



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:58 PM UTC

PDB ID : 6JUM / pdb_00006jum
Title : MsDpo4-DNA complex 2
Authors : Nair, D.T.; Johnson, M.J.
Deposited on : 2019-04-15
Resolution : 1.78 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:

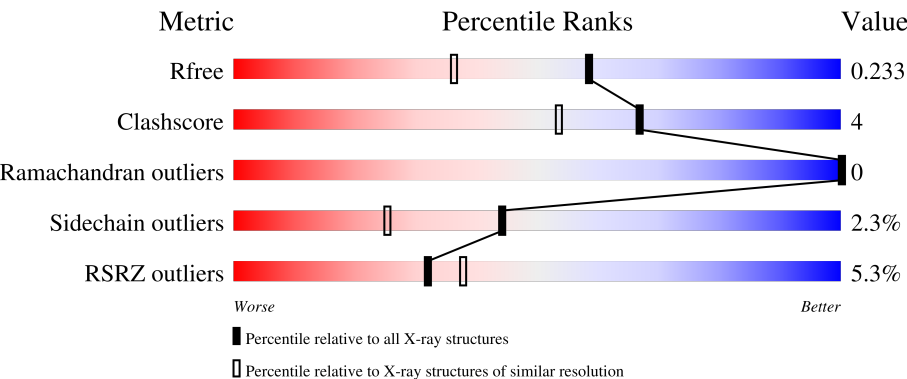
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	347	5% 79% 19% .
1	F	347	4% 84% 14% .
2	B	18	22% 56% 17% 28%
2	C	18	39% 17% 44%
2	G	18	11% 28% 39% 33%

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Mol	Chain	Length	Quality of chain
2	H	18	17% 17% 11% 56%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6928 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 DNA polymerase IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	0	0	0
			2646	1664	465	507	10			
1	F	347	Total	C	N	O	S	0	0	0
			2646	1664	465	507	10			

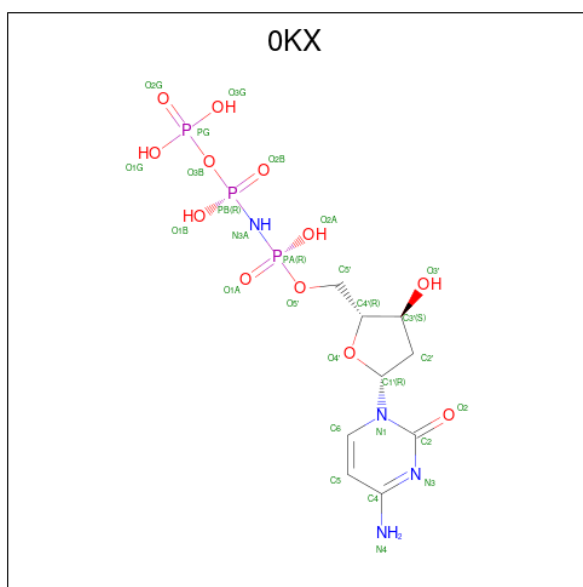
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	THR	CYS	engineered mutation	UNP A0QR77
F	47	THR	CYS	engineered mutation	UNP A0QR77

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*AP*GP*GP*AP*CP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	8	Total	C	N	O	P	0	0	0
			163	77	31	47	8			
2	G	12	Total	C	N	O	P	0	0	0
			248	117	45	74	12			
2	C	10	Total	C	N	O	P	0	0	0
			201	95	37	59	10			
2	B	13	Total	C	N	O	P	0	0	0
			270	127	50	80	13			

- Molecule 3 is 2'-deoxy-5'-O-[(R)-hydroxy{[(R)-hydroxy(phosphonooxy)phosphoryl]amino}phosphoryl]cytidine (CCD ID: 0KX) (formula: C₉H₁₇N₄O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			28	9	4	12	3		
3	F	1	Total	C	N	O	P	0	0
			28	9	4	12	3		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mg	0	0
			2	2		
4	F	2	Total	Mg	0	0
			2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	295	Total	O	0	0
			295	295		
5	F	290	Total	O	0	0
			290	290		
5	H	22	Total	O	0	0
			22	22		
5	G	41	Total	O	0	0
			41	41		
5	C	17	Total	O	0	0
			17	17		

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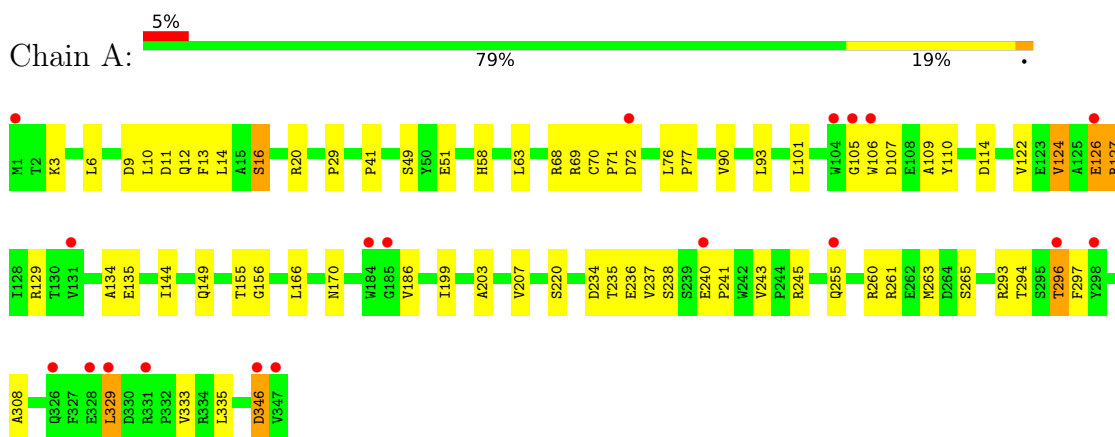
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	29	Total	O	0	0
			29	29		

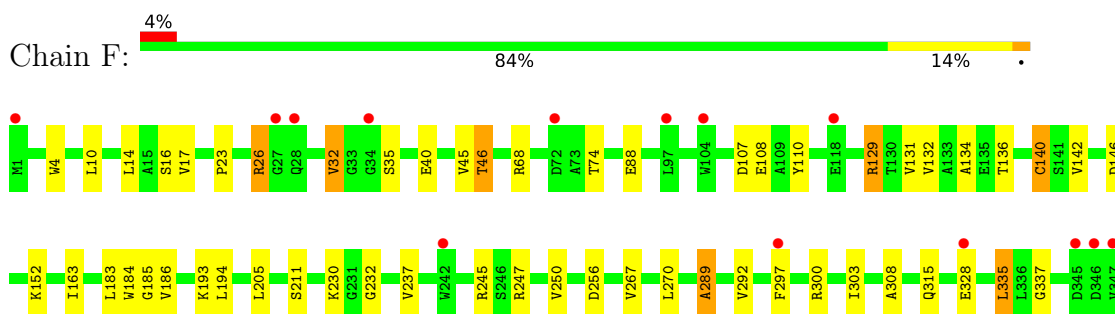
3 Residue-property plots

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.

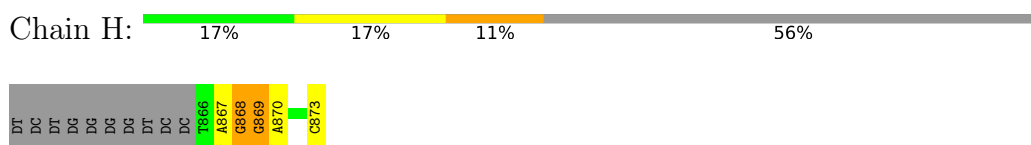
• Molecule 1: DNA polymerase IV



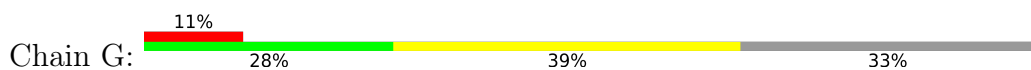
• Molecule 1: DNA polymerase IV



• Molecule 2: DNA (5'-D(P*TP*AP*GP*GP*AP*CP*CP*C)-3')

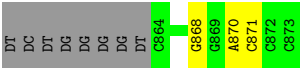


• Molecule 2: DNA (5'-D(P*TP*AP*GP*GP*AP*CP*CP*C)-3')

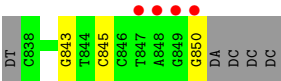




● Molecule 2: DNA (5'-D(P*TP*AP*GP*GP*AP*CP*CP*C)-3')



● Molecule 2: DNA (5'-D(P*TP*AP*GP*GP*AP*CP*CP*C)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.02Å 80.96Å 211.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.96 – 1.78 80.96 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.7 (80.96-1.78) 99.7 (80.96-1.78)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.195 , 0.234 (Not available) , 0.233	Depositor DCC
R_{free} test set	4627 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6928	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% 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: MG, 0KX

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	1.85	43/2699 (1.6%)	1.37	9/3682 (0.2%)
1	F	1.76	32/2699 (1.2%)	1.34	10/3682 (0.3%)
2	B	0.77	0/302	1.16	2/465 (0.4%)
2	C	0.70	0/224	1.19	1/342 (0.3%)
2	G	0.79	0/277	1.25	3/426 (0.7%)
2	H	0.86	1/182 (0.5%)	1.44	4/278 (1.4%)
All	All	1.69	76/6383 (1.2%)	1.34	29/8875 (0.3%)

All (76) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	238	SER	C-O	-14.80	1.06	1.24
1	A	234	ASP	C-O	-13.09	1.08	1.23
1	A	126	GLU	C-O	-12.57	1.09	1.24
1	A	236	GLU	C-O	-12.17	1.09	1.24
1	A	241	PRO	C-O	-10.48	1.12	1.23
1	A	237	VAL	C-O	-9.96	1.12	1.24
1	F	193	LYS	CA-C	8.96	1.64	1.52
1	F	183	LEU	N-CA	8.29	1.56	1.45
1	F	16	SER	N-CA	7.85	1.55	1.46
1	A	155	THR	C-O	7.67	1.33	1.24
1	A	13	PHE	N-CA	7.59	1.55	1.46
1	F	152	LYS	N-CA	-7.08	1.37	1.46
1	F	134	ALA	N-CA	7.03	1.55	1.46
1	A	234	ASP	CG-OD2	-7.02	1.12	1.25
1	F	146	ASP	CA-C	6.98	1.61	1.52
1	A	170	ASN	N-CA	-6.91	1.36	1.45
1	A	156	GLY	CA-C	6.72	1.59	1.52
1	A	77	PRO	C-O	-6.57	1.15	1.23
1	A	234	ASP	CG-OD1	-6.53	1.12	1.25
1	F	270	LEU	N-CA	6.50	1.54	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	74	THR	CA-C	-6.46	1.44	1.52
1	F	17	VAL	CA-C	-6.30	1.45	1.52
1	A	90	VAL	C-O	-6.25	1.16	1.24
2	H	870	DA	O3'-P	-6.19	1.51	1.61
1	A	110	TYR	CA-C	6.16	1.60	1.52
1	F	256	ASP	N-CA	-6.12	1.38	1.46
1	F	10	LEU	CA-C	6.11	1.60	1.52
1	A	236	GLU	N-CA	-6.06	1.38	1.46
1	A	166	LEU	N-CA	-6.01	1.39	1.46
1	F	136	THR	C-O	-6.01	1.16	1.24
1	F	194	LEU	CA-C	5.96	1.60	1.52
1	A	149	GLN	N-CA	5.95	1.53	1.46
1	A	16	SER	CA-C	5.88	1.60	1.52
1	A	235	THR	C-N	-5.86	1.25	1.33
1	F	4	TRP	N-CA	5.83	1.53	1.45
1	A	41	PRO	CA-C	5.83	1.59	1.52
1	F	110	TYR	C-O	-5.80	1.17	1.24
1	F	136	THR	CA-CB	5.80	1.62	1.54
1	A	10	LEU	C-O	-5.78	1.17	1.23
1	F	184	TRP	N-CA	-5.77	1.39	1.46
1	A	207	VAL	CA-CB	5.77	1.60	1.54
1	A	245	ARG	C-O	5.72	1.31	1.24
1	F	245	ARG	CA-C	5.71	1.60	1.52
1	F	140	CYS	C-O	5.66	1.31	1.23
1	A	203	ALA	CA-CB	5.64	1.62	1.53
1	F	129	ARG	CD-NE	-5.62	1.38	1.46
1	F	46	THR	CB-CG2	-5.61	1.34	1.52
1	A	76	LEU	CA-C	-5.59	1.45	1.52
1	A	134	ALA	N-CA	5.53	1.53	1.46
1	F	132	VAL	CA-CB	5.52	1.60	1.54
1	A	144	ILE	C-O	5.50	1.30	1.24
1	F	247	ARG	C-O	5.48	1.30	1.23
1	A	265	SER	CA-C	5.42	1.59	1.52
1	A	114	ASP	CA-CB	-5.38	1.45	1.53
1	A	3	LYS	CA-C	5.38	1.59	1.52
1	A	261	ARG	CA-C	5.37	1.60	1.52
1	F	232	GLY	N-CA	5.35	1.51	1.45
1	F	32	VAL	C-O	5.34	1.30	1.24
1	F	205	LEU	N-CA	5.33	1.52	1.46
1	A	308	ALA	C-O	5.32	1.28	1.24
1	F	292	VAL	C-O	5.31	1.29	1.24
1	A	109	ALA	CA-C	-5.27	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	129	ARG	CA-C	5.27	1.59	1.52
1	A	51	GLU	CD-OE1	5.27	1.35	1.25
1	A	199	ILE	C-O	-5.26	1.18	1.24
1	A	9	ASP	CG-OD1	-5.23	1.15	1.25
1	A	124	VAL	CA-C	5.23	1.59	1.52
1	A	63	LEU	N-CA	-5.18	1.40	1.46
1	F	108	GLU	CD-OE1	-5.15	1.15	1.25
1	F	289	ALA	C-O	5.13	1.30	1.23
1	F	237	VAL	C-O	-5.09	1.18	1.24
1	F	185	GLY	CA-C	5.07	1.58	1.51
1	A	101	LEU	C-O	5.05	1.29	1.24
1	A	243	VAL	N-CA	5.05	1.50	1.46
1	A	105	GLY	C-N	-5.02	1.27	1.33
1	F	45	VAL	N-CA	-5.00	1.39	1.46

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	868	DG	C4'-C3'-O3'	11.29	126.93	110.00
1	F	26	ARG	NE-CZ-NH2	-8.50	111.55	119.20
2	C	868	DG	C2'-C3'-O3'	-8.09	99.36	111.50
1	A	106	TRP	N-CA-CB	-8.06	98.23	110.16
1	A	106	TRP	N-CA-C	7.81	119.87	111.36
2	H	868	DG	C2'-C3'-O3'	-7.57	100.14	111.50
1	F	129	ARG	NE-CZ-NH2	-6.99	112.91	119.20
1	F	267	VAL	N-CA-C	6.43	116.59	110.42
1	A	6	LEU	CB-CG-CD2	6.41	129.93	110.70
1	A	49	SER	N-CA-C	-5.94	102.69	110.53
2	B	843	DG	O5'-C5'-C4'	-5.88	101.98	110.80
1	A	20	ARG	CG-CD-NE	-5.83	99.17	112.00
2	B	845	DC	C4'-C3'-O3'	-5.79	101.31	110.00
1	A	127	ARG	N-CA-C	5.52	117.30	111.28
1	F	308	ALA	O-C-N	5.44	125.75	121.88
2	H	869	DG	C2'-C3'-O3'	5.42	119.64	111.50
1	A	126	GLU	CB-CG-CD	5.42	121.81	112.60
2	G	847	DT	C4'-C3'-O3'	-5.41	101.88	110.00
1	F	26	ARG	NE-CZ-NH1	5.34	126.84	121.50
1	F	315	GLN	N-CA-C	5.27	117.10	111.36
1	A	346	ASP	N-CA-C	5.25	119.74	112.45
2	H	873	DC	N1-C1'-C2'	5.24	121.35	113.50
2	G	839	DT	C2'-C3'-O3'	5.21	119.31	111.50
1	F	131	VAL	CB-CA-C	-5.13	105.41	111.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	88	GLU	N-CA-C	5.12	117.53	111.33
2	G	845	DC	C2'-C3'-O3'	5.12	119.18	111.50
1	F	131	VAL	N-CA-C	5.12	115.33	110.42
1	A	186	VAL	N-CA-C	5.02	115.54	108.36
1	F	211	SER	CA-CB-OG	-5.02	101.06	111.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2646	0	2661	20	0
1	F	2646	0	2661	15	0
2	B	270	0	147	1	0
2	C	201	0	112	2	0
2	G	248	0	136	5	0
2	H	163	0	89	3	0
3	A	28	0	16	0	0
3	F	28	0	13	0	0
4	A	2	0	0	0	0
4	F	2	0	0	0	0
5	A	295	0	0	6	0
5	B	29	0	0	0	0
5	C	17	0	0	2	0
5	F	290	0	0	5	0
5	G	41	0	0	2	0
5	H	22	0	0	0	0
All	All	6928	0	5835	44	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 (44) 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:263:MET:SD	5:A:720:HOH:O	2.23	0.94
1:F:23:PRO:O	1:F:26:ARG:HD3	1.72	0.89
1:A:29:PRO:HG2	1:A:72:ASP:O	1.83	0.76
1:A:68:ARG:NH1	5:A:503:HOH:O	2.17	0.75
1:A:263:MET:HE3	1:A:333:VAL:HG21	1.72	0.71
1:A:329:LEU:O	1:A:329:LEU:HG	1.91	0.71
2:G:842:DG:O6	5:G:901:HOH:O	2.09	0.69
1:F:40:GLU:OE1	5:F:501:HOH:O	2.14	0.64
2:H:868:DG:H4'	2:H:869:DG:OP1	2.00	0.62
1:A:16:SER:OG	5:A:502:HOH:O	2.16	0.61
1:A:329:LEU:O	1:A:329:LEU:CG	2.49	0.61
1:A:260:ARG:HH11	1:A:329:LEU:HD22	1.68	0.58
1:F:250:VAL:HG12	1:F:337:GLY:HA3	1.86	0.57
1:F:32:VAL:O	1:F:46:THR:HG22	2.04	0.57
2:G:849:DG:O3'	5:G:902:HOH:O	2.18	0.55
1:F:335:LEU:C	1:F:335:LEU:HD23	2.32	0.55
1:A:70:CYS:N	1:A:71:PRO:HD3	2.24	0.53
2:C:871:DC:O2	5:C:901:HOH:O	2.14	0.53
1:F:129:ARG:HD2	1:F:140:CYS:O	2.11	0.51
2:H:867:DA:C2	2:G:848:DA:C2	2.98	0.51
1:A:293:ARG:HB3	1:A:335:LEU:HB3	1.93	0.50
1:F:230:LYS:HD3	5:F:536:HOH:O	2.12	0.49
2:G:838:DC:H5''	2:G:838:DC:O2	2.14	0.48
1:F:186:VAL:O	5:F:502:HOH:O	2.20	0.48
1:F:300:ARG:HD2	2:H:868:DG:OP2	2.13	0.48
1:A:58:HIS:HD2	5:A:739:HOH:O	1.98	0.47
1:F:328:GLU:CD	1:F:328:GLU:N	2.73	0.46
1:A:240:GLU:O	5:A:504:HOH:O	2.20	0.46
1:A:11:ASP:O	1:A:12:GLN:C	2.59	0.45
1:A:93:LEU:HD11	1:A:135:GLU:HB2	1.99	0.45
1:A:69:ARG:C	1:A:71:PRO:HD3	2.43	0.44
1:A:124:VAL:HG22	1:A:127:ARG:HH22	1.82	0.44
1:F:40:GLU:CD	5:F:501:HOH:O	2.60	0.44
1:A:263:MET:HE1	1:A:329:LEU:HB2	1.99	0.44
1:A:294:THR:OG1	1:A:296:THR:HG23	2.18	0.44
5:A:636:HOH:O	2:G:838:DC:H5	2.00	0.43
2:B:850:DG:H8	2:B:850:DG:O5'	2.02	0.43
1:F:289:ALA:HB2	1:F:303:ILE:HD12	2.00	0.43
1:F:68:ARG:NH2	5:F:507:HOH:O	2.43	0.43
1:A:29:PRO:CG	1:A:72:ASP:O	2.60	0.42
1:F:328:GLU:CD	1:F:328:GLU:H	2.27	0.42
1:F:142:VAL:O	1:F:163:ILE:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:870:DA:H2'	5:C:915:HOH:O	2.20	0.41
1:A:122:VAL:O	1:A:126:GLU:HG3	2.21	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	345/347 (99%)	339 (98%)	6 (2%)	0	100	100
1	F	345/347 (99%)	339 (98%)	6 (2%)	0	100	100
All	All	690/694 (99%)	678 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	284/284 (100%)	276 (97%)	8 (3%)	38	17
1	F	284/284 (100%)	279 (98%)	5 (2%)	51	33
All	All	568/568 (100%)	555 (98%)	13 (2%)	44	25

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	107	ASP
1	A	220	SER
1	A	255	GLN
1	A	296	THR
1	A	297	PHE
1	A	329	LEU
1	A	346	ASP
1	F	14	LEU
1	F	35	SER
1	F	107	ASP
1	F	297	PHE
1	F	335	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	F	99	HIS
1	F	255	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	OKX	A	401	4	28,29,29	2.84	11 (39%)	39,45,45	1.93	7 (17%)
3	OKX	F	401	4	28,29,29	2.94	14 (50%)	39,45,45	1.63	8 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OKX	A	401	4	-	4/19/34/34	0/2/2/2
3	OKX	F	401	4	-	6/19/34/34	0/2/2/2

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	OKX	C2-N1	7.42	1.55	1.40
3	F	401	OKX	C2-N3	5.91	1.48	1.36
3	F	401	OKX	C6-C5	5.89	1.48	1.35
3	F	401	OKX	PA-O1A	5.53	1.54	1.46
3	F	401	OKX	PA-O2A	-5.46	1.42	1.56
3	A	401	OKX	C6-C5	5.06	1.46	1.35
3	F	401	OKX	C2'-C1'	-4.39	1.40	1.52
3	A	401	OKX	C2-N3	4.32	1.44	1.36
3	F	401	OKX	O4'-C1'	4.25	1.51	1.42
3	A	401	OKX	C3'-C4'	-4.23	1.41	1.53
3	A	401	OKX	O4'-C1'	4.05	1.51	1.42
3	A	401	OKX	C2'-C3'	3.98	1.63	1.52
3	A	401	OKX	C5-C4	3.44	1.50	1.42
3	A	401	OKX	C2'-C1'	-3.38	1.43	1.52
3	A	401	OKX	PB-O3B	-3.23	1.55	1.59
3	F	401	OKX	C3'-C4'	-3.11	1.44	1.53
3	F	401	OKX	PB-O1B	-3.08	1.48	1.56
3	A	401	OKX	C4-N3	3.07	1.40	1.34
3	F	401	OKX	O3'-C3'	2.89	1.49	1.43
3	F	401	OKX	C4-N3	2.72	1.40	1.34
3	A	401	OKX	PG-O3G	-2.58	1.45	1.54
3	F	401	OKX	C2'-C3'	2.39	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	401	0KX	C5-C4	2.21	1.48	1.42
3	F	401	0KX	PG-O3G	-2.10	1.47	1.54
3	F	401	0KX	O2-C2	-2.01	1.20	1.23

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	0KX	O2A-PA-O1A	7.03	124.95	109.87
3	F	401	0KX	O5'-PA-O1A	-4.68	100.39	114.27
3	A	401	0KX	O5'-PA-O1A	-3.54	103.75	114.27
3	F	401	0KX	C4'-O4'-C1'	-3.39	101.46	109.51
3	A	401	0KX	O2A-PA-O5'	-3.31	97.89	106.69
3	A	401	0KX	O5'-C5'-C4'	3.07	119.46	108.99
3	A	401	0KX	C2'-C3'-C4'	-2.93	96.86	102.80
3	A	401	0KX	O3G-PG-O2G	2.77	121.61	110.83
3	F	401	0KX	C2'-C3'-C4'	-2.62	97.49	102.80
3	F	401	0KX	O4'-C1'-N1	-2.36	103.68	107.86
3	A	401	0KX	C1'-N1-C2	-2.22	114.01	117.83
3	F	401	0KX	O2A-PA-O1A	-2.09	105.38	109.87
3	F	401	0KX	C4-N3-C2	2.04	123.48	120.26
3	F	401	0KX	O4'-C4'-C3'	2.02	110.25	105.65
3	F	401	0KX	O1G-PG-O2G	2.02	118.69	110.83

There are no chirality outliers.

All (10) torsion outliers are listed below:

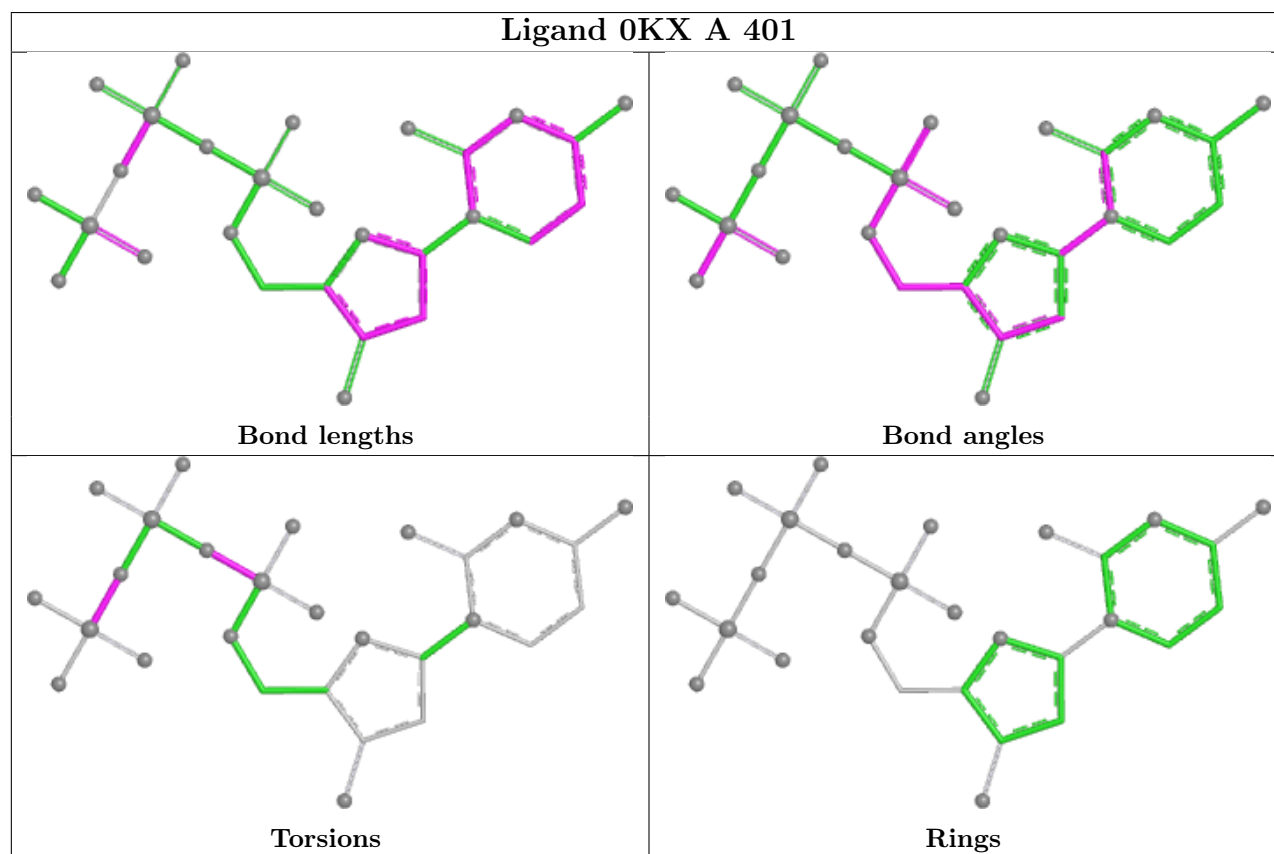
Mol	Chain	Res	Type	Atoms
3	A	401	0KX	PB-N3A-PA-O5'
3	F	401	0KX	PB-O3B-PG-O1G
3	F	401	0KX	PA-N3A-PB-O2B
3	F	401	0KX	PB-N3A-PA-O5'
3	A	401	0KX	PB-O3B-PG-O1G
3	F	401	0KX	PB-O3B-PG-O2G
3	F	401	0KX	C5'-O5'-PA-O1A
3	A	401	0KX	PB-O3B-PG-O3G
3	F	401	0KX	PB-O3B-PG-O3G
3	A	401	0KX	PB-O3B-PG-O2G

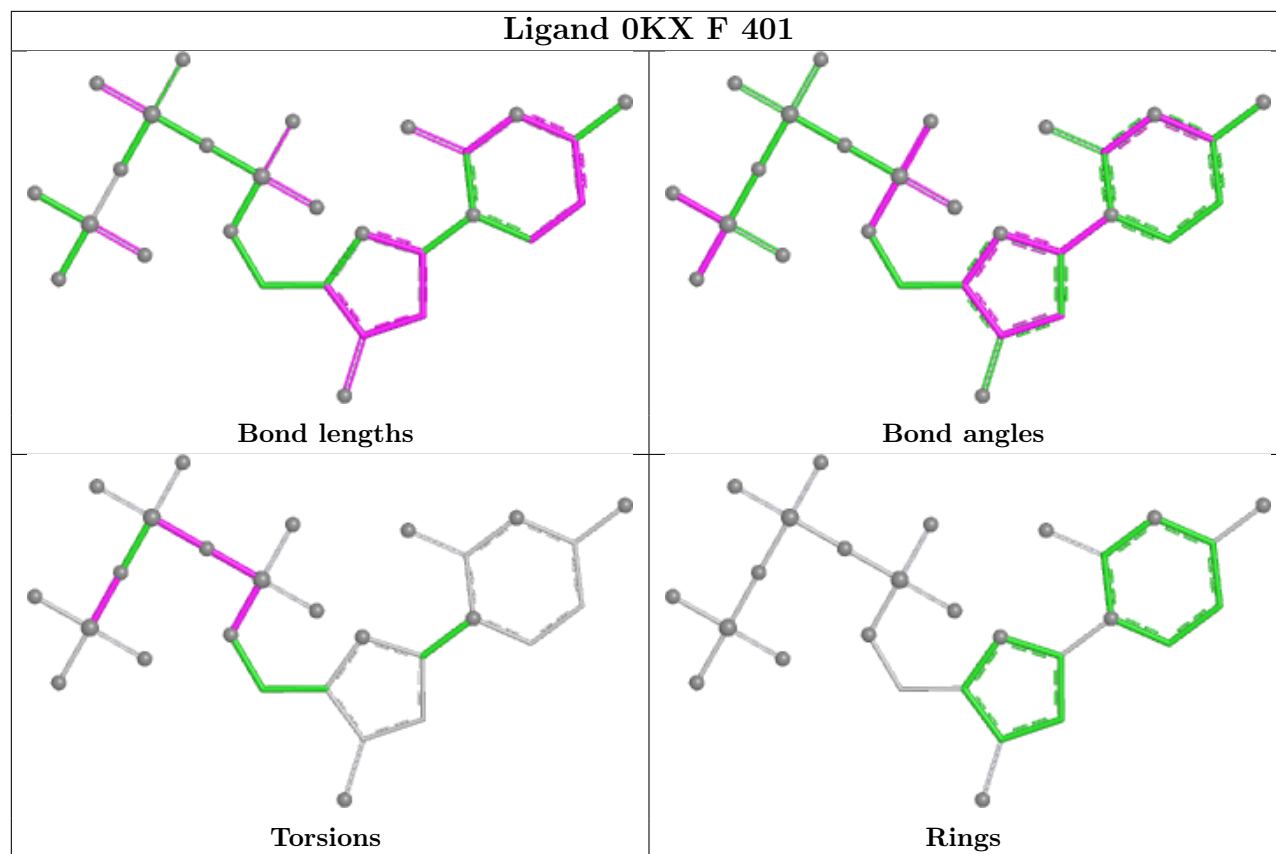
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	347/347 (100%)	0.47	19 (5%) 30 36	17, 28, 49, 108	0
1	F	347/347 (100%)	0.39	14 (4%) 42 48	18, 27, 47, 90	0
2	B	13/18 (72%)	0.91	4 (30%) 1 1	28, 38, 87, 93	0
2	C	10/18 (55%)	0.68	0 100 100	30, 52, 66, 80	0
2	G	12/18 (66%)	0.49	2 (16%) 4 4	23, 35, 89, 107	0
2	H	8/18 (44%)	0.40	0 100 100	24, 33, 58, 73	0
All	All	737/766 (96%)	0.44	39 (5%) 32 38	17, 28, 53, 108	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	347	VAL	10.0
1	A	329	LEU	7.4
1	F	347	VAL	6.8
1	A	72	ASP	6.3
1	A	184	TRP	4.7
1	F	1	MET	3.8
1	F	104	TRP	3.7
1	F	97	LEU	3.7
1	A	1	MET	3.6
1	A	104	TRP	3.2
1	A	106	TRP	3.2
1	F	242	TRP	3.2
1	F	34	GLY	3.1
1	A	346	ASP	3.1
1	F	27	GLY	3.0
2	G	849	DG	2.8
2	B	849	DG	2.8
2	G	848	DA	2.6
1	F	297	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	331	ARG	2.6
1	A	105	GLY	2.6
1	F	345	ASP	2.6
1	F	72	ASP	2.5
2	B	847	DT	2.5
2	B	848	DA	2.5
2	B	850	DG	2.4
1	A	131	VAL	2.4
1	F	118	GLU	2.4
1	A	296	THR	2.3
1	F	346	ASP	2.3
1	A	126	GLU	2.3
1	A	328	GLU	2.2
1	A	240	GLU	2.1
1	A	185	GLY	2.1
1	A	255	GLN	2.1
1	A	326	GLN	2.1
1	F	28	GLN	2.1
1	F	328	GLU	2.1
1	A	298	TYR	2.1

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.

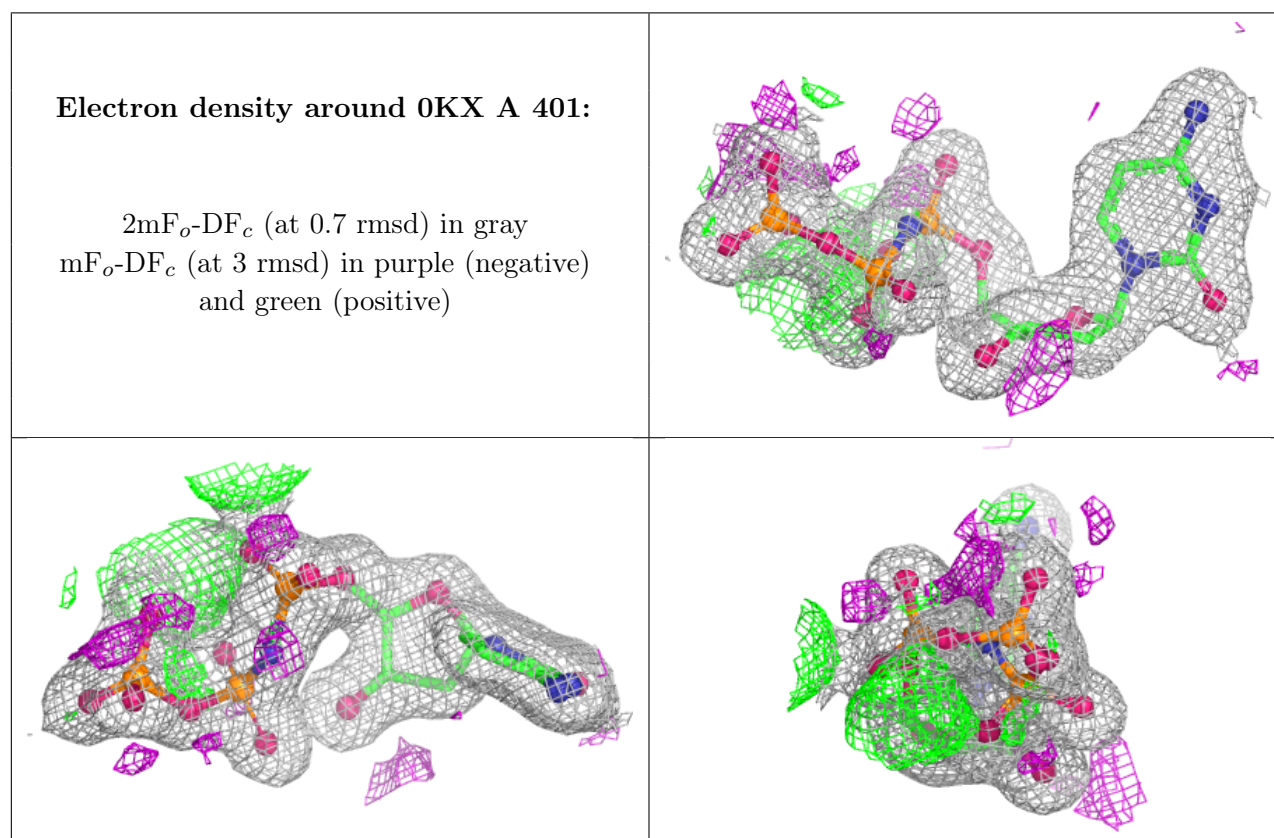
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MG	A	402	1/1	0.92	0.37	23,23,23,23	0
4	MG	A	403	1/1	0.95	0.34	22,22,22,22	0
3	OKX	A	401	28/28	0.96	0.07	25,27,29,29	0

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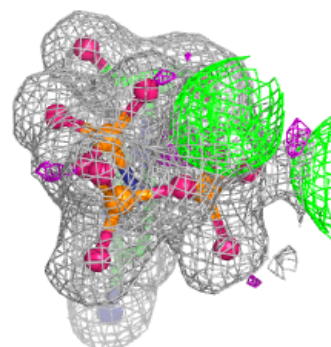
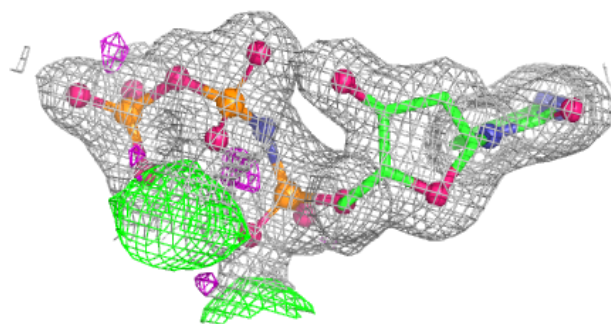
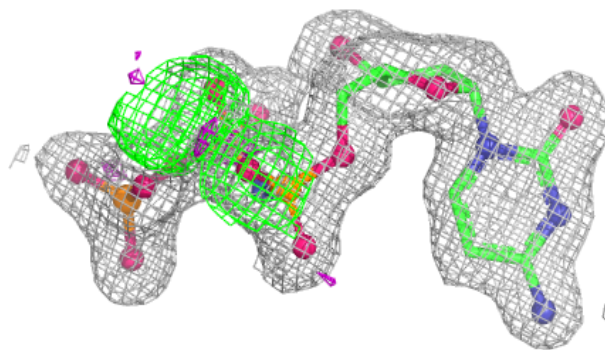
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	OKX	F	401	28/28	0.98	0.05	19,22,24,24	0
4	MG	F	403	1/1	0.98	0.30	17,17,17,17	0
4	MG	F	402	1/1	0.99	0.29	18,18,18,18	0

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 0KX F 401:

$2mF_o-DF_c$ (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.