



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 14, 2020 – 04:30 am BST

PDB ID : 1F52
Title : CRYSTAL STRUCTURE OF GLUTAMINE SYNTHETASE FROM
SALMONELLA TYPHIMURIUM CO-CRYSTALLIZED WITH ADP
Authors : Gill, H.S.; Pfluegl, G.M.U.; Eisenberg, D.
Deposited on : 2000-06-12
Resolution : 2.49 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

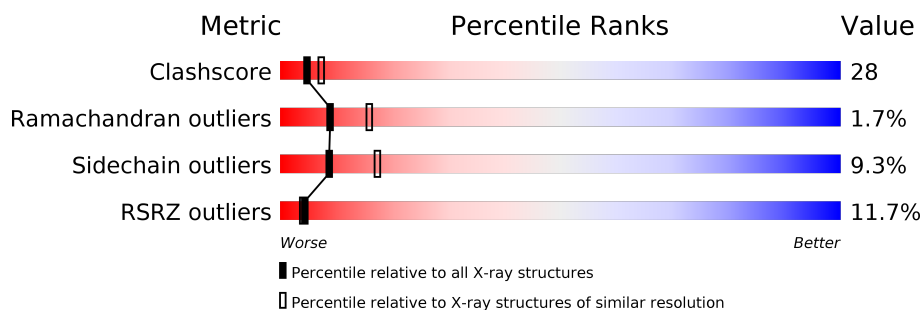
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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.



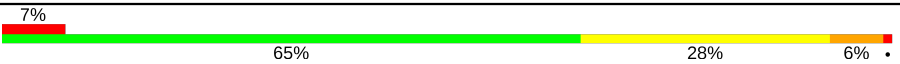


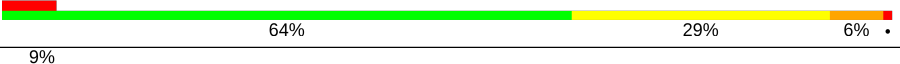

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 on 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	<div> <div>31%</div> <div>65% 28% 6%</div> </div>
1	B	468	<div> <div>15%</div> <div>65% 28% 6%</div> </div>
1	C	468	<div> <div>14%</div> <div>65% 28% 6%</div> </div>
1	D	468	<div> <div>10%</div> <div>66% 27% 6%</div> </div>
1	E	468	<div> <div>15%</div> <div>65% 28% 6%</div> </div>
1	F	468	<div> <div>10%</div> <div>63% 29% 6%</div> </div>
1	G	468	<div> <div>9%</div> <div>65% 28% 6%</div> </div>

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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
3	ADP	A	4471	-	-	-	X
3	ADP	B	4472	-	-	-	X
3	ADP	F	4476	-	-	-	X
3	ADP	I	4479	-	-	-	X
3	ADP	K	4481	-	-	-	X
3	ADP	L	4482	-	-	-	X
4	MPD	A	5472	-	-	X	X
4	MPD	A	5481	-	-	X	-
4	MPD	B	5471	-	-	X	X
4	MPD	B	5474	-	-	X	X
4	MPD	C	5473	-	-	X	-
4	MPD	C	5476	-	-	X	X
4	MPD	D	5475	-	-	X	-
4	MPD	D	5478	-	-	X	X
4	MPD	E	5477	-	-	X	-
4	MPD	E	5480	-	-	X	X
4	MPD	F	5479	-	-	X	-
4	MPD	F	5482	-	-	X	-
4	MPD	G	5484	-	-	X	X
4	MPD	G	5485	-	-	X	-
4	MPD	H	5486	-	-	X	X
4	MPD	H	5487	-	-	X	-
4	MPD	I	5488	-	-	X	X
4	MPD	I	5489	-	-	X	-
4	MPD	J	5490	-	-	X	X
4	MPD	J	5491	-	-	X	-
4	MPD	K	5492	-	-	X	X
4	MPD	K	5493	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MPD	L	5483	-	-	X	-
4	MPD	L	5494	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 47688 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 GLUTAMINE SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	B	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	C	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	D	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	E	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	F	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	G	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	H	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	I	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	J	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	K	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			
1	L	468	Total	C	N	O	S	8	0	0
			3637	2301	624	692	20			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

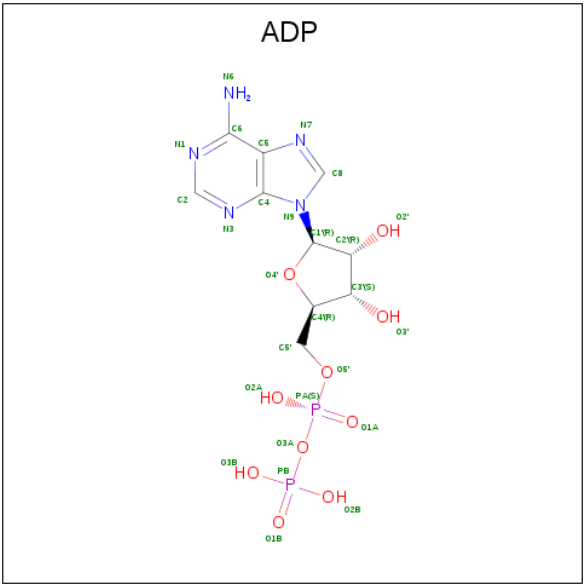
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	2	Total	Mn	0	0
			2	2		
2	J	2	Total	Mn	0	0
			2	2		

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

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



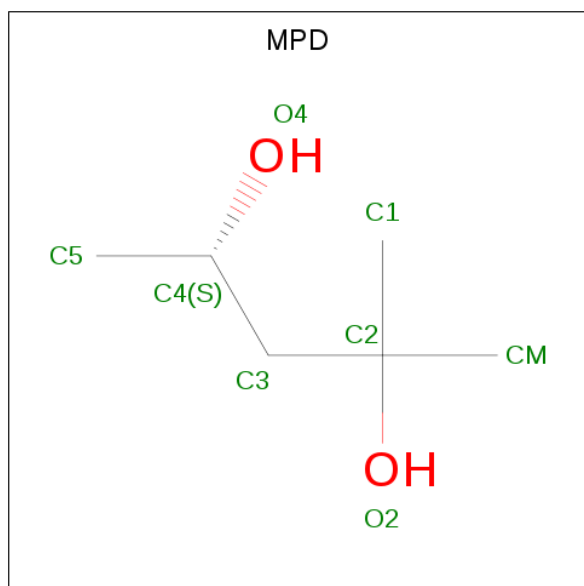
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O P	0	0
			27	10	5	10 2		

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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 (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		
4	A	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		
4	C	1	Total	C	O	0	0
			8	6	2		
4	C	1	Total	C	O	0	0
			8	6	2		
4	D	1	Total	C	O	0	0
			8	6	2		
4	D	1	Total	C	O	0	0
			8	6	2		
4	E	1	Total	C	O	0	0
			8	6	2		
4	E	1	Total	C	O	0	0
			8	6	2		
4	F	1	Total	C	O	0	0
			8	6	2		
4	F	1	Total	C	O	0	0
			8	6	2		
4	G	1	Total	C	O	0	0
			8	6	2		
4	G	1	Total	C	O	0	0
			8	6	2		
4	H	1	Total	C	O	0	0
			8	6	2		
4	H	1	Total	C	O	0	0
			8	6	2		
4	I	1	Total	C	O	0	0
			8	6	2		
4	I	1	Total	C	O	0	0
			8	6	2		
4	J	1	Total	C	O	0	0
			8	6	2		
4	J	1	Total	C	O	0	0
			8	6	2		
4	K	1	Total	C	O	0	0
			8	6	2		
4	K	1	Total	C	O	0	0
			8	6	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	L	1	Total	C	O	0	0
			8	6	2		
4	L	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	294	Total	O		0	0
			294	294			
5	B	297	Total	O		0	0
			297	297			
5	C	293	Total	O		0	0
			293	293			
5	D	295	Total	O		0	0
			295	295			
5	E	294	Total	O		0	0
			294	294			
5	F	293	Total	O		0	0
			293	293			
5	G	288	Total	O		0	0
			288	288			
5	H	288	Total	O		0	0
			288	288			
5	I	295	Total	O		0	0
			295	295			
5	J	287	Total	O		0	0
			287	287			
5	K	288	Total	O		0	0
			288	288			
5	L	292	Total	O		0	0
			292	292			

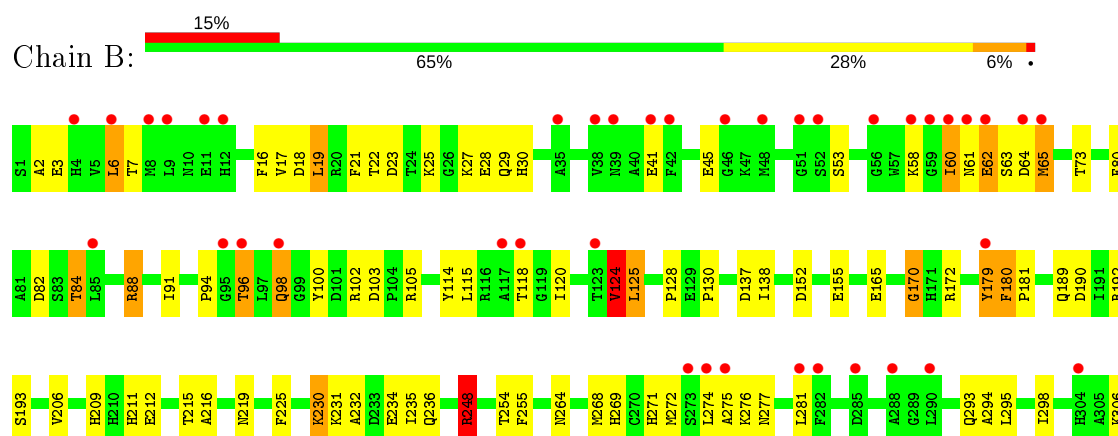
3 Residue-property plots

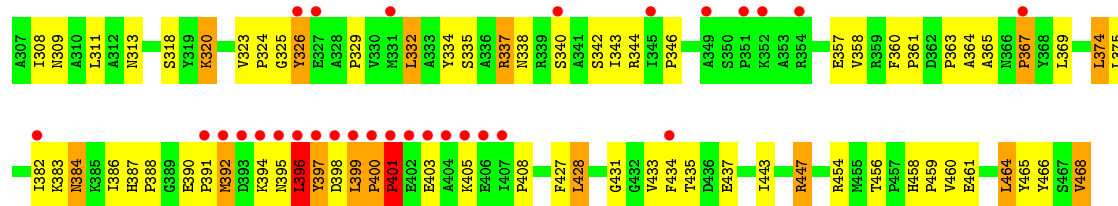
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

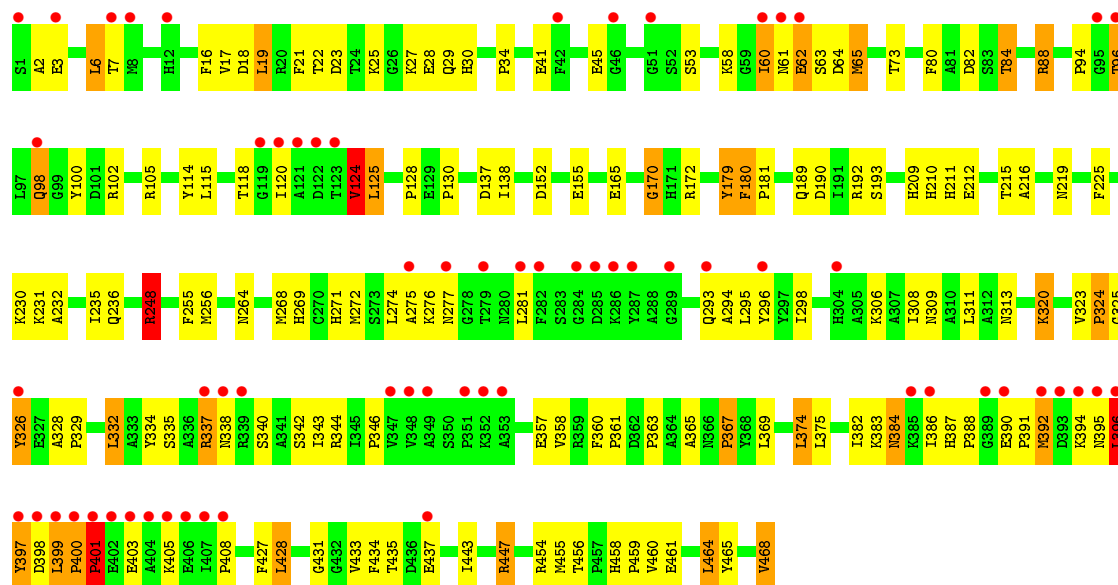


• Molecule 1: GLUTAMINE SYNTHETASE

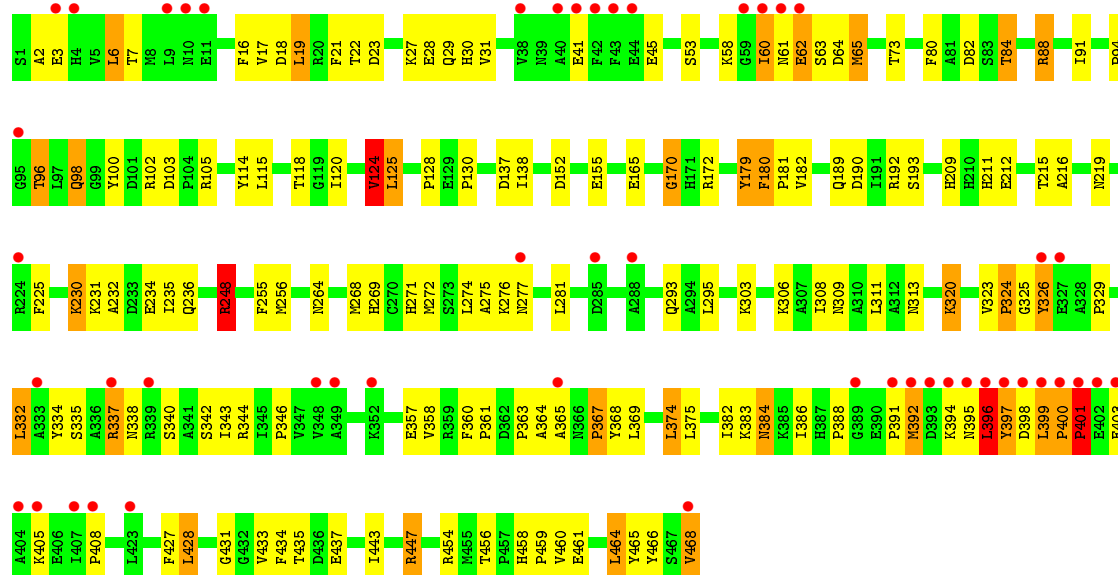




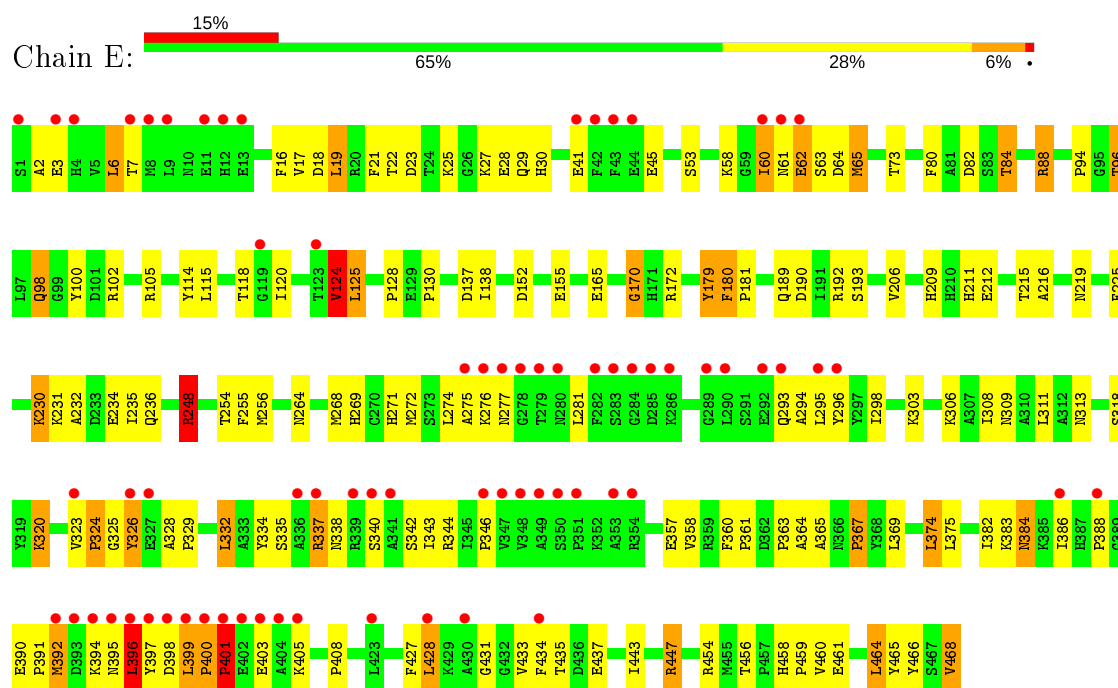
• Molecule 1: GLUTAMINE SYNTHETASE



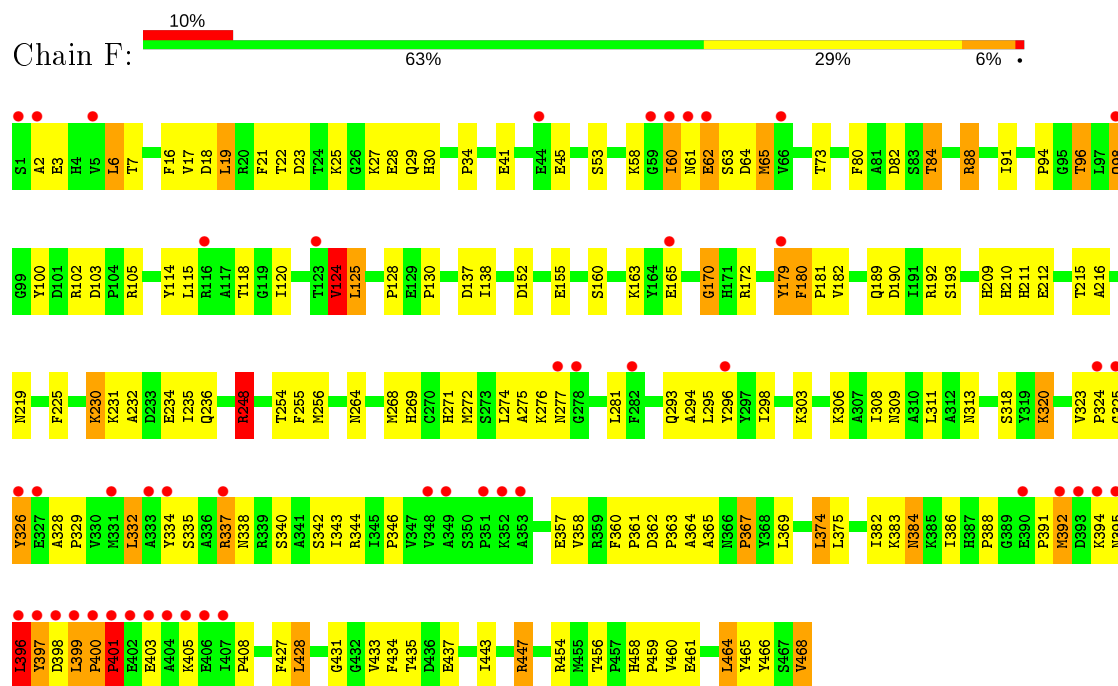
• Molecule 1: GLUTAMINE SYNTHETASE



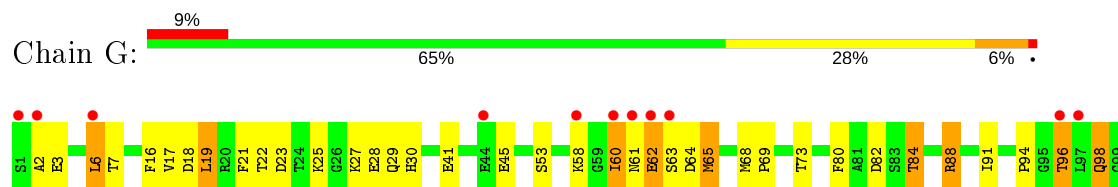
• Molecule 1: GLUTAMINE SYNTHETASE

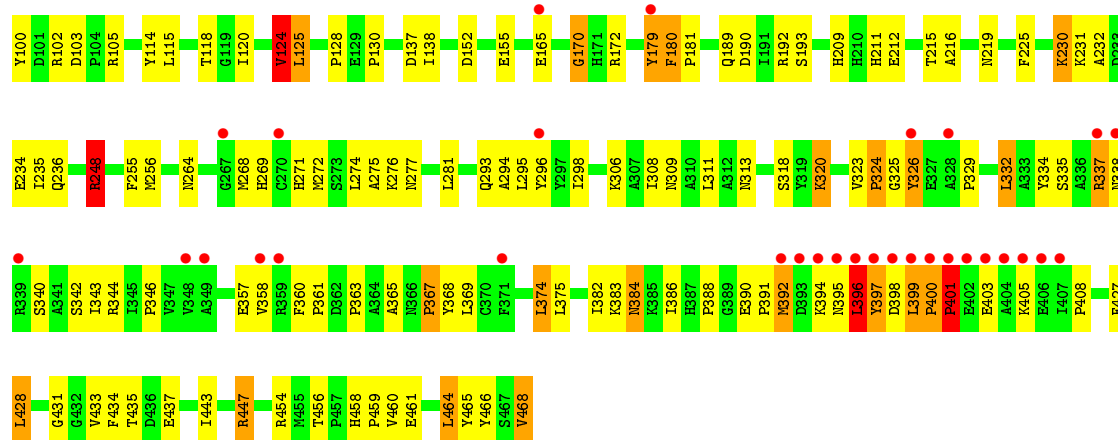


• Molecule 1: GLUTAMINE SYNTHETASE

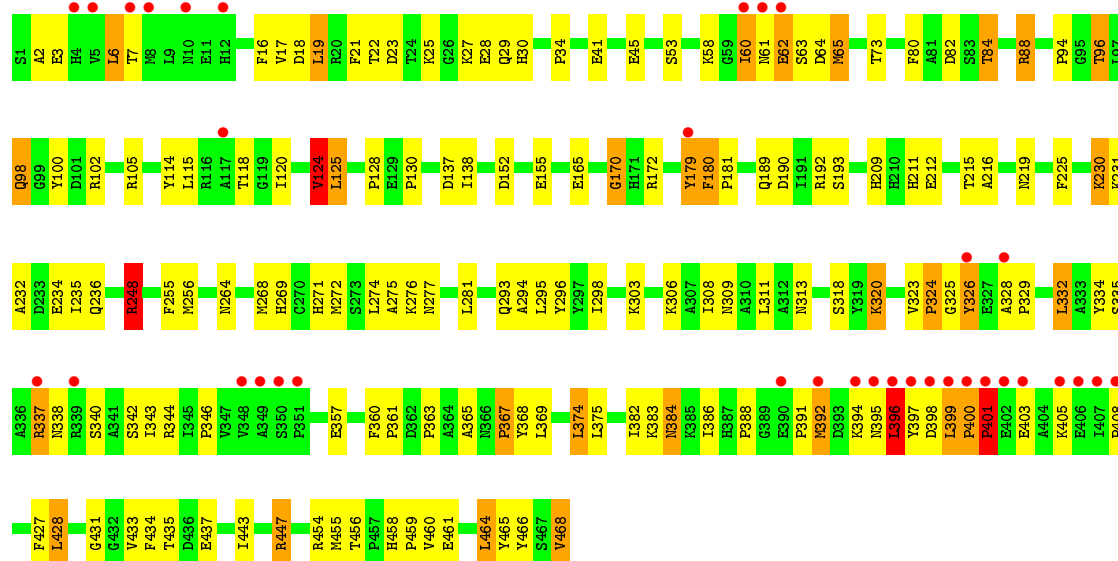


• Molecule 1: GLUTAMINE SYNTHETASE

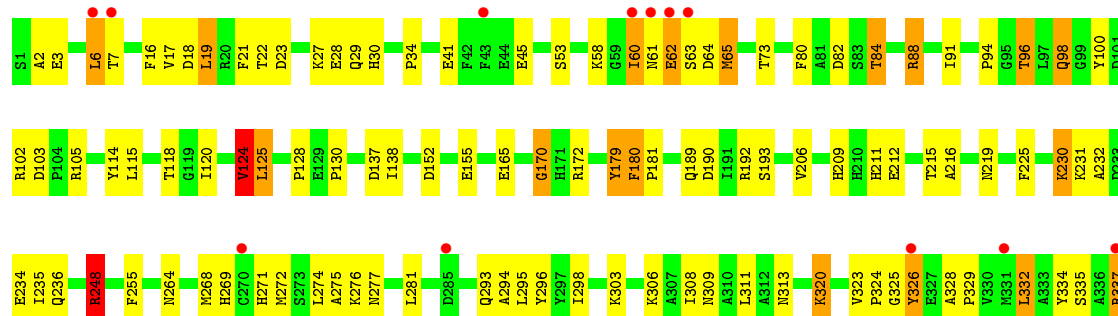




• Molecule 1: GLUTAMINE SYNTHETASE

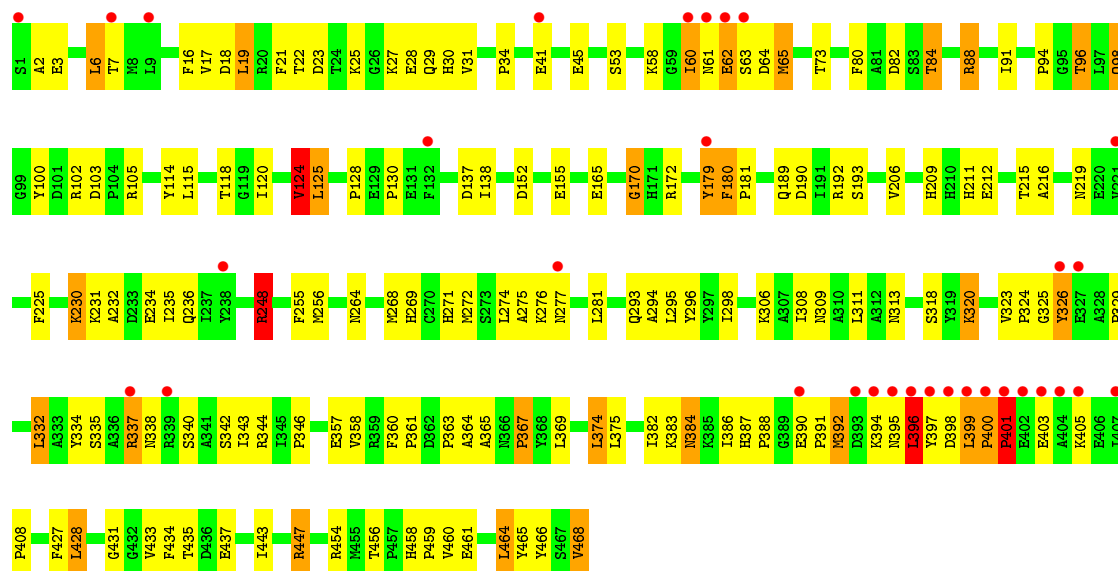


• Molecule 1: GLUTAMINE SYNTHETASE

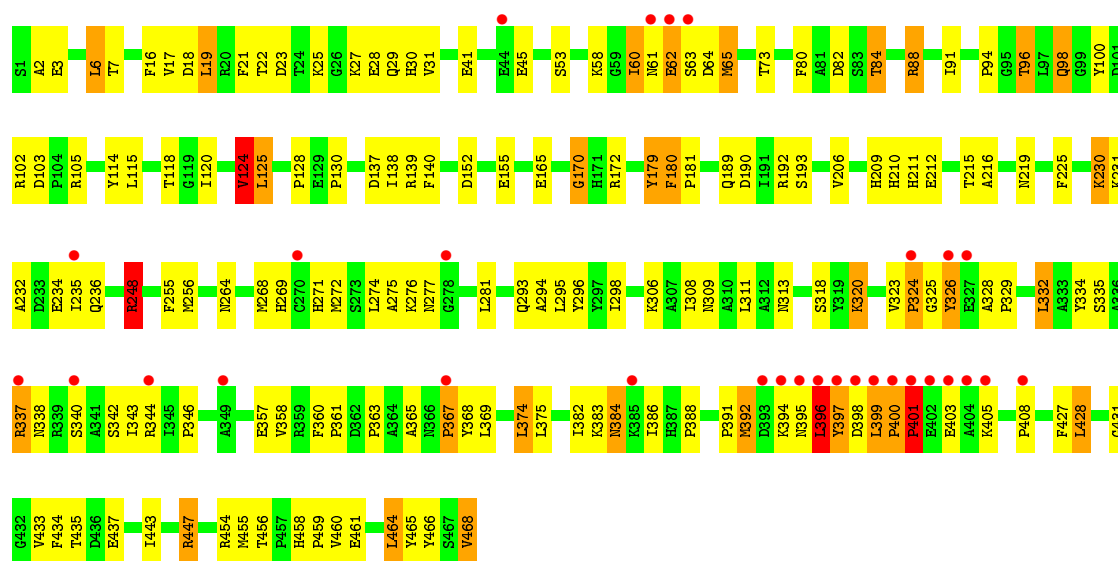




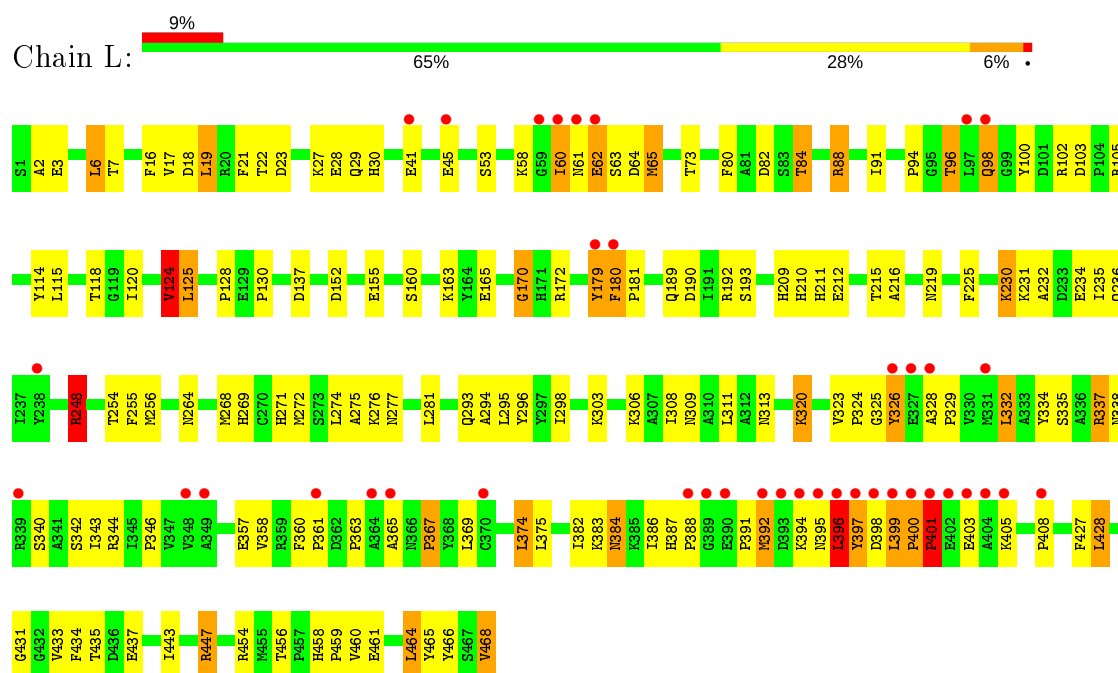
• Molecule 1: GLUTAMINE SYNTHETASE



• Molecule 1: GLUTAMINE SYNTHETASE



• Molecule 1: 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	230.60 Å 132.50 Å 195.90 Å 90.00° 102.40° 90.00°	Depositor
Resolution (Å)	34.90 – 2.49 34.90 – 2.49	Depositor EDS
% Data completeness (in resolution range)	98.2 (34.90-2.49) 97.9 (34.90-2.49)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.67 (at 2.48 Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.243 , 0.257 0.261 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	36.0	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 57.6	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	47688	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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: MPD, MN, ADP

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	0.53	0/3724	0.85	4/5043 (0.1%)
1	B	0.53	0/3724	0.85	4/5043 (0.1%)
1	C	0.53	0/3724	0.85	4/5043 (0.1%)
1	D	0.53	0/3724	0.85	4/5043 (0.1%)
1	E	0.53	0/3724	0.85	4/5043 (0.1%)
1	F	0.53	0/3724	0.85	4/5043 (0.1%)
1	G	0.53	0/3724	0.85	4/5043 (0.1%)
1	H	0.53	0/3724	0.85	4/5043 (0.1%)
1	I	0.53	0/3724	0.85	4/5043 (0.1%)
1	J	0.53	0/3724	0.85	4/5043 (0.1%)
1	K	0.53	0/3724	0.85	4/5043 (0.1%)
1	L	0.53	0/3724	0.85	4/5043 (0.1%)
All	All	0.53	0/44688	0.85	48/60516 (0.1%)

There are no bond length outliers.

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	401	PRO	CA-N-CD	-6.91	101.83	111.50
1	J	401	PRO	CA-N-CD	-6.90	101.84	111.50
1	I	401	PRO	CA-N-CD	-6.89	101.86	111.50
1	L	401	PRO	CA-N-CD	-6.89	101.86	111.50
1	F	401	PRO	CA-N-CD	-6.88	101.86	111.50

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	3544	210	0
1	B	3637	0	3544	204	0
1	C	3637	0	3544	207	0
1	D	3637	0	3544	205	0
1	E	3637	0	3544	199	0
1	F	3637	0	3544	218	0
1	G	3637	0	3544	205	0
1	H	3637	0	3544	213	0
1	I	3637	0	3544	211	0
1	J	3637	0	3544	221	0
1	K	3637	0	3544	220	0
1	L	3637	0	3544	216	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	1	0
3	B	27	0	10	1	0
3	C	27	0	10	1	0
3	D	27	0	10	1	0
3	E	27	0	10	1	0
3	F	27	0	10	1	0
3	G	27	0	10	1	0
3	H	27	0	10	1	0
3	I	27	0	10	1	0
3	J	27	0	10	1	0
3	K	27	0	10	1	0
3	L	27	0	10	1	0
4	A	16	0	27	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	16	0	27	60	0
4	C	16	0	27	62	0
4	D	16	0	27	61	0
4	E	16	0	27	54	0
4	F	16	0	27	62	0
4	G	16	0	27	60	0
4	H	16	0	27	65	0
4	I	16	0	27	62	0
4	J	16	0	27	68	0
4	K	16	0	27	66	0
4	L	16	0	27	65	0
5	A	294	0	0	6	0
5	B	297	0	0	7	0
5	C	293	0	0	8	0
5	D	295	0	0	7	0
5	E	294	0	0	8	0
5	F	293	0	0	8	0
5	G	288	0	0	8	0
5	H	288	0	0	7	0
5	I	295	0	0	7	0
5	J	287	0	0	8	0
5	K	288	0	0	7	0
5	L	292	0	0	7	0
All	All	47688	0	42972	2421	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 28.

The worst 5 of 2421 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:J:84:THR:HG21	4:J:5491:MPD:C5	1.53	1.36
1:F:84:THR:HG21	4:F:5479:MPD:C5	1.57	1.32
1:J:84:THR:CG2	4:J:5491:MPD:H52	1.60	1.32
1:L:84:THR:HG21	4:L:5483:MPD:C5	1.60	1.31
1:I:61:ASN:O	1:J:337:ARG:HB2	1.29	1.29

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%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	B	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	C	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	D	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	E	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	F	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	G	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	H	466/468 (100%)	427 (92%)	31 (7%)	8 (2%)	9	16
1	I	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	J	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
1	K	466/468 (100%)	427 (92%)	31 (7%)	8 (2%)	9	16
1	L	466/468 (100%)	426 (91%)	32 (7%)	8 (2%)	9	16
All	All	5592/5616 (100%)	5114 (92%)	382 (7%)	96 (2%)	9	16

5 of 96 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	PHE
1	A	400	PRO
1	A	401	PRO
1	B	180	PHE
1	B	400	PRO

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	384/384 (100%)	348 (91%)	36 (9%)	8	17
1	B	384/384 (100%)	349 (91%)	35 (9%)	9	18
1	C	384/384 (100%)	348 (91%)	36 (9%)	8	17
1	D	384/384 (100%)	348 (91%)	36 (9%)	8	17
1	E	384/384 (100%)	348 (91%)	36 (9%)	8	17
1	F	384/384 (100%)	349 (91%)	35 (9%)	9	18
1	G	384/384 (100%)	348 (91%)	36 (9%)	8	17
1	H	384/384 (100%)	348 (91%)	36 (9%)	8	17
1	I	384/384 (100%)	349 (91%)	35 (9%)	9	18
1	J	384/384 (100%)	349 (91%)	35 (9%)	9	18
1	K	384/384 (100%)	348 (91%)	36 (9%)	8	17
1	L	384/384 (100%)	349 (91%)	35 (9%)	9	18
All	All	4608/4608 (100%)	4181 (91%)	427 (9%)	9	17

5 of 427 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	165	GLU
1	G	374	LEU
1	L	60	ILE
1	F	264	ASN
1	G	60	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	244	ASN
1	G	313	ASN
1	L	30	HIS
1	F	264	ASN
1	G	30	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 60 ligands modelled in this entry, 24 are monoatomic - leaving 36 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	MPD	K	5492	-	7,7,7	3.31	4 (57%)	9,10,10	1.56	1 (11%)
4	MPD	B	5471	-	7,7,7	1.55	2 (28%)	9,10,10	1.00	0
3	ADP	F	4476	2	24,29,29	2.92	8 (33%)	29,45,45	3.33	11 (37%)
4	MPD	E	5480	-	7,7,7	3.32	4 (57%)	9,10,10	1.57	1 (11%)
4	MPD	I	5489	-	7,7,7	1.55	2 (28%)	9,10,10	1.00	0
3	ADP	A	4471	2	24,29,29	2.91	8 (33%)	29,45,45	3.34	11 (37%)
3	ADP	H	4478	2	24,29,29	2.91	8 (33%)	29,45,45	3.34	11 (37%)
4	MPD	D	5478	-	7,7,7	3.31	4 (57%)	9,10,10	1.56	1 (11%)
3	ADP	C	4473	2	24,29,29	2.91	8 (33%)	29,45,45	3.33	11 (37%)
4	MPD	K	5493	-	7,7,7	1.54	2 (28%)	9,10,10	1.00	0
4	MPD	J	5491	-	7,7,7	1.54	2 (28%)	9,10,10	1.00	0
4	MPD	I	5488	-	7,7,7	3.31	4 (57%)	9,10,10	1.57	1 (11%)
4	MPD	C	5476	-	7,7,7	3.31	4 (57%)	9,10,10	1.57	1 (11%)
4	MPD	G	5484	-	7,7,7	3.31	4 (57%)	9,10,10	1.57	1 (11%)
4	MPD	A	5472	-	7,7,7	3.31	4 (57%)	9,10,10	1.56	1 (11%)
3	ADP	E	4475	2	24,29,29	2.91	8 (33%)	29,45,45	3.34	12 (41%)
4	MPD	C	5473	-	7,7,7	1.54	2 (28%)	9,10,10	1.00	0
4	MPD	E	5477	-	7,7,7	1.55	2 (28%)	9,10,10	1.00	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ADP	K	4481	2	24,29,29	2.92	8 (33%)	29,45,45	3.33	11 (37%)
4	MPD	H	5486	-	7,7,7	3.31	4 (57%)	9,10,10	1.56	1 (11%)
3	ADP	G	4477	2	24,29,29	2.91	8 (33%)	29,45,45	3.34	11 (37%)
4	MPD	A	5481	-	7,7,7	1.55	2 (28%)	9,10,10	1.00	0
4	MPD	L	5483	-	7,7,7	1.54	2 (28%)	9,10,10	1.00	0
4	MPD	J	5490	-	7,7,7	3.31	4 (57%)	9,10,10	1.57	1 (11%)
4	MPD	F	5482	-	7,7,7	3.31	4 (57%)	9,10,10	1.57	1 (11%)
3	ADP	I	4479	2	24,29,29	2.91	8 (33%)	29,45,45	3.34	12 (41%)
3	ADP	L	4482	2	24,29,29	2.92	8 (33%)	29,45,45	3.34	11 (37%)
4	MPD	L	5494	-	7,7,7	3.32	4 (57%)	9,10,10	1.56	1 (11%)
3	ADP	B	4472	2	24,29,29	2.90	8 (33%)	29,45,45	3.34	11 (37%)
3	ADP	J	4480	2	24,29,29	2.91	8 (33%)	29,45,45	3.34	11 (37%)
4	MPD	D	5475	-	7,7,7	1.54	2 (28%)	9,10,10	1.00	0
4	MPD	B	5474	-	7,7,7	3.32	4 (57%)	9,10,10	1.56	1 (11%)
3	ADP	D	4474	2	24,29,29	2.92	8 (33%)	29,45,45	3.33	11 (37%)
4	MPD	H	5487	-	7,7,7	1.55	2 (28%)	9,10,10	1.00	0
4	MPD	G	5485	-	7,7,7	1.55	2 (28%)	9,10,10	1.00	0
4	MPD	F	5479	-	7,7,7	1.55	2 (28%)	9,10,10	1.00	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
4	MPD	K	5492	-	-	3/5/5/5	-
4	MPD	B	5471	-	-	0/5/5/5	-
3	ADP	F	4476	2	-	3/12/32/32	0/3/3/3
4	MPD	E	5480	-	-	3/5/5/5	-
4	MPD	I	5489	-	-	0/5/5/5	-
3	ADP	A	4471	2	-	3/12/32/32	0/3/3/3
3	ADP	H	4478	2	-	3/12/32/32	0/3/3/3
4	MPD	D	5478	-	-	3/5/5/5	-
3	ADP	C	4473	2	-	3/12/32/32	0/3/3/3
4	MPD	K	5493	-	-	0/5/5/5	-
4	MPD	J	5491	-	-	0/5/5/5	-
4	MPD	I	5488	-	-	3/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MPD	C	5476	-	-	3/5/5/5	-
4	MPD	G	5484	-	-	3/5/5/5	-
4	MPD	A	5472	-	-	3/5/5/5	-
3	ADP	E	4475	2	-	3/12/32/32	0/3/3/3
4	MPD	C	5473	-	-	0/5/5/5	-
4	MPD	E	5477	-	-	0/5/5/5	-
3	ADP	K	4481	2	-	3/12/32/32	0/3/3/3
4	MPD	H	5486	-	-	3/5/5/5	-
3	ADP	G	4477	2	-	3/12/32/32	0/3/3/3
4	MPD	A	5481	-	-	0/5/5/5	-
4	MPD	L	5483	-	-	0/5/5/5	-
4	MPD	J	5490	-	-	3/5/5/5	-
4	MPD	F	5482	-	-	3/5/5/5	-
3	ADP	I	4479	2	-	3/12/32/32	0/3/3/3
3	ADP	L	4482	2	-	3/12/32/32	0/3/3/3
4	MPD	L	5494	-	-	3/5/5/5	-
3	ADP	B	4472	2	-	3/12/32/32	0/3/3/3
3	ADP	J	4480	2	-	3/12/32/32	0/3/3/3
4	MPD	D	5475	-	-	0/5/5/5	-
4	MPD	B	5474	-	-	3/5/5/5	-
3	ADP	D	4474	2	-	3/12/32/32	0/3/3/3
4	MPD	H	5487	-	-	0/5/5/5	-
4	MPD	G	5485	-	-	0/5/5/5	-
4	MPD	F	5479	-	-	0/5/5/5	-

The worst 5 of 168 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	4481	ADP	O4'-C1'	8.85	1.53	1.41
3	L	4482	ADP	O4'-C1'	8.83	1.53	1.41
3	F	4476	ADP	O4'-C1'	8.82	1.53	1.41
3	C	4473	ADP	O4'-C1'	8.81	1.53	1.41
3	D	4474	ADP	O4'-C1'	8.80	1.53	1.41

The worst 5 of 146 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	4477	ADP	O4'-C1'-C2'	-10.30	91.87	106.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	4478	ADP	O4'-C1'-C2'	-10.30	91.87	106.93
3	K	4481	ADP	O4'-C1'-C2'	-10.29	91.89	106.93
3	J	4480	ADP	O4'-C1'-C2'	-10.29	91.89	106.93
3	A	4471	ADP	O4'-C1'-C2'	-10.29	91.89	106.93

There are no chirality outliers.

5 of 72 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	4476	ADP	C4'-C5'-O5'-PA
4	E	5480	MPD	C1-C2-C3-C4
4	E	5480	MPD	O2-C2-C3-C4
4	E	5480	MPD	C2-C3-C4-O4
3	A	4471	ADP	C4'-C5'-O5'-PA

There are no ring outliers.

36 monomers are involved in 753 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	K	5492	MPD	30	0
4	B	5471	MPD	30	0
3	F	4476	ADP	1	0
4	E	5480	MPD	29	0
4	I	5489	MPD	31	0
3	A	4471	ADP	1	0
3	H	4478	ADP	1	0
4	D	5478	MPD	30	0
3	C	4473	ADP	1	0
4	K	5493	MPD	36	0
4	J	5491	MPD	39	0
4	I	5488	MPD	31	0
4	C	5476	MPD	30	0
4	G	5484	MPD	32	0
4	A	5472	MPD	29	0
3	E	4475	ADP	1	0
4	C	5473	MPD	32	0
4	E	5477	MPD	25	0
3	K	4481	ADP	1	0
4	H	5486	MPD	30	0
3	G	4477	ADP	1	0
4	A	5481	MPD	27	0

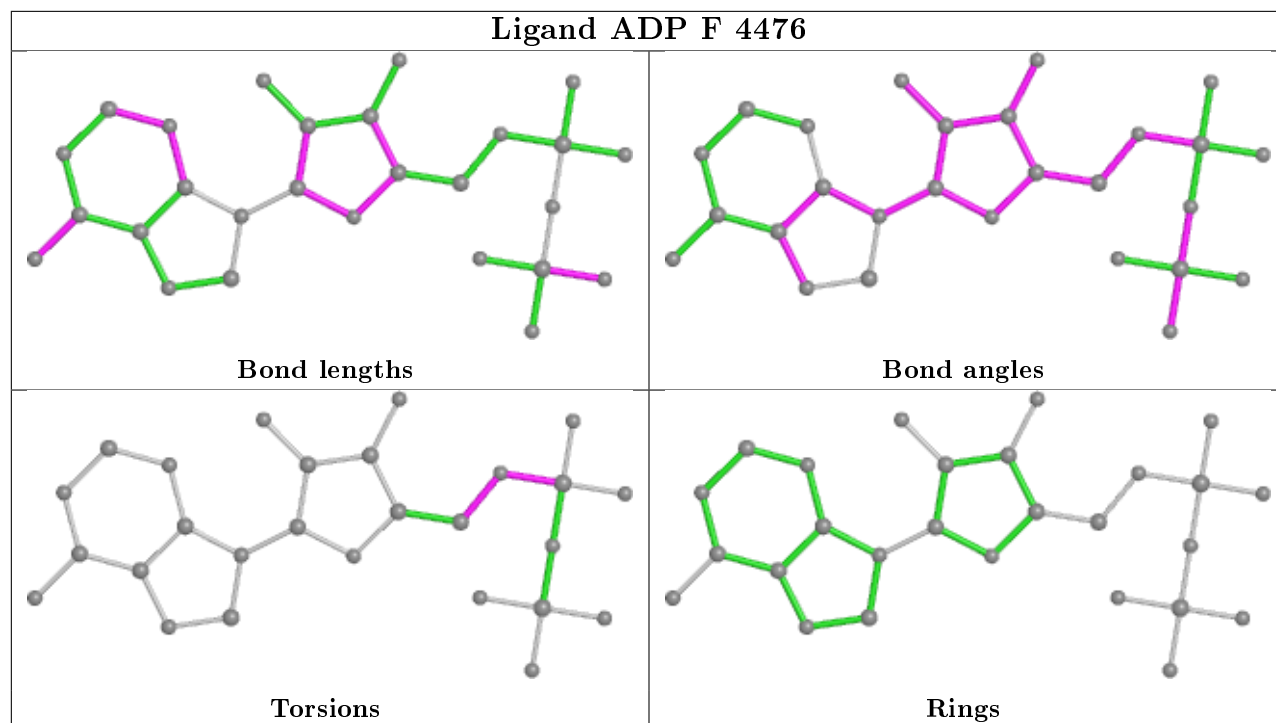
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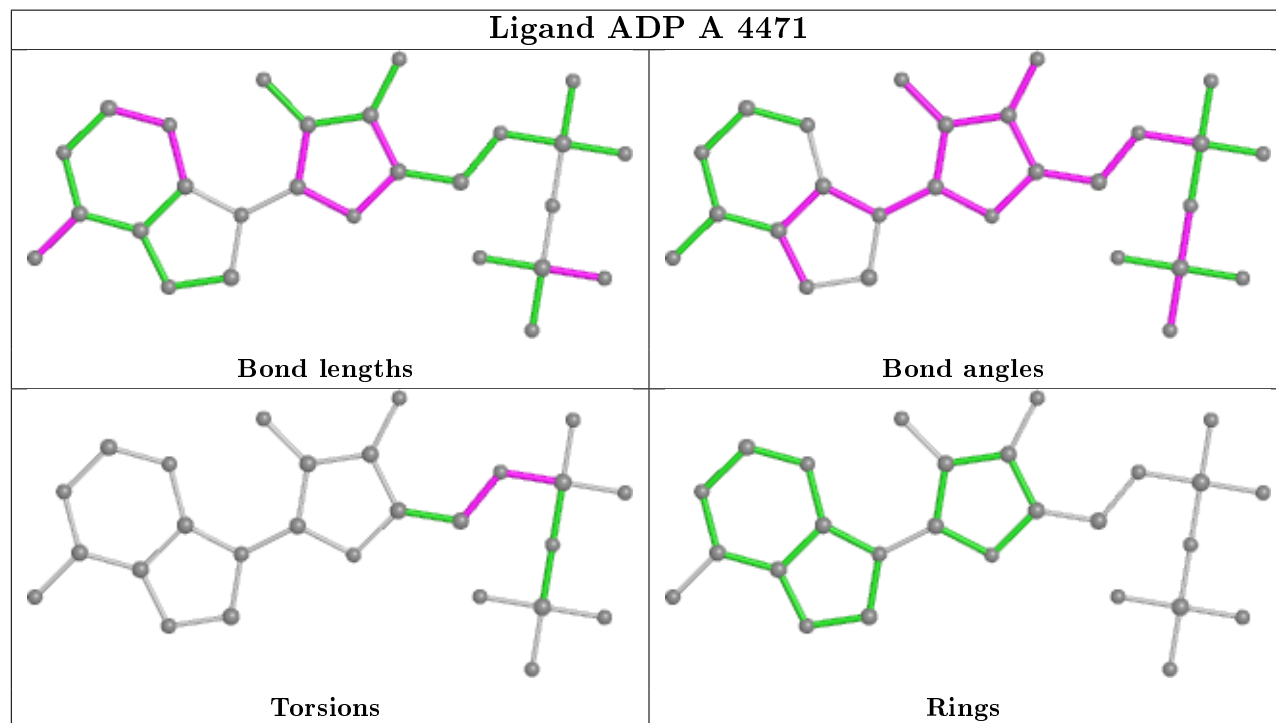
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	5483	MPD	35	0
4	J	5490	MPD	29	0
4	F	5482	MPD	29	0
3	I	4479	ADP	1	0
3	L	4482	ADP	1	0
4	L	5494	MPD	30	0
3	B	4472	ADP	1	0
3	J	4480	ADP	1	0
4	D	5475	MPD	31	0
4	B	5474	MPD	30	0
3	D	4474	ADP	1	0
4	H	5487	MPD	35	0
4	G	5485	MPD	28	0
4	F	5479	MPD	33	0

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.

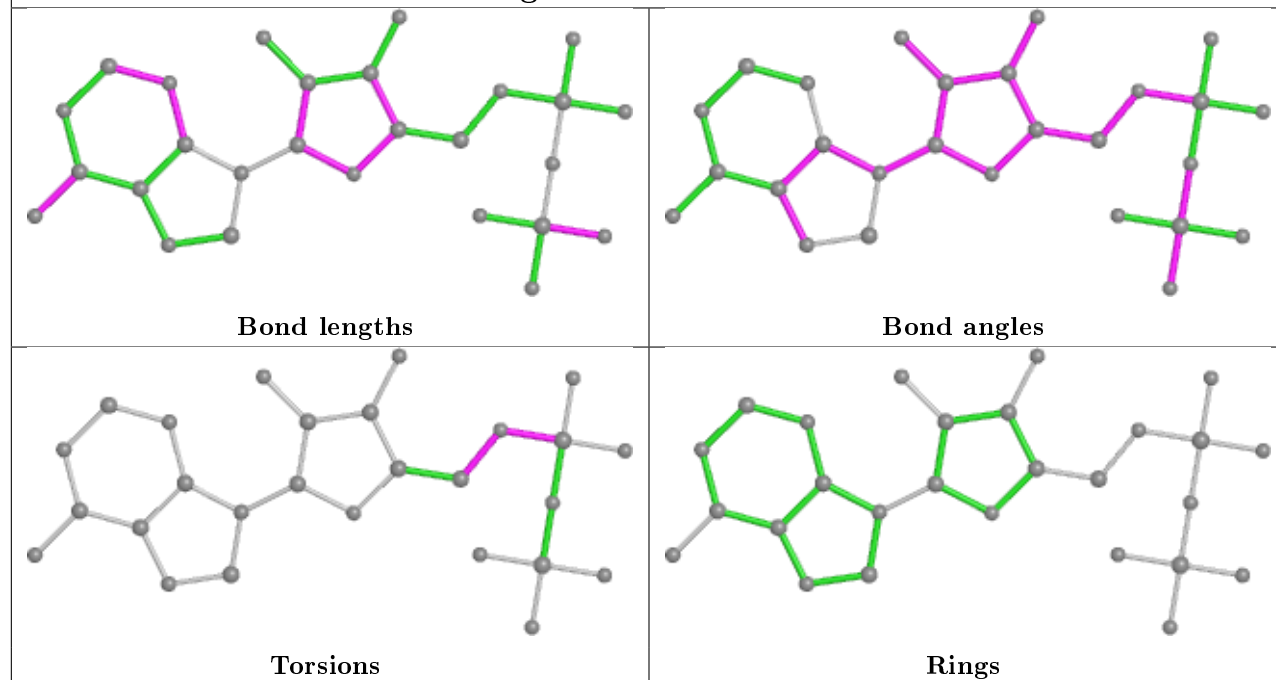
Ligand ADP F 4476



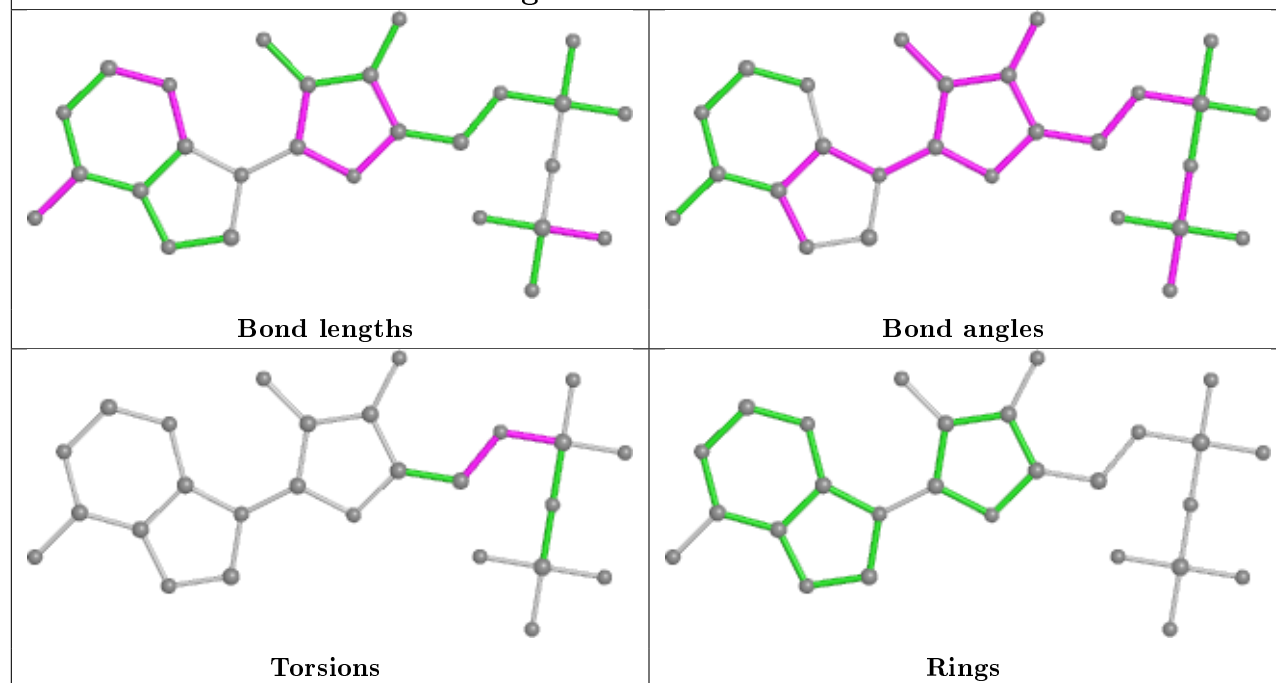
Ligand ADP A 4471



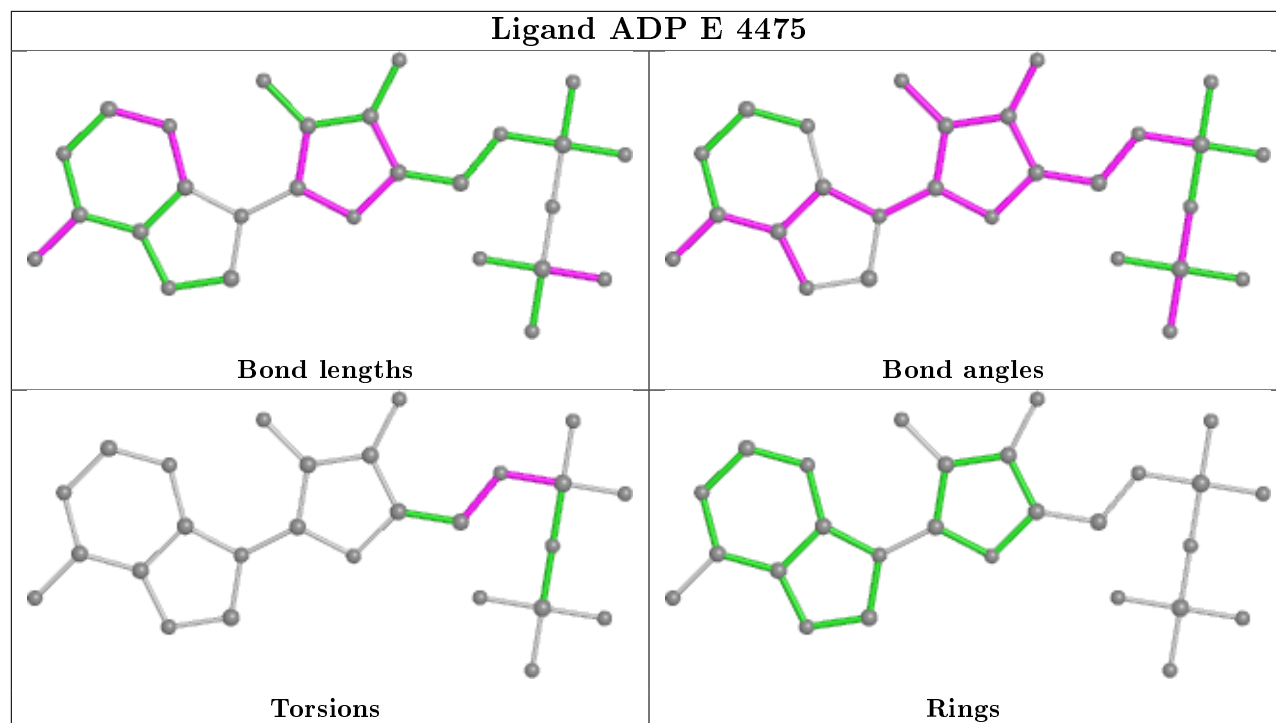
Ligand ADP H 4478



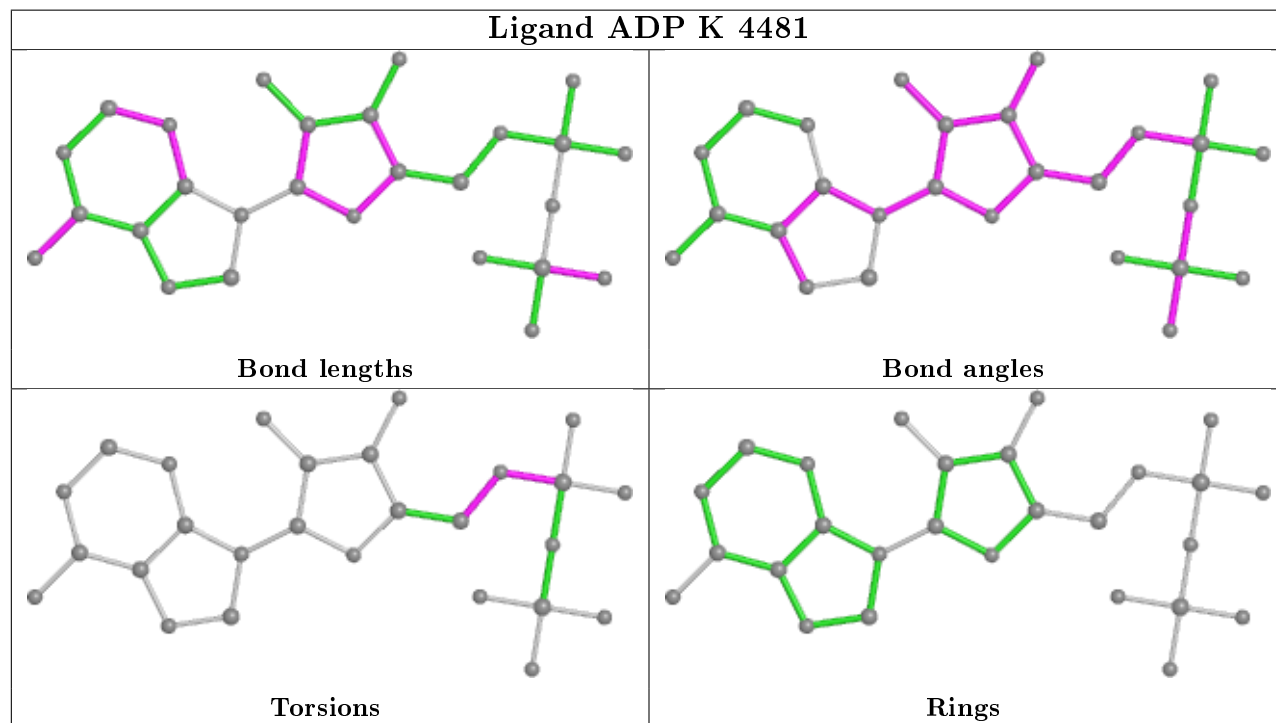
Ligand ADP C 4473



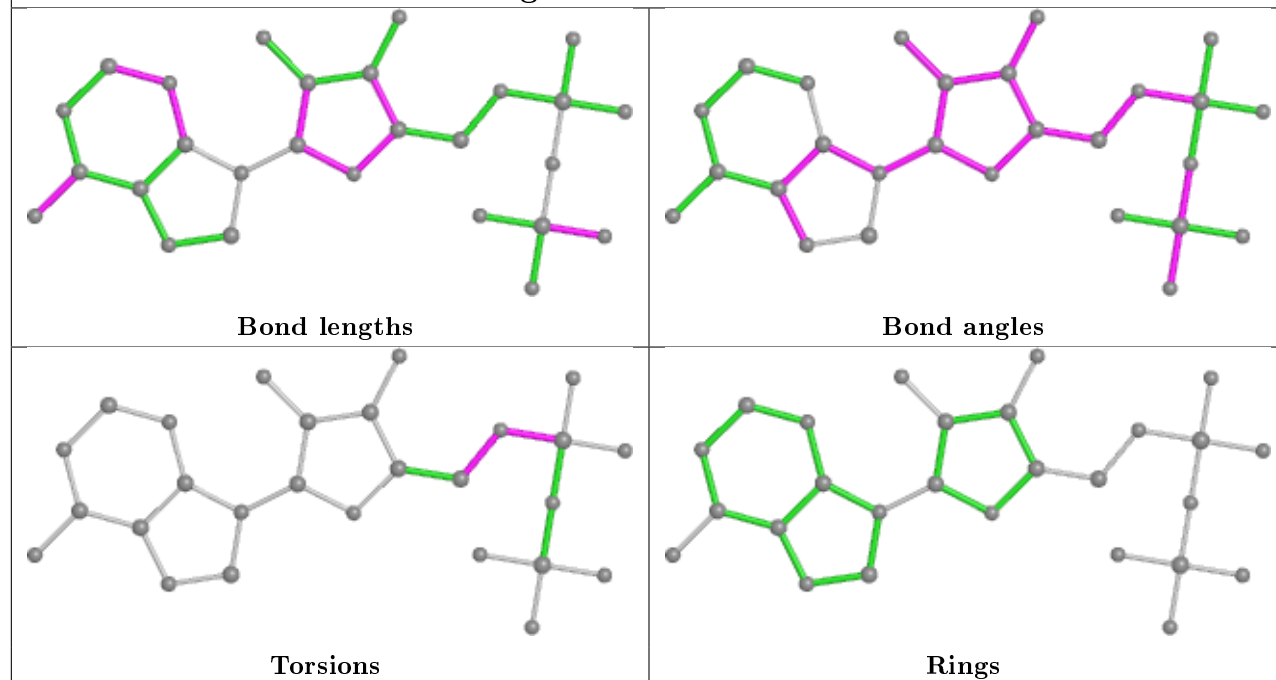
Ligand ADP E 4475



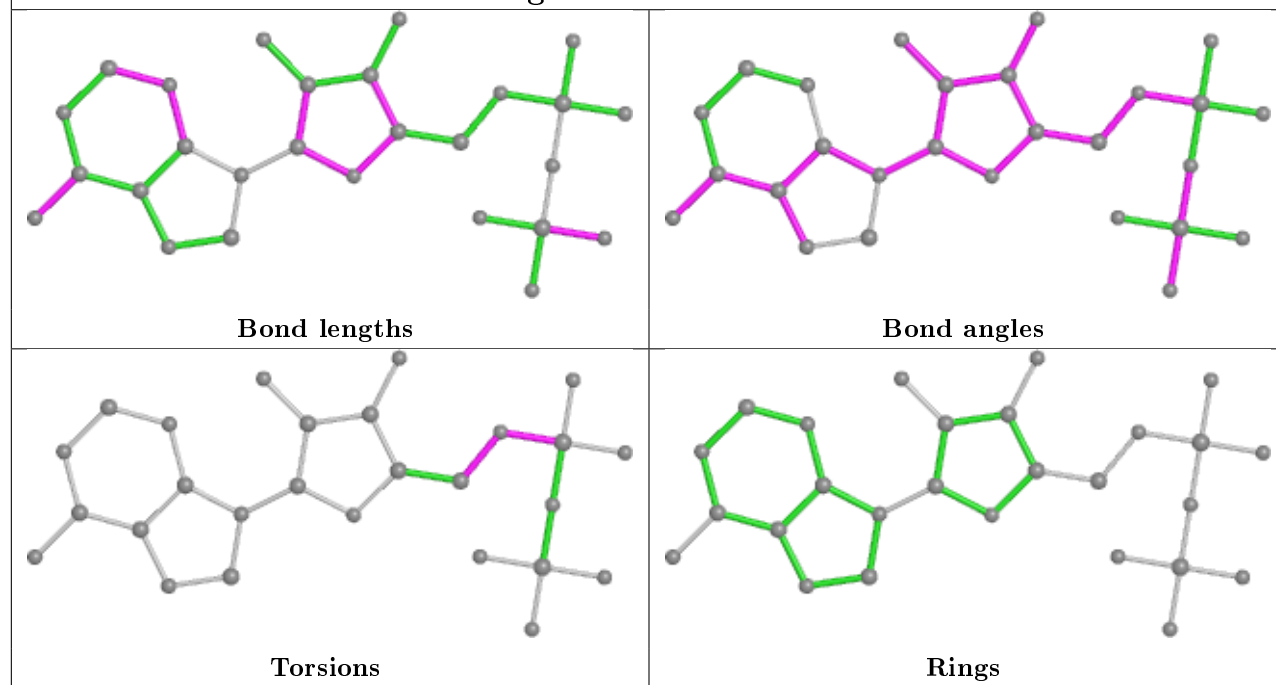
Ligand ADP K 4481



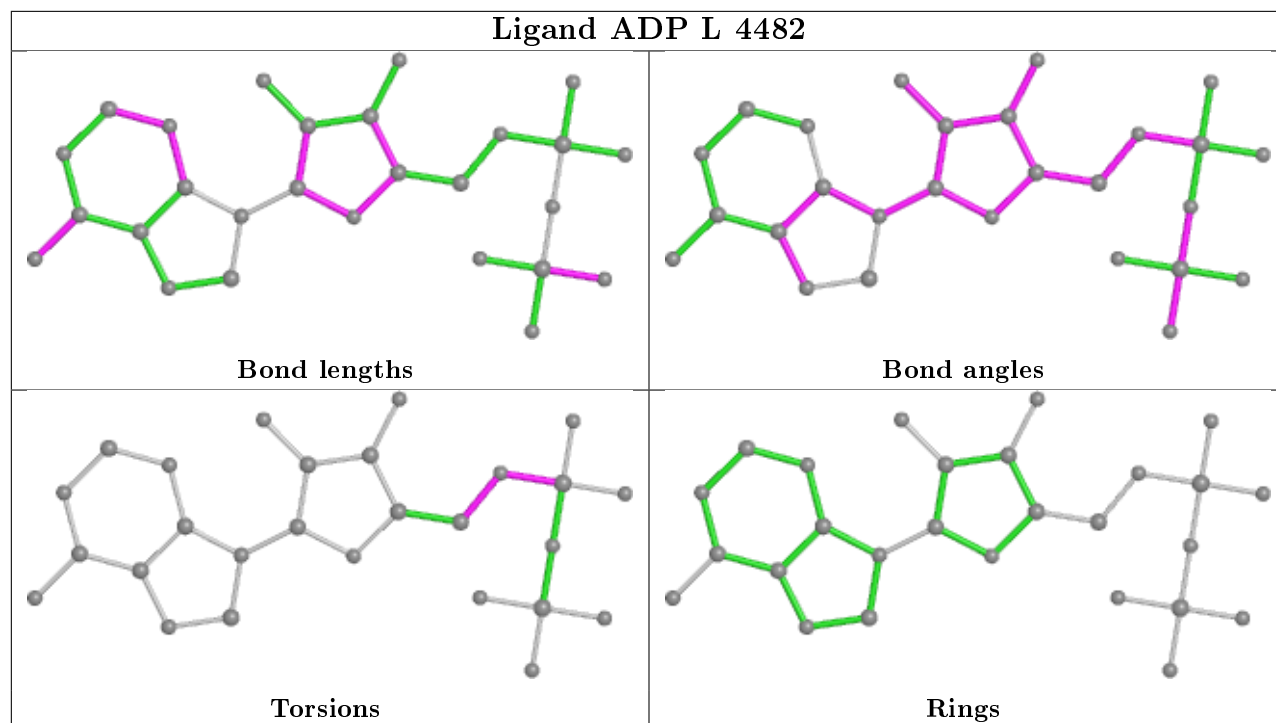
Ligand ADP G 4477



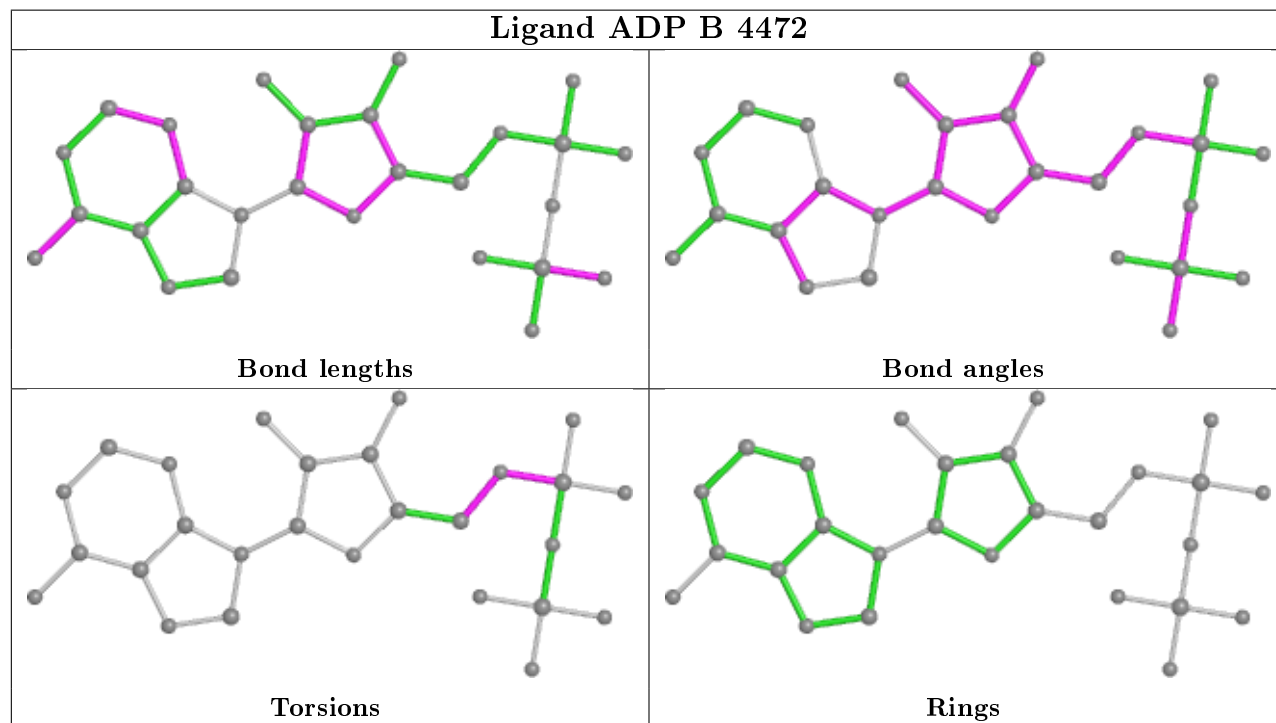
Ligand ADP I 4479

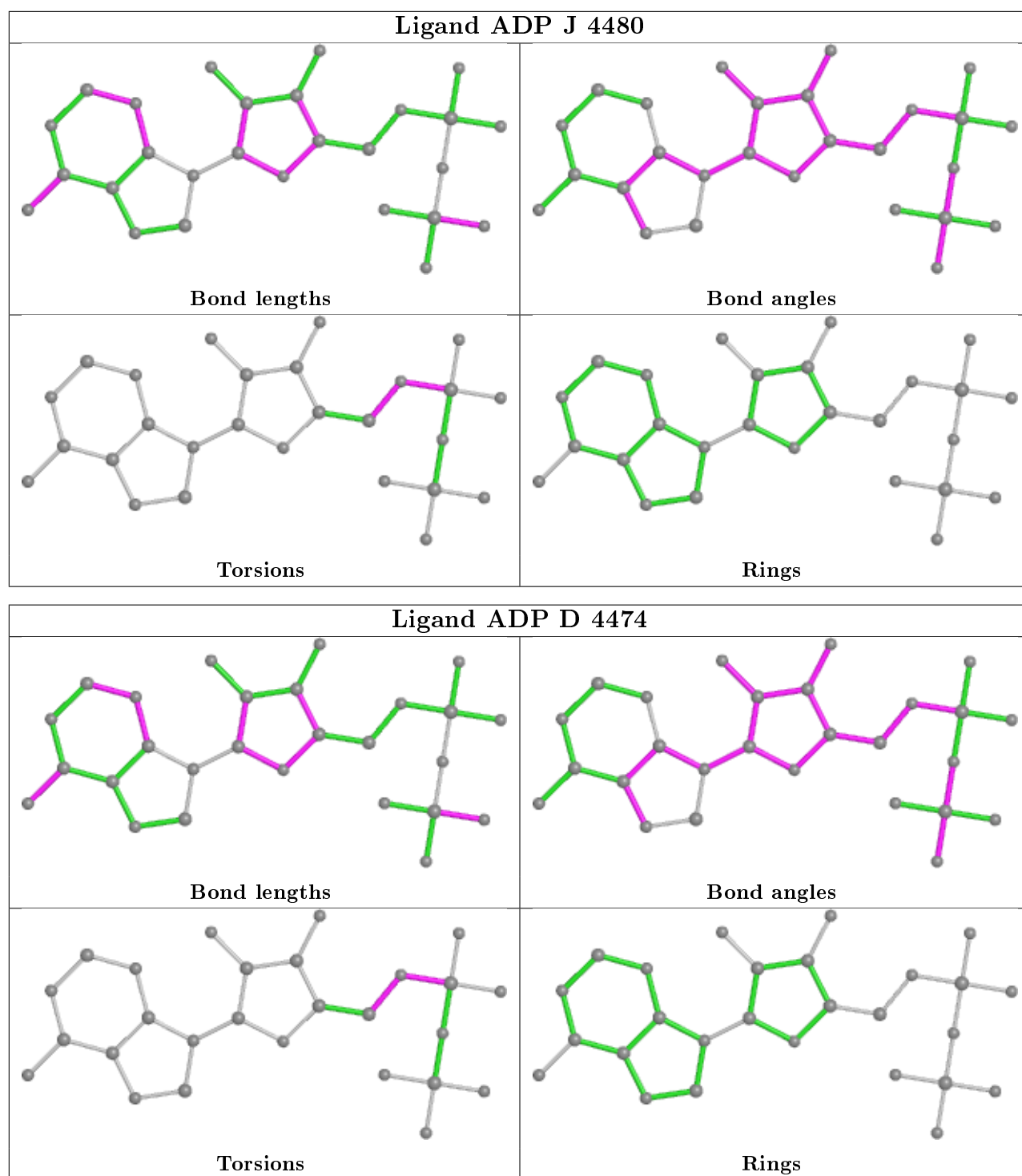


Ligand ADP L 4482



Ligand ADP B 4472





5.7 Other polymers [i](#)

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 [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	468/468 (100%)	1.47	145 (30%) 0 0	28, 48, 96, 100	19 (4%)
1	B	468/468 (100%)	0.84	69 (14%) 2 2	28, 48, 96, 100	19 (4%)
1	C	468/468 (100%)	0.76	64 (13%) 3 2	28, 48, 96, 100	19 (4%)
1	D	468/468 (100%)	0.44	49 (10%) 6 6	28, 48, 96, 100	19 (4%)
1	E	468/468 (100%)	0.77	71 (15%) 2 1	28, 48, 96, 100	19 (4%)
1	F	468/468 (100%)	0.78	48 (10%) 6 6	28, 48, 96, 100	19 (4%)
1	G	468/468 (100%)	0.52	42 (8%) 9 9	28, 48, 96, 100	19 (4%)
1	H	468/468 (100%)	0.51	35 (7%) 14 14	28, 48, 96, 100	19 (4%)
1	I	468/468 (100%)	0.46	33 (7%) 16 16	28, 48, 96, 100	19 (4%)
1	J	468/468 (100%)	0.48	32 (6%) 17 17	28, 48, 96, 100	19 (4%)
1	K	468/468 (100%)	0.40	30 (6%) 19 20	28, 48, 96, 100	19 (4%)
1	L	468/468 (100%)	0.63	40 (8%) 10 10	28, 48, 96, 100	19 (4%)
All	All	5616/5616 (100%)	0.67	658 (11%) 4 4	28, 48, 96, 100	228 (4%)

The worst 5 of 658 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	397	TYR	13.5
1	A	397	TYR	12.8
1	J	397	TYR	12.7
1	B	397	TYR	12.5
1	A	398	ASP	12.5

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ADP	A	4471	27/27	0.51	0.54	38,77,100,100	27
4	MPD	B	5474	8/8	0.58	0.47	63,68,75,98	8
4	MPD	C	5476	8/8	0.59	0.45	63,68,75,98	8
4	MPD	A	5472	8/8	0.63	0.48	63,68,75,98	8
3	ADP	B	4472	27/27	0.64	0.45	38,77,100,100	27
4	MPD	H	5486	8/8	0.65	0.52	63,68,75,98	8
3	ADP	F	4476	27/27	0.70	0.41	38,77,100,100	27
3	ADP	E	4475	27/27	0.71	0.36	38,77,100,100	27
3	ADP	L	4482	27/27	0.71	0.44	38,77,100,100	27
3	ADP	K	4481	27/27	0.73	0.40	38,77,100,100	27
3	ADP	I	4479	27/27	0.73	0.41	38,77,100,100	27
4	MPD	B	5471	8/8	0.74	0.46	37,50,65,66	8
4	MPD	G	5484	8/8	0.74	0.51	63,68,75,98	8
4	MPD	J	5490	8/8	0.75	0.49	63,68,75,98	8
3	ADP	G	4477	27/27	0.75	0.39	38,77,100,100	27
3	ADP	D	4474	27/27	0.75	0.34	38,77,100,100	27
4	MPD	E	5480	8/8	0.76	0.48	63,68,75,98	8
4	MPD	I	5488	8/8	0.77	0.55	63,68,75,98	8
3	ADP	C	4473	27/27	0.77	0.34	38,77,100,100	27
4	MPD	D	5478	8/8	0.78	0.49	63,68,75,98	8
4	MPD	F	5482	8/8	0.78	0.36	63,68,75,98	8
3	ADP	H	4478	27/27	0.80	0.33	38,77,100,100	27
4	MPD	K	5492	8/8	0.80	0.50	63,68,75,98	8
3	ADP	J	4480	27/27	0.81	0.39	38,77,100,100	27
4	MPD	L	5494	8/8	0.82	0.52	63,68,75,98	8
4	MPD	A	5481	8/8	0.82	0.38	37,50,65,66	8
4	MPD	D	5475	8/8	0.83	0.36	37,50,65,66	8
4	MPD	F	5479	8/8	0.83	0.45	37,50,65,66	8
2	MN	A	470	1/1	0.87	0.07	46,46,46,46	0
4	MPD	E	5477	8/8	0.87	0.40	37,50,65,66	8
4	MPD	I	5489	8/8	0.88	0.40	37,50,65,66	8

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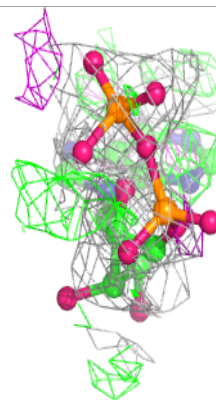
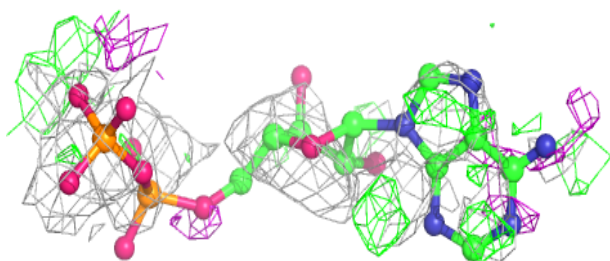
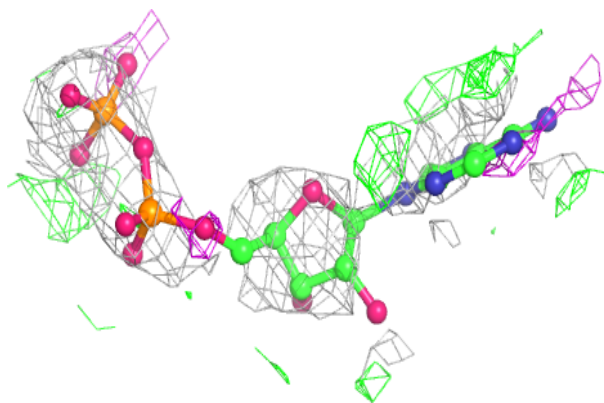
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MPD	C	5473	8/8	0.88	0.39	37,50,65,66	8
4	MPD	H	5487	8/8	0.88	0.44	37,50,65,66	8
4	MPD	L	5483	8/8	0.89	0.42	37,50,65,66	8
4	MPD	G	5485	8/8	0.89	0.44	37,50,65,66	8
2	MN	A	469	1/1	0.91	0.07	47,47,47,47	0
4	MPD	J	5491	8/8	0.92	0.43	37,50,65,66	8
2	MN	L	469	1/1	0.92	0.16	47,47,47,47	0
2	MN	C	469	1/1	0.93	0.07	47,47,47,47	0
4	MPD	K	5493	8/8	0.93	0.43	37,50,65,66	8
2	MN	D	470	1/1	0.93	0.04	46,46,46,46	0
2	MN	E	470	1/1	0.94	0.06	46,46,46,46	0
2	MN	B	470	1/1	0.94	0.07	46,46,46,46	0
2	MN	H	469	1/1	0.95	0.15	47,47,47,47	0
2	MN	F	469	1/1	0.95	0.07	47,47,47,47	0
2	MN	B	469	1/1	0.96	0.06	47,47,47,47	0
2	MN	H	470	1/1	0.96	0.08	46,46,46,46	0
2	MN	K	469	1/1	0.97	0.15	47,47,47,47	0
2	MN	I	470	1/1	0.97	0.08	46,46,46,46	0
2	MN	G	470	1/1	0.97	0.10	46,46,46,46	0
2	MN	J	469	1/1	0.97	0.16	47,47,47,47	0
2	MN	C	470	1/1	0.97	0.04	46,46,46,46	0
2	MN	E	469	1/1	0.97	0.03	47,47,47,47	0
2	MN	I	469	1/1	0.97	0.12	47,47,47,47	0
2	MN	J	470	1/1	0.98	0.10	46,46,46,46	0
2	MN	F	470	1/1	0.98	0.04	46,46,46,46	0
2	MN	L	470	1/1	0.98	0.13	46,46,46,46	0
2	MN	D	469	1/1	0.98	0.09	47,47,47,47	0
2	MN	K	470	1/1	0.99	0.12	46,46,46,46	0
2	MN	G	469	1/1	0.99	0.10	47,47,47,47	0

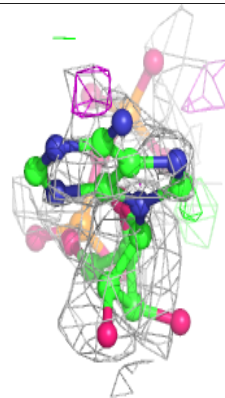
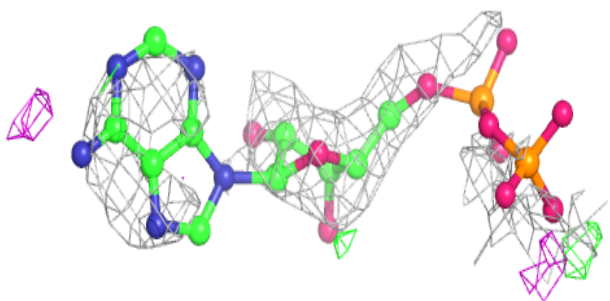
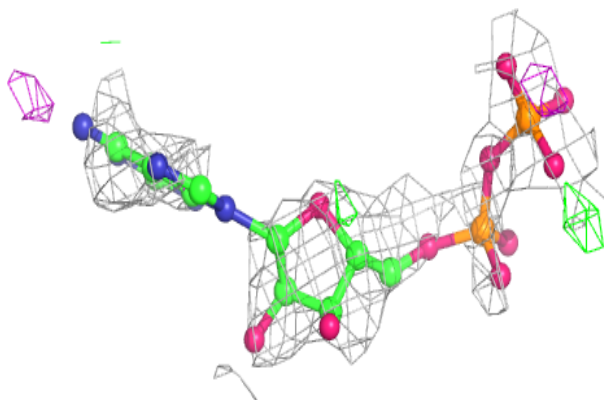
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ADP A 4471:

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

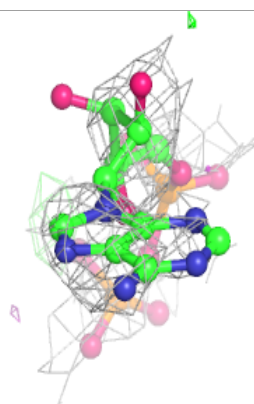
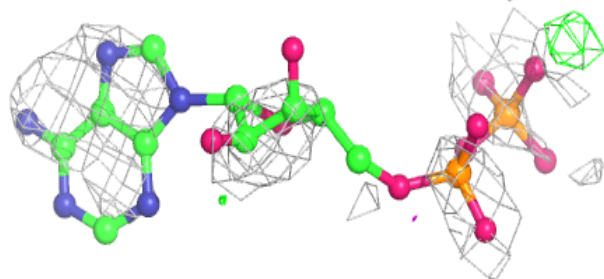
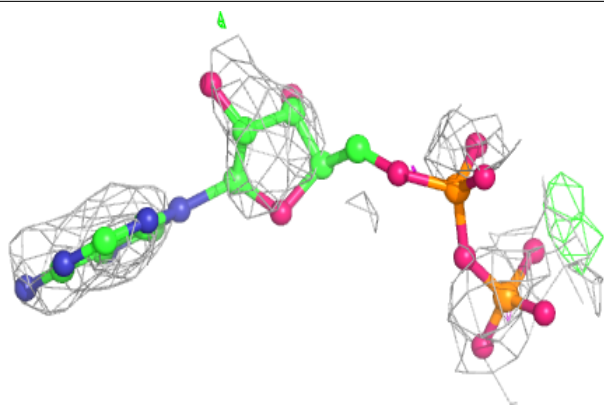
**Electron density around ADP B 4472:**

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

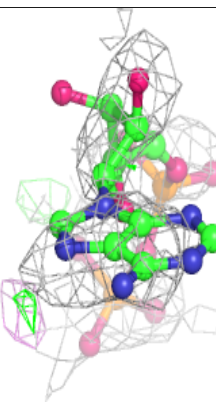
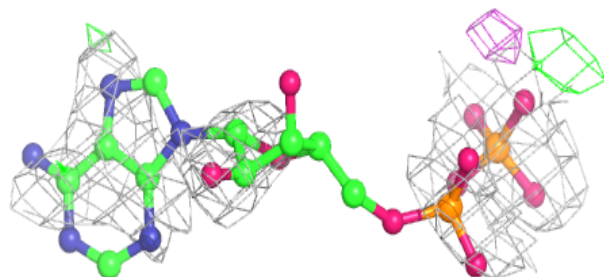
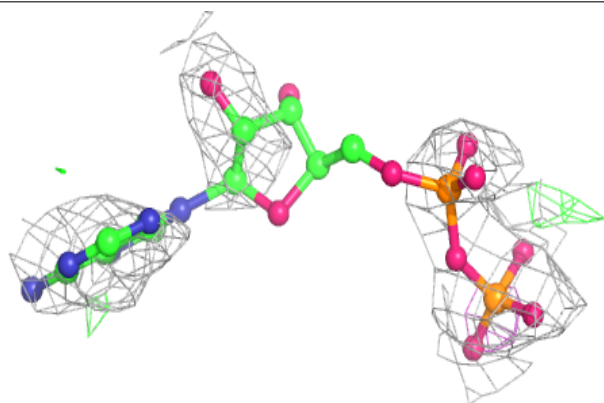


Electron density around ADP F 4476:

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

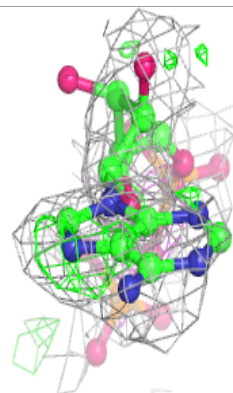
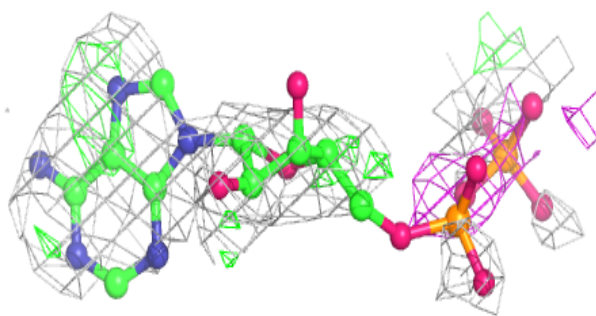
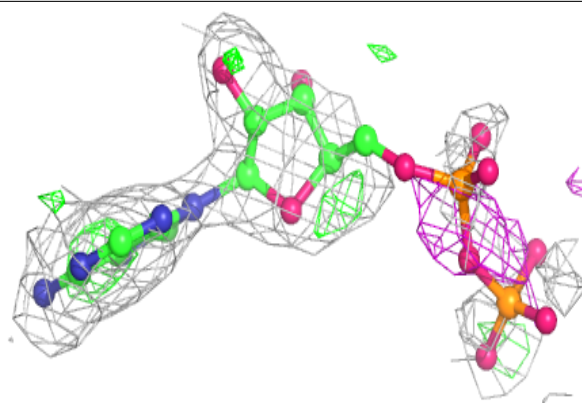
**Electron density around ADP E 4475:**

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

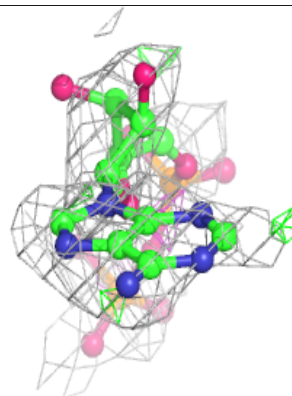
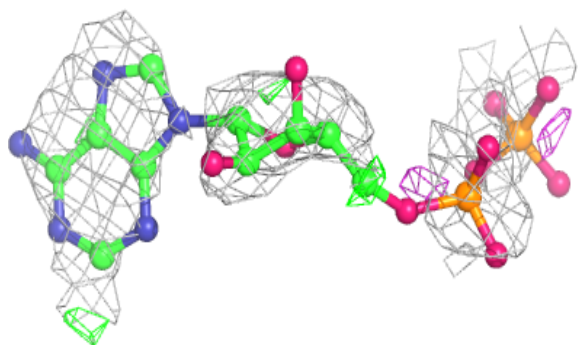
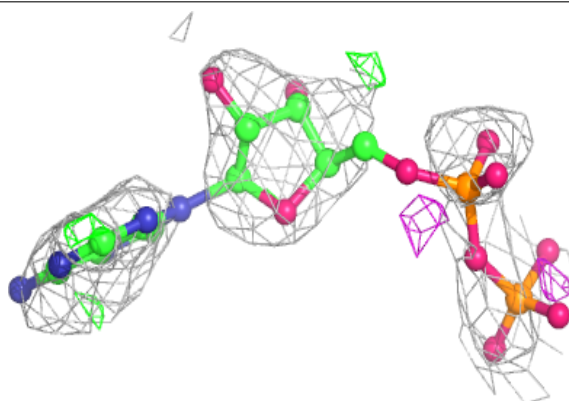


Electron density around ADP L 4482:

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

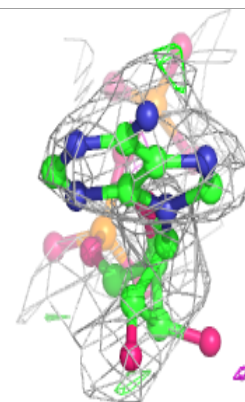
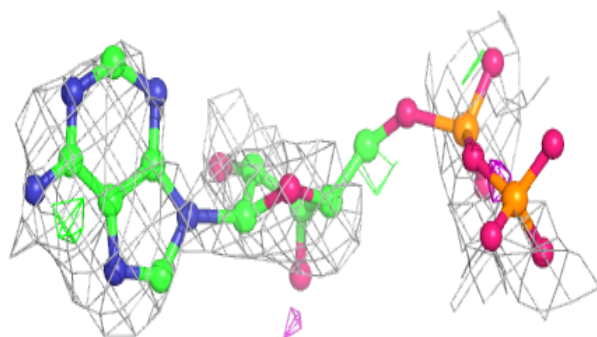
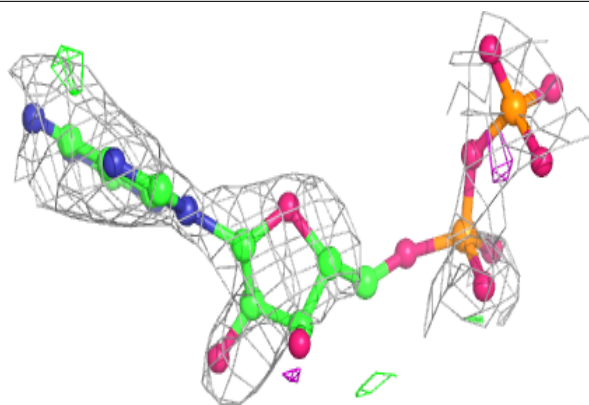
**Electron density around ADP K 4481:**

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

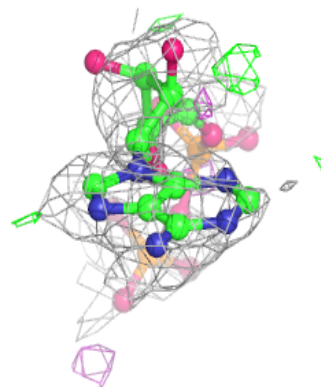
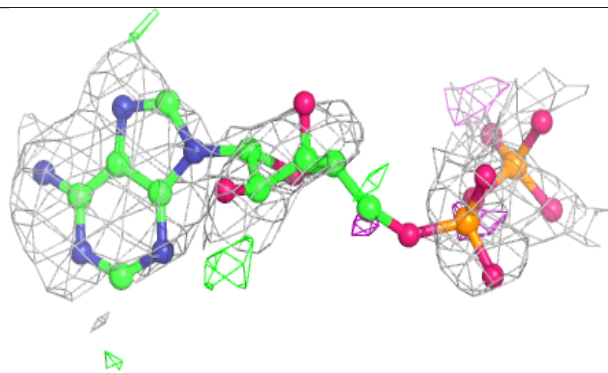
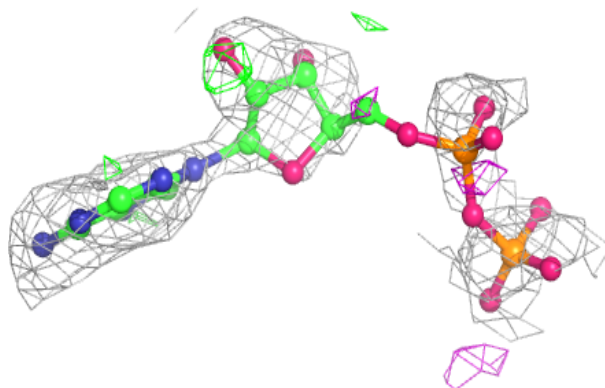


Electron density around ADP I 4479:

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

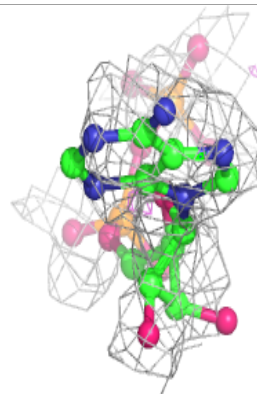
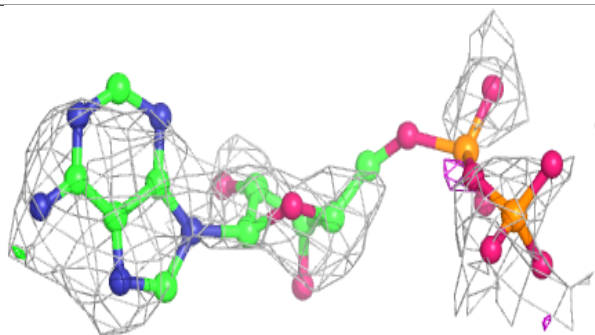
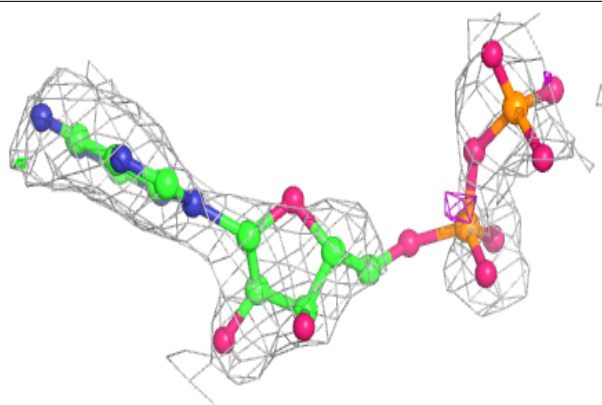
**Electron density around ADP G 4477:**

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

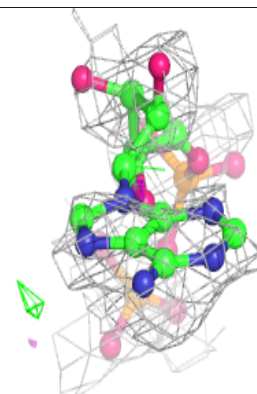
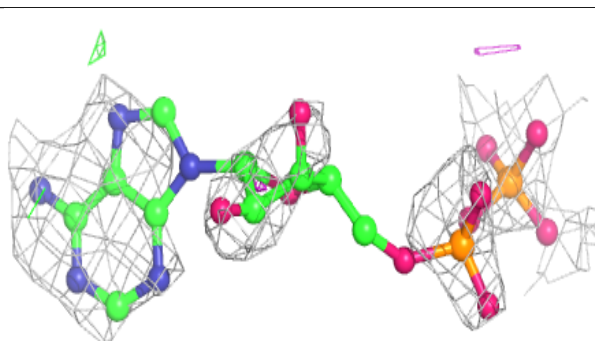
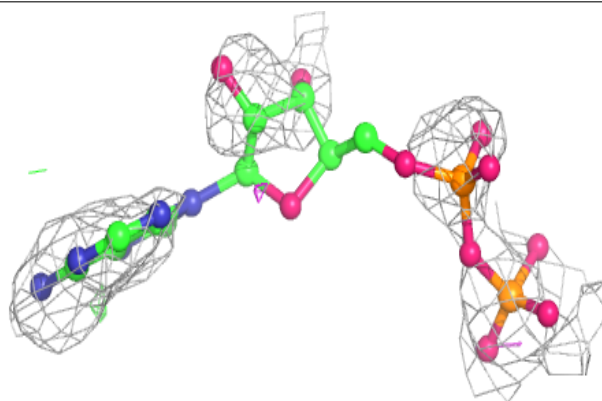


Electron density around ADP D 4474:

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

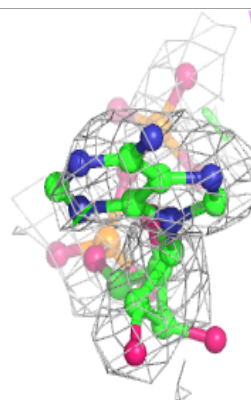
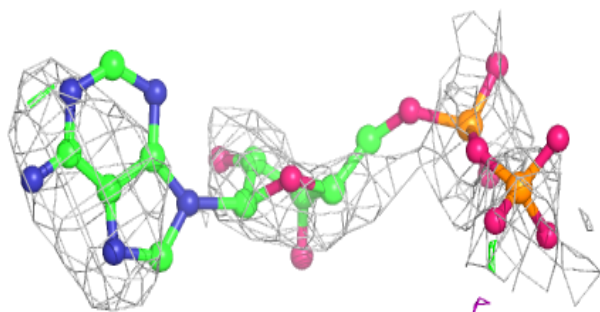
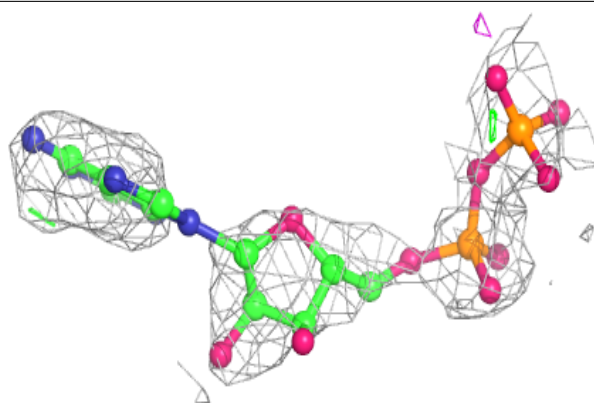
**Electron density around ADP C 4473:**

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

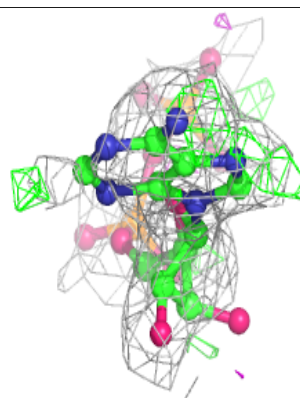
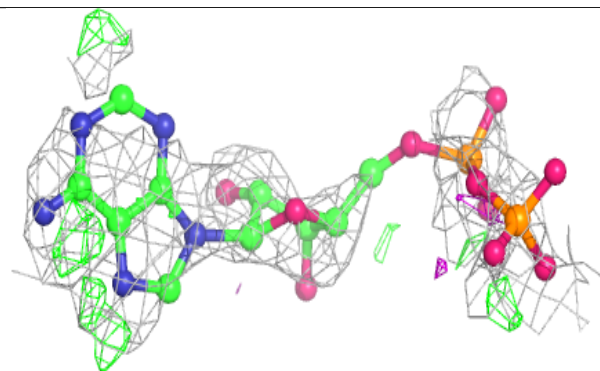
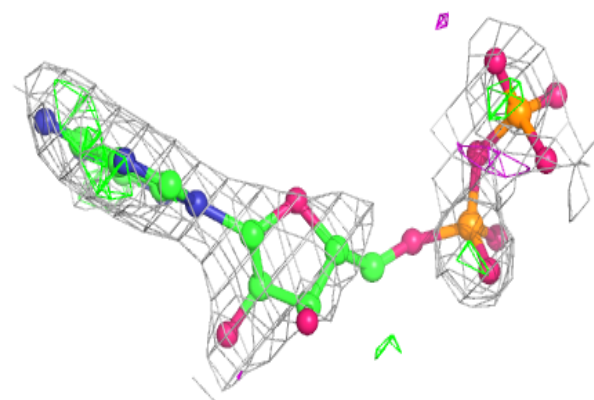


Electron density around ADP H 4478:

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

**Electron density around ADP J 4480:**

$2mF_o-DF_c$ (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.