



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 02:46 PM EDT

PDB ID : 8HZY / pdb_00008hzy
Title : The crystal structure of a Radical SAM Enzyme DesII
Authors : Hou, X.L.; Zhou, J.H.
Deposited on : 2023-01-10
Resolution : 2.04 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

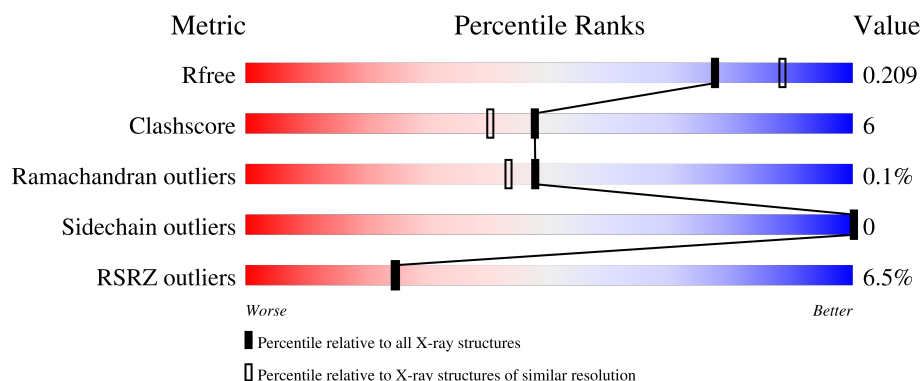
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	510	
1	B	510	

2 Entry composition [i](#)

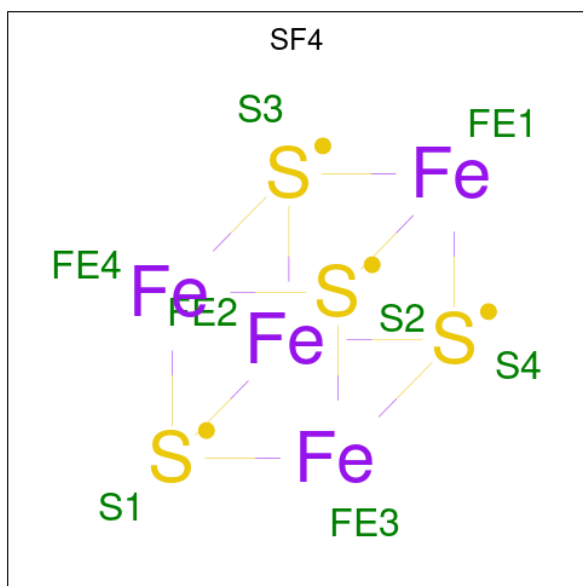
There are 4 unique types of molecules in this entry. The entry contains 7857 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DesII.

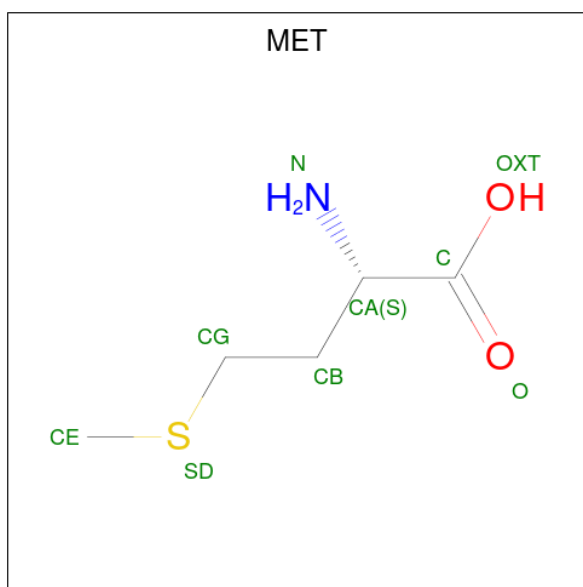
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	462	Total	C	N	O	S	0	0	0
			3581	2248	652	672	9			
1	B	458	Total	C	N	O	S	0	0	0
			3554	2232	651	662	9			

- Molecule 2 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



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

- Molecule 3 is METHIONINE (CCD ID: MET) (formula: $\text{C}_5\text{H}_{11}\text{NO}_2\text{S}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			9	5	1	2	1		

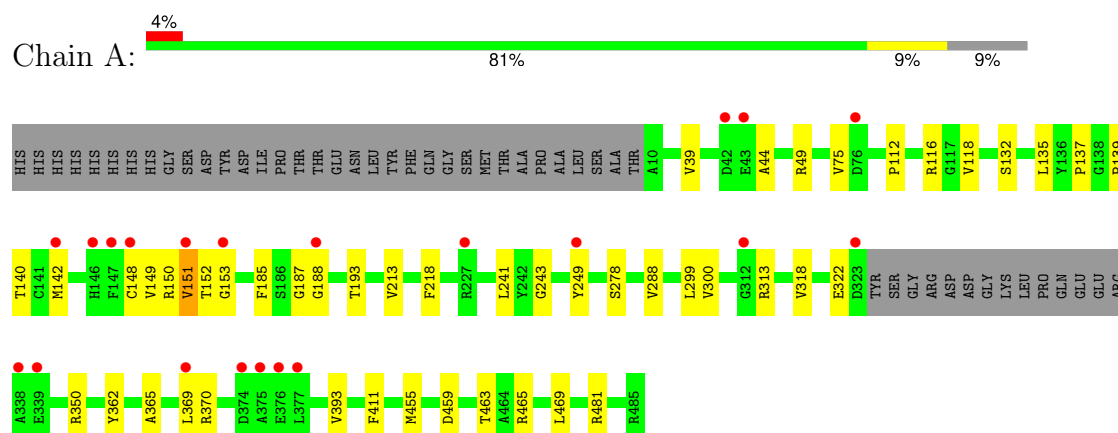
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	388	Total	O	0	0
			388	388		
4	B	309	Total	O	0	0
			309	309		

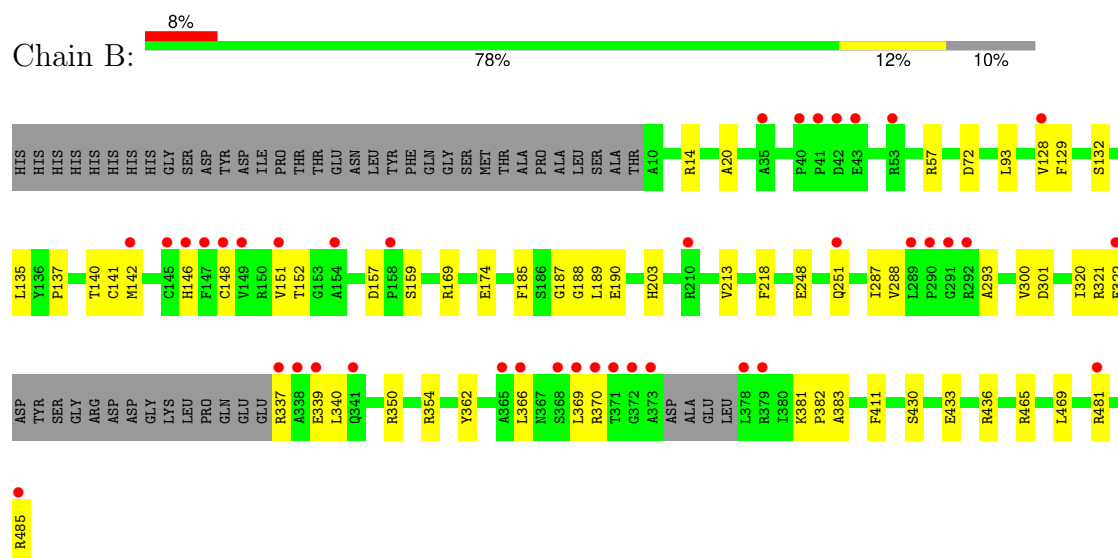
3 Residue-property plots

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 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: DesII



• Molecule 1: DesII



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α , β , γ	97.09Å 105.19Å 118.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.98 – 2.04 32.98 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.9 (32.98-2.04) 99.1 (32.98-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.12_2829, PHENIX 1.12_2829	Depositor
R, R_{free}	0.205 , 0.244 0.207 , 0.209	Depositor DCC
R_{free} test set	4021 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	17.1	Xtriage
Anisotropy	0.682	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7857	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 32.58 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.1867e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 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	0.27	0/3660	0.48	2/4975 (0.0%)
1	B	0.25	0/3632	0.47	0/4934
All	All	0.26	0/7292	0.47	2/9909 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	75	VAL	CA-C-N	5.28	128.58	120.82
1	A	75	VAL	C-N-CA	5.28	128.58	120.82

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	187	GLY	Peptide
1	B	187	GLY	Peptide

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	3581	0	3488	38	0
1	B	3554	0	3470	41	0
2	A	8	0	0	0	0
2	B	8	0	0	1	0
3	B	9	0	8	1	0
4	A	388	0	0	2	0
4	B	309	0	0	2	0
All	All	7857	0	6966	79	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 6.

All (79) 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:381:LYS:HG2	1:B:382:PRO:HD2	1.64	0.80
1:B:190:GLU:OE2	3:B:501:MET:N	2.17	0.77
1:B:322:GLU:HB3	1:B:366:LEU:HG	1.73	0.71
1:B:140:THR:HG22	1:B:141:CYS:H	1.56	0.70
1:A:365:ALA:O	1:A:369:LEU:CD2	2.40	0.69
1:B:301:ASP:OD2	1:B:354:ARG:NH2	2.26	0.68
1:A:365:ALA:O	1:A:369:LEU:HD23	1.96	0.66
1:A:241:LEU:HD12	1:A:249:TYR:OH	1.97	0.65
1:B:169:ARG:NH1	4:B:601:HOH:O	1.98	0.65
1:A:469:LEU:HD22	1:A:481:ARG:HG2	1.79	0.64
1:B:185:PHE:HB2	1:B:213:VAL:HG22	1.79	0.63
1:A:243:GLY:O	1:A:249:TYR:HE2	1.81	0.62
1:B:469:LEU:HD22	1:B:481:ARG:HH11	1.65	0.62
1:A:365:ALA:C	1:A:369:LEU:HD23	2.25	0.61
1:A:278:SER:O	1:A:313:ARG:NH1	2.25	0.60
1:A:188:GLY:HA2	1:A:411:PHE:CZ	2.37	0.59
1:B:169:ARG:HG2	1:B:203:HIS:CD2	2.37	0.59
1:B:57:ARG:NH1	1:B:72:ASP:OD1	2.31	0.58
1:B:146:HIS:HA	1:B:151:VAL:HG11	1.85	0.57
1:A:150:ARG:C	1:A:152:THR:H	2.12	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:CYS:O	1:A:151:VAL:HG22	2.06	0.56
1:A:152:THR:HG22	1:A:153:GLY:H	1.71	0.56
1:B:370:ARG:HH21	1:B:370:ARG:HG3	1.69	0.56
1:A:140:THR:H	1:A:193:THR:HG21	1.71	0.55
1:B:169:ARG:HG2	1:B:203:HIS:CG	2.42	0.55
1:A:112:PRO:O	1:A:116:ARG:HG3	2.07	0.55
1:A:142:MET:HG3	1:A:218:PHE:CD1	2.42	0.54
1:B:362:TYR:CE2	1:B:370:ARG:HD2	2.44	0.53
1:A:139:PRO:HD2	1:A:193:THR:HG22	1.90	0.53
1:B:300:VAL:HG11	1:B:350:ARG:HG3	1.91	0.53
1:B:465:ARG:O	1:B:469:LEU:HG	2.07	0.53
1:B:381:LYS:HE2	1:B:383:ALA:H	1.75	0.52
1:B:132:SER:HB2	4:B:836:HOH:O	2.09	0.52
1:B:188:GLY:HA2	1:B:411:PHE:CZ	2.45	0.52
1:A:185:PHE:HB2	1:A:213:VAL:HG22	1.92	0.51
1:B:148:CYS:O	1:B:151:VAL:HG22	2.10	0.51
1:A:300:VAL:HG11	1:A:350:ARG:HG3	1.91	0.51
1:A:148:CYS:SG	1:A:149:VAL:N	2.84	0.51
1:A:365:ALA:O	1:A:369:LEU:HD22	2.09	0.51
1:A:455:MET:HE1	1:A:463:THR:OG1	2.11	0.51
1:B:433:GLU:HG2	1:B:436:ARG:HH22	1.75	0.50
1:B:433:GLU:HG2	1:B:436:ARG:NH2	2.26	0.50
1:B:469:LEU:HD22	1:B:481:ARG:NH1	2.25	0.50
1:B:142:MET:HG3	1:B:218:PHE:CD1	2.47	0.49
1:A:465:ARG:O	1:A:469:LEU:HG	2.13	0.49
1:A:132:SER:HB2	4:A:767:HOH:O	2.12	0.49
1:A:39:VAL:HG21	1:A:44:ALA:HA	1.95	0.48
1:B:14:ARG:HH22	1:B:20:ALA:HA	1.77	0.48
1:B:248:GLU:HA	1:B:251:GLN:HG2	1.96	0.48
1:A:49:ARG:NH1	4:A:622:HOH:O	2.48	0.47
1:A:135:LEU:O	1:A:137:PRO:HD3	2.13	0.47
1:B:151:VAL:HG23	1:B:152:THR:HG23	1.96	0.47
1:B:287:ILE:HD11	1:B:321:ARG:CZ	2.44	0.47
1:A:139:PRO:HG2	1:A:193:THR:HG22	1.98	0.46
1:B:337:ARG:C	1:B:339:GLU:H	2.22	0.46
1:A:362:TYR:CD1	1:A:370:ARG:HD2	2.51	0.46
1:A:142:MET:SD	1:A:142:MET:N	2.81	0.45
1:B:135:LEU:O	1:B:137:PRO:HD3	2.17	0.45
1:B:128:VAL:HG12	1:B:129:PHE:O	2.17	0.45
1:A:243:GLY:O	1:A:249:TYR:CE2	2.66	0.44
1:A:369:LEU:HD22	1:A:369:LEU:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:340:LEU:HD23	1:B:369:LEU:CD2	2.47	0.44
1:B:140:THR:HG22	1:B:141:CYS:N	2.29	0.44
1:B:189:LEU:HA	2:B:502:SF4:S2	2.58	0.44
1:A:118:VAL:HG12	1:A:393:VAL:HG22	1.99	0.43
1:A:150:ARG:HA	1:A:150:ARG:HD2	1.77	0.43
1:B:340:LEU:HD23	1:B:369:LEU:HD21	1.99	0.43
1:B:320:ILE:HG22	1:B:366:LEU:CD1	2.49	0.43
1:A:299:LEU:HD21	1:A:318:VAL:HG21	2.01	0.43
1:B:288:VAL:HG23	1:B:293:ALA:HA	2.01	0.42
1:A:455:MET:HE2	1:A:459:ASP:HB3	2.01	0.42
1:A:455:MET:HE2	1:A:455:MET:HB3	1.94	0.42
1:A:139:PRO:CD	1:A:193:THR:HG22	2.50	0.41
1:A:313:ARG:HA	1:A:313:ARG:HD2	1.85	0.41
1:B:157:ASP:OD2	1:B:159:SER:OG	2.30	0.41
1:B:174:GLU:CD	1:B:430:SER:HB2	2.46	0.41
1:B:93:LEU:HA	1:B:93:LEU:HD23	1.84	0.41
1:A:288:VAL:HG22	1:A:322:GLU:HA	2.03	0.40
1:B:485:ARG:HH21	1:B:485:ARG:HG3	1.87	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	458/510 (90%)	446 (97%)	11 (2%)	1 (0%)	43	37
1	B	452/510 (89%)	443 (98%)	9 (2%)	0	100	100
All	All	910/1020 (89%)	889 (98%)	20 (2%)	1 (0%)	48	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	VAL

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	362/403 (90%)	362 (100%)	0	100	100
1	B	359/403 (89%)	359 (100%)	0	100	100
All	All	721/806 (90%)	721 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	HIS
1	A	89	GLN
1	A	271	GLN
1	B	265	ASN
1	B	345	ASN
1	B	467	ASN

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 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	SF4	B	502	1	0,12,12	-	-	-		
2	SF4	A	501	1,4	0,12,12	-	-	-		
3	MET	B	501	-	7,8,8	0.83	0	5,9,9	1.10	1 (20%)

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	MET	B	501	-	-	2/8/8/8	-
2	SF4	A	501	1,4	-	-	0/6/5/5
2	SF4	B	502	1	-	-	0/6/5/5

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	MET	OXT-C-O	-2.25	118.98	124.08

There are no chirality outliers.

All (2) torsion outliers are listed below:

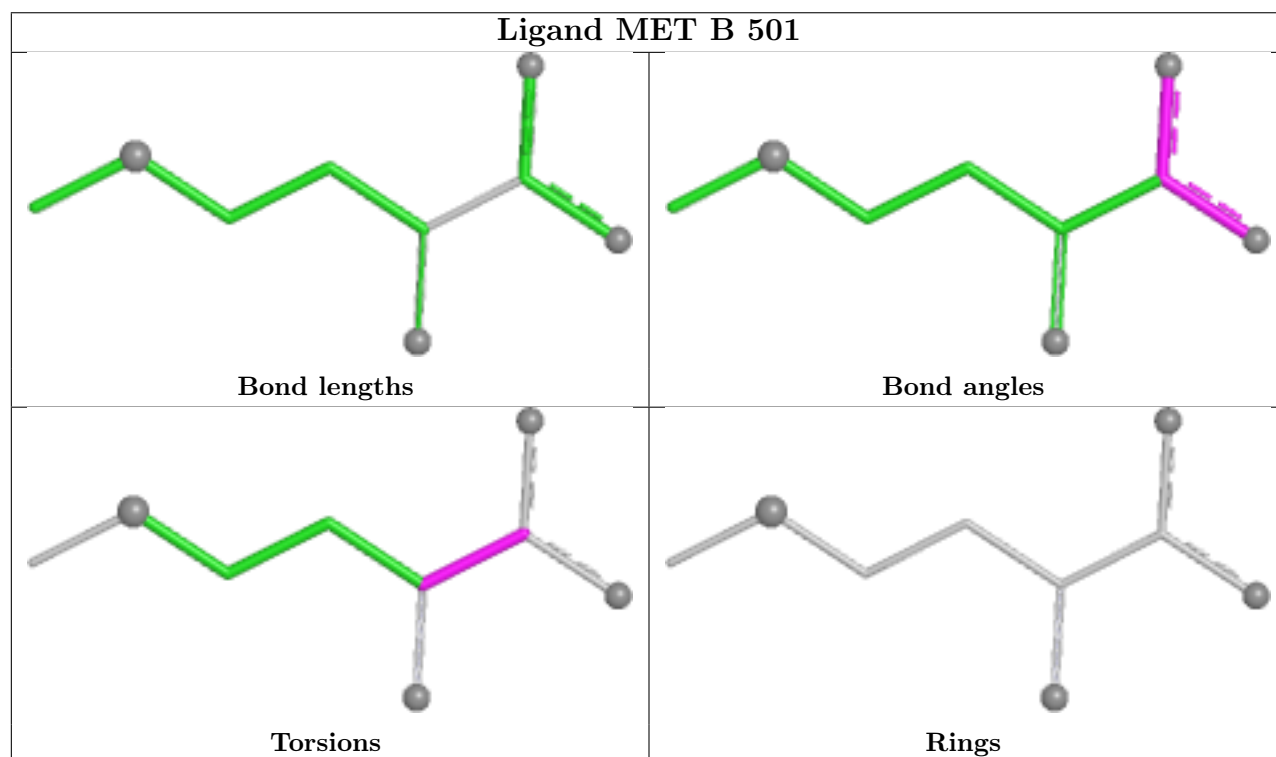
Mol	Chain	Res	Type	Atoms
3	B	501	MET	O-C-CA-N
3	B	501	MET	OXT-C-CA-N

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	502	SF4	1	0
3	B	501	MET	1	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	462/510 (90%)	0.01	21 (4%) 38 38	10, 18, 37, 73	0
1	B	458/510 (89%)	0.26	39 (8%) 16 17	12, 21, 43, 67	0
All	All	920/1020 (90%)	0.13	60 (6%) 25 24	10, 19, 41, 73	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	147	PHE	6.9
1	A	338	ALA	6.4
1	B	373	ALA	6.4
1	B	371	THR	6.2
1	B	368	SER	5.9
1	A	146	HIS	5.6
1	B	338	ALA	5.5
1	B	372	GLY	4.8
1	A	153	GLY	4.5
1	A	151	VAL	4.3
1	B	369	LEU	4.2
1	A	148	CYS	4.1
1	A	377	LEU	4.1
1	B	41	PRO	3.9
1	B	379	ARG	3.9
1	B	337	ARG	3.8
1	B	146	HIS	3.6
1	B	42	ASP	3.4
1	B	142	MET	3.4
1	A	376	GLU	3.3
1	A	227	ARG	3.1
1	B	339	GLU	3.1
1	A	312	GLY	3.0
1	B	40	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	145	CYS	3.0
1	B	366	LEU	3.0
1	B	148	CYS	3.0
1	A	42	ASP	3.0
1	B	341	GLN	3.0
1	B	35	ALA	2.9
1	A	76	ASP	2.8
1	B	251	GLN	2.8
1	B	43	GLU	2.8
1	B	147	PHE	2.8
1	B	151	VAL	2.8
1	A	339	GLU	2.7
1	B	481	ARG	2.7
1	A	249	TYR	2.7
1	A	369	LEU	2.6
1	A	375	ALA	2.6
1	B	378	LEU	2.6
1	A	43	GLU	2.6
1	B	210	ARG	2.5
1	B	322	GLU	2.5
1	B	365	ALA	2.5
1	A	188	GLY	2.5
1	B	370	ARG	2.5
1	A	374	ASP	2.4
1	B	158	PRO	2.3
1	B	292	ARG	2.3
1	B	128	VAL	2.2
1	B	154	ALA	2.2
1	A	142	MET	2.1
1	A	323	ASP	2.1
1	B	289	LEU	2.1
1	B	149	VAL	2.1
1	B	485	ARG	2.0
1	B	291	GLY	2.0
1	B	53	ARG	2.0
1	B	290	PRO	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 [i](#)

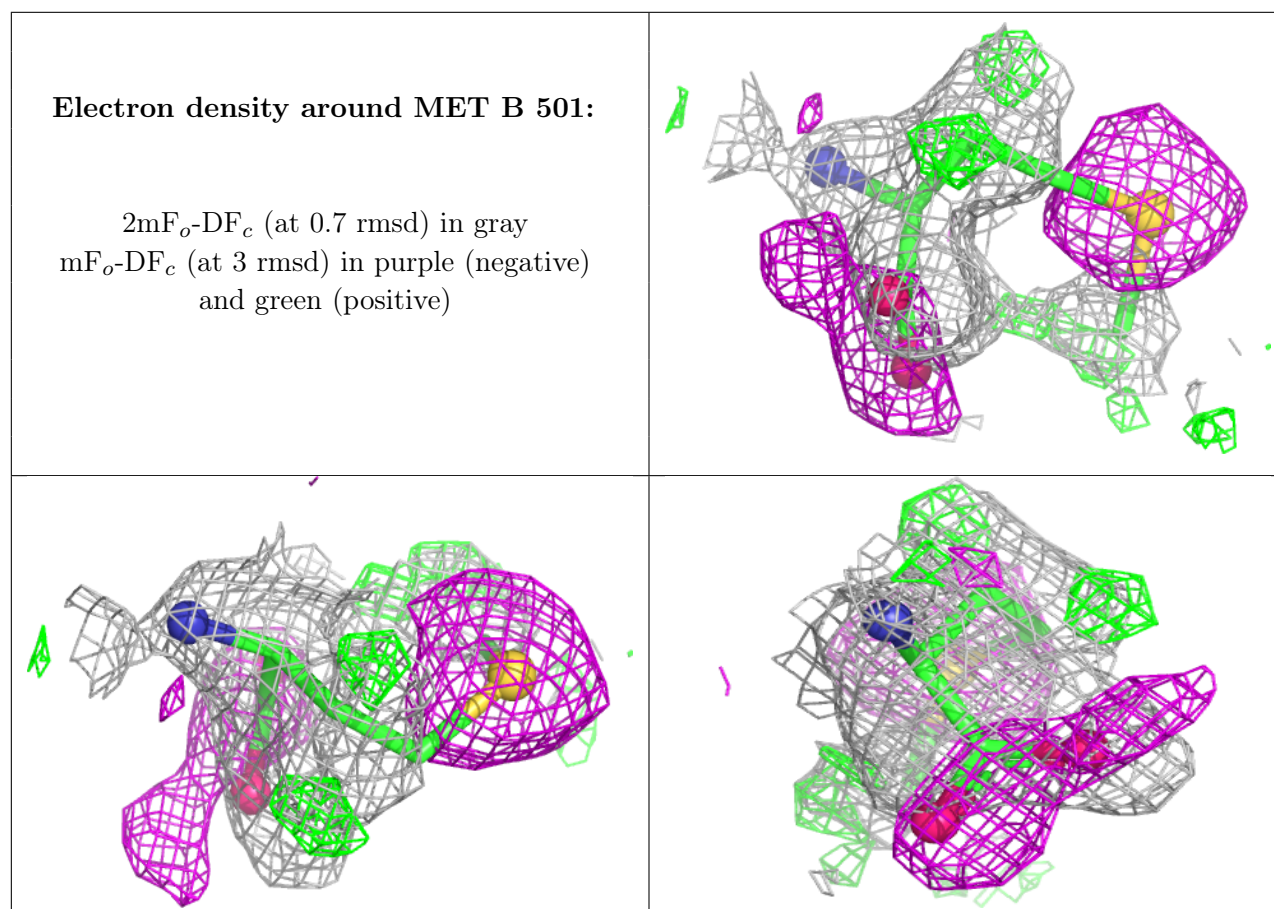
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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
3	MET	B	501	9/9	0.32	0.32	31,38,50,51	0
2	SF4	A	501	8/8	0.94	0.10	23,34,47,62	0
2	SF4	B	502	8/8	0.96	0.09	25,28,35,46	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.