



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 07:51 AM UTC

PDB ID : 6HJG / pdb_00006hjc
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 ⓘ 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) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

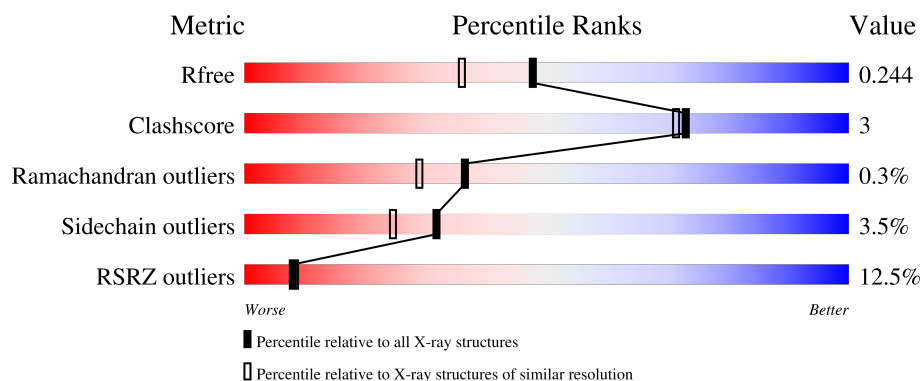
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (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 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 $\leq 5\%$. 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	14% 79% 6% 15%
1	B	414	7% 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:

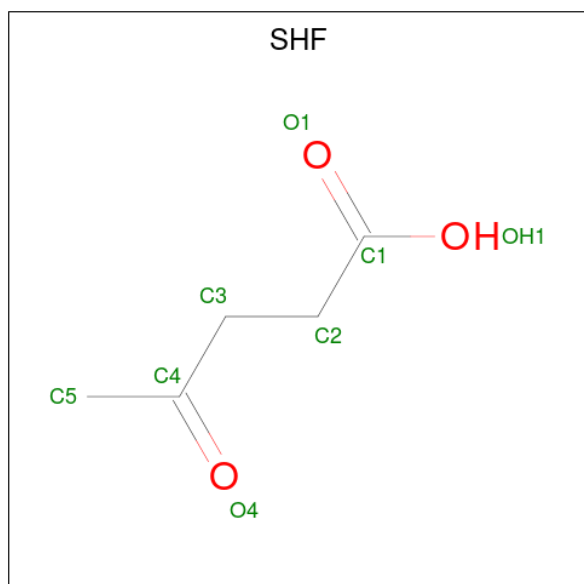
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q4DA80
A	118	ILE	MET	conflict	UNP Q4DA80
A	394	TYR	-	expression tag	UNP Q4DA80
A	395	ILE	-	expression tag	UNP Q4DA80
A	396	TRP	-	expression tag	UNP Q4DA80
A	397	SER	-	expression tag	UNP Q4DA80
A	398	SER	-	expression tag	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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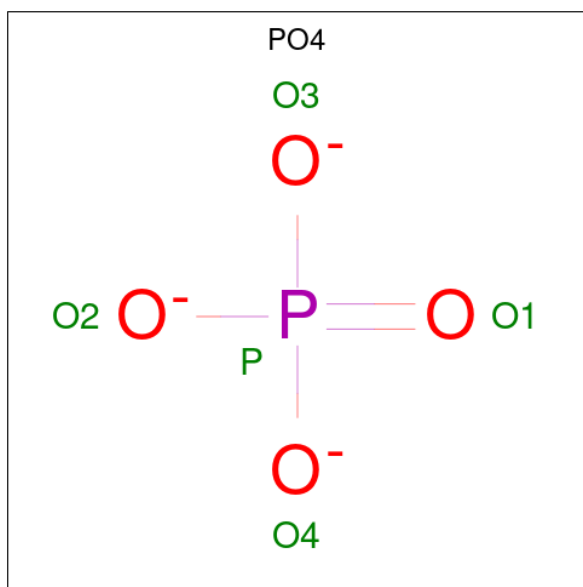
Chain	Residue	Modelled	Actual	Comment	Reference
B	394	TYR	-	expression tag	UNP Q4DA80
B	395	ILE	-	expression tag	UNP Q4DA80
B	396	TRP	-	expression tag	UNP Q4DA80
B	397	SER	-	expression tag	UNP Q4DA80
B	398	SER	-	expression tag	UNP Q4DA80
B	399	SER	-	expression tag	UNP Q4DA80
B	400	VAL	-	expression tag	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 (CCD ID: SHF) (formula: $C_5H_8O_3$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

- Molecule 4 is water.

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

- Molecule 1: Proline racemase A



4 Data and refinement statistics

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 41.24 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.1 (41.24-1.90) 97.1 (41.24-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ 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 (1.93%)	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 , 48.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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	0.78	0/2749	0.88	0/3729
1	B	0.81	0/2948	0.89	0/4000
All	All	0.80	0/5697	0.88	0/7729

There are no bond length outliers.

There are no bond angle outliers.

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	16	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	35	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 (35) 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:B:304:THR:HG22	1:B:308:MET:HE2	1.92	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: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:67:HIS:HE1	4:A:733:HOH:O	2.00	0.45
1:A:198:VAL:HG11	1:A:255:VAL:HG21	1.98	0.45
1:A:266:ASN:HD22	1:A:266:ASN:H	1.65	0.45
1:A:377[B]:MET:HE3	1:A:377[B]:MET:HB2	1.79	0.45
1:A:279:ASN:OD1	1:A:279:ASN:C	2.60	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

5.3.1 Protein backbone

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%)	21	13
1	B	378/414 (91%)	371 (98%)	7 (2%)	0	100	100
All	All	730/828 (88%)	716 (98%)	12 (2%)	2 (0%)	36	29

All (2) Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains

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%)	281 (97%)	10 (3%)	32	25
1	B	309/347 (89%)	298 (96%)	11 (4%)	31	23
All	All	600/694 (86%)	579 (96%)	21 (4%)	32	24

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	MET
1	A	129	MET
1	A	133	ASN
1	A	200	VAL

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Mol	Chain	Res	Type
1	A	234	VAL
1	A	235	GLN
1	A	266	ASN
1	A	325	TYR
1	A	349	PRO
1	A	353	ASP
1	B	38	GLU
1	B	43	LYS
1	B	129	MET
1	B	133	ASN
1	B	200	VAL
1	B	208	GLU
1	B	286	ASN
1	B	325	TYR
1	B	340	GLU
1	B	364	GLU
1	B	393	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	241	GLN
1	A	266	ASN
1	A	316	GLN
1	B	128	ASN
1	B	133	ASN
1	B	195	GLN
1	B	236	ASN
1	B	241	GLN
1	B	264	HIS
1	B	266	ASN
1	B	294	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 ⓘ

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 ⓘ

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	-	3,3,7	1.16	0	3,3,8	0.22	0
3	PO4	B	501	-	4,4,4	1.11	0	6,6,6	0.51	0
2	SHF	B	502	-	4,4,7	1.05	0	4,4,8	0.52	0

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	-	-	2/2/2/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

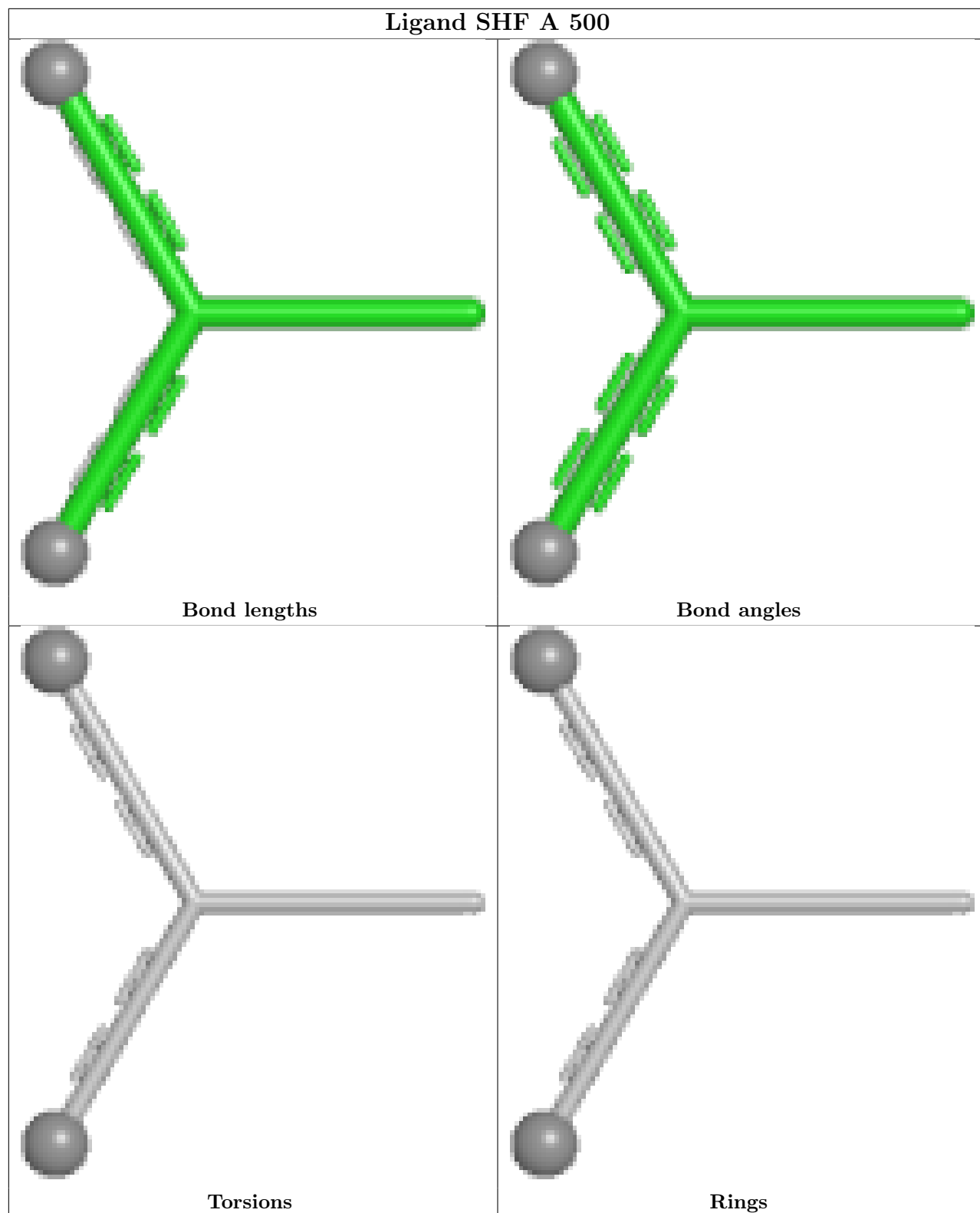
Mol	Chain	Res	Type	Atoms
2	B	502	SHF	O1-C1-C2-C3
2	B	502	SHF	OH1-C1-C2-C3

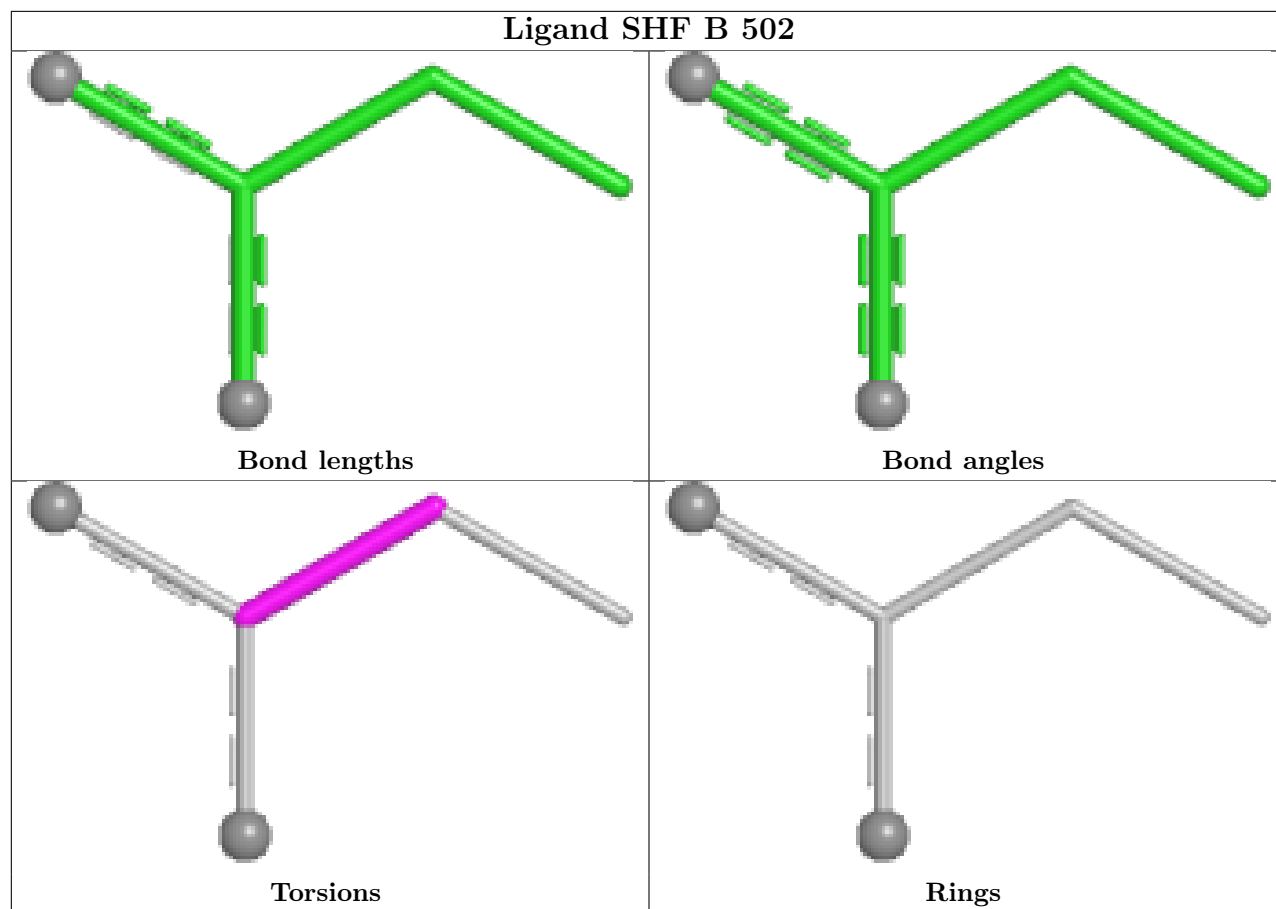
There are no ring outliers.

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 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

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, 95th 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%)	0.74	60 (17%) 4 4	13, 32, 69, 92	4 (1%)
1	B	376/414 (90%)	0.43	31 (8%) 17 18	13, 29, 67, 83	4 (1%)
All	All	728/828 (87%)	0.58	91 (12%) 8 8	13, 30, 68, 92	8 (1%)

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	201	VAL	5.1
1	A	202	LEU	4.9
1	B	395	ILE	4.6
1	B	25	ASN	4.5
1	A	209	VAL	4.5
1	A	211	VAL	4.3
1	A	230	ILE	4.3
1	B	264	HIS	4.1
1	A	229	GLY	4.1
1	B	396	TRP	3.8
1	A	240	LEU	3.7
1	A	353	ASP	3.7
1	B	206	TYR	3.6
1	B	394	TYR	3.4
1	A	228	LEU	3.4
1	B	262	LEU	3.4
1	B	22	LYS	3.3
1	A	394	TYR	3.3
1	A	225	ALA	3.2
1	B	42	PHE	3.2
1	B	21	GLU	3.2
1	B	200	VAL	3.2
1	A	232	ILE	3.1
1	A	199	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	178	GLU	3.1
1	B	344	PRO	3.1
1	B	343	ILE	3.0
1	A	262	LEU	3.0
1	A	241	GLN	2.9
1	B	39	ILE	2.9
1	A	40	MET	2.9
1	B	356	GLU	2.9
1	A	257	VAL	2.8
1	A	198	VAL	2.8
1	A	264	HIS	2.8
1	A	231	ASP	2.8
1	A	254	SER	2.7
1	A	176	GLY	2.7
1	A	246	LEU	2.7
1	A	255	VAL	2.7
1	A	177	THR	2.6
1	A	268	VAL	2.6
1	A	242	GLU	2.6
1	A	251	ILE	2.6
1	A	244	GLY	2.6
1	B	260	PRO	2.5
1	B	263	PRO	2.5
1	B	265	ILE	2.5
1	A	200	VAL	2.5
1	B	209	VAL	2.5
1	A	154	THR	2.5
1	A	243	ALA	2.5
1	A	357	GLY	2.5
1	A	236	ASN	2.5
1	A	224	PRO	2.5
1	A	263	PRO	2.5
1	B	354	ALA	2.4
1	A	223	VAL	2.4
1	B	266	ASN	2.4
1	A	210	ARG	2.4
1	B	23	LYS	2.4
1	B	251	ILE	2.3
1	A	277	PRO	2.3
1	A	328	ILE	2.3
1	A	318	ARG	2.3
1	B	255	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	237	LEU	2.3
1	B	28	ALA	2.2
1	A	197	ASP	2.2
1	B	40	MET	2.2
1	A	278	THR	2.2
1	A	293	ARG	2.2
1	B	176	GLY	2.2
1	B	254	SER	2.2
1	A	354	ALA	2.2
1	A	196	GLN	2.2
1	A	235	GLN	2.2
1	B	203	PRO	2.2
1	A	174	GLN	2.1
1	A	149	VAL	2.1
1	A	152	LYS	2.1
1	B	33	HIS	2.1
1	A	291	GLY	2.1
1	B	149	VAL	2.1
1	A	253	ARG	2.1
1	A	270	CYS	2.1
1	A	151	ALA	2.1
1	A	179	SER	2.0
1	A	258	GLN	2.0
1	A	280	PRO	2.0
1	A	234	VAL	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

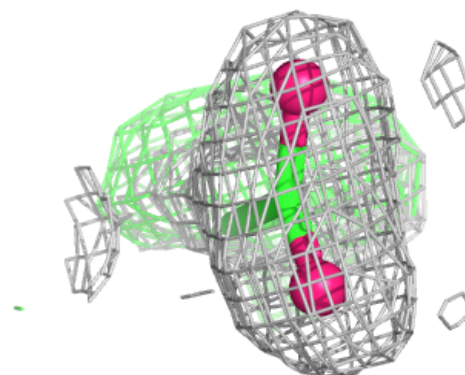
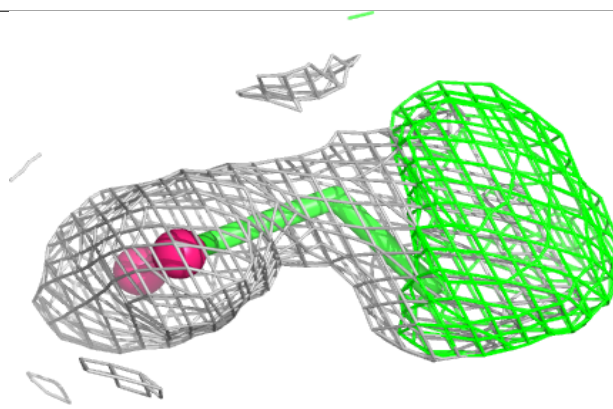
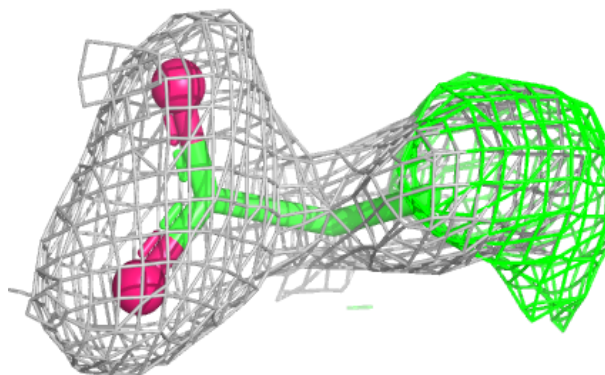
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SHF	B	502	5/8	0.75	0.21	29,32,36,39	1
3	PO4	B	501	5/5	0.81	0.10	63,73,75,83	0
2	SHF	A	500	4/8	0.85	0.10	28,29,30,38	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.

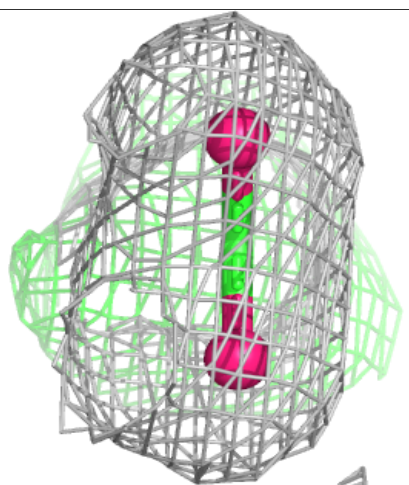
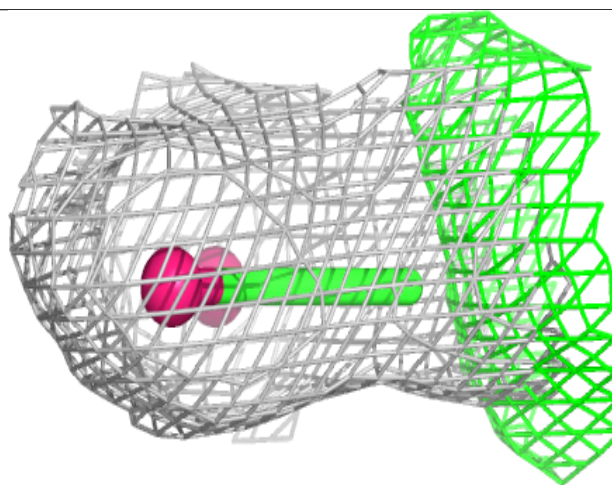
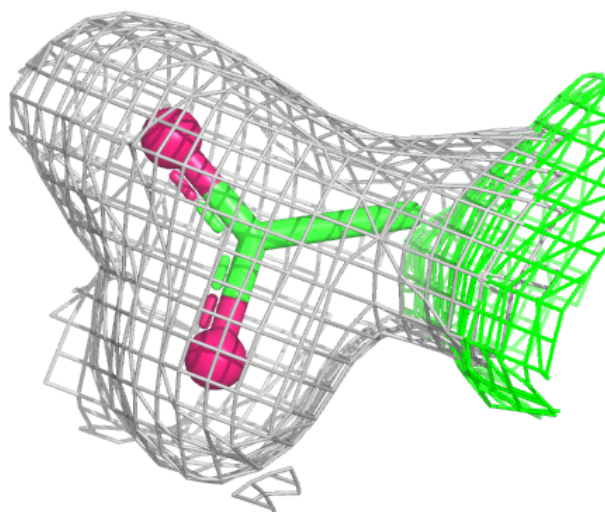
Electron density around SHF B 502:

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 [i](#)

There are no such residues in this entry.