



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 20, 2026 – 02:46 pm BST

PDB ID : 9RYY / pdb_00009ryy
Title : Alpha-Methylacyl-CoA racemase from Mycobacterium tuberculosis in complex with 2-(3-Benzoyloxyphenylthio)propanoyl-CoA
Authors : Mojanaga, O.O.; Acharya, K.R.
Deposited on : 2025-07-15
Resolution : 2.00 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 : 1.8.4, CSD as541be (2020)
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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

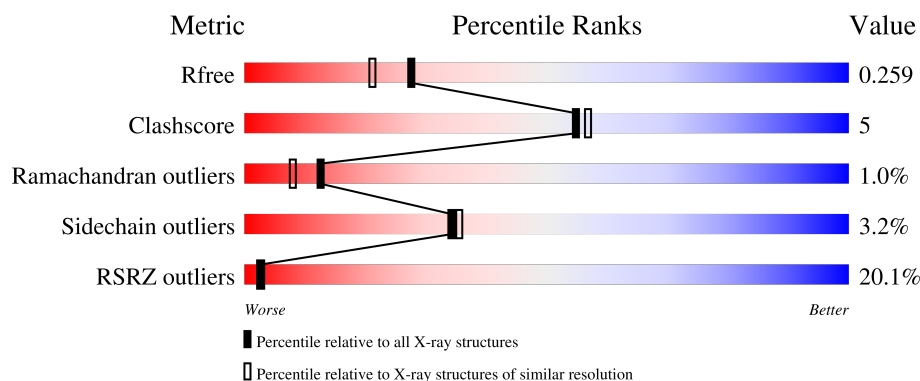
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	364	
1	B	364	
1	C	364	
1	D	364	
1	E	364	

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Mol	Chain	Length	Quality of chain
1	F	364	
1	G	364	
1	H	364	
1	I	364	
1	J	364	
1	K	364	
1	L	364	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34603 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 Alpha-methylacyl-CoA racemase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	2	0
			2706	1696	484	510	16			
1	B	355	Total	C	N	O	S	0	2	0
			2698	1693	484	505	16			
1	C	359	Total	C	N	O	S	0	2	0
			2714	1702	486	510	16			
1	D	359	Total	C	N	O	S	0	1	0
			2715	1703	486	510	16			
1	E	356	Total	C	N	O	S	0	2	0
			2698	1692	483	507	16			
1	F	357	Total	C	N	O	S	0	1	0
			2703	1695	484	508	16			
1	G	358	Total	C	N	O	S	0	2	0
			2710	1700	485	509	16			
1	H	357	Total	C	N	O	S	0	1	0
			2703	1697	484	506	16			
1	I	359	Total	C	N	O	S	0	3	0
			2727	1709	488	514	16			
1	J	357	Total	C	N	O	S	0	1	0
			2700	1694	484	506	16			
1	K	356	Total	C	N	O	S	0	3	0
			2704	1696	484	508	16			
1	L	359	Total	C	N	O	S	0	1	0
			2715	1703	486	510	16			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	361	GLY	-	expression tag	UNP O06543
A	362	SER	-	expression tag	UNP O06543
A	363	GLY	-	expression tag	UNP O06543
A	364	CYS	-	expression tag	UNP O06543
B	361	GLY	-	expression tag	UNP O06543

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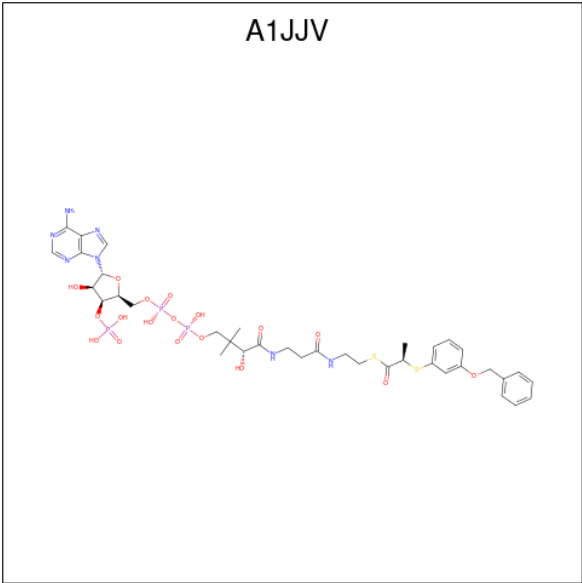
Chain	Residue	Modelled	Actual	Comment	Reference
B	362	SER	-	expression tag	UNP O06543
B	363	GLY	-	expression tag	UNP O06543
B	364	CYS	-	expression tag	UNP O06543
C	361	GLY	-	expression tag	UNP O06543
C	362	SER	-	expression tag	UNP O06543
C	363	GLY	-	expression tag	UNP O06543
C	364	CYS	-	expression tag	UNP O06543
D	361	GLY	-	expression tag	UNP O06543
D	362	SER	-	expression tag	UNP O06543
D	363	GLY	-	expression tag	UNP O06543
D	364	CYS	-	expression tag	UNP O06543
E	361	GLY	-	expression tag	UNP O06543
E	362	SER	-	expression tag	UNP O06543
E	363	GLY	-	expression tag	UNP O06543
E	364	CYS	-	expression tag	UNP O06543
F	361	GLY	-	expression tag	UNP O06543
F	362	SER	-	expression tag	UNP O06543
F	363	GLY	-	expression tag	UNP O06543
F	364	CYS	-	expression tag	UNP O06543
G	361	GLY	-	expression tag	UNP O06543
G	362	SER	-	expression tag	UNP O06543
G	363	GLY	-	expression tag	UNP O06543
G	364	CYS	-	expression tag	UNP O06543
H	361	GLY	-	expression tag	UNP O06543
H	362	SER	-	expression tag	UNP O06543
H	363	GLY	-	expression tag	UNP O06543
H	364	CYS	-	expression tag	UNP O06543
I	361	GLY	-	expression tag	UNP O06543
I	362	SER	-	expression tag	UNP O06543
I	363	GLY	-	expression tag	UNP O06543
I	364	CYS	-	expression tag	UNP O06543
J	361	GLY	-	expression tag	UNP O06543
J	362	SER	-	expression tag	UNP O06543
J	363	GLY	-	expression tag	UNP O06543
J	364	CYS	-	expression tag	UNP O06543
K	361	GLY	-	expression tag	UNP O06543
K	362	SER	-	expression tag	UNP O06543
K	363	GLY	-	expression tag	UNP O06543
K	364	CYS	-	expression tag	UNP O06543
L	361	GLY	-	expression tag	UNP O06543
L	362	SER	-	expression tag	UNP O06543
L	363	GLY	-	expression tag	UNP O06543

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Chain	Residue	Modelled	Actual	Comment	Reference
L	364	CYS	-	expression tag	UNP O06543

- Molecule 2 is 2-((3-(benzyloxy)phenyl)thio)propanoyl-CoA (CCD ID: A1JJV) (formula: C₃₇H₅₀N₇O₁₈P₃S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	B	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	C	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	D	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	E	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	F	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	G	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	H	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	I	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	J	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	K	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		
2	L	1	Total	C	N	O	P	S	0	0
			67	37	7	18	3	2		

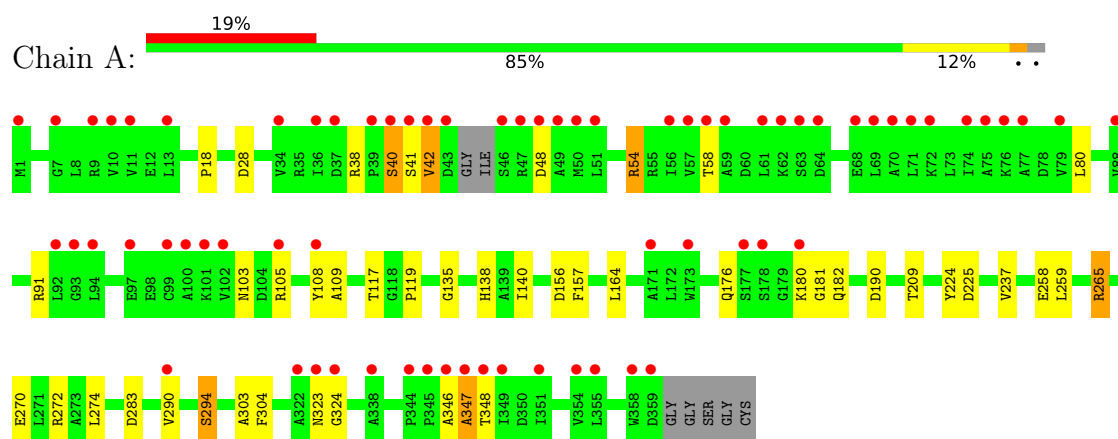
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total	O	0	0
			106	106		
3	B	88	Total	O	0	0
			88	88		
3	C	114	Total	O	0	0
			114	114		
3	D	119	Total	O	0	0
			119	119		
3	E	111	Total	O	0	0
			111	111		
3	F	107	Total	O	0	0
			107	107		
3	G	86	Total	O	0	0
			86	86		
3	H	113	Total	O	0	0
			113	113		
3	I	117	Total	O	0	0
			117	117		
3	J	106	Total	O	0	0
			106	106		
3	K	115	Total	O	0	0
			115	115		
3	L	124	Total	O	0	0
			124	124		

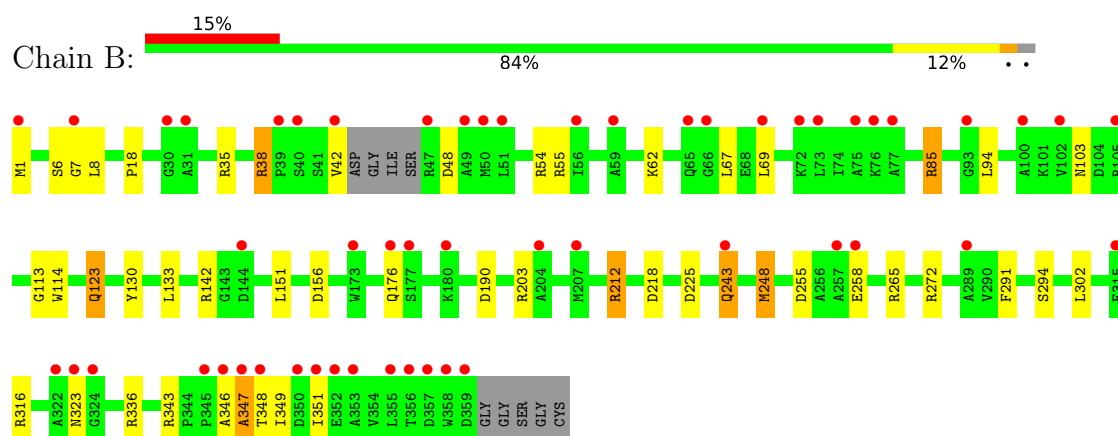
3 Residue-property plots [i](#)

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.

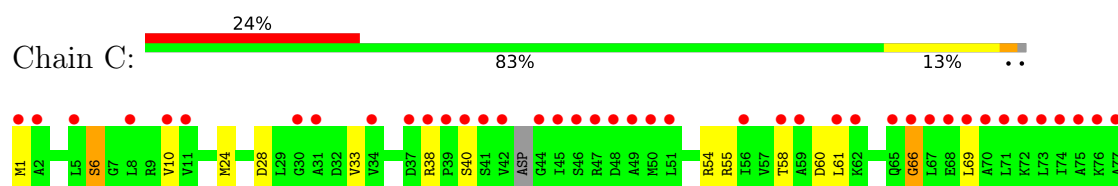
• Molecule 1: Alpha-methylacyl-CoA racemase

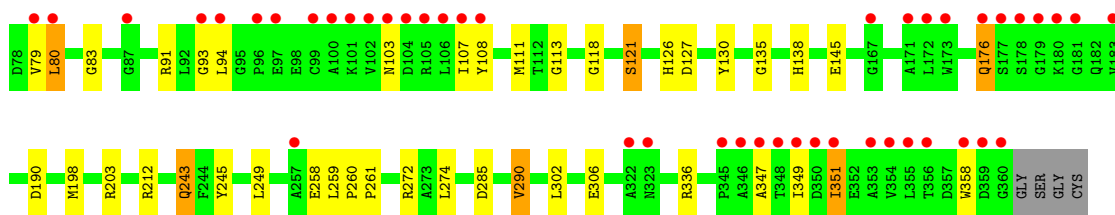


• Molecule 1: Alpha-methylacyl-CoA racemase

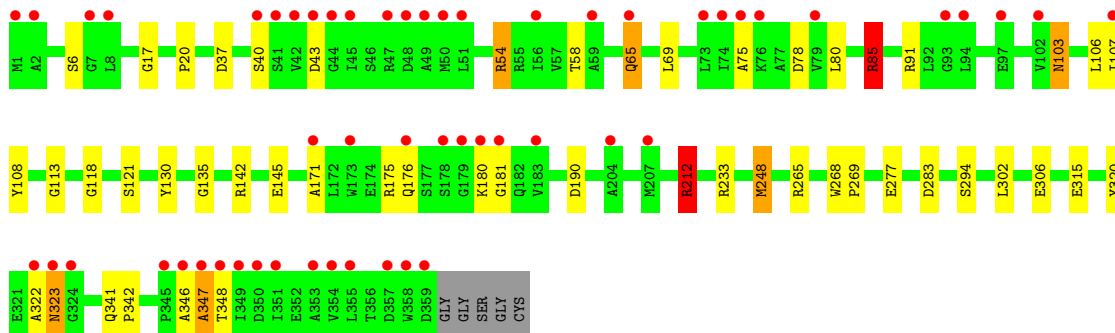
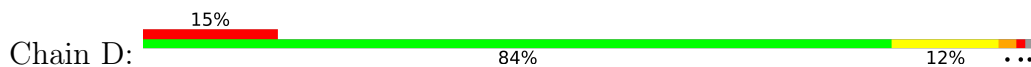


• Molecule 1: Alpha-methylacyl-CoA racemase

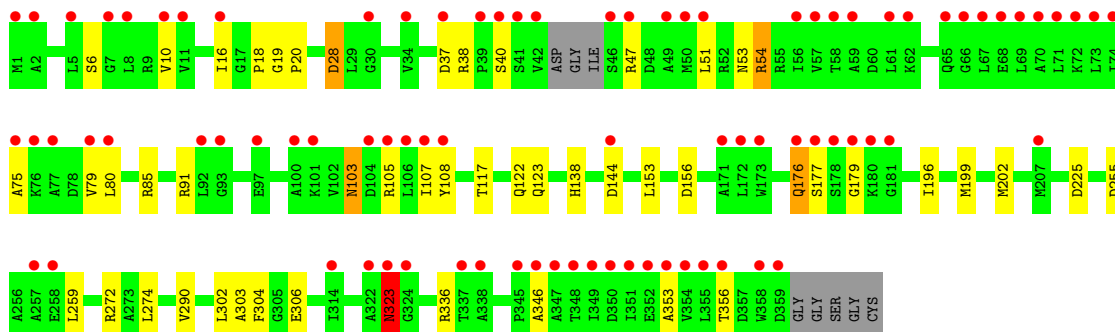
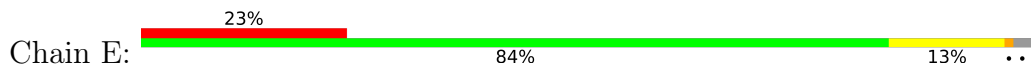




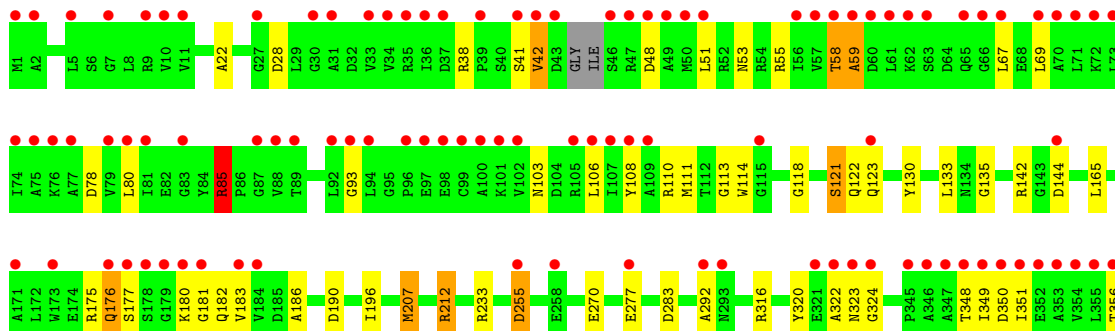
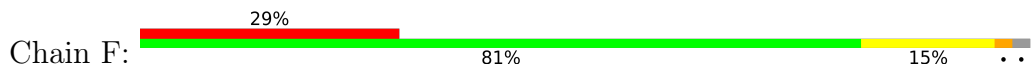
● Molecule 1: Alpha-methylacyl-CoA racemase

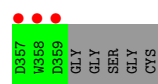


● Molecule 1: Alpha-methylacyl-CoA racemase

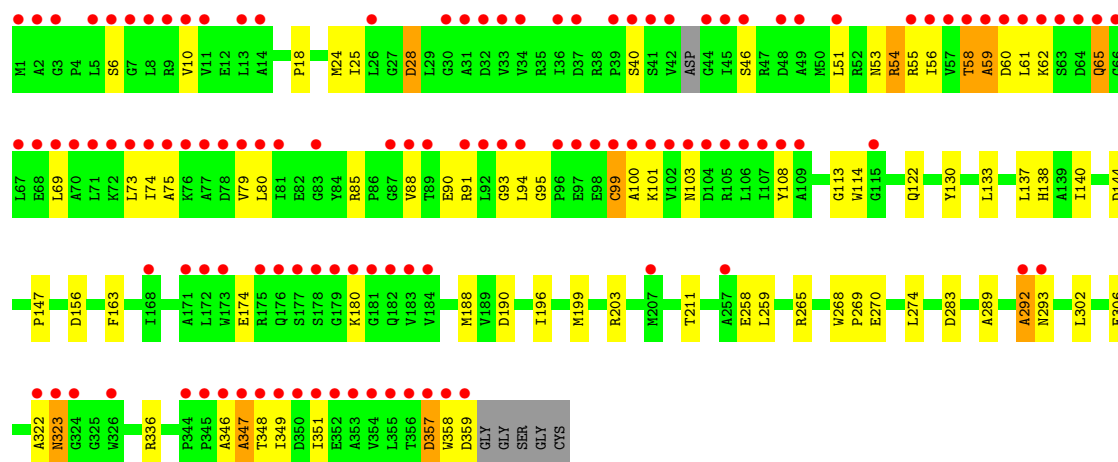
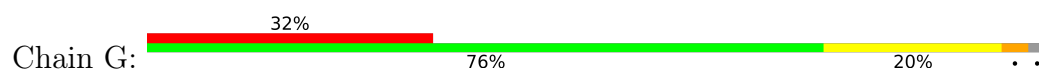


● Molecule 1: Alpha-methylacyl-CoA racemase

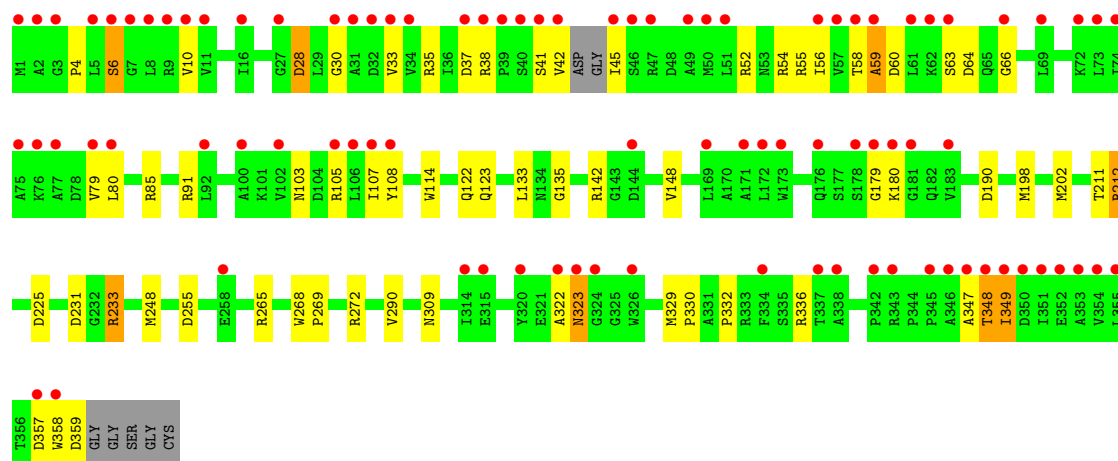
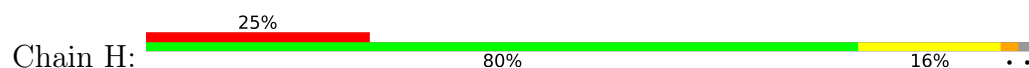




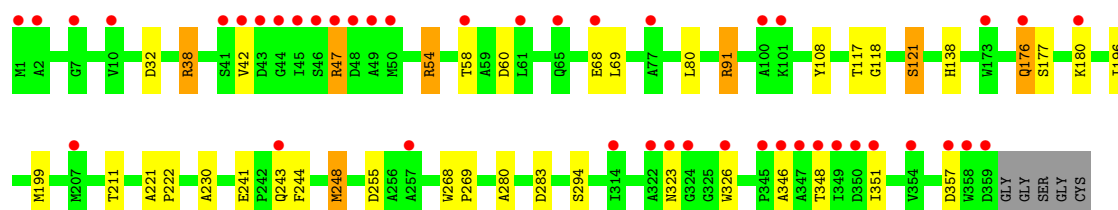
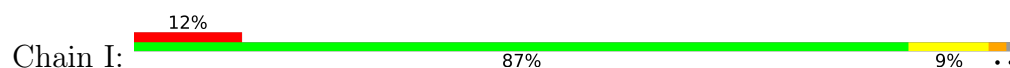
● Molecule 1: Alpha-methylacyl-CoA racemase



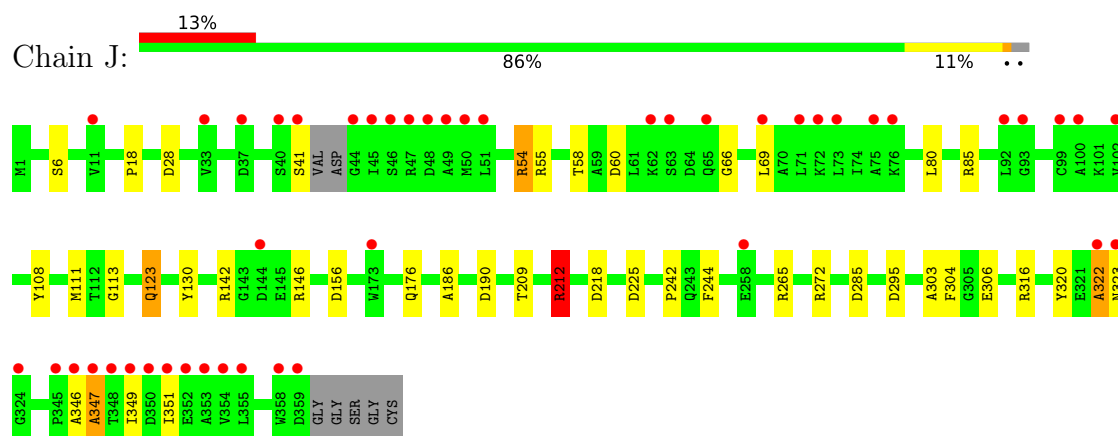
● Molecule 1: Alpha-methylacyl-CoA racemase



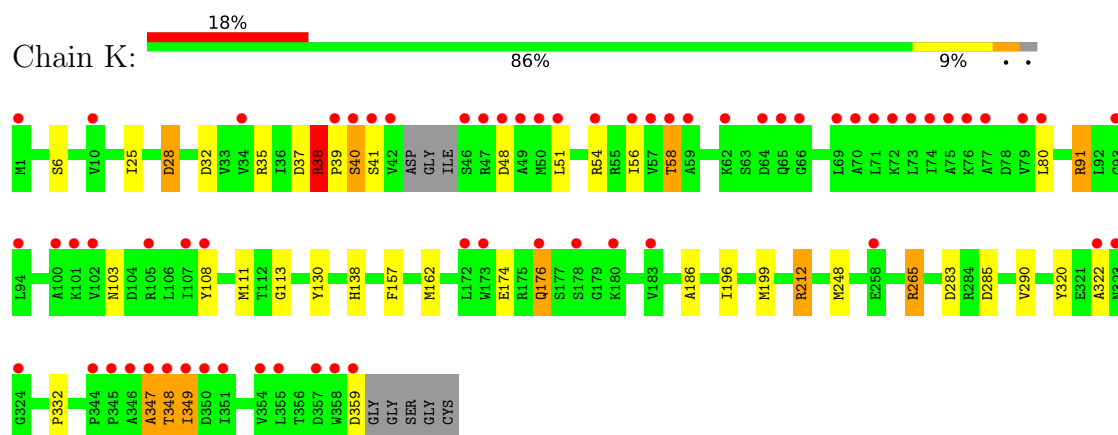
● Molecule 1: Alpha-methylacyl-CoA racemase



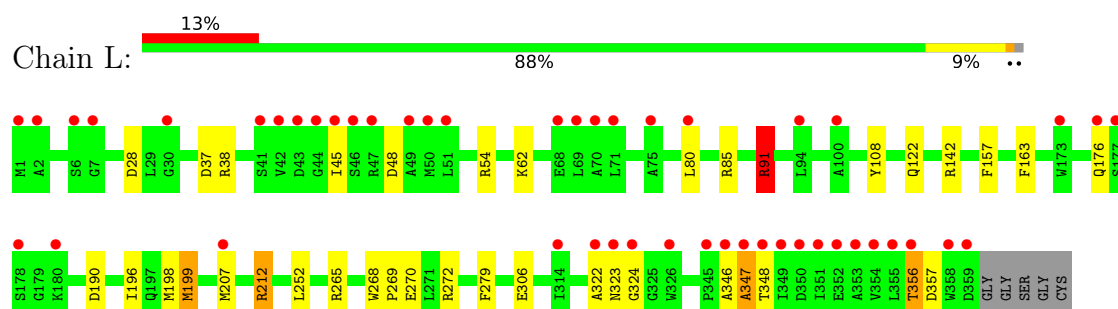
- Molecule 1: Alpha-methylacyl-CoA racemase



- Molecule 1: Alpha-methylacyl-CoA racemase



- Molecule 1: Alpha-methylacyl-CoA racemase



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	276.13Å 276.13Å 392.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	196.02 – 2.00 196.02 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (196.02-2.00) 99.8 (196.02-2.00)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.88)	Depositor
R, R_{free}	0.216 , 0.250 0.227 , 0.259	Depositor DCC
R_{free} test set	25172 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	33.0	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.008 for $-1/2^*h-1/2^*k-1/2^*l, -1/2^*h-1/2^*k+1/2^*l, -h+k$ 0.006 for $-1/2^*h+1/2^*k-1/2^*l, 1/2^*h-1/2^*k-1/2^*l, -h-k$	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	34603	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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: A1JJV

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	0.66	0/2778	1.12	7/3778 (0.2%)
1	B	0.67	0/2764	1.20	11/3759 (0.3%)
1	C	0.67	0/2786	1.19	10/3788 (0.3%)
1	D	0.69	0/2782	1.21	11/3785 (0.3%)
1	E	0.66	0/2770	1.15	5/3767 (0.1%)
1	F	0.66	0/2769	1.19	7/3766 (0.2%)
1	G	0.65	0/2782	1.19	8/3783 (0.2%)
1	H	0.65	0/2769	1.20	9/3766 (0.2%)
1	I	0.66	0/2800	1.14	10/3809 (0.3%)
1	J	0.68	0/2766	1.17	10/3761 (0.3%)
1	K	0.68	0/2779	1.18	9/3779 (0.2%)
1	L	0.68	0/2782	1.17	5/3785 (0.1%)
All	All	0.67	0/33327	1.18	102/45326 (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	A	0	1
1	B	0	3
1	C	0	2
1	D	0	5
1	F	0	4
1	G	0	3
1	H	0	6
1	J	0	4
1	K	0	3
1	L	0	5
All	All	0	36

There are no bond length outliers.

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	203	ARG	CB-CA-C	-10.34	93.62	110.79
1	C	203	ARG	CB-CA-C	-9.78	94.23	110.85
1	J	123	GLN	CB-CA-C	9.51	125.34	109.84
1	D	248	MET	CG-SD-CE	9.12	120.96	100.90
1	B	203	ARG	N-CA-CB	7.92	121.76	110.12

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	54	ARG	Sidechain
1	B	212	ARG	Sidechain
1	B	35	ARG	Sidechain
1	B	38	ARG	Sidechain
1	C	91	ARG	Sidechain

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	2706	0	2643	27	0
1	B	2698	0	2643	29	0
1	C	2714	0	2656	30	0
1	D	2715	0	2660	27	0
1	E	2698	0	2639	32	0
1	F	2703	0	2645	35	0
1	G	2710	0	2653	47	0
1	H	2703	0	2652	31	0
1	I	2727	0	2665	24	0
1	J	2700	0	2646	19	0
1	K	2704	0	2647	24	0
1	L	2715	0	2660	17	0
2	A	67	0	0	2	0
2	B	67	0	0	4	0
2	C	67	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	67	0	0	4	0
2	E	67	0	0	5	0
2	F	67	0	0	4	0
2	G	67	0	0	2	0
2	H	67	0	0	1	0
2	I	67	0	0	1	0
2	J	67	0	0	1	0
2	K	67	0	0	0	0
2	L	67	0	0	0	0
3	A	106	0	0	6	0
3	B	88	0	0	3	0
3	C	114	0	0	3	0
3	D	119	0	0	1	0
3	E	111	0	0	3	0
3	F	107	0	0	2	0
3	G	86	0	0	3	0
3	H	113	0	0	2	0
3	I	117	0	0	6	0
3	J	106	0	0	0	0
3	K	115	0	0	4	0
3	L	124	0	0	4	0
All	All	34603	0	31809	314	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 5.

The worst 5 of 314 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:F:85:ARG:HD3	2:F:401:A1JJV:O10	1.73	0.87
1:G:80:LEU:HD23	1:G:108:TYR:CE1	2.12	0.85
1:G:259:LEU:HD22	1:G:274:LEU:HD13	1.59	0.81
1:K:40:SER:OG	3:K:501:HOH:O	1.99	0.81
1:B:48:ASP:OD1	3:B:501:HOH:O	1.98	0.80

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	355/364 (98%)	329 (93%)	21 (6%)	5 (1%)	9	4
1	B	353/364 (97%)	334 (95%)	16 (4%)	3 (1%)	16	11
1	C	357/364 (98%)	337 (94%)	17 (5%)	3 (1%)	16	11
1	D	358/364 (98%)	336 (94%)	18 (5%)	4 (1%)	11	7
1	E	354/364 (97%)	334 (94%)	17 (5%)	3 (1%)	16	11
1	F	354/364 (97%)	325 (92%)	22 (6%)	7 (2%)	6	2
1	G	356/364 (98%)	325 (91%)	22 (6%)	9 (2%)	4	1
1	H	354/364 (97%)	332 (94%)	17 (5%)	5 (1%)	9	4
1	I	360/364 (99%)	346 (96%)	14 (4%)	0	100	100
1	J	354/364 (97%)	338 (96%)	15 (4%)	1 (0%)	36	35
1	K	355/364 (98%)	333 (94%)	19 (5%)	3 (1%)	16	11
1	L	358/364 (98%)	337 (94%)	20 (6%)	1 (0%)	36	35
All	All	4268/4368 (98%)	4006 (94%)	218 (5%)	44 (1%)	12	8

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	VAL
1	B	347	ALA
1	C	103	ASN
1	C	347	ALA
1	D	347	ALA

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	276/277 (100%)	270 (98%)	6 (2%)	45	50
1	B	274/277 (99%)	267 (97%)	7 (3%)	40	44
1	C	276/277 (100%)	266 (96%)	10 (4%)	31	31
1	D	276/277 (100%)	269 (98%)	7 (2%)	42	45
1	E	275/277 (99%)	266 (97%)	9 (3%)	33	34
1	F	275/277 (99%)	265 (96%)	10 (4%)	31	31
1	G	276/277 (100%)	265 (96%)	11 (4%)	28	27
1	H	275/277 (99%)	266 (97%)	9 (3%)	33	34
1	I	278/277 (100%)	267 (96%)	11 (4%)	28	27
1	J	274/277 (99%)	269 (98%)	5 (2%)	51	58
1	K	276/277 (100%)	264 (96%)	12 (4%)	26	25
1	L	276/277 (100%)	269 (98%)	7 (2%)	42	45
All	All	3307/3324 (100%)	3203 (97%)	104 (3%)	34	37

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	293	ASN
1	I	54	ARG
1	L	45	ILE
1	G	357	ASP
1	H	290	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	327	GLN
1	J	243	GLN
1	I	116	GLN
1	I	263	ASN
1	J	286	HIS

5.3.3 RNA ⓘ

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](#)

12 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	A1JJV	G	401	-	65,71,71	0.61	1 (1%)	88,103,103	1.33	10 (11%)
2	A1JJV	J	401	-	65,71,71	0.68	1 (1%)	88,103,103	1.01	6 (6%)
2	A1JJV	C	401	-	65,71,71	0.69	0	88,103,103	0.92	5 (5%)
2	A1JJV	F	401	-	65,71,71	0.70	2 (3%)	88,103,103	1.22	6 (6%)
2	A1JJV	L	401	-	65,71,71	0.74	2 (3%)	88,103,103	1.31	9 (10%)
2	A1JJV	B	401	-	65,71,71	0.83	3 (4%)	88,103,103	1.02	4 (4%)
2	A1JJV	K	401	-	65,71,71	0.87	2 (3%)	88,103,103	1.31	13 (14%)
2	A1JJV	H	401	-	65,71,71	1.09	5 (7%)	88,103,103	1.02	6 (6%)
2	A1JJV	I	401	-	65,71,71	0.89	3 (4%)	88,103,103	1.19	6 (6%)
2	A1JJV	E	401	-	65,71,71	0.80	3 (4%)	88,103,103	1.28	11 (12%)
2	A1JJV	A	401	-	65,71,71	0.66	1 (1%)	88,103,103	1.22	9 (10%)
2	A1JJV	D	401	-	65,71,71	0.76	1 (1%)	88,103,103	1.38	8 (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
2	A1JJV	G	401	-	-	9/63/80/80	0/5/5/5
2	A1JJV	J	401	-	-	9/63/80/80	0/5/5/5
2	A1JJV	C	401	-	-	10/63/80/80	0/5/5/5
2	A1JJV	F	401	-	-	9/63/80/80	0/5/5/5
2	A1JJV	L	401	-	-	10/63/80/80	0/5/5/5
2	A1JJV	B	401	-	-	6/63/80/80	0/5/5/5
2	A1JJV	K	401	-	-	13/63/80/80	0/5/5/5
2	A1JJV	H	401	-	-	6/63/80/80	0/5/5/5
2	A1JJV	I	401	-	-	14/63/80/80	0/5/5/5
2	A1JJV	E	401	-	-	19/63/80/80	0/5/5/5
2	A1JJV	A	401	-	-	8/63/80/80	0/5/5/5
2	A1JJV	D	401	-	-	12/63/80/80	0/5/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	401	A1JJV	C2-S1	4.40	1.90	1.83
2	D	401	A1JJV	P3-O15	3.87	1.66	1.59
2	H	401	A1JJV	O2-C16	3.63	1.26	1.20
2	H	401	A1JJV	C16-S2	3.46	1.86	1.75
2	K	401	A1JJV	C2-S1	3.35	1.88	1.83

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	A1JJV	O2-C16-S2	-6.54	115.00	123.80
2	D	401	A1JJV	C36-C37-C29	-6.16	92.31	103.22
2	L	401	A1JJV	C36-C37-C29	-6.09	92.44	103.22
2	G	401	A1JJV	O7-P1-O8	5.42	139.03	112.24
2	I	401	A1JJV	C36-C37-C29	-5.22	93.97	103.22

There are no chirality outliers.

5 of 125 torsion outliers are listed below:

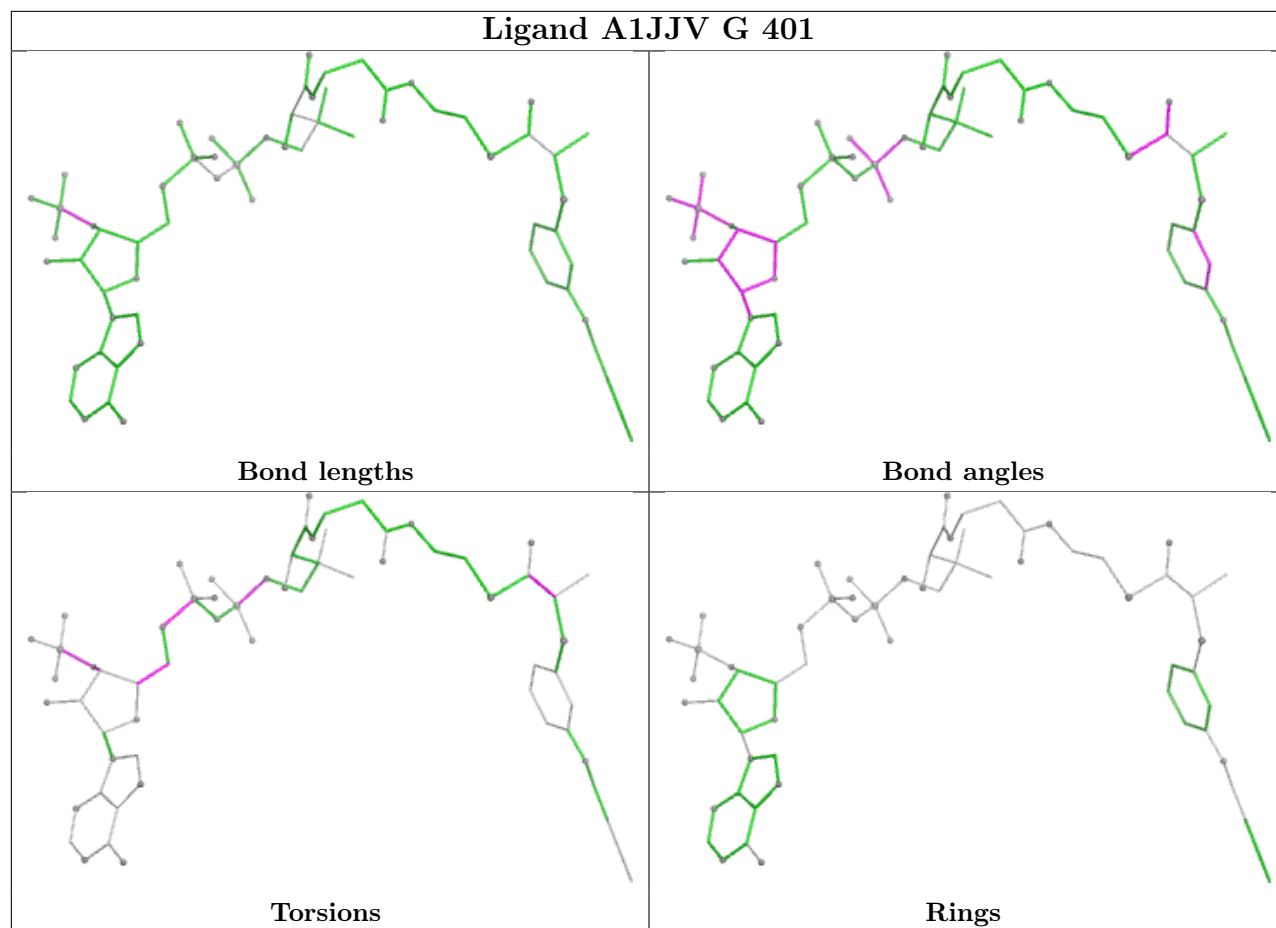
Mol	Chain	Res	Type	Atoms
2	A	401	A1JJV	C19-C20-C21-N2
2	A	401	A1JJV	C28-O12-P2-O9
2	A	401	A1JJV	C28-O12-P2-O10
2	B	401	A1JJV	C28-O12-P2-O9
2	B	401	A1JJV	C28-O12-P2-O10

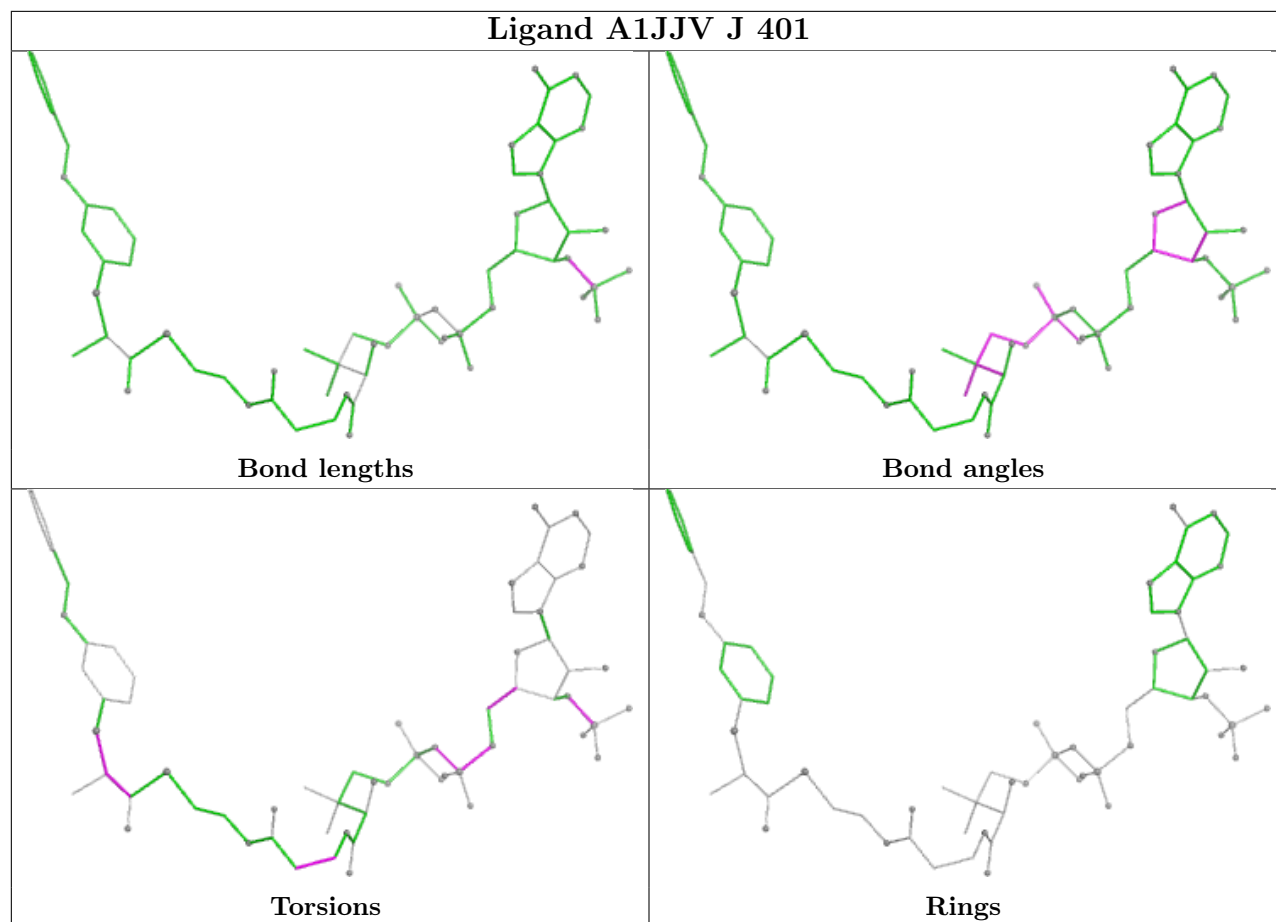
There are no ring outliers.

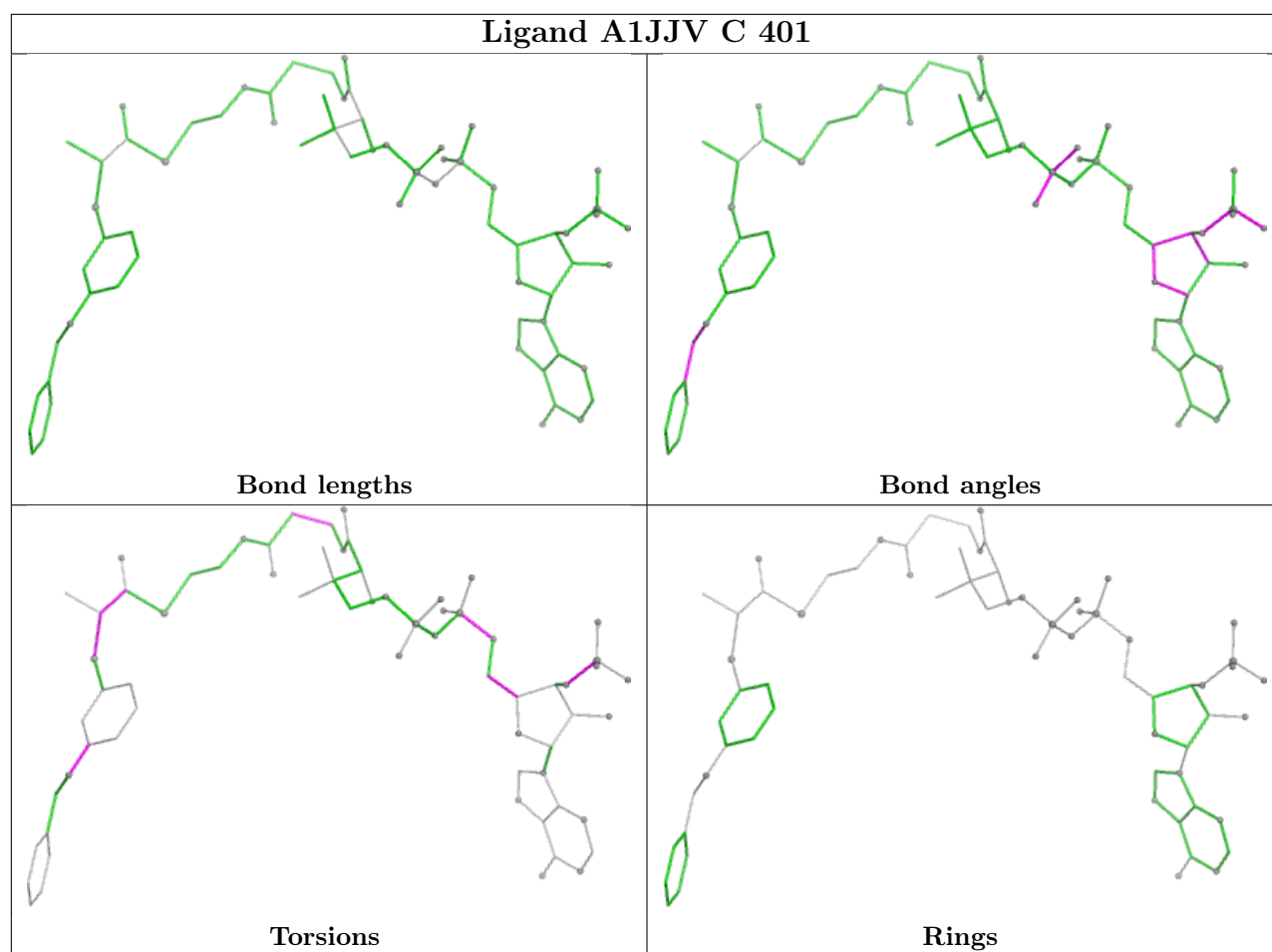
9 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	401	A1JJV	2	0
2	J	401	A1JJV	1	0
2	F	401	A1JJV	4	0
2	B	401	A1JJV	4	0
2	H	401	A1JJV	1	0
2	I	401	A1JJV	1	0
2	E	401	A1JJV	5	0
2	A	401	A1JJV	2	0
2	D	401	A1JJV	4	0

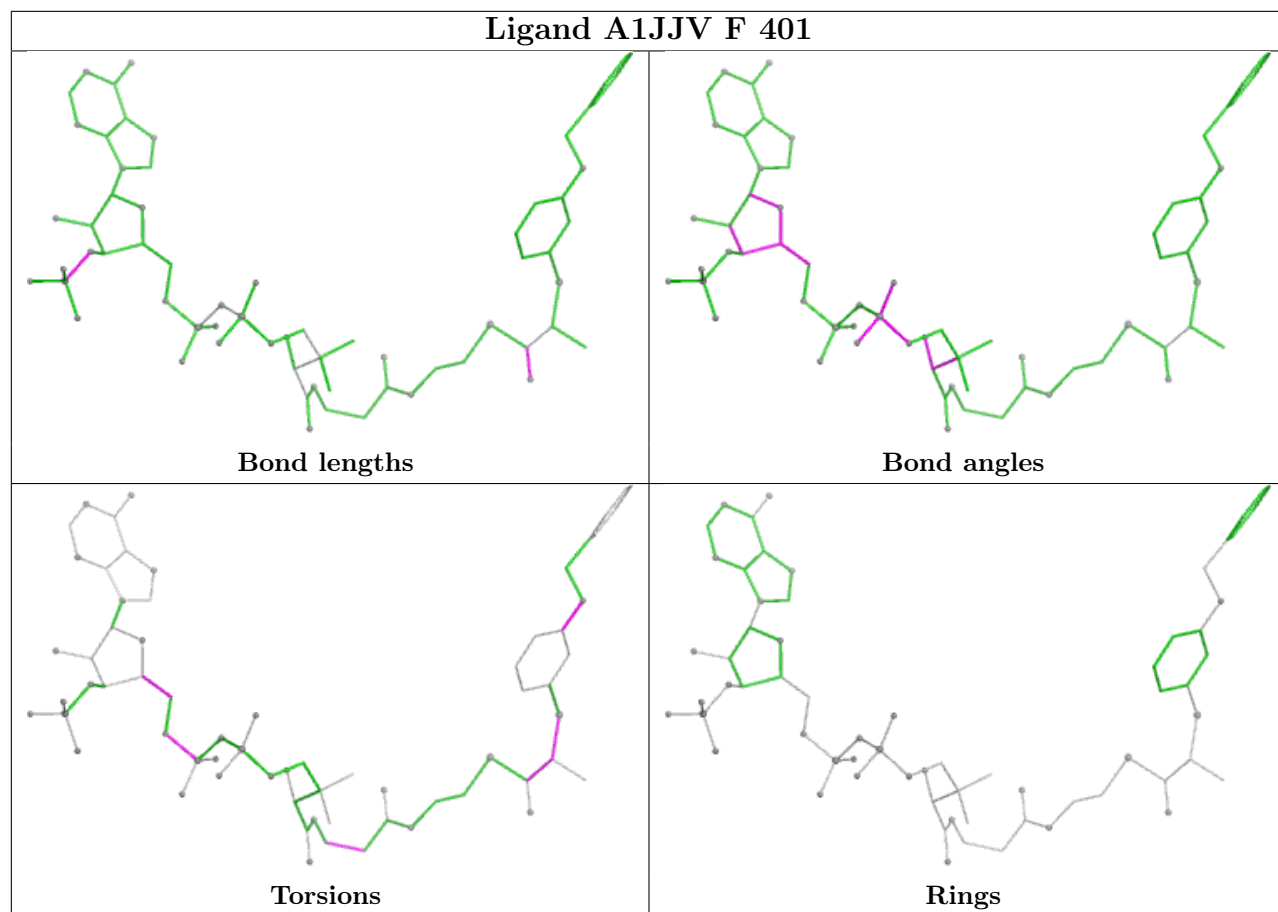
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

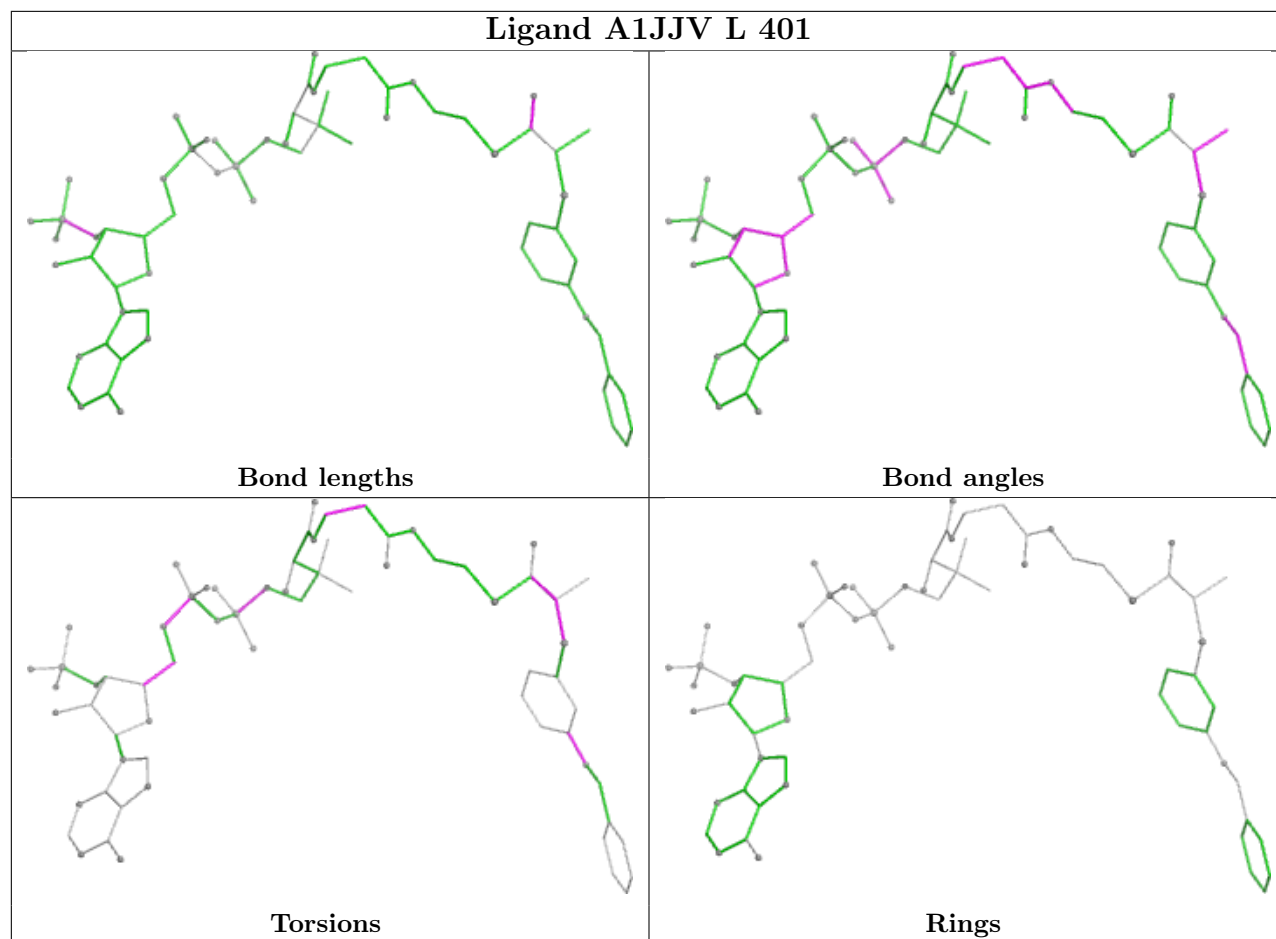


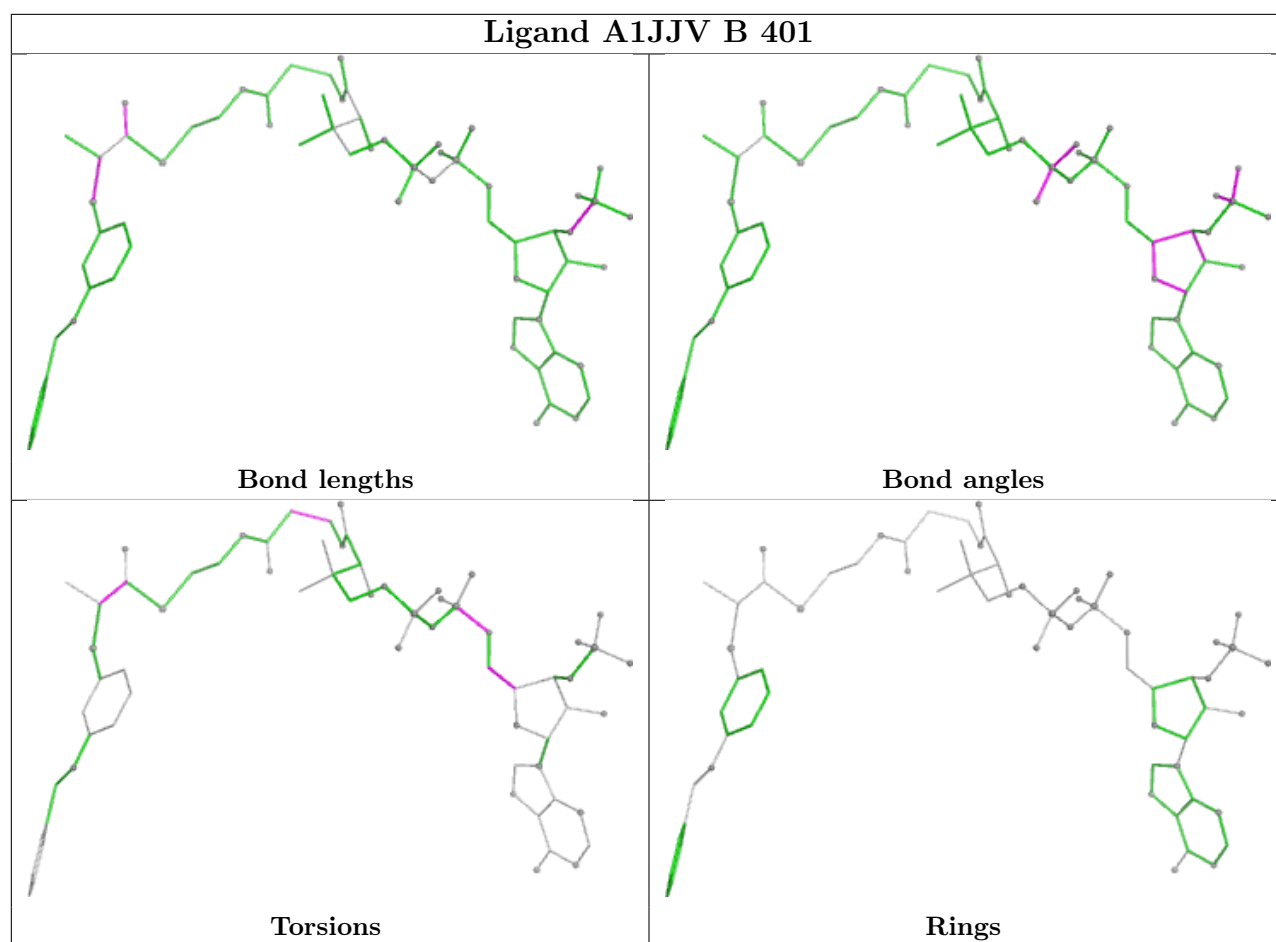




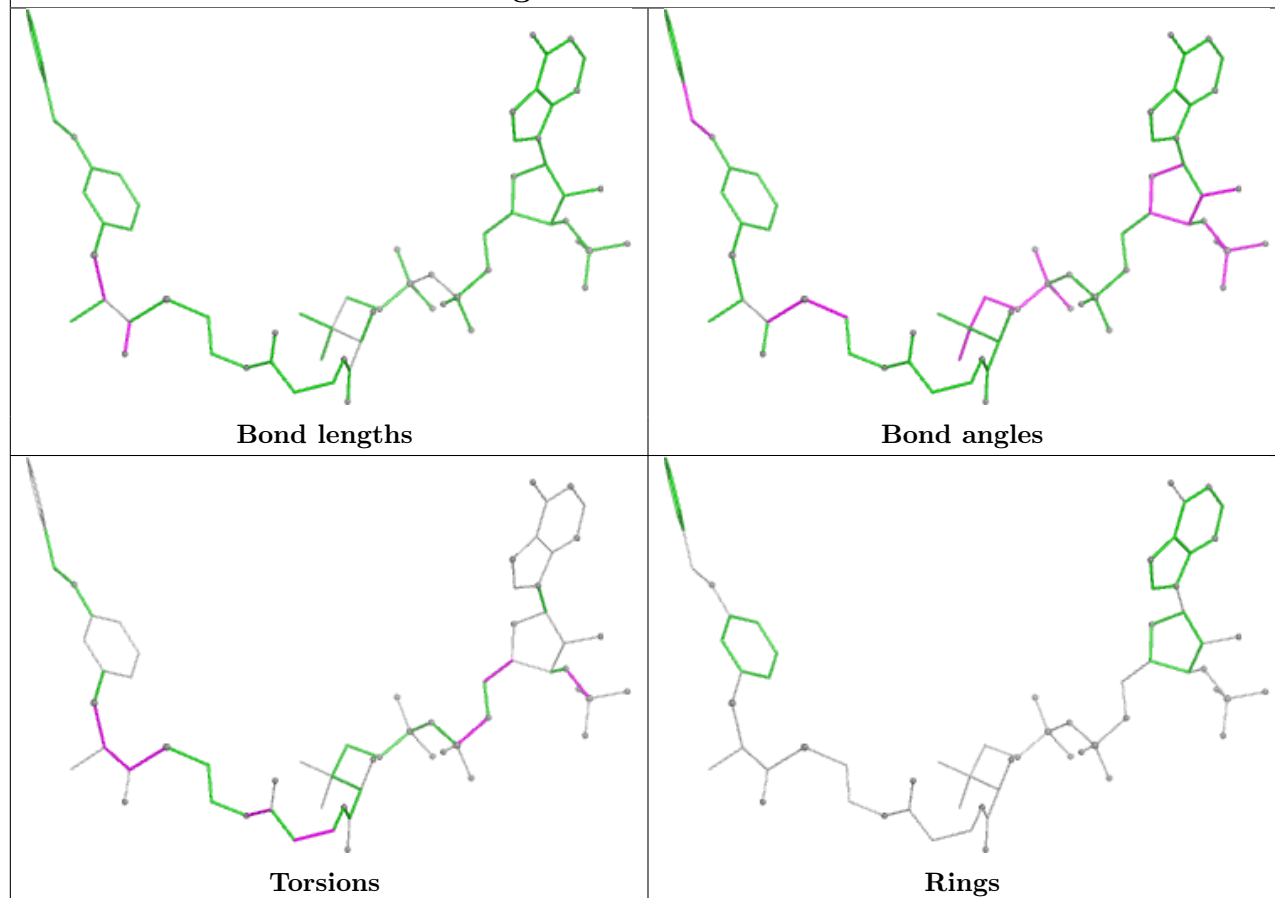
Ligand A1JJV F 401



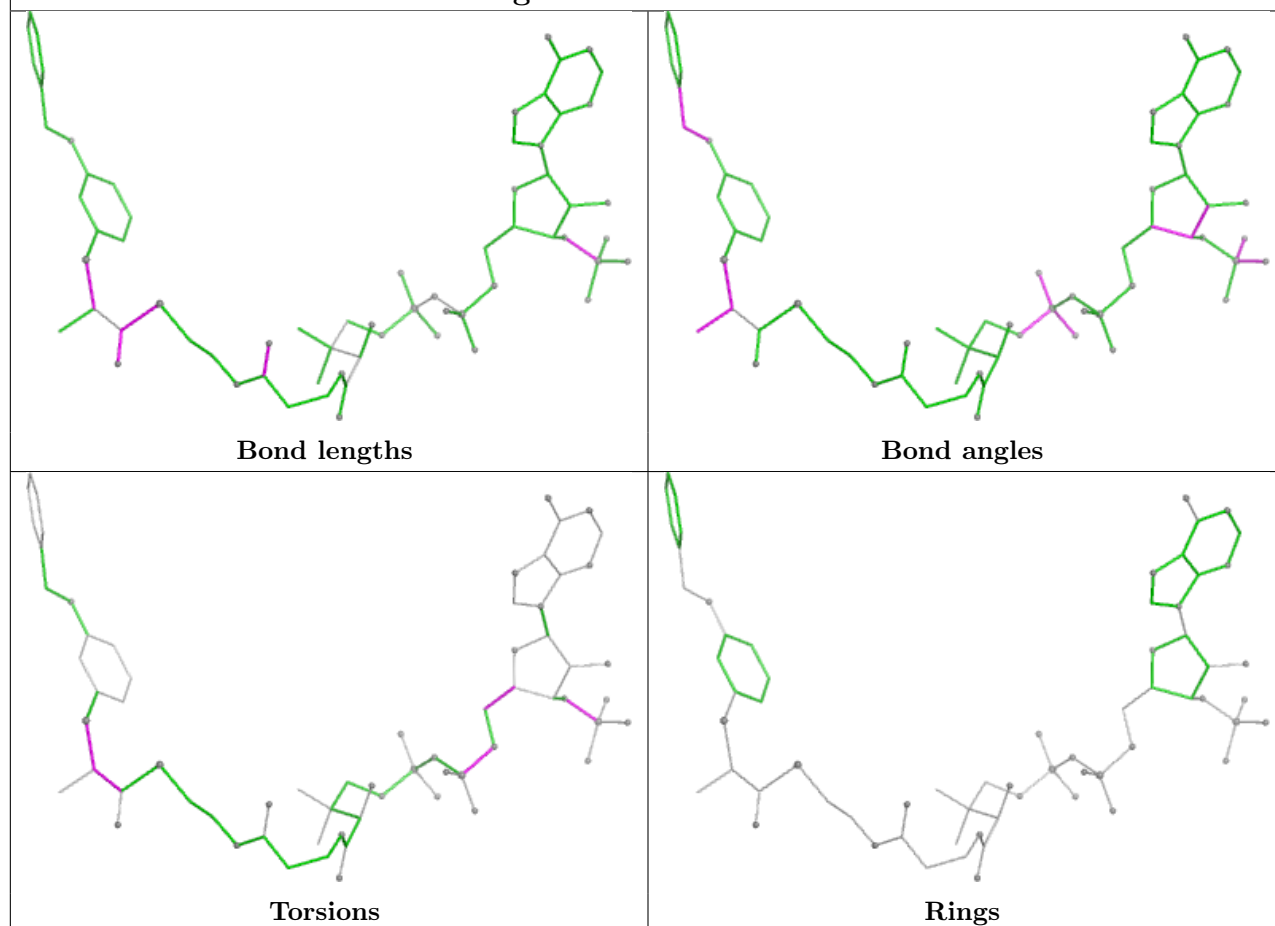


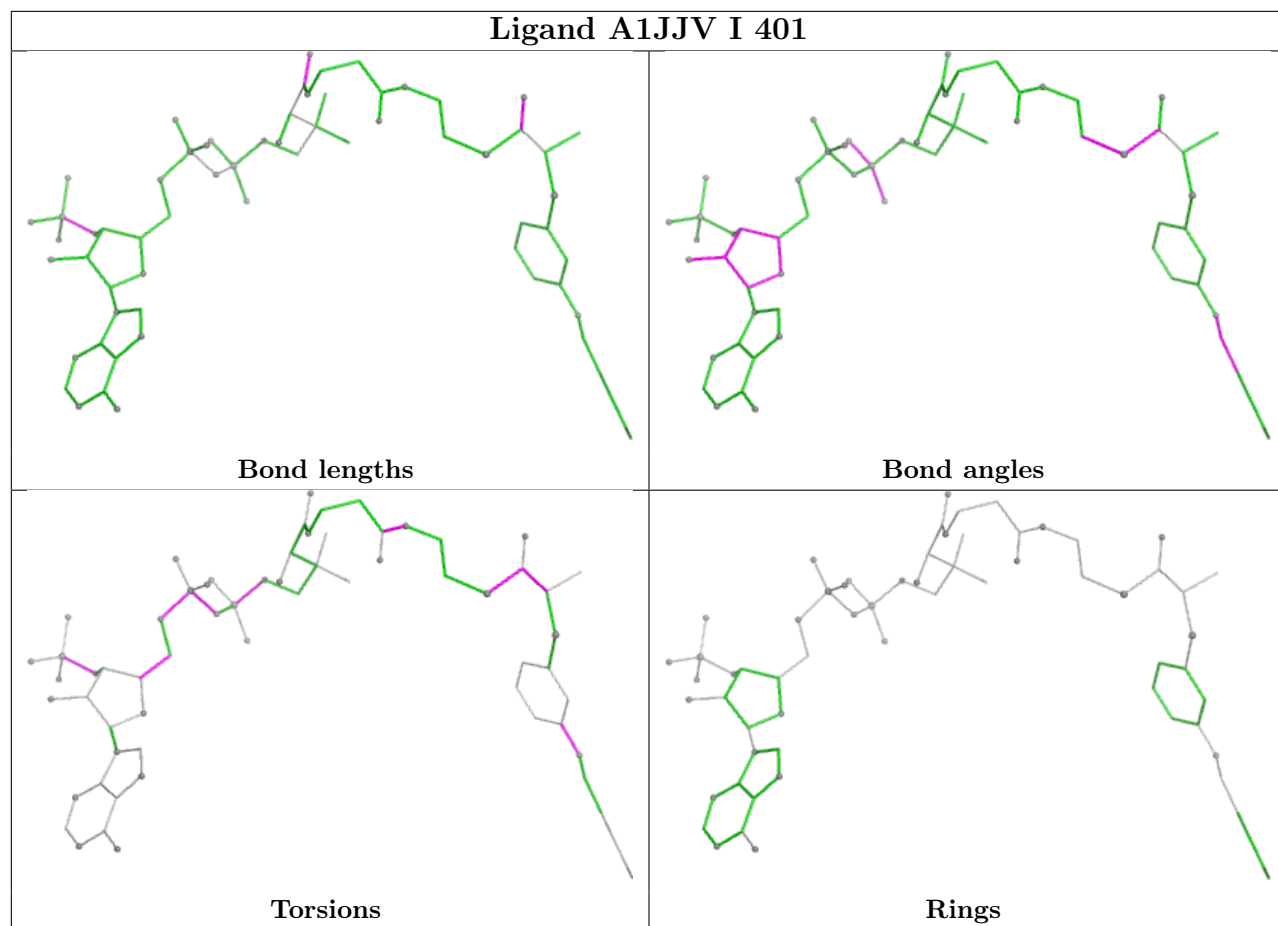


Ligand A1JJV K 401

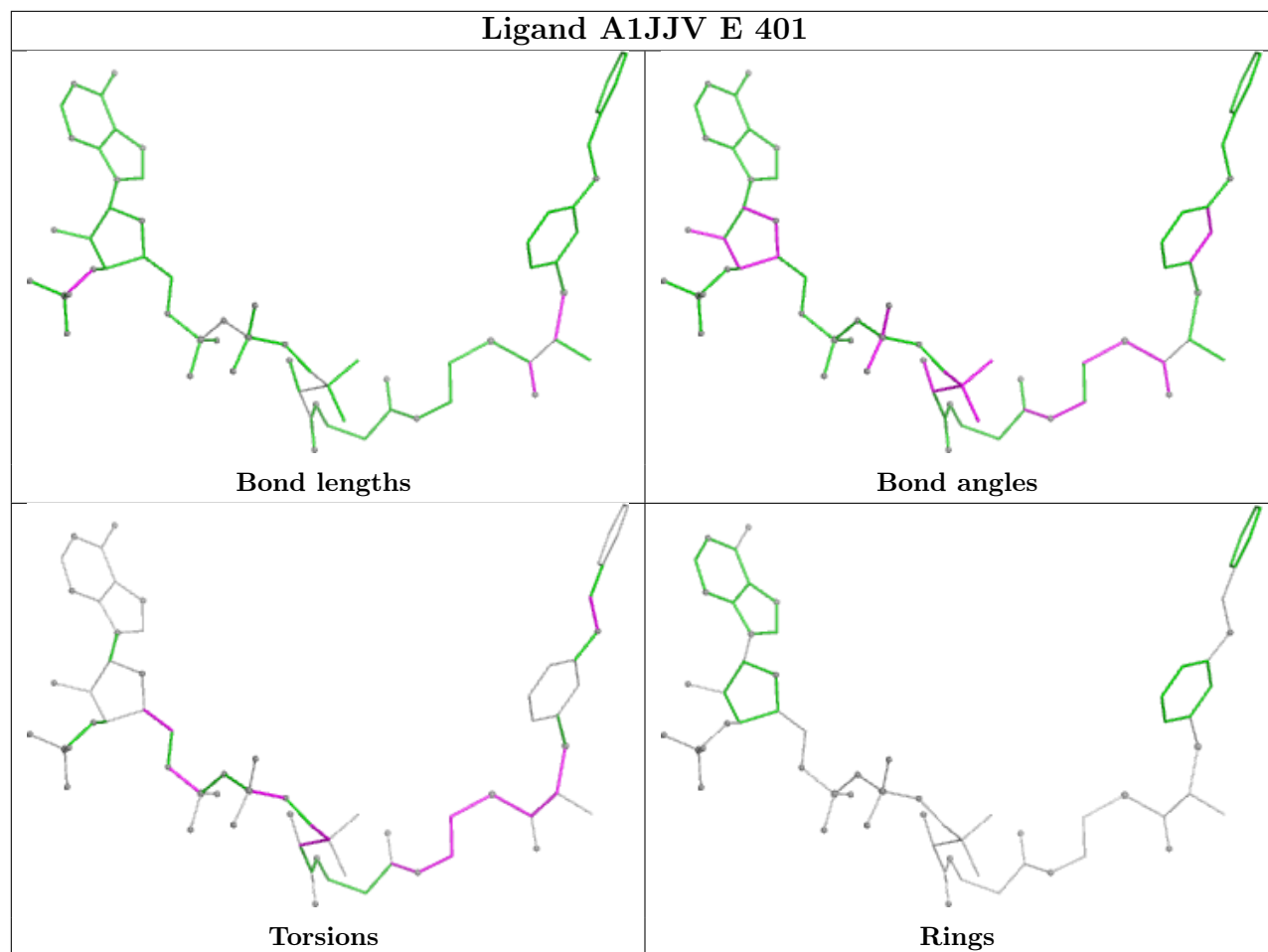


Ligand A1JJV H 401

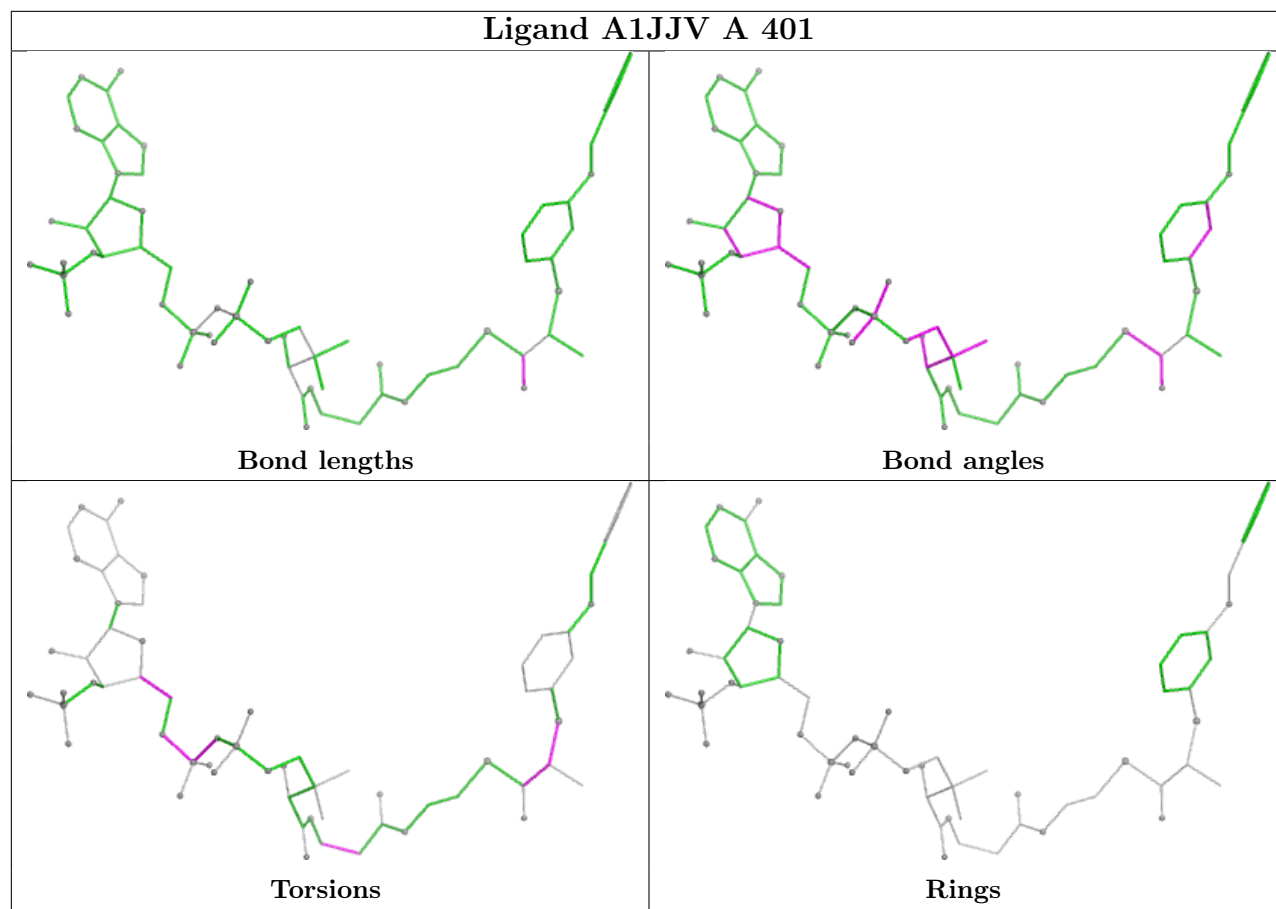


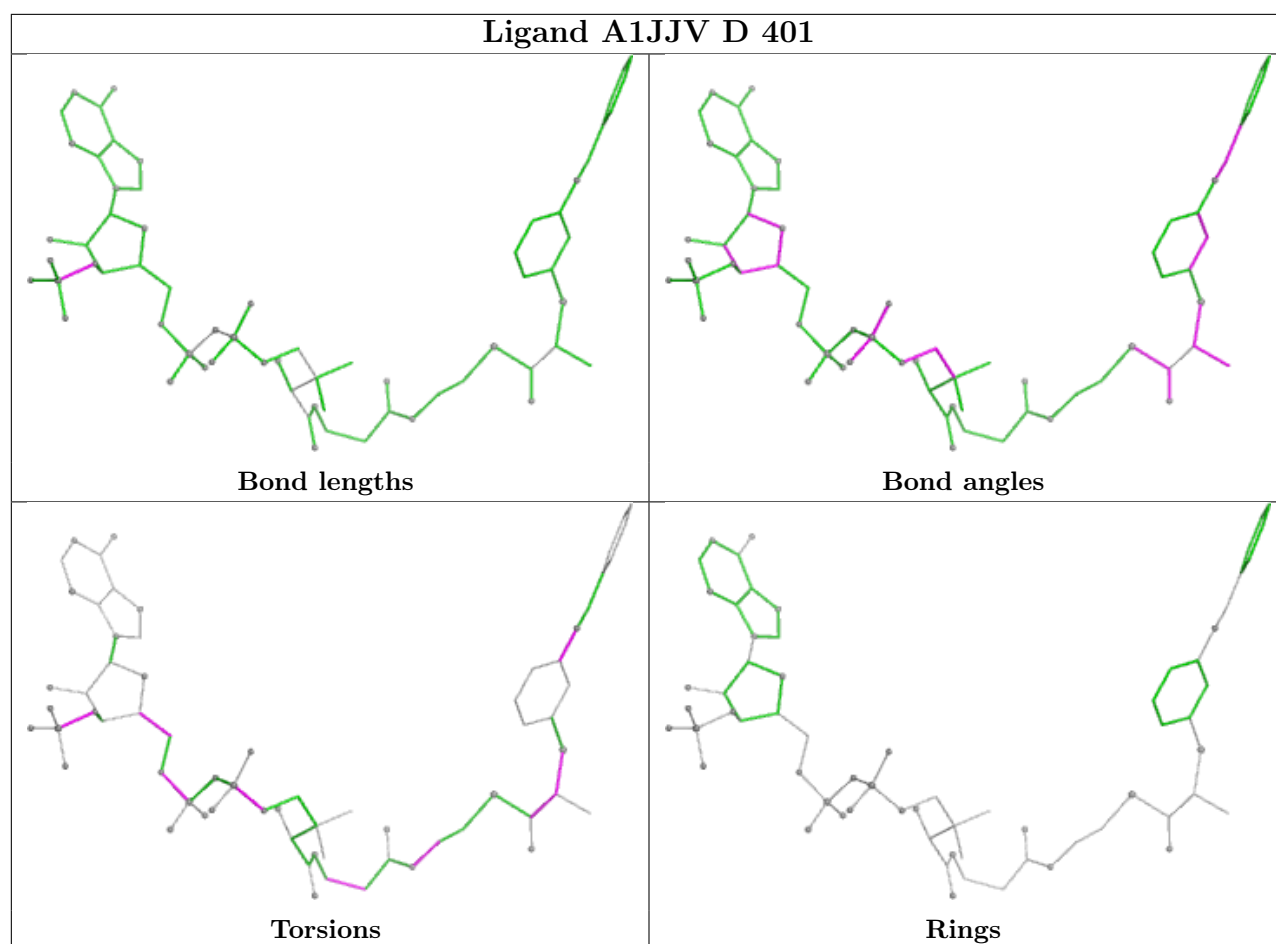


Ligand A1JJV E 401



Ligand A1JJV A 401





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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	357/364 (98%)	0.95	70 (19%) 3 3	22, 38, 76, 118	2 (0%)
1	B	355/364 (97%)	0.84	53 (14%) 5 5	16, 38, 77, 107	2 (0%)
1	C	359/364 (98%)	1.00	86 (23%) 2 2	21, 37, 78, 115	2 (0%)
1	D	359/364 (98%)	0.76	54 (15%) 5 5	21, 36, 74, 113	1 (0%)
1	E	356/364 (97%)	1.04	84 (23%) 2 2	23, 39, 83, 118	2 (0%)
1	F	357/364 (98%)	1.25	104 (29%) 1 1	22, 40, 83, 121	1 (0%)
1	G	358/364 (98%)	1.41	118 (32%) 1 1	22, 41, 89, 115	2 (0%)
1	H	357/364 (98%)	1.18	90 (25%) 1 1	22, 40, 87, 116	1 (0%)
1	I	359/364 (98%)	0.68	43 (11%) 9 8	17, 35, 70, 113	3 (0%)
1	J	357/364 (98%)	0.69	46 (12%) 7 6	23, 35, 71, 119	1 (0%)
1	K	356/364 (97%)	0.82	64 (17%) 3 3	16, 36, 74, 107	3 (0%)
1	L	359/364 (98%)	0.72	48 (13%) 7 6	22, 36, 75, 109	1 (0%)
All	All	4289/4368 (98%)	0.95	860 (20%) 3 2	16, 37, 79, 121	21 (0%)

The worst 5 of 860 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	42	VAL	8.7
1	A	346	ALA	7.5
1	E	42	VAL	7.4
1	H	45	ILE	7.2
1	C	346	ALA	7.1

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](#)

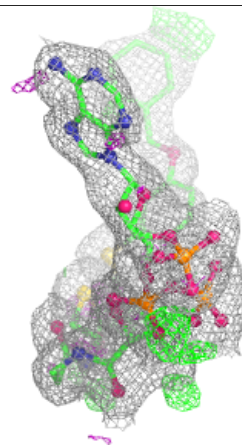
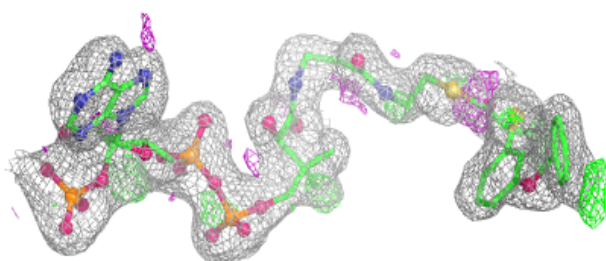
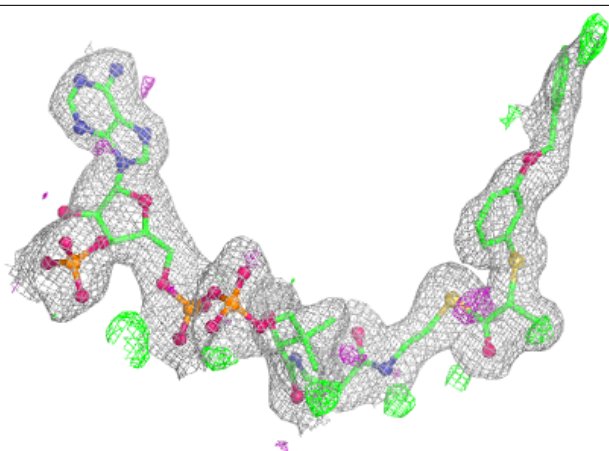
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	A1JJV	H	401	67/67	0.90	0.15	34,61,88,95	0
2	A1JJV	E	401	67/67	0.91	0.15	37,55,93,101	0
2	A1JJV	F	401	67/67	0.94	0.12	25,49,76,83	0
2	A1JJV	G	401	67/67	0.94	0.13	25,49,86,93	0
2	A1JJV	A	401	67/67	0.94	0.12	28,45,68,74	0
2	A1JJV	C	401	67/67	0.95	0.12	27,47,94,97	0
2	A1JJV	J	401	67/67	0.95	0.12	25,44,92,94	0
2	A1JJV	K	401	67/67	0.95	0.11	27,45,78,87	0
2	A1JJV	B	401	67/67	0.96	0.10	28,45,88,101	0
2	A1JJV	I	401	67/67	0.96	0.10	23,38,67,76	0
2	A1JJV	L	401	67/67	0.96	0.10	22,36,73,90	0
2	A1JJV	D	401	67/67	0.97	0.09	25,35,65,69	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.

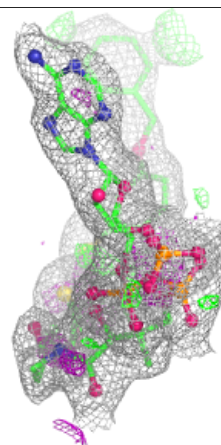
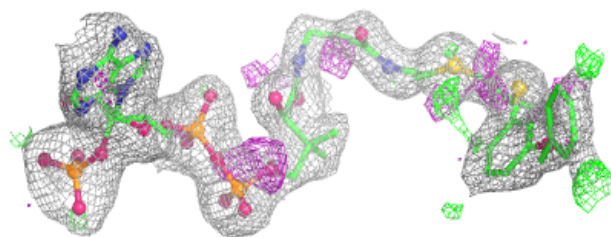
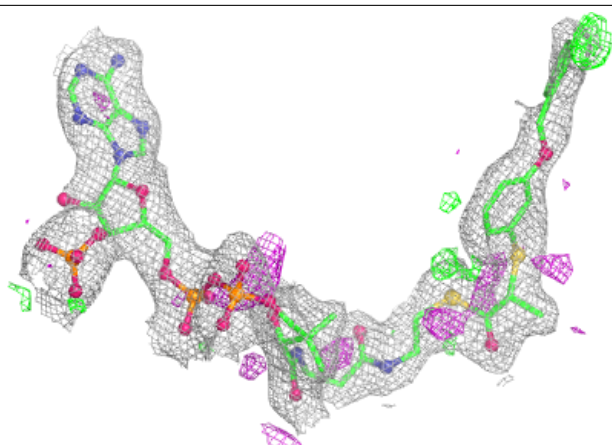
Electron density around A1JJV H 401:

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



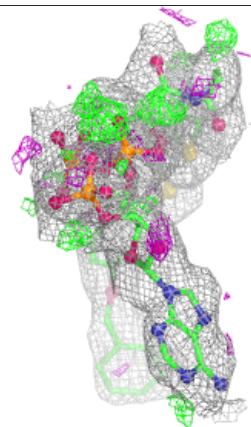
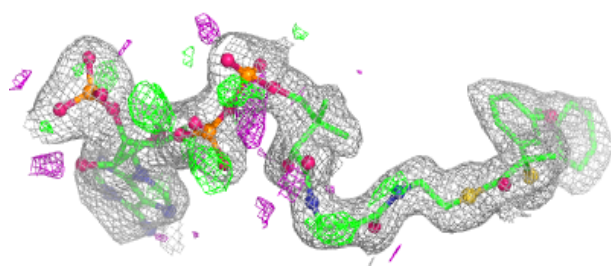
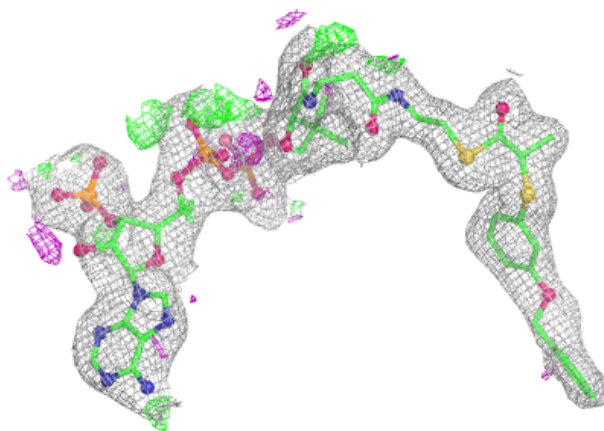
Electron density around A1JJV E 401:

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



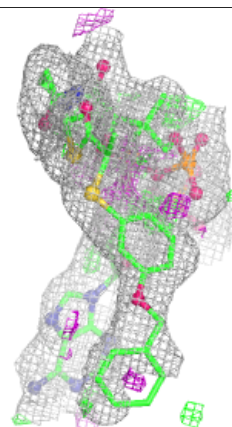
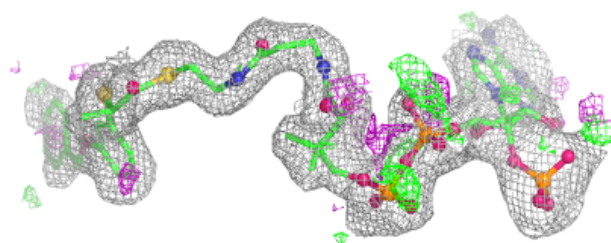
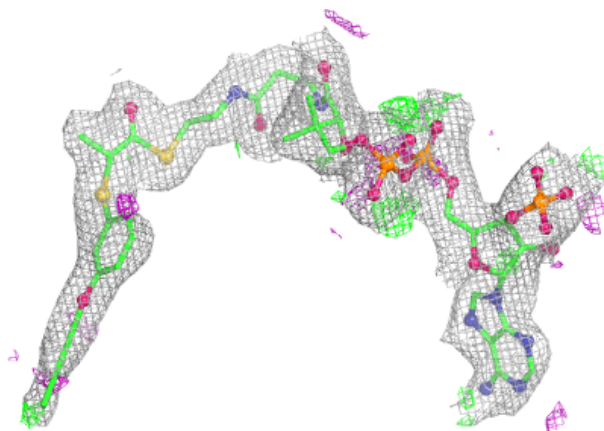
Electron density around A1JJV F 401:

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



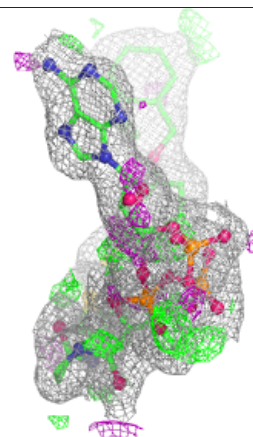
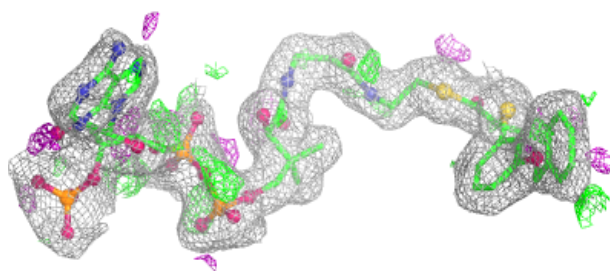
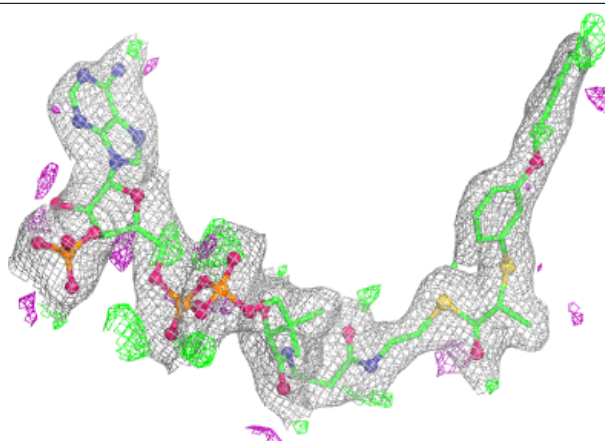
Electron density around A1JJV G 401:

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



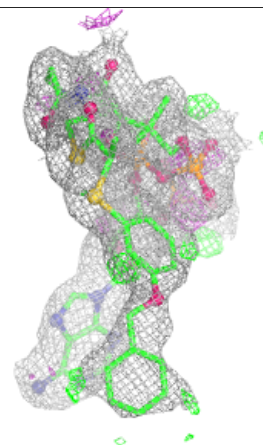
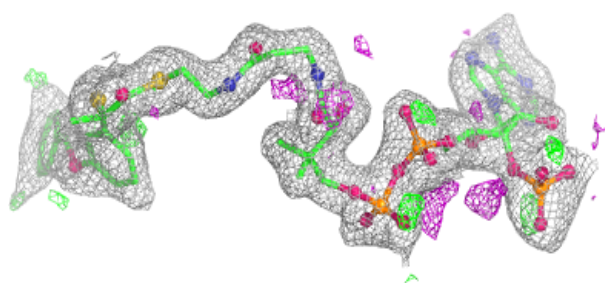
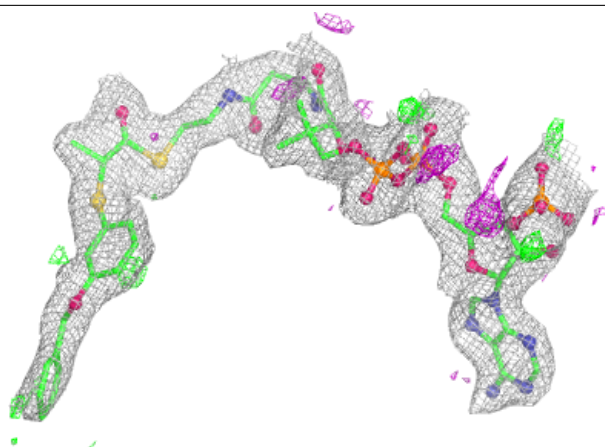
Electron density around A1JJV A 401:

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

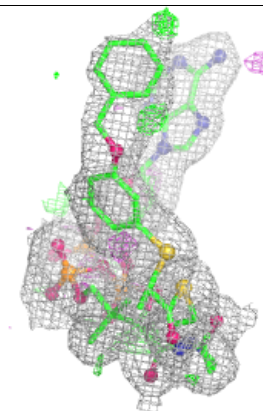
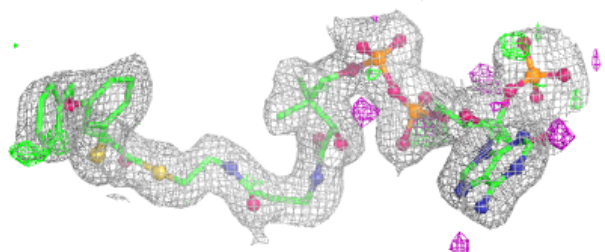
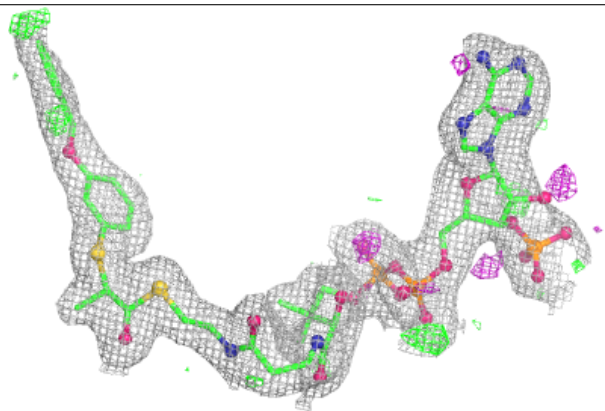


Electron density around A1JJV C 401:

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

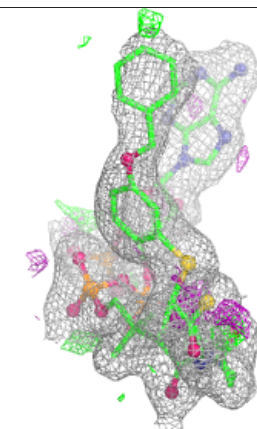
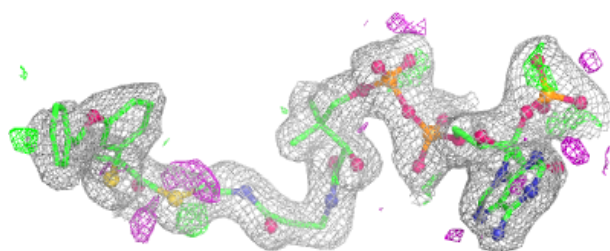
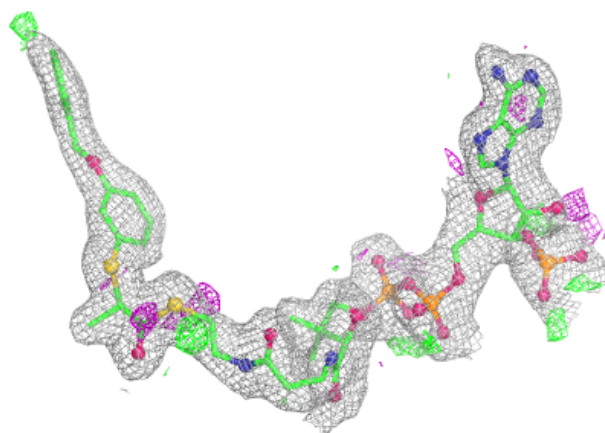
**Electron density around A1JJV J 401:**

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

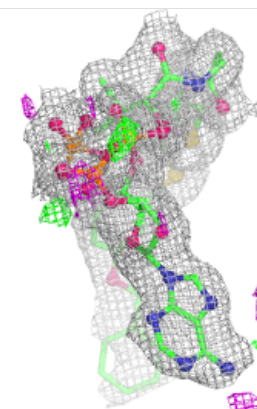
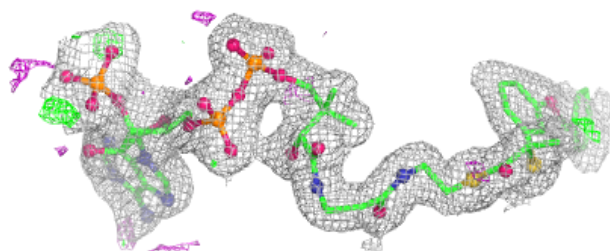
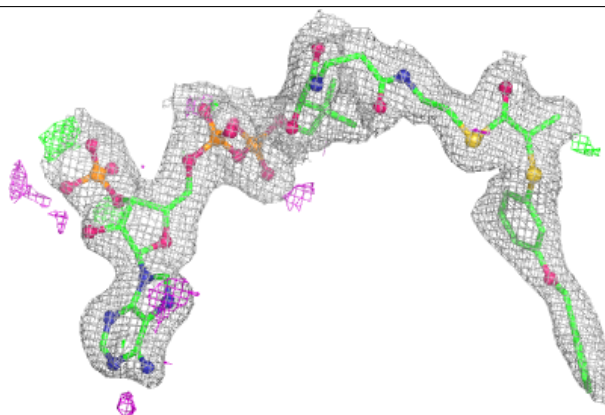


Electron density around A1JJV K 401:

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

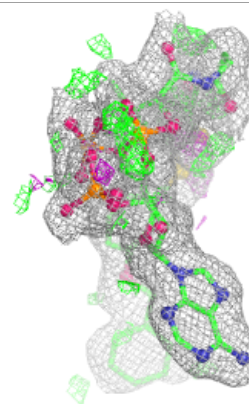
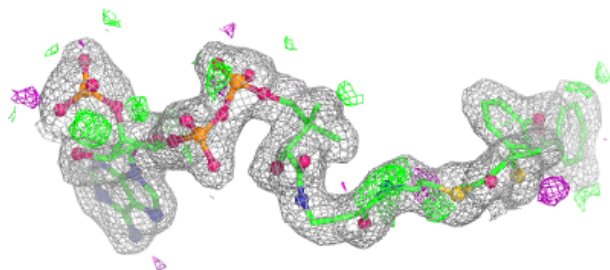
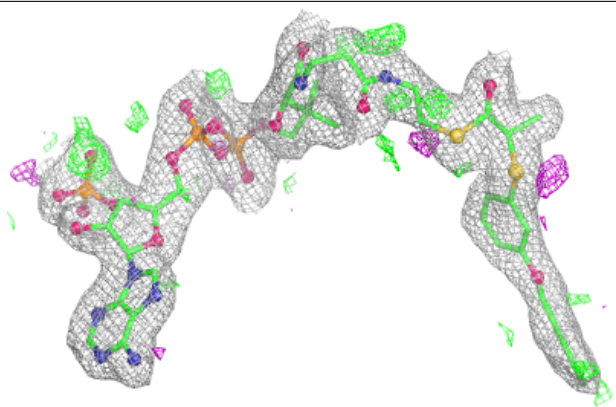
**Electron density around A1JJV B 401:**

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

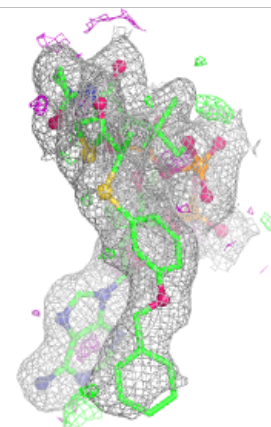
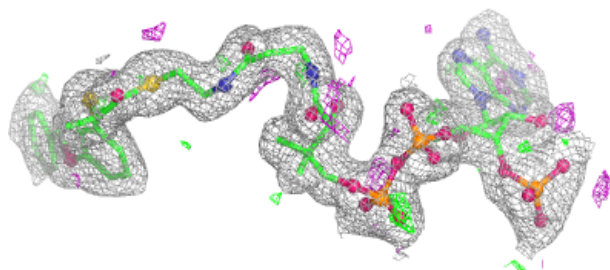
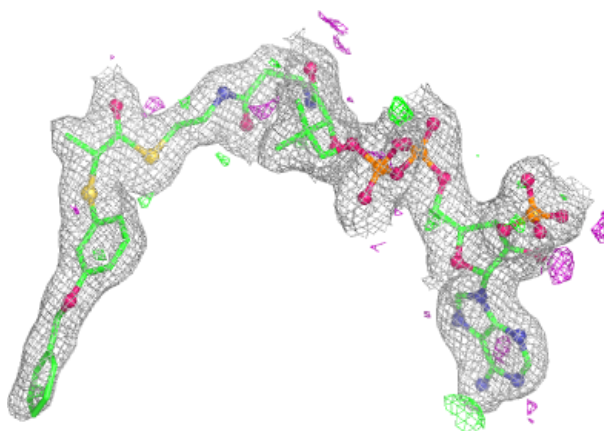


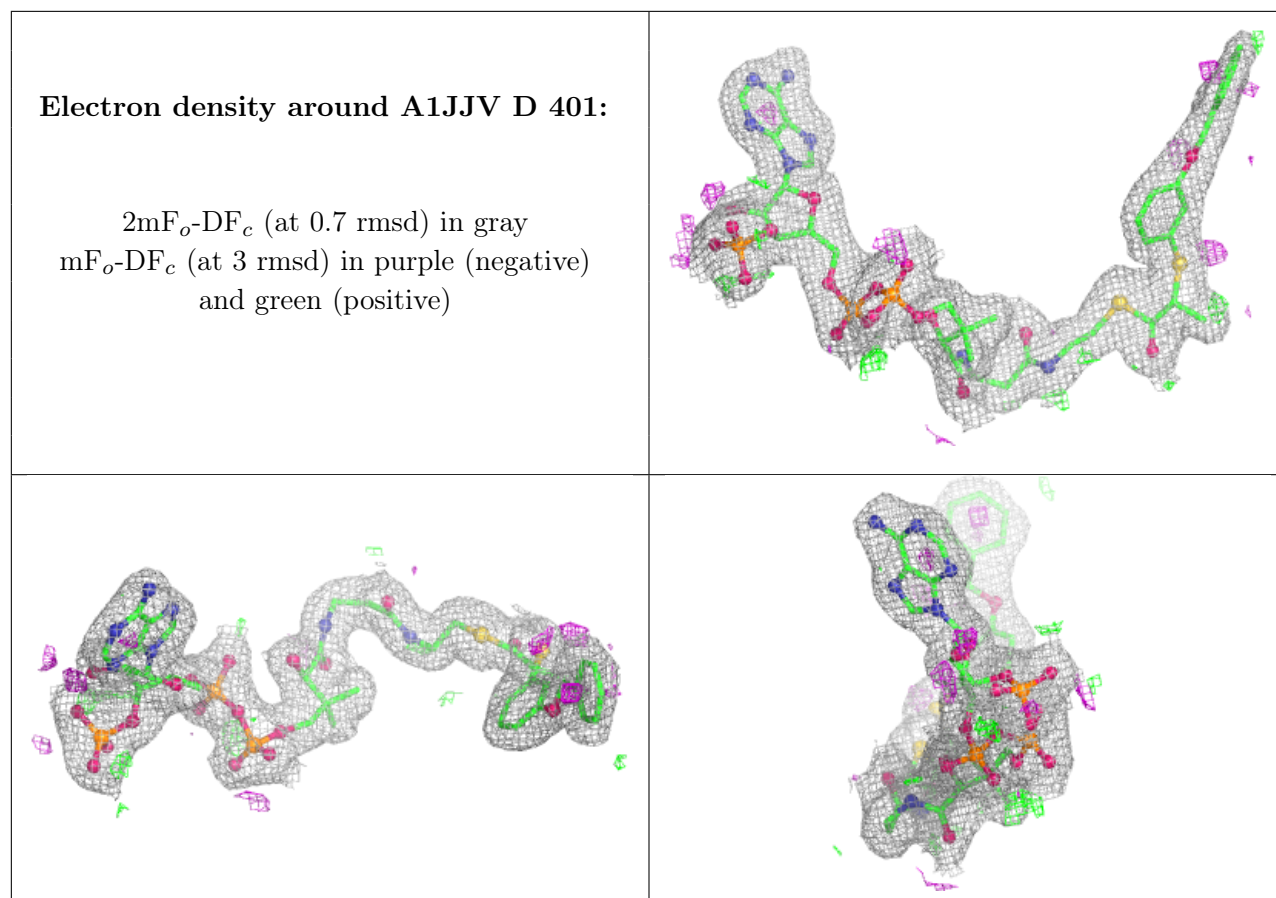
Electron density around A1JJV I 401:

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

**Electron density around A1JJV L 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 ⓘ

There are no such residues in this entry.