



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 03:38 pm BST

PDB ID : 4BE7
Title : MUTANT (K220R) OF THE HSDR SUBUNIT OF THE ECOR124I RESTRICTION ENZYME IN COMPLEX WITH ATP
Authors : Csefalvay, E.; Lapkouski, M.; Guzanova, A.; Csefalvay, L.; Baikova, T.; Shevelev, I.; Janscak, P.; Smatanova, I.K.; Panjikar, S.; Carey, J.; Weiserova, M.; Ettrich, R.
Deposited on : 2013-03-06
Resolution : 2.74 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

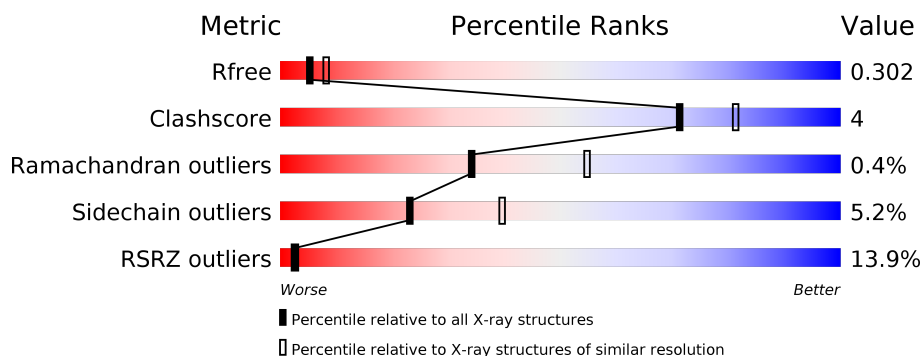
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.74 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	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	B	1038	<div> <div>9%</div> <div> <div></div> <div>71%</div> <div>8%</div> <div>19%</div> </div> </div>
1	D	1038	<div> <div>13%</div> <div> <div></div> <div>70%</div> <div>9%</div> <div>20%</div> </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 13387 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.

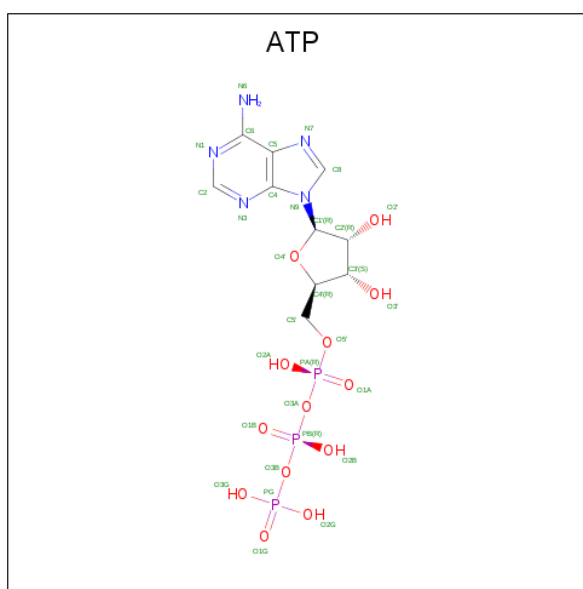
- Molecule 1 is a protein called TYPE I RESTRICTION ENZYME ECOR124II R PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	837	Total	C	N	O	S	0	0	0
			6631	4226	1112	1277	16			
1	D	835	Total	C	N	O	S	0	0	0
			6594	4204	1106	1268	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	220	ARG	LYS	engineered mutation	UNP Q304R3
D	220	ARG	LYS	engineered mutation	UNP Q304R3

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



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

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

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



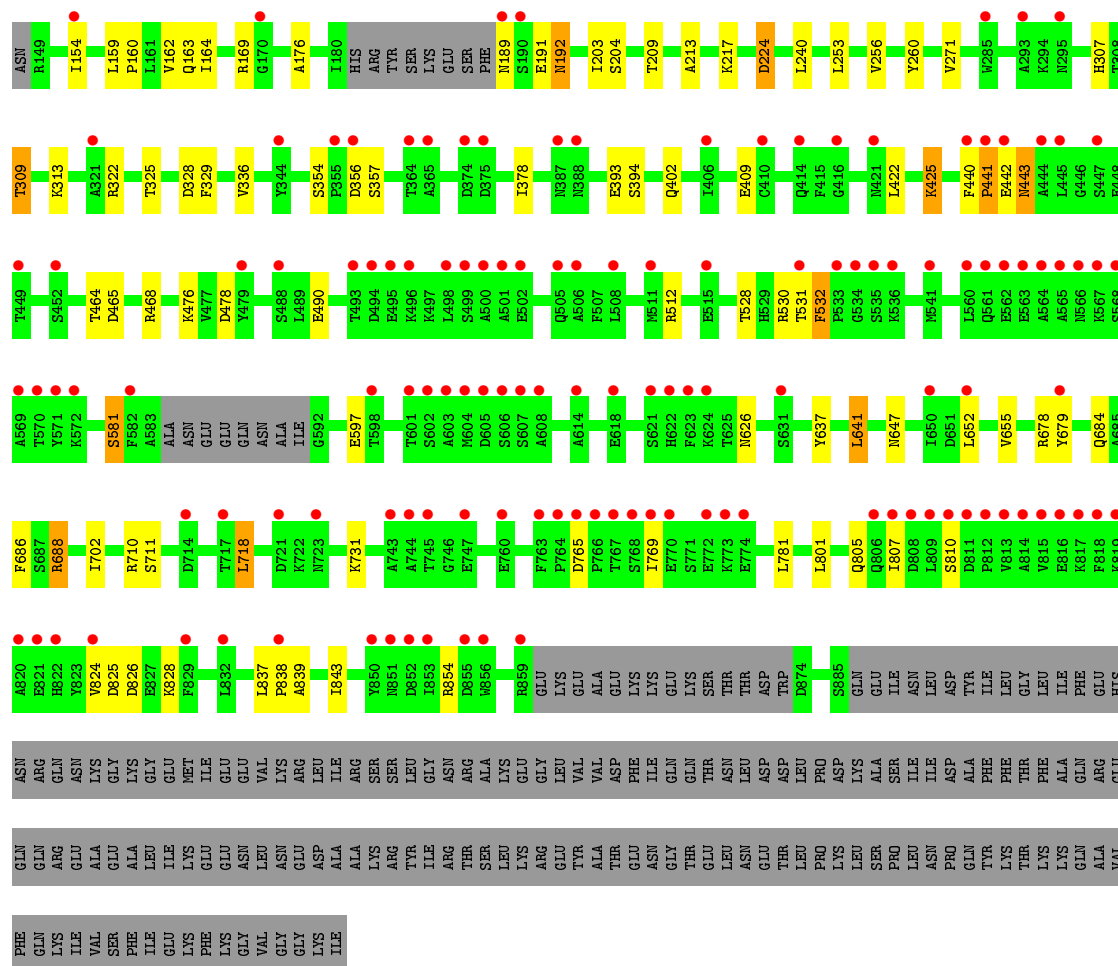
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	45	Total 45	O 45	0	0
5	D	33	Total 33	O 33	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.05Å 124.35Å 128.01Å 90.00° 108.86° 90.00°	Depositor
Resolution (Å)	32.36 – 2.74 33.73 – 2.74	Depositor EDS
% Data completeness (in resolution range)	93.2 (32.36-2.74) 93.5 (33.73-2.74)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.76Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.249 , 0.292 0.263 , 0.302	Depositor DCC
R_{free} test set	3200 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	42.1	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	13387	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.14% 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, PO4, 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	B	0.27	0/6760	0.52	1/9146 (0.0%)
1	D	0.27	0/6721	0.53	3/9097 (0.0%)
All	All	0.27	0/13481	0.53	4/18243 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	441	PRO	C-N-CA	6.15	137.08	121.70
1	D	441	PRO	CA-C-N	5.29	128.83	117.20
1	B	769	ILE	N-CA-C	-5.26	96.79	111.00
1	D	826	ASP	C-N-CA	5.03	134.27	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	B	6631	0	6305	44	0
1	D	6594	0	6268	47	0
2	B	31	0	12	1	0
2	D	31	0	12	1	0
3	B	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	10	0	0	0	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
5	B	45	0	0	1	0
5	D	33	0	0	1	0
All	All	13387	0	12597	91	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 4.

All (91) 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:824:VAL:HG13	1:D:828:LYS:HB3	1.54	0.90
1:D:27:GLY:HA2	1:D:28:ASP:HB2	1.59	0.85
1:D:169:ARG:HG3	1:D:169:ARG:HH11	1.52	0.73
1:D:465:ASP:OD1	1:D:468:ARG:NH2	2.22	0.71
1:D:322:ARG:NH2	5:D:2021:HOH:O	2.25	0.69
1:B:770:GLU:N	1:B:770:GLU:OE1	2.25	0.68
1:D:440:PHE:O	1:D:443:ASN:ND2	2.28	0.66
1:D:801:LEU:HG	1:D:837:LEU:HD11	1.78	0.65
1:B:322:ARG:NH2	5:B:2025:HOH:O	2.29	0.65
1:B:769:ILE:HG22	1:B:770:GLU:HA	1.79	0.65
1:B:213:ALA:HB2	1:B:271:VAL:HG23	1.81	0.63
1:D:440:PHE:N	1:D:443:ASN:OD1	2.29	0.62
1:D:54:VAL:HG11	1:D:60:MET:HG3	1.82	0.62
1:B:226:THR:O	1:B:471:LYS:NZ	2.30	0.62
1:D:684:GLN:O	1:D:688:ARG:NH1	2.32	0.62
1:D:213:ALA:HB2	1:D:271:VAL:HG23	1.82	0.62
1:D:688:ARG:NH2	2:D:1887:ATP:O1G	2.30	0.61
1:B:154:ILE:HB	1:B:162:VAL:HB	1.81	0.60
1:D:154:ILE:HB	1:D:162:VAL:HB	1.83	0.60
1:D:678:ARG:NH1	1:D:711:SER:OG	2.34	0.60
1:B:298:LYS:O	1:B:301:SER:OG	2.21	0.58
1:B:65:ARG:HG3	1:B:81:TRP:CD2	2.39	0.58
1:B:110:ASP:HB2	1:B:118:LEU:HD21	1.86	0.57
1:B:313:LYS:NZ	1:B:409:GLU:OE1	2.32	0.57
1:B:443:ASN:HB3	1:B:718:LEU:HD11	1.86	0.57
1:D:309:THR:HA	1:D:313:LYS:HE2	1.86	0.56
1:B:13:ASN:HD22	1:B:13:ASN:N	2.04	0.56
1:B:89:LEU:O	1:B:99:LYS:NZ	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:313:LYS:NZ	1:D:409:GLU:OE1	2.37	0.55
1:D:54:VAL:HG11	1:D:60:MET:CG	2.37	0.55
1:B:44:LEU:HD13	1:B:136:ILE:HG21	1.89	0.54
1:B:54:VAL:HG11	1:B:60:MET:HG3	1.90	0.53
1:B:688:ARG:NH2	2:B:1887:ATP:O1G	2.34	0.53
1:B:824:VAL:HG13	1:B:828:LYS:HB3	1.89	0.53
1:B:838:PRO:HG2	1:B:843:ILE:HD11	1.92	0.52
1:D:189:ASN:HA	1:D:192:ASN:OD1	2.10	0.51
1:B:801:LEU:HG	1:B:837:LEU:HD11	1.91	0.51
1:B:101:ARG:NH1	1:B:106:ASP:OD2	2.38	0.51
1:B:54:VAL:HG11	1:B:60:MET:CG	2.41	0.51
1:B:204:SER:HB2	1:B:209:THR:HG23	1.94	0.50
1:D:325:THR:HG21	1:D:378:ILE:HB	1.94	0.50
1:D:88:TYR:CE1	1:D:109:CYS:HB2	2.47	0.49
1:D:125:ASP:OD2	1:D:131:ARG:NH1	2.45	0.49
1:B:686:PHE:CZ	1:B:702:ILE:HG21	2.49	0.48
1:D:110:ASP:HB2	1:D:118:LEU:HD21	1.95	0.48
1:B:26:THR:OG1	1:B:27:GLY:HA2	2.13	0.48
1:D:679:TYR:CD1	1:D:718:LEU:HD12	2.49	0.48
1:B:256:VAL:HA	1:B:260:TYR:HB2	1.94	0.47
1:D:581:SER:O	1:D:597:GLU:HB3	2.15	0.47
1:D:528:THR:OG1	1:D:530:ARG:HD2	2.14	0.46
1:B:125:ASP:OD2	1:B:131:ARG:NH1	2.48	0.46
1:D:256:VAL:HA	1:D:260:TYR:HB2	1.96	0.46
1:B:112:ILE:HD13	1:B:118:LEU:HD23	1.98	0.46
1:D:531:THR:HG23	1:D:532:PHE:H	1.80	0.46
1:D:441:PRO:HB2	1:D:442:GLU:HB2	1.98	0.46
1:D:825:ASP:O	1:D:828:LYS:HB2	2.15	0.46
1:D:224:ASP:N	1:D:224:ASP:OD1	2.48	0.46
1:D:838:PRO:HG2	1:D:843:ILE:HD11	1.98	0.46
1:D:686:PHE:CZ	1:D:702:ILE:HG21	2.52	0.45
1:D:328:ASP:OD1	1:D:329:PHE:N	2.49	0.45
1:B:684:GLN:O	1:B:688:ARG:NH1	2.47	0.45
1:D:89:LEU:HD21	1:D:159:LEU:HD21	1.98	0.44
1:D:354:SER:HB3	1:D:357:SER:OG	2.17	0.44
1:D:637:TYR:O	1:D:641:LEU:HB2	2.18	0.44
1:B:342:LEU:O	1:B:638:TYR:OH	2.32	0.44
1:B:57:GLN:OE1	1:B:192:ASN:HB3	2.17	0.44
1:B:637:TYR:O	1:B:641:LEU:HB2	2.18	0.44
1:B:99:LYS:HD2	1:B:197:TYR:CZ	2.52	0.44
1:B:440:PHE:N	1:B:443:ASN:OD1	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:ALA:HB1	1:D:203:ILE:HD11	1.99	0.43
1:B:704:THR:HG21	1:B:708:LEU:HD12	2.01	0.43
1:B:769:ILE:CG2	1:B:770:GLU:HA	2.46	0.43
1:B:99:LYS:HD2	1:B:197:TYR:CE2	2.52	0.43
1:D:204:SER:HB2	1:D:209:THR:HG23	1.99	0.43
1:D:57:GLN:HB2	1:D:191:GLU:O	2.19	0.43
1:B:60:MET:HE2	1:B:194:LEU:HD13	2.01	0.43
1:D:394:SER:HA	1:D:425:LYS:NZ	2.33	0.43
1:D:839:ALA:O	1:D:843:ILE:HG12	2.19	0.43
1:B:763:PHE:HA	1:B:768:SER:CB	2.49	0.43
1:B:544:VAL:HA	1:B:674:ASP:O	2.19	0.42
1:D:60:MET:HE1	1:D:160:PRO:HD3	2.02	0.42
1:D:490:GLU:HG2	1:D:512:ARG:HH21	1.83	0.42
1:B:763:PHE:HA	1:B:768:SER:HB3	2.01	0.42
1:D:44:LEU:HD13	1:D:136:ILE:HG21	2.02	0.42
1:B:640:ASP:OD2	1:B:644:ARG:NE	2.50	0.41
1:D:40:LEU:HD11	1:D:164:ILE:HG21	2.01	0.41
1:B:847:ARG:NH2	1:B:886:GLN:OE1	2.40	0.41
1:D:65:ARG:HG3	1:D:81:TRP:CD2	2.54	0.41
1:D:476:LYS:NZ	1:D:478:ASP:OD2	2.48	0.41
1:B:679:TYR:CD1	1:B:718:LEU:HD12	2.56	0.40
1:B:60:MET:HE1	1:B:160:PRO:HD3	2.03	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	B	827/1038 (80%)	798 (96%)	26 (3%)	3 (0%)	34 55
1	D	825/1038 (80%)	785 (95%)	37 (4%)	3 (0%)	34 55
All	All	1652/2076 (80%)	1583 (96%)	63 (4%)	6 (0%)	34 55

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	810	SER
1	B	807	ILE
1	B	810	SER
1	D	807	ILE
1	B	769	ILE
1	D	769	ILE

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	B	690/927 (74%)	656 (95%)	34 (5%)	25	43
1	D	684/927 (74%)	647 (95%)	37 (5%)	22	38
All	All	1374/1854 (74%)	1303 (95%)	71 (5%)	23	39

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	13	ASN
1	B	21	ILE
1	B	40	LEU
1	B	65	ARG
1	B	71	LEU
1	B	89	LEU
1	B	118	LEU
1	B	165	GLU
1	B	169	ARG
1	B	221	ASN
1	B	240	LEU
1	B	253	LEU
1	B	282	ARG
1	B	298	LYS
1	B	301	SER
1	B	307	HIS
1	B	332	LYS

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Mol	Chain	Res	Type
1	B	336	VAL
1	B	346	THR
1	B	356	ASP
1	B	393	GLU
1	B	402	GLN
1	B	422	LEU
1	B	464	THR
1	B	641	LEU
1	B	652	LEU
1	B	655	VAL
1	B	688	ARG
1	B	718	LEU
1	B	722	LYS
1	B	731	LYS
1	B	765	ASP
1	B	781	LEU
1	B	840	ASP
1	D	21	ILE
1	D	26	THR
1	D	40	LEU
1	D	89	LEU
1	D	118	LEU
1	D	134	VAL
1	D	163	GLN
1	D	192	ASN
1	D	217	LYS
1	D	224	ASP
1	D	240	LEU
1	D	253	LEU
1	D	307	HIS
1	D	309	THR
1	D	336	VAL
1	D	356	ASP
1	D	393	GLU
1	D	402	GLN
1	D	422	LEU
1	D	425	LYS
1	D	443	ASN
1	D	464	THR
1	D	532	PHE
1	D	581	SER
1	D	626	ASN

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Mol	Chain	Res	Type
1	D	641	LEU
1	D	647	ASN
1	D	652	LEU
1	D	655	VAL
1	D	688	ARG
1	D	710	ARG
1	D	718	LEU
1	D	731	LYS
1	D	765	ASP
1	D	781	LEU
1	D	805	GLN
1	D	854	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	91	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	PO4	B	1888	-	4,4,4	0.89	0	6,6,6	0.42	0
3	PO4	B	1889	-	4,4,4	0.92	0	6,6,6	0.36	0
2	ATP	B	1887	4	26,33,33	0.92	1 (3%)	31,52,52	1.46	4 (12%)
2	ATP	D	1887	4	26,33,33	0.91	1 (3%)	31,52,52	1.45	5 (16%)
3	PO4	D	1889	-	4,4,4	0.89	0	6,6,6	0.37	0
3	PO4	D	1890	-	4,4,4	0.94	0	6,6,6	0.44	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
2	ATP	B	1887	4	-	0/18/38/38	0/3/3/3
2	ATP	D	1887	4	-	1/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1887	ATP	C5-C4	2.39	1.47	1.40
2	D	1887	ATP	C5-C4	2.38	1.47	1.40

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1887	ATP	PA-O3A-PB	-3.66	120.28	132.83
2	D	1887	ATP	PA-O3A-PB	-3.47	120.91	132.83
2	D	1887	ATP	N3-C2-N1	-3.21	123.66	128.68
2	B	1887	ATP	N3-C2-N1	-3.09	123.84	128.68
2	D	1887	ATP	PB-O3B-PG	-2.72	123.49	132.83
2	B	1887	ATP	PB-O3B-PG	-2.67	123.66	132.83
2	B	1887	ATP	C4-C5-N7	-2.56	106.73	109.40
2	D	1887	ATP	C4-C5-N7	-2.52	106.78	109.40
2	D	1887	ATP	C3'-C2'-C1'	2.10	104.14	100.98

There are no chirality outliers.

All (1) torsion outliers are listed below:

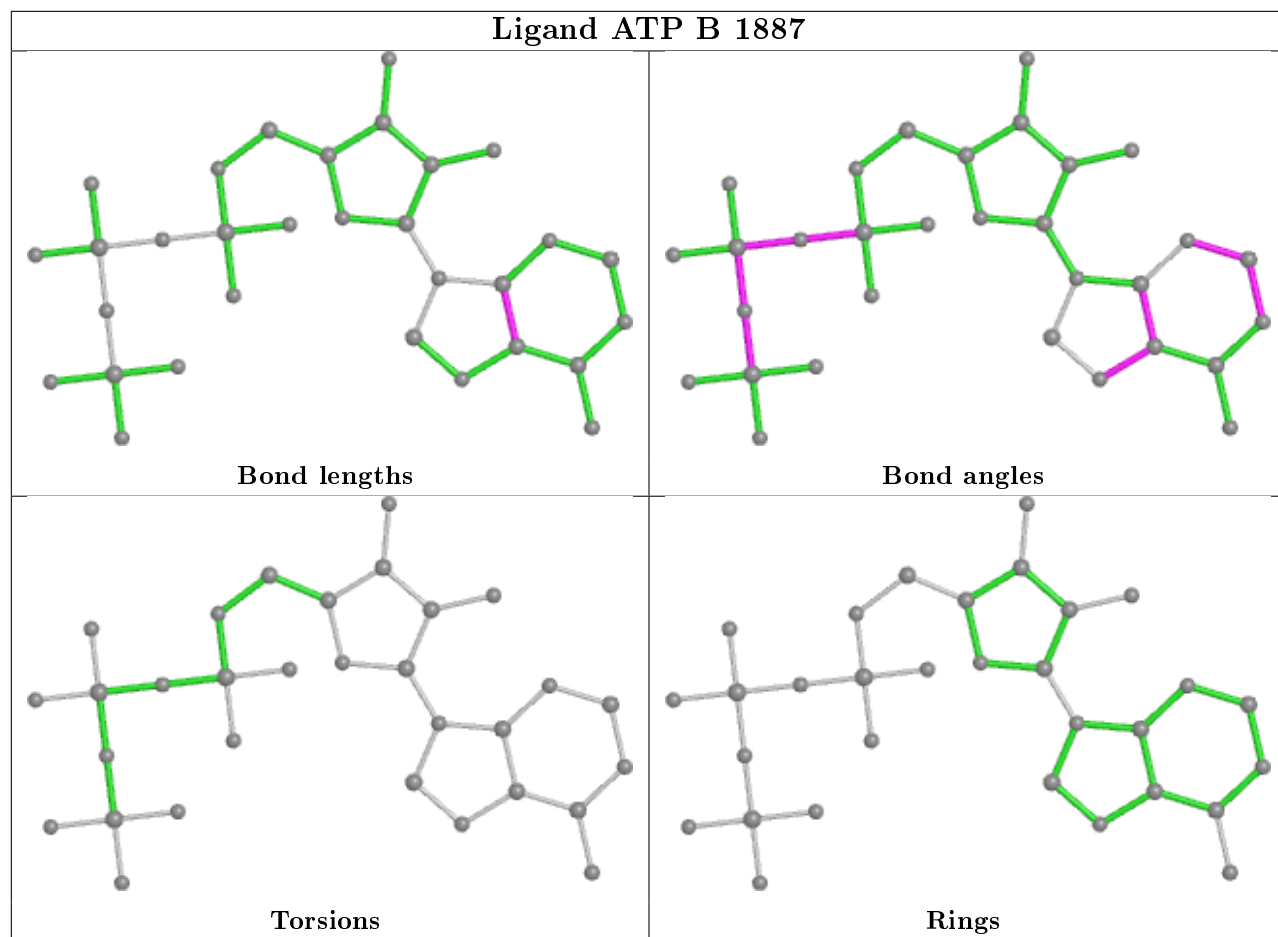
Mol	Chain	Res	Type	Atoms
2	D	1887	ATP	PB-O3B-PG-O1G

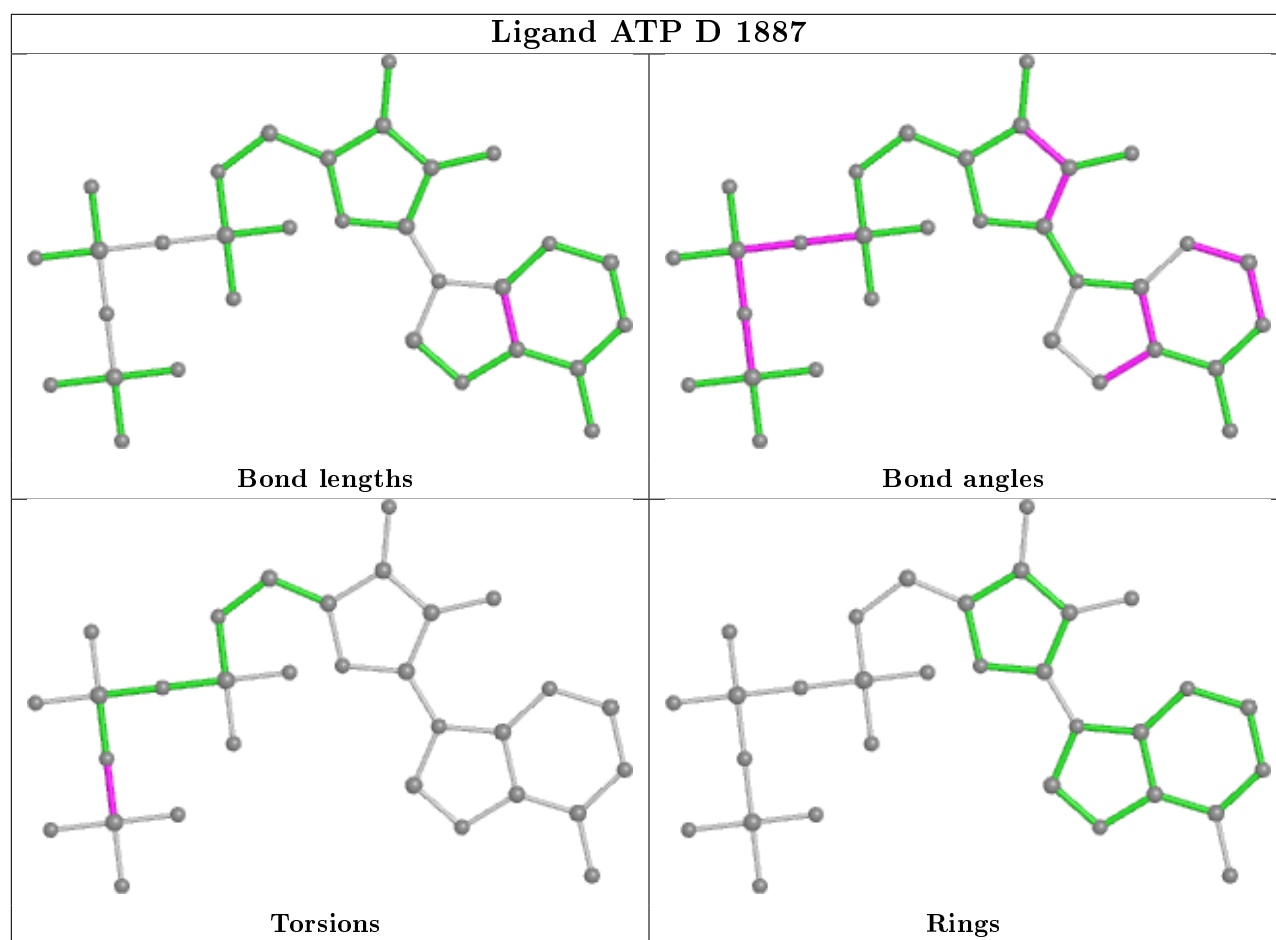
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1887	ATP	1	0
2	D	1887	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.





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	B	837/1038 (80%)	0.80	96 (11%) 4 4	13, 33, 71, 121	0
1	D	835/1038 (80%)	0.96	137 (16%) 1 1	17, 40, 84, 114	0
All	All	1672/2076 (80%)	0.88	233 (13%) 2 3	13, 36, 78, 121	0

All (233) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	809	LEU	14.0
1	B	807	ILE	8.3
1	B	808	ASP	8.3
1	D	604	MET	7.8
1	B	813	VAL	7.7
1	D	566	ASN	7.6
1	D	809	LEU	7.5
1	B	566	ASN	7.1
1	D	534	GLY	7.0
1	B	745	THR	6.9
1	B	568	SER	6.8
1	D	768	SER	6.7
1	D	569	ALA	6.6
1	D	565	ALA	6.6
1	D	818	PHE	6.6
1	D	808	ASP	6.6
1	B	812	PRO	6.5
1	B	814	ALA	6.5
1	D	816	GLU	6.4
1	B	564	ALA	6.3
1	D	603	ALA	6.3
1	D	533	PRO	6.2
1	D	570	THR	6.0
1	B	506	ALA	6.0

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Mol	Chain	Res	Type	RSRZ
1	B	567	LYS	6.0
1	D	807	ILE	5.6
1	D	819	LYS	5.5
1	D	769	ILE	5.4
1	B	820	ALA	5.4
1	D	563	GLU	5.3
1	D	511	MET	5.2
1	D	810	SER	5.1
1	D	813	VAL	5.1
1	D	767	THR	5.1
1	B	498	LEU	4.9
1	D	495	GLU	4.9
1	B	170	GLY	4.8
1	B	565	ALA	4.6
1	B	744	ALA	4.6
1	D	623	PHE	4.5
1	D	773	LYS	4.5
1	D	811	ASP	4.5
1	D	723	ASN	4.5
1	B	826	ASP	4.5
1	D	562	GLU	4.4
1	B	722	LYS	4.4
1	B	604	MET	4.4
1	D	441	PRO	4.4
1	D	506	ALA	4.3
1	D	772	GLU	4.3
1	D	814	ALA	4.3
1	D	567	LYS	4.3
1	D	568	SER	4.2
1	D	853	ILE	4.2
1	D	502	GLU	4.2
1	B	723	ASN	4.2
1	B	855	ASP	4.1
1	D	717	THR	4.1
1	B	356	ASP	4.1
1	B	511	MET	4.0
1	B	494	ASP	3.9
1	D	815	VAL	3.9
1	D	820	ALA	3.9
1	D	855	ASP	3.9
1	D	743	ALA	3.9
1	D	745	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	744	ALA	3.8
1	D	714	ASP	3.8
1	D	765	ASP	3.8
1	B	818	PHE	3.8
1	D	421	ASN	3.8
1	D	602	SER	3.8
1	B	563	GLU	3.7
1	D	498	LEU	3.7
1	B	606	SER	3.7
1	D	560	LEU	3.7
1	D	535	SER	3.6
1	B	718	LEU	3.6
1	D	564	ALA	3.6
1	B	621	SER	3.6
1	D	499	SER	3.5
1	B	819	LYS	3.5
1	B	509	HIS	3.5
1	B	570	THR	3.5
1	D	766	PRO	3.4
1	B	449	THR	3.4
1	D	774	GLU	3.4
1	B	824	VAL	3.4
1	D	501	ALA	3.4
1	D	582	PHE	3.4
1	D	355	PRO	3.4
1	D	374	ASP	3.4
1	D	406	ILE	3.3
1	B	825	ASP	3.3
1	D	479	TYR	3.3
1	B	441	PRO	3.3
1	B	508	LEU	3.3
1	B	770	GLU	3.2
1	D	812	PRO	3.2
1	D	601	THR	3.2
1	D	817	LYS	3.2
1	D	770	GLU	3.2
1	B	829	PHE	3.2
1	B	150	TYR	3.2
1	D	344	TYR	3.2
1	B	618	GLU	3.1
1	B	827	GLU	3.1
1	D	824	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	571	TYR	3.1
1	D	606	SER	3.1
1	B	605	ASP	3.1
1	D	605	ASP	3.1
1	D	764	PRO	3.1
1	D	500	ALA	3.1
1	B	571	TYR	3.1
1	D	622	HIS	3.1
1	D	806	GLN	3.1
1	B	496	LYS	3.1
1	B	190	SER	3.1
1	B	743	ALA	3.0
1	B	502	GLU	3.0
1	D	822	HIS	3.0
1	B	357	SER	3.0
1	B	444	ALA	3.0
1	D	821	GLU	2.9
1	D	170	GLY	2.9
1	B	806	GLN	2.9
1	D	679	TYR	2.9
1	B	627	PHE	2.8
1	D	32	SER	2.8
1	D	572	LYS	2.8
1	D	721	ASP	2.8
1	B	290	SER	2.8
1	D	508	LEU	2.8
1	B	355	PRO	2.8
1	D	850	TYR	2.8
1	B	445	LEU	2.8
1	D	365	ALA	2.7
1	D	444	ALA	2.7
1	D	447	SER	2.7
1	B	623	PHE	2.7
1	B	533	PRO	2.7
1	B	854	ARG	2.7
1	D	189	ASN	2.7
1	B	505	GLN	2.7
1	D	493	THR	2.7
1	D	505	GLN	2.7
1	D	28	ASP	2.7
1	D	614	ALA	2.7
1	D	356	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	829	PHE	2.6
1	D	608	ALA	2.6
1	B	817	LYS	2.6
1	D	440	PHE	2.6
1	B	446	GLY	2.6
1	B	560	LEU	2.6
1	B	742	ASP	2.6
1	D	375	ASP	2.6
1	B	420	LYS	2.5
1	D	496	LYS	2.5
1	B	569	ALA	2.5
1	D	536	LYS	2.5
1	D	295	ASN	2.5
1	B	501	ALA	2.5
1	D	852	ASP	2.5
1	D	515	GLU	2.5
1	D	387	ASN	2.5
1	D	452	SER	2.5
1	D	832	LEU	2.5
1	B	535	SER	2.5
1	B	218	ARG	2.5
1	D	416	GLY	2.5
1	B	541	MET	2.4
1	B	811	ASP	2.4
1	B	717	THR	2.4
1	B	291	PHE	2.4
1	B	626	ASN	2.4
1	D	747	GLU	2.4
1	D	838	PRO	2.4
1	B	534	GLY	2.4
1	D	442	GLU	2.4
1	D	410	CYS	2.4
1	B	816	GLU	2.4
1	B	661	THR	2.4
1	D	110	ASP	2.4
1	D	494	ASP	2.4
1	B	852	ASP	2.4
1	D	650	ILE	2.4
1	D	859	ARG	2.4
1	B	189	ASN	2.3
1	D	488	SER	2.3
1	D	285	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	874	ASP	2.3
1	D	624	LYS	2.3
1	D	763	PHE	2.3
1	D	760	GLU	2.3
1	B	375	ASP	2.3
1	D	293	ALA	2.3
1	B	219	ASP	2.3
1	D	856	TRP	2.2
1	B	830	ALA	2.2
1	B	828	LYS	2.2
1	D	445	LEU	2.2
1	D	531	THR	2.2
1	D	190	SER	2.2
1	B	620	ASN	2.2
1	D	851	ASN	2.2
1	D	598	THR	2.2
1	B	447	SER	2.2
1	D	388	ASN	2.2
1	B	388	ASN	2.2
1	D	449	THR	2.1
1	D	618	GLU	2.1
1	D	414	GLN	2.1
1	B	660	LEU	2.1
1	B	448	GLU	2.1
1	B	815	VAL	2.1
1	D	154	ILE	2.1
1	B	856	TRP	2.1
1	D	652	LEU	2.1
1	D	561	GLN	2.1
1	D	321	ALA	2.1
1	D	364	THR	2.1
1	D	621	SER	2.1
1	B	769	ILE	2.0
1	D	21	ILE	2.0
1	B	370	ASN	2.0
1	D	607	SER	2.0
1	D	541	MET	2.0
1	B	391	LYS	2.0
1	B	581	SER	2.0
1	B	721	ASP	2.0
1	D	631	SER	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 carbohydrates in this entry.

6.4 Ligands [i](#)

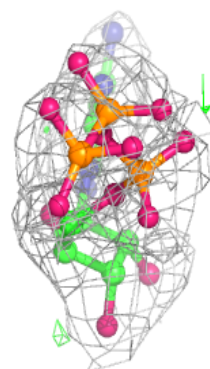
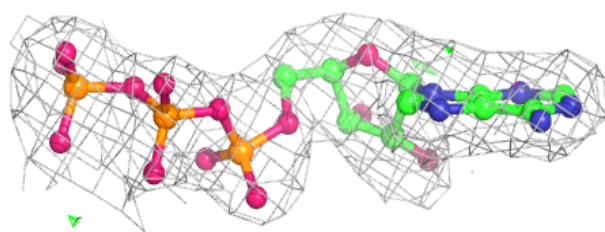
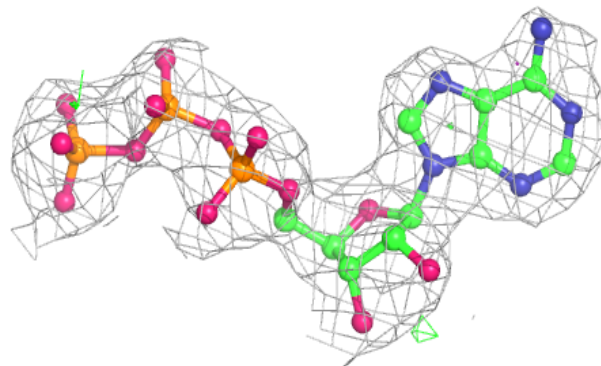
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PO4	D	1889	5/5	0.86	0.17	36,53,55,82	0
4	MG	D	1886	1/1	0.87	0.28	25,25,25,25	0
3	PO4	B	1889	5/5	0.89	0.17	52,55,69,83	0
4	MG	B	1890	1/1	0.92	0.34	23,23,23,23	0
2	ATP	B	1887	31/31	0.97	0.16	11,18,23,25	0
2	ATP	D	1887	31/31	0.97	0.17	13,21,27,33	0
3	PO4	D	1890	5/5	0.98	0.14	16,17,21,23	0
3	PO4	B	1888	5/5	0.98	0.13	24,24,27,32	0

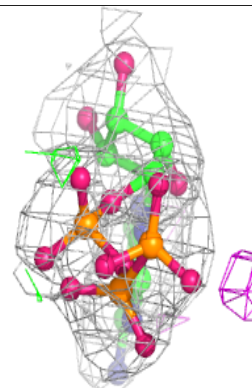
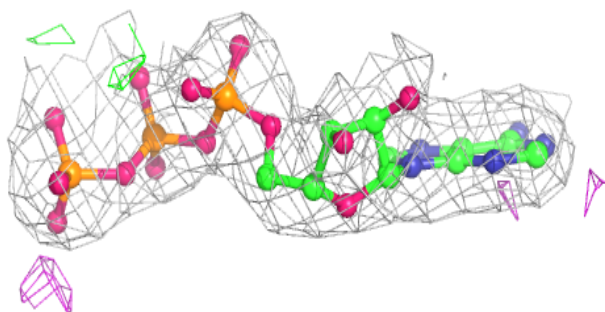
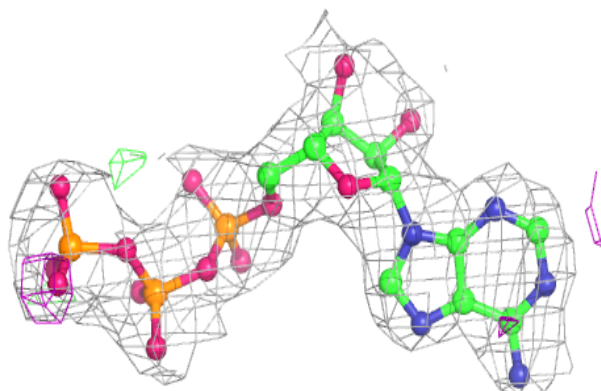
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP B 1887:

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

**Electron density around ATP D 1887:**

$2mF_o-DF_c$ (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.