Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 09:32 AM EDT

PDB ID	:	1FEH / pdb_00001feh
Title	:	FE-ONLY HYDROGENASE FROM CLOSTRIDIUM PASTEURIANUM
Authors	:	Peters, J.W.; Lanzilotta, W.N.; Lemon, B.J.; Seefeldt, L.C.
Deposited on	:	1998-10-28
Resolution	:	1.80 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 ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

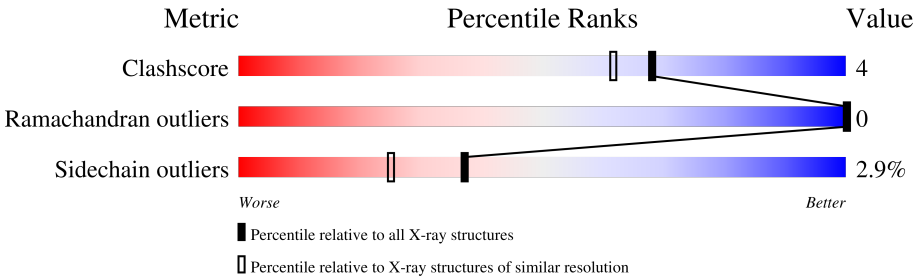
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

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 1.80 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	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	574	89% 9% .

2 Entry composition

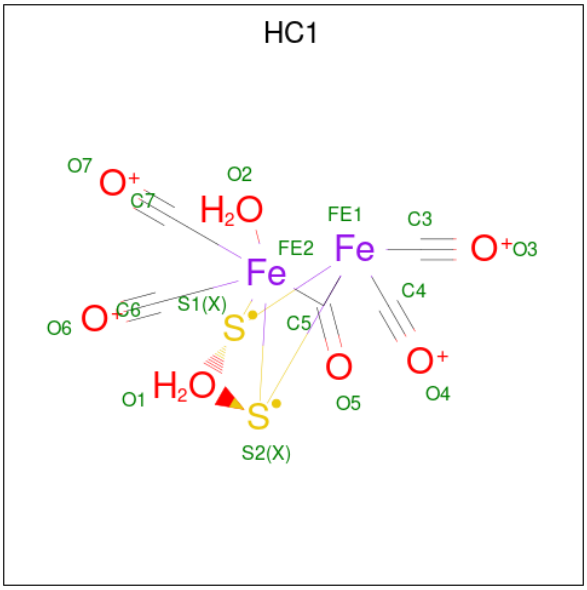
There are 5 unique types of molecules in this entry. The entry contains 5289 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PROTEIN (PERIPLASMIC HYDROGENASE 1).

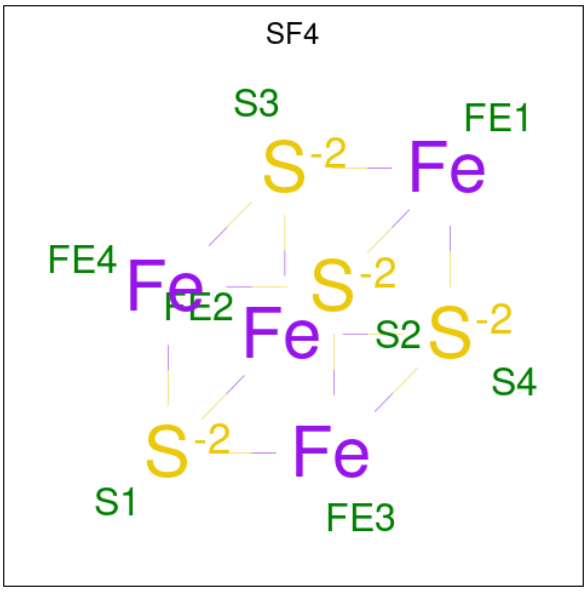
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	574	4461	2795	767	859	40	0	0	0

- Molecule 2 is 2 IRON/2 SULFUR/5 CARBONYL/2 WATER INORGANIC CLUSTER (CCD ID: HC1) (formula: $C_5H_4Fe_2O_7S_2$).



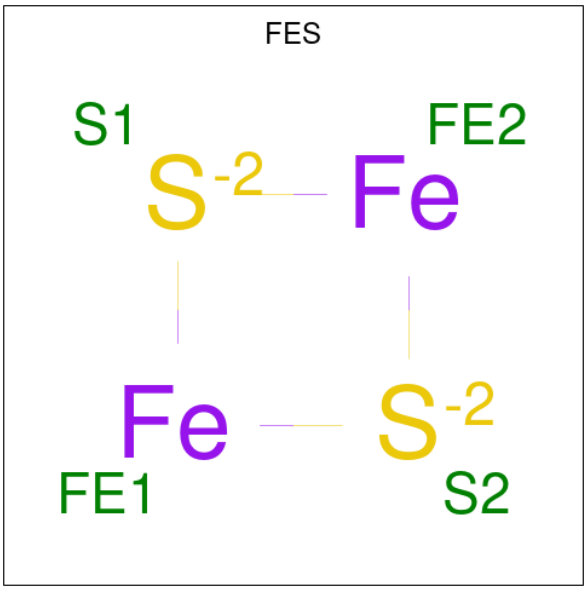
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Fe	O	S		
2	A	1	16	5	2	7	2	0	0

- Molecule 3 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Fe S 8 4 4	0	0
3	A	1	Total Fe S 8 4 4	0	0
3	A	1	Total Fe S 8 4 4	0	0
3	A	1	Total Fe S 8 4 4	0	0

- Molecule 4 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	776	Total	O	0	0
			776	776		

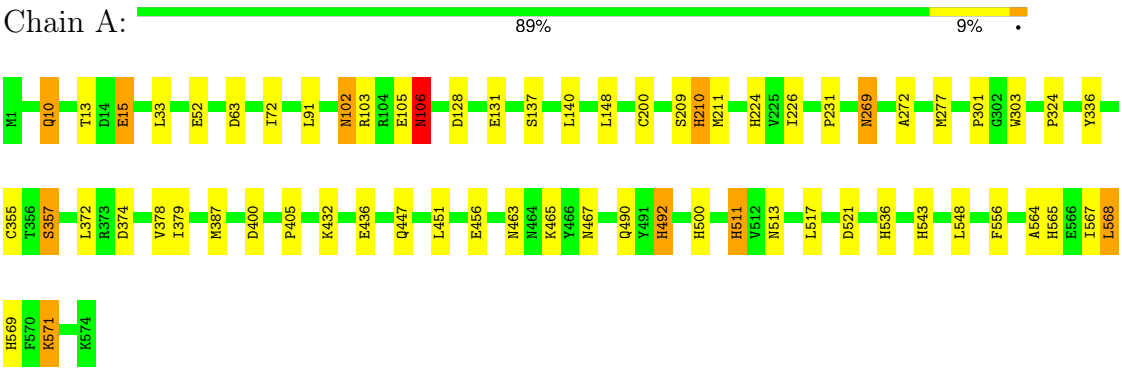
3 Residue-property plots (i)

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: PROTEIN (PERIPLASMIC HYDROGENASE 1)

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 42 21 2	Depositor
Cell constants a, b, c, α, β, γ	111.60Å 111.60Å 103.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.80	Depositor
% Data completeness (in resolution range)	86.3 (20.00-1.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.180 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5289	wwPDB-VP
Average B, all atoms (Å^2)	18.0	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: FES, HC1, SF4

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	0.72	9/4534 (0.2%)	1.30	23/6103 (0.4%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	210	HIS	CD2-NE2	-6.89	1.30	1.37
1	A	492	HIS	CD2-NE2	-6.61	1.30	1.37
1	A	511	HIS	CD2-NE2	-6.48	1.30	1.37
1	A	536	HIS	CD2-NE2	-6.39	1.30	1.37
1	A	569	HIS	CD2-NE2	-6.39	1.30	1.37
1	A	565	HIS	CD2-NE2	-6.25	1.30	1.37
1	A	543	HIS	CD2-NE2	-6.25	1.30	1.37
1	A	500	HIS	CD2-NE2	-6.18	1.31	1.37
1	A	224	HIS	CD2-NE2	-6.10	1.31	1.37

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	102	ASN	CA-CB-CG	8.26	120.86	112.60
1	A	15	GLU	N-CA-C	8.21	122.67	110.52
1	A	513	ASN	CA-CB-CG	7.44	120.04	112.60
1	A	269	ASN	CA-CB-CG	6.28	118.88	112.60
1	A	569	HIS	CB-CG-CD2	-5.99	123.42	131.20
1	A	405	PRO	N-CA-C	5.93	121.34	113.57
1	A	63	ASP	CA-CB-CG	5.59	118.19	112.60
1	A	210	HIS	CB-CG-CD2	-5.56	123.98	131.20
1	A	106	ASN	CA-CB-CG	5.55	118.15	112.60
1	A	209	SER	N-CA-C	5.46	118.24	110.10
1	A	303	TRP	CB-CG-CD1	-5.41	118.79	126.90
1	A	200	CYS	CA-C-N	5.40	125.01	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	200	CYS	C-N-CA	5.40	125.01	119.56
1	A	492	HIS	CB-CG-CD2	-5.35	124.25	131.20
1	A	374	ASP	CA-CB-CG	5.32	117.92	112.60
1	A	463	ASN	N-CA-C	5.31	119.34	112.86
1	A	400	ASP	CA-CB-CG	5.31	117.91	112.60
1	A	303	TRP	CG-CD2-CE3	5.17	139.07	133.90
1	A	521	ASP	CA-CB-CG	5.17	117.77	112.60
1	A	565	HIS	CB-CG-CD2	-5.11	124.56	131.20
1	A	536	HIS	CB-CG-CD2	-5.10	124.57	131.20
1	A	513	ASN	CA-C-N	5.04	125.31	119.47
1	A	513	ASN	C-N-CA	5.04	125.31	119.47

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	4461	0	4430	30	0
2	A	16	0	0	2	0
3	A	32	0	0	1	0
4	A	4	0	0	0	0
5	A	776	0	0	4	2
All	All	5289	0	4430	32	2

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 4.

All (32) 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:556:PHE:HE1	1:A:567:ILE:HD11	1.58	0.69
1:A:467:ASN:H	1:A:492:HIS:HD2	1.44	0.66
1:A:210:HIS:HD2	1:A:378:VAL:H	1.45	0.64
1:A:211:MET:HE1	1:A:387:MET:HE2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:MET:SD	1:A:387:MET:HE2	2.40	0.61
1:A:567:ILE:HG13	1:A:568:LEU:HD13	1.89	0.55
2:A:580:HC1:S2	2:A:580:HC1:O1	2.64	0.55
1:A:277:MET:HG3	1:A:548:LEU:HD21	1.89	0.54
1:A:379:ILE:HD13	1:A:387:MET:HE1	1.90	0.53
1:A:210:HIS:CD2	1:A:378:VAL:H	2.27	0.52
1:A:432:LYS:O	1:A:436:GLU:HG2	2.11	0.51
1:A:33:LEU:HD21	1:A:148:LEU:HD13	1.94	0.50
1:A:103:ARG:HE	1:A:106:ASN:ND2	2.09	0.50
1:A:211:MET:CE	1:A:387:MET:HE2	2.42	0.50
1:A:564:ALA:HA	1:A:568:LEU:HD22	1.95	0.49
2:A:580:HC1:O1	2:A:580:HC1:S1	2.70	0.49
1:A:355:CYS:HB2	3:A:581:SF4:S3	2.53	0.48
1:A:128:ASP:O	1:A:131:GLU:HG2	2.15	0.47
1:A:210:HIS:HE1	5:A:962:HOH:O	1.97	0.47
1:A:13:THR:OG1	1:A:15:GLU:HG2	2.15	0.47
1:A:301:PRO:HG2	1:A:357:SER:HB3	1.96	0.47
1:A:52:GLU:O	1:A:72:ILE:HA	2.15	0.46
1:A:105:GLU:HG2	5:A:967:HOH:O	2.16	0.45
1:A:564:ALA:O	1:A:568:LEU:HB2	2.16	0.45
1:A:272:ALA:HA	1:A:324:PRO:HG3	1.98	0.45
1:A:10:GLN:NE2	1:A:10:GLN:H	2.17	0.43
1:A:231:PRO:HG3	1:A:269:ASN:ND2	2.33	0.42
1:A:571:LYS:HB2	1:A:571:LYS:HE2	1.92	0.42
1:A:137:SER:HB3	1:A:140:LEU:O	2.19	0.41
1:A:226:ILE:HD11	1:A:336:TYR:CD2	2.56	0.40
1:A:301:PRO:HB2	5:A:679:HOH:O	2.21	0.40
1:A:511:HIS:HD2	5:A:603:HOH:O	2.04	0.40

All (2) 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)
5:A:1059:HOH:O	5:A:1250:HOH:O[8_666]	2.16	0.04
5:A:693:HOH:O	5:A:1335:HOH:O[8_666]	2.17	0.03

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	572/574 (100%)	558 (98%)	14 (2%)	0	100 100

There are no Ramachandran outliers to report.

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	490/490 (100%)	476 (97%)	14 (3%)	37 25

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	91	LEU
1	A	102	ASN
1	A	106	ASN
1	A	357	SER
1	A	372	LEU
1	A	447	GLN
1	A	451	LEU
1	A	456	GLU
1	A	465	LYS
1	A	490	GLN
1	A	517	LEU
1	A	568	LEU

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Mol	Chain	Res	Type
1	A	571	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	12	ASN
1	A	37	ASN
1	A	73	ASN
1	A	75	ASN
1	A	89	GLN
1	A	106	ASN
1	A	189	ASN
1	A	210	HIS
1	A	224	HIS
1	A	269	ASN
1	A	326	GLN
1	A	447	GLN
1	A	490	GLN
1	A	492	HIS
1	A	511	HIS
1	A	536	HIS
1	A	554	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry

6 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	$\#\|Z\| > 2$
3	SF4	A	581	1	0,12,12	-	-	-		
3	SF4	A	582	1	0,12,12	-	-	-		
4	FES	A	585	1	0,4,4	-	-	-		
3	SF4	A	583	1	0,12,12	-	-	-		
2	HC1	A	580	1	7,18,18	1.98	2 (28%)	0,39,39	-	-
3	SF4	A	584	1	0,12,12	-	-	-		

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	SF4	A	581	1	-	-	0/6/5/5
3	SF4	A	582	1	-	-	0/6/5/5
4	FES	A	585	1	-	-	0/1/1/1
3	SF4	A	583	1	-	-	0/6/5/5
2	HC1	A	580	1	-	-	0/5/3/3
3	SF4	A	584	1	-	-	0/6/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	580	HC1	O5-C5	-4.38	1.10	1.17
2	A	580	HC1	C3-FE1	2.13	1.86	1.79

There are no bond angle outliers.

There are no chirality outliers.

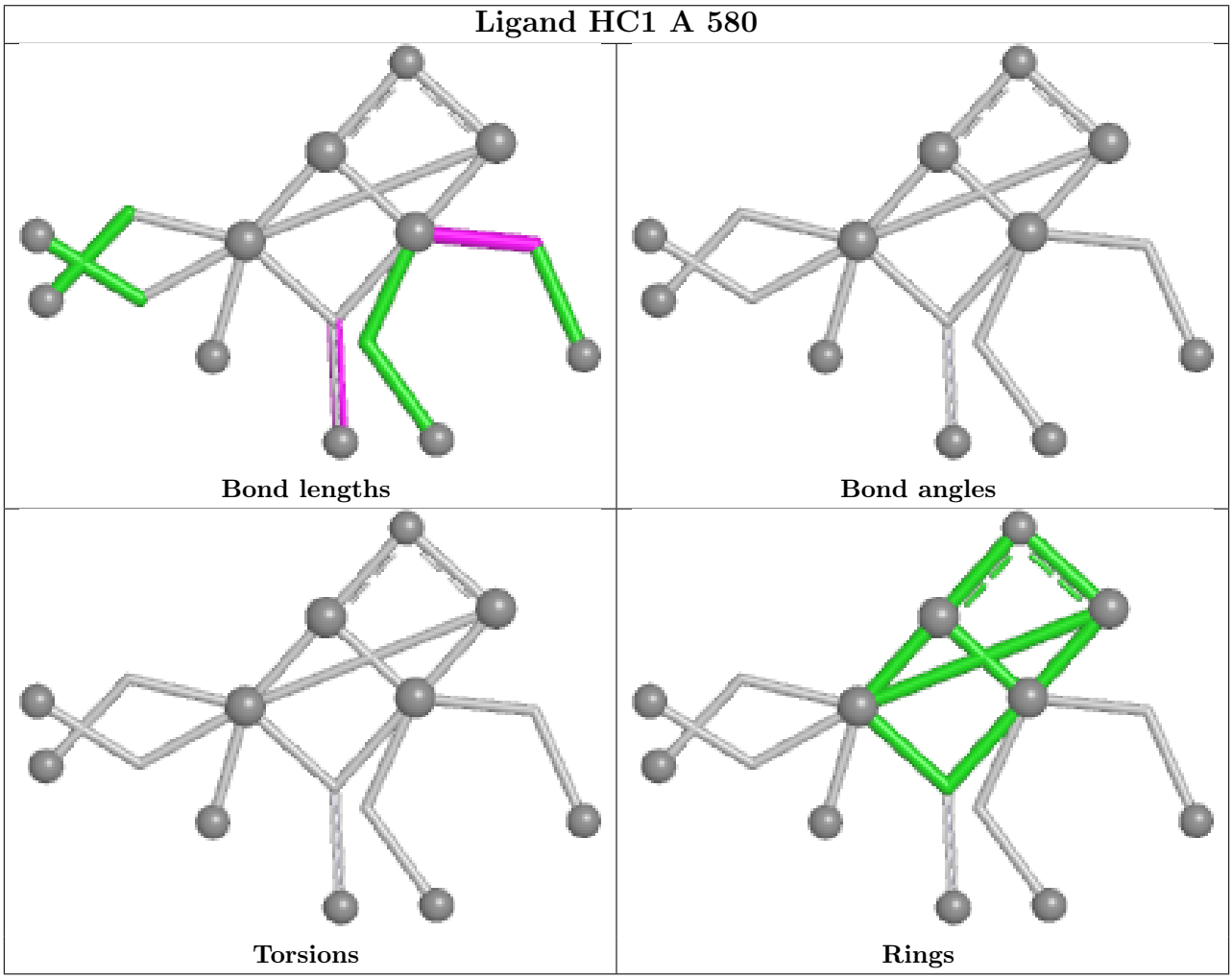
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	581	SF4	1	0
2	A	580	HC1	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 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.



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.