



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 3, 2023 – 09:44 am GMT

PDB ID : 1H0H
Title : Tungsten containing Formate Dehydrogenase from *Desulfovibrio Gigas*
Authors : Raaijmakers, H.C.A.
Deposited on : 2002-06-19
Resolution : 1.80 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

<https://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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtrriage (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

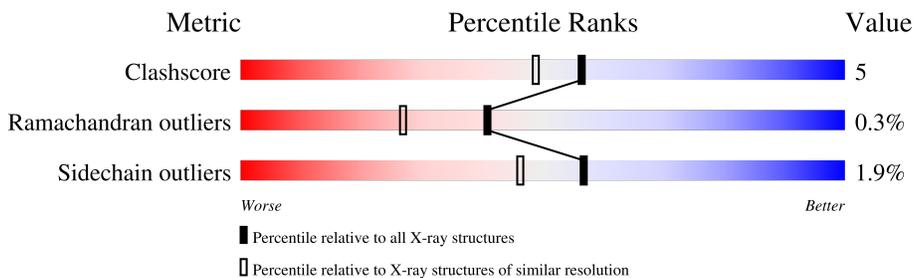
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	977	
1	K	977	
2	B	214	
2	L	214	

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
4	2MD	A	1001	X	-	-	-
4	2MD	K	1001	X	-	-	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 21055 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 FORMATE DEHYDROGENASE SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S				Se
1	A	977	7857	5002	1349	1458	47	1	4	28	0
1	K	977	7836	4992	1341	1455	47	1	6	23	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	959	ASN	ASP	conflict	UNP Q934F5
K	959	ASN	ASP	conflict	UNP Q934F5

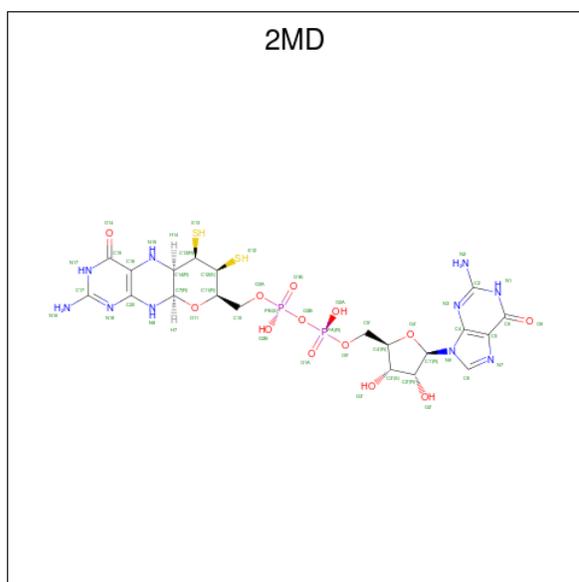
- Molecule 2 is a protein called FORMATE DEHYDROGENASE SUBUNIT BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	214	1697	1051	293	332	21	0	8	0
2	L	214	1669	1037	287	323	22	0	2	0

- Molecule 3 is TUNGSTEN ION (three-letter code: W) (formula: W).

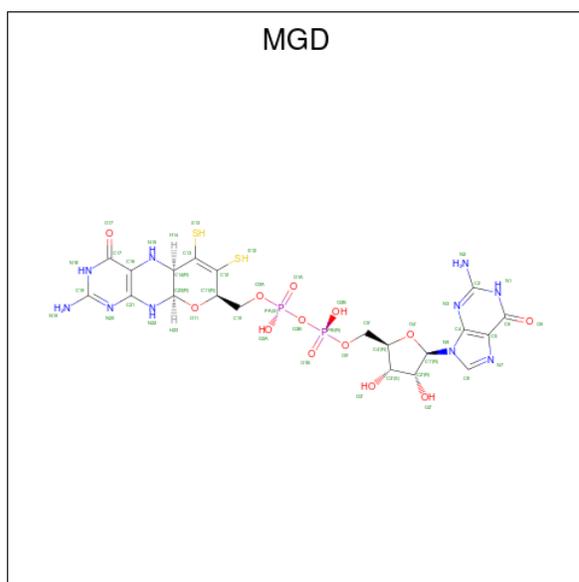
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total W 1 1	0	0
3	K	1	Total W 1 1	0	0

- Molecule 4 is GUANYLATE-O'-PHOSPHORIC ACID MONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,5,6,7,8A,9,10,10A-OCTAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (three-letter code: 2MD) (formula: C₂₀H₂₈N₁₀O₁₃P₂S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
4	A	1	47	20	10	13	2	2	0	0
4	K	1	47	20	10	13	2	2	0	0

- Molecule 5 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: MGD) (formula: C₂₀H₂₆N₁₀O₁₃P₂S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
5	A	1	47	20	10	13	2	2	0	0

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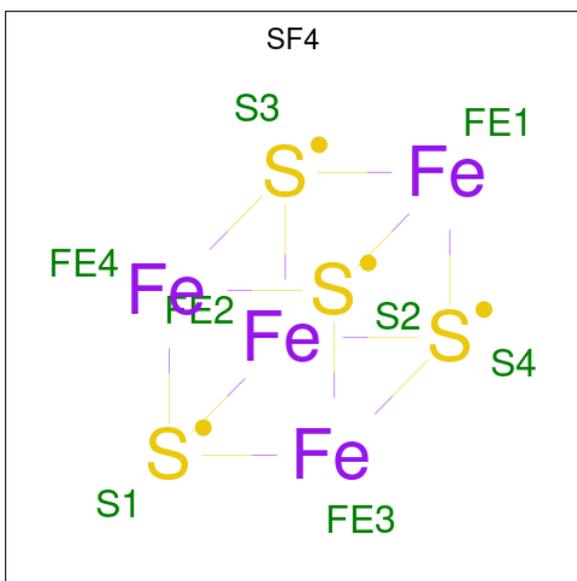
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
5	K	1	47	20	10	13	2	2	0	0

- Molecule 6 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total X 1 1	0	0
6	K	1	Total X 1 1	0	0

- Molecule 7 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Fe S 8 4 4	0	0
7	B	1	Total Fe S 8 4 4	0	0
7	B	1	Total Fe S 8 4 4	0	0
7	B	1	Total Fe S 8 4 4	0	0
7	K	1	Total Fe S 8 4 4	0	0
7	L	1	Total Fe S 8 4 4	0	0

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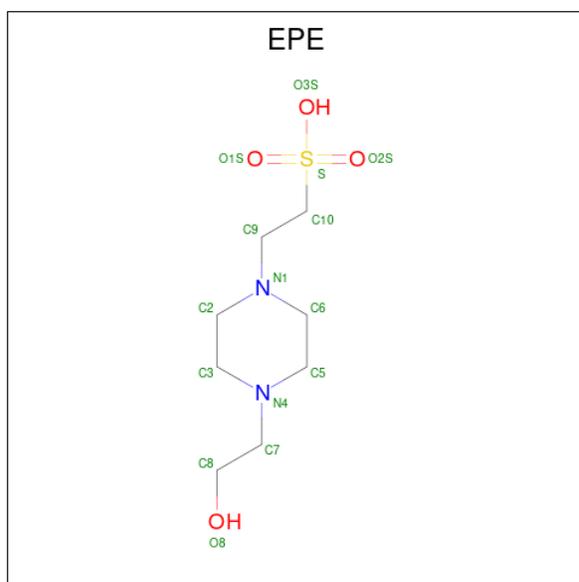
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	L	1	Total	Fe	S	0	0
			8	4	4		
7	L	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Ca	0	0
			1	1		
8	K	1	Total	Ca	0	0
			1	1		

- Molecule 9 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
9	K	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 10 is water.

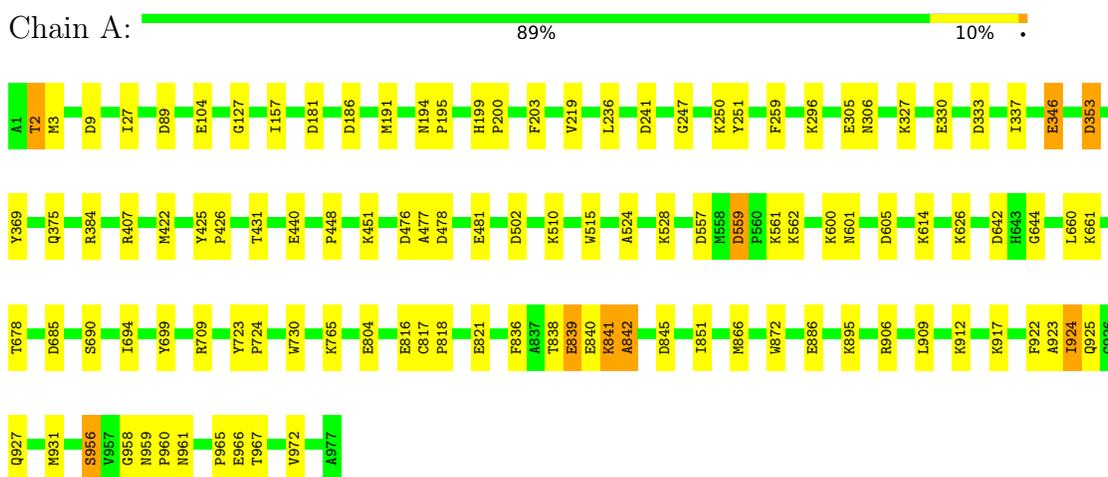
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	704	Total 704	O 704	0	0
10	B	188	Total 188	O 188	0	0
10	K	623	Total 623	O 623	0	0
10	L	193	Total 193	O 193	0	0

3 Residue-property plots [i](#)

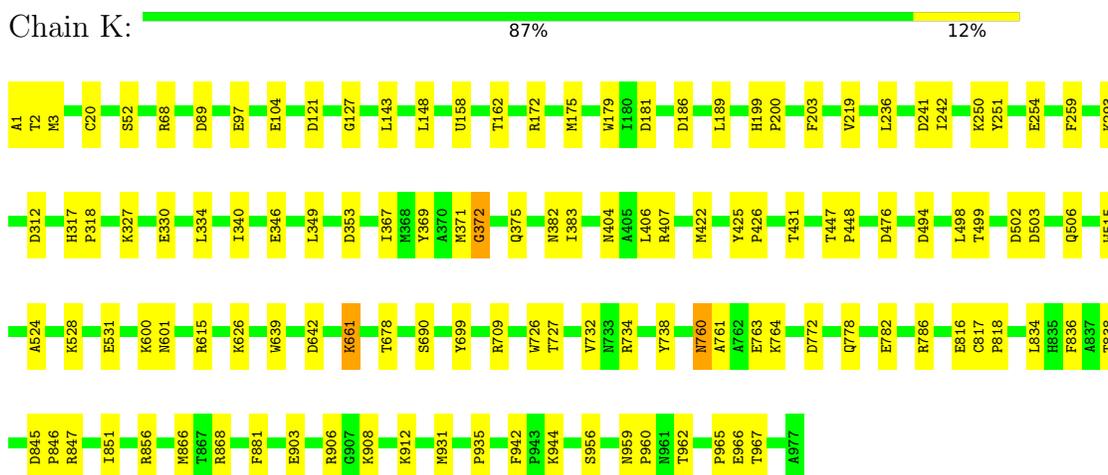
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: FORMATE DEHYDROGENASE SUBUNIT ALPHA

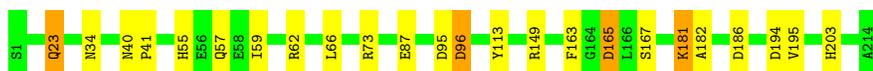


- Molecule 1: FORMATE DEHYDROGENASE SUBUNIT ALPHA



- Molecule 2: FORMATE DEHYDROGENASE SUBUNIT BETA





- Molecule 2: FORMATE DEHYDROGENASE SUBUNIT BETA

Chain L:  90% 9%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.41Å 110.40Å 156.19Å 90.00° 93.53° 90.00°	Depositor
Resolution (Å)	35.00 – 1.80	Depositor
% Data completeness (in resolution range)	95.7 (35.00-1.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.167 , 0.201	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	21055	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: W, SEC, UNX, CA, 2MD, SF4, EPE, MGD

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	0.59	0/8171	0.83	18/11073 (0.2%)
1	K	0.55	0/8120	0.82	8/11010 (0.1%)
2	B	0.55	0/1771	0.87	7/2404 (0.3%)
2	L	0.57	0/1720	0.88	6/2334 (0.3%)
All	All	0.57	0/19782	0.83	39/26821 (0.1%)

There are no bond length outliers.

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	186	ASP	CB-CG-OD2	7.17	124.75	118.30
1	A	685	ASP	CB-CG-OD2	6.85	124.47	118.30
1	K	121	ASP	CB-CG-OD2	6.46	124.11	118.30
2	B	194	ASP	CB-CG-OD2	6.34	124.01	118.30
1	K	89	ASP	CB-CG-OD2	6.29	123.96	118.30

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	7857	0	7657	78	0
1	K	7836	0	7633	80	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1697	0	1575	19	1
2	L	1669	0	1570	16	0
3	A	1	0	0	0	0
3	K	1	0	0	0	0
4	A	47	0	23	2	0
4	K	47	0	22	2	0
5	A	47	0	22	0	0
5	K	47	0	22	0	0
6	A	1	0	0	0	0
6	K	1	0	0	0	0
7	A	8	0	0	0	0
7	B	24	0	0	0	0
7	K	8	0	0	0	0
7	L	24	0	0	0	0
8	A	1	0	0	0	0
8	K	1	0	0	0	0
9	A	15	0	17	1	0
9	K	15	0	17	1	0
10	A	704	0	0	6	0
10	B	188	0	0	5	0
10	K	623	0	0	12	0
10	L	193	0	0	5	0
All	All	21055	0	18558	189	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 5.

The worst 5 of 189 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:839[B]:GLU:HG2	1:A:840[B]:GLU:OE1	1.01	1.17
1:K:531:GLU:HG3	10:K:2066:HOH:O	1.41	1.16
1:A:839[B]:GLU:CG	1:A:840[B]:GLU:OE1	1.96	1.12
2:L:168:GLU:OE1	10:L:2152:HOH:O	1.78	1.01
2:L:62:ARG:HH11	2:L:62:ARG:HG3	1.27	0.97

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)
2:B:96[A]:ASP:OD2	1:K:847:ARG:NH1[1_545]	2.18	0.02

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	1002/977 (103%)	968 (97%)	29 (3%)	5 (0%)	29	15
1	K	997/977 (102%)	965 (97%)	28 (3%)	4 (0%)	34	21
2	B	220/214 (103%)	213 (97%)	7 (3%)	0	100	100
2	L	214/214 (100%)	207 (97%)	7 (3%)	0	100	100
All	All	2433/2382 (102%)	2353 (97%)	71 (3%)	9 (0%)	41	21

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	841[A]	LYS
1	A	841[B]	LYS
1	A	842[A]	ALA
1	A	842[B]	ALA
1	K	838	THR

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	836/809 (103%)	817 (98%)	19 (2%)	50	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	829/809 (102%)	814 (98%)	15 (2%)	59	48
2	B	190/182 (104%)	188 (99%)	2 (1%)	73	68
2	L	184/182 (101%)	180 (98%)	4 (2%)	52	39
All	All	2039/1982 (103%)	1999 (98%)	40 (2%)	57	44

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	407	ARG
1	K	906	ARG
1	K	422	MET
1	K	699	TYR
2	L	62	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	55	HIS
1	K	12	GLN
2	L	55	HIS
1	K	760	ASN
1	A	927	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

Of 20 ligands modelled in this entry, 4 are monoatomic and 2 are unknown - leaving 14 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	MGD	A	1002	3	41,52,52	1.41	7 (17%)	40,81,81	1.81	10 (25%)
7	SF4	L	1011	2	0,12,12	-	-	-	-	-
7	SF4	L	1013	2	0,12,12	-	-	-	-	-
4	2MD	A	1001	3	42,52,52	1.41	8 (19%)	47,81,81	1.67	10 (21%)
7	SF4	A	1010	1	0,12,12	-	-	-	-	-
5	MGD	K	1002	3	41,52,52	1.35	3 (7%)	40,81,81	1.79	11 (27%)
7	SF4	K	1010	1	0,12,12	-	-	-	-	-
7	SF4	L	1012	2	0,12,12	-	-	-	-	-
7	SF4	B	1012	2	0,12,12	-	-	-	-	-
7	SF4	B	1013	2	0,12,12	-	-	-	-	-
7	SF4	B	1011	2	0,12,12	-	-	-	-	-
9	EPE	K	1200	-	15,15,15	0.97	1 (6%)	18,20,20	1.84	4 (22%)
9	EPE	A	1200	-	15,15,15	0.97	1 (6%)	18,20,20	1.86	6 (33%)
4	2MD	K	1001	3	42,52,52	1.27	5 (11%)	47,81,81	1.99	8 (17%)

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	MGD	A	1002	3	-	1/18/66/66	0/6/6/6
7	SF4	L	1011	2	-	-	0/6/5/5
7	SF4	L	1013	2	-	-	0/6/5/5
4	2MD	A	1001	3	1/1/11/13	5/18/66/66	0/6/6/6
7	SF4	A	1010	1	-	-	0/6/5/5
5	MGD	K	1002	3	-	1/18/66/66	0/6/6/6
7	SF4	K	1010	1	-	-	0/6/5/5
7	SF4	L	1012	2	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	SF4	B	1012	2	-	-	0/6/5/5
7	SF4	B	1013	2	-	-	0/6/5/5
7	SF4	B	1011	2	-	-	0/6/5/5
9	EPE	K	1200	-	-	1/9/19/19	0/1/1/1
9	EPE	A	1200	-	-	1/9/19/19	0/1/1/1
4	2MD	K	1001	3	2/2/11/13	6/18/66/66	0/6/6/6

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1002	MGD	C19-N19	3.49	1.42	1.34
9	K	1200	EPE	C10-S	3.37	1.82	1.77
4	A	1001	2MD	C15-N17	-3.35	1.32	1.38
5	K	1002	MGD	C19-N19	3.32	1.42	1.34
9	A	1200	EPE	C10-S	3.32	1.82	1.77

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	1001	2MD	C11-C12-S12	6.71	126.48	110.16
4	K	1001	2MD	O4'-C1'-C2'	-6.04	98.09	106.93
4	A	1001	2MD	O4'-C1'-C2'	-5.85	98.37	106.93
9	K	1200	EPE	C5-N4-C3	5.02	120.12	108.83
4	K	1001	2MD	O11-C7-C14	-4.34	106.00	108.97

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1001	2MD	C12
4	K	1001	2MD	C12
4	K	1001	2MD	C13

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1001	2MD	C4'-C5'-O5'-PA
4	K	1001	2MD	C5'-O5'-PA-O1A
4	K	1001	2MD	C4'-C5'-O5'-PA
4	K	1001	2MD	O4'-C4'-C5'-O5'
5	A	1002	MGD	PA-O3B-PB-O5'

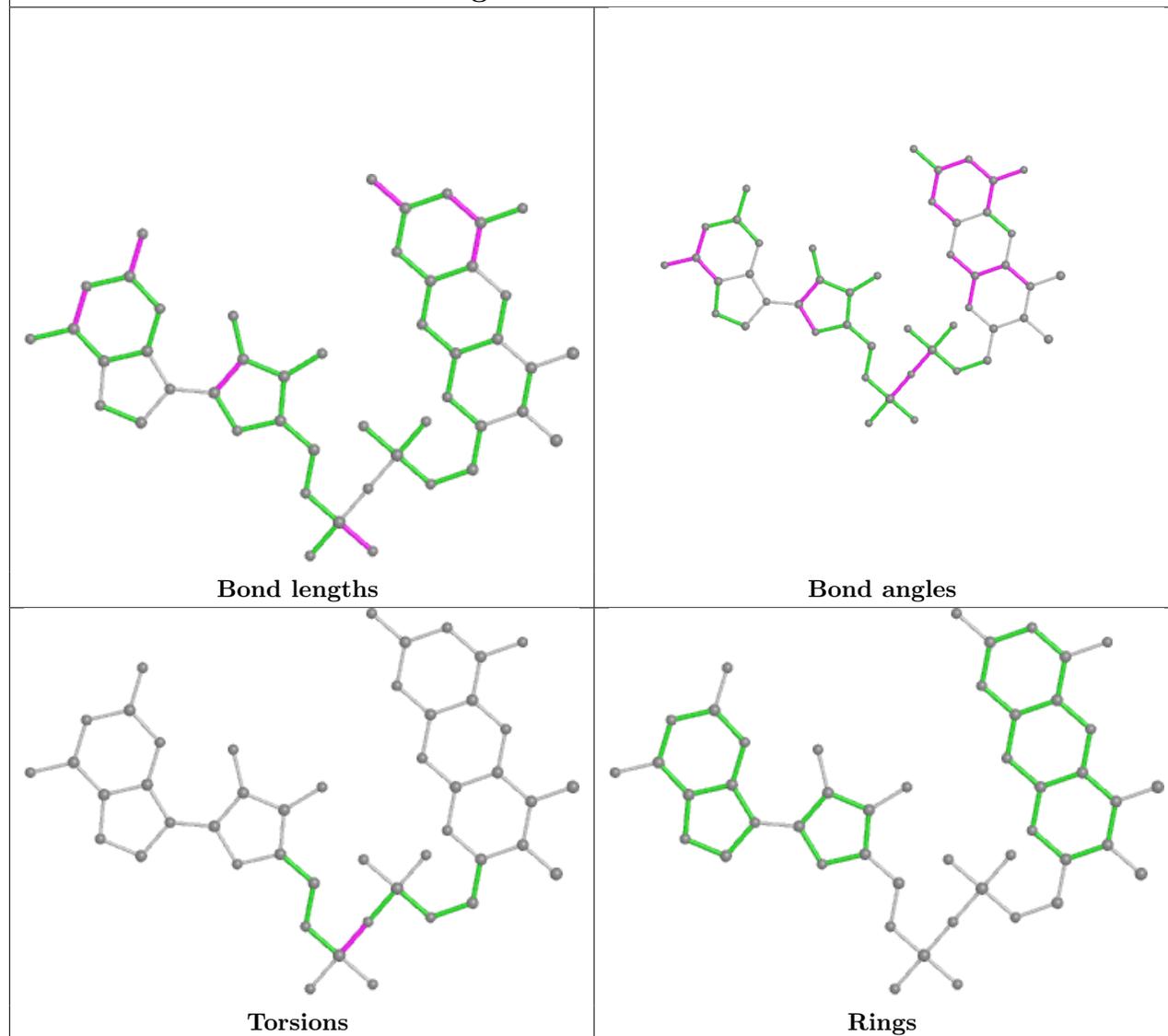
There are no ring outliers.

4 monomers are involved in 6 short contacts:

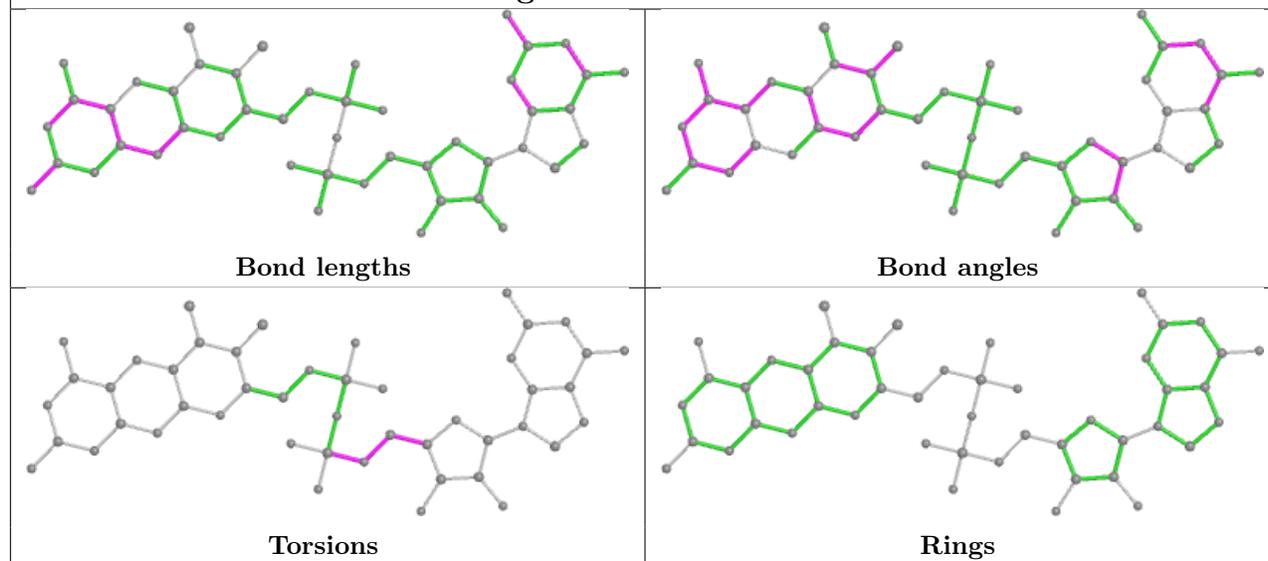
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001	2MD	2	0
9	K	1200	EPE	1	0
9	A	1200	EPE	1	0
4	K	1001	2MD	2	0

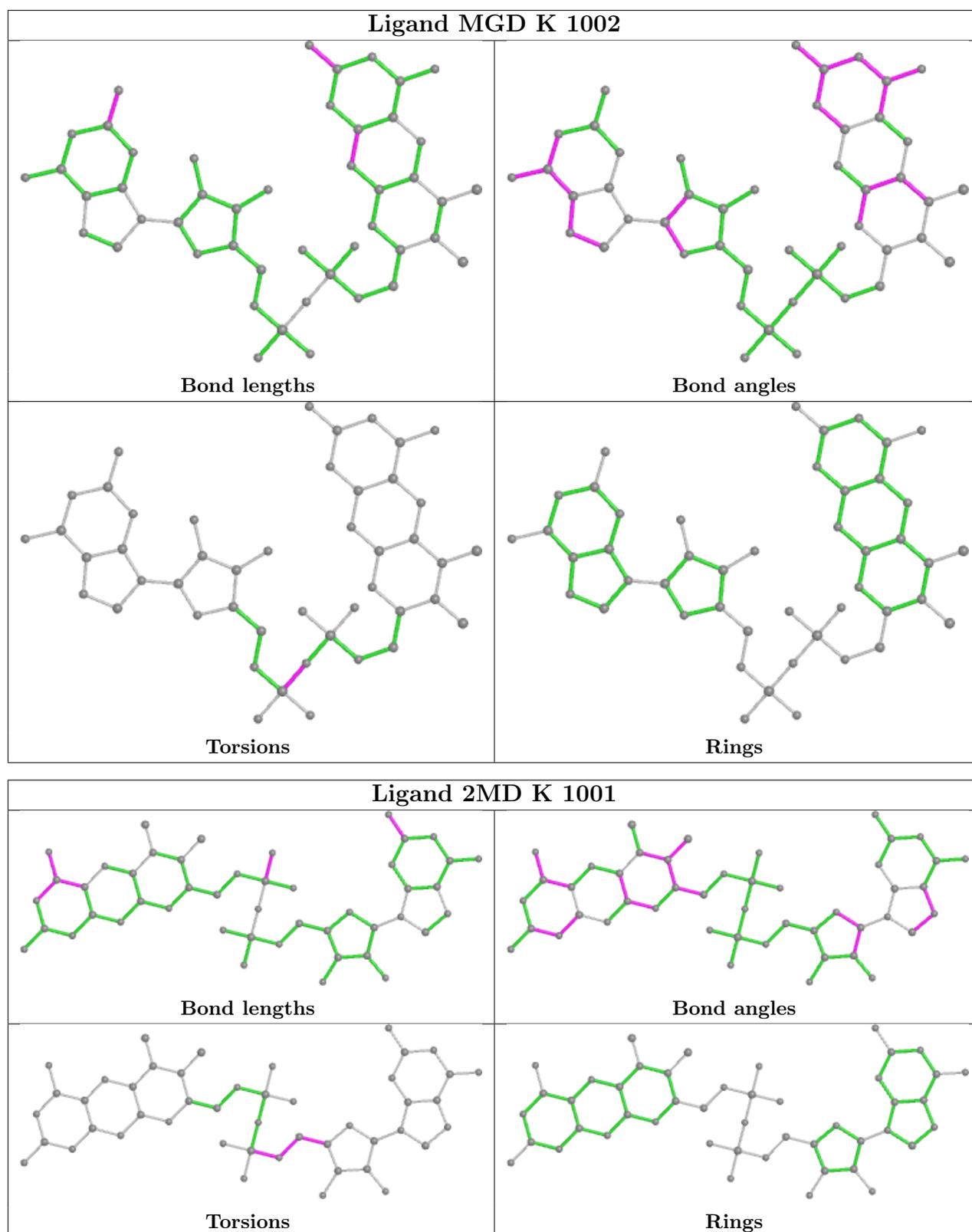
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

Ligand MGD A 1002



Ligand 2MD A 1001





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

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.