



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 3, 2024 – 03:01 am GMT

PDB ID : 4XJX
Title : STRUCTURE OF MUTANT (E165H) OF THE HSDR SUBUNIT OF THE ECOR124I RESTRICTION ENZYME IN COMPLEX WITH ATP
Authors : Baikova, T.; Stsiapanava, A.; Moche, M.; Degtjarik, O.; Kuta-Smatanova, I.; Ettrich, R.
Deposited on : 2015-01-09
Resolution : 2.40 Å(reported)

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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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

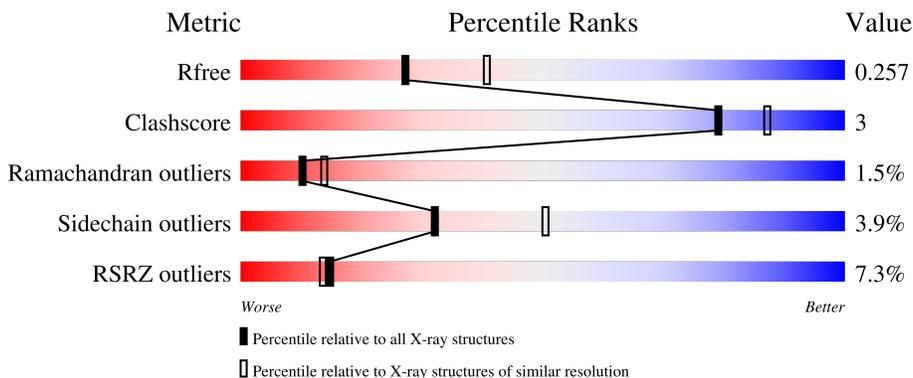
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	1038	 6% 75% 7% • 17%
1	B	1038	 6% 75% 7% • 17%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 14686 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 HsdR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	861	7062	4486	1195	1365	16	0	1	0
1	B	863	7089	4502	1204	1367	16	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	165	HIS	GLU	engineered mutation	UNP Q304R3
B	165	HIS	GLU	engineered mutation	UNP Q304R3

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
2	A	1	1	1	0	0
2	B	1	1	1	0	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.22Å 124.54Å 128.54Å 90.00° 107.77° 90.00°	Depositor
Resolution (Å)	49.09 – 2.40 49.09 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.09-2.40) 99.3 (49.09-2.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 2.39Å)	Xtrriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.208 , 0.243 0.224 , 0.257	Depositor DCC
R_{free} test set	4977 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtrriage
Anisotropy	0.676	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.021 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14686	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.80% 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: 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	0.50	0/7204	0.67	0/9719
1	B	0.50	0/7230	0.69	2/9753 (0.0%)
All	All	0.50	0/14434	0.68	2/19472 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	808	ASP	C-N-CA	6.58	138.16	121.70
1	B	806	GLN	C-N-CA	5.01	134.23	121.70

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	7062	0	6914	39	0
1	B	7089	0	6942	39	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	31	0	12	0	0
3	B	31	0	12	0	0
4	A	220	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	251	0	0	3	0
All	All	14686	0	13880	78	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 (78) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:765:ASP:HB3	1:B:766:PRO:HD3	1.35	1.05
1:A:322:ARG:HH11	1:A:322:ARG:HG2	1.30	0.95
1:B:765:ASP:HB3	1:B:766:PRO:CD	2.03	0.88
1:B:54:VAL:HG11	1:B:60:MET:HG3	1.63	0.80
1:A:139:GLN:HG2	1:A:151:ASP:H	1.46	0.79
1:A:811:ASP:HB3	1:A:812:PRO:HD3	1.63	0.79
1:A:54:VAL:HG11	1:A:60:MET:HG3	1.65	0.78
1:A:811:ASP:HB3	1:A:812:PRO:CD	2.13	0.78
1:A:272:MET:CE	1:A:319:LYS:HG2	2.24	0.68
1:B:559:ARG:HD2	4:B:1249:HOH:O	1.94	0.68
1:B:765:ASP:CB	1:B:766:PRO:HD3	2.21	0.67
1:B:272:MET:CE	1:B:319:LYS:HG2	2.23	0.67
1:A:809:LEU:HB2	1:A:813:VAL:HG11	1.79	0.63
1:B:54:VAL:HG11	1:B:60:MET:CG	2.29	0.63
1:A:813:VAL:HG22	1:A:814:ALA:H	1.64	0.62
1:A:591:ILE:HG12	1:A:678:ARG:HG3	1.79	0.62
1:B:272:MET:HE1	1:B:319:LYS:HG2	1.80	0.62
1:A:541:MET:HG3	1:A:668:LEU:HD11	1.83	0.60
1:A:227:MET:HE3	1:A:273:ARG:HG3	1.84	0.59
1:A:322:ARG:HH11	1:A:322:ARG:CG	2.10	0.58
1:A:272:MET:HE1	1:A:319:LYS:HG2	1.84	0.58
1:B:227:MET:HE3	1:B:273:ARG:HG3	1.86	0.58
1:B:541:MET:HG3	1:B:668:LEU:HD11	1.85	0.58
1:B:586:GLU:HG2	1:B:589:ASN:HA	1.86	0.57
1:B:57:GLN:HG3	1:B:194:LEU:HD22	1.86	0.57
1:B:592:GLY:HA2	1:B:678:ARG:HB2	1.87	0.56
1:A:272:MET:HE2	1:A:319:LYS:HG2	1.89	0.55
1:A:554:TYR:HB3	1:A:611:PHE:HZ	1.73	0.54
1:A:811:ASP:CB	1:A:812:PRO:HD3	2.37	0.54
1:A:824:VAL:HG13	1:A:828:LYS:HB3	1.90	0.54
1:A:113:PHE:HE1	1:A:119:GLU:HB2	1.74	0.53
1:B:272:MET:HE2	1:B:319:LYS:HG2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:554:TYR:HB3	1:B:611:PHE:HZ	1.74	0.52
1:A:412:ARG:HA	1:A:415:PHE:HB3	1.93	0.50
1:B:113:PHE:HE1	1:B:119:GLU:HB2	1.76	0.50
1:B:753:MET:HA	1:B:753:MET:CE	2.41	0.50
1:A:19:LYS:HE3	1:A:20:TYR:H	1.77	0.50
1:B:824:VAL:HG13	1:B:828:LYS:HB3	1.93	0.50
1:A:809:LEU:HB2	1:A:813:VAL:CG1	2.42	0.49
1:B:19:LYS:HE3	1:B:20:TYR:H	1.77	0.49
1:B:91:ASN:HB3	4:B:1269:HOH:O	2.13	0.49
1:B:745:THR:OG1	1:B:747:GLU:HG2	2.13	0.49
1:B:641:LEU:HD11	1:B:653:LEU:HD13	1.95	0.49
1:B:765:ASP:CB	1:B:766:PRO:CD	2.87	0.48
1:A:641:LEU:HD11	1:A:653:LEU:HD13	1.95	0.47
1:A:770:GLU:HB3	1:A:771:SER:H	1.52	0.47
1:A:769:ILE:HG23	1:A:770:GLU:H	1.80	0.47
1:B:244:THR:HA	1:B:248:PHE:HB2	1.98	0.45
1:A:559:ARG:HD2	4:A:1237:HOH:O	2.17	0.45
1:A:244:THR:HA	1:A:248:PHE:HB2	1.99	0.45
1:A:390:MET:HE1	1:A:426:PHE:CE2	2.52	0.45
1:A:227:MET:CE	1:A:273:ARG:HG3	2.45	0.45
1:B:227:MET:CE	1:B:273:ARG:HG3	2.46	0.44
1:A:21:ILE:O	1:A:21:ILE:HG13	2.18	0.44
1:A:547:VAL:O	1:A:551:LYS:HG3	2.17	0.44
1:B:893:ILE:H	1:B:893:ILE:HG13	1.70	0.44
1:B:412:ARG:H	1:B:412:ARG:HD2	1.82	0.44
1:B:695:ALA:HB3	1:B:881:ASP:HB2	2.00	0.44
1:B:769:ILE:HG22	1:B:775:LYS:HG2	2.00	0.43
1:A:44:LEU:HD13	1:A:136:ILE:HG21	1.99	0.43
1:B:44:LEU:HD13	1:B:136:ILE:HG21	2.00	0.43
1:B:412:ARG:HD3	1:B:439:ILE:HD11	2.00	0.43
1:A:886:GLN:HB2	1:A:887:GLU:H	1.60	0.43
1:B:231:LYS:HE2	4:B:1414:HOH:O	2.18	0.43
1:A:110:ASP:HB3	1:A:118:LEU:HD11	2.01	0.43
1:B:29:SER:O	1:B:35:ASP:HB3	2.19	0.42
1:B:807:ILE:HG23	1:B:808:ASP:N	2.34	0.42
1:B:591:ILE:HG22	1:B:678:ARG:CG	2.49	0.42
1:A:60:MET:HE1	1:A:195:PHE:HE2	1.85	0.41
1:A:832:LEU:HA	1:A:835:ILE:HD12	2.02	0.41
1:B:832:LEU:HA	1:B:835:ILE:HD12	2.02	0.41
1:A:20:TYR:HB3	1:A:231[A]:LYS:HD3	2.02	0.41
1:B:154:ILE:HB	1:B:162:VAL:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:890:LEU:C	1:B:892:TYR:H	2.23	0.41
1:A:371:LEU:HD22	1:A:398:VAL:HG21	2.02	0.41
1:B:547:VAL:O	1:B:551:LYS:HG3	2.21	0.41
1:A:89:LEU:HD11	1:A:159:LEU:HD21	2.03	0.40
1:A:322:ARG:HG2	1:A:322:ARG:NH1	2.11	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	856/1038 (82%)	790 (92%)	51 (6%)	15 (2%)	8	10
1	B	857/1038 (83%)	792 (92%)	54 (6%)	11 (1%)	12	17
All	All	1713/2076 (82%)	1582 (92%)	105 (6%)	26 (2%)	10	14

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	411	HIS
1	A	767	THR
1	A	770	GLU
1	A	811	ASP
1	A	886	GLN
1	A	891	ASP
1	B	411	HIS
1	B	585	ASN
1	B	765	ASP
1	B	807	ILE
1	A	591	ILE
1	A	813	VAL
1	A	889	ASN

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Mol	Chain	Res	Type
1	B	140	PHE
1	B	190	SER
1	B	768	SER
1	A	769	ILE
1	A	871	THR
1	A	884	LYS
1	B	412	ARG
1	B	584	ALA
1	B	769	ILE
1	B	891	ASP
1	A	412	ARG
1	A	589	ASN
1	A	855	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	775/927 (84%)	745 (96%)	30 (4%)	32	50
1	B	777/927 (84%)	746 (96%)	31 (4%)	31	49
All	All	1552/1854 (84%)	1491 (96%)	61 (4%)	32	50

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	19	LYS
1	A	38	ARG
1	A	39	GLU
1	A	139	GLN
1	A	181	HIS
1	A	270	LEU
1	A	322	ARG
1	A	393	GLU
1	A	472	VAL

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Mol	Chain	Res	Type
1	A	655	VAL
1	A	747	GLU
1	A	749	LYS
1	A	750	ARG
1	A	765	ASP
1	A	767	THR
1	A	770	GLU
1	A	772	GLU
1	A	777	ASP
1	A	806	GLN
1	A	807	ILE
1	A	811	ASP
1	A	836	ARG
1	A	841	ARG
1	A	842	LYS
1	A	854	ARG
1	A	882	LEU
1	A	886	GLN
1	A	890	LEU
1	A	891	ASP
1	B	19	LYS
1	B	117	ARG
1	B	179	GLN
1	B	180	ILE
1	B	191	GLU
1	B	194	LEU
1	B	217	LYS
1	B	224	ASP
1	B	270	LEU
1	B	393	GLU
1	B	412	ARG
1	B	472	VAL
1	B	511	MET
1	B	531	THR
1	B	575	ARG
1	B	586	GLU
1	B	587	GLU
1	B	655	VAL
1	B	722	LYS
1	B	749	LYS
1	B	750	ARG
1	B	769	ILE

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Mol	Chain	Res	Type
1	B	806	GLN
1	B	809	LEU
1	B	816	GLU
1	B	828	LYS
1	B	841	ARG
1	B	860	GLU
1	B	890	LEU
1	B	893	ILE
1	B	896	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	ATP	B	1102	2	26,33,33	0.75	0	31,52,52	0.93	1 (3%)
3	ATP	A	1102	2	26,33,33	0.70	0	31,52,52	0.88	2 (6%)

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	ATP	B	1102	2	-	1/18/38/38	0/3/3/3
3	ATP	A	1102	2	-	0/18/38/38	0/3/3/3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1102	ATP	O3G-PG-O2G	2.45	117.02	107.64
3	B	1102	ATP	C5-C6-N6	2.04	123.46	120.35
3	A	1102	ATP	C5-C6-N6	2.01	123.41	120.35

There are no chirality outliers.

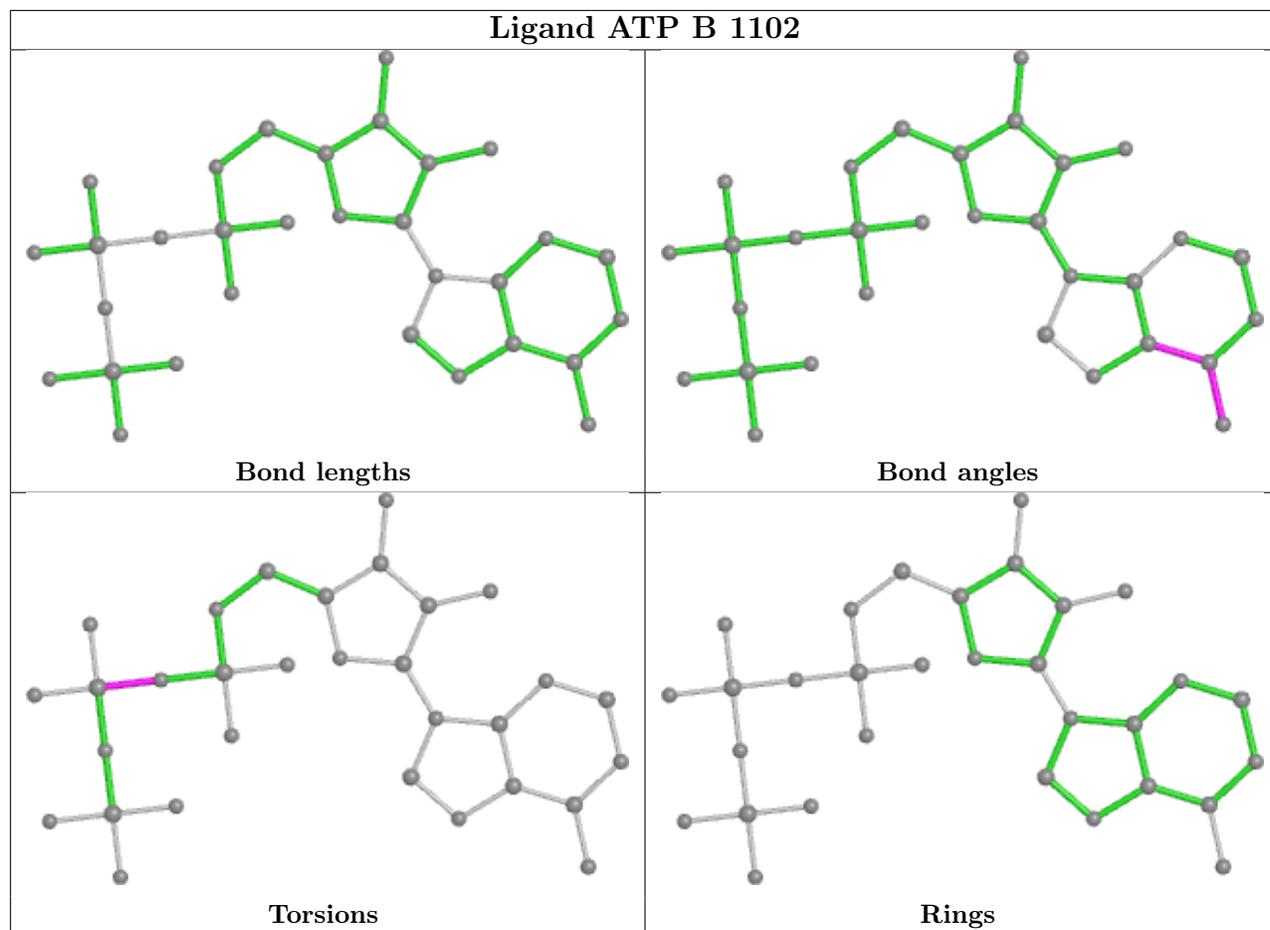
All (1) torsion outliers are listed below:

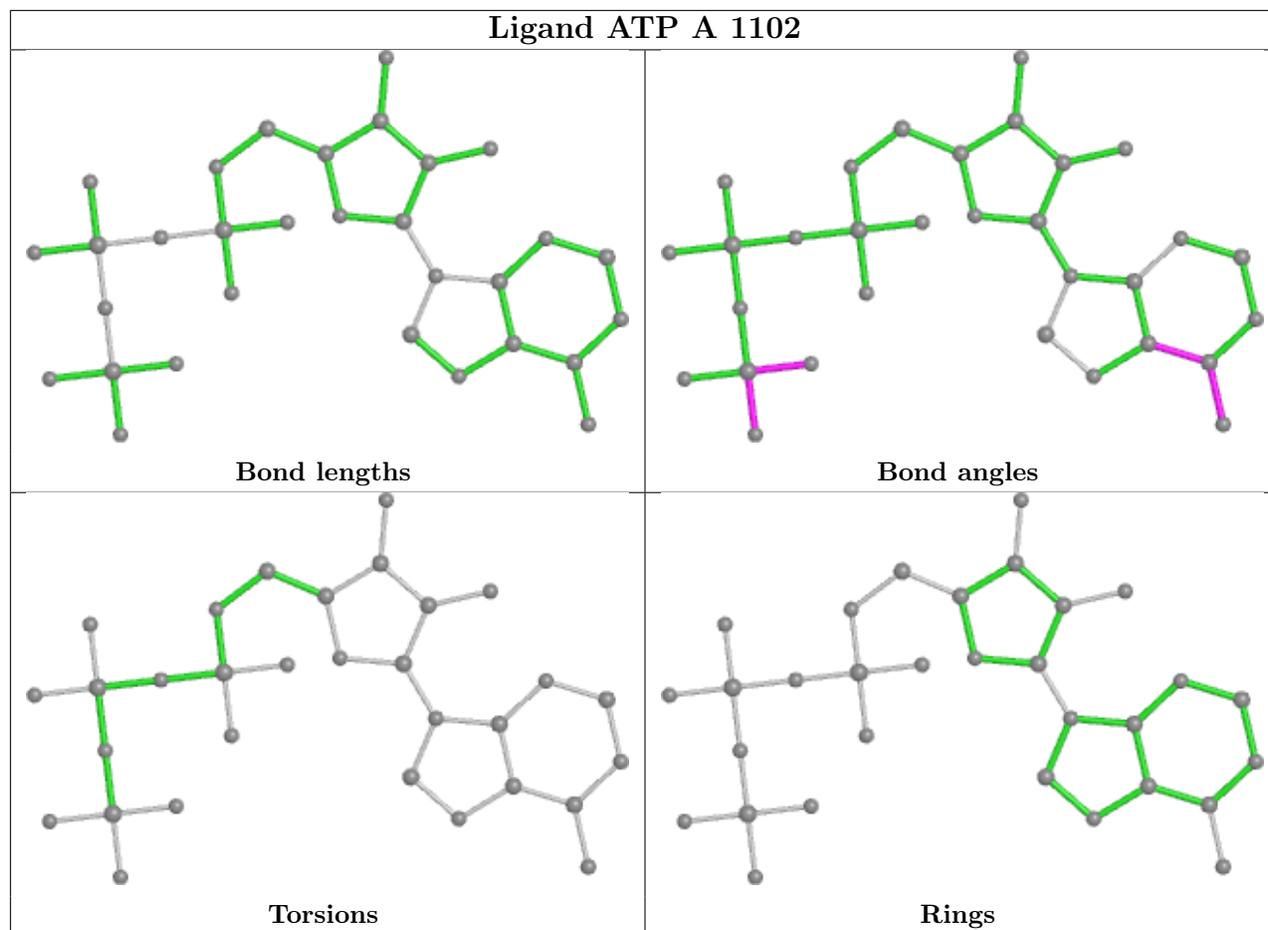
Mol	Chain	Res	Type	Atoms
3	B	1102	ATP	PA-O3A-PB-O2B

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	861/1038 (82%)	0.33	66 (7%) 13 12	29, 50, 102, 134	0
1	B	863/1038 (83%)	0.17	60 (6%) 16 15	25, 46, 95, 129	0
All	All	1724/2076 (83%)	0.25	126 (7%) 15 13	25, 48, 99, 134	0

All (126) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	810	SER	16.0
1	A	445	LEU	11.5
1	A	813	VAL	10.5
1	A	811	ASP	8.2
1	A	766	PRO	8.0
1	A	183	TYR	7.6
1	A	888	ILE	7.4
1	B	896	LEU	7.3
1	B	813	VAL	7.2
1	A	812	PRO	6.7
1	A	592	GLY	6.4
1	B	768	SER	6.4
1	A	446	GLY	6.3
1	A	767	THR	6.1
1	B	809	LEU	5.8
1	B	890	LEU	5.8
1	A	182	ARG	5.2
1	B	587	GLU	5.1
1	A	856	TRP	5.1
1	B	589	ASN	5.1
1	B	894	LEU	5.1
1	A	588	GLN	5.1
1	B	810	SER	5.0
1	A	412	ARG	4.9

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Mol	Chain	Res	Type	RSRZ
1	B	588	GLN	4.8
1	B	592	GLY	4.7
1	A	441	PRO	4.6
1	A	814	ALA	4.5
1	A	829	PHE	4.5
1	B	892	TYR	4.4
1	A	892	TYR	4.3
1	A	807	ILE	4.2
1	B	893	ILE	4.2
1	B	812	PRO	4.1
1	B	181	HIS	4.1
1	B	814	ALA	4.0
1	B	570	THR	4.0
1	A	854	ARG	4.0
1	B	586	GLU	4.0
1	A	809	LEU	3.9
1	A	444	ALA	3.9
1	A	808	ASP	3.9
1	A	591	ILE	3.9
1	A	190	SER	3.8
1	A	818	PHE	3.8
1	A	570	THR	3.8
1	A	587	GLU	3.8
1	B	141	GLU	3.8
1	B	769	ILE	3.7
1	A	890	LEU	3.6
1	B	446	GLY	3.6
1	A	851	ASN	3.5
1	B	815	VAL	3.5
1	B	889	ASN	3.5
1	B	891	ASP	3.4
1	A	887	GLU	3.4
1	A	768	SER	3.3
1	B	818	PHE	3.3
1	B	871	THR	3.3
1	A	848	SER	3.3
1	A	148	ASN	3.3
1	A	769	ILE	3.3
1	B	856	TRP	3.3
1	B	585	ASN	3.2
1	A	889	ASN	3.2
1	B	807	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	189	ASN	3.1
1	B	584	ALA	3.1
1	A	498	LEU	3.1
1	A	184	SER	3.1
1	A	871	THR	3.1
1	B	770	GLU	3.0
1	A	584	ALA	3.0
1	B	829	PHE	3.0
1	B	23	ALA	3.0
1	A	569	ALA	2.9
1	B	411	HIS	2.9
1	A	586	GLU	2.8
1	B	412	ARG	2.8
1	B	21	ILE	2.8
1	A	891	ASP	2.8
1	A	185	LYS	2.8
1	B	820	ALA	2.8
1	A	589	ASN	2.8
1	B	441	PRO	2.8
1	A	774	GLU	2.7
1	B	744	ALA	2.7
1	A	770	GLU	2.7
1	B	687	SER	2.6
1	B	495	GLU	2.6
1	A	296	TRP	2.6
1	B	765	ASP	2.6
1	A	838	PRO	2.5
1	A	440	PHE	2.5
1	A	411	HIS	2.5
1	A	853	ILE	2.5
1	B	568	SER	2.5
1	B	26	THR	2.5
1	B	745	THR	2.5
1	A	772	GLU	2.4
1	B	445	LEU	2.4
1	B	27	GLY	2.4
1	B	895	GLY	2.3
1	B	190	SER	2.2
1	B	569	ALA	2.2
1	A	181	HIS	2.2
1	A	839	ALA	2.2
1	B	888	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	806	GLN	2.2
1	A	374	ASP	2.2
1	A	447	SER	2.2
1	A	23	ALA	2.1
1	B	533	PRO	2.1
1	A	687	SER	2.1
1	B	148	ASN	2.1
1	A	765	ASP	2.1
1	B	572	LYS	2.1
1	B	808	ASP	2.1
1	B	883	LEU	2.1
1	B	92	PRO	2.0
1	A	171	VAL	2.0
1	B	292	THR	2.0
1	B	443	ASN	2.0
1	B	853	ILE	2.0
1	A	775	LYS	2.0
1	A	397	PRO	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](#)

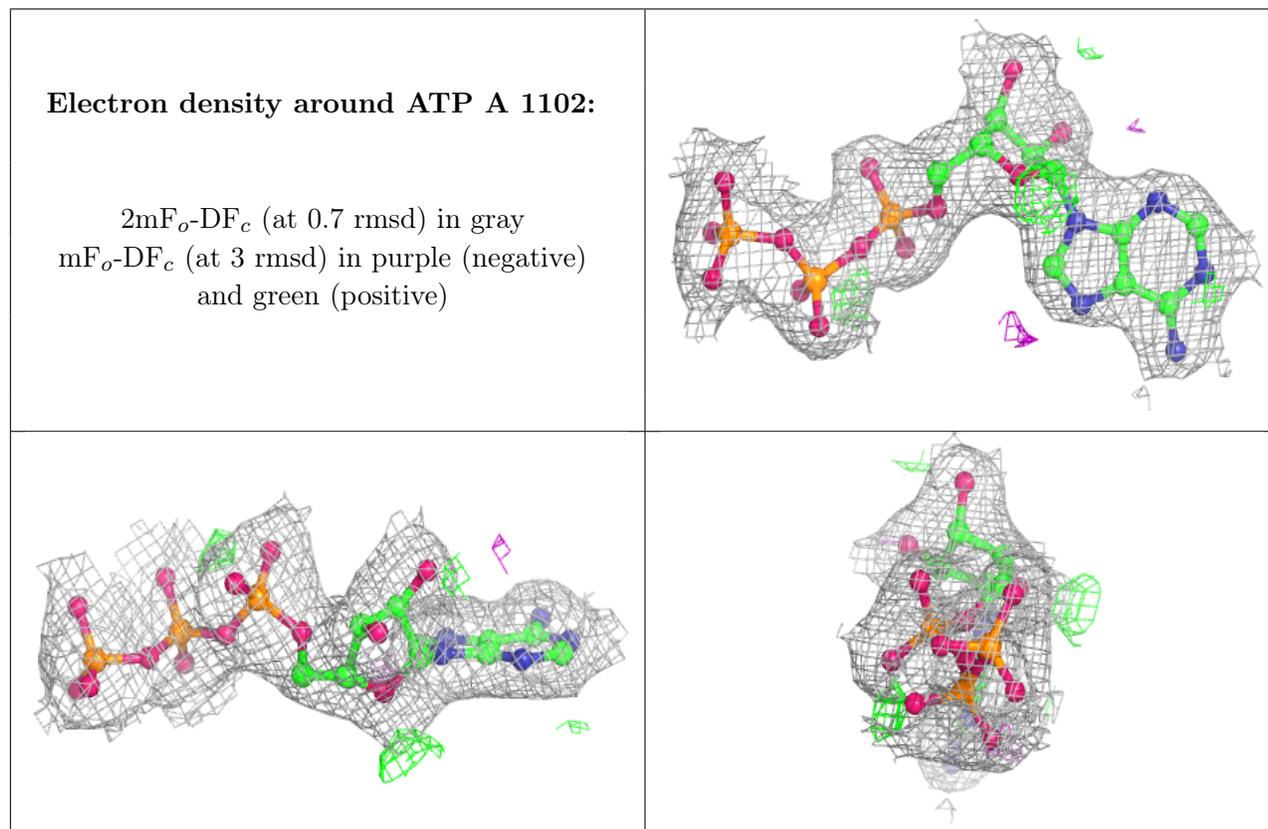
There are no monosaccharides in this entry.

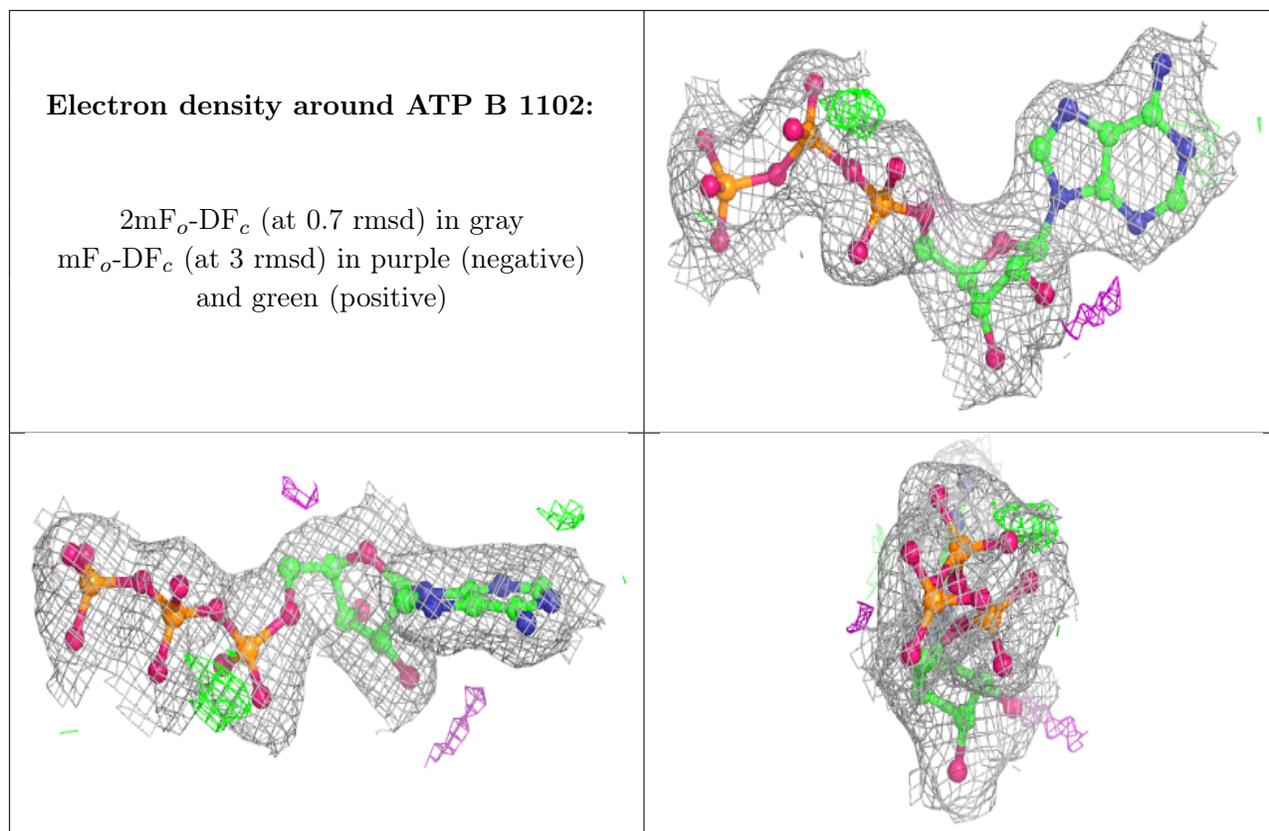
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
2	MG	A	1101	1/1	0.97	0.15	40,40,40,40	0
2	MG	B	1101	1/1	0.97	0.17	33,33,33,33	0
3	ATP	A	1102	31/31	0.98	0.18	26,35,40,41	0
3	ATP	B	1102	31/31	0.98	0.18	25,33,38,38	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.