



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 29, 2019 – 01:37 PM EDT

PDB ID : 4A4Z  
Title : CRYSTAL STRUCTURE OF THE S. CEREVISIAE DEXH HELICASE SKI2  
BOUND TO AMPPNP  
Authors : Halbach, F.; Rode, M.; Conti, E.  
Deposited on : 2011-10-20  
Resolution : 2.40 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.4  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

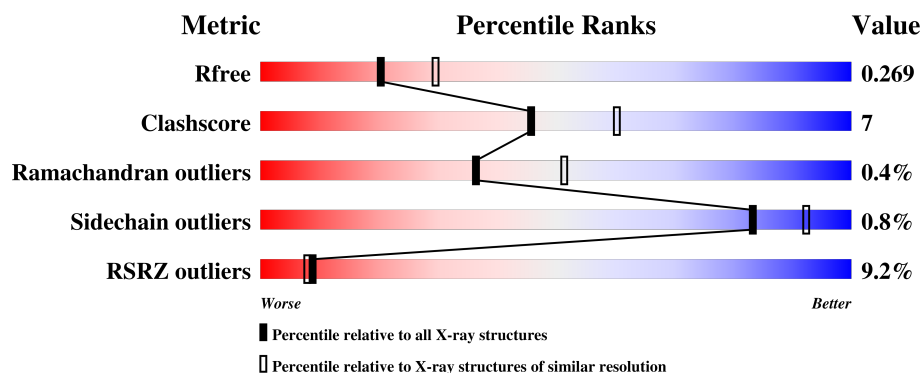
# 1 Overall quality at a glance

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))
$R_{free}$	111664	3481 (2.40-2.40)
Clashscore	122126	3956 (2.40-2.40)
Ramachandran outliers	120053	3897 (2.40-2.40)
Sidechain outliers	120020	3898 (2.40-2.40)
RSRZ outliers	108989	3386 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	997	<div> <div>8%</div> <div>74%</div> <div>13%</div> <div>12%</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6683 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.

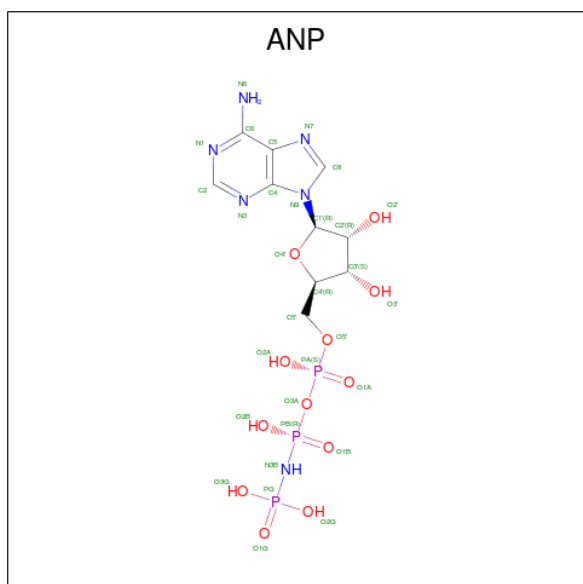
- Molecule 1 is a protein called ANTIVIRAL HELICASE SKI2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	874	6503	4155	1123	1196	29	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

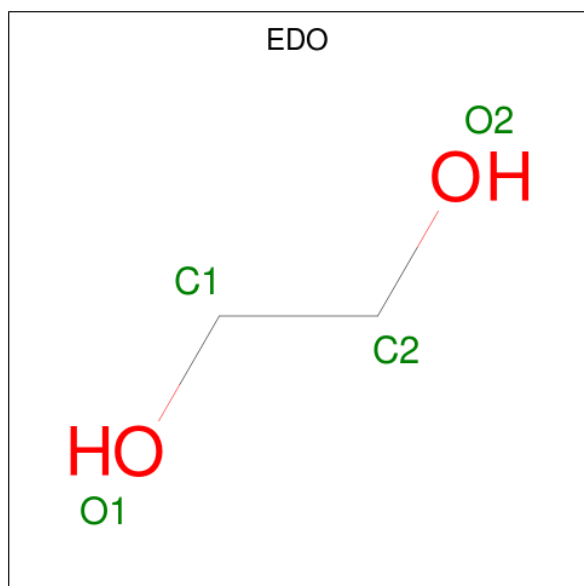
Chain	Residue	Modelled	Actual	Comment	Reference
A	291	GLY	-	expression tag	UNP P35207
A	292	PRO	-	expression tag	UNP P35207
A	293	ASP	-	expression tag	UNP P35207
A	294	SER	-	expression tag	UNP P35207
A	295	MET	-	expression tag	UNP P35207

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula:  $C_{10}H_{17}N_6O_{12}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	133	Total	O	0	0
			133	133		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.79Å 118.55Å 129.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.43 – 2.40 51.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.43-2.40) 99.7 (51.00-2.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.75 (at 2.39Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.1_743)	Depositor
R, $R_{free}$	0.238 , 0.275 0.229 , 0.269	Depositor DCC
$R_{free}$ test set	2565 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	50.3	Xtriage
Anisotropy	0.535	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 50.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6683	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: ANP, EDO

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	0.23	0/6620	0.40	0/8997

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6503	0	6077	87	0
2	A	31	0	13	1	0
3	A	16	0	24	0	0
4	A	133	0	0	9	0
All	All	6683	0	6114	87	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 7.

All (87) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:GLN:NE2	1:A:730:ASN:OD1	2.16	0.78
1:A:419:MET:HE1	1:A:424:LEU:HA	1.70	0.73
1:A:1206:ARG:O	4:A:2121:HOH:O	2.06	0.72
1:A:1140:SER:OG	4:A:2108:HOH:O	2.07	0.71
1:A:819:ALA:O	4:A:2092:HOH:O	2.09	0.70
1:A:1216:TYR:CE2	1:A:1220:ARG:HD2	2.27	0.70
1:A:751:GLU:HG2	1:A:788:THR:HG23	1.74	0.69
1:A:459:GLU:O	1:A:462:ILE:HG22	1.95	0.66
1:A:1226:GLU:OE1	4:A:2123:HOH:O	2.15	0.65
1:A:454:ARG:NH2	1:A:1122:ASN:O	2.29	0.64
1:A:762:GLY:O	4:A:2079:HOH:O	2.15	0.63
1:A:745:ASP:O	1:A:748:GLY:N	2.33	0.61
1:A:1155:TYR:CE2	1:A:1157:GLY:HA2	2.35	0.61
1:A:670:ARG:NH1	1:A:1283:ALA:O	2.34	0.61
1:A:419:MET:HE3	1:A:423:ILE:HG22	1.81	0.60
1:A:419:MET:HE1	1:A:424:LEU:CA	2.31	0.60
1:A:428:LEU:HD23	1:A:435:ILE:HD13	1.83	0.60
1:A:355:ALA:HA	1:A:505:PRO:HG2	1.85	0.59
1:A:353:THR:O	1:A:354:SER:OG	2.18	0.57
1:A:390:ARG:NH2	1:A:391:ASP:OD1	2.38	0.57
1:A:818:GLU:HB3	1:A:821:ARG:HG2	1.85	0.57
1:A:384:LEU:HD12	1:A:387:GLN:HB3	1.86	0.56
1:A:1268:MET:HE2	1:A:1268:MET:HA	1.88	0.56
1:A:681:ILE:O	1:A:685:ARG:HG3	2.07	0.55
1:A:1062:VAL:N	1:A:1063:PRO:HD2	2.22	0.55
1:A:353:THR:O	1:A:354:SER:CB	2.55	0.54
1:A:909:ASP:HB2	1:A:910:PRO:HD2	1.89	0.54
1:A:513:TRP:CZ2	1:A:516:LYS:HA	2.43	0.54
1:A:619:ASN:O	1:A:623:LYS:HG2	2.07	0.53
1:A:451:ASP:OD1	1:A:452:GLN:N	2.44	0.51
1:A:745:ASP:O	1:A:747:ASN:N	2.45	0.50
1:A:503:LYS:O	4:A:2027:HOH:O	2.19	0.50
1:A:466:PRO:HG2	1:A:469:VAL:HG23	1.94	0.48
1:A:378:THR:OG1	4:A:2007:HOH:O	2.20	0.48
1:A:744:HIS:ND1	1:A:744:HIS:C	2.66	0.48
1:A:1097:ALA:HB1	1:A:1192:HIS:CE1	2.48	0.48
1:A:1167:VAL:HG13	1:A:1168:THR:HG23	1.94	0.48
1:A:743:LYS:NZ	1:A:756:GLU:OE2	2.46	0.48
1:A:463:ILE:HD11	1:A:829:SER:HA	1.95	0.47
1:A:389:PHE:CD1	1:A:403:LEU:HB2	2.50	0.47
1:A:425:ARG:HG3	1:A:464:MET:HE1	1.96	0.47
1:A:401:ILE:HG22	1:A:416:CYS:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:ASN:N	1:A:412:PRO:HD3	2.29	0.47
1:A:1089:LEU:HB2	1:A:1090:PRO:HD3	1.96	0.46
1:A:353:THR:HB	1:A:504:ARG:NH1	2.31	0.46
1:A:353:THR:HG23	2:A:2288:ANP:O1G	2.15	0.46
1:A:818:GLU:HG2	4:A:2091:HOH:O	2.15	0.45
1:A:434:LEU:C	1:A:434:LEU:HD12	2.35	0.45
1:A:909:ASP:HB2	1:A:910:PRO:CD	2.47	0.45
1:A:332:THR:O	1:A:336:GLU:HG2	2.17	0.45
1:A:933:THR:O	1:A:970:PHE:HA	2.16	0.45
1:A:632:PHE:CZ	1:A:726:ALA:HB2	2.51	0.45
1:A:352:HIS:CE1	1:A:477:THR:HG21	2.51	0.44
1:A:1117:VAL:HG13	1:A:1255:ALA:HB1	1.98	0.44
1:A:536:HIS:CG	1:A:537:LYS:N	2.85	0.44
1:A:363:TYR:O	1:A:366:ALA:HB3	2.18	0.44
1:A:1225:LYS:HD2	4:A:2124:HOH:O	2.18	0.44
1:A:333:PHE:CE1	1:A:334:GLN:HG3	2.53	0.43
1:A:1277:ARG:NH1	1:A:1278:ASP:OD2	2.52	0.43
1:A:424:LEU:HD23	1:A:461:VAL:HG11	1.99	0.43
1:A:532:ASN:O	1:A:535:LYS:HB3	2.18	0.43
1:A:352:HIS:CG	1:A:477:THR:HG21	2.54	0.43
1:A:1154:VAL:HB	1:A:1244:TRP:CE3	2.54	0.42
1:A:363:TYR:O	1:A:364:ALA:C	2.57	0.42
1:A:1152:VAL:HG23	1:A:1208:ARG:HB3	2.01	0.42
1:A:462:ILE:HD11	1:A:471:PHE:CD1	2.54	0.42
1:A:420:THR:OG1	1:A:423:ILE:HG12	2.19	0.42
1:A:1214:VAL:HG13	1:A:1227:ILE:HG23	2.00	0.42
1:A:378:THR:HA	1:A:419:MET:O	2.20	0.42
1:A:839:GLN:CB	1:A:840:PRO:CD	2.98	0.42
1:A:694:VAL:O	1:A:707:ILE:HD13	2.20	0.41
1:A:646:LEU:O	1:A:690:ARG:NH2	2.53	0.41
1:A:638:ARG:HD2	1:A:642:TYR:OH	2.21	0.41
1:A:745:ASP:O	1:A:746:GLY:C	2.57	0.41
1:A:404:ILE:HD13	1:A:409:GLN:HG3	2.01	0.41
1:A:694:VAL:HA	1:A:720:PHE:O	2.20	0.41
1:A:1217:GLU:HB3	1:A:1222:LEU:HD12	2.02	0.41
1:A:434:LEU:HD12	1:A:435:ILE:N	2.36	0.41
1:A:491:THR:HG23	1:A:828:TYR:CD2	2.55	0.41
1:A:1104:PHE:CZ	1:A:1127:LEU:HD22	2.56	0.41
1:A:377:TYR:HB3	1:A:418:ILE:HD13	2.02	0.41
1:A:712:SER:HB3	1:A:731:LEU:CD2	2.50	0.41
1:A:919:VAL:HA	1:A:931:ILE:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:744:HIS:HA	1:A:748:GLY:O	2.21	0.40
1:A:923:SER:O	1:A:927:ALA:N	2.54	0.40
1:A:1062:VAL:HB	1:A:1063:PRO:CD	2.52	0.40
1:A:696:HIS:O	1:A:704:LYS:HE3	2.22	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	852/997 (86%)	801 (94%)	48 (6%)	3 (0%)	36	51

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	354	SER
1	A	746	GLY
1	A	1017	LYS

### 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	623/881 (71%)	618 (99%)	5 (1%)	83	92

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	348	PHE
1	A	536	HIS
1	A	686	SER
1	A	744	HIS
1	A	1196	LEU

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

### 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 ⓘ

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	ANP	A	2288	-	28,33,33	1.73	10 (35%)	29,52,52	1.98	7 (24%)
3	EDO	A	2289	-	3,3,3	0.47	0	2,2,2	0.31	0
3	EDO	A	2290	-	3,3,3	0.46	0	2,2,2	0.32	0
3	EDO	A	2291	-	3,3,3	0.47	0	2,2,2	0.30	0
3	EDO	A	2292	-	3,3,3	0.46	0	2,2,2	0.36	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	ANP	A	2288	-	-	5/13/38/38	0/3/3/3
3	EDO	A	2289	-	-	0/1/1/1	-
3	EDO	A	2290	-	-	0/1/1/1	-
3	EDO	A	2291	-	-	0/1/1/1	-
3	EDO	A	2292	-	-	0/1/1/1	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2288	ANP	PB-O1B	3.56	1.50	1.46
2	A	2288	ANP	C6-N6	2.94	1.45	1.34
2	A	2288	ANP	PG-O1G	2.81	1.49	1.46
2	A	2288	ANP	PG-O3G	-2.57	1.49	1.56
2	A	2288	ANP	C2-N3	2.48	1.36	1.32
2	A	2288	ANP	PG-O2G	-2.46	1.50	1.56
2	A	2288	ANP	PB-O2B	-2.31	1.50	1.56
2	A	2288	ANP	O3'-C3'	-2.21	1.37	1.43
2	A	2288	ANP	C2'-C3'	-2.11	1.48	1.53
2	A	2288	ANP	O4'-C4'	-2.01	1.40	1.45

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2288	ANP	N3-C2-N1	-4.51	121.42	128.68
2	A	2288	ANP	O3G-PG-O1G	-3.97	103.32	113.43
2	A	2288	ANP	O2B-PB-O1B	-3.96	101.70	109.87
2	A	2288	ANP	PA-O3A-PB	-3.71	119.47	132.46
2	A	2288	ANP	O2G-PG-O1G	-3.36	104.87	113.43
2	A	2288	ANP	C4'-O4'-C1'	-2.59	107.13	109.83
2	A	2288	ANP	O3A-PB-N3B	2.08	112.35	106.59

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2288	ANP	PB-N3B-PG-O1G
2	A	2288	ANP	PG-N3B-PB-O1B

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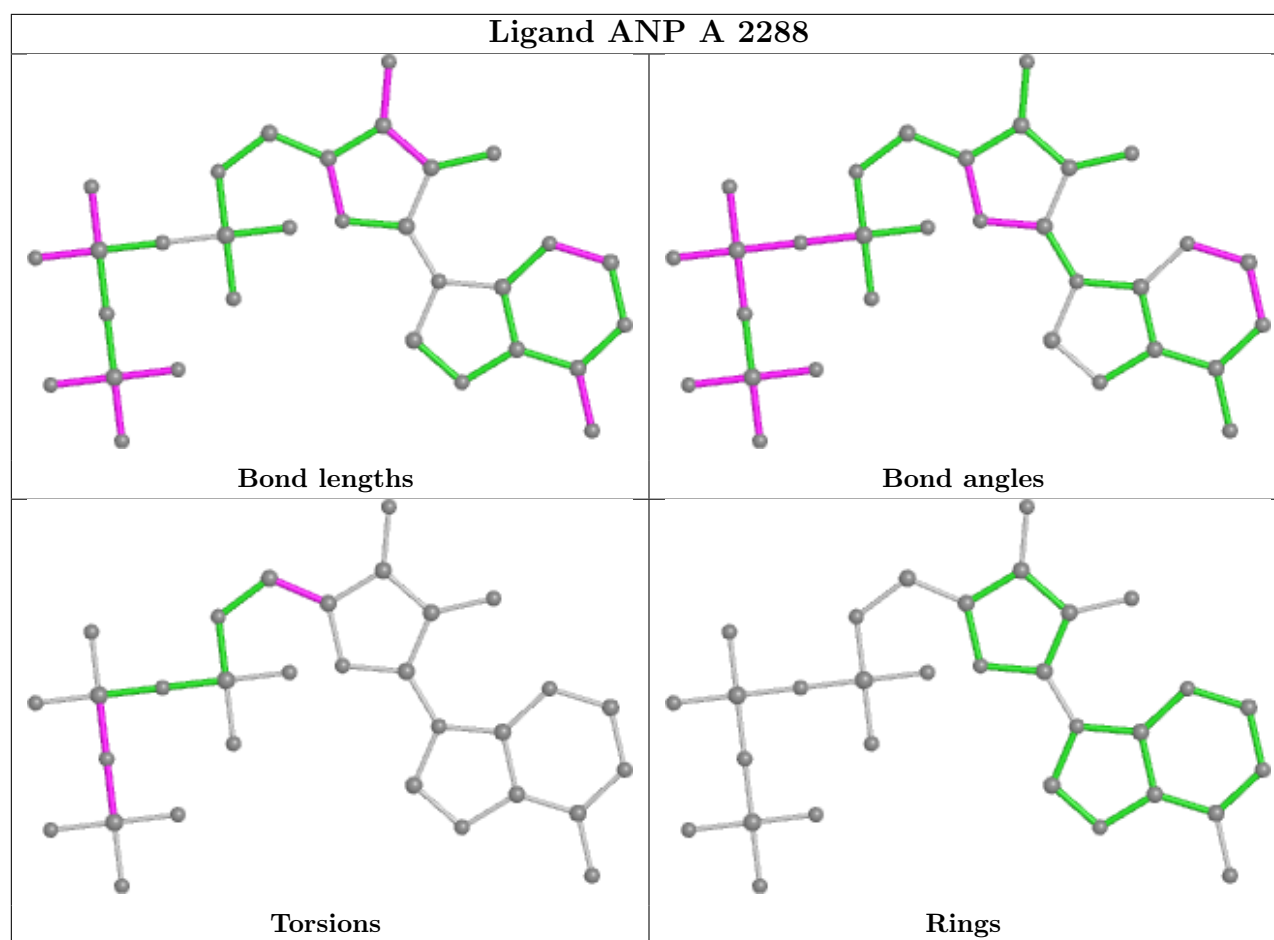
Mol	Chain	Res	Type	Atoms
2	A	2288	ANP	O4'-C4'-C5'-O5'
2	A	2288	ANP	C3'-C4'-C5'-O5'
2	A	2288	ANP	PG-N3B-PB-O3A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2288	ANP	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	874/997 (87%)	0.44	80 (9%) 9 8	27, 59, 136, 182	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1058	SER	7.5
1	A	876	LEU	6.8
1	A	871	PHE	6.5
1	A	1061	ILE	6.5
1	A	872	LEU	6.1
1	A	1063	PRO	6.0
1	A	924	LEU	5.4
1	A	1065	PHE	4.9
1	A	892	SER	4.8
1	A	1062	VAL	4.7
1	A	961	ASN	4.6
1	A	1014	LEU	4.6
1	A	855	THR	4.6
1	A	977	VAL	4.5
1	A	962	PHE	4.5
1	A	873	GLU	4.4
1	A	854	GLN	4.4
1	A	1039	ARG	4.2
1	A	894	SER	4.2
1	A	935	THR	4.1
1	A	882	THR	4.0
1	A	883	VAL	4.0
1	A	954	ALA	4.0
1	A	932	MET	3.9
1	A	951	PHE	3.9
1	A	878	TYR	3.9
1	A	920	PHE	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	1067	ALA	3.8
1	A	315	PHE	3.8
1	A	853	LEU	3.6
1	A	875	MET	3.6
1	A	851	GLU	3.6
1	A	874	LEU	3.5
1	A	607	ASP	3.5
1	A	889	MET	3.2
1	A	1043	ARG	3.2
1	A	959	ARG	3.2
1	A	879	LYS	3.1
1	A	1074	ILE	3.0
1	A	1064	LYS	3.0
1	A	923	SER	3.0
1	A	887	GLN	2.9
1	A	922	VAL	2.9
1	A	988	PHE	2.9
1	A	1006	PHE	2.9
1	A	950	TYR	2.8
1	A	957	TYR	2.8
1	A	1068	HIS	2.8
1	A	918	PHE	2.8
1	A	1040	THR	2.8
1	A	886	MET	2.8
1	A	925	LYS	2.8
1	A	960	ARG	2.7
1	A	1072	LYS	2.7
1	A	1035	ILE	2.6
1	A	1038	ASP	2.6
1	A	384	LEU	2.6
1	A	913	CYS	2.6
1	A	1019	LEU	2.6
1	A	877	ALA	2.5
1	A	890	VAL	2.5
1	A	1060	HIS	2.5
1	A	1042	ILE	2.4
1	A	891	LYS	2.4
1	A	953	LYS	2.4
1	A	1079	HIS	2.4
1	A	899	LEU	2.3
1	A	462	ILE	2.3
1	A	907	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1034	GLN	2.3
1	A	434	LEU	2.3
1	A	1044	ASP	2.2
1	A	906	ALA	2.2
1	A	1002	ALA	2.1
1	A	1244	TRP	2.1
1	A	989	ALA	2.1
1	A	1071	LYS	2.1
1	A	1078	TYR	2.1
1	A	895	ILE	2.1
1	A	310	HIS	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](#)

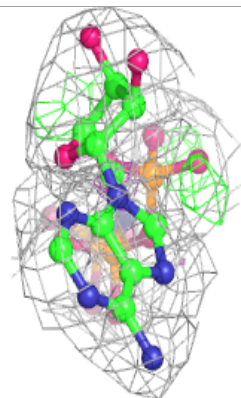
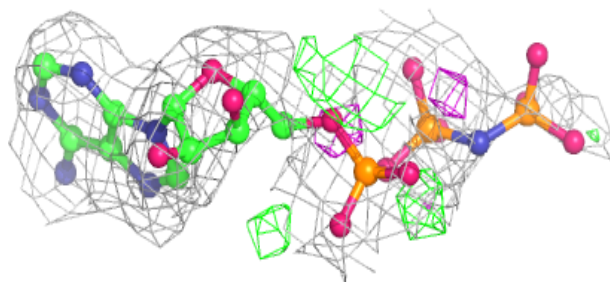
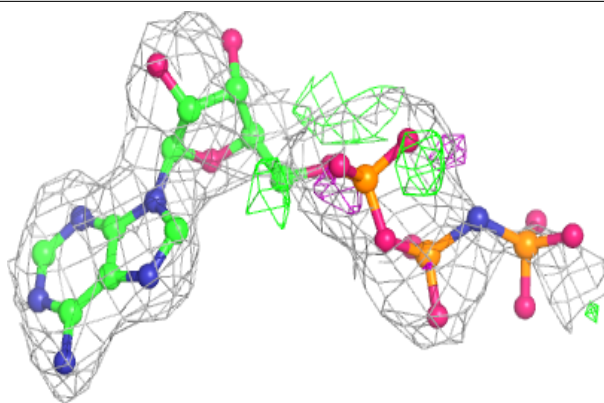
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	A	2291	4/4	0.79	0.39	72,72,73,73	0
3	EDO	A	2289	4/4	0.85	0.25	58,58,59,59	0
2	ANP	A	2288	31/31	0.87	0.20	75,82,85,87	3
3	EDO	A	2290	4/4	0.87	0.27	55,55,56,56	0
3	EDO	A	2292	4/4	0.89	0.24	56,56,56,56	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 ANP A 2288:**

$2mF_o-DF_c$  (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.