



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:27 PM UTC

PDB ID : 1XFV / pdb_00001xfv
Title : Crystal structure of anthrax edema factor (EF) in complex with calmodulin and 3' deoxy-ATP
Authors : Shen, Q.; Zhukovskaya, N.L.; Guo, Q.; Florian, J.; Tang, W.J.
Deposited on : 2004-09-15
Resolution : 3.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

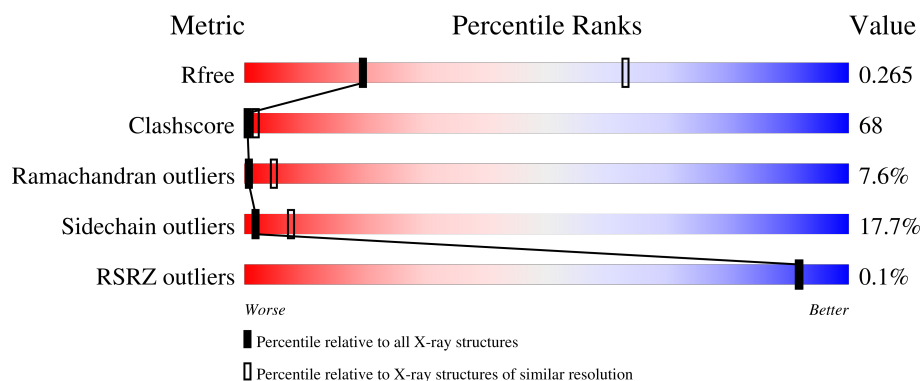
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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	1099 (3.40-3.32)
Clashscore	190562	1116 (3.40-3.32)
Ramachandran outliers	187476	1101 (3.40-3.32)
Sidechain outliers	187428	1101 (3.40-3.32)
RSRZ outliers	180081	1099 (3.40-3.32)

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	777	19% 54% 19% • 5%
1	B	777	19% 54% 20% • 5%
1	C	777	19% 55% 19% • 5%
1	D	777	18% 53% 21% • 5%
1	E	777	18% 54% 21% • 5%

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Mol	Chain	Length	Quality of chain
1	F	777	
2	O	149	
2	P	149	
2	Q	149	
2	R	149	
2	S	149	
2	T	149	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 43044 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 Calmodulin-sensitive adenylate cyclase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	B	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	C	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	D	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	E	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	F	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	MET	-	initiating methionine	UNP P40136
A	25	HIS	-	expression tag	UNP P40136
A	26	HIS	-	expression tag	UNP P40136
A	27	HIS	-	expression tag	UNP P40136
A	28	HIS	-	expression tag	UNP P40136
A	29	HIS	-	expression tag	UNP P40136
A	30	HIS	-	expression tag	UNP P40136
A	31	ALA	-	cloning artifact	UNP P40136
A	32	ALA	-	cloning artifact	UNP P40136
B	24	MET	-	initiating methionine	UNP P40136
B	25	HIS	-	expression tag	UNP P40136
B	26	HIS	-	expression tag	UNP P40136
B	27	HIS	-	expression tag	UNP P40136
B	28	HIS	-	expression tag	UNP P40136
B	29	HIS	-	expression tag	UNP P40136
B	30	HIS	-	expression tag	UNP P40136
B	31	ALA	-	cloning artifact	UNP P40136

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Chain	Residue	Modelled	Actual	Comment	Reference
B	32	ALA	-	cloning artifact	UNP P40136
C	24	MET	-	initiating methionine	UNP P40136
C	25	HIS	-	expression tag	UNP P40136
C	26	HIS	-	expression tag	UNP P40136
C	27	HIS	-	expression tag	UNP P40136
C	28	HIS	-	expression tag	UNP P40136
C	29	HIS	-	expression tag	UNP P40136
C	30	HIS	-	expression tag	UNP P40136
C	31	ALA	-	cloning artifact	UNP P40136
C	32	ALA	-	cloning artifact	UNP P40136
D	24	MET	-	initiating methionine	UNP P40136
D	25	HIS	-	expression tag	UNP P40136
D	26	HIS	-	expression tag	UNP P40136
D	27	HIS	-	expression tag	UNP P40136
D	28	HIS	-	expression tag	UNP P40136
D	29	HIS	-	expression tag	UNP P40136
D	30	HIS	-	expression tag	UNP P40136
D	31	ALA	-	cloning artifact	UNP P40136
D	32	ALA	-	cloning artifact	UNP P40136
E	24	MET	-	initiating methionine	UNP P40136
E	25	HIS	-	expression tag	UNP P40136
E	26	HIS	-	expression tag	UNP P40136
E	27	HIS	-	expression tag	UNP P40136
E	28	HIS	-	expression tag	UNP P40136
E	29	HIS	-	expression tag	UNP P40136
E	30	HIS	-	expression tag	UNP P40136
E	31	ALA	-	cloning artifact	UNP P40136
E	32	ALA	-	cloning artifact	UNP P40136
F	24	MET	-	initiating methionine	UNP P40136
F	25	HIS	-	expression tag	UNP P40136
F	26	HIS	-	expression tag	UNP P40136
F	27	HIS	-	expression tag	UNP P40136
F	28	HIS	-	expression tag	UNP P40136
F	29	HIS	-	expression tag	UNP P40136
F	30	HIS	-	expression tag	UNP P40136
F	31	ALA	-	cloning artifact	UNP P40136
F	32	ALA	-	cloning artifact	UNP P40136

- Molecule 2 is a protein called Calmodulin 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			

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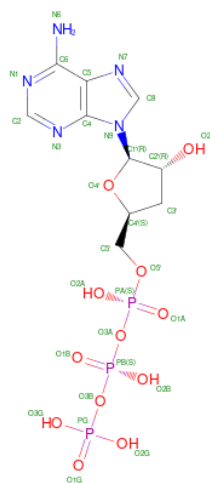
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	Q	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	R	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	S	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	T	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		
3	D	2	Total	Mg	0	0
			2	2		
3	E	2	Total	Mg	0	0
			2	2		
3	F	2	Total	Mg	0	0
			2	2		

- Molecule 4 is 3'-DEOXYADENOSINE-5'-TRIPHOSPHATE (CCD ID: 3AT) (formula: C₁₀H₁₆N₅O₁₂P₃).

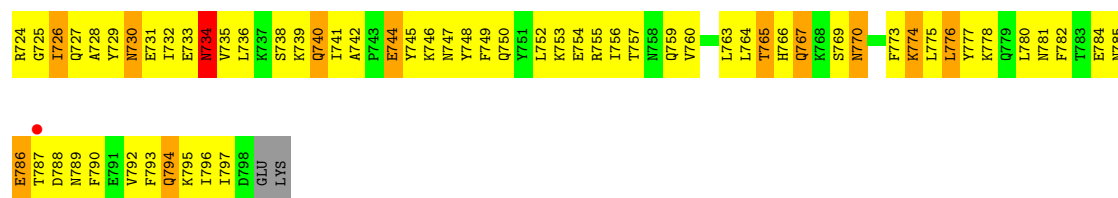


- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).



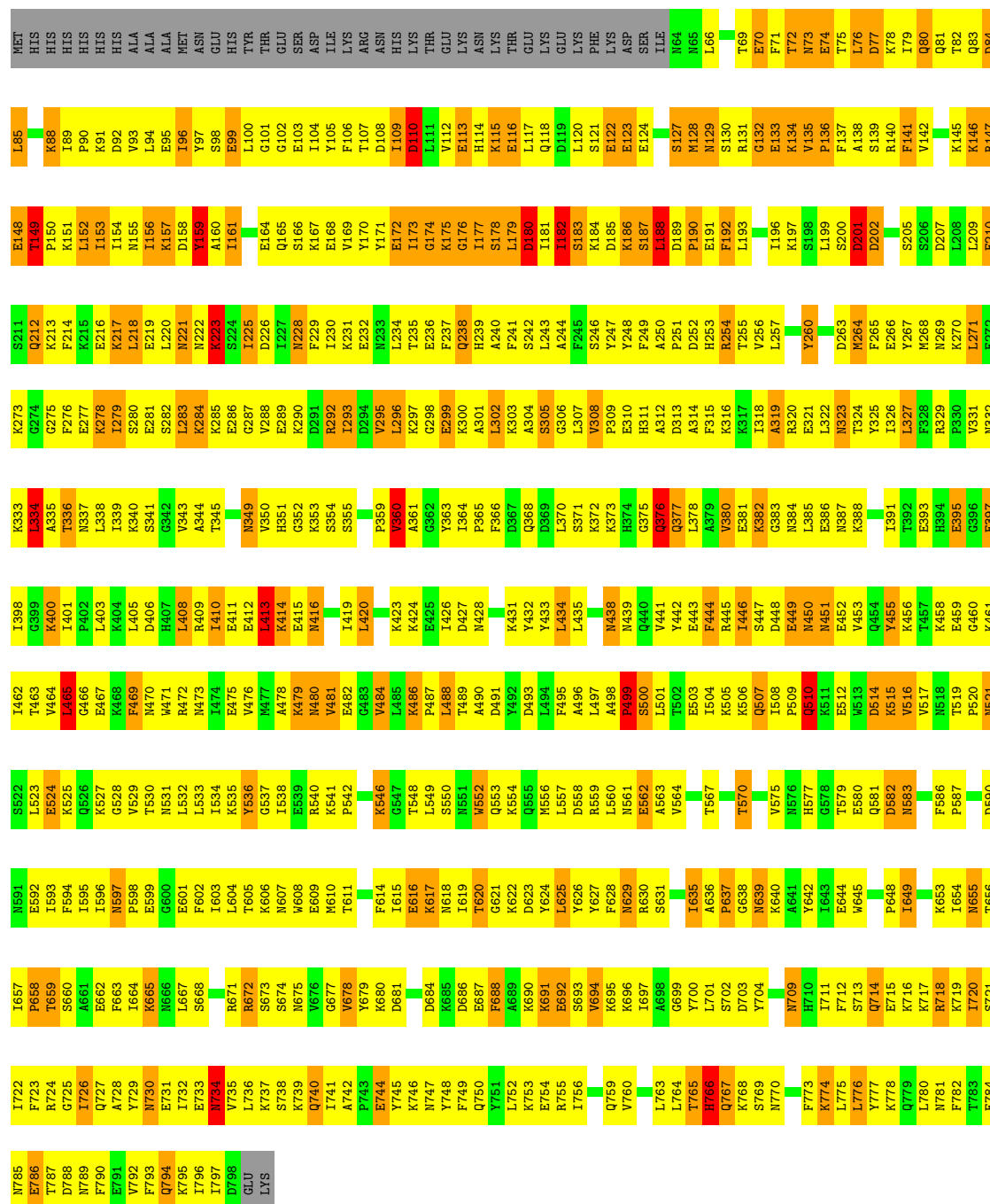
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total 1	O 1	0	0
6	B	1	Total 1	O 1	0	0
6	C	1	Total 1	O 1	0	0
6	D	1	Total 1	O 1	0	0
6	E	1	Total 1	O 1	0	0
6	F	1	Total 1	O 1	0	0

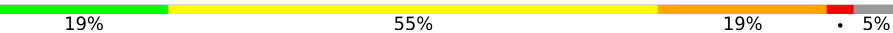


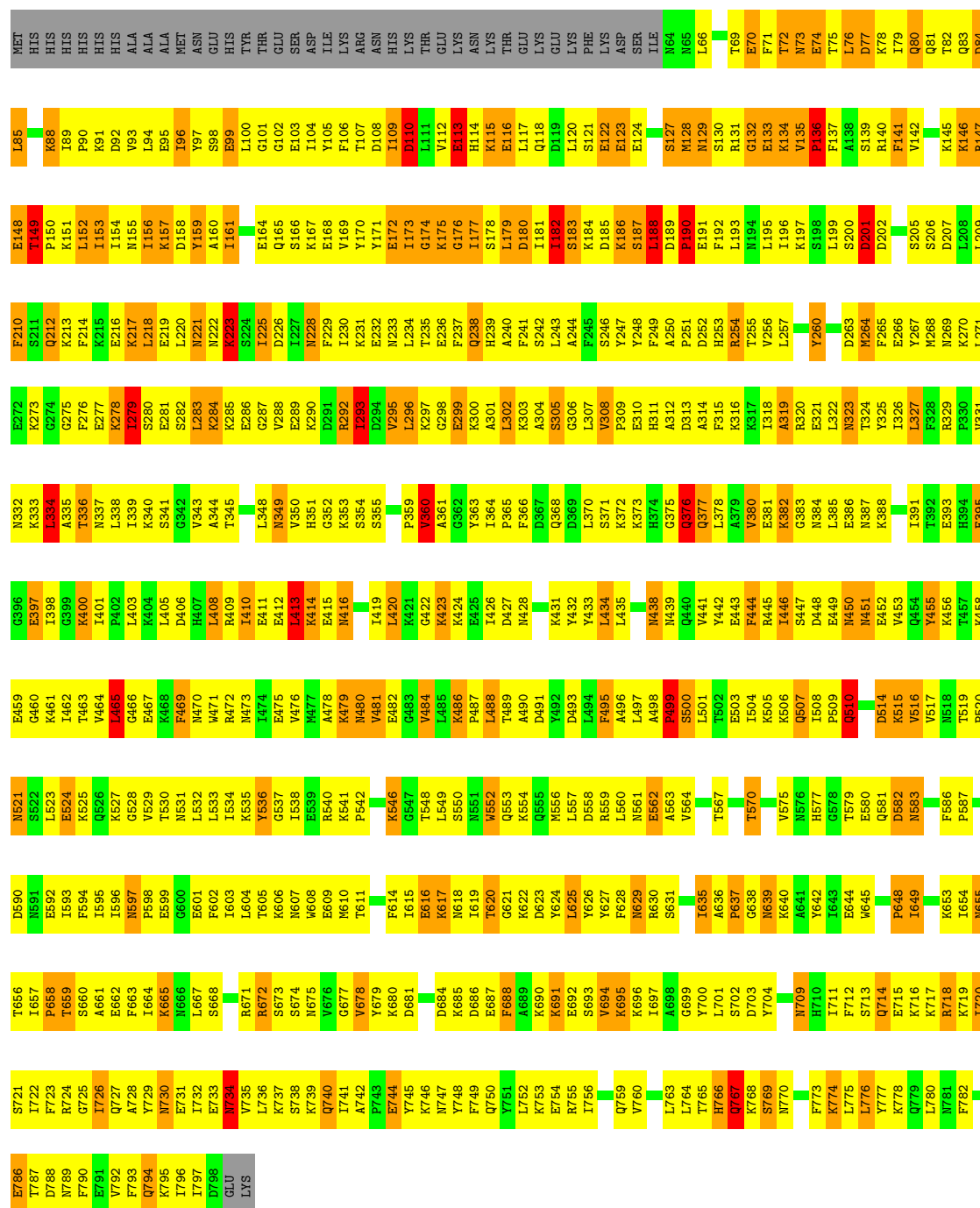
● Molecule 1: Calmodulin-sensitive adenylate cyclase

Chain B: 19% 54% 20% 5%



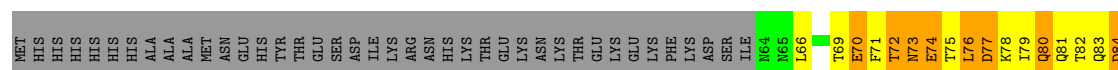
• Molecule 1: Calmodulin-sensitive adenylate cyclase

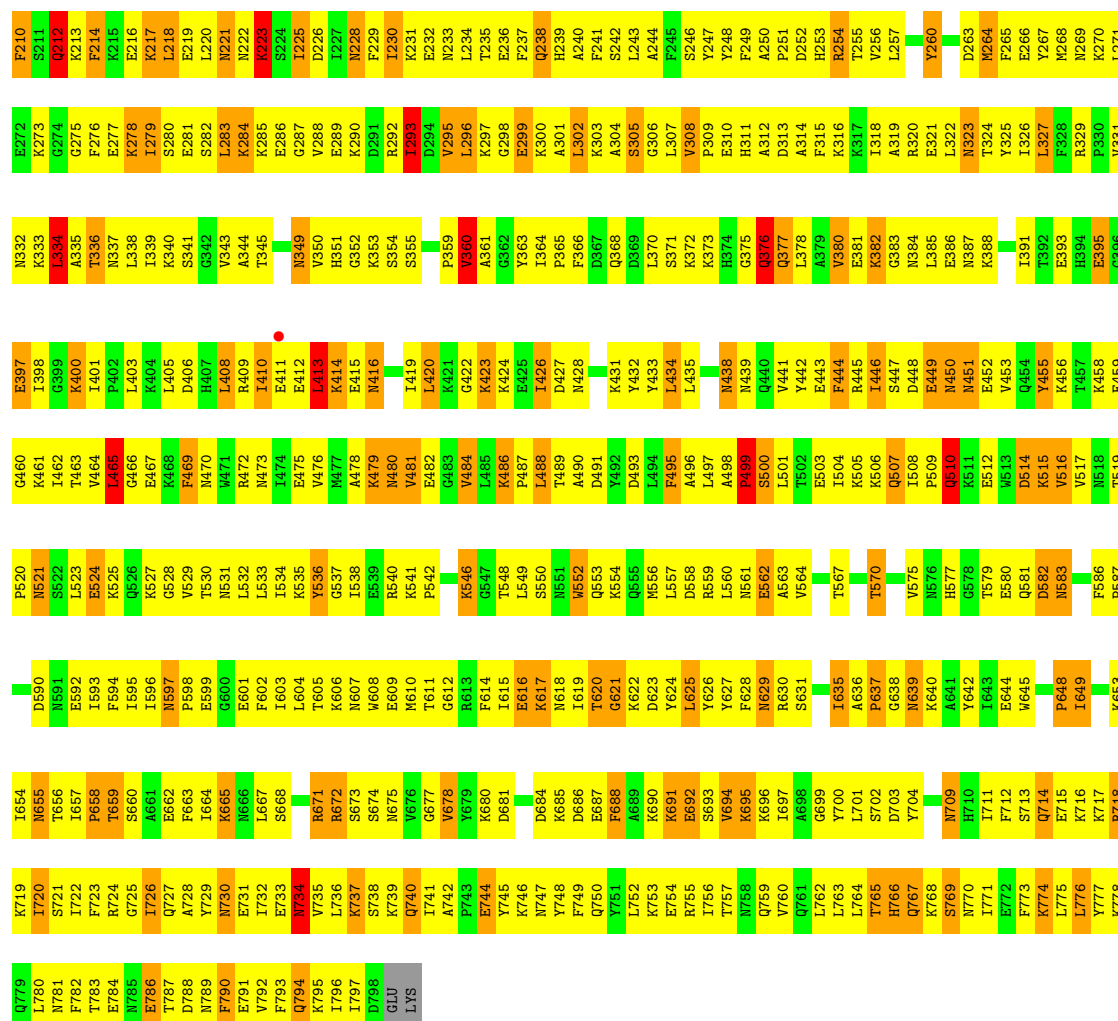
Chain C:  19% 55% 19% 5%



• Molecule 1: Calmodulin-sensitive adenylate cyclase

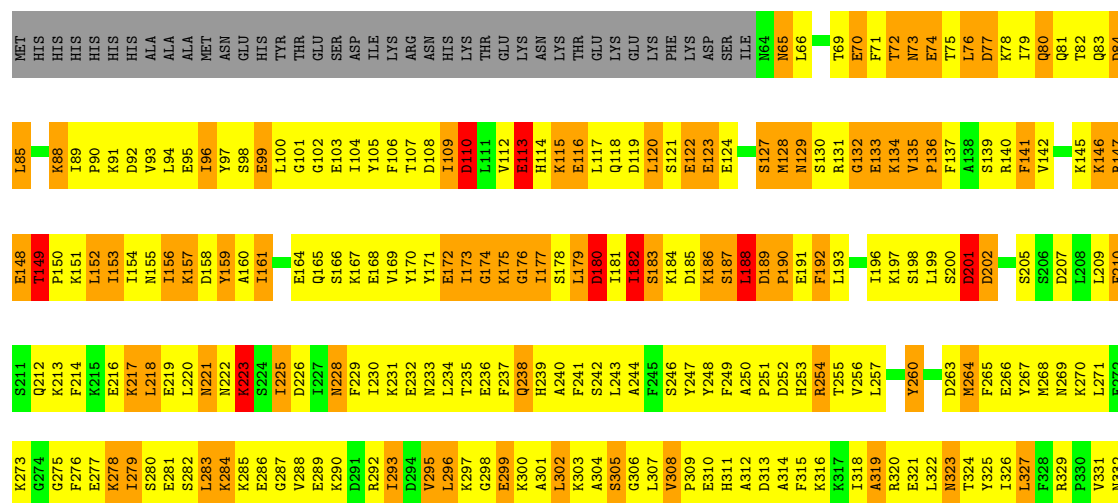
Chain D:  18% 53% 21% 5%

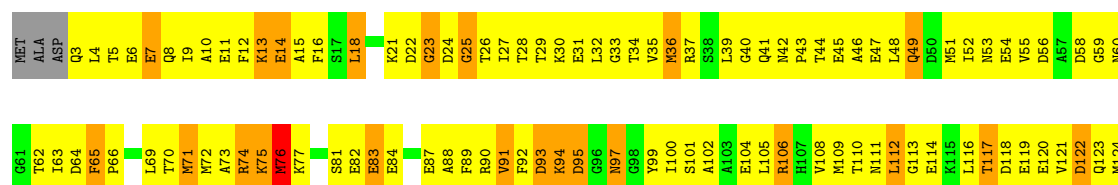


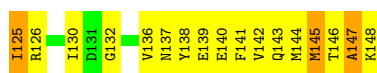


• Molecule 1: Calmodulin-sensitive adenylate cyclase

Chain F: 19% 54% 20% 5%



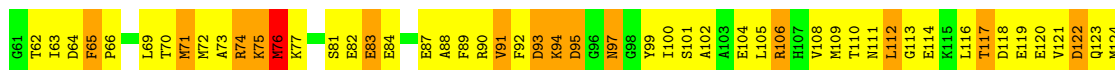
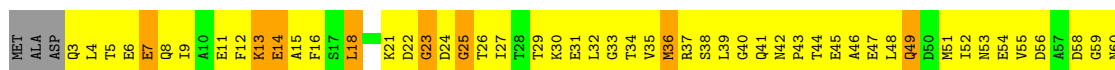




● Molecule 2: Calmodulin 2

Chain Q:

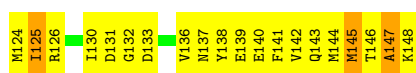
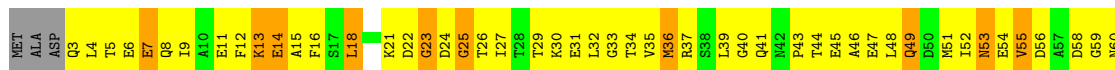
18% 62% 17% ..



● Molecule 2: Calmodulin 2

Chain R:

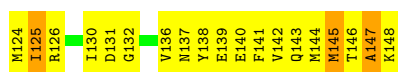
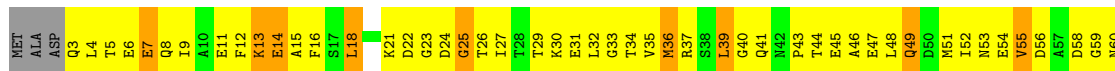
17% 62% 18% ..



● Molecule 2: Calmodulin 2

Chain S:

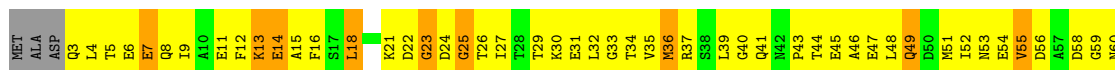
18% 62% 16% ..

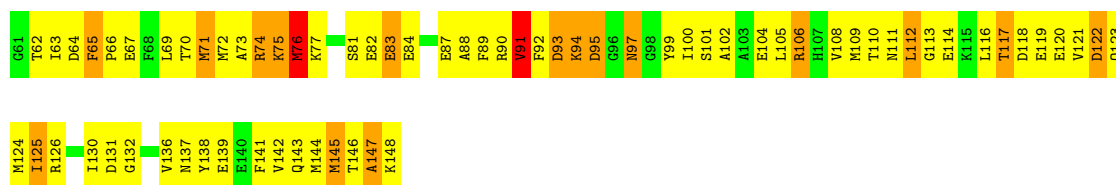


● Molecule 2: Calmodulin 2

Chain T:

19% 61% 17% ..





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	184.60Å 319.29Å 142.05Å 90.00° 90.22° 90.00°	Depositor
Resolution (Å)	29.57 – 3.35 29.57 – 3.35	Depositor EDS
% Data completeness (in resolution range)	92.6 (29.57-3.35) 91.7 (29.57-3.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 3.32Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.263 , 0.282 0.250 , 0.265	Depositor DCC
R_{free} test set	5790 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	97.5	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 156.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.458 for -1/2*h+1/2*k,3/2*h+1/2*k,-l 0.458 for -1/2*h-1/2*k,-3/2*h+1/2*k,-l 0.440 for 1/2*h+1/2*k,3/2*h-1/2*k,-l 0.447 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.439 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	43044	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.41% 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: 3AT, CA, 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	A	0.70	12/6104 (0.2%)	1.27	84/8208 (1.0%)
1	B	0.72	13/6104 (0.2%)	1.28	89/8208 (1.1%)
1	C	0.76	18/6104 (0.3%)	1.33	100/8208 (1.2%)
1	D	0.76	21/6104 (0.3%)	1.30	95/8208 (1.2%)
1	E	0.76	17/6104 (0.3%)	1.31	97/8208 (1.2%)
1	F	0.72	11/6104 (0.2%)	1.29	93/8208 (1.1%)
2	O	0.66	0/1158	1.12	11/1553 (0.7%)
2	P	0.67	0/1158	1.14	8/1553 (0.5%)
2	Q	0.68	0/1158	1.13	8/1553 (0.5%)
2	R	0.70	0/1158	1.14	10/1553 (0.6%)
2	S	0.72	2/1158 (0.2%)	1.14	7/1553 (0.5%)
2	T	0.72	1/1158 (0.1%)	1.14	8/1553 (0.5%)
All	All	0.73	95/43572 (0.2%)	1.27	610/58566 (1.0%)

The worst 5 of 95 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	740	GLN	C-N	-9.88	1.20	1.33
1	D	784	GLU	C-N	9.20	1.46	1.33
1	C	766	HIS	C-N	-9.16	1.20	1.33
1	D	621	GLY	C-N	8.64	1.46	1.33
1	E	784	GLU	C-N	8.61	1.45	1.33

The worst 5 of 610 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	766	HIS	O-C-N	-16.86	98.42	122.36
1	E	147	ARG	N-CA-C	14.34	126.63	111.14
1	C	147	ARG	N-CA-C	14.34	126.62	111.14
1	B	147	ARG	N-CA-C	14.32	126.61	111.14
1	D	147	ARG	N-CA-C	14.28	126.56	111.14

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	5992	0	6010	825	2
1	B	5992	0	6010	818	2
1	C	5992	0	6010	826	2
1	D	5992	0	6010	831	3
1	E	5992	0	6010	837	3
1	F	5992	0	6010	821	1
2	O	1146	0	1071	159	0
2	P	1146	0	1071	164	0
2	Q	1146	0	1071	165	0
2	R	1146	0	1071	168	0
2	S	1146	0	1071	174	0
2	T	1146	0	1071	167	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	2	0	0	0	0
4	A	30	0	12	1	0
4	B	30	0	12	1	0
4	C	30	0	12	1	0
4	D	30	0	12	1	0
4	E	30	0	12	1	0
4	F	30	0	12	1	0
5	O	3	0	0	0	0
5	P	3	0	0	0	0
5	Q	3	0	0	0	0
5	R	3	0	0	0	0
5	S	3	0	0	0	0
5	T	3	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
All	All	43044	0	42558	5798	8

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 68.

The worst 5 of 5798 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:E:179:LEU:O	1:E:183:SER:CB	1.74	1.36
1:D:179:LEU:O	1:D:183:SER:CB	1.77	1.30
1:F:179:LEU:O	1:F:183:SER:CB	1.80	1.30
1:C:179:LEU:O	1:C:183:SER:CB	1.77	1.30
1:B:179:LEU:O	1:B:183:SER:HB2	1.18	1.27

The worst 5 of 8 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)
1:D:685:LYS:NZ	1:D:685:LYS:NZ[2_657]	2.03	0.17
1:A:75:THR:CG2	1:E:786:GLU:O[4_556]	2.09	0.11
1:B:786:GLU:O	1:D:75:THR:CG2[4_656]	2.12	0.08
1:F:75:THR:CG2	1:F:786:GLU:O[2_557]	2.13	0.07
1:B:75:THR:CG2	1:D:786:GLU:O[4_656]	2.14	0.06

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	733/777 (94%)	497 (68%)	179 (24%)	57 (8%)	1	4
1	B	733/777 (94%)	494 (67%)	183 (25%)	56 (8%)	1	5
1	C	733/777 (94%)	491 (67%)	187 (26%)	55 (8%)	1	5
1	D	733/777 (94%)	492 (67%)	187 (26%)	54 (7%)	1	5
1	E	733/777 (94%)	490 (67%)	186 (25%)	57 (8%)	1	4
1	F	733/777 (94%)	492 (67%)	186 (25%)	55 (8%)	1	5
2	O	144/149 (97%)	103 (72%)	30 (21%)	11 (8%)	1	5
2	P	144/149 (97%)	103 (72%)	30 (21%)	11 (8%)	1	5
2	Q	144/149 (97%)	103 (72%)	30 (21%)	11 (8%)	1	5
2	R	144/149 (97%)	103 (72%)	29 (20%)	12 (8%)	0	4
2	S	144/149 (97%)	103 (72%)	30 (21%)	11 (8%)	1	5
2	T	144/149 (97%)	103 (72%)	30 (21%)	11 (8%)	1	5
All	All	5262/5556 (95%)	3574 (68%)	1287 (24%)	401 (8%)	1	5

5 of 401 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176	GLY
1	A	183	SER
1	A	302	LEU
1	A	787	THR
1	B	137	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	664/705 (94%)	550 (83%)	114 (17%)	2	8
1	B	664/705 (94%)	548 (82%)	116 (18%)	2	8
1	C	664/705 (94%)	548 (82%)	116 (18%)	2	8
1	D	664/705 (94%)	549 (83%)	115 (17%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	664/705 (94%)	549 (83%)	115 (17%)	2	8
1	F	664/705 (94%)	546 (82%)	118 (18%)	2	7
2	O	123/127 (97%)	100 (81%)	23 (19%)	1	6
2	P	123/127 (97%)	100 (81%)	23 (19%)	1	6
2	Q	123/127 (97%)	100 (81%)	23 (19%)	1	6
2	R	123/127 (97%)	99 (80%)	24 (20%)	1	5
2	S	123/127 (97%)	99 (80%)	24 (20%)	1	5
2	T	123/127 (97%)	100 (81%)	23 (19%)	1	6
All	All	4722/4992 (95%)	3888 (82%)	834 (18%)	2	8

5 of 834 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	77	ASP
1	E	776	LEU
2	S	62	THR
1	E	135	VAL
1	E	72	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 270 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	740	GLN
1	F	781	ASN
2	S	41	GLN
1	C	507	GLN
1	C	387	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 36 ligands modelled in this entry, 30 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
4	3AT	D	906	3	30,32,32	2.32	5 (16%)	42,50,50	1.45	4 (9%)
4	3AT	A	903	3	30,32,32	2.30	4 (13%)	42,50,50	1.46	4 (9%)
4	3AT	F	908	3	30,32,32	2.20	4 (13%)	42,50,50	1.49	4 (9%)
4	3AT	B	904	3	30,32,32	2.33	4 (13%)	42,50,50	1.48	4 (9%)
4	3AT	C	905	3	30,32,32	2.42	5 (16%)	42,50,50	1.47	4 (9%)
4	3AT	E	907	3	30,32,32	2.33	5 (16%)	42,50,50	1.43	4 (9%)

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	3AT	D	906	3	-	7/22/34/34	0/3/3/3
4	3AT	A	903	3	-	7/22/34/34	0/3/3/3
4	3AT	F	908	3	-	7/22/34/34	0/3/3/3
4	3AT	B	904	3	-	7/22/34/34	0/3/3/3
4	3AT	C	905	3	-	7/22/34/34	0/3/3/3
4	3AT	E	907	3	-	7/22/34/34	0/3/3/3

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	905	3AT	PB-O3B	10.31	1.70	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	904	3AT	PB-O3B	10.09	1.70	1.59
4	E	907	3AT	PB-O3B	9.79	1.70	1.59
4	D	906	3AT	PB-O3B	9.77	1.70	1.59
4	A	903	3AT	PB-O3B	9.37	1.69	1.59

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	908	3AT	O4'-C1'-C2'	-5.97	100.89	106.51
4	B	904	3AT	O4'-C1'-C2'	-5.85	101.01	106.51
4	C	905	3AT	O4'-C1'-C2'	-5.71	101.14	106.51
4	A	903	3AT	O4'-C1'-C2'	-5.57	101.27	106.51
4	E	907	3AT	O4'-C1'-C2'	-5.46	101.38	106.51

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	903	3AT	PB-O3B-PG-O2G
4	A	903	3AT	O4'-C4'-C5'-O5'
4	A	903	3AT	C3'-C4'-C5'-O5'
4	B	904	3AT	PB-O3B-PG-O2G
4	B	904	3AT	O4'-C4'-C5'-O5'

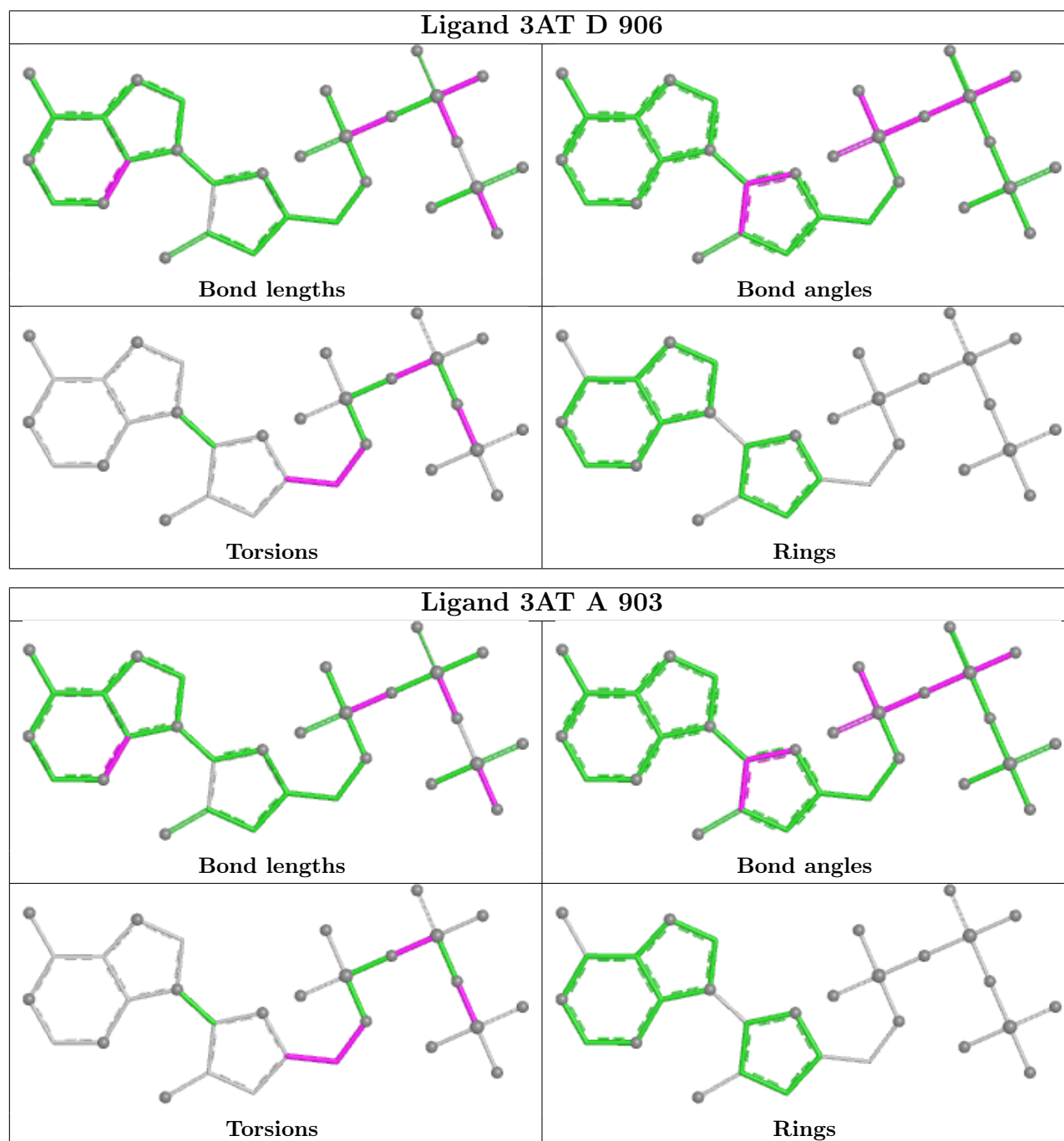
There are no ring outliers.

6 monomers are involved in 6 short contacts:

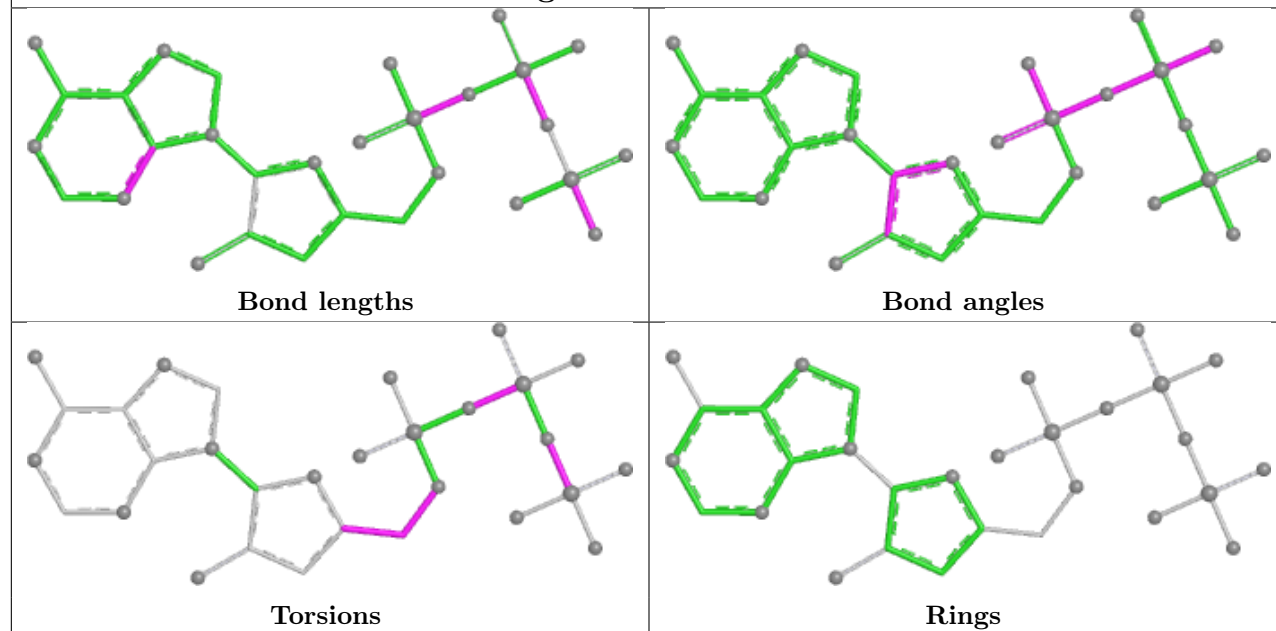
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	906	3AT	1	0
4	A	903	3AT	1	0
4	F	908	3AT	1	0
4	B	904	3AT	1	0
4	C	905	3AT	1	0
4	E	907	3AT	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

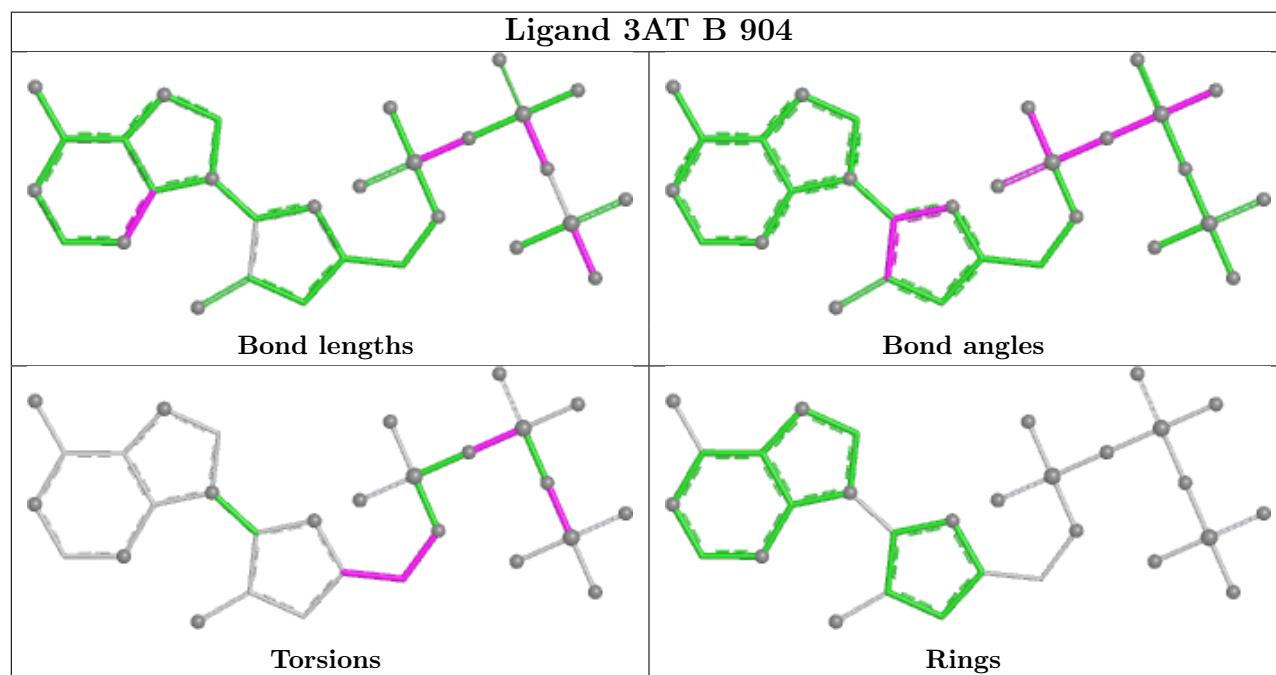
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

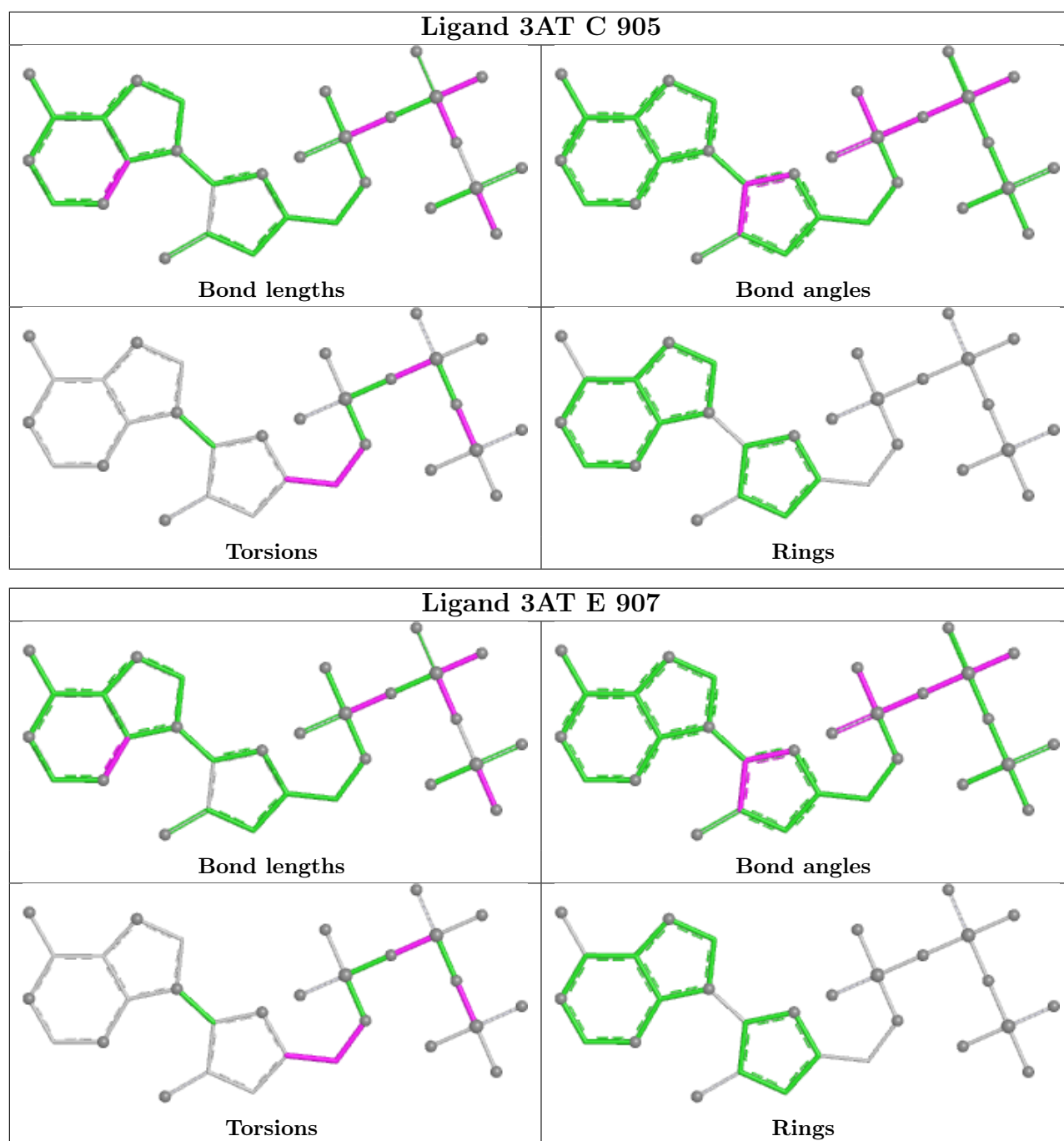


Ligand 3AT F 908



Ligand 3AT B 904





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	735/777 (94%)	-1.03	2 (0%) 90 84	26, 80, 136, 148	0
1	B	735/777 (94%)	-1.06	0 100 100	27, 80, 136, 148	0
1	C	735/777 (94%)	-1.08	0 100 100	27, 80, 136, 148	0
1	D	735/777 (94%)	-1.05	1 (0%) 92 92	27, 80, 136, 150	0
1	E	735/777 (94%)	-1.07	2 (0%) 90 84	26, 80, 136, 148	0
1	F	735/777 (94%)	-1.06	1 (0%) 92 92	27, 80, 136, 148	0
2	O	146/149 (97%)	-1.08	0 100 100	33, 63, 124, 131	0
2	P	146/149 (97%)	-1.15	0 100 100	33, 63, 124, 131	0
2	Q	146/149 (97%)	-1.15	0 100 100	33, 62, 124, 131	0
2	R	146/149 (97%)	-1.03	0 100 100	33, 63, 124, 131	0
2	S	146/149 (97%)	-1.13	0 100 100	32, 62, 124, 131	0
2	T	146/149 (97%)	-1.13	0 100 100	33, 62, 124, 131	0
All	All	5286/5556 (95%)	-1.07	6 (0%) 92 92	26, 76, 134, 150	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	163	SER	3.9
1	A	283	LEU	2.4
1	E	411	GLU	2.2
1	D	450	ASN	2.1
1	A	787	THR	2.1

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	3AT	B	904	30/30	0.98	0.05	58,73,93,94	0
4	3AT	D	906	30/30	0.98	0.05	58,74,94,95	0
4	3AT	E	907	30/30	0.98	0.04	60,74,96,97	0
5	CA	P	703	1/1	0.98	0.04	62,62,62,62	0
5	CA	R	707	1/1	0.98	0.10	62,62,62,62	0
5	CA	S	709	1/1	0.98	0.05	57,57,57,57	0
4	3AT	A	903	30/30	0.99	0.05	60,74,93,94	0
4	3AT	F	908	30/30	0.99	0.05	61,75,94,95	0
5	CA	O	701	1/1	0.99	0.03	51,51,51,51	0
3	MG	A	902	1/1	0.99	0.02	28,28,28,28	0
5	CA	P	804	1/1	0.99	0.02	52,52,52,52	0
5	CA	Q	806	1/1	0.99	0.04	57,57,57,57	0
4	3AT	C	905	30/30	0.99	0.04	62,73,94,95	0
3	MG	E	906	1/1	0.99	0.05	26,26,26,26	0
3	MG	C	903	1/1	1.00	0.02	9,9,9,9	0
3	MG	C	904	1/1	1.00	0.06	26,26,26,26	0
3	MG	D	904	1/1	1.00	0.05	8,8,8,8	0
3	MG	D	905	1/1	1.00	0.06	43,43,43,43	0
3	MG	E	905	1/1	1.00	0.02	20,20,20,20	0
5	CA	O	801	1/1	1.00	0.02	30,30,30,30	0
5	CA	O	802	1/1	1.00	0.02	52,52,52,52	0
3	MG	A	901	1/1	1.00	0.02	5,5,5,5	0
5	CA	P	803	1/1	1.00	0.02	31,31,31,31	0
3	MG	F	906	1/1	1.00	0.03	11,11,11,11	0
5	CA	Q	705	1/1	1.00	0.02	55,55,55,55	0
5	CA	Q	805	1/1	1.00	0.03	27,27,27,27	0
3	MG	F	907	1/1	1.00	0.02	34,34,34,34	0
3	MG	B	902	1/1	1.00	0.02	17,17,17,17	0
5	CA	R	807	1/1	1.00	0.02	33,33,33,33	0
5	CA	R	808	1/1	1.00	0.01	54,54,54,54	0
3	MG	B	903	1/1	1.00	0.08	25,25,25,25	0
5	CA	S	809	1/1	1.00	0.02	26,26,26,26	0

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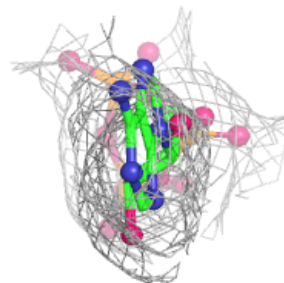
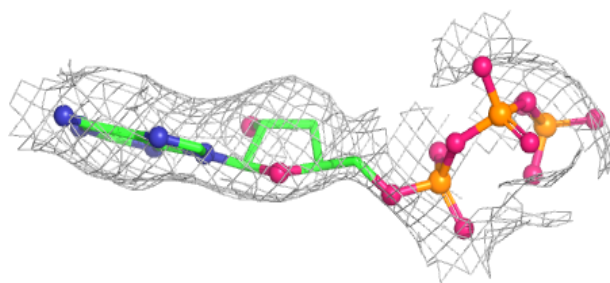
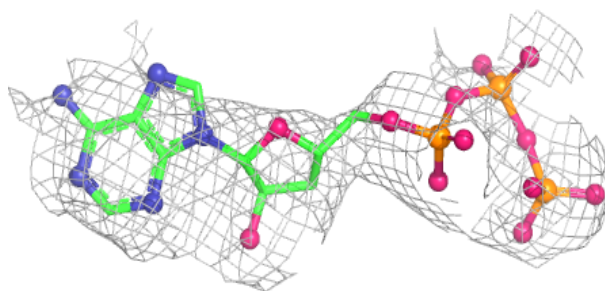
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	CA	S	810	1/1	1.00	0.01	56,56,56,56	0
5	CA	T	711	1/1	1.00	0.01	55,55,55,55	0
5	CA	T	811	1/1	1.00	0.03	33,33,33,33	0
5	CA	T	812	1/1	1.00	0.03	49,49,49,49	0

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.

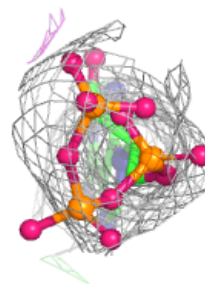
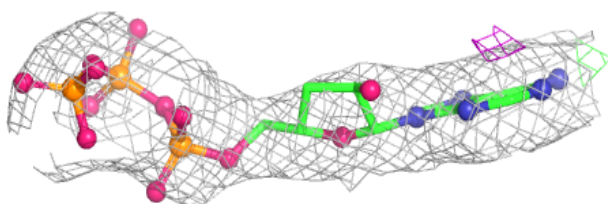
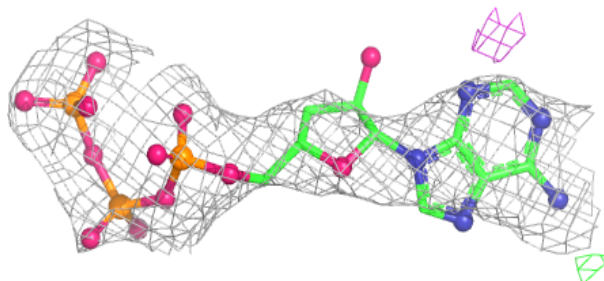
Electron density around 3AT B 904:

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

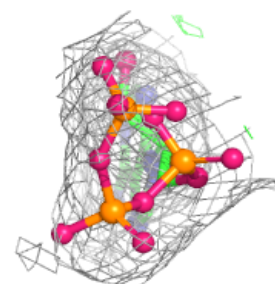
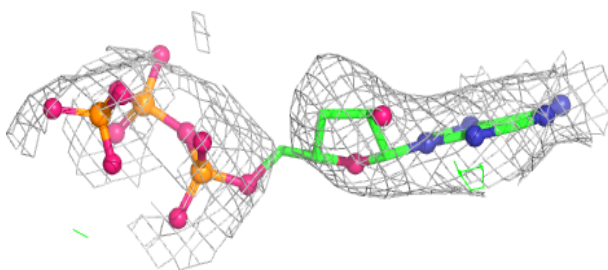
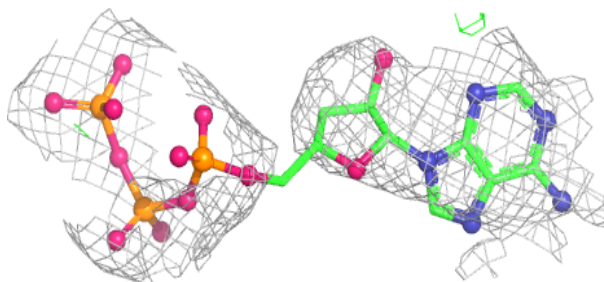


Electron density around 3AT D 906:

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

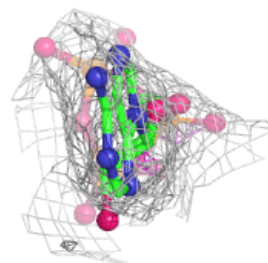
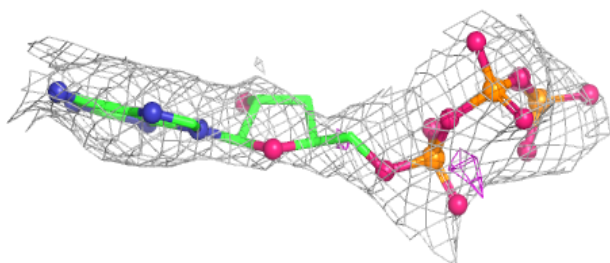
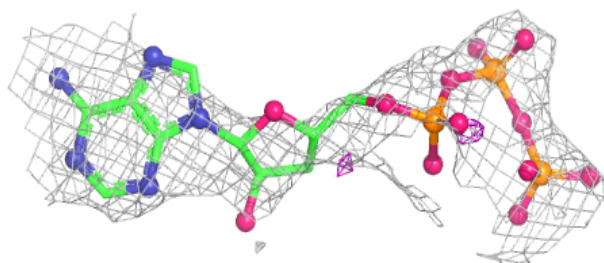
**Electron density around 3AT E 907:**

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and green (positive)

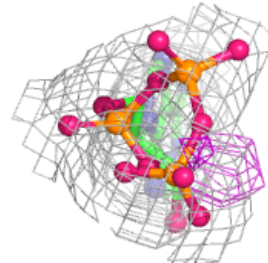
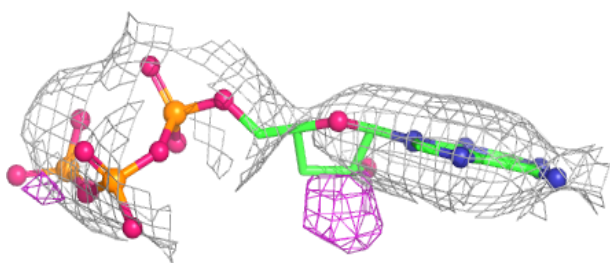
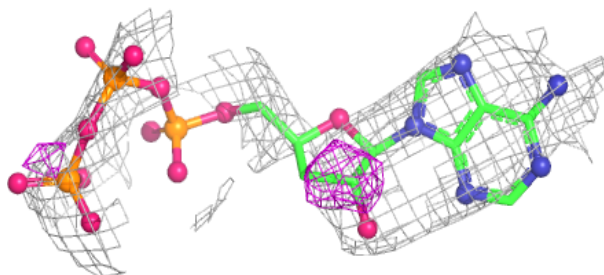


Electron density around 3AT A 903:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

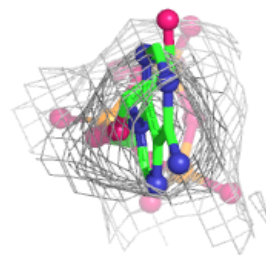
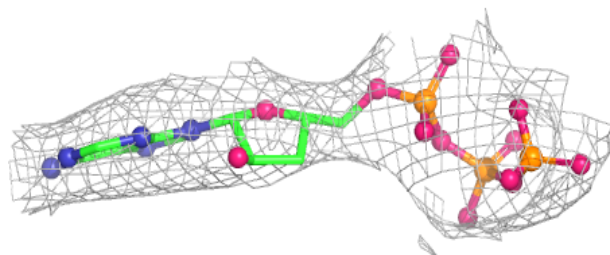
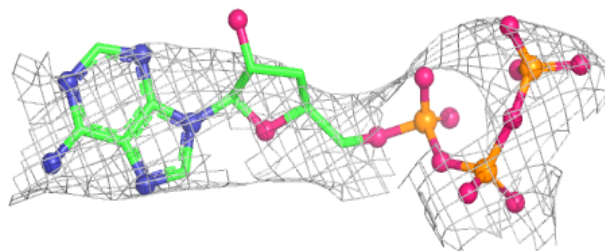
**Electron density around 3AT F 908:**

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



Electron density around 3AT C 905:

$2mF_o-DF_c$ (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.