Full wwPDB X-ray Structure Validation Report (i)

Dec 2, 2023 – 03:00 pm GMT

PDB ID	:	1HE3
Title	:	Human biliverdin IX beta reductase: NADP/mesobiliverdin IV alpha ternary complex
Authors	:	Pereira, P.J.B.; Macedo-Ribeiro, S.; Parraga, A.; Perez-Luque, R.; Cunningham, O.; Darcy, K.; Mantle, T.J.; Coll, M.
Deposited on	:	2000-11-18
Resolution	:	1.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

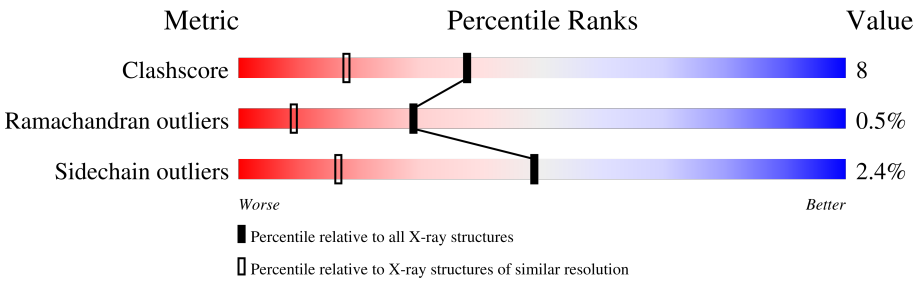
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.40 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	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	206	84% 12% • ••

2 Entry composition (i)

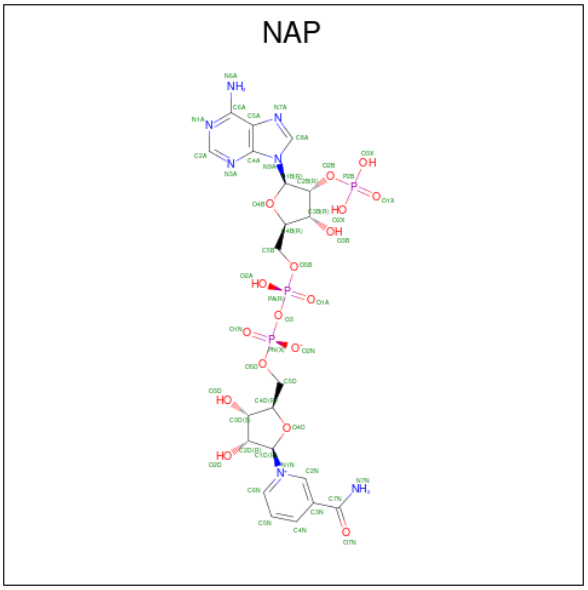
There are 4 unique types of molecules in this entry. The entry contains 1953 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BILIVERDIN IX BETA REDUCTASE.

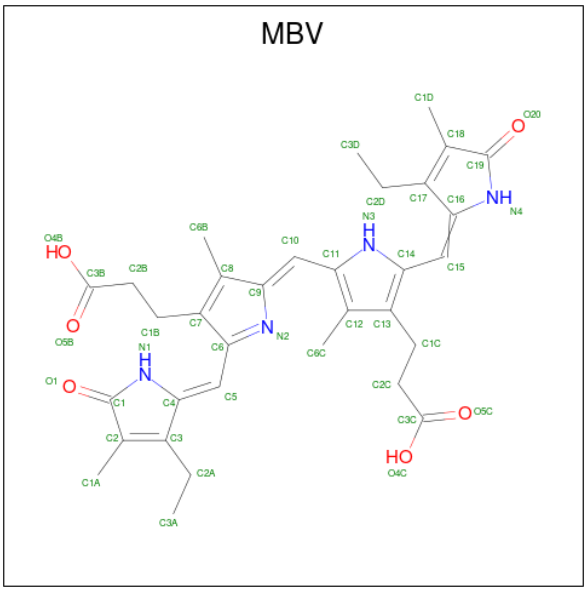
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	204	1573	988	277	299	9	16	12	0

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	48	21	7	17	3	0	0

- Molecule 3 is MESOBILIVERDIN IV ALPHA (three-letter code: MBV) (formula: $C_{33}H_{38}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	43	33	4	6	14	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	289	289	289	0	16

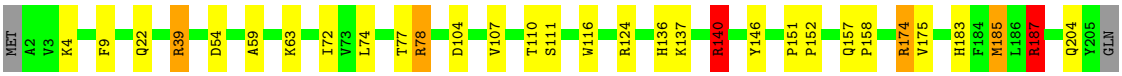
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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: BILIVERDIN IX BETA REDUCTASE

Chain A:



4 Data and refinement statistics (i)

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	40.20Å 49.40Å 107.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.40	Depositor
% Data completeness (in resolution range)	98.3 (20.00-1.40)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.138 , 0.181	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1953	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MBV, NAP

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	0.58	0/1651	1.24	13/2249 (0.6%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	39	ARG	CD-NE-CZ	12.80	141.52	123.60
1	A	78	ARG	NE-CZ-NH2	-11.91	114.34	120.30
1	A	39	ARG	NE-CZ-NH1	10.82	125.71	120.30
1	A	187	ARG	CD-NE-CZ	9.44	136.81	123.60
1	A	140	ARG	NE-CZ-NH2	9.01	124.81	120.30
1	A	146	TYR	CB-CG-CD1	7.71	125.63	121.00
1	A	140	ARG	NE-CZ-NH1	-7.66	116.47	120.30
1	A	185[A]	MET	CA-CB-CG	6.54	124.42	113.30
1	A	185[B]	MET	CA-CB-CG	6.54	124.42	113.30
1	A	54	ASP	CB-CG-OD1	6.35	124.01	118.30
1	A	174	ARG	CD-NE-CZ	5.71	131.60	123.60
1	A	174	ARG	NE-CZ-NH2	5.17	122.89	120.30
1	A	9	PHE	CB-CG-CD1	-5.16	117.19	120.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1573	0	1567	25	1
2	A	48	0	25	2	0
3	A	43	0	36	4	0
4	A	289	0	0	3	0
All	All	1953	0	1628	25	1

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 8.

All (25) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104[B]:ASP:OD2	4:A:2186[B]:HOH:O	1.66	1.10
1:A:157:GLN:HE22	1:A:175[A]:VAL:HG21	1.55	0.71
1:A:110:THR:O	2:A:1206:NAP:H6N	1.98	0.63
1:A:78:ARG:HB3	4:A:2155:HOH:O	2.05	0.55
1:A:74:LEU:HD21	1:A:185[B]:MET:SD	2.49	0.53
1:A:4:LYS:HG3	4:A:2063:HOH:O	2.08	0.53
1:A:187:ARG:HH11	1:A:187:ARG:HG3	1.74	0.53
1:A:116:TRP:CH2	3:A:1207:MBV:H1B1	2.46	0.51
1:A:116:TRP:CH2	1:A:174:ARG:HD3	2.45	0.51
1:A:116:TRP:CZ2	1:A:174:ARG:HD3	2.48	0.48
1:A:77:THR:OG1	3:A:1207:MBV:O5C	2.32	0.48
1:A:157:GLN:HB3	1:A:158:PRO:HD2	1.94	0.48
1:A:59:ALA:O	1:A:63:LYS:HG3	2.14	0.47
1:A:72[B]:ILE:HD13	1:A:107:VAL:HB	1.96	0.47
1:A:137:LYS:HA	1:A:140:ARG:HG2	1.96	0.47
1:A:63:LYS:HZ2	1:A:63:LYS:HB3	1.81	0.46
1:A:22:GLN:HE22	1:A:183:HIS:HB2	1.81	0.46
1:A:78:ARG:O	3:A:1207:MBV:O4C	2.34	0.45
1:A:151:PRO:O	2:A:1206:NAP:H5N	2.17	0.44
1:A:63:LYS:HB3	1:A:63:LYS:NZ	2.34	0.43
1:A:136:HIS:CD2	1:A:140:ARG:HH12	2.37	0.42
1:A:140:ARG:HG2	1:A:140:ARG:HH11	1.86	0.40
1:A:116:TRP:HH2	3:A:1207:MBV:H1B1	1.85	0.40
1:A:187:ARG:HH11	1:A:187:ARG:CG	2.34	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:ARG:NH1	1:A:204:GLN:NE2[4_545]	2.06	0.14

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	214/206 (104%)	210 (98%)	3 (1%)	1 (0%)	29 9

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	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	178/169 (105%)	174 (98%)	4 (2%)	52 19

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ARG
1	A	111	SER
1	A	140	ARG
1	A	187	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAP	A	1206	-	45,52,52	2.27	9 (20%)	56,80,80	2.16	17 (30%)
3	MBV	A	1207	-	42,46,46	2.59	16 (38%)	54,67,67	1.98	14 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAP	A	1206	-	-	7/31/67/67	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MBV	A	1207	-	-	13/26/74/74	0/4/4/4

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1206	NAP	C2N-N1N	9.99	1.47	1.35
3	A	1207	MBV	C3-C2	6.49	1.50	1.36
3	A	1207	MBV	C17-C18	-5.80	1.24	1.36
3	A	1207	MBV	C4-C3	-5.80	1.34	1.45
3	A	1207	MBV	C4-N1	5.36	1.46	1.37
2	A	1206	NAP	C4N-C3N	4.81	1.47	1.39
3	A	1207	MBV	C6-N2	4.51	1.47	1.36
3	A	1207	MBV	C13-C12	4.40	1.50	1.37
2	A	1206	NAP	O4D-C1D	4.37	1.47	1.41
2	A	1206	NAP	C6N-C5N	3.92	1.47	1.38
3	A	1207	MBV	C1-N1	3.74	1.45	1.38
2	A	1206	NAP	C4A-N3A	3.70	1.40	1.35
3	A	1207	MBV	C9-N2	3.52	1.46	1.38
3	A	1207	MBV	C1D-C18	3.30	1.57	1.50
3	A	1207	MBV	C5-C4	3.15	1.45	1.38
3	A	1207	MBV	C16-C17	3.07	1.50	1.45
2	A	1206	NAP	C2A-N1A	2.95	1.39	1.33
3	A	1207	MBV	C6-C7	2.87	1.50	1.45
3	A	1207	MBV	C5-C6	-2.85	1.33	1.40
2	A	1206	NAP	C6N-N1N	2.60	1.41	1.35
2	A	1206	NAP	C3N-C7N	2.49	1.54	1.50
2	A	1206	NAP	C2D-C1D	-2.34	1.50	1.53
3	A	1207	MBV	C9-C8	2.19	1.50	1.45
3	A	1207	MBV	C1-C2	-2.06	1.42	1.47
3	A	1207	MBV	O1-C1	2.03	1.27	1.23

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1206	NAP	O7N-C7N-N7N	7.77	133.62	122.58
2	A	1206	NAP	O7N-C7N-C3N	-6.67	111.65	119.63
3	A	1207	MBV	C2D-C17-C18	-5.83	117.55	127.53
3	A	1207	MBV	C3D-C2D-C17	5.50	127.59	112.43
3	A	1207	MBV	C16-C17-C18	4.92	112.46	107.82
2	A	1206	NAP	C5A-C6A-N6A	4.32	126.92	120.35
2	A	1206	NAP	O4B-C1B-C2B	-4.31	99.11	106.59
3	A	1207	MBV	C2D-C17-C16	4.16	129.99	124.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1207	MBV	C11-C10-C9	-3.62	124.48	128.81
2	A	1206	NAP	C3N-C2N-N1N	-3.52	116.99	120.43
2	A	1206	NAP	C2N-C3N-C4N	3.16	121.84	118.26
3	A	1207	MBV	C1D-C18-C17	3.04	134.38	126.12
2	A	1206	NAP	C5A-C6A-N1A	-2.91	113.75	120.35
2	A	1206	NAP	N3A-C2A-N1A	-2.90	124.14	128.68
3	A	1207	MBV	C2C-C1C-C13	-2.87	107.72	112.62
3	A	1207	MBV	C5-C4-N1	-2.83	119.97	126.06
2	A	1206	NAP	O4D-C1D-C2D	-2.72	102.95	106.93
2	A	1206	NAP	C3N-C7N-N7N	-2.61	114.62	117.75
2	A	1206	NAP	C1B-N9A-C4A	-2.57	122.12	126.64
3	A	1207	MBV	C17-C16-N4	-2.55	103.58	107.30
2	A	1206	NAP	C2A-N1A-C6A	2.51	123.05	118.75
3	A	1207	MBV	C4-N1-C1	-2.44	107.56	110.67
2	A	1206	NAP	C6N-N1N-C2N	2.44	124.20	121.97
3	A	1207	MBV	C9-C8-C7	2.37	109.23	106.51
2	A	1206	NAP	O2A-PA-O1A	2.37	123.95	112.24
2	A	1206	NAP	O3X-P2B-O2X	2.27	116.32	107.64
3	A	1207	MBV	C1C-C2C-C3C	-2.19	107.61	113.76
2	A	1206	NAP	C5N-C6N-N1N	-2.19	117.26	120.40
3	A	1207	MBV	C1A-C2-C1	2.16	126.47	121.39
2	A	1206	NAP	O5B-C5B-C4B	-2.07	101.86	108.99
3	A	1207	MBV	C19-C18-C17	-2.04	106.15	108.07

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1206	NAP	O4D-C1D-N1N-C2N
2	A	1206	NAP	O4D-C1D-N1N-C6N
2	A	1206	NAP	C2D-C1D-N1N-C2N
2	A	1206	NAP	C2D-C1D-N1N-C6N
3	A	1207	MBV	N3-C14-C15-C16
3	A	1207	MBV	C13-C14-C15-C16
3	A	1207	MBV	C14-C15-C16-N4
3	A	1207	MBV	C14-C15-C16-C17
3	A	1207	MBV	C7-C1B-C2B-C3B
3	A	1207	MBV	C13-C1C-C2C-C3C
3	A	1207	MBV	C2B-C1B-C7-C6
3	A	1207	MBV	C2B-C1B-C7-C8
3	A	1207	MBV	C14-C13-C1C-C2C
3	A	1207	MBV	C12-C13-C1C-C2C

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Mol	Chain	Res	Type	Atoms
3	A	1207	MBV	C1C-C2C-C3C-O4C
3	A	1207	MBV	C1C-C2C-C3C-O5C
2	A	1206	NAP	C2B-O2B-P2B-O2X
2	A	1206	NAP	O4B-C4B-C5B-O5B
2	A	1206	NAP	PN-O3-PA-O1A
3	A	1207	MBV	C1B-C2B-C3B-O4B

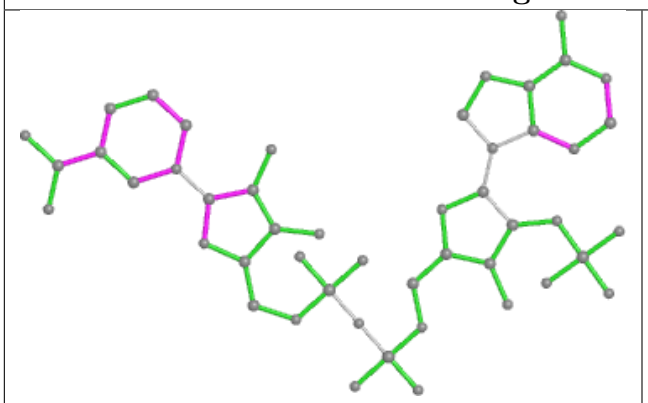
There are no ring outliers.

2 monomers are involved in 6 short contacts:

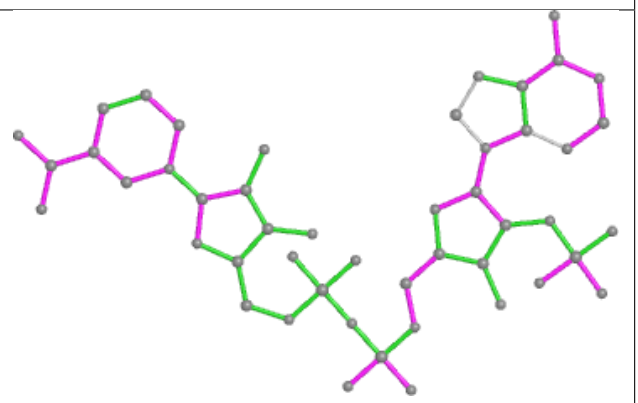
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1206	NAP	2	0
3	A	1207	MBV	4	0

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

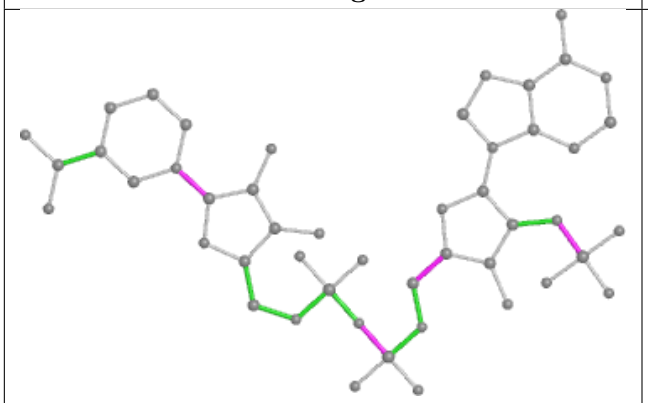
Ligand NAP A 1206



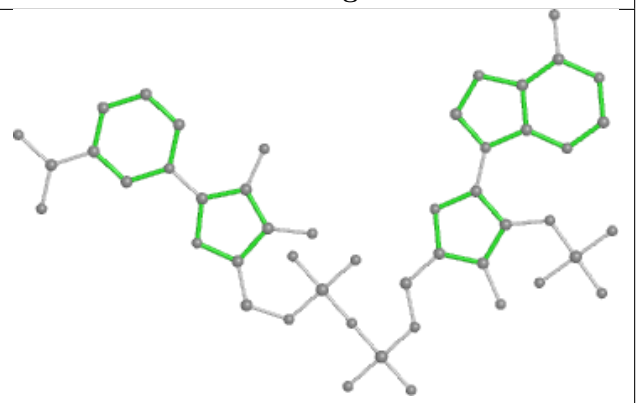
Bond lengths



Bond angles

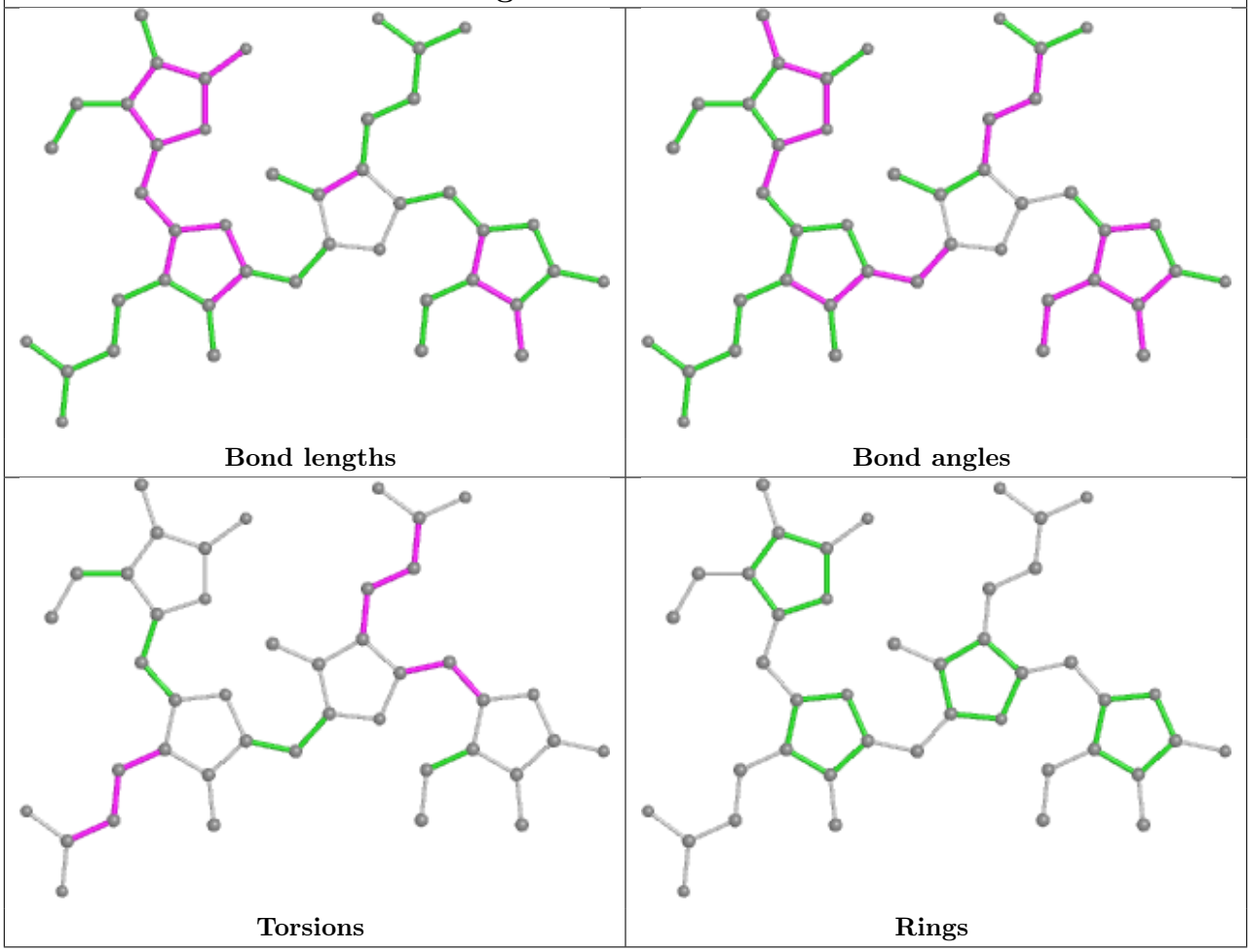


Torsions



Rings

Ligand MBV A 1207



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.