346	VAL	2.4
1	A	37	ARG	2.2
1	C	335	ILE	2.2
1	D	321	ALA	2.2
1	B	346	VAL	2.1
1	B	227[A]	PHE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
6	EDO	A	413	4/4	0.78	0.40	57,64,65,78	4
6	EDO	B	409	4/4	0.79	0.14	57,63,83,100	0
6	EDO	B	407	4/4	0.81	0.12	62,80,85,106	0
7	PEG	D	415	7/7	0.81	0.30	45,64,79,82	7
6	EDO	A	405	4/4	0.83	0.23	54,59,66,74	0
6	EDO	B	411	4/4	0.85	0.16	88,89,97,118	0
6	EDO	A	412	4/4	0.85	0.18	68,74,85,98	0
6	EDO	D	407	4/4	0.86	0.13	61,75,78,95	0
6	EDO	C	407	4/4	0.86	0.15	47,51,55,57	0
6	EDO	D	410	4/4	0.87	0.14	63,65,67,79	0
6	EDO	C	408	4/4	0.87	0.16	50,55,72,88	0
6	EDO	A	408	4/4	0.88	0.12	68,71,81,82	0
6	EDO	A	406	4/4	0.88	0.15	54,61,66,68	0
6	EDO	A	407	4/4	0.88	0.16	54,58,58,69	0
6	EDO	D	411	4/4	0.88	0.18	51,57,58,59	0
6	EDO	A	414	4/4	0.88	0.12	78,78,92,93	0
6	EDO	B	410	4/4	0.89	0.14	76,80,86,87	0
6	EDO	T	101	4/4	0.89	0.12	65,65,69,74	0
7	PEG	C	411	7/7	0.89	0.21	57,63,70,70	7
6	EDO	C	405	4/4	0.89	0.14	63,64,65,66	0
6	EDO	R	101	4/4	0.90	0.12	75,80,88,108	0
6	EDO	A	411	4/4	0.90	0.23	53,66,67,73	0
6	EDO	B	408	4/4	0.90	0.10	52,61,63,63	0
6	EDO	C	410	4/4	0.90	0.14	77,83,84,95	0
7	PEG	D	416	7/7	0.90	0.14	36,50,55,70	7
6	EDO	B	405	4/4	0.91	0.11	52,54,61,73	0
6	EDO	D	409	4/4	0.91	0.11	59,69,74,85	0

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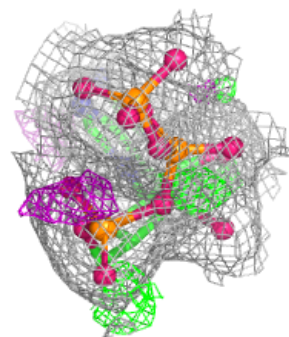
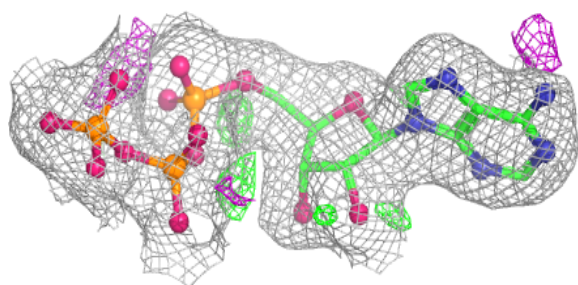
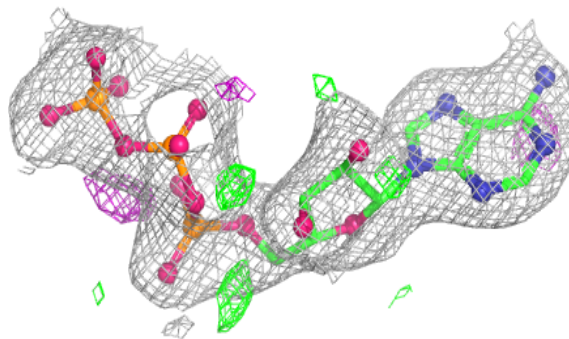
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	D	412	4/4	0.91	0.13	69,75,79,93	0
6	EDO	D	413	4/4	0.91	0.09	63,68,71,77	0
6	EDO	D	414	4/4	0.91	0.13	45,49,62,68	0
6	EDO	D	408	4/4	0.92	0.12	65,67,74,76	0
6	EDO	B	406	4/4	0.92	0.09	48,48,51,60	0
6	EDO	D	406	4/4	0.92	0.15	53,70,80,89	0
6	EDO	C	406	4/4	0.92	0.10	53,69,71,73	0
6	EDO	A	410	4/4	0.93	0.07	53,57,58,71	0
6	EDO	D	405	4/4	0.93	0.11	64,67,68,70	0
6	EDO	C	409	4/4	0.95	0.10	36,37,50,62	0
6	EDO	A	409	4/4	0.96	0.08	37,41,63,65	0
3	ATP	C	401	31/31	0.97	0.06	29,42,47,54	0
3	ATP	B	401	31/31	0.98	0.05	30,35,42,43	0
3	ATP	D	401	31/31	0.98	0.05	28,36,41,46	0
5	ZN	B	403	1/1	0.99	0.02	45,45,45,45	0
5	ZN	C	403	1/1	0.99	0.02	47,47,47,47	0
3	ATP	A	401	31/31	0.99	0.04	26,35,40,41	0
4	MG	A	402	1/1	0.99	0.07	37,37,37,37	0
4	MG	A	404	1/1	0.99	0.02	35,35,35,35	0
4	MG	B	404	1/1	0.99	0.04	36,36,36,36	0
4	MG	C	402	1/1	0.99	0.06	45,45,45,45	0
4	MG	D	402	1/1	0.99	0.05	37,37,37,37	0
4	MG	D	404	1/1	0.99	0.03	34,34,34,34	0
5	ZN	A	403	1/1	0.99	0.02	42,42,42,42	0
5	ZN	D	403	1/1	1.00	0.02	40,40,40,40	0
4	MG	C	404	1/1	1.00	0.03	37,37,37,37	0
4	MG	B	402	1/1	1.00	0.03	38,38,38,38	0

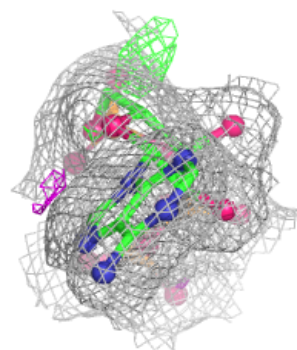
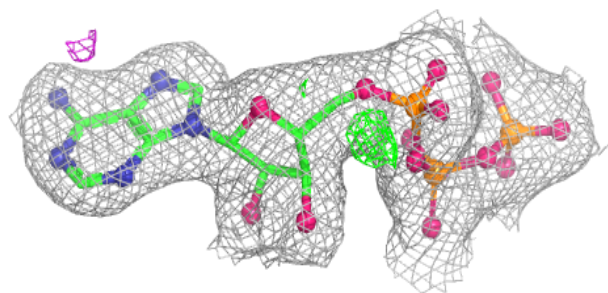
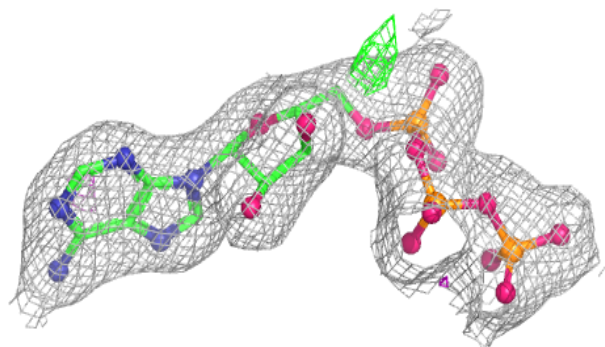
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP 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)

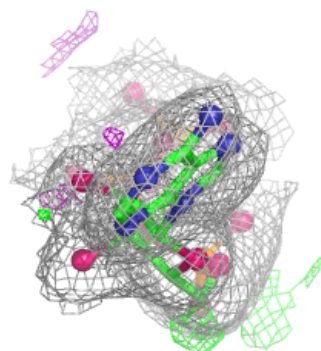
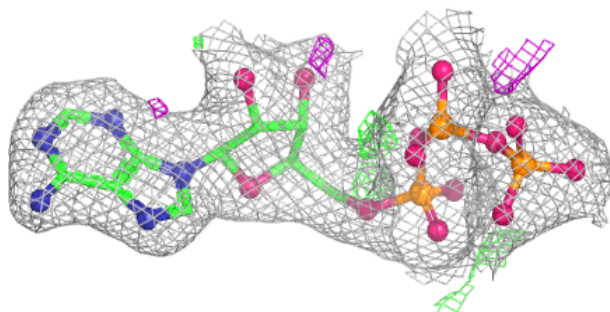
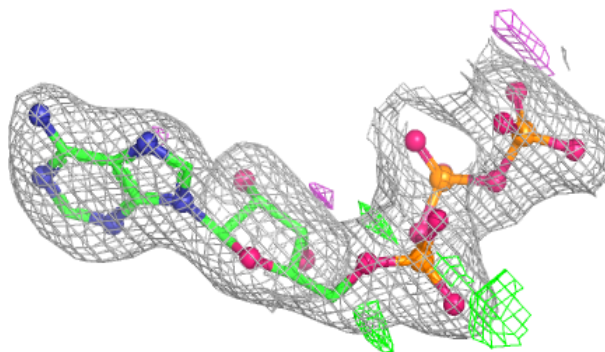
**Electron density around ATP B 401:**

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

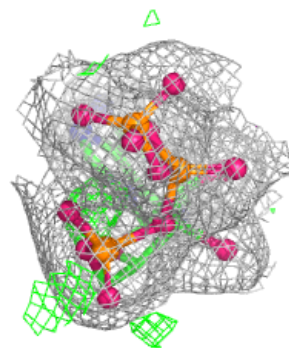
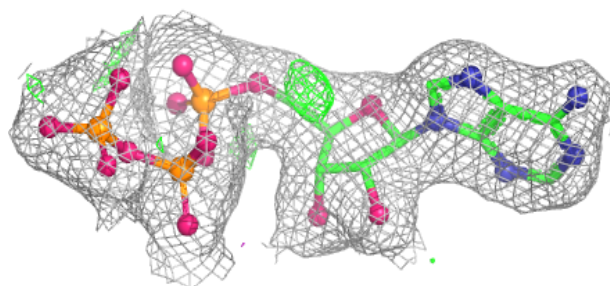
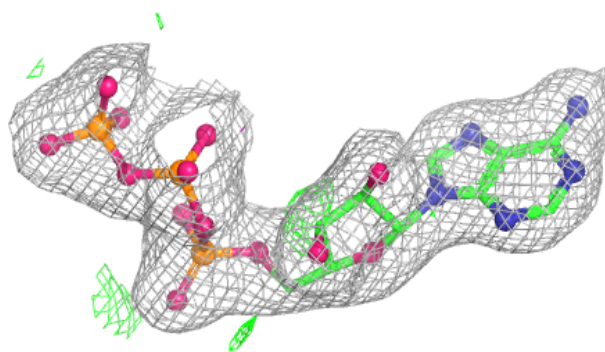


Electron density around ATP D 401:

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

**Electron density around ATP 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 [i](#)

There are no such residues in this entry.