



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:20 PM UTC

PDB ID : 1F4L / pdb_00001f4l
Title : CRYSTAL STRUCTURE OF THE E.COLI METHIONYL-TRNA SYN-
THETASE COMPLEXED WITH METHIONINE
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Deposited on : 2000-06-08
Resolution : 1.85 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
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

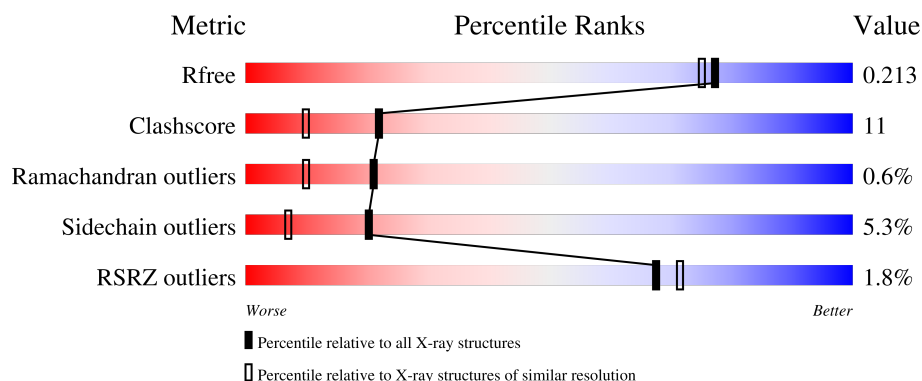
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

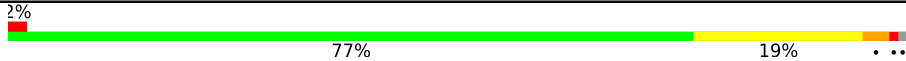
The reported resolution of this entry is 1.85 Å.

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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	551	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4893 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.

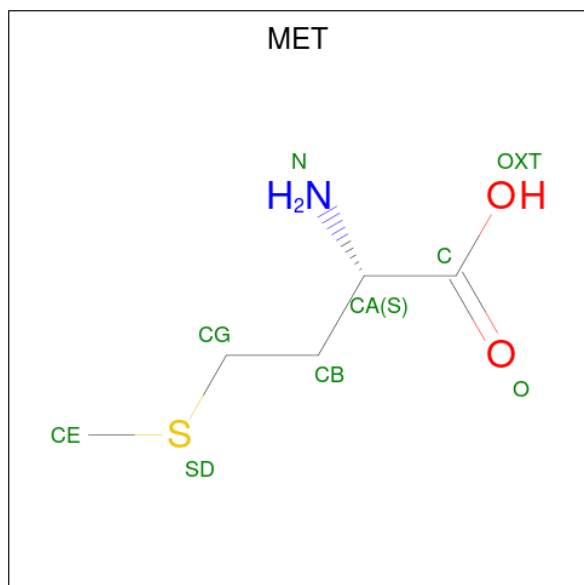
- Molecule 1 is a protein called METHIONYL-TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	545	4446	2837	754	829	26	0	23	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S).



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

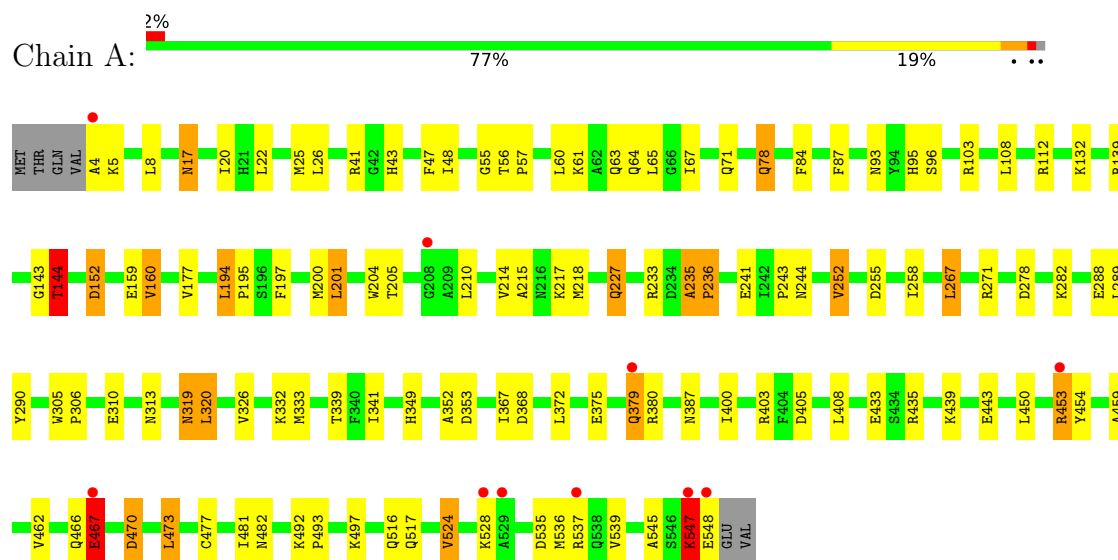
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	437	Total 437	O 437	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 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: METHIONYL-TRNA SYNTHETASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.40Å 45.16Å 86.31Å 90.00° 107.91° 90.00°	Depositor
Resolution (Å)	20.00 – 1.85 20.00 – 1.86	Depositor EDS
% Data completeness (in resolution range)	91.2 (20.00-1.85) 91.9 (20.00-1.86)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.47 (at 1.86Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.182 , 0.239 (Not available) , 0.213	Depositor DCC
R_{free} test set	4532 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	13.6	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 61.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4893	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.30% 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: ZN

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	0.65	0/4683	1.53	49/6333 (0.8%)

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	3

There are no bond length outliers.

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	235	ALA	CA-C-O	-26.41	99.13	119.46
1	A	435	ARG	CD-NE-CZ	22.23	155.51	124.40
1	A	467	GLU	CB-CG-CD	11.42	132.01	112.60
1	A	379	GLN	CB-CG-CD	9.67	129.03	112.60
1	A	236	PRO	N-CA-CB	9.63	113.37	103.25
1	A	252	VAL	CB-CA-C	-9.60	95.55	111.29
1	A	103	ARG	CD-NE-CZ	9.35	137.50	124.40
1	A	103	ARG	NE-CZ-NH2	9.11	127.40	119.20
1	A	435	ARG	NE-CZ-NH2	9.05	127.34	119.20
1	A	435	ARG	NE-CZ-NH1	-8.82	112.68	121.50
1	A	236	PRO	CA-N-CD	-8.78	99.71	112.00
1	A	160	VAL	CA-C-O	-8.35	112.45	120.30
1	A	524	VAL	N-CA-CB	-8.20	97.35	112.43
1	A	159	GLU	CA-C-N	-7.82	115.07	122.66
1	A	159	GLU	C-N-CA	-7.82	115.07	122.66
1	A	375	GLU	CB-CG-CD	7.76	125.78	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	467	GLU	N-CA-C	7.55	126.89	110.80
1	A	547	LYS	N-CA-C	-7.53	103.01	111.07
1	A	41	ARG	NE-CZ-NH2	7.38	125.85	119.20
1	A	524	VAL	CB-CA-C	7.17	121.44	111.19
1	A	139	ARG	CD-NE-CZ	7.15	134.41	124.40
1	A	233	ARG	NE-CZ-NH2	6.84	125.36	119.20
1	A	547	LYS	CA-CB-CG	6.80	127.69	114.10
1	A	387	ASN	CA-CB-CG	-6.46	106.14	112.60
1	A	387	ASN	OD1-CG-ND2	6.36	128.96	122.60
1	A	227	GLN	CB-CG-CD	6.34	123.38	112.60
1	A	349	HIS	CA-CB-CG	-6.04	107.76	113.80
1	A	470	ASP	CA-CB-CG	5.93	118.53	112.60
1	A	47	PHE	CA-CB-CG	5.78	119.58	113.80
1	A	177	VAL	N-CA-C	5.77	115.95	110.53
1	A	152	ASP	CA-CB-CG	-5.71	106.89	112.60
1	A	319	ASN	CA-CB-CG	-5.57	107.03	112.60
1	A	103	ARG	NE-CZ-NH1	-5.55	115.95	121.50
1	A	144	THR	N-CA-CB	5.54	119.61	110.69
1	A	17	ASN	CA-CB-CG	5.53	118.13	112.60
1	A	453	ARG	CD-NE-CZ	5.46	132.05	124.40
1	A	143	GLY	CA-C-N	-5.43	115.06	122.93
1	A	143	GLY	C-N-CA	-5.43	115.06	122.93
1	A	41	ARG	NE-CZ-NH1	-5.41	116.09	121.50
1	A	235	ALA	N-CA-C	5.30	117.27	109.42
1	A	55	GLY	N-CA-C	5.29	117.42	112.08
1	A	467	GLU	CA-C-O	-5.28	112.95	120.51
1	A	258	ILE	CA-C-O	5.27	126.41	120.03
1	A	517	GLN	CA-CB-CG	5.27	124.64	114.10
1	A	547	LYS	CA-C-N	5.26	131.16	121.70
1	A	547	LYS	C-N-CA	5.26	131.16	121.70
1	A	78	GLN	CB-CG-CD	5.20	121.44	112.60
1	A	387	ASN	N-CA-C	5.18	119.65	113.23
1	A	482	ASN	OD1-CG-ND2	-5.01	117.59	122.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	235	ALA	Peptide,Mainchain
1	A	467	GLU	Mainchain

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	4446	0	4309	95	0
2	A	1	0	0	0	0
3	A	9	0	8	0	0
4	A	437	0	0	9	0
All	All	4893	0	4317	95	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 11.

All (95) 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:25[A]:MET:HE1	1:A:84:PHE:CE2	1.68	1.25
1:A:25[A]:MET:CE	1:A:84:PHE:HE2	1.69	1.04
1:A:450[A]:LEU:HD11	1:A:453:ARG:NH1	1.81	0.95
1:A:352:ALA:N	1:A:497:LYS:HZ1	1.64	0.94
1:A:25[A]:MET:HE1	1:A:84:PHE:HE2	1.07	0.94
1:A:333[A]:MET:HE2	1:A:339:THR:O	1.68	0.92
1:A:450[A]:LEU:CD1	1:A:453:ARG:NH1	2.32	0.92
1:A:352:ALA:H	1:A:497:LYS:HZ1	1.17	0.92
1:A:205:THR:HG23	1:A:218:MET:HE3	1.54	0.89
1:A:400[A]:ILE:HD12	1:A:481:ILE:CD1	2.02	0.89
1:A:25[A]:MET:HE1	1:A:84:PHE:CD2	2.10	0.86
1:A:25[A]:MET:CE	1:A:84:PHE:CE2	2.49	0.83
1:A:352:ALA:H	1:A:497:LYS:NZ	1.77	0.82
1:A:400[A]:ILE:HD12	1:A:481:ILE:HD12	1.62	0.80
1:A:400[A]:ILE:HD13	1:A:408:LEU:HD23	1.62	0.80
1:A:67:ILE:HD12	1:A:71[B]:GLN:HG2	1.65	0.79
1:A:200[A]:MET:SD	1:A:310:GLU:OE2	2.41	0.78
1:A:93:ASN:HB2	1:A:267:LEU:HG	1.68	0.76
1:A:215:ALA:HA	1:A:218:MET:HE2	1.69	0.74
1:A:215:ALA:HA	1:A:218:MET:CE	2.19	0.72
1:A:17:ASN:HB2	1:A:61:LYS:HE3	1.74	0.68
1:A:210:LEU:HD21	1:A:320:LEU:HD13	1.76	0.68
1:A:204:TRP:HH2	1:A:320:LEU:HD11	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400[A]:ILE:CD1	1:A:481:ILE:HD12	2.25	0.66
1:A:210:LEU:HD12	1:A:218:MET:HE1	1.76	0.65
1:A:453:ARG:HH21	1:A:454:TYR:HB2	1.62	0.64
1:A:536:MET:HA	1:A:539:VAL:HG22	1.80	0.63
1:A:333[A]:MET:CE	1:A:341:ILE:H	2.13	0.62
1:A:450[A]:LEU:HD12	1:A:453:ARG:NH1	2.15	0.62
1:A:535:ASP:OD2	1:A:537:ARG:HB2	2.01	0.61
1:A:152:ASP:HB2	4:A:896:HOH:O	2.00	0.60
1:A:450[A]:LEU:HD11	1:A:453:ARG:HH11	1.66	0.60
1:A:22:LEU:HD12	1:A:333[A]:MET:HE3	1.83	0.60
1:A:144:THR:HG21	4:A:855:HOH:O	2.01	0.59
1:A:305:TRP:HB3	1:A:306:PRO:HD3	1.85	0.58
1:A:352:ALA:HB3	1:A:497:LYS:NZ	2.18	0.58
1:A:547:LYS:O	1:A:548:GLU:HB2	2.04	0.57
1:A:497:LYS:HG3	4:A:785:HOH:O	2.03	0.57
1:A:8[A]:LEU:HD11	1:A:48:ILE:HG13	1.87	0.57
1:A:210:LEU:CD1	1:A:218:MET:HE1	2.34	0.56
1:A:497:LYS:HD2	4:A:1086:HOH:O	2.06	0.56
1:A:278:ASP:O	1:A:282[B]:LYS:HG3	2.05	0.56
1:A:60:LEU:O	1:A:64:GLN:HG3	2.09	0.53
1:A:320:LEU:N	1:A:320:LEU:HD12	2.25	0.52
1:A:536:MET:SD	1:A:539:VAL:HG21	2.50	0.51
1:A:227:GLN:HG2	4:A:760:HOH:O	2.10	0.51
1:A:26:LEU:HD22	1:A:326:VAL:HG22	1.91	0.51
1:A:353:ASP:H	1:A:497:LYS:HE2	1.76	0.51
1:A:466:GLN:HB3	1:A:467:GLU:OE2	2.11	0.51
1:A:352:ALA:HB3	1:A:497:LYS:HZ3	1.73	0.50
1:A:204:TRP:CH2	1:A:320:LEU:HD11	2.44	0.50
1:A:56:THR:HB	1:A:57:PRO:HD3	1.93	0.50
1:A:467:GLU:HA	4:A:1105:HOH:O	2.12	0.50
1:A:545:ALA:O	1:A:548:GLU:HA	2.12	0.50
1:A:22:LEU:HD12	1:A:333[A]:MET:CE	2.42	0.49
1:A:63:GLN:HE22	1:A:132:LYS:NZ	2.09	0.49
1:A:352:ALA:CA	1:A:497:LYS:HZ1	2.26	0.49
1:A:95:HIS:CG	1:A:96:SER:H	2.30	0.49
1:A:353:ASP:H	1:A:497:LYS:CE	2.26	0.48
1:A:459:ALA:O	1:A:462[A]:VAL:HG22	2.13	0.48
1:A:5:LYS:H	1:A:43:HIS:CD2	2.31	0.48
1:A:194:LEU:N	1:A:195:PRO:CD	2.76	0.47
1:A:450[A]:LEU:CD1	1:A:453:ARG:HH11	2.20	0.47
1:A:353:ASP:OD2	1:A:497:LYS:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:333[A]:MET:HE2	1:A:341:ILE:H	1.80	0.46
1:A:439:LYS:NZ	1:A:443:GLU:HG2	2.30	0.46
1:A:450[A]:LEU:HD11	1:A:453:ARG:HH12	1.71	0.46
1:A:108[A]:LEU:HD11	1:A:112:ARG:CZ	2.46	0.46
1:A:288:GLU:HG2	1:A:290:TYR:OH	2.16	0.45
1:A:205:THR:HG23	1:A:218:MET:CE	2.36	0.45
1:A:333[A]:MET:HE1	1:A:341:ILE:H	1.81	0.45
1:A:320:LEU:N	1:A:320:LEU:CD1	2.81	0.44
1:A:403:ARG:NH2	1:A:470:ASP:OD2	2.40	0.44
1:A:467:GLU:CG	4:A:954:HOH:O	2.66	0.44
1:A:25[B]:MET:HE2	1:A:87:PHE:CG	2.53	0.43
1:A:210:LEU:CD2	1:A:320:LEU:HD13	2.46	0.43
1:A:132:LYS:HE3	4:A:880:HOH:O	2.18	0.43
1:A:4:ALA:N	1:A:43:HIS:HD2	2.16	0.43
1:A:243:PRO:O	1:A:244:ASN:HB2	2.18	0.43
1:A:400[A]:ILE:HD13	1:A:408:LEU:CD2	2.42	0.43
1:A:197:PHE:O	1:A:201[B]:LEU:HD22	2.18	0.42
1:A:4:ALA:N	1:A:43:HIS:CD2	2.87	0.42
1:A:492:LYS:N	1:A:493:PRO:CD	2.83	0.42
1:A:215:ALA:CA	1:A:218:MET:HE2	2.46	0.42
1:A:319:ASN:C	1:A:320:LEU:HD12	2.45	0.42
1:A:20:ILE:CG2	1:A:25[A]:MET:HE3	2.50	0.42
1:A:5:LYS:H	1:A:43:HIS:HD2	1.68	0.41
1:A:473:LEU:HD22	1:A:477:CYS:SG	2.61	0.41
1:A:516:GLN:NE2	4:A:1066:HOH:O	2.53	0.41
1:A:8[A]:LEU:HD11	1:A:48:ILE:CG1	2.50	0.41
1:A:67:ILE:CD1	1:A:71[B]:GLN:HG2	2.45	0.41
1:A:22:LEU:HD13	1:A:372[B]:LEU:HD12	2.02	0.41
1:A:214:VAL:CG2	1:A:367:ILE:HD11	2.51	0.41

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	566/551 (103%)	555 (98%)	8 (1%)	3 (0%)	24 13

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	528	LYS
1	A	467	GLU
1	A	236	PRO

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	492/475 (104%)	463 (94%)	29 (6%)	18 5

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	LEU
1	A	78	GLN
1	A	144	THR
1	A	160	VAL
1	A	194	LEU
1	A	201[A]	LEU
1	A	201[B]	LEU
1	A	217[A]	LYS
1	A	217[B]	LYS
1	A	241	GLU
1	A	252	VAL
1	A	255	ASP
1	A	267	LEU
1	A	271	ARG
1	A	289	LEU
1	A	313[A]	ASN
1	A	313[B]	ASN
1	A	320	LEU

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Mol	Chain	Res	Type
1	A	332	LYS
1	A	368	ASP
1	A	379	GLN
1	A	380[A]	ARG
1	A	380[B]	ARG
1	A	405	ASP
1	A	433	GLU
1	A	467	GLU
1	A	473	LEU
1	A	524	VAL
1	A	547	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	A	63	GLN
1	A	78	GLN
1	A	88	ASN
1	A	379	GLN
1	A	391	ASN
1	A	401	ASN
1	A	458	GLN
1	A	507	ASN
1	A	525	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 [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
3	MET	A	601	-	7,8,8	1.06	1 (14%)	5,9,9	0.59	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
3	MET	A	601	-	-	0/8/8/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	MET	OXT-C	-2.53	1.22	1.30

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	545/551 (98%)	-0.13	10 (1%) 67 71	6, 14, 28, 52	22 (4%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	467	GLU	6.2
1	A	4	ALA	5.3
1	A	529	ALA	3.9
1	A	548	GLU	3.2
1	A	379	GLN	2.9
1	A	537	ARG	2.6
1	A	208	GLY	2.6
1	A	528	LYS	2.5
1	A	453	ARG	2.5
1	A	547	LYS	2.3

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 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	A	601	9/9	0.98	0.06	7,10,14,16	0
2	ZN	A	701	1/1	1.00	0.01	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.