



wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 07:14 am BST

PDB ID : 1LVU
Title : Crystal structure of calf spleen purine nucleoside phosphorylase in a new space group with full trimer in the asymmetric unit
Authors : Bzowska, A.; Koellner, G.; Wielgus-Kutrowska, B.; Stroh, A.; Raszewski, G.; Holy, A.; Steiner, T.; Frank, J.
Deposited on : 2002-05-29
Resolution : 2.05 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

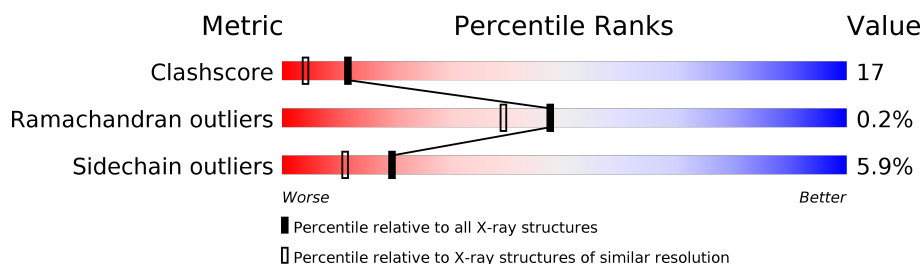
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	289	62% 29% • 6%
1	B	289	75% 18% • •
1	C	289	67% 24% • • 6%
1	D	289	73% 21% • •
1	E	289	61% 29% • 7%
1	F	289	67% 22% • 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14809 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 Purine nucleoside phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	272	Total	C	N	O	S	0	0	0
			2131	1352	374	390	15			
1	B	277	Total	C	N	O	S	0	0	0
			2174	1379	381	399	15			
1	C	273	Total	C	N	O	S	0	0	0
			2140	1357	376	391	16			
1	D	279	Total	C	N	O	S	0	0	0
			2189	1387	384	403	15			
1	E	268	Total	C	N	O	S	0	0	0
			2104	1337	370	382	15			
1	F	269	Total	C	N	O	S	0	0	0
			2112	1341	370	385	16			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	144	GLN	GLU	CONFLICT	UNP P55859
B	1144	GLN	GLU	CONFLICT	UNP P55859
C	2144	GLN	GLU	CONFLICT	UNP P55859
D	144	GLN	GLU	CONFLICT	UNP P55859
E	1144	GLN	GLU	CONFLICT	UNP P55859
F	2144	GLN	GLU	CONFLICT	UNP P55859

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

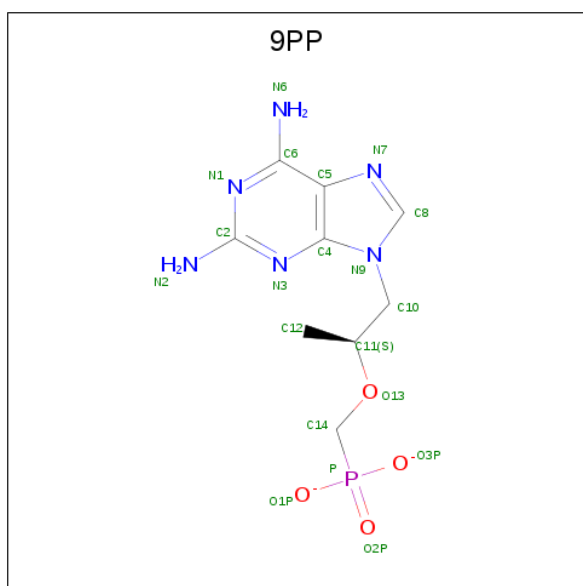
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Ca	0	0
			1	1		
2	E	1	Total	Ca	0	0
			1	1		
2	B	3	Total	Ca	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	1	Total	Ca	0	0
			1	1		
2	A	2	Total	Ca	0	0
			2	2		
2	F	2	Total	Ca	0	0
			2	2		

- Molecule 3 is 2,6-DIAMINO-(S)-9-[2-(PHOSPHONOMETHOXY)PROPYL]PURINE (three-letter code: 9PP) (formula: C₉H₁₃N₆O₄P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			20	9	6	4	1		
3	B	1	Total	C	N	O	P	0	0
			20	9	6	4	1		
3	C	1	Total	C	N	O	P	0	0
			20	9	6	4	1		
3	D	1	Total	C	N	O	P	0	0
			20	9	6	4	1		
3	E	1	Total	C	N	O	P	0	0
			20	9	6	4	1		
3	F	1	Total	C	N	O	P	0	0
			20	9	6	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	251	Total 251	O 251	0	0
4	B	331	Total 331	O 331	0	0
4	C	272	Total 272	O 272	0	0
4	D	350	Total 350	O 350	0	0
4	E	315	Total 315	O 315	0	0
4	F	310	Total 310	O 310	0	0

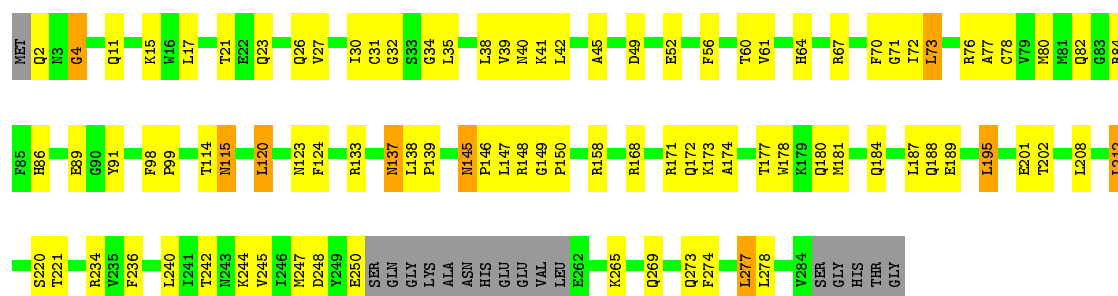
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

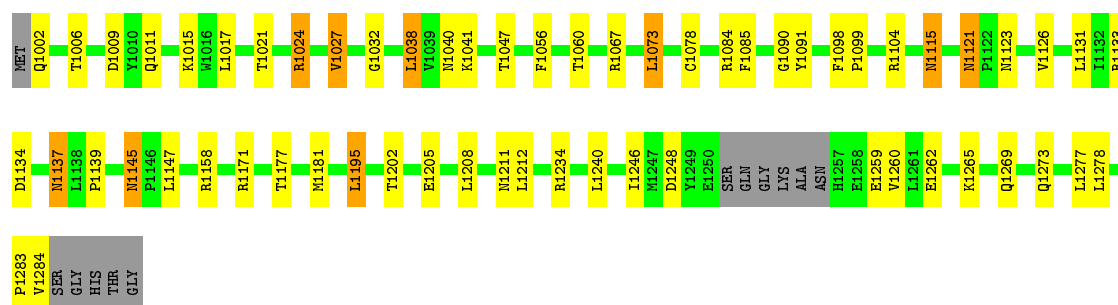
• Molecule 1: Purine nucleoside phosphorylase

Chain A: 



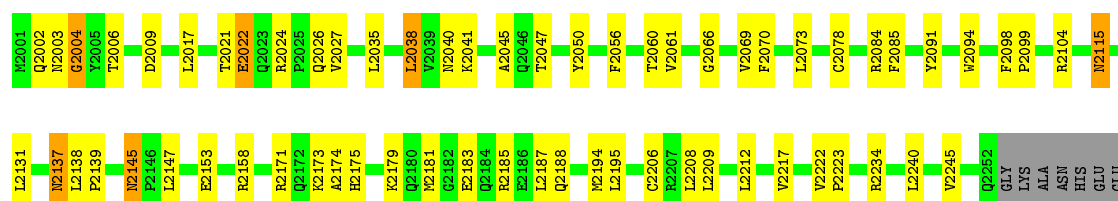
• Molecule 1: Purine nucleoside phosphorylase

Chain B: 



• Molecule 1: Purine nucleoside phosphorylase

Chain C: 





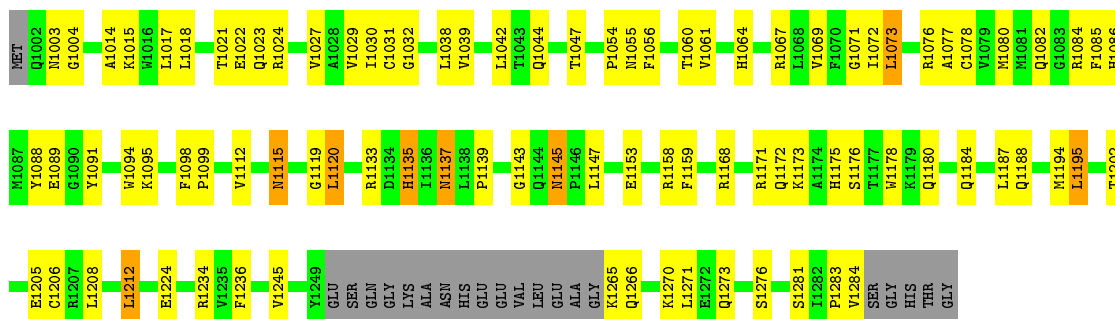
• Molecule 1: Purine nucleoside phosphorylase

Chain D: 73% 21%



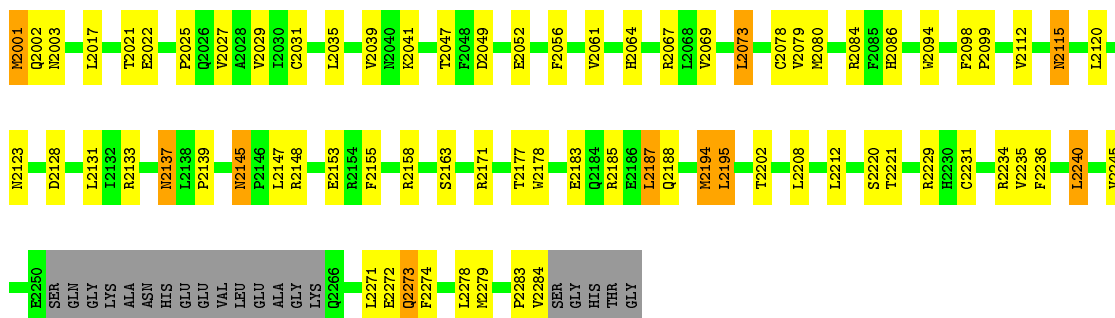
• Molecule 1: Purine nucleoside phosphorylase

Chain E: 61% 29% 7%



• Molecule 1: Purine nucleoside phosphorylase

Chain F: 67% 22% 7%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.01Å 132.62Å 177.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.05	Depositor
% Data completeness (in resolution range)	98.7 (20.00-2.05)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.188 , 0.244	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14809	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 9PP

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	0.37	1/2179 (0.0%)	0.64	1/2948 (0.0%)
1	B	0.34	0/2223	0.63	0/3008
1	C	0.39	2/2188 (0.1%)	0.91	6/2959 (0.2%)
1	D	0.34	0/2238	0.63	1/3028 (0.0%)
1	E	0.33	0/2152	0.63	1/2912 (0.0%)
1	F	0.34	0/2160	0.63	0/2923
All	All	0.35	3/13140 (0.0%)	0.69	9/17778 (0.1%)

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	C	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4	GLY	N-CA	8.71	1.59	1.46
1	C	2004	GLY	N-CA	7.07	1.56	1.46
1	C	2265	LYS	C-N	5.25	1.46	1.34

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2266	GLN	N-CA-C	-20.94	54.47	111.00
1	C	2265	LYS	O-C-N	-17.94	93.99	122.70
1	C	2265	LYS	C-N-CA	-13.92	86.91	121.70
1	C	2265	LYS	CA-C-N	12.89	145.57	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2266	GLN	N-CA-CB	12.43	132.97	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	2265	LYS	Peptide

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	2131	0	2091	91	0
1	B	2174	0	2130	58	0
1	C	2140	0	2102	76	0
1	D	2189	0	2143	69	0
1	E	2104	0	2071	86	0
1	F	2112	0	2073	77	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	2	0	0	0	0
3	A	20	0	13	2	0
3	B	20	0	13	1	0
3	C	20	0	13	0	0
3	D	20	0	13	2	0
3	E	20	0	13	2	0
3	F	20	0	13	2	0
4	A	251	0	0	7	0
4	B	331	0	0	12	0
4	C	272	0	0	11	0
4	D	350	0	0	12	0
4	E	315	0	0	20	0
4	F	310	0	0	7	0
All	All	14809	0	12688	449	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 17.

The worst 5 of 449 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:C:2265:LYS:HB3	1:C:2266:GLN:OE1	1.30	1.29
1:C:2265:LYS:CB	1:C:2266:GLN:OE1	1.86	1.23
1:A:27:VAL:HG13	1:A:78:CYS:HB3	1.35	1.06
1:E:1206:CYS:HB3	4:E:8161:HOH:O	1.57	1.05
1:E:1145:ASN:HD22	1:E:1147:LEU:H	1.09	0.96

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	268/289 (93%)	256 (96%)	11 (4%)	1 (0%)	34	24
1	B	273/289 (94%)	266 (97%)	7 (3%)	0	100	100
1	C	269/289 (93%)	258 (96%)	9 (3%)	2 (1%)	22	12
1	D	275/289 (95%)	267 (97%)	8 (3%)	0	100	100
1	E	264/289 (91%)	258 (98%)	6 (2%)	0	100	100
1	F	265/289 (92%)	257 (97%)	8 (3%)	0	100	100
All	All	1614/1734 (93%)	1562 (97%)	49 (3%)	3 (0%)	47	39

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	GLY
1	C	2266	GLN
1	C	2004	GLY

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	226/239 (95%)	214 (95%)	12 (5%)	22	14
1	B	231/239 (97%)	217 (94%)	14 (6%)	18	10
1	C	228/239 (95%)	217 (95%)	11 (5%)	25	18
1	D	233/239 (98%)	218 (94%)	15 (6%)	17	9
1	E	224/239 (94%)	209 (93%)	15 (7%)	16	9
1	F	225/239 (94%)	212 (94%)	13 (6%)	20	11
All	All	1367/1434 (95%)	1287 (94%)	80 (6%)	19	11

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	2266	GLN
1	D	145	ASN
1	F	2187	LEU
1	D	38	LEU
1	D	115	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	2199	ASN
1	D	180	GLN
1	F	2144	GLN
1	C	2273	GLN
1	D	137	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 10 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	9PP	B	6200	-	18,21,21	3.84	9 (50%)	17,31,31	3.41	4 (23%)
3	9PP	F	6600	-	18,21,21	3.90	7 (38%)	17,31,31	3.42	4 (23%)
3	9PP	C	6300	-	18,21,21	3.89	7 (38%)	17,31,31	3.47	4 (23%)
3	9PP	E	6500	-	18,21,21	3.87	9 (50%)	17,31,31	3.45	4 (23%)
3	9PP	D	6400	-	18,21,21	3.79	8 (44%)	17,31,31	3.50	4 (23%)
3	9PP	A	6100	-	18,21,21	3.95	9 (50%)	17,31,31	3.48	4 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	9PP	B	6200	-	-	1/8/10/10	0/2/2/2
3	9PP	F	6600	-	-	1/8/10/10	0/2/2/2
3	9PP	C	6300	-	-	0/8/10/10	0/2/2/2
3	9PP	E	6500	-	-	1/8/10/10	0/2/2/2
3	9PP	D	6400	-	-	0/8/10/10	0/2/2/2
3	9PP	A	6100	-	-	1/8/10/10	0/2/2/2

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	6300	9PP	P-C14	-10.94	1.52	1.80
3	F	6600	9PP	P-C14	-10.87	1.53	1.80
3	A	6100	9PP	P-C14	-10.82	1.53	1.80
3	B	6200	9PP	P-C14	-10.72	1.53	1.80
3	E	6500	9PP	P-C14	-10.48	1.53	1.80

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	6100	9PP	C5-C6-N1	-12.38	112.88	121.01
3	D	6400	9PP	C5-C6-N1	-12.34	112.91	121.01
3	C	6300	9PP	C5-C6-N1	-12.21	113.00	121.01
3	E	6500	9PP	C5-C6-N1	-12.13	113.04	121.01
3	F	6600	9PP	C5-C6-N1	-11.98	113.14	121.01

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	6600	9PP	C12-C11-O13-C14
3	E	6500	9PP	C12-C11-O13-C14
3	A	6100	9PP	C12-C11-O13-C14
3	B	6200	9PP	C12-C11-O13-C14

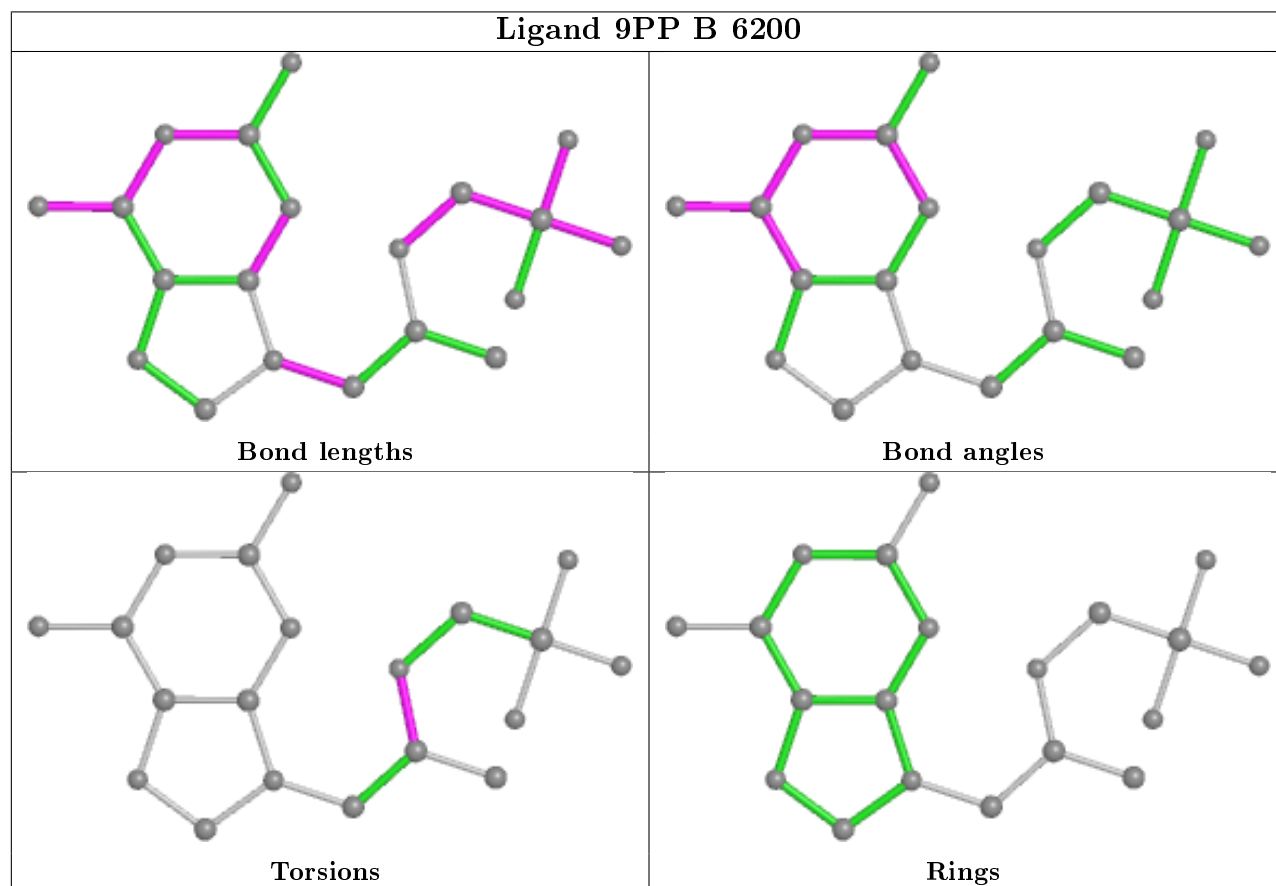
There are no ring outliers.

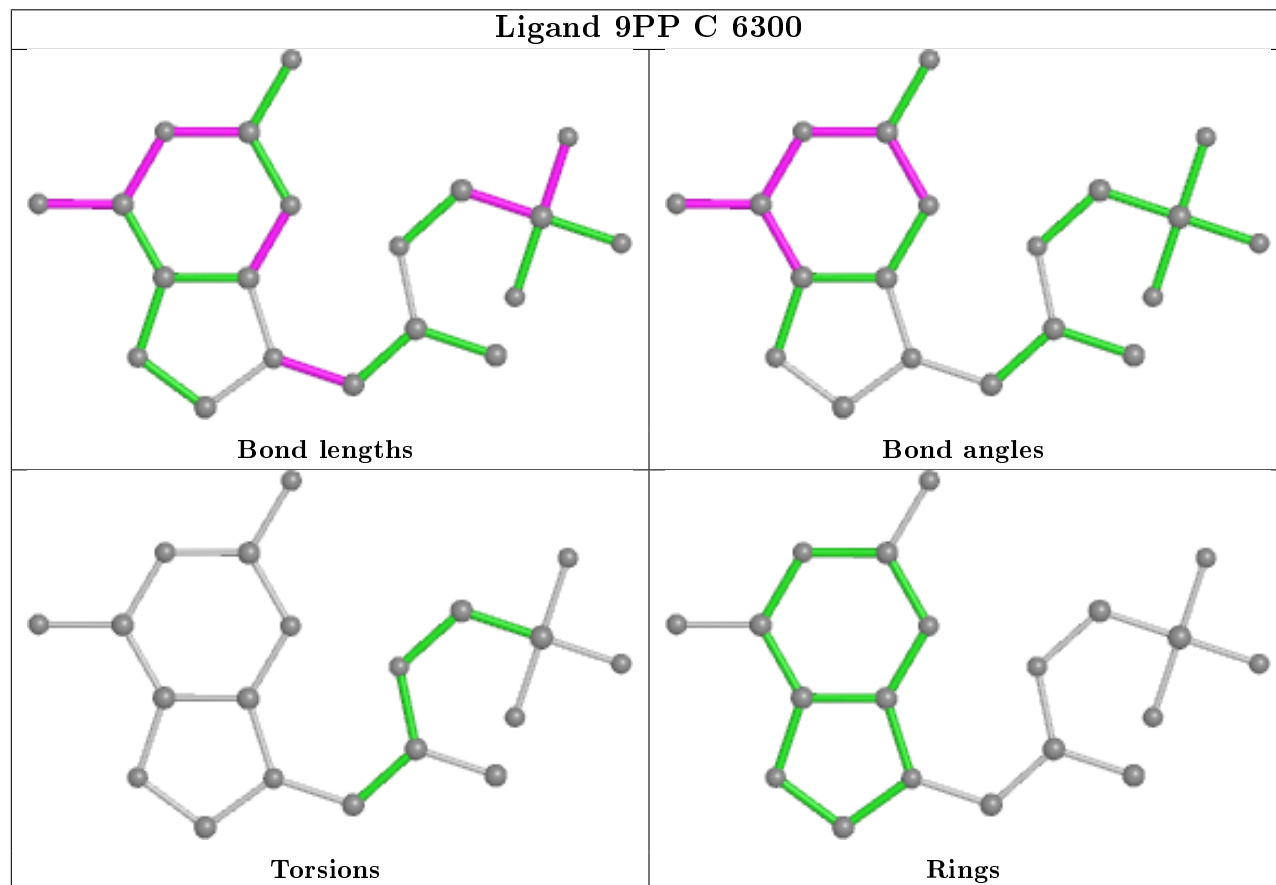
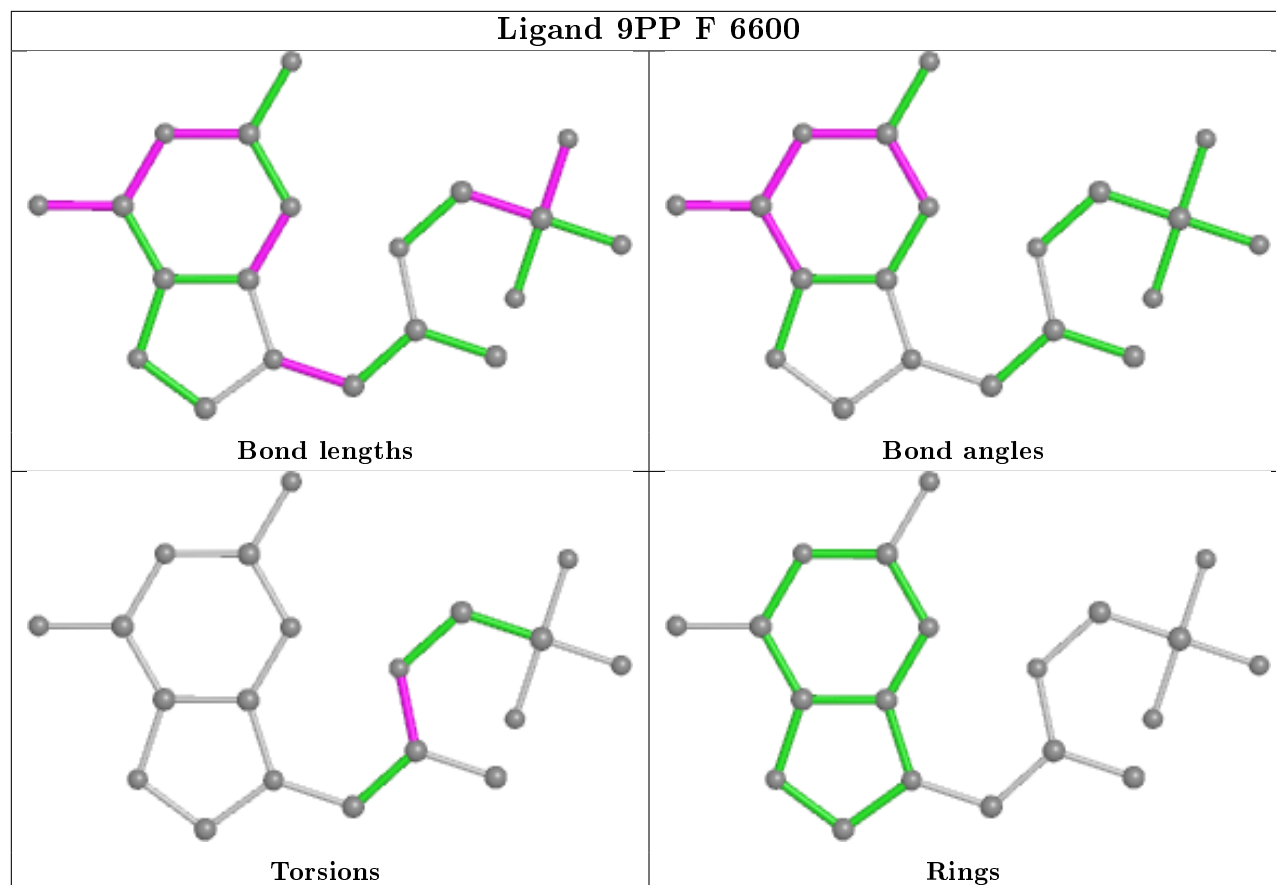
5 monomers are involved in 9 short contacts:

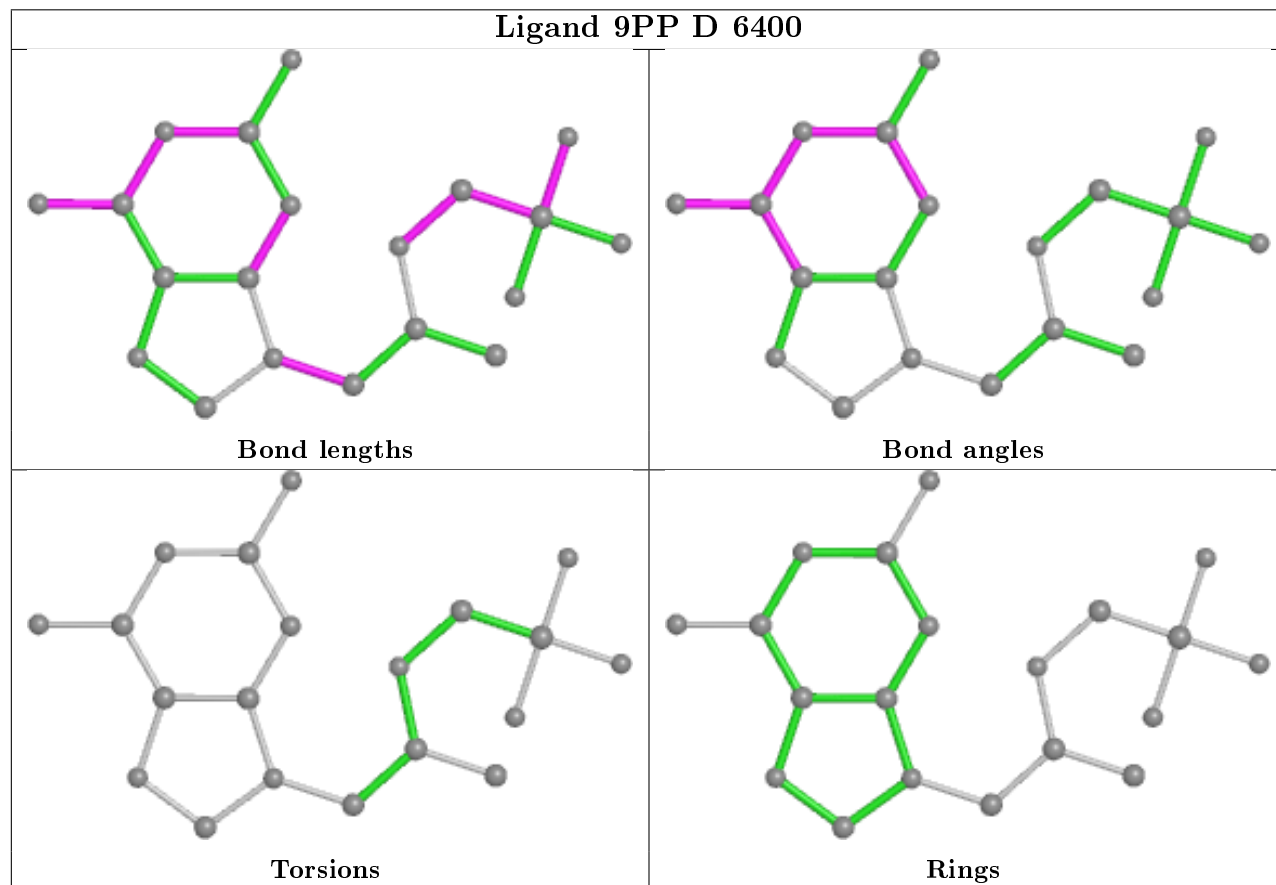
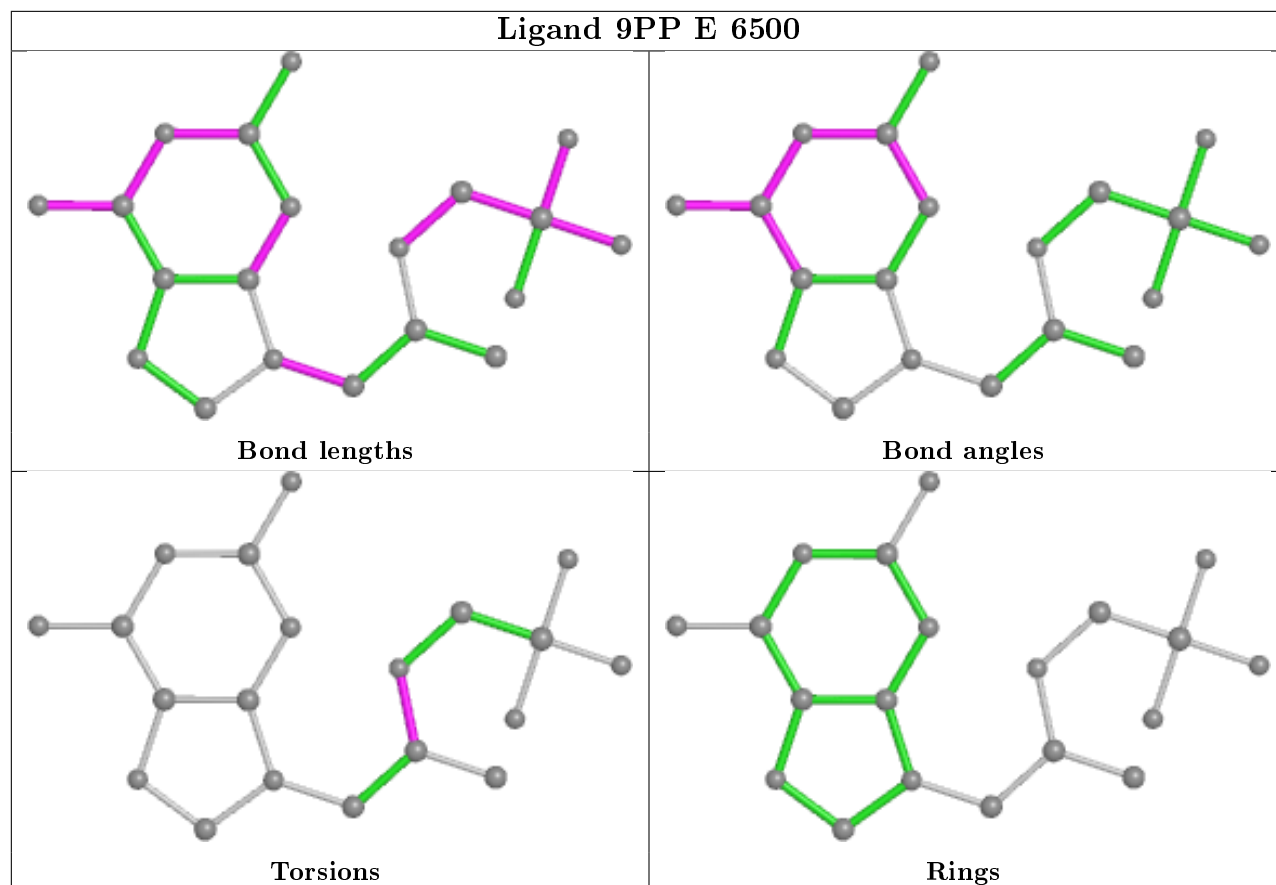
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	6200	9PP	1	0
3	F	6600	9PP	2	0
3	E	6500	9PP	2	0
3	D	6400	9PP	2	0
3	A	6100	9PP	2	0

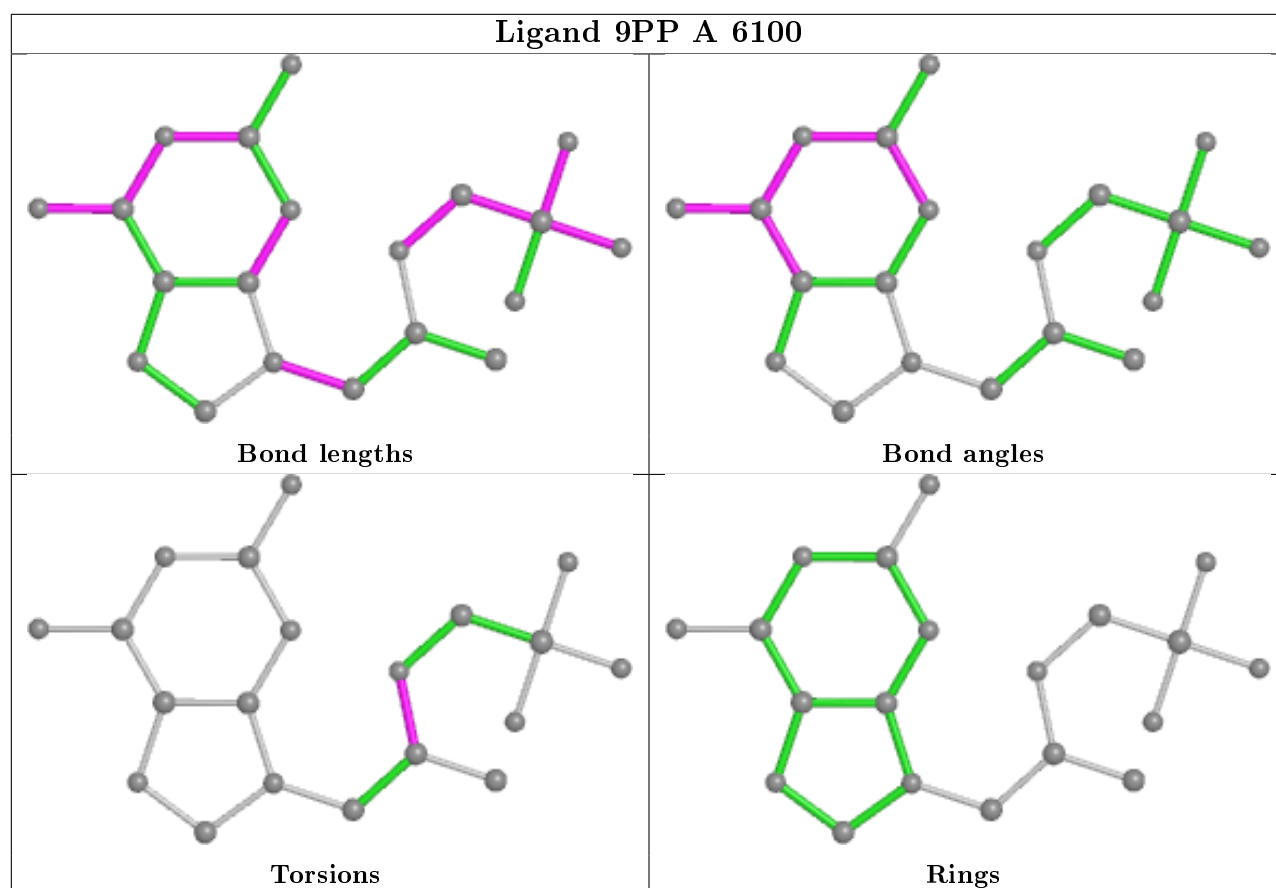
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.