



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 05:05 AM UTC

PDB ID : 3MYK / pdb_00003myk
Title : Insights into the Importance of Hydrogen Bonding in the Gamma-Phosphate Binding Pocket of Myosin: Structural and Functional Studies of Ser236
Authors : Frye, J.J.; Klenchin, V.A.; Bagshaw, C.R.; Rayment, I.
Deposited on : 2010-05-10
Resolution : 1.84 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

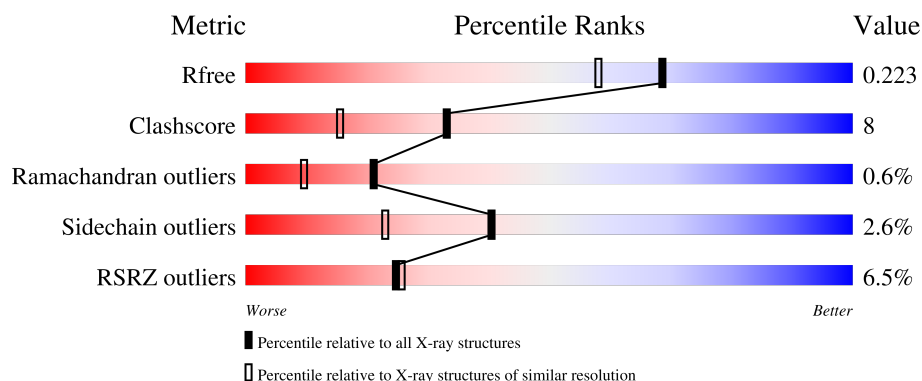
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	X	762	6% 78% 12% 7%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6061 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.

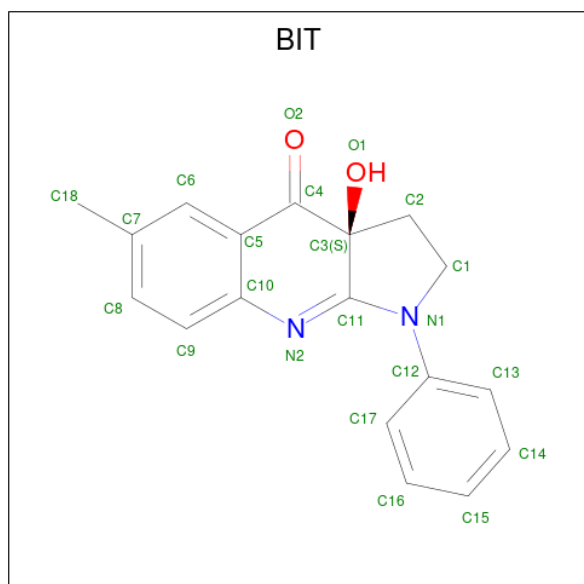
- Molecule 1 is a protein called Myosin-2 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	X	706	5562	3550	938	1058	16	0	4	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	1	GLY	-	expression tag	UNP P08799
X	236	ALA	SER	engineered mutation	UNP P08799
X	760	LEU	-	expression tag	UNP P08799
X	761	PRO	-	expression tag	UNP P08799
X	762	ASN	-	expression tag	UNP P08799

- Molecule 2 is (-)-1-PHENYL-1,2,3,4-TETRAHYDRO-4-HYDROXYPYRROLO[2,3-B]-7-METHYLQUINOLIN-4-ONE (CCD ID: BIT) (formula: C₁₈H₁₆N₂O₂).

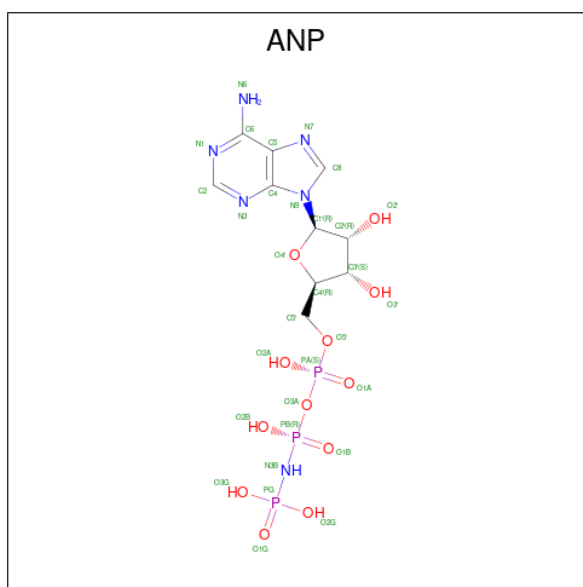


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	X	1	Total	C	N	O	0	0
			22	18	2	2		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	X	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



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

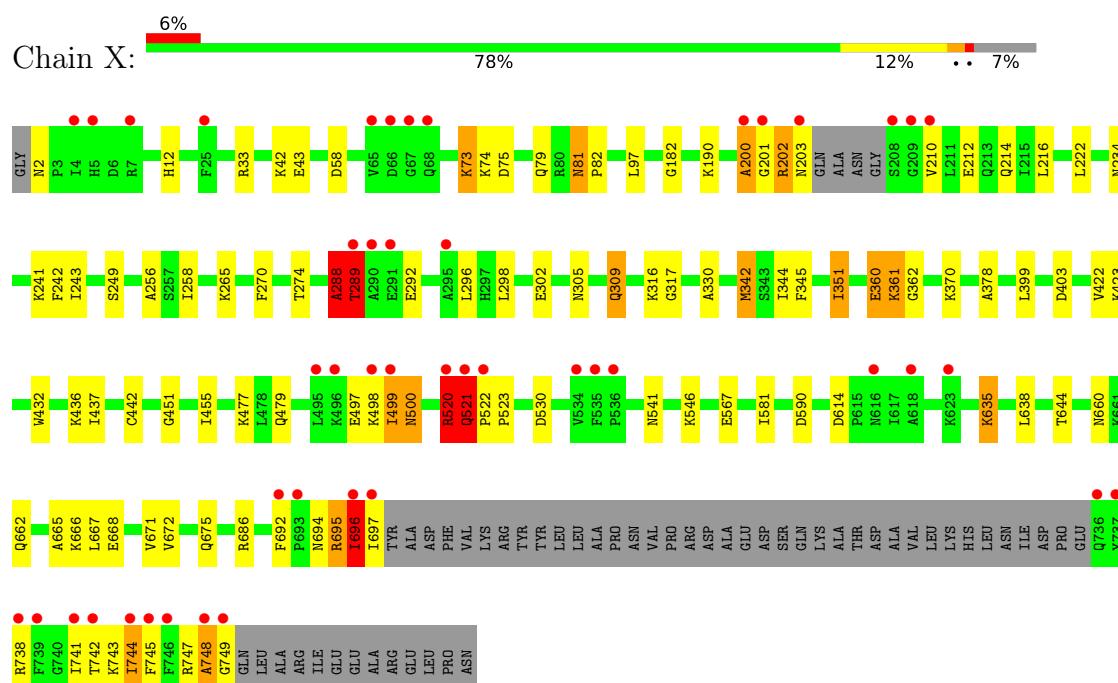
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	X	445	Total	O	0	0
			445	445		

3 Residue-property plots

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: Myosin-2 heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	88.00Å 147.02Å 153.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.91 – 1.84 28.91 – 1.84	Depositor EDS
% Data completeness (in resolution range)	98.6 (28.91-1.84) 98.6 (28.91-1.84)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.64 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.193 , 0.230 0.188 , 0.223	Depositor DCC
R_{free} test set	4234 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtriage
Anisotropy	0.519	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.020 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6061	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BIT, ANP, MG

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	X	1.40	18/5682 (0.3%)	1.22	19/7673 (0.2%)

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	X	0	4

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	274	THR	CA-CB	7.51	1.63	1.54
1	X	437	ILE	CA-CB	7.22	1.63	1.54
1	X	590	ASP	CA-C	7.14	1.58	1.53
1	X	590	ASP	C-O	6.87	1.27	1.23
1	X	644	THR	C-O	6.78	1.31	1.24
1	X	330	ALA	CA-CB	6.59	1.63	1.53
1	X	567	GLU	N-CA	6.46	1.54	1.45
1	X	581	ILE	CA-CB	5.45	1.60	1.54
1	X	344	ILE	N-CA	5.32	1.52	1.46
1	X	378	ALA	CA-CB	5.26	1.61	1.53
1	X	200	ALA	CA-CB	5.17	1.61	1.53
1	X	675	GLN	N-CA	5.14	1.52	1.46
1	X	455	ILE	N-CA	5.09	1.53	1.46
1	X	672	VAL	CA-CB	5.08	1.60	1.54
1	X	635	LYS	CG-CD	5.06	1.67	1.52
1	X	222	LEU	N-CA	5.04	1.52	1.46
1	X	665	ALA	CA-CB	5.01	1.60	1.53
1	X	351	ILE	CA-C	-5.00	1.46	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	520	ARG	N-CA-C	11.35	128.22	112.45
1	X	201	GLY	N-CA-C	10.08	124.67	112.48
1	X	288	ALA	N-CA-C	-6.40	100.43	109.96
1	X	541	ASN	N-CA-C	6.38	118.31	111.36
1	X	289	THR	CB-CA-C	6.36	123.08	110.42
1	X	521	GLN	C-N-CD	-5.99	107.42	120.60
1	X	692	PHE	CA-C-N	5.89	126.03	119.32
1	X	692	PHE	C-N-CA	5.89	126.03	119.32
1	X	499	ILE	N-CA-C	5.56	120.91	109.34
1	X	479	GLN	N-CA-C	-5.48	105.31	111.28
1	X	81	ASN	N-CA-C	5.38	116.47	109.64
1	X	289	THR	N-CA-CB	5.35	119.53	110.49
1	X	288	ALA	CA-C-N	5.34	131.73	121.54
1	X	288	ALA	C-N-CA	5.34	131.73	121.54
1	X	521	GLN	N-CA-C	5.28	125.77	111.00
1	X	42	LYS	N-CA-C	-5.26	106.37	112.89
1	X	694	ASN	N-CA-C	5.23	117.42	108.90
1	X	309	GLN	CB-CA-C	-5.09	101.16	109.56
1	X	345	PHE	N-CA-C	5.09	117.72	111.82

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	200	ALA	Peptide
1	X	288	ALA	Peptide
1	X	520	ARG	Peptide
1	X	696	ILE	Peptide

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	X	5562	0	5386	86	0
2	X	22	0	16	0	0
3	X	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	X	31	0	13	2	0
5	X	445	0	0	8	2
All	All	6061	0	5415	86	2

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 8.

All (86) 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:X:748:ALA:CB	1:X:749:GLY:HA2	1.57	1.30
1:X:748:ALA:HB3	1:X:749:GLY:HA2	1.30	1.05
1:X:748:ALA:HB1	1:X:749:GLY:HA2	1.34	1.05
1:X:288:ALA:HA	1:X:289:THR:HG22	1.42	1.01
1:X:748:ALA:CB	1:X:749:GLY:CA	2.43	0.96
1:X:2:ASN:N	5:X:1474:HOH:O	1.99	0.95
1:X:182:GLY:H	4:X:999:ANP:HNB1	1.14	0.94
1:X:696:ILE:HG22	1:X:697:ILE:HA	1.50	0.91
1:X:696:ILE:O	1:X:744:ILE:HD13	1.70	0.91
1:X:73:LYS:HE2	1:X:75:ASP:H	1.34	0.90
1:X:73:LYS:HE2	1:X:74:LYS:N	1.91	0.84
1:X:748:ALA:HB1	1:X:749:GLY:CA	2.05	0.84
1:X:58:ASP:O	1:X:73:LYS:HE3	1.76	0.83
1:X:288:ALA:HA	1:X:289:THR:CG2	2.07	0.83
1:X:289:THR:HG21	1:X:292:GLU:OE1	1.79	0.82
1:X:497:GLU:HG3	1:X:745:PHE:CZ	2.14	0.81
1:X:289:THR:HG21	1:X:292:GLU:CD	2.07	0.80
1:X:498:LYS:HB2	1:X:741:ILE:CD1	2.12	0.80
1:X:520:ARG:CD	5:X:1541:HOH:O	2.30	0.79
1:X:289:THR:HG23	1:X:292:GLU:HB2	1.64	0.77
1:X:520:ARG:HD2	5:X:1541:HOH:O	1.82	0.77
1:X:265:LYS:HE3	1:X:423:LYS:HB3	1.67	0.77
1:X:497:GLU:HG3	1:X:745:PHE:HZ	1.46	0.77
1:X:73:LYS:CE	1:X:75:ASP:H	2.01	0.73
1:X:289:THR:CG2	1:X:292:GLU:HB2	2.18	0.73
1:X:361:LYS:HE3	1:X:362:GLY:O	1.89	0.72
1:X:234:ASN:H	1:X:662:GLN:HE22	1.37	0.72
1:X:520:ARG:NE	5:X:1541:HOH:O	2.21	0.72
1:X:43:GLU:HB2	5:X:1355:HOH:O	1.90	0.70
1:X:73:LYS:HE2	1:X:75:ASP:N	2.07	0.69
1:X:342:MET:HA	1:X:342:MET:HE3	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:498:LYS:HB2	1:X:741:ILE:HD12	1.74	0.69
1:X:316:LYS:HD2	1:X:317:GLY:N	2.10	0.67
1:X:33:ARG:HH21	1:X:79:GLN:HE22	1.42	0.66
1:X:498:LYS:HB2	1:X:741:ILE:HD11	1.77	0.65
1:X:360:GLU:HG3	1:X:370:LYS:HE2	1.79	0.63
1:X:696:ILE:CG2	1:X:697:ILE:HA	2.25	0.63
1:X:747:ARG:HG3	5:X:1535:HOH:O	1.98	0.62
1:X:614:ASP:OD1	1:X:614:ASP:C	2.43	0.62
1:X:73:LYS:HD3	1:X:75:ASP:HB2	1.81	0.61
1:X:243:ILE:CD1	1:X:258:ILE:HG12	2.32	0.59
1:X:342:MET:O	1:X:342:MET:CE	2.51	0.59
1:X:289:THR:HG23	1:X:292:GLU:CB	2.33	0.58
1:X:243:ILE:HD12	1:X:258:ILE:HG12	1.85	0.57
1:X:342:MET:O	1:X:342:MET:HE2	2.05	0.57
1:X:499:ILE:HB	1:X:738:ARG:HB3	1.87	0.56
1:X:288:ALA:CA	1:X:289:THR:CG2	2.81	0.55
1:X:270:PHE:HA	1:X:309:GLN:HE22	1.74	0.53
1:X:202:ARG:O	1:X:203:ASN:O	2.27	0.52
1:X:477:LYS:HG3	1:X:638:LEU:HD21	1.92	0.52
1:X:741:ILE:HG22	1:X:742:THR:HG23	1.92	0.51
1:X:748:ALA:HB3	1:X:749:GLY:CA	2.20	0.51
1:X:666:LYS:HE2	1:X:668:GLU:OE2	2.12	0.50
1:X:697:ILE:H	1:X:743:LYS:HA	1.77	0.50
1:X:497:GLU:HG3	1:X:745:PHE:CE1	2.47	0.49
1:X:432:TRP:CZ2	1:X:436:LYS:HE2	2.48	0.49
1:X:696:ILE:O	1:X:744:ILE:CD1	2.51	0.49
1:X:288:ALA:HB1	1:X:289:THR:HG23	1.96	0.48
1:X:305[A]:ASN:ND2	5:X:1323:HOH:O	2.46	0.47
1:X:747:ARG:CG	1:X:748:ALA:N	2.77	0.47
1:X:499:ILE:O	1:X:500:ASN:O	2.32	0.47
1:X:289:THR:CG2	1:X:292:GLU:CB	2.91	0.47
1:X:695:ARG:C	1:X:696:ILE:HG12	2.41	0.45
1:X:256:ALA:O	1:X:442:CYS:HB2	2.18	0.44
1:X:296:LEU:HB2	1:X:298:LEU:HG	2.00	0.44
1:X:73:LYS:CE	1:X:74:LYS:N	2.74	0.43
1:X:97:LEU:CD2	1:X:686:ARG:HG2	2.48	0.43
1:X:242:PHE:CZ	1:X:451:GLY:HA3	2.53	0.43
1:X:499:ILE:HB	1:X:738:ARG:CB	2.47	0.43
1:X:302:GLU:H	1:X:302:GLU:CD	2.27	0.43
1:X:351:ILE:HG23	1:X:422:VAL:HG13	2.01	0.43
1:X:342:MET:HE3	1:X:342:MET:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:530:ASP:OD2	1:X:635:LYS:NZ	2.51	0.42
1:X:399:LEU:HA	1:X:403:ASP:O	2.19	0.41
1:X:316:LYS:HD2	1:X:317:GLY:H	1.85	0.41
1:X:660[B]:ASN:HD21	1:X:671:VAL:HG22	1.85	0.41
1:X:522:PRO:HA	1:X:523:PRO:HD3	1.90	0.41
1:X:182:GLY:N	4:X:999:ANP:HNB1	1.98	0.41
1:X:190:LYS:HG3	5:X:1421:HOH:O	2.21	0.41
1:X:747:ARG:HG2	1:X:748:ALA:N	2.35	0.41
1:X:212:GLU:H	1:X:212:GLU:CD	2.28	0.41
1:X:241:LYS:HD2	1:X:243:ILE:HD11	2.02	0.41
1:X:288:ALA:CA	1:X:289:THR:HG22	2.30	0.41
1:X:73:LYS:HE2	1:X:74:LYS:H	1.81	0.40
1:X:81:ASN:O	1:X:82:PRO:C	2.60	0.40
1:X:210:VAL:O	1:X:214:GLN:HG3	2.21	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:1518:HOH:O	5:X:1518:HOH:O[3_654]	1.99	0.21
5:X:1303:HOH:O	5:X:1303:HOH:O[3_654]	2.05	0.15

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	X	704/762 (92%)	686 (97%)	14 (2%)	4 (1%)	21 9

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	202	ARG

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Mol	Chain	Res	Type
1	X	521	GLN
1	X	748	ALA
1	X	500	ASN

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	X	582/664 (88%)	567 (97%)	15 (3%)	40	23

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	12	HIS
1	X	73	LYS
1	X	216	LEU
1	X	249	SER
1	X	289	THR
1	X	342	MET
1	X	360	GLU
1	X	361	LYS
1	X	520	ARG
1	X	521	GLN
1	X	546	LYS
1	X	667	LEU
1	X	695	ARG
1	X	696	ILE
1	X	744	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	79	GLN
1	X	173	GLN
1	X	188	ASN

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Mol	Chain	Res	Type
1	X	234	ASN
1	X	283	GLN
1	X	309	GLN
1	X	439	ASN
1	X	443	GLN
1	X	500	ASN
1	X	606	ASN
1	X	616	ASN
1	X	649	ASN
1	X	662	GLN
1	X	679	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is 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
4	ANP	X	999	3	33,33,33	1.92	8 (24%)	45,52,52	1.79	12 (26%)
2	BIT	X	800	-	23,25,25	2.72	8 (34%)	29,38,38	2.66	13 (44%)

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
4	ANP	X	999	3	-	3/18/38/38	0/3/3/3
2	BIT	X	800	-	-	0/4/34/34	0/3/4/4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	X	800	BIT	C5-C4	-6.29	1.39	1.48
2	X	800	BIT	C11-N2	5.48	1.36	1.29
2	X	800	BIT	O1-C3	5.41	1.51	1.42
4	X	999	ANP	PG-O1G	4.81	1.53	1.46
2	X	800	BIT	C9-C8	4.36	1.45	1.38
4	X	999	ANP	C5-C4	4.24	1.46	1.39
4	X	999	ANP	C8-N7	4.00	1.39	1.31
4	X	999	ANP	PB-O3A	3.99	1.64	1.59
2	X	800	BIT	C13-C12	3.54	1.46	1.39
2	X	800	BIT	C5-C10	3.41	1.44	1.40
4	X	999	ANP	C4-N9	-2.98	1.31	1.37
2	X	800	BIT	C8-C7	2.54	1.44	1.38
4	X	999	ANP	PB-O1B	2.32	1.49	1.46
4	X	999	ANP	PB-O2B	-2.28	1.50	1.56
4	X	999	ANP	C5-C6	2.20	1.47	1.41
2	X	800	BIT	O2-C4	2.07	1.25	1.21

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	800	BIT	C9-C10-C5	5.73	124.78	119.14
2	X	800	BIT	C8-C7-C6	5.71	126.38	117.96
2	X	800	BIT	C18-C7-C6	-5.05	114.08	120.92
2	X	800	BIT	C9-C8-C7	-5.02	115.58	121.37
4	X	999	ANP	O1B-PB-N3B	4.26	118.04	111.77
4	X	999	ANP	N3-C2-N1	-4.21	122.20	128.58
2	X	800	BIT	C17-C12-N1	3.75	125.58	120.18
2	X	800	BIT	C13-C12-N1	-3.68	114.87	120.18
4	X	999	ANP	C5-C4-N3	-3.53	121.85	126.72
4	X	999	ANP	O2B-PB-O1B	3.42	117.21	109.87
2	X	800	BIT	C10-N2-C11	3.41	121.39	116.41
4	X	999	ANP	C2-N1-C6	3.38	124.28	118.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	800	BIT	O2-C4-C5	3.02	126.74	122.36
2	X	800	BIT	C9-C10-N2	-2.89	114.93	118.61
4	X	999	ANP	C4-N9-C8	2.79	108.66	105.74
4	X	999	ANP	O2'-C2'-C1'	-2.73	100.69	110.10
4	X	999	ANP	C2-N3-C4	2.72	118.47	111.83
4	X	999	ANP	N3-C4-N9	2.71	131.78	127.17
2	X	800	BIT	C5-C6-C7	-2.69	117.57	121.65
4	X	999	ANP	O2A-PA-O3A	2.47	113.96	107.27
2	X	800	BIT	C5-C10-N2	-2.18	120.22	122.41
4	X	999	ANP	N6-C6-N1	2.13	123.12	118.38
2	X	800	BIT	C1-N1-C11	-2.10	109.48	112.70
4	X	999	ANP	O1G-PG-N3B	-2.06	108.74	111.77
2	X	800	BIT	C6-C5-C10	-2.04	117.91	120.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

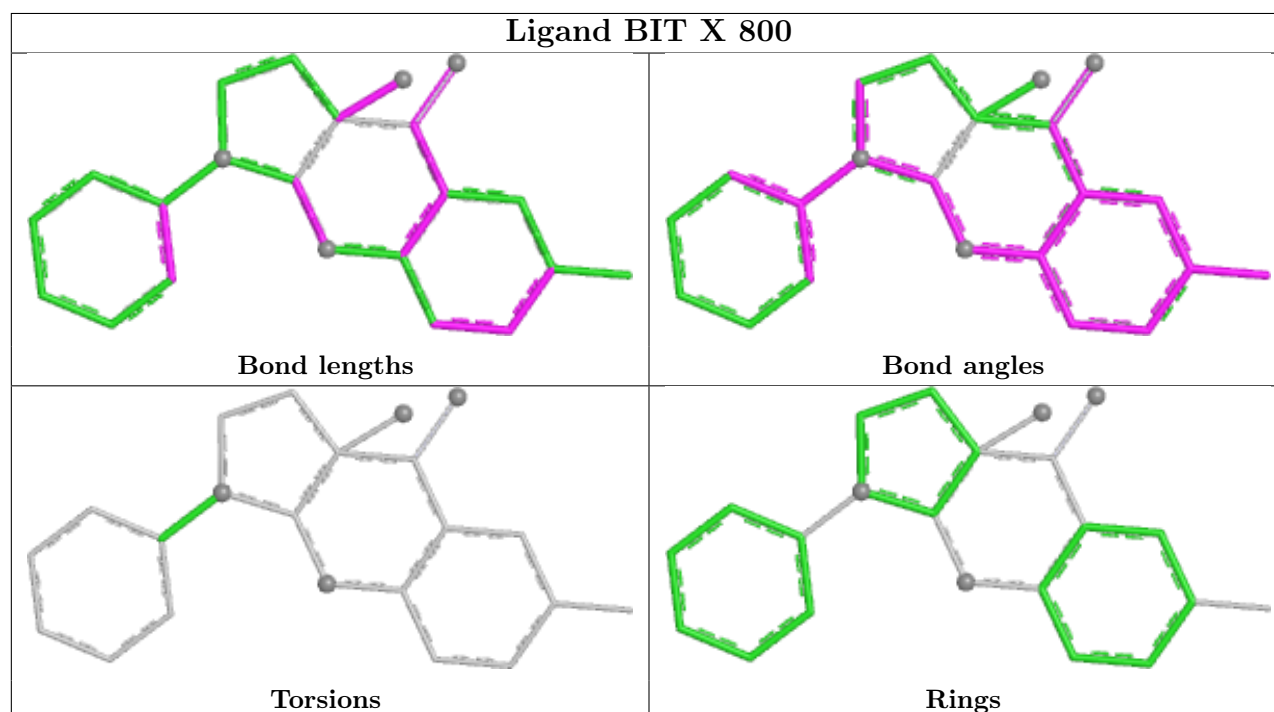
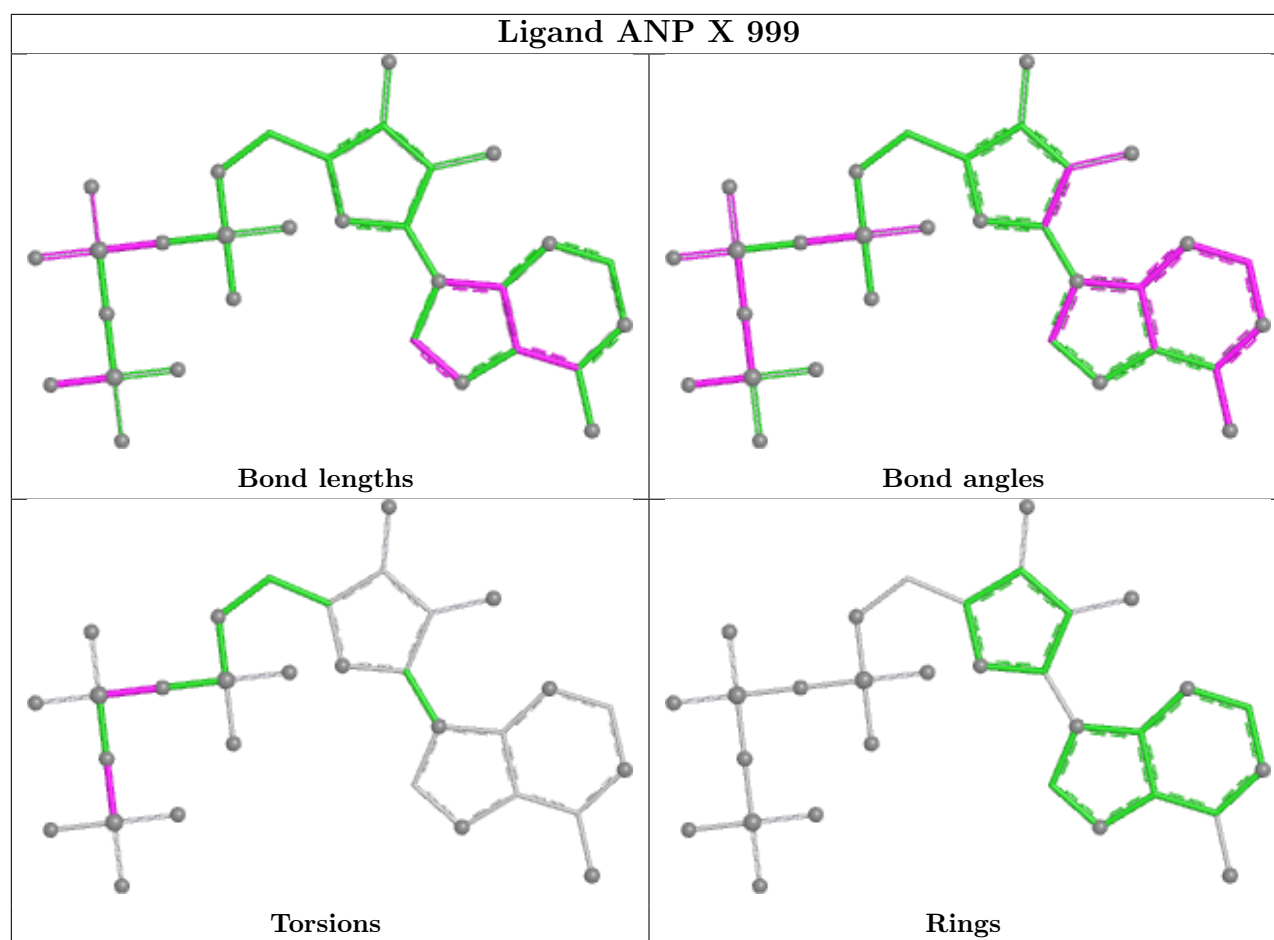
Mol	Chain	Res	Type	Atoms
4	X	999	ANP	PB-N3B-PG-O1G
4	X	999	ANP	PA-O3A-PB-O2B
4	X	999	ANP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	X	999	ANP	2	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	X	706/762 (92%)	0.18	46 (6%) 25 26	11, 25, 49, 66	4 (0%)

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	X	67	GLY	9.2
1	X	746	PHE	8.0
1	X	696	ILE	5.8
1	X	201	GLY	5.4
1	X	744	ILE	5.1
1	X	289	THR	4.9
1	X	737	TYR	4.4
1	X	697	ILE	4.4
1	X	68	GLN	4.1
1	X	741	ILE	4.0
1	X	209	GLY	4.0
1	X	290	ALA	3.9
1	X	498	LYS	3.9
1	X	65	VAL	3.9
1	X	748	ALA	3.7
1	X	496	LYS	3.6
1	X	739	PHE	3.4
1	X	203	ASN	3.3
1	X	66	ASP	3.2
1	X	736	GLN	3.2
1	X	693	PRO	3.1
1	X	499	ILE	3.1
1	X	745	PHE	3.1
1	X	208	SER	3.1
1	X	749	GLY	3.1
1	X	522	PRO	3.0
1	X	534	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	X	742	THR	2.9
1	X	520	ARG	2.8
1	X	692	PHE	2.7
1	X	4	ILE	2.7
1	X	291	GLU	2.7
1	X	495	LEU	2.6
1	X	200	ALA	2.5
1	X	521	GLN	2.5
1	X	295	ALA	2.3
1	X	623	LYS	2.3
1	X	618	ALA	2.2
1	X	738	ARG	2.2
1	X	536	PRO	2.2
1	X	535	PHE	2.2
1	X	5	HIS	2.1
1	X	7	ARG	2.1
1	X	210	VAL	2.1
1	X	25	PHE	2.0
1	X	616	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

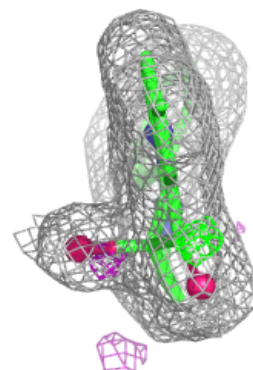
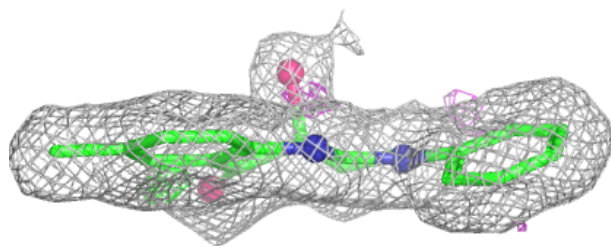
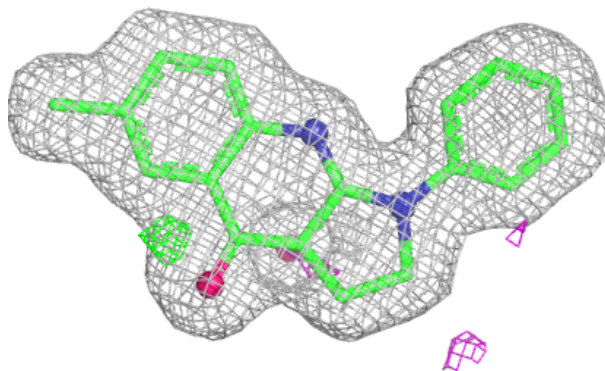
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

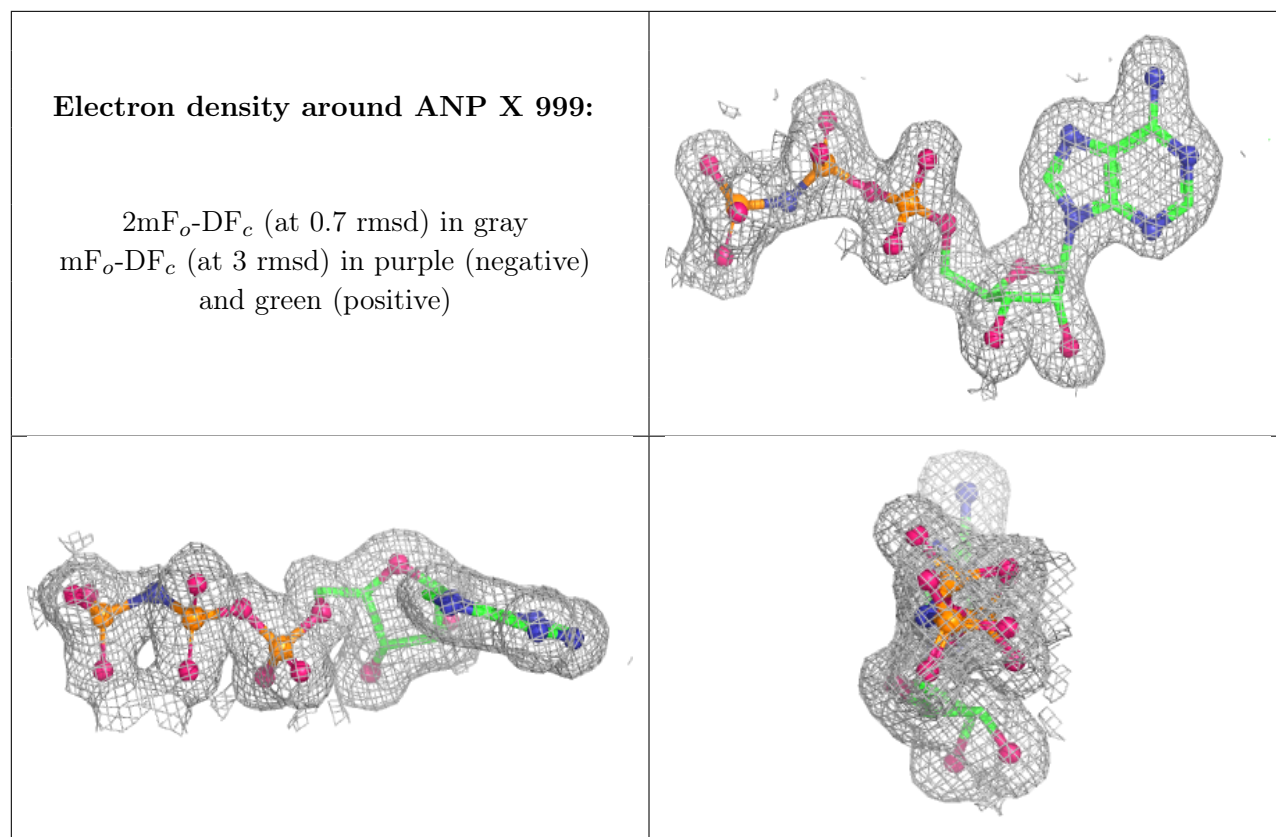
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BIT	X	800	22/22	0.96	0.06	13,19,21,23	0
3	MG	X	998	1/1	0.99	0.04	14,14,14,14	0
4	ANP	X	999	31/31	0.99	0.04	12,16,20,21	0

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 BIT X 800:

$2mF_o-DF_c$ (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.