Full wwPDB X-ray Structure Validation Report (i)

May 15, 2020 – 06:20 pm BST

PDB ID	:	6HJG
Title	:	Trypanosoma cruzi proline racemase in complex with inhibitor OxoPA
Authors	:	Saul, F.; Haouz, A.; Uriac, P.; Blondel, A.; Minoprio, P.
Deposited on	:	2018-09-03
Resolution	:	1.90 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 following versions of software and data (see references (i)) were used in the production of this report:

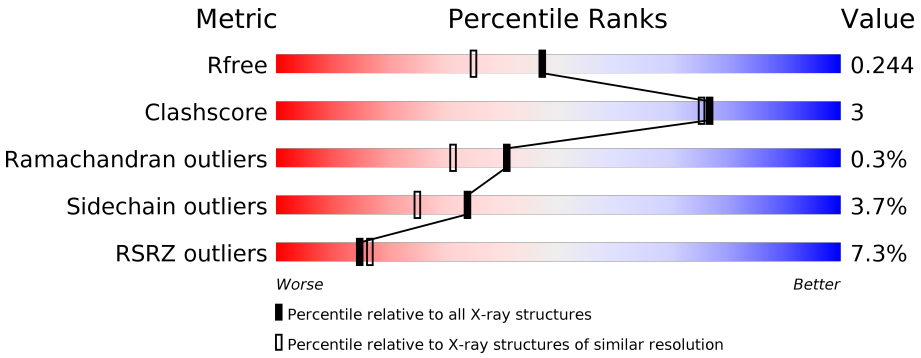
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.90 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))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 <=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	414	8% 79% 6% • 15%
1	B	414	5% 81% 9% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5925 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 Proline racemase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	4	0
			2686	1704	455	509	18			
1	B	376	Total	C	N	O	S	0	4	0
			2878	1823	494	543	18			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q4DA80
A	118	ILE	MET	conflict	UNP Q4DA80
A	394	TYR	-	expression tag	UNP Q4DA80
A	395	ILE	-	expression tag	UNP Q4DA80
A	396	TRP	-	expression tag	UNP Q4DA80
A	397	SER	-	expression tag	UNP Q4DA80
A	398	SER	-	expression tag	UNP Q4DA80
A	399	SER	-	expression tag	UNP Q4DA80
A	400	VAL	-	expression tag	UNP Q4DA80
A	401	ASP	-	expression tag	UNP Q4DA80
A	402	LYS	-	expression tag	UNP Q4DA80
A	403	LEU	-	expression tag	UNP Q4DA80
A	404	ALA	-	expression tag	UNP Q4DA80
A	405	ALA	-	expression tag	UNP Q4DA80
A	406	ALA	-	expression tag	UNP Q4DA80
A	407	LEU	-	expression tag	UNP Q4DA80
A	408	GLU	-	expression tag	UNP Q4DA80
A	409	HIS	-	expression tag	UNP Q4DA80
A	410	HIS	-	expression tag	UNP Q4DA80
A	411	HIS	-	expression tag	UNP Q4DA80
A	412	HIS	-	expression tag	UNP Q4DA80
A	413	HIS	-	expression tag	UNP Q4DA80
A	414	HIS	-	expression tag	UNP Q4DA80
B	1	MET	-	initiating methionine	UNP Q4DA80
B	118	ILE	MET	conflict	UNP Q4DA80

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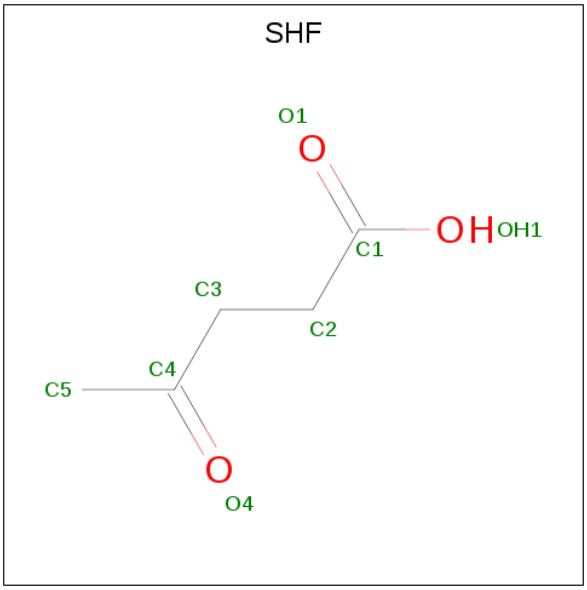
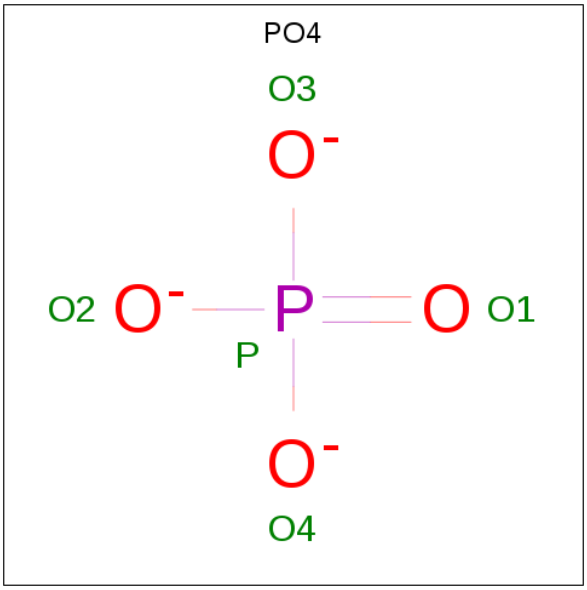
Chain	Residue	Modelled	Actual	Comment	Reference
B	394	TYR	-	expression tag	UNP Q4DA80
B	395	ILE	-	expression tag	UNP Q4DA80
B	396	TRP	-	expression tag	UNP Q4DA80
B	397	SER	-	expression tag	UNP Q4DA80
B	398	SER	-	expression tag	UNP Q4DA80
B	399	SER	-	expression tag	UNP Q4DA80
B	400	VAL	-	expression tag	UNP Q4DA80
B	401	ASP	-	expression tag	UNP Q4DA80
B	402	LYS	-	expression tag	UNP Q4DA80
B	403	LEU	-	expression tag	UNP Q4DA80
B	404	ALA	-	expression tag	UNP Q4DA80
B	405	ALA	-	expression tag	UNP Q4DA80
B	406	ALA	-	expression tag	UNP Q4DA80
B	407	LEU	-	expression tag	UNP Q4DA80
B	408	GLU	-	expression tag	UNP Q4DA80
B	409	HIS	-	expression tag	UNP Q4DA80
B	410	HIS	-	expression tag	UNP Q4DA80
B	411	HIS	-	expression tag	UNP Q4DA80
B	412	HIS	-	expression tag	UNP Q4DA80
B	413	HIS	-	expression tag	UNP Q4DA80
B	414	HIS	-	expression tag	UNP Q4DA80

- Molecule 2 is LAEVULINIC ACID (three-letter code: SHF) (formula: $C_5H_8O_3$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	B	1	Total C O 5 3 2	0	0

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O P 5 4 1	0	0

- Molecule 4 is water.

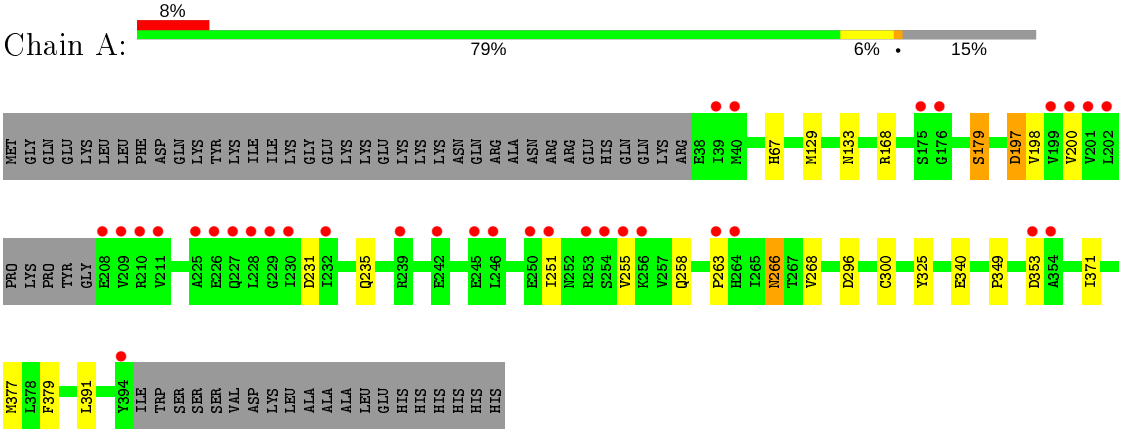
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	147	Total O 147 147	0	0
4	B	200	Total O 200 200	0	0

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 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.

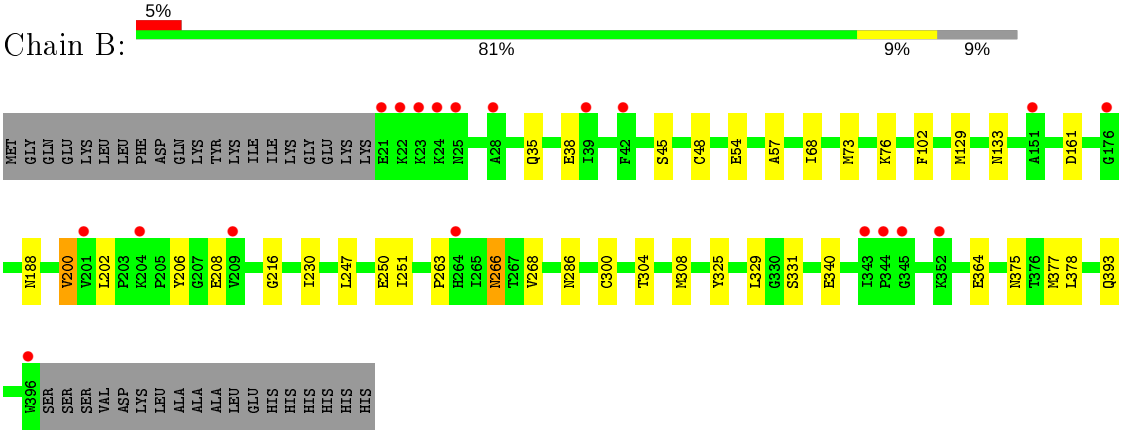
- Molecule 1: Proline racemase A

Chain A:



- Molecule 1: Proline racemase A

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	129.24Å 91.33Å 85.63Å 90.00° 126.45° 90.00°	Depositor
Resolution (Å)	41.24 – 1.90 41.20 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.1 (41.24-1.90) 97.1 (41.20-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.63 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.189 , 0.239 0.195 , 0.244	Depositor DCC
R_{free} test set	1224 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å^2)	23.7	Xtriage
Anisotropy	0.464	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 56.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5925	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: PO4, SHF

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	0/2749	0.73	1/3729 (0.0%)
1	B	0.59	0/2948	0.73	0/4000
All	All	0.58	0/5697	0.73	1/7729 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	296	ASP	CB-CG-OD1	5.73	123.45	118.30

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	2686	0	2671	14	0
1	B	2878	0	2846	23	0
2	A	4	0	0	1	0
2	B	5	0	2	2	0
3	B	5	0	0	0	0
4	A	147	0	0	2	0
4	B	200	0	0	1	0
All	All	5925	0	5519	33	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 3.

All (33) 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:B:300:CYS:SG	2:B:502:SHF:H22	2.24	0.78
1:B:300:CYS:SG	2:B:502:SHF:C2	2.79	0.70
1:A:179:SER:HB3	1:B:35:GLN:HG2	1.81	0.62
1:B:48[A]:CYS:SG	1:B:377[A]:MET:SD	3.04	0.56
1:A:371:ILE:HG22	1:B:378:LEU:HD12	1.88	0.54
1:A:391:LEU:HD21	1:B:329:LEU:HD21	1.90	0.52
1:B:68:ILE:O	1:B:76:LYS:NZ	2.44	0.51
1:B:76:LYS:HE3	4:B:606:HOH:O	2.11	0.51
1:A:266:ASN:HD22	1:A:266:ASN:N	2.09	0.50
1:B:54:GLU:HB3	1:B:331:SER:HB3	1.95	0.49
1:B:48[B]:CYS:SG	1:B:375:ASN:HB3	2.52	0.49
1:B:206:TYR:HE1	1:B:230:ILE:HD11	1.76	0.49
1:A:258:GLN:HE22	1:A:263:PRO:HA	1.77	0.49
1:B:188:ASN:ND2	1:B:216:GLY:O	2.41	0.48
1:B:202:LEU:HD23	1:B:250:GLU:OE1	2.13	0.48
1:B:206:TYR:CE1	1:B:230:ILE:HD11	2.49	0.48
1:B:304:THR:HG22	1:B:308:MET:HE2	1.96	0.48
1:B:200:VAL:HG21	1:B:247:LEU:HD11	1.97	0.46
1:A:168:ARG:HD2	4:A:724:HOH:O	2.15	0.46
1:A:300:CYS:SG	2:A:500:SHF:C2	3.02	0.46
1:A:258:GLN:NE2	1:A:263:PRO:HA	2.31	0.45
1:B:251:ILE:HG21	1:B:268:VAL:HG21	1.98	0.45
1:A:198:VAL:HG11	1:A:255:VAL:HG21	1.98	0.45
1:A:67:HIS:HE1	4:A:733:HOH:O	2.00	0.45
1:A:266:ASN:HD22	1:A:266:ASN:H	1.65	0.45
1:B:200:VAL:HG12	1:B:250:GLU:HG2	2.00	0.44
1:A:377[B]:MET:HG2	1:A:379:PHE:CE1	2.54	0.43
1:A:251:ILE:HG21	1:A:268:VAL:HG21	2.00	0.43
1:B:263:PRO:O	1:B:266:ASN:OD1	2.38	0.42
1:A:371:ILE:CG2	1:B:378:LEU:HD12	2.48	0.42
1:B:73:MET:HG3	1:B:161:ASP:O	2.20	0.41
1:B:57:ALA:O	1:B:102:PHE:HB2	2.21	0.40

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	352/414 (85%)	345 (98%)	5 (1%)	2 (1%)	25 15
1	B	378/414 (91%)	371 (98%)	7 (2%)	0	100 100
All	All	730/828 (88%)	716 (98%)	12 (2%)	2 (0%)	41 31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	179	SER
1	A	197	ASP

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	291/347 (84%)	280 (96%)	11 (4%)	33 24
1	B	309/347 (89%)	298 (96%)	11 (4%)	35 26
All	All	600/694 (86%)	578 (96%)	22 (4%)	34 25

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	129	MET
1	A	133	ASN
1	A	197	ASP
1	A	200	VAL

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Mol	Chain	Res	Type
1	A	231	ASP
1	A	235	GLN
1	A	266	ASN
1	A	325	TYR
1	A	340	GLU
1	A	349	PRO
1	A	353	ASP
1	B	38	GLU
1	B	129	MET
1	B	133	ASN
1	B	200	VAL
1	B	208	GLU
1	B	266	ASN
1	B	286	ASN
1	B	325	TYR
1	B	340	GLU
1	B	364	GLU
1	B	393	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	155	ASN
1	A	195	GLN
1	A	266	ASN
1	A	387	ASN
1	B	35	GLN
1	B	155	ASN
1	B	195	GLN
1	B	196	GLN
1	B	236	ASN
1	B	241	GLN
1	B	387	ASN

5.3.3 RNA

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)

3 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	SHF	A	500	-	1,3,7	3.97	1 (100%)	0,3,8	0.00	-
3	PO4	B	501	-	4,4,4	1.06	0	6,6,6	0.48	0
2	SHF	B	502	-	1,4,7	0.52	0	1,4,8	2.10	1 (100%)

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	SHF	B	502	-	-	0/0/2/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	SHF	C2-C1	3.97	1.53	1.48

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	502	SHF	C3-C2-C1	-2.10	109.68	112.59

There are no chirality outliers.

There are no torsion outliers.

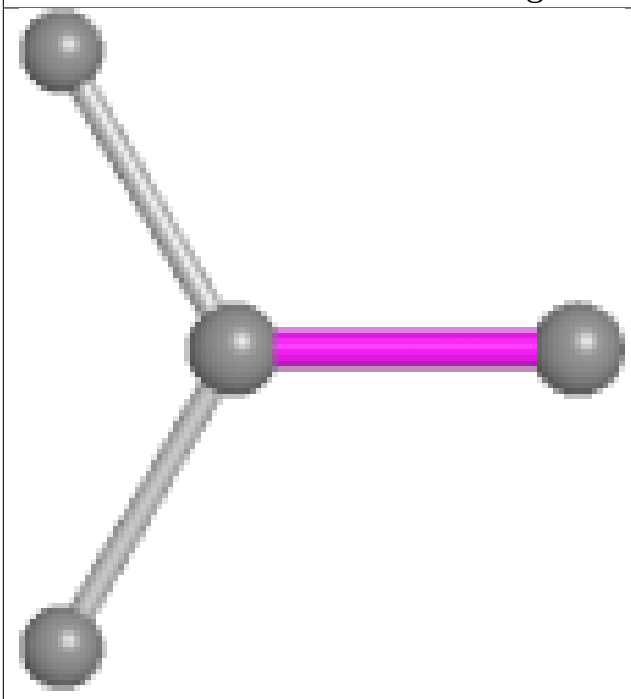
There are no ring outliers.

2 monomers are involved in 3 short contacts:

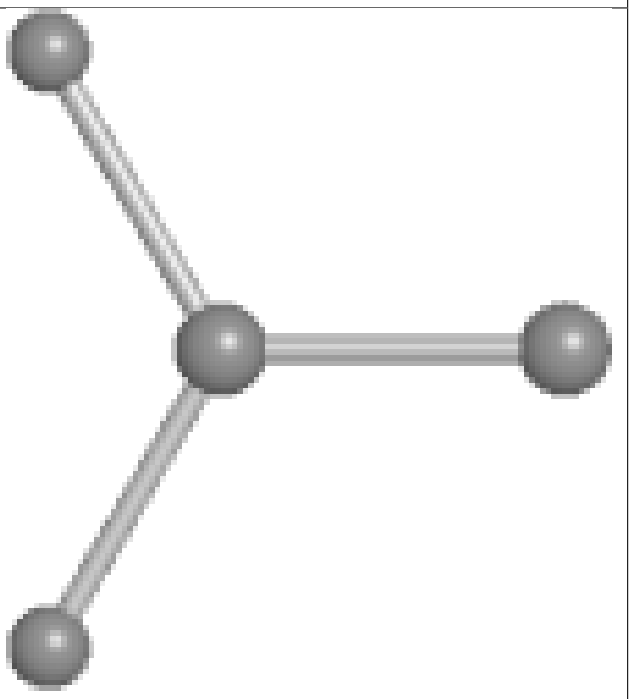
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	SHF	1	0
2	B	502	SHF	2	0

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.

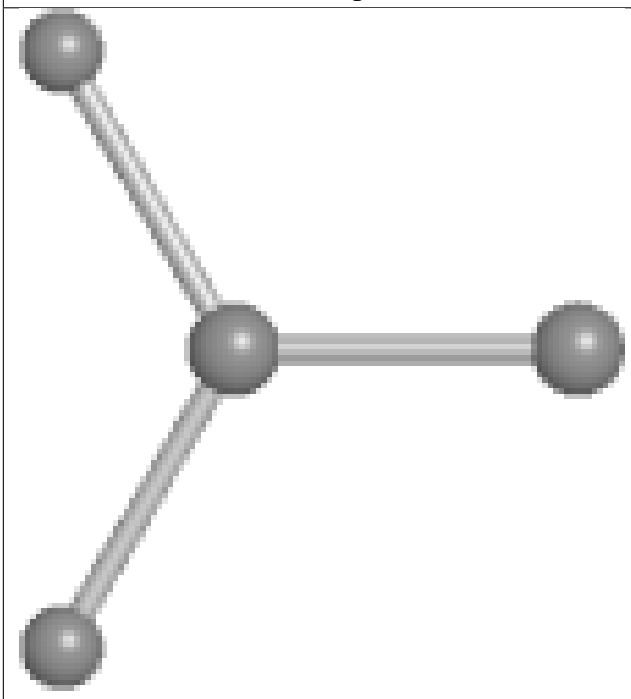
Ligand SHF A 500



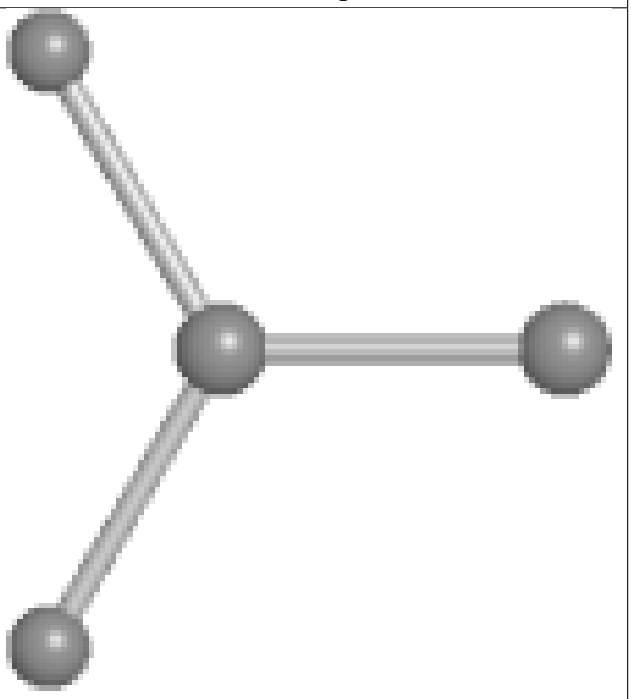
Bond lengths



Bond angles

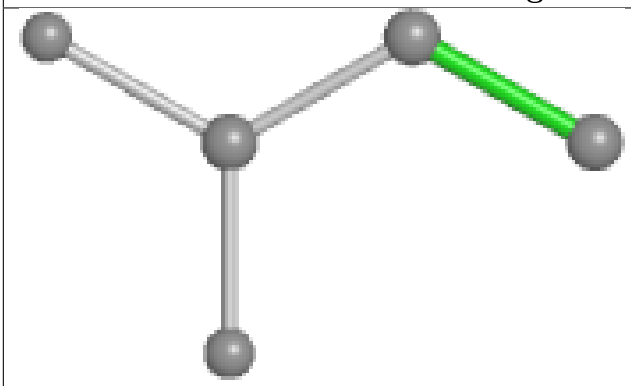


Torsions

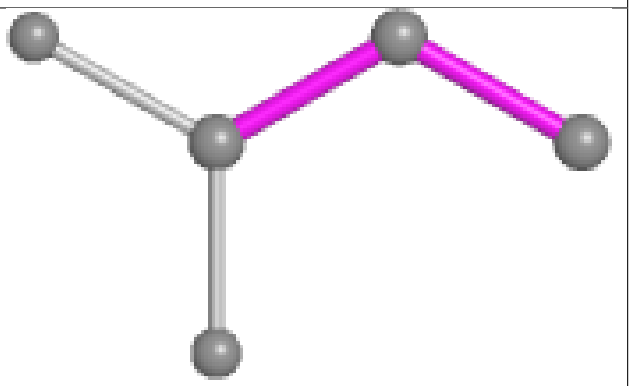


Rings

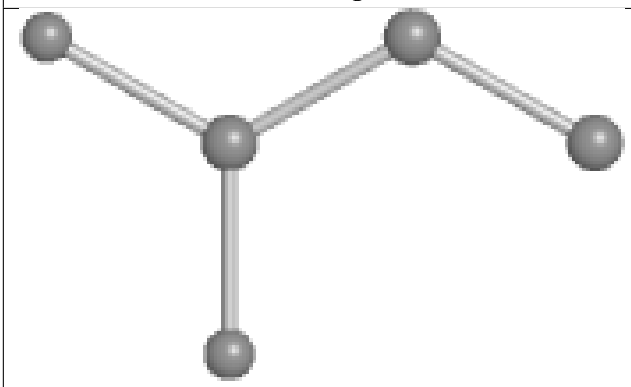
Ligand SHF B 502



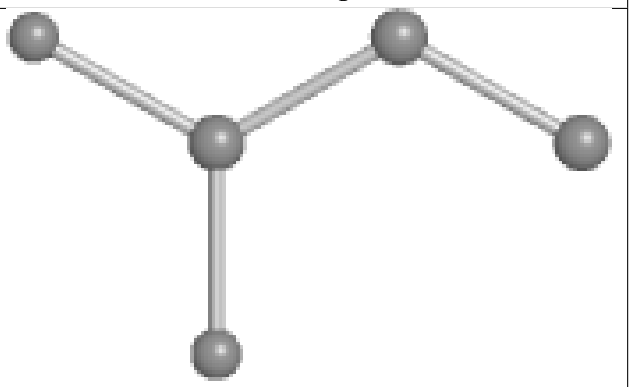
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

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

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, 95^{th} 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	352/414 (85%)	0.32	34 (9%)	7	9	16, 32, 69, 92	0
1	B	376/414 (90%)	0.10	19 (5%)	28	31	13, 29, 67, 83	0
All	All	728/828 (87%)	0.20	53 (7%)	15	16	13, 30, 68, 92	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	202	LEU	8.4
1	A	228	LEU	6.8
1	A	201	VAL	6.6
1	A	200	VAL	6.3
1	B	42	PHE	6.1
1	A	229	GLY	5.5
1	A	394	TYR	5.2
1	A	199	VAL	5.1
1	B	176	GLY	4.4
1	A	209	VAL	4.3
1	B	24	LYS	3.7
1	A	230	ILE	3.6
1	B	151	ALA	3.6
1	A	175	SER	3.5
1	B	352	LYS	3.4
1	B	25	ASN	3.3
1	A	246	LEU	3.3
1	A	210	ARG	3.3
1	A	354	ALA	3.2
1	A	256	LYS	3.2
1	A	251	ILE	3.1
1	A	226	GLU	3.0
1	B	344	PRO	3.0
1	B	21	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	201	VAL	3.0
1	A	263	PRO	2.9
1	A	211	VAL	2.8
1	A	253	ARG	2.7
1	A	39	ILE	2.6
1	A	255	VAL	2.5
1	B	209	VAL	2.5
1	B	396	TRP	2.5
1	A	250	GLU	2.5
1	B	345	GLY	2.5
1	B	22	LYS	2.4
1	B	264	HIS	2.4
1	A	225	ALA	2.4
1	B	28	ALA	2.4
1	A	264	HIS	2.4
1	A	208	GLU	2.4
1	A	254	SER	2.4
1	B	39	ILE	2.3
1	A	40	MET	2.3
1	A	232	ILE	2.3
1	B	23	LYS	2.2
1	A	239	ARG	2.2
1	A	242	GLU	2.1
1	A	176	GLY	2.1
1	A	353	ASP	2.1
1	B	343	ILE	2.1
1	B	204	LYS	2.0
1	A	227	GLN	2.0
1	A	245	GLU	2.0

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 (i)

There are no carbohydrates in this entry.

6.4 Ligands

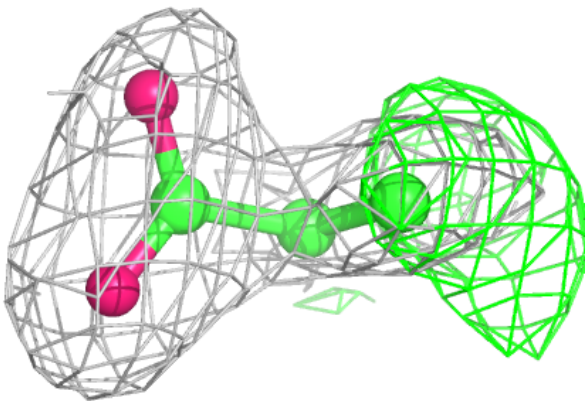
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

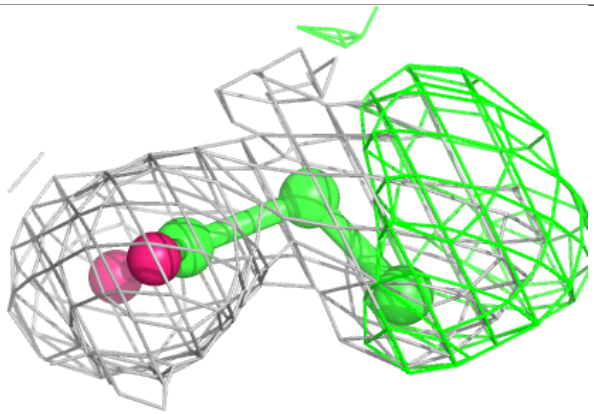
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SHF	B	502	5/8	0.89	0.21	29,32,36,39	1
2	SHF	A	500	4/8	0.93	0.10	28,29,30,38	0
3	PO4	B	501	5/5	0.95	0.18	63,73,75,83	0

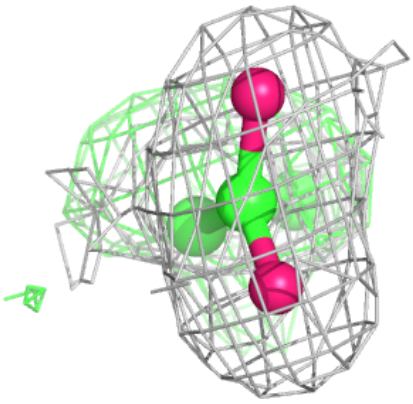
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SHF B 502:

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

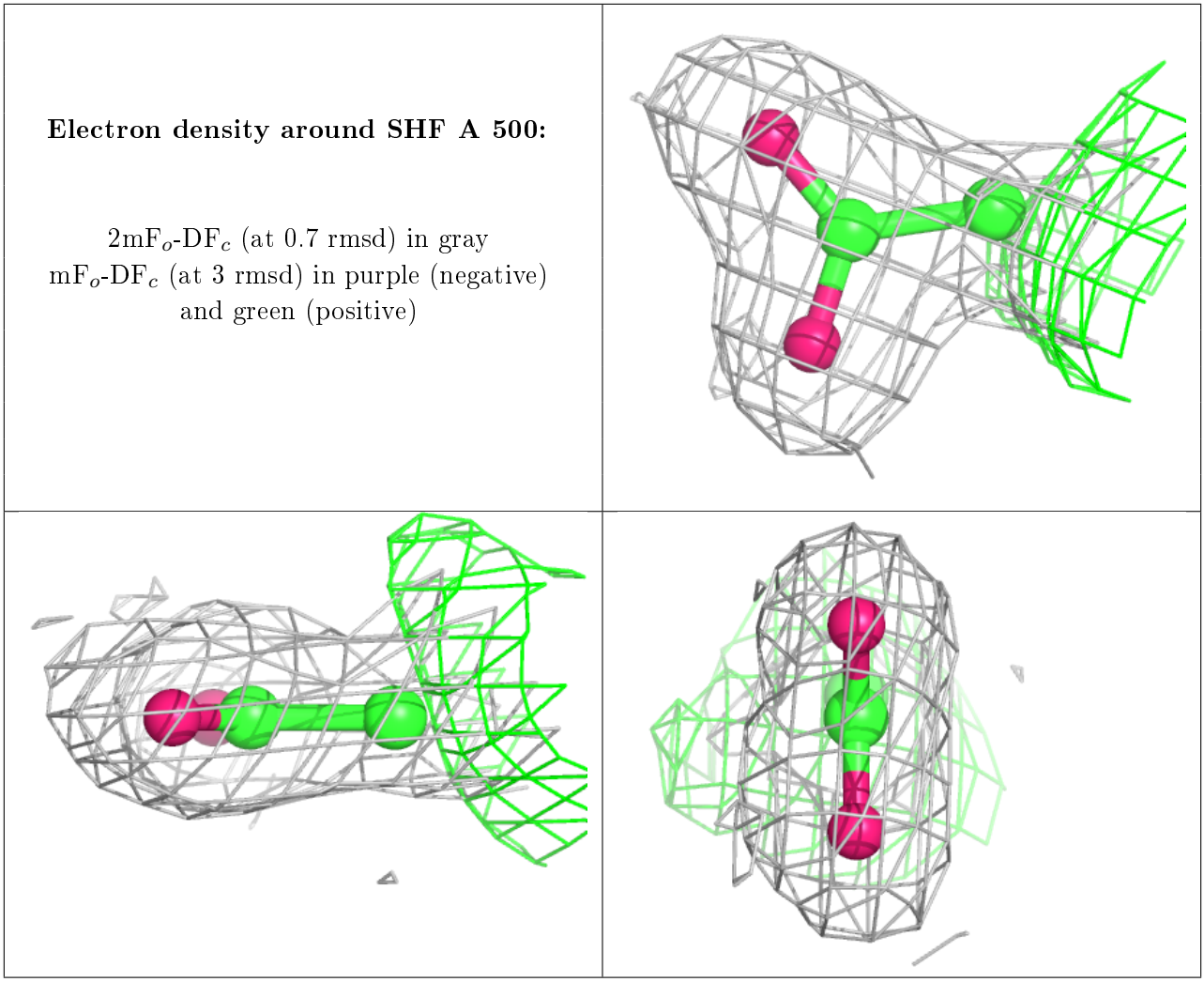






Electron density around SHF A 500:

$2mF_o$-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.