



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 10:38 PM UTC

PDB ID : 1F1H / pdb_00001f1h
Title : CRYSTAL STRUCTURE OF GLUTAMINE SYNTHETASE FROM
SALMONELLA TYPHIMURIUM WITH THALLIUM IONS
Authors : Gill, H.S.; Eisenberg, D.
Deposited on : 2000-05-19
Resolution : 2.67 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

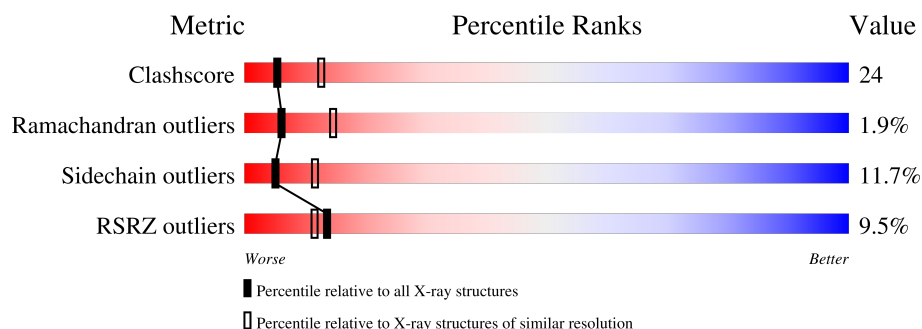
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 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))
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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	468	17% 66% 25% 7%
1	B	468	8% 67% 24% 7%
1	C	468	9% 66% 25% 7%
1	D	468	6% 66% 24% 7%
1	E	468	7% 66% 24% 7%
1	F	468	7% 66% 25% 7%
1	G	468	7% 67% 24% 8%

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Mol	Chain	Length	Quality of chain
1	H	468	
1	I	468	
1	J	468	
1	K	468	
1	L	468	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MPD	A	1483	-	-	X	-
5	MPD	B	1484	-	-	X	-
5	MPD	C	1485	-	-	X	-
5	MPD	D	1486	-	-	X	-
5	MPD	E	1487	-	-	X	-
5	MPD	F	1488	-	-	X	-
5	MPD	G	1489	-	-	X	-
5	MPD	H	1490	-	-	X	-
5	MPD	I	1491	-	-	X	-
5	MPD	J	1492	-	-	X	-
5	MPD	K	1493	-	-	X	-
5	MPD	L	1494	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 45564 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 PROTEIN (GLUTAMINE SYNTHETASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	B	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	C	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	D	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	E	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	F	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	G	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	H	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	I	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	J	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	K	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			
1	L	468	Total	C	N	O	S	0	0	0
			3637	2301	624	692	20			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

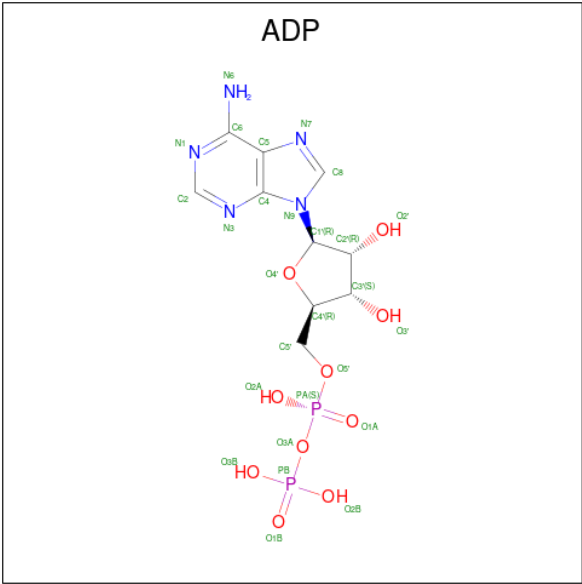
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		
2	B	2	Total	Mn	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	2	Total	Mn	0	0
			2	2		
2	D	2	Total	Mn	0	0
			2	2		
2	E	2	Total	Mn	0	0
			2	2		
2	F	2	Total	Mn	0	0
			2	2		
2	G	2	Total	Mn	0	0
			2	2		
2	H	2	Total	Mn	0	0
			2	2		
2	I	2	Total	Mn	0	0
			2	2		
2	J	2	Total	Mn	0	0
			2	2		
2	K	2	Total	Mn	0	0
			2	2		
2	L	2	Total	Mn	0	0
			2	2		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	I	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	J	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	K	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	L	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is THALLIUM (I) ION (CCD ID: TL) (formula: Tl).

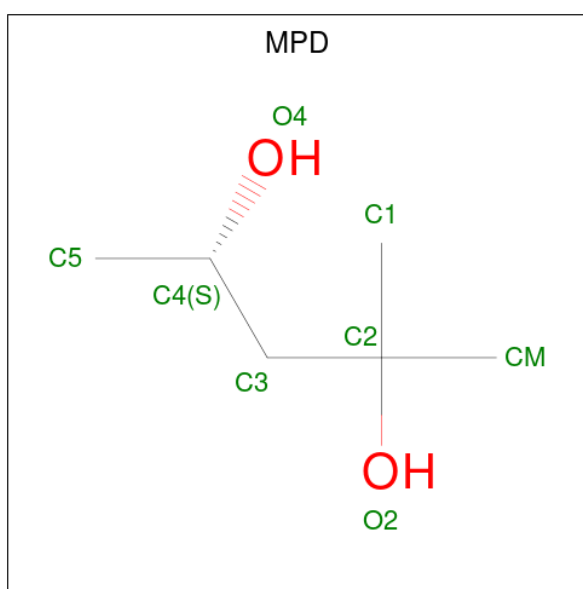
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Tl	0	0
			2	2		
4	B	2	Total	Tl	0	0
			2	2		
4	C	2	Total	Tl	0	0
			2	2		
4	D	2	Total	Tl	0	0
			2	2		
4	E	2	Total	Tl	0	0
			2	2		
4	F	2	Total	Tl	0	0
			2	2		
4	G	2	Total	Tl	0	0
			2	2		
4	H	2	Total	Tl	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	2	Total 2	Tl 2	0	0
4	J	2	Total 2	Tl 2	0	0
4	K	2	Total 2	Tl 2	0	0
4	L	2	Total 2	Tl 2	0	0

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 8	C 6	O 2	0	0
5	B	1	Total 8	C 6	O 2	0	0
5	C	1	Total 8	C 6	O 2	0	0
5	D	1	Total 8	C 6	O 2	0	0
5	E	1	Total 8	C 6	O 2	0	0
5	F	1	Total 8	C 6	O 2	0	0
5	G	1	Total 8	C 6	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	H	1	Total	C	O	0	0
			8	6	2		
5	I	1	Total	C	O	0	0
			8	6	2		
5	J	1	Total	C	O	0	0
			8	6	2		
5	K	1	Total	C	O	0	0
			8	6	2		
5	L	1	Total	C	O	0	0
			8	6	2		

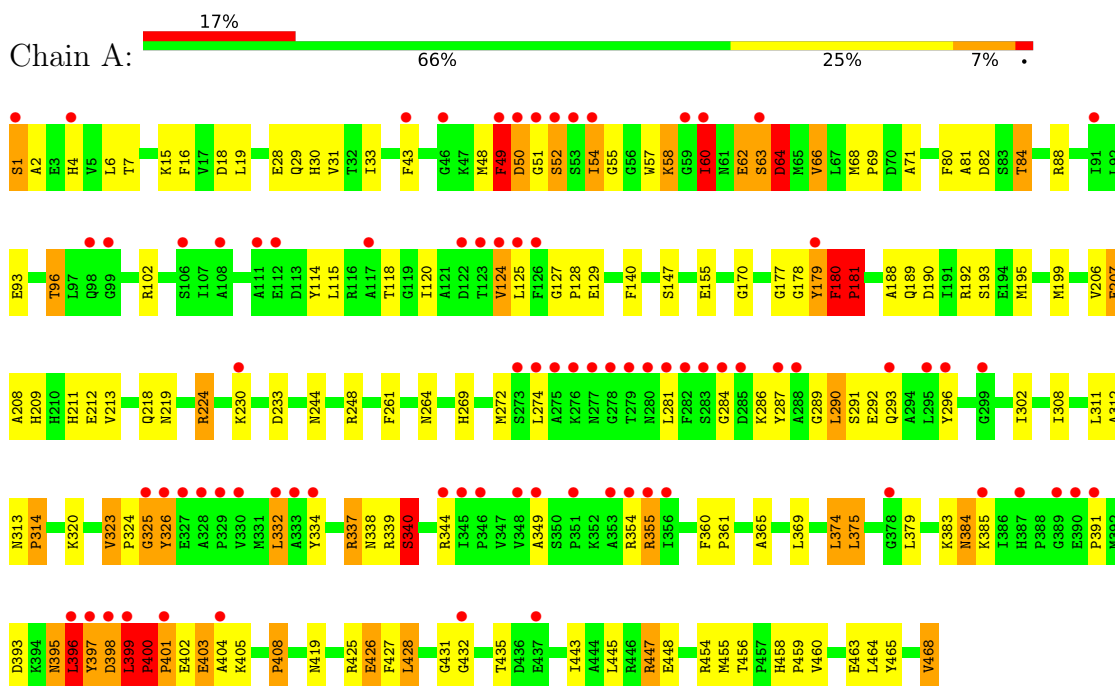
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	120	Total	O	0	0
			120	120		
6	B	121	Total	O	0	0
			121	121		
6	C	119	Total	O	0	0
			119	119		
6	D	122	Total	O	0	0
			122	122		
6	E	122	Total	O	0	0
			122	122		
6	F	121	Total	O	0	0
			121	121		
6	G	122	Total	O	0	0
			122	122		
6	H	121	Total	O	0	0
			121	121		
6	I	122	Total	O	0	0
			122	122		
6	J	120	Total	O	0	0
			120	120		
6	K	123	Total	O	0	0
			123	123		
6	L	119	Total	O	0	0
			119	119		

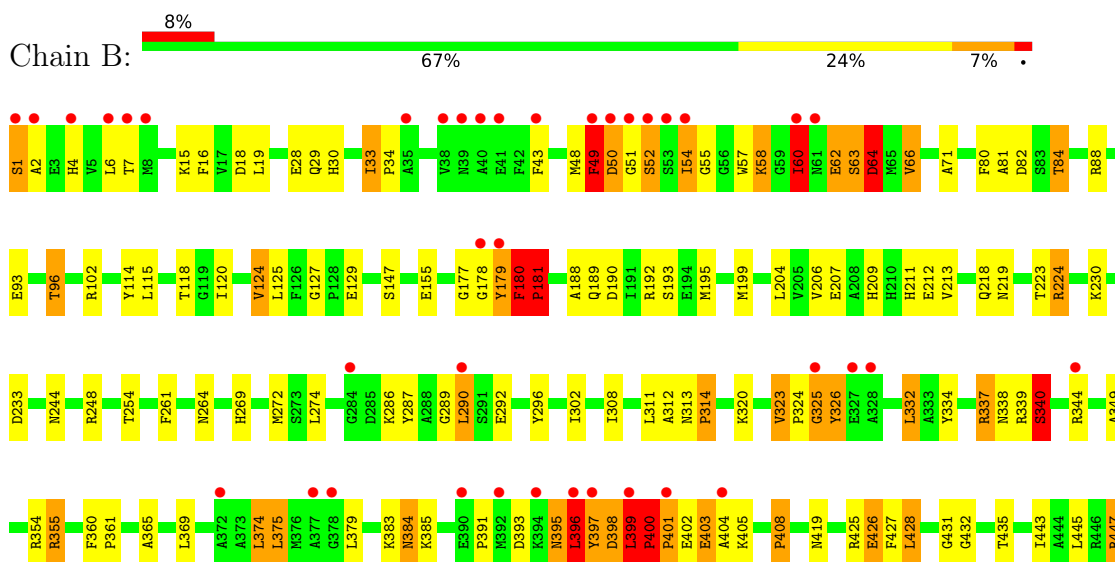
3 Residue-property plots

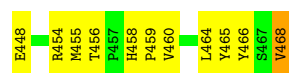
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: PROTEIN (GLUTAMINE SYNTHETASE)

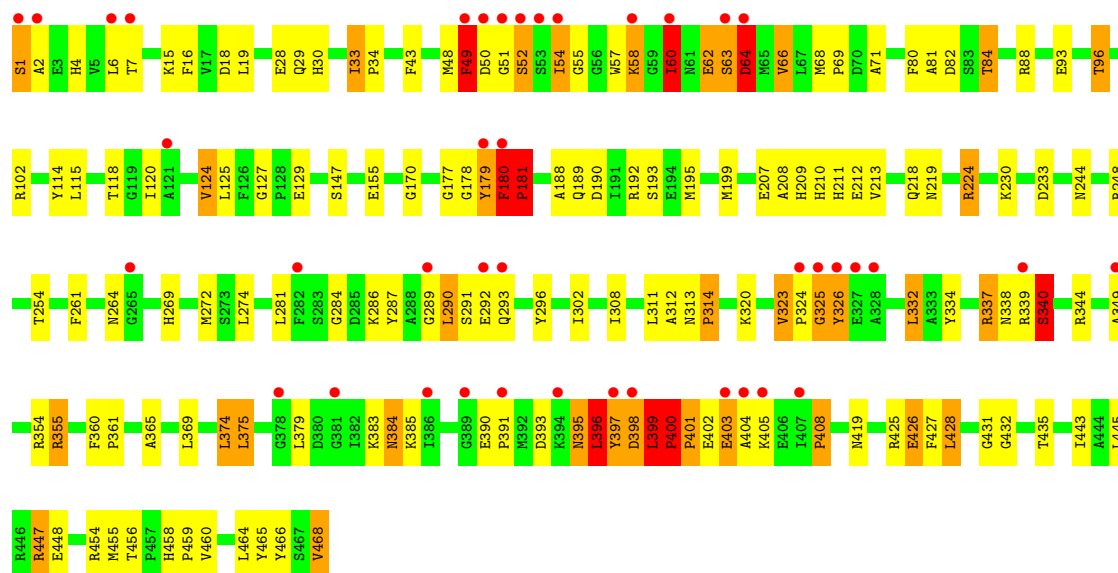


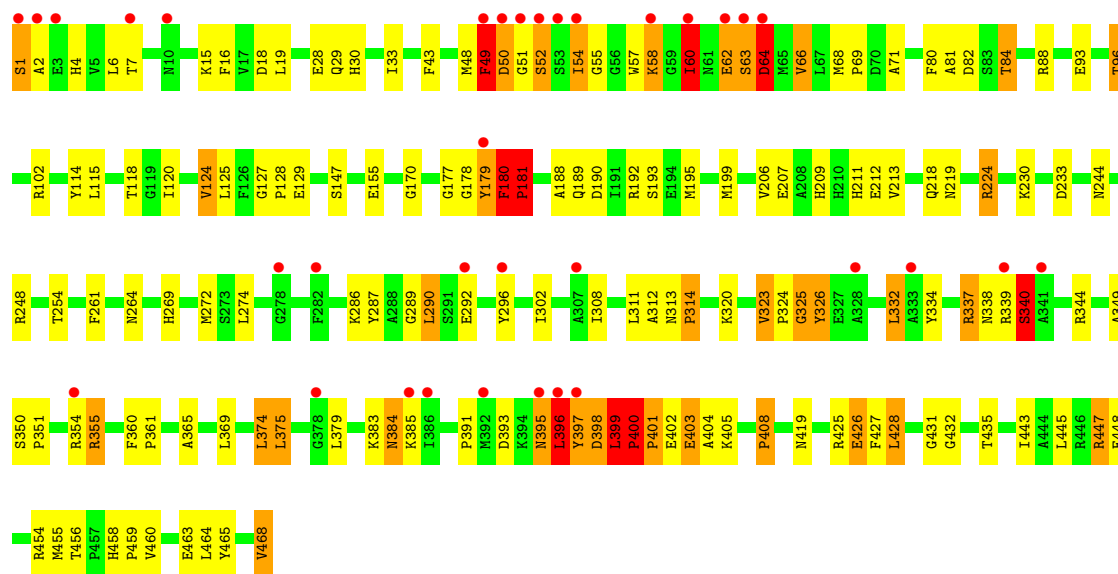
• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)



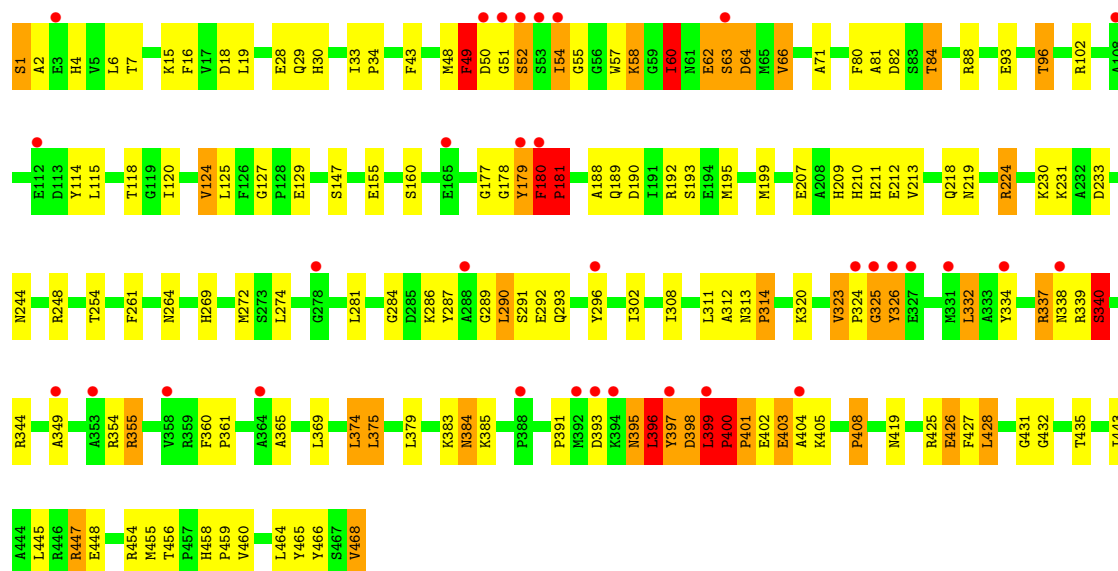


• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)

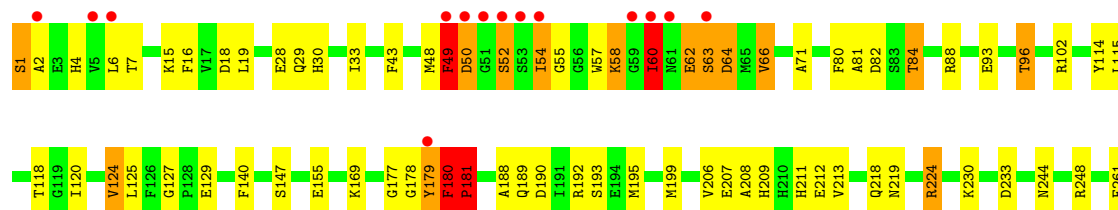


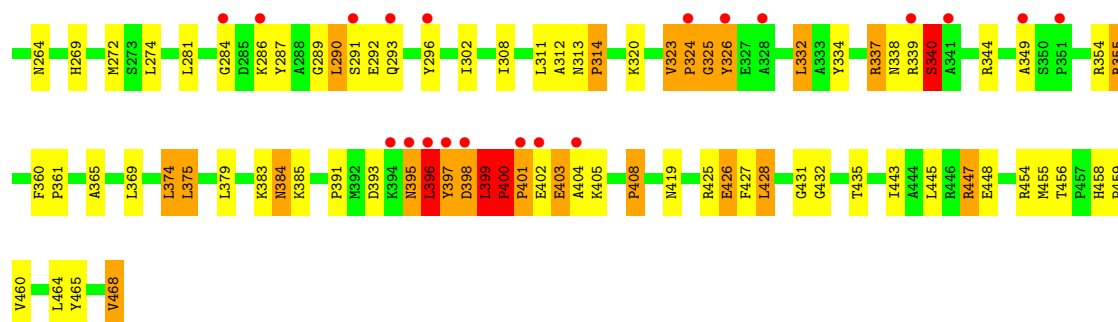


• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)

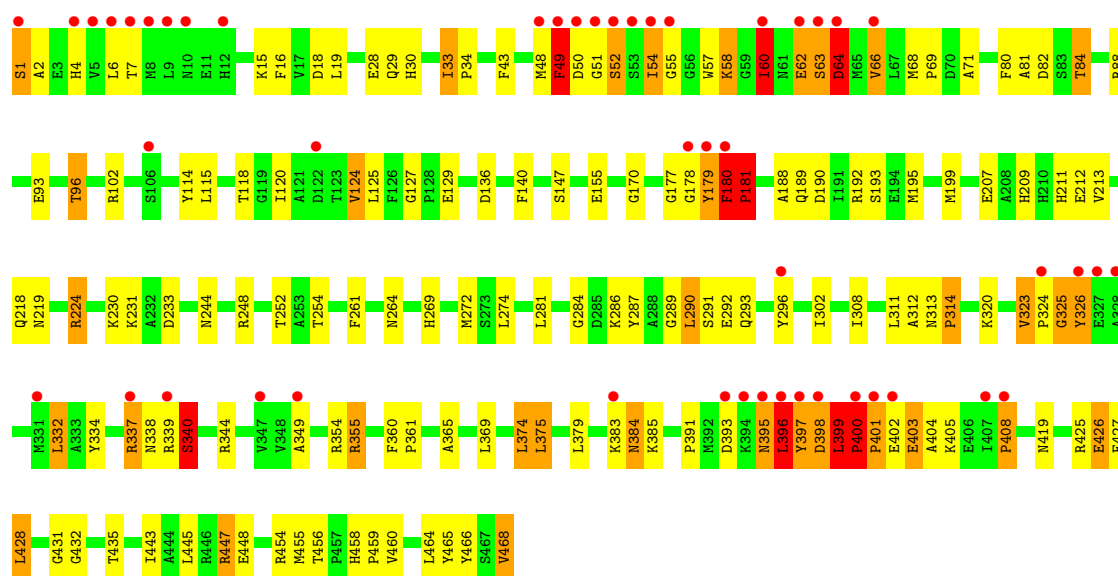


• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)

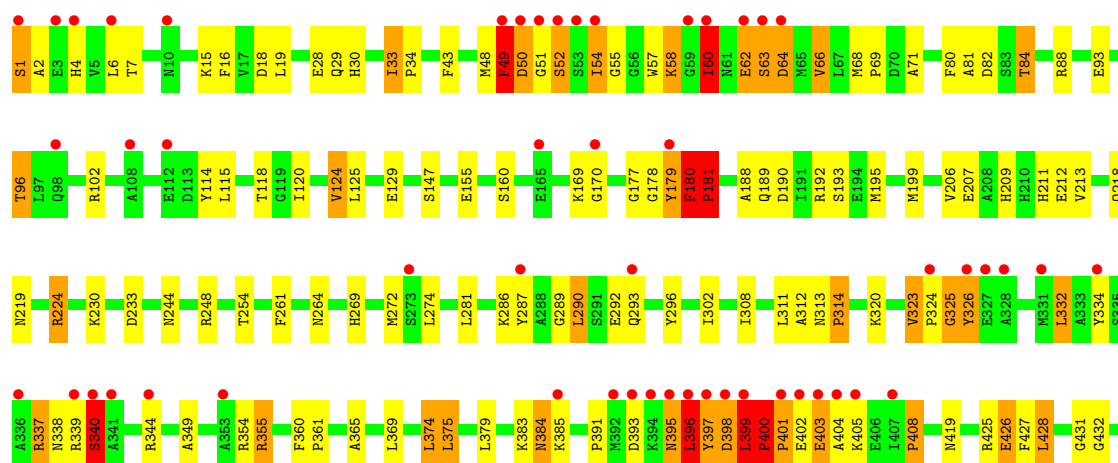




• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)

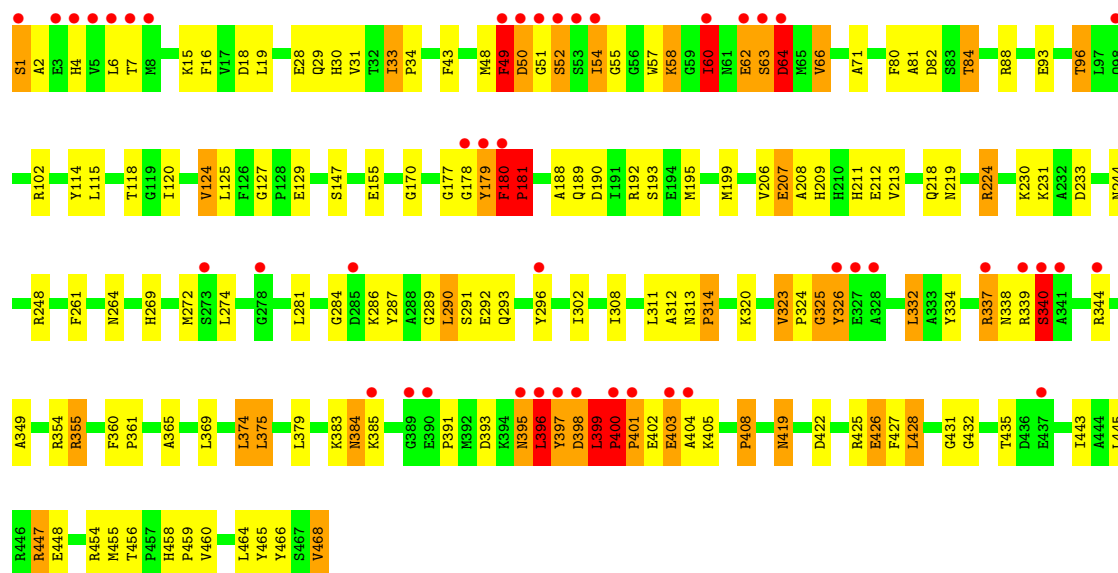


• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)

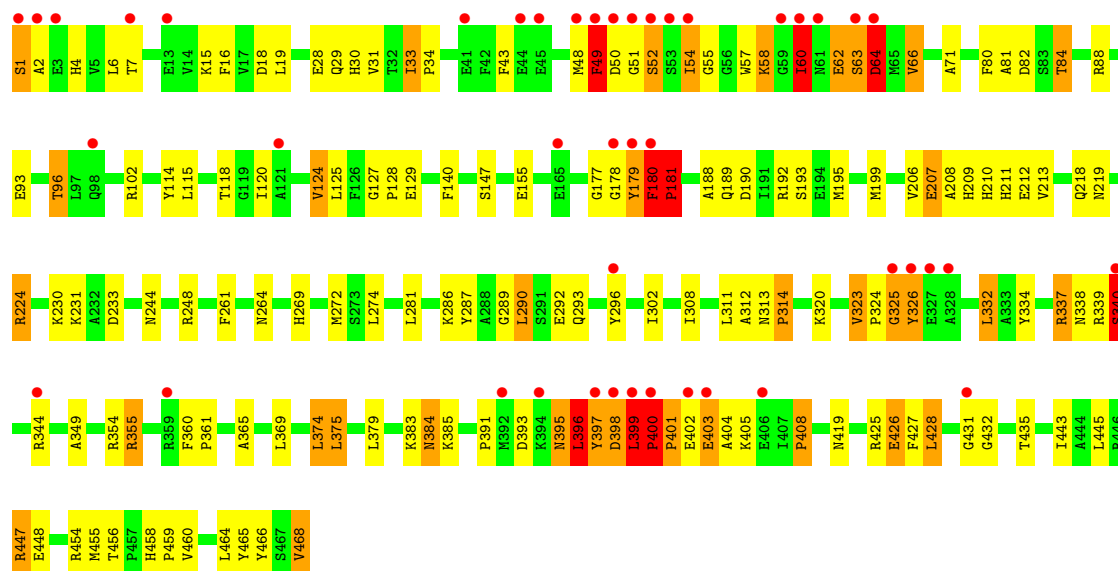




• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)

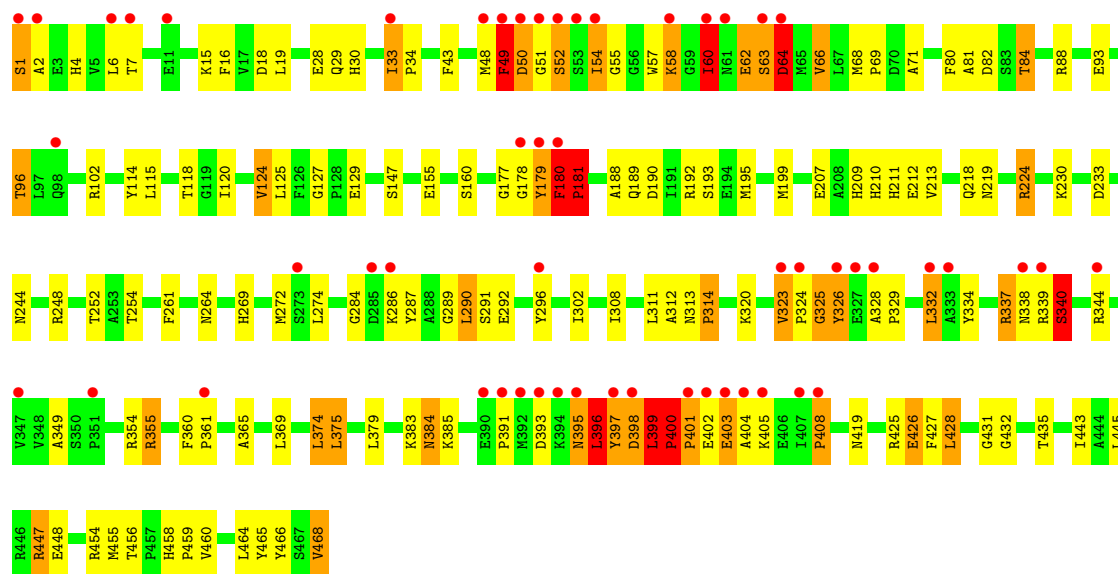


• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)



• Molecule 1: PROTEIN (GLUTAMINE SYNTHETASE)





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	231.13Å 132.79Å 196.78Å 90.00° 102.44° 90.00°	Depositor
Resolution (Å)	32.00 – 2.67 32.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	82.0 (32.00-2.67) 81.9 (32.00-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.68Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.232 , 0.263 0.231 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	45564	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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: MN, ADP, TL, MPD

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	0.64	1/3724 (0.0%)	1.25	35/5043 (0.7%)
1	B	0.64	1/3724 (0.0%)	1.25	33/5043 (0.7%)
1	C	0.64	1/3724 (0.0%)	1.25	35/5043 (0.7%)
1	D	0.64	1/3724 (0.0%)	1.25	35/5043 (0.7%)
1	E	0.64	1/3724 (0.0%)	1.25	37/5043 (0.7%)
1	F	0.64	1/3724 (0.0%)	1.25	33/5043 (0.7%)
1	G	0.64	1/3724 (0.0%)	1.25	33/5043 (0.7%)
1	H	0.64	1/3724 (0.0%)	1.25	37/5043 (0.7%)
1	I	0.64	1/3724 (0.0%)	1.25	35/5043 (0.7%)
1	J	0.64	1/3724 (0.0%)	1.25	35/5043 (0.7%)
1	K	0.64	1/3724 (0.0%)	1.25	33/5043 (0.7%)
1	L	0.64	1/3724 (0.0%)	1.25	33/5043 (0.7%)
All	All	0.64	12/44688 (0.0%)	1.25	414/60516 (0.7%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	54	ILE	CA-C	5.20	1.57	1.52
1	D	54	ILE	CA-C	5.19	1.57	1.52
1	G	54	ILE	CA-C	5.17	1.57	1.52
1	H	54	ILE	CA-C	5.17	1.57	1.52
1	K	54	ILE	CA-C	5.16	1.57	1.52

The worst 5 of 414 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	213	VAL	N-CA-C	9.11	119.91	110.62
1	H	213	VAL	N-CA-C	9.08	119.88	110.62
1	E	213	VAL	N-CA-C	9.07	119.87	110.62
1	A	213	VAL	N-CA-C	9.07	119.87	110.62
1	D	213	VAL	N-CA-C	9.07	119.87	110.62

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	3637	0	3542	186	0
1	B	3637	0	3543	187	0
1	C	3637	0	3543	189	0
1	D	3637	0	3542	180	0
1	E	3637	0	3543	177	0
1	F	3637	0	3543	175	0
1	G	3637	0	3542	182	0
1	H	3637	0	3543	185	0
1	I	3637	0	3542	190	0
1	J	3637	0	3543	194	0
1	K	3637	0	3543	188	0
1	L	3637	0	3543	181	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
3	A	27	0	10	4	0
3	B	27	0	10	4	0
3	C	27	0	10	4	0
3	D	27	0	10	4	0
3	E	27	0	10	4	0
3	F	27	0	10	4	0
3	G	27	0	10	4	0
3	H	27	0	10	4	0
3	I	27	0	10	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	27	0	10	4	0
3	K	27	0	10	4	0
3	L	27	0	10	4	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
4	G	2	0	0	0	0
4	H	2	0	0	0	0
4	I	2	0	0	0	0
4	J	2	0	0	0	0
4	K	2	0	0	0	0
4	L	2	0	0	0	0
5	A	8	0	14	28	0
5	B	8	0	14	33	0
5	C	8	0	14	32	0
5	D	8	0	14	33	0
5	E	8	0	14	28	0
5	F	8	0	14	33	0
5	G	8	0	14	30	0
5	H	8	0	14	32	0
5	I	8	0	14	34	0
5	J	8	0	14	33	0
5	K	8	0	14	32	0
5	L	8	0	14	31	0
6	A	120	0	0	7	0
6	B	121	0	0	6	0
6	C	119	0	0	5	0
6	D	122	0	0	6	0
6	E	122	0	0	7	0
6	F	121	0	0	5	0
6	G	122	0	0	6	0
6	H	121	0	0	5	0
6	I	122	0	0	6	0
6	J	120	0	0	6	0
6	K	123	0	0	6	0
6	L	119	0	0	6	0
All	All	45564	0	42800	2078	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 24.

The worst 5 of 2078 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)
3:K:1481:ADP:N9	3:K:1481:ADP:C1'	1.71	1.54
3:I:1479:ADP:N9	3:I:1479:ADP:C1'	1.71	1.54
3:B:1472:ADP:N9	3:B:1472:ADP:C1'	1.71	1.52
3:F:1476:ADP:N9	3:F:1476:ADP:C1'	1.71	1.52
3:E:1475:ADP:N9	3:E:1475:ADP:C1'	1.71	1.51

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	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	B	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	C	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	D	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	E	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	F	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	G	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	H	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	I	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	J	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	K	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
1	L	466/468 (100%)	429 (92%)	28 (6%)	9 (2%)	6	15
All	All	5592/5616 (100%)	5148 (92%)	336 (6%)	108 (2%)	6	15

5 of 108 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	SER
1	A	62	GLU
1	A	180	PHE
1	A	399	LEU
1	A	400	PRO

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	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	B	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	C	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	D	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	E	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	F	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	G	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	H	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	I	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	J	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	K	384/384 (100%)	339 (88%)	45 (12%)	5	12
1	L	384/384 (100%)	339 (88%)	45 (12%)	5	12
All	All	4608/4608 (100%)	4068 (88%)	540 (12%)	5	12

5 of 540 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	102	ARG
1	K	323	VAL
1	K	96	THR
1	L	290	LEU
1	E	115	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 144 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	338	ASN
1	L	458	HIS
1	J	458	HIS
1	K	409	GLN
1	E	10	ASN

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 72 ligands modelled in this entry, 48 are monoatomic - leaving 24 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	$\# Z > 2$
5	MPD	L	1494	-	7,7,7	1.17	0	9,10,10	0.73	0
3	ADP	I	1479	-	28,29,29	3.43	12 (42%)	43,45,45	3.02	16 (37%)
3	ADP	G	1477	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
5	MPD	G	1489	-	7,7,7	1.17	0	9,10,10	0.72	0
3	ADP	B	1472	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
3	ADP	J	1480	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	MPD	C	1485	-	7,7,7	1.18	0	9,10,10	0.72	0
3	ADP	C	1473	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
5	MPD	A	1483	-	7,7,7	1.17	0	9,10,10	0.73	0
3	ADP	E	1475	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
5	MPD	H	1490	-	7,7,7	1.18	0	9,10,10	0.72	0
5	MPD	K	1493	-	7,7,7	1.17	0	9,10,10	0.72	0
3	ADP	L	1482	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
3	ADP	D	1474	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
5	MPD	J	1492	-	7,7,7	1.17	0	9,10,10	0.72	0
3	ADP	H	1478	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
5	MPD	F	1488	-	7,7,7	1.18	0	9,10,10	0.73	0
5	MPD	D	1486	-	7,7,7	1.17	0	9,10,10	0.72	0
5	MPD	I	1491	-	7,7,7	1.17	0	9,10,10	0.72	0
3	ADP	A	1471	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
3	ADP	F	1476	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
3	ADP	K	1481	-	28,29,29	3.42	12 (42%)	43,45,45	3.02	16 (37%)
5	MPD	B	1484	-	7,7,7	1.17	0	9,10,10	0.72	0
5	MPD	E	1487	-	7,7,7	1.16	0	9,10,10	0.73	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MPD	L	1494	-	-	3/5/5/5	-
3	ADP	I	1479	-	-	7/16/32/32	0/3/3/3
3	ADP	G	1477	-	-	7/16/32/32	0/3/3/3
5	MPD	G	1489	-	-	3/5/5/5	-
3	ADP	B	1472	-	-	7/16/32/32	0/3/3/3
3	ADP	J	1480	-	-	7/16/32/32	0/3/3/3
5	MPD	C	1485	-	-	3/5/5/5	-
3	ADP	C	1473	-	-	7/16/32/32	0/3/3/3
5	MPD	A	1483	-	-	3/5/5/5	-
3	ADP	E	1475	-	-	7/16/32/32	0/3/3/3
5	MPD	H	1490	-	-	3/5/5/5	-
5	MPD	K	1493	-	-	3/5/5/5	-
3	ADP	L	1482	-	-	7/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	D	1474	-	-	7/16/32/32	0/3/3/3
5	MPD	J	1492	-	-	3/5/5/5	-
3	ADP	H	1478	-	-	7/16/32/32	0/3/3/3
5	MPD	F	1488	-	-	3/5/5/5	-
5	MPD	D	1486	-	-	3/5/5/5	-
5	MPD	I	1491	-	-	3/5/5/5	-
3	ADP	A	1471	-	-	7/16/32/32	0/3/3/3
3	ADP	F	1476	-	-	7/16/32/32	0/3/3/3
3	ADP	K	1481	-	-	7/16/32/32	0/3/3/3
5	MPD	B	1484	-	-	3/5/5/5	-
5	MPD	E	1487	-	-	3/5/5/5	-

The worst 5 of 144 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	1479	ADP	C1'-N9	9.00	1.71	1.46
3	L	1482	ADP	C1'-N9	8.99	1.71	1.46
3	H	1478	ADP	C1'-N9	8.98	1.71	1.46
3	D	1474	ADP	C1'-N9	8.98	1.71	1.46
3	C	1473	ADP	C1'-N9	8.98	1.71	1.46

The worst 5 of 192 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	1481	ADP	O5'-C5'-C4'	8.10	136.58	108.99
3	J	1480	ADP	O5'-C5'-C4'	8.10	136.56	108.99
3	E	1475	ADP	O5'-C5'-C4'	8.10	136.56	108.99
3	D	1474	ADP	O5'-C5'-C4'	8.10	136.56	108.99
3	L	1482	ADP	O5'-C5'-C4'	8.10	136.56	108.99

There are no chirality outliers.

5 of 120 torsion outliers are listed below:

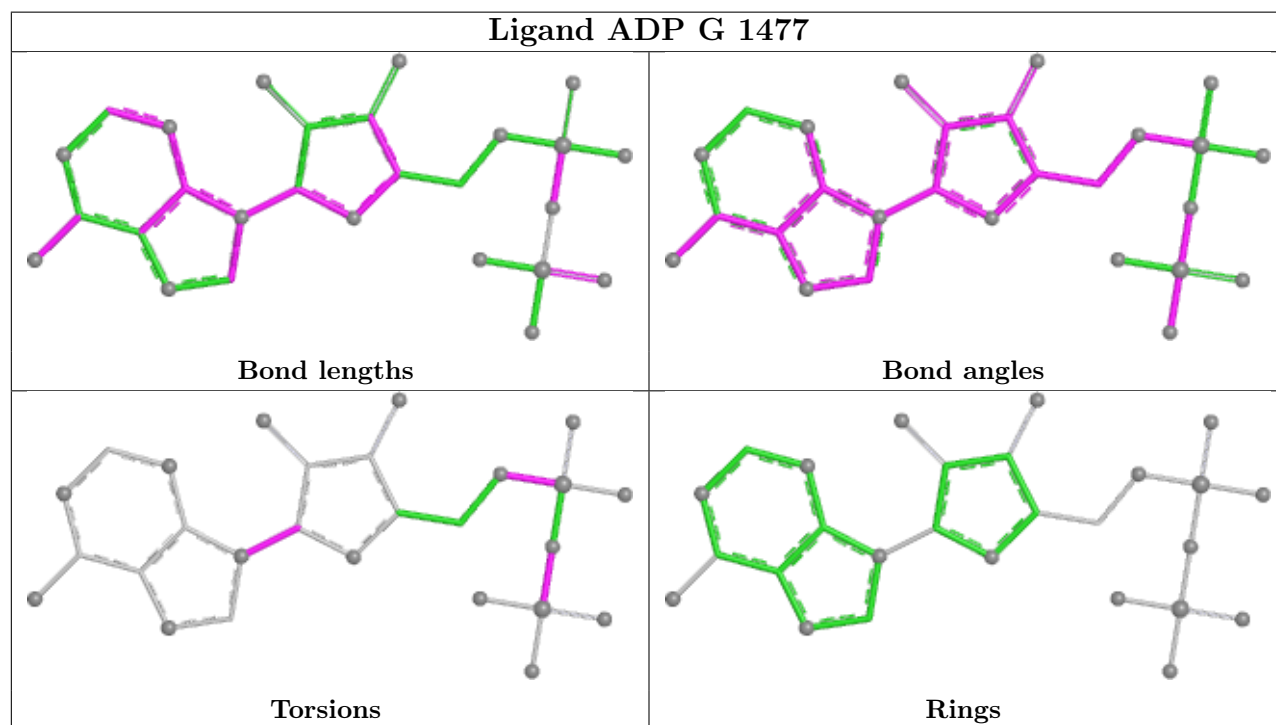
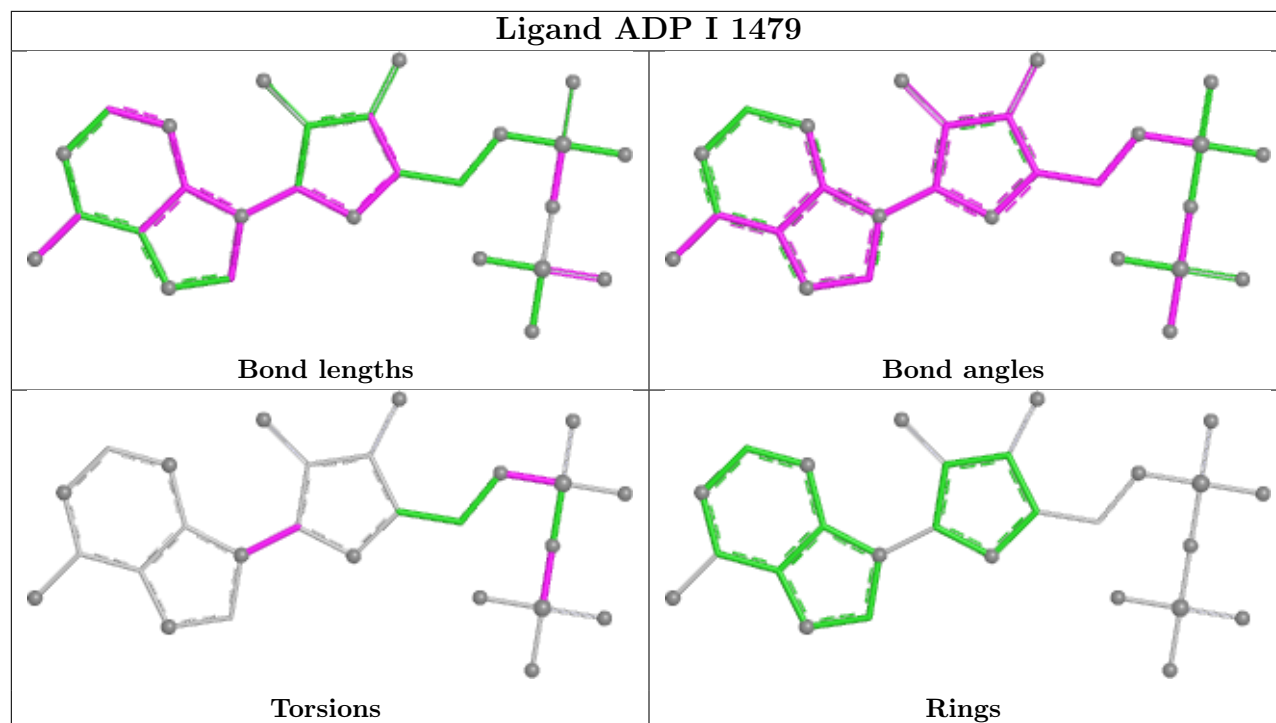
Mol	Chain	Res	Type	Atoms
3	A	1471	ADP	PA-O3A-PB-O3B
3	B	1472	ADP	PA-O3A-PB-O3B
3	C	1473	ADP	PA-O3A-PB-O3B
3	D	1474	ADP	PA-O3A-PB-O3B
3	E	1475	ADP	PA-O3A-PB-O3B

There are no ring outliers.

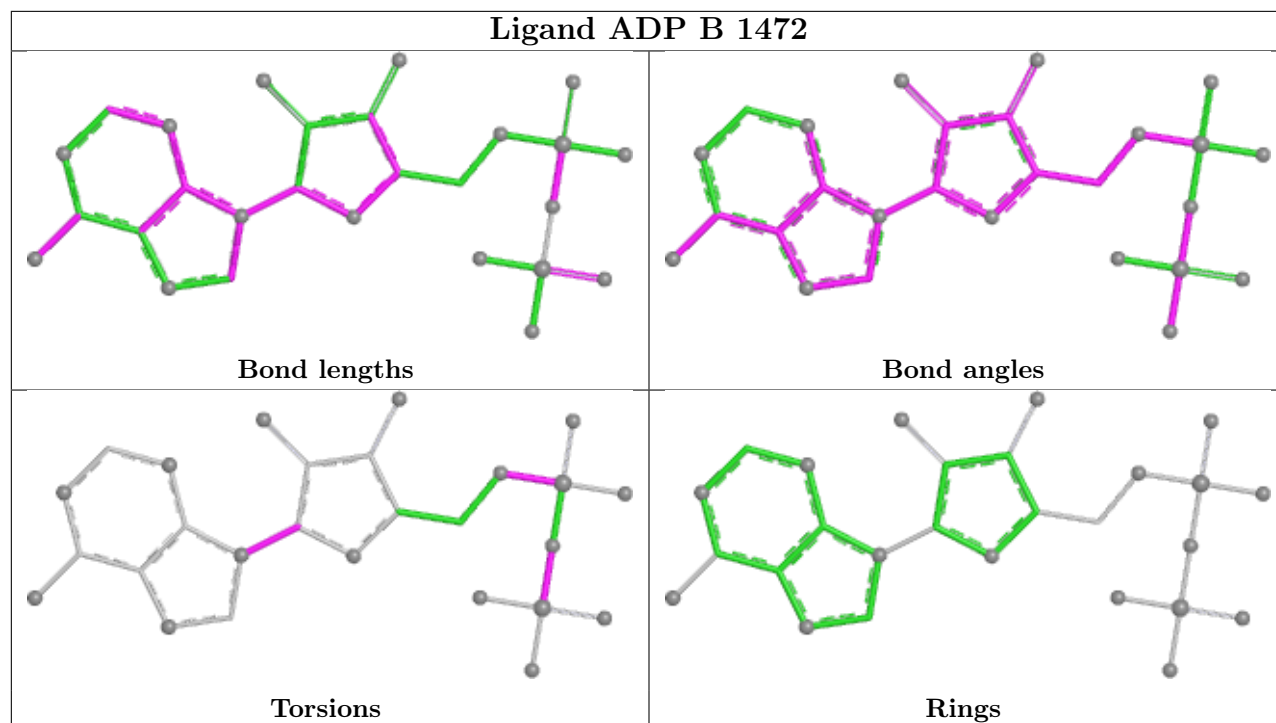
24 monomers are involved in 426 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	1494	MPD	31	0
3	I	1479	ADP	3	0
3	G	1477	ADP	4	0
5	G	1489	MPD	30	0
3	B	1472	ADP	4	0
3	J	1480	ADP	4	0
5	C	1485	MPD	32	0
3	C	1473	ADP	4	0
5	A	1483	MPD	28	0
3	E	1475	ADP	4	0
5	H	1490	MPD	32	0
5	K	1493	MPD	32	0
3	L	1482	ADP	4	0
3	D	1474	ADP	4	0
5	J	1492	MPD	33	0
3	H	1478	ADP	4	0
5	F	1488	MPD	33	0
5	D	1486	MPD	33	0
5	I	1491	MPD	34	0
3	A	1471	ADP	4	0
3	F	1476	ADP	4	0
3	K	1481	ADP	4	0
5	B	1484	MPD	33	0
5	E	1487	MPD	28	0

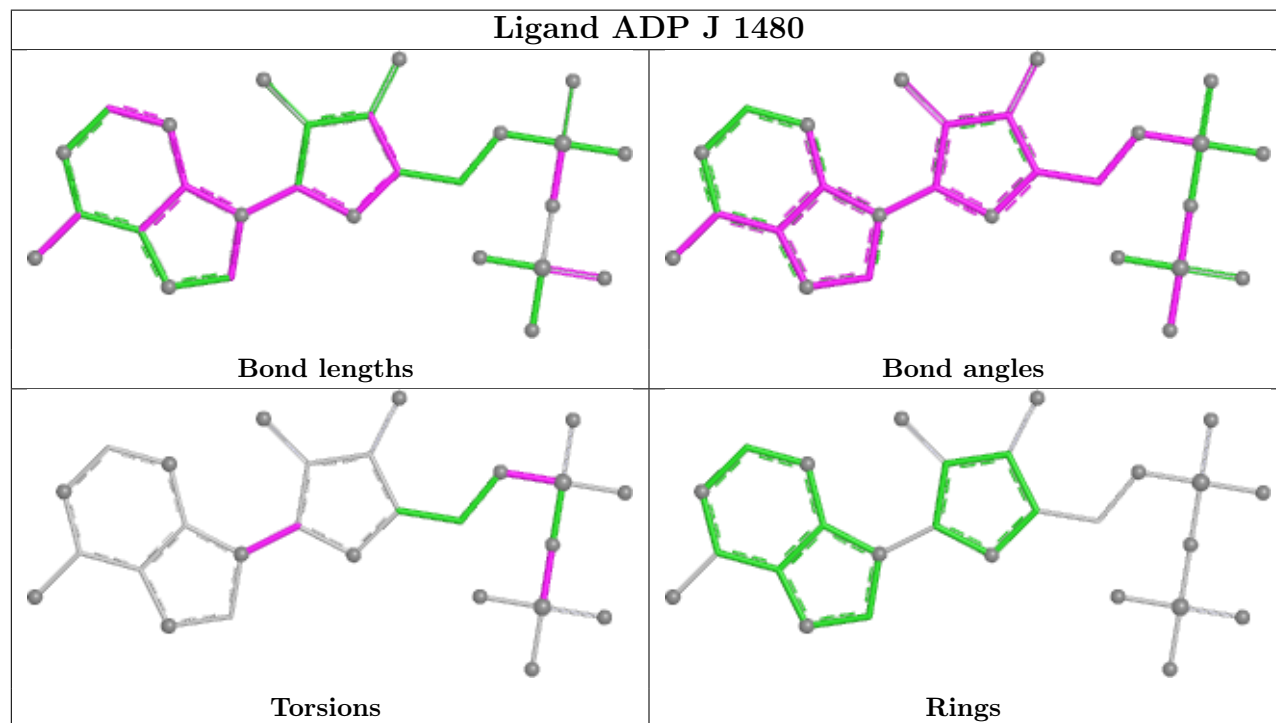
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



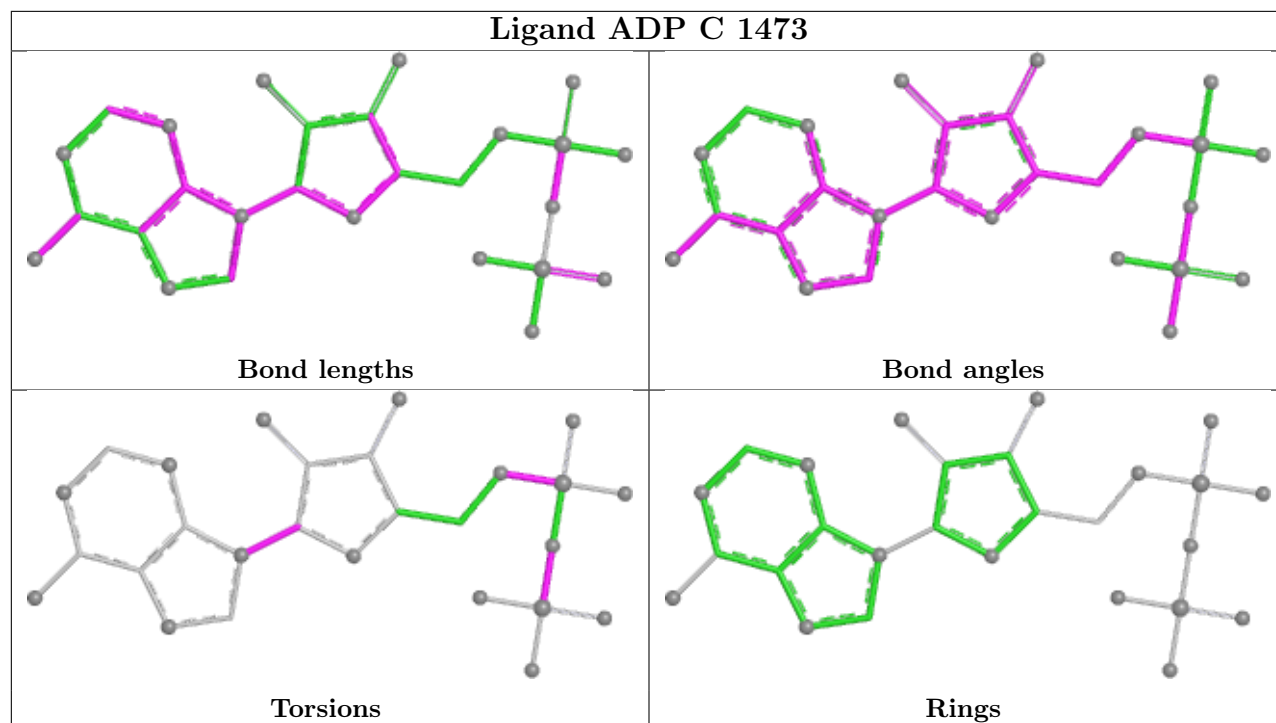
Ligand ADP B 1472



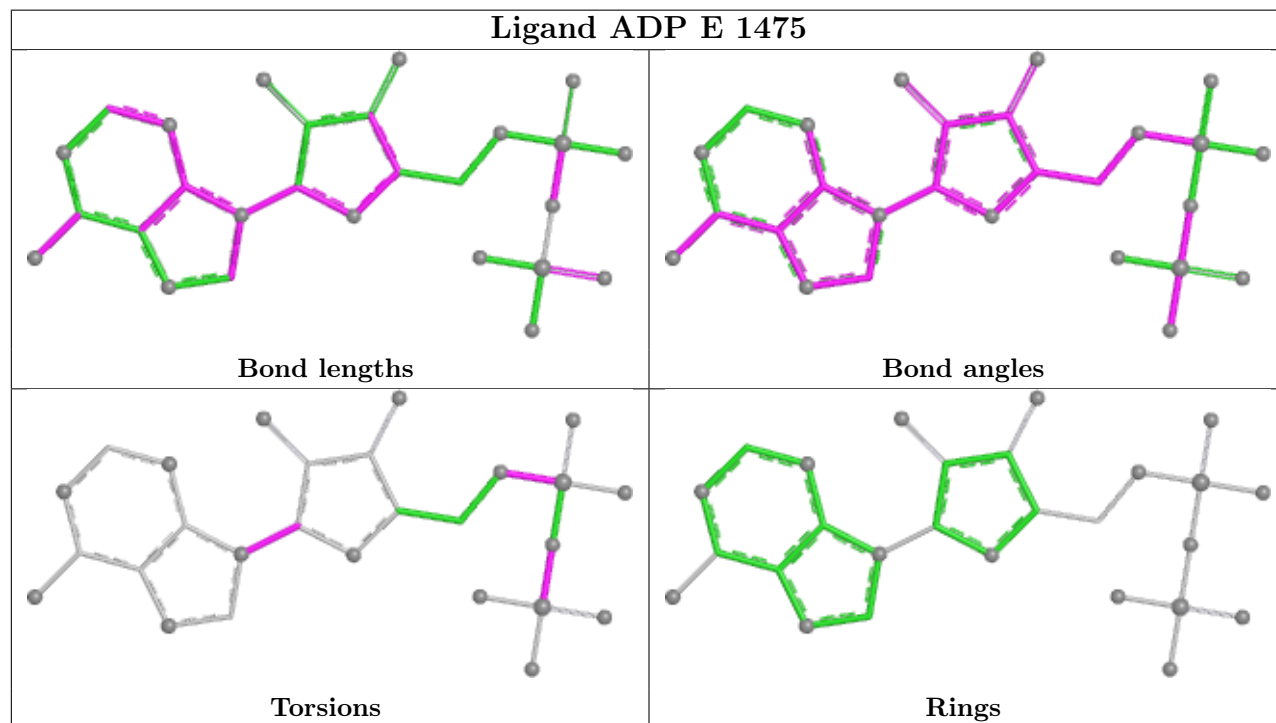
Ligand ADP J 1480

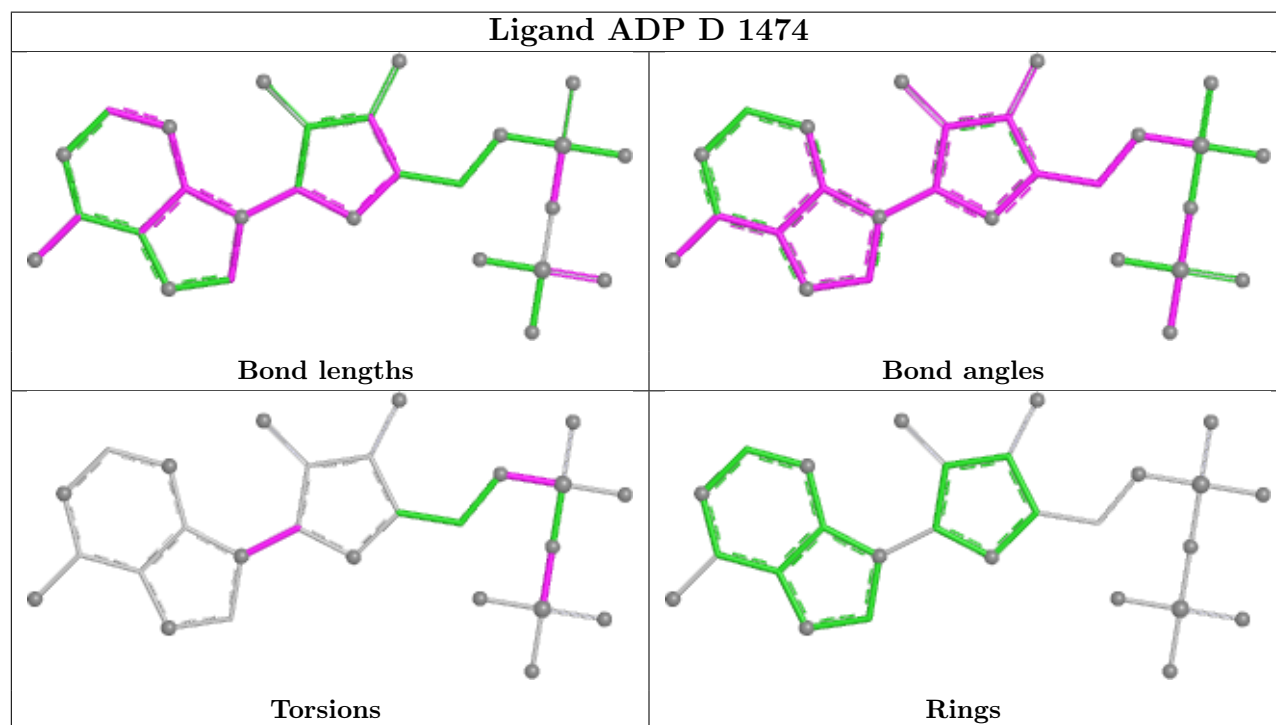
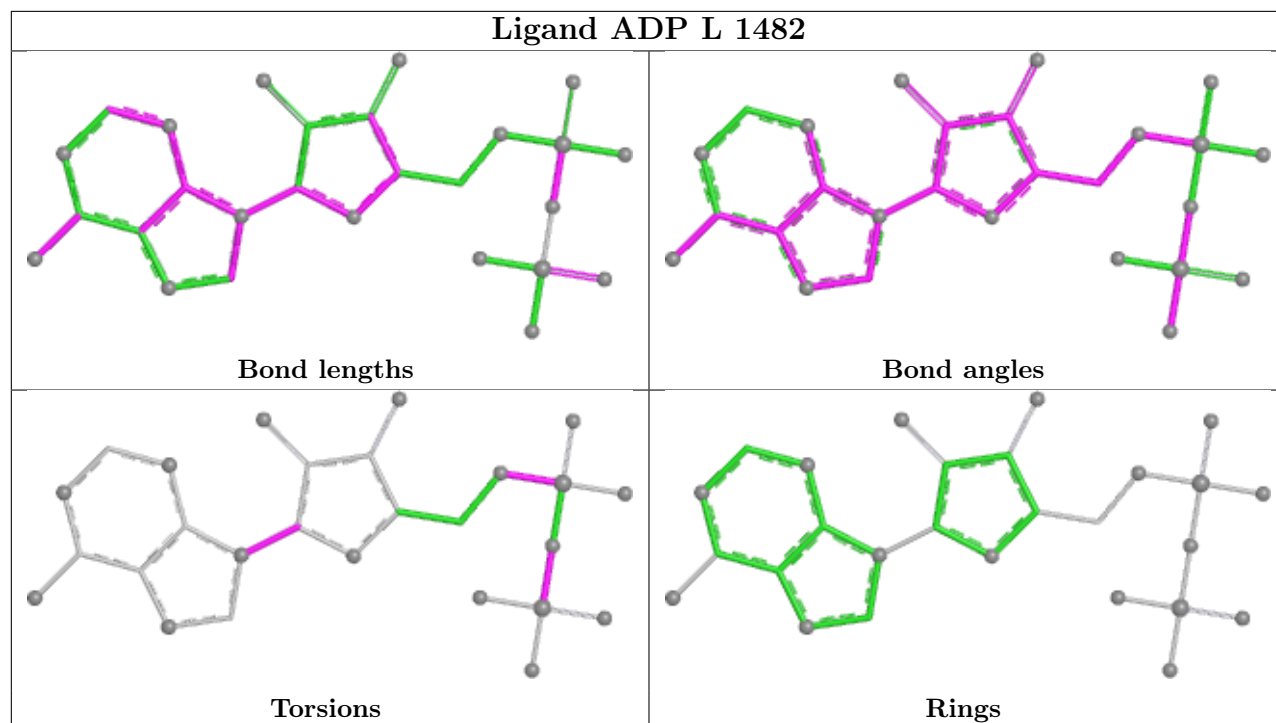


Ligand ADP C 1473

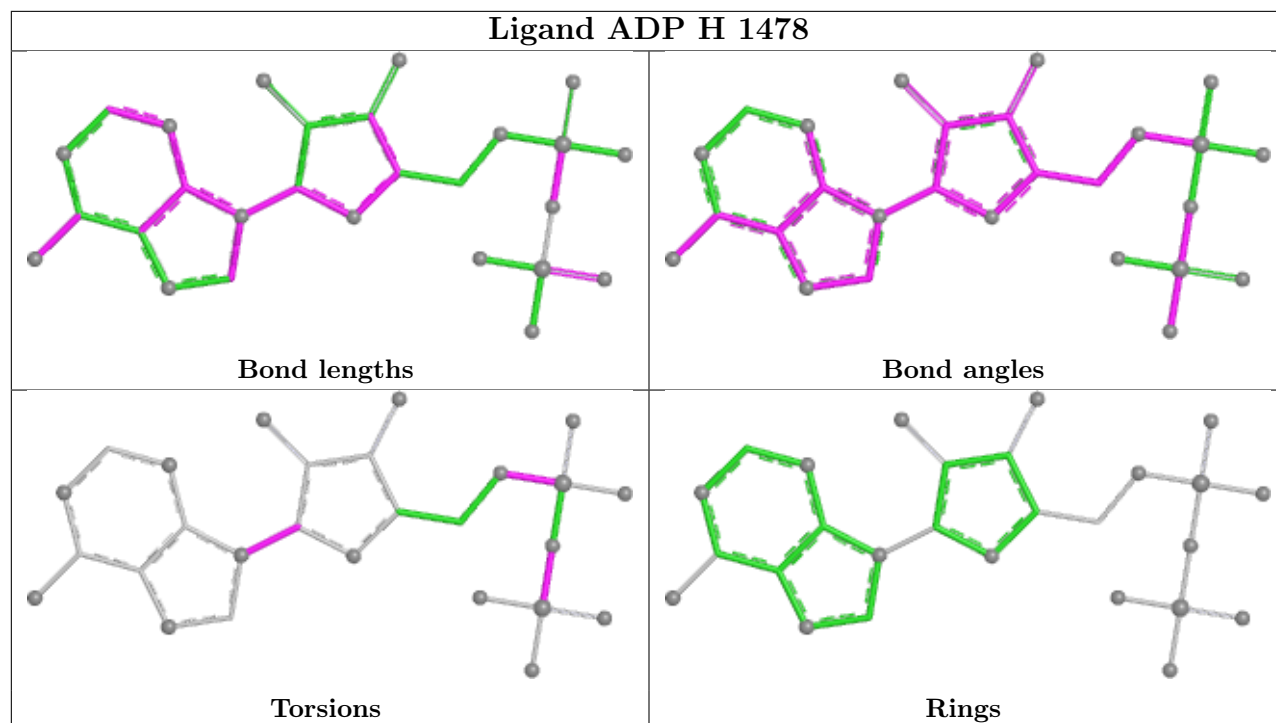


Ligand ADP E 1475

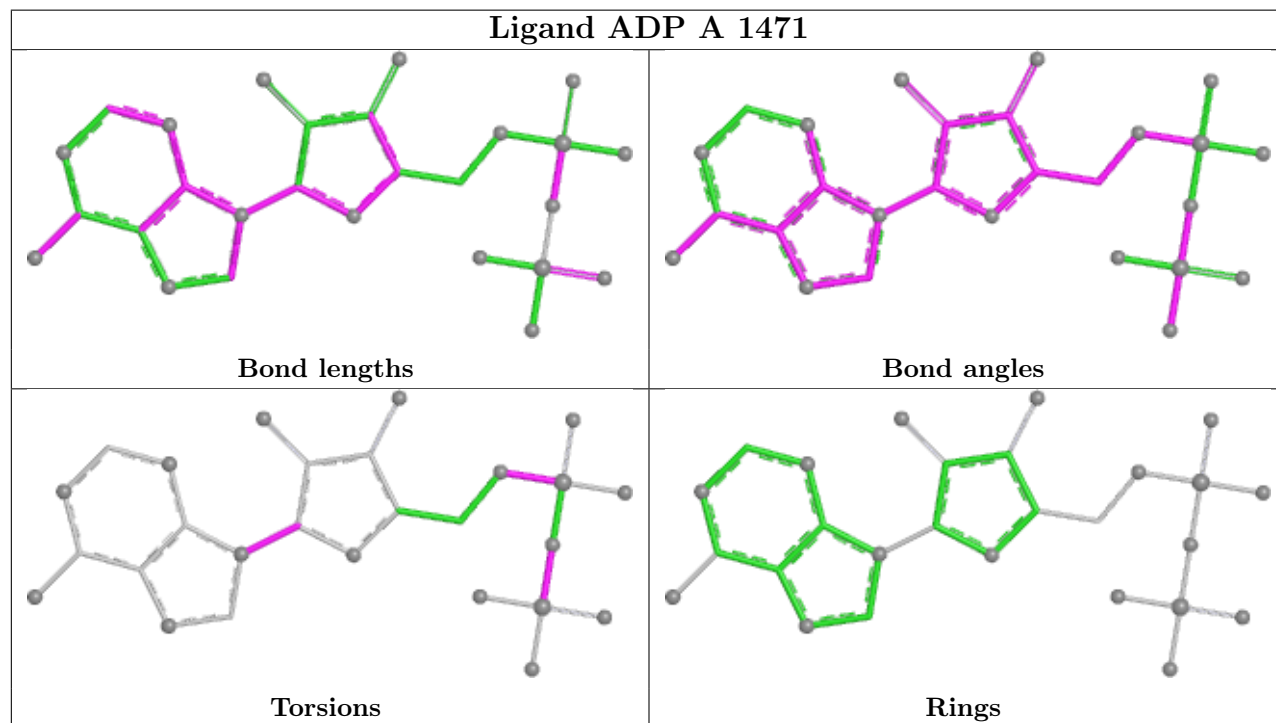


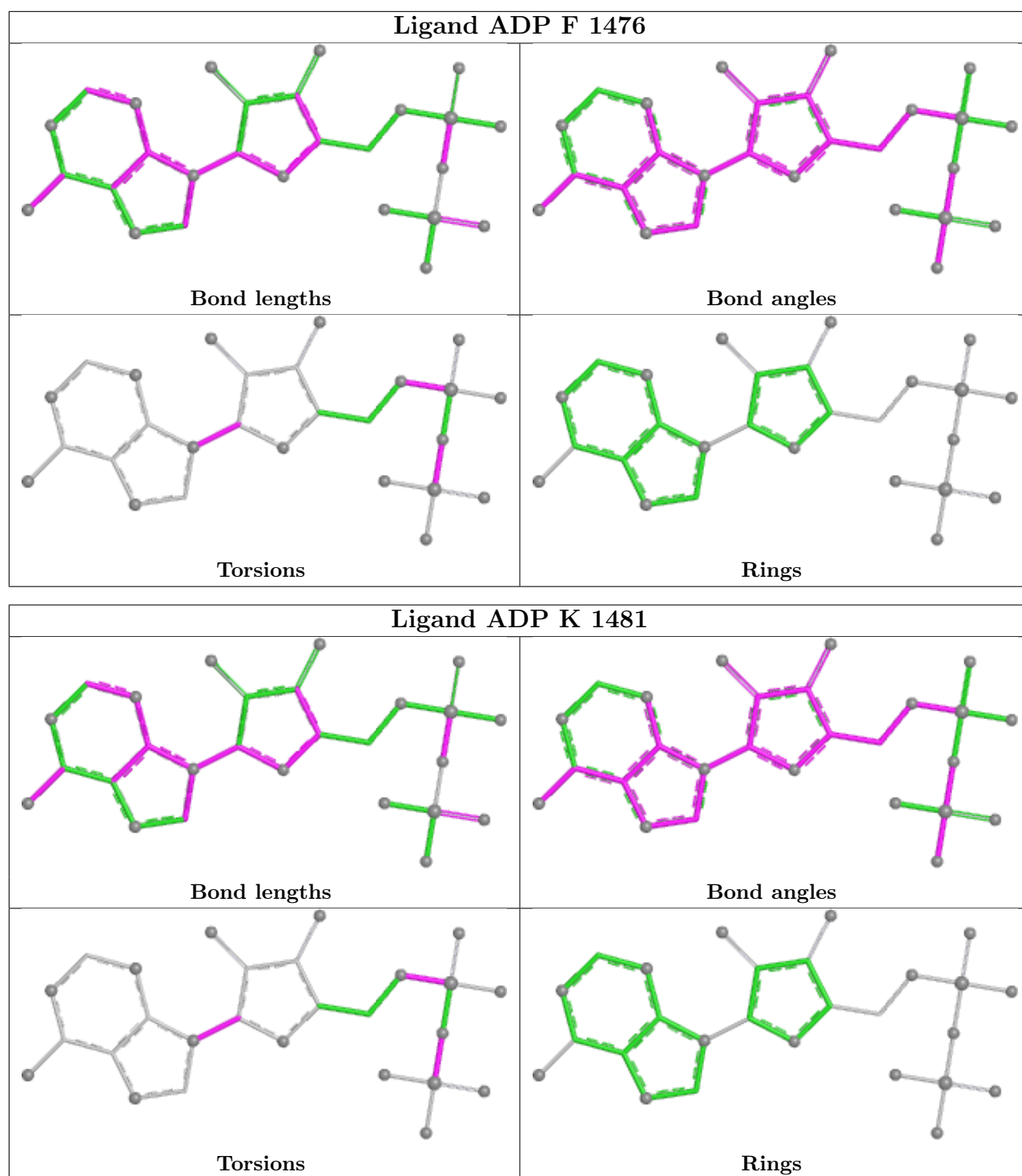


Ligand ADP H 1478



Ligand ADP A 1471





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	468/468 (100%)	0.90	80 (17%) 4 3	12, 39, 82, 100	29 (6%)
1	B	468/468 (100%)	0.63	39 (8%) 17 14	12, 39, 82, 100	29 (6%)
1	C	468/468 (100%)	0.51	41 (8%) 15 13	12, 39, 82, 100	29 (6%)
1	D	468/468 (100%)	0.34	28 (5%) 27 24	12, 39, 82, 100	29 (6%)
1	E	468/468 (100%)	0.45	34 (7%) 21 18	12, 39, 82, 100	29 (6%)
1	F	468/468 (100%)	0.58	33 (7%) 22 18	12, 39, 82, 100	29 (6%)
1	G	468/468 (100%)	0.48	34 (7%) 21 18	12, 39, 82, 100	29 (6%)
1	H	468/468 (100%)	0.57	49 (10%) 11 9	12, 39, 82, 100	29 (6%)
1	I	468/468 (100%)	0.57	52 (11%) 10 8	12, 39, 82, 100	29 (6%)
1	J	468/468 (100%)	0.53	45 (9%) 13 11	12, 39, 82, 100	29 (6%)
1	K	468/468 (100%)	0.53	44 (9%) 14 12	12, 39, 82, 100	29 (6%)
1	L	468/468 (100%)	0.65	54 (11%) 9 8	12, 39, 82, 100	29 (6%)
All	All	5616/5616 (100%)	0.56	533 (9%) 14 11	12, 39, 82, 100	348 (6%)

The worst 5 of 533 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	179	TYR	9.0
1	K	50	ASP	8.7
1	G	50	ASP	8.6
1	I	51	GLY	8.1
1	B	53	SER	7.9

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($\text{\AA}^2$)	Q<0.9
3	ADP	F	1476	27/27	0.64	0.20	20,78,100,100	27
3	ADP	I	1479	27/27	0.66	0.23	20,78,100,100	27
3	ADP	L	1482	27/27	0.71	0.23	20,78,100,100	27
3	ADP	B	1472	27/27	0.72	0.21	20,78,100,100	27
3	ADP	C	1473	27/27	0.73	0.20	20,78,100,100	27
3	ADP	A	1471	27/27	0.74	0.20	20,78,100,100	27
3	ADP	E	1475	27/27	0.75	0.17	20,78,100,100	27
3	ADP	D	1474	27/27	0.75	0.23	20,78,100,100	27
4	TL	I	473	1/1	0.75	0.25	67,67,67,67	1
3	ADP	K	1481	27/27	0.76	0.22	20,78,100,100	27
4	TL	L	473	1/1	0.77	0.21	67,67,67,67	1
3	ADP	H	1478	27/27	0.78	0.21	20,78,100,100	27
5	MPD	B	1484	8/8	0.81	0.32	16,43,64,74	8
4	TL	J	474	1/1	0.82	0.10	75,75,75,75	1
3	ADP	G	1477	27/27	0.83	0.20	20,78,100,100	27
3	ADP	J	1480	27/27	0.83	0.23	20,78,100,100	27
4	TL	A	473	1/1	0.84	0.19	67,67,67,67	1
4	TL	K	473	1/1	0.84	0.12	67,67,67,67	1
4	TL	F	473	1/1	0.85	0.14	67,67,67,67	1
5	MPD	D	1486	8/8	0.86	0.32	16,43,64,74	8
5	MPD	I	1491	8/8	0.86	0.28	16,43,64,74	8
5	MPD	A	1483	8/8	0.87	0.32	16,43,64,74	8
4	TL	C	474	1/1	0.87	0.08	75,75,75,75	1
4	TL	H	473	1/1	0.88	0.18	67,67,67,67	1
5	MPD	C	1485	8/8	0.88	0.27	16,43,64,74	8
5	MPD	E	1487	8/8	0.90	0.25	16,43,64,74	8
5	MPD	H	1490	8/8	0.91	0.26	16,43,64,74	8
5	MPD	F	1488	8/8	0.91	0.23	16,43,64,74	8
4	TL	A	474	1/1	0.92	0.07	75,75,75,75	1
5	MPD	G	1489	8/8	0.92	0.29	16,43,64,74	8
5	MPD	J	1492	8/8	0.92	0.28	16,43,64,74	8
5	MPD	K	1493	8/8	0.92	0.23	16,43,64,74	8

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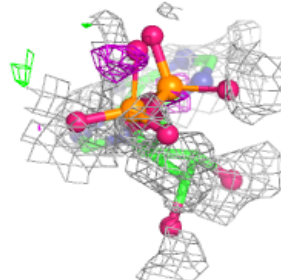
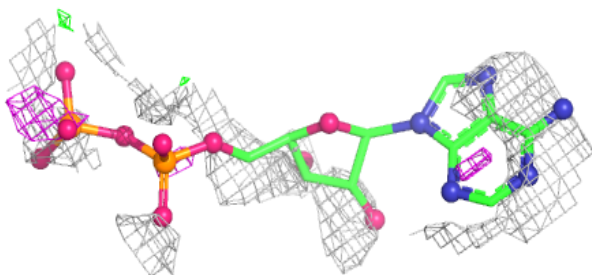
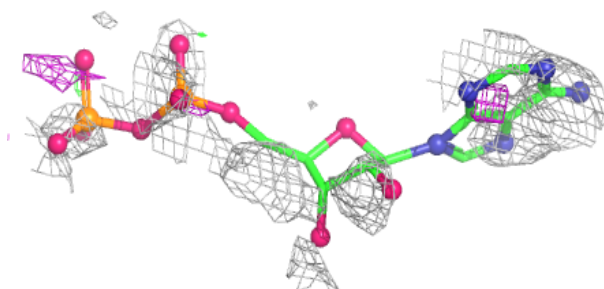
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	TL	E	473	1/1	0.93	0.09	67,67,67,67	1
5	MPD	L	1494	8/8	0.93	0.24	16,43,64,74	8
2	MN	F	470	1/1	0.94	0.08	41,41,41,41	0
4	TL	G	474	1/1	0.94	0.08	75,75,75,75	1
4	TL	D	473	1/1	0.94	0.07	67,67,67,67	1
4	TL	H	474	1/1	0.94	0.06	75,75,75,75	1
4	TL	B	473	1/1	0.94	0.08	67,67,67,67	1
4	TL	J	473	1/1	0.94	0.22	67,67,67,67	1
4	TL	E	474	1/1	0.94	0.07	75,75,75,75	1
4	TL	D	474	1/1	0.95	0.06	75,75,75,75	1
4	TL	B	474	1/1	0.95	0.06	75,75,75,75	1
2	MN	A	469	1/1	0.95	0.08	34,34,34,34	0
2	MN	B	469	1/1	0.95	0.06	34,34,34,34	0
4	TL	G	473	1/1	0.96	0.09	67,67,67,67	1
4	TL	I	474	1/1	0.96	0.07	75,75,75,75	1
2	MN	A	470	1/1	0.96	0.07	41,41,41,41	0
4	TL	L	474	1/1	0.96	0.07	75,75,75,75	1
2	MN	C	469	1/1	0.97	0.05	34,34,34,34	0
4	TL	F	474	1/1	0.97	0.06	75,75,75,75	1
4	TL	C	473	1/1	0.97	0.12	67,67,67,67	1
4	TL	K	474	1/1	0.97	0.05	75,75,75,75	1
2	MN	H	469	1/1	0.97	0.03	34,34,34,34	0
2	MN	I	470	1/1	0.97	0.06	41,41,41,41	0
2	MN	C	470	1/1	0.97	0.04	41,41,41,41	0
2	MN	D	470	1/1	0.97	0.04	41,41,41,41	0
2	MN	F	469	1/1	0.97	0.07	34,34,34,34	0
2	MN	E	469	1/1	0.98	0.04	34,34,34,34	0
2	MN	G	470	1/1	0.98	0.07	41,41,41,41	0
2	MN	E	470	1/1	0.98	0.03	41,41,41,41	0
2	MN	B	470	1/1	0.98	0.04	41,41,41,41	0
2	MN	J	469	1/1	0.98	0.07	34,34,34,34	0
2	MN	J	470	1/1	0.98	0.06	41,41,41,41	0
2	MN	K	469	1/1	0.98	0.05	34,34,34,34	0
2	MN	L	470	1/1	0.98	0.11	41,41,41,41	0
2	MN	G	469	1/1	0.99	0.03	34,34,34,34	0
2	MN	H	470	1/1	0.99	0.04	41,41,41,41	0
2	MN	I	469	1/1	0.99	0.02	34,34,34,34	0
2	MN	K	470	1/1	0.99	0.10	41,41,41,41	0
2	MN	L	469	1/1	0.99	0.04	34,34,34,34	0
2	MN	D	469	1/1	0.99	0.02	34,34,34,34	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.

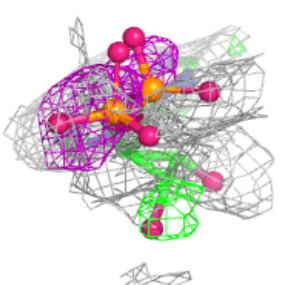
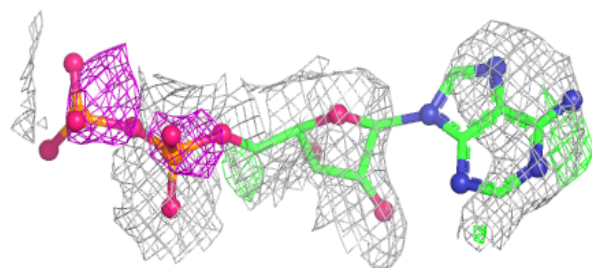
Electron density around ADP F 1476:

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



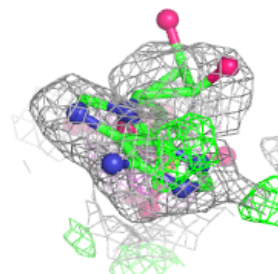
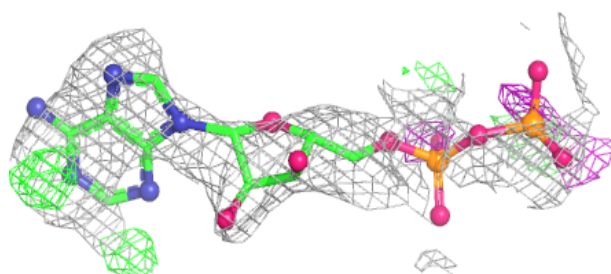
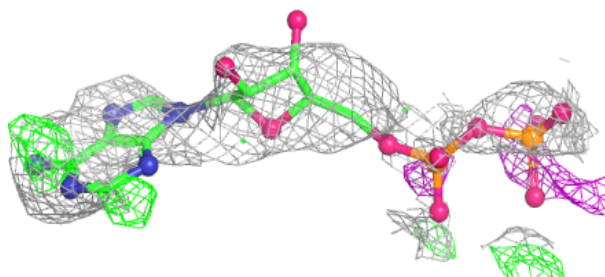
Electron density around ADP I 1479:

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

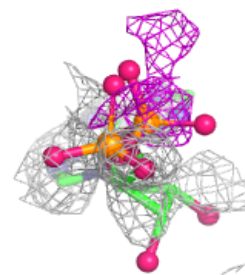
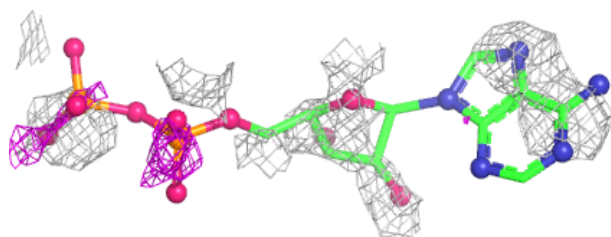
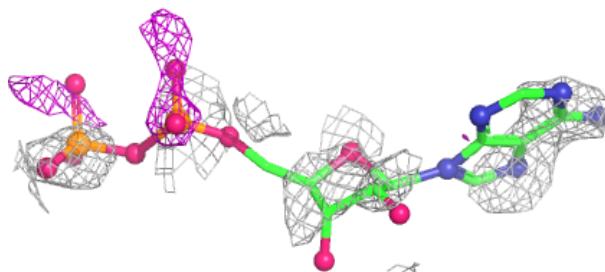


Electron density around ADP L 1482:

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

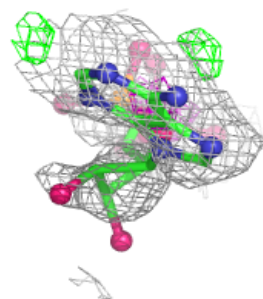
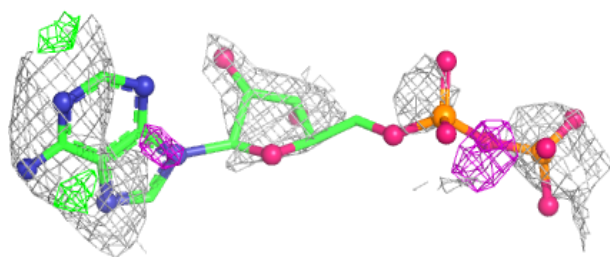
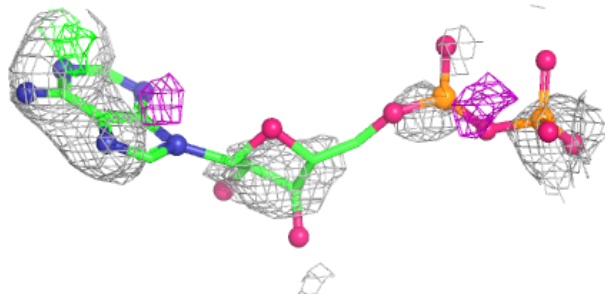
**Electron density around ADP B 1472:**

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

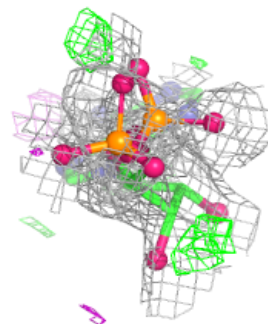
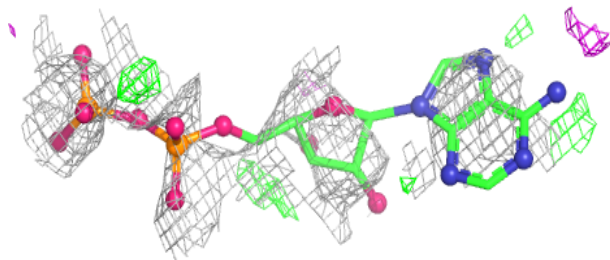
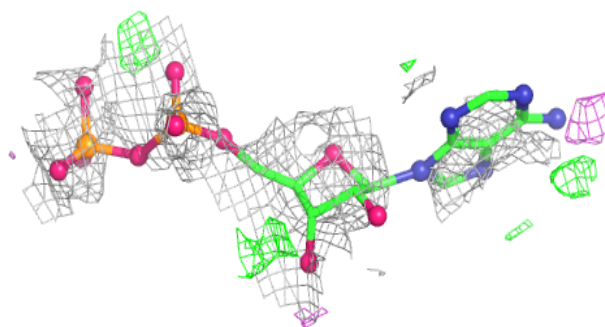


Electron density around ADP C 1473:

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

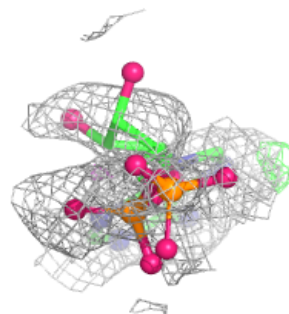
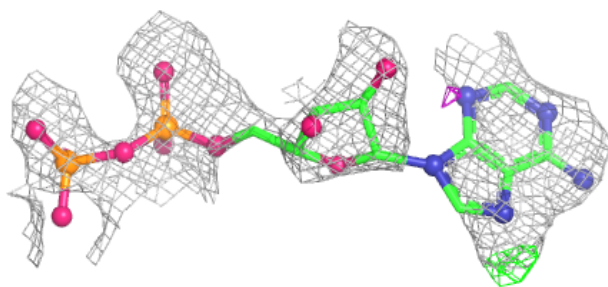
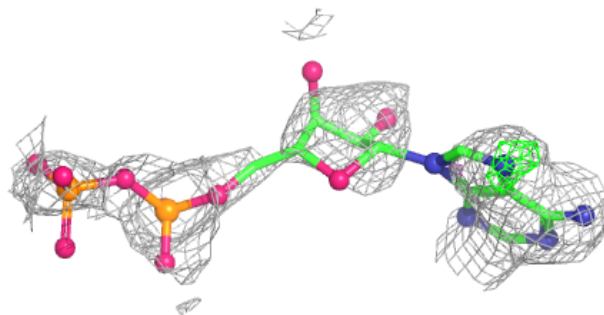
**Electron density around ADP A 1471:**

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

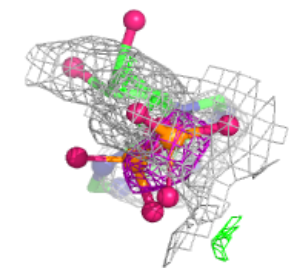
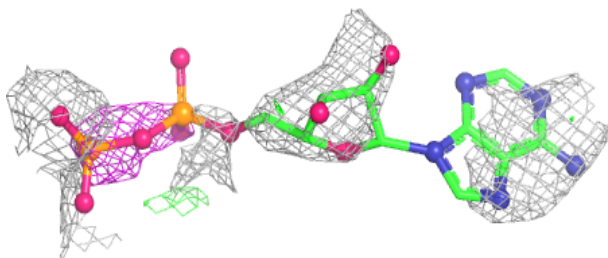
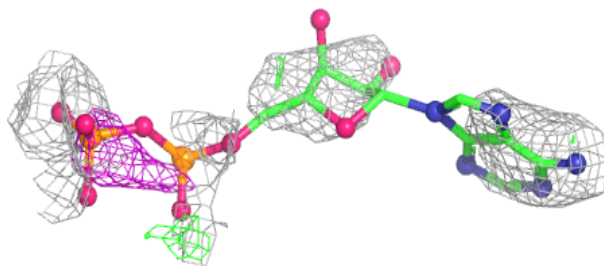


Electron density around ADP E 1475:

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

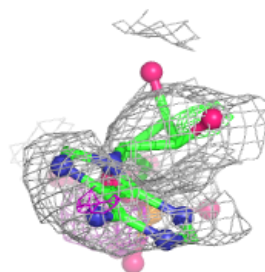
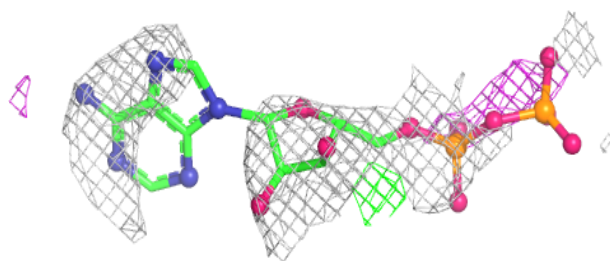
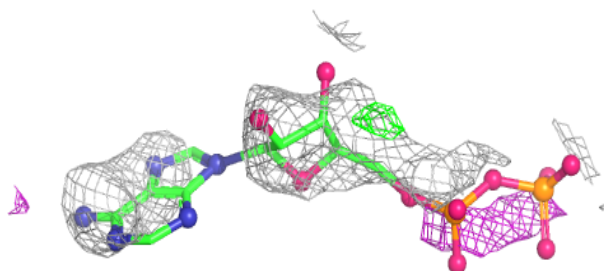
**Electron density around ADP D 1474:**

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

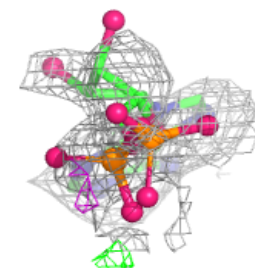
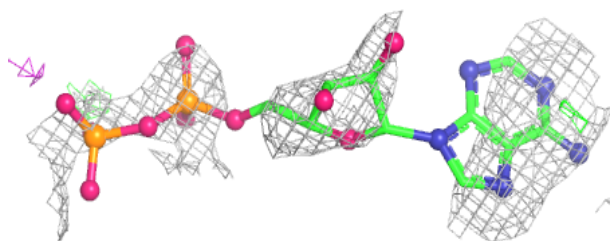
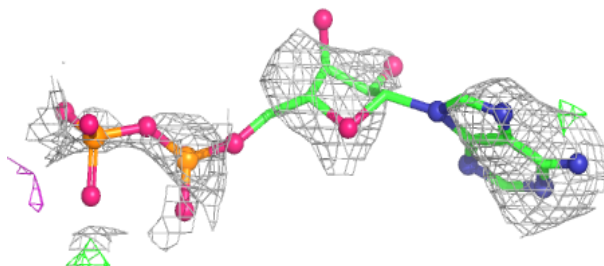


Electron density around ADP K 1481:

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

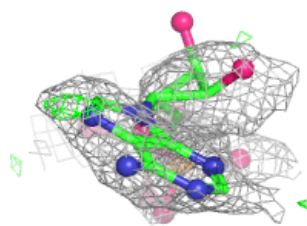
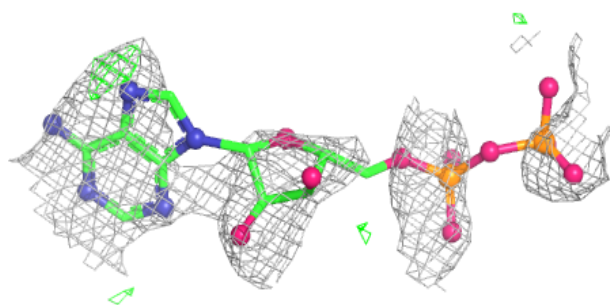
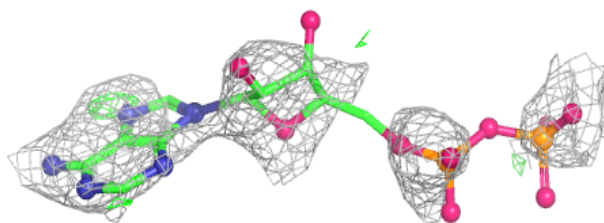
**Electron density around ADP H 1478:**

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

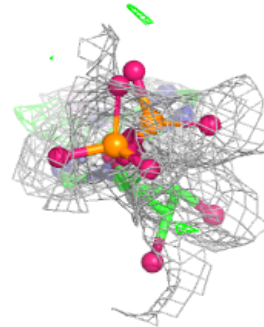
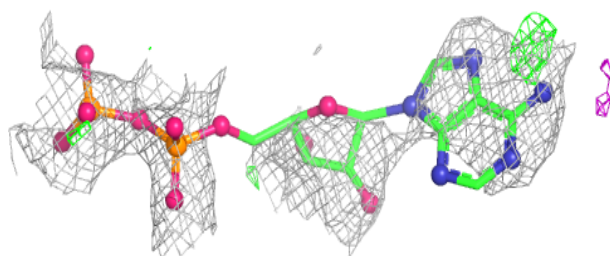
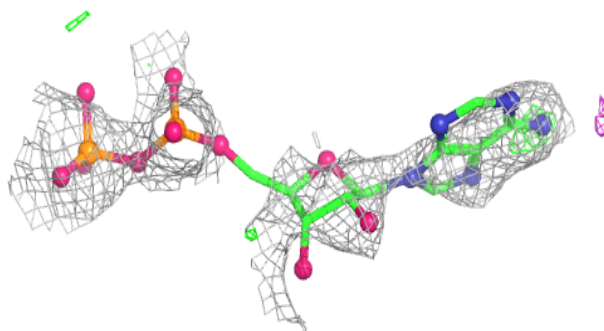


Electron density around ADP G 1477:

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

**Electron density around ADP J 1480:**

$2mF_o-DF_c$ (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.