



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:30 PM UTC

PDB ID : 3D6V / pdb_00003d6v
Title : Crystal structure of 4-(trifluoromethyldiaziriny)phenylalanyl-tRNA synthetase
Authors : Liu, W.; Tippmann, E.; Mack, A.V.; Schultz, P.G.
Deposited on : 2008-05-20
Resolution : 2.20 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

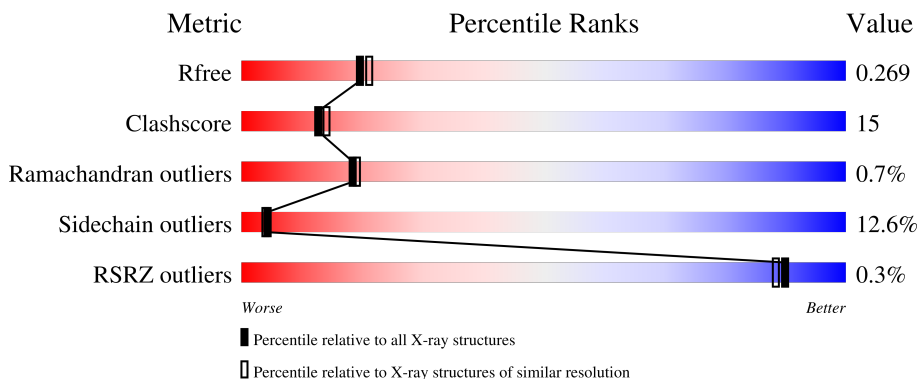
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	314	 66% 24% 8% ...

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2689 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.

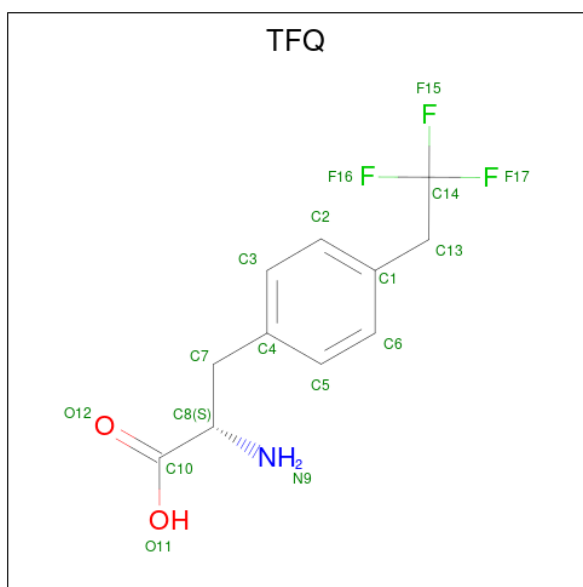
- Molecule 1 is a protein called Tyrosyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	308	2499	1604	420	461	14	0	4	0

There are 15 discrepancies between the modelled and reference sequences:

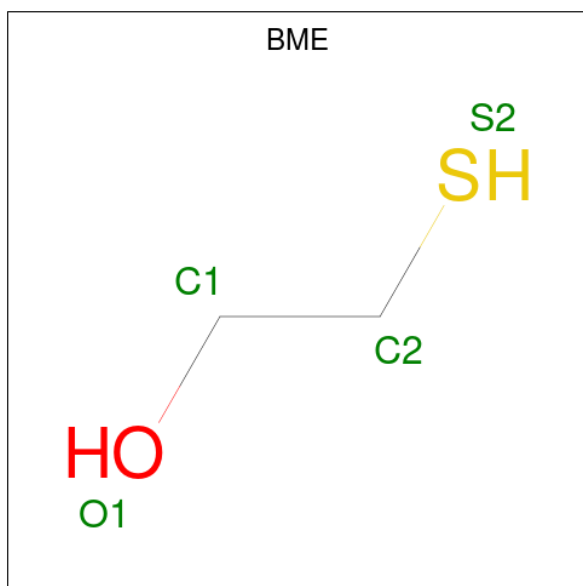
Chain	Residue	Modelled	Actual	Comment	Reference
A	32	ILE	TYR	engineered mutation	UNP Q57834
A	70	PHE	HIS	engineered mutation	UNP Q57834
A	107	SER	GLU	engineered mutation	UNP Q57834
A	109	MET	GLN	engineered mutation	UNP Q57834
A	158	PRO	ASP	engineered mutation	UNP Q57834
A	159	LEU	ILE	engineered mutation	UNP Q57834
A	162	GLU	LEU	engineered mutation	UNP Q57834
A	307	LEU	-	expression tag	UNP Q57834
A	308	GLU	-	expression tag	UNP Q57834
A	309	HIS	-	expression tag	UNP Q57834
A	310	HIS	-	expression tag	UNP Q57834
A	311	HIS	-	expression tag	UNP Q57834
A	312	HIS	-	expression tag	UNP Q57834
A	313	HIS	-	expression tag	UNP Q57834
A	314	HIS	-	expression tag	UNP Q57834

- Molecule 2 is 4-(2,2,2-TRIFLUOROETHYL)-L-PHENYLALANINE (CCD ID: TFQ) (formula: C₁₁H₁₂F₃NO₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			17	11	3	1	2		

- Molecule 3 is BETA-MERCAPTOETHANOL (CCD ID: BME) (formula: C_2H_6OS).



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

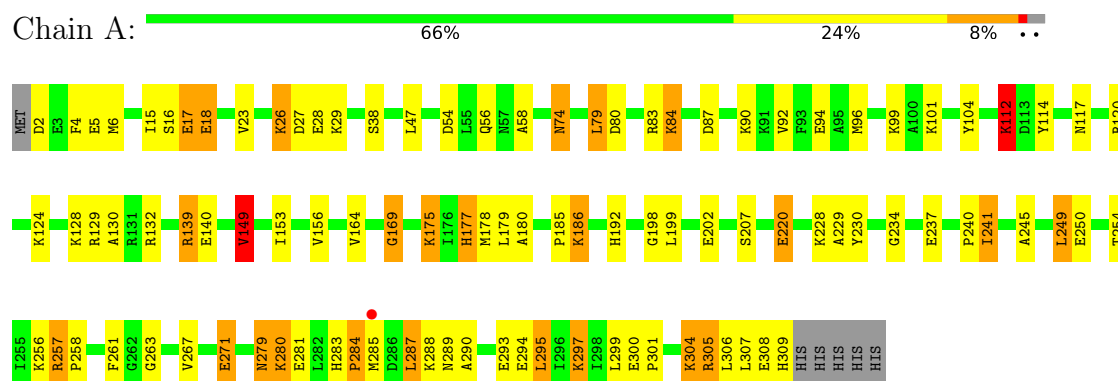
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	169	Total 169	O 169	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: Tyrosyl-tRNA synthetase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	104.16Å 104.16Å 70.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.92 – 2.20 38.92 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.6 (38.92-2.20) 98.5 (38.92-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.193 , 0.270 0.193 , 0.269	Depositor DCC
R_{free} test set	1021 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	52.3	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2689	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.05% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: BME, TFQ

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	1.50	8/2554 (0.3%)	1.35	10/3429 (0.3%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	241	ILE	CA-CB	6.72	1.63	1.54
1	A	164	VAL	CA-CB	6.13	1.61	1.54
1	A	104	TYR	C-O	-5.59	1.17	1.24
1	A	38	SER	C-O	5.33	1.30	1.24
1	A	114	TYR	N-CA	-5.25	1.40	1.46
1	A	177	HIS	CA-C	-5.20	1.46	1.52
1	A	169	GLY	N-CA	5.10	1.50	1.45
1	A	153	ILE	N-CA	-5.01	1.39	1.46

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	LEU	N-CA-C	5.96	119.38	111.75
1	A	17	GLU	N-CA-C	5.84	117.64	111.28
1	A	198	GLY	N-CA-C	-5.77	104.86	112.82
1	A	149	VAL	CB-CA-C	5.53	119.14	110.95
1	A	80	ASP	CA-C-N	5.52	127.67	120.28
1	A	80	ASP	C-N-CA	5.52	127.67	120.28
1	A	299	LEU	N-CA-C	5.42	119.15	112.54
1	A	117	ASN	N-CA-C	5.17	116.92	111.28
1	A	112	LYS	CB-CG-CD	-5.11	99.56	111.30
1	A	79	LEU	N-CA-C	5.07	116.81	111.28

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	2499	0	2585	78	1
2	A	17	0	11	0	0
3	A	4	0	5	0	0
4	A	169	0	0	10	1
All	All	2689	0	2601	78	1

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 15.

All (78) 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:56:GLN:NE2	1:A:99:LYS:HB2	1.65	1.12
1:A:90:LYS:O	1:A:94:GLU:HG3	1.74	0.86
1:A:56:GLN:HE22	1:A:99:LYS:HB2	1.42	0.83
1:A:279:ASN:HD21	1:A:281:GLU:HG3	1.43	0.83
1:A:56:GLN:HE22	1:A:99:LYS:CB	1.94	0.80
1:A:279:ASN:C	1:A:279:ASN:HD22	1.90	0.79
1:A:258:PRO:HG2	1:A:261:PHE:HD1	1.49	0.77
1:A:2:ASP:N	4:A:538:HOH:O	2.18	0.74
1:A:83:ARG:HD3	4:A:515:HOH:O	1.86	0.74
1:A:56:GLN:NE2	1:A:99:LYS:CB	2.46	0.74
1:A:290:ALA:O	1:A:294:GLU:HG2	1.91	0.71
1:A:6:MET:CE	1:A:58:ALA:HB2	2.24	0.68
1:A:300:GLU:HG2	1:A:304:LYS:HE3	1.76	0.66
1:A:220:GLU:HG3	4:A:445:HOH:O	1.94	0.65
1:A:156:VAL:HG12	1:A:180:ALA:HB2	1.79	0.65
1:A:56:GLN:HE21	1:A:99:LYS:HB2	1.58	0.64
1:A:258:PRO:HG2	1:A:261:PHE:CD1	2.31	0.64
1:A:6:MET:CE	1:A:54:ASP:O	2.45	0.64
1:A:6:MET:HE3	1:A:54:ASP:O	1.97	0.64
1:A:128:LYS:O	1:A:132[A]:ARG:HG3	1.97	0.64
1:A:245:ALA:HA	1:A:249:LEU:HD22	1.79	0.64
1:A:289:ASN:O	1:A:293:GLU:HG2	1.98	0.64
1:A:92:VAL:HG12	1:A:96:MET:HE3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18[B]:GLU:H	1:A:18[B]:GLU:CD	2.11	0.58
1:A:6:MET:HE1	1:A:58:ALA:HB2	1.84	0.58
1:A:241:ILE:HG22	1:A:287:LEU:HD13	1.86	0.57
1:A:279:ASN:C	1:A:279:ASN:ND2	2.57	0.57
1:A:271:GLU:H	1:A:271:GLU:CD	2.11	0.56
1:A:257:ARG:CD	1:A:263:GLY:O	2.54	0.56
1:A:301:PRO:O	1:A:305:ARG:HD2	2.06	0.54
1:A:74:ASN:HD21	1:A:139:ARG:H	1.55	0.53
1:A:279:ASN:ND2	1:A:281:GLU:HG3	2.20	0.52
1:A:257:ARG:HD3	1:A:263:GLY:O	2.10	0.52
1:A:130:ALA:CB	1:A:149:VAL:HG22	2.40	0.52
1:A:294:GLU:HA	1:A:297:LYS:HG3	1.91	0.52
1:A:129:ARG:HD2	1:A:132[A]:ARG:NH2	2.25	0.51
1:A:56:GLN:HE22	1:A:99:LYS:H	1.57	0.51
1:A:220:GLU:CG	4:A:445:HOH:O	2.57	0.51
1:A:284:PRO:O	1:A:288:LYS:HG3	2.11	0.51
1:A:23:VAL:O	1:A:26:LYS:HG3	2.11	0.51
1:A:285[B]:MET:HE3	1:A:288:LYS:HD2	1.93	0.50
1:A:241:ILE:CG2	1:A:287:LEU:HD13	2.42	0.49
1:A:130:ALA:HB3	1:A:149:VAL:HG22	1.94	0.49
1:A:234:GLY:HA3	1:A:280:LYS:HE2	1.94	0.48
1:A:257:ARG:HD2	1:A:263:GLY:O	2.14	0.48
1:A:4:PHE:HZ	1:A:17:GLU:HG2	1.80	0.47
1:A:229:ALA:CB	1:A:241:ILE:HD11	2.44	0.47
1:A:293:GLU:O	1:A:297:LYS:CG	2.62	0.47
1:A:175:LYS:HD3	4:A:507:HOH:O	2.15	0.46
1:A:229:ALA:HB3	1:A:241:ILE:HD11	1.98	0.45
1:A:308:GLU:O	1:A:309:HIS:CD2	2.70	0.45
1:A:169:GLY:O	1:A:192:HIS:HA	2.17	0.45
1:A:297:LYS:HB3	1:A:297:LYS:HE2	1.70	0.45
1:A:177:HIS:CE1	4:A:557:HOH:O	2.70	0.44
1:A:92:VAL:HA	1:A:306:LEU:HD21	2.00	0.44
1:A:101:LYS:HG2	4:A:440:HOH:O	2.16	0.44
1:A:304:LYS:HB2	4:A:584:HOH:O	2.17	0.44
1:A:283[A]:HIS:CG	1:A:284:PRO:HD2	2.53	0.44
1:A:293:GLU:O	1:A:297:LYS:HG3	2.17	0.43
1:A:74:ASN:HD22	1:A:74:ASN:HA	1.65	0.43
1:A:307:LEU:HD23	1:A:307:LEU:HA	1.67	0.43
1:A:178:MET:HE2	1:A:178:MET:HA	2.01	0.43
1:A:56:GLN:HE22	1:A:99:LYS:CA	2.31	0.42
1:A:186:LYS:H	1:A:186:LYS:HG2	1.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:TYR:O	1:A:240:PRO:HD2	2.19	0.42
1:A:120:ARG:NH1	1:A:124:LYS:NZ	2.68	0.42
1:A:156:VAL:CG1	1:A:180:ALA:HB2	2.47	0.42
1:A:15:ILE:HA	1:A:16:SER:HA	1.73	0.42
1:A:84:LYS:HE3	1:A:84:LYS:HB3	1.43	0.42
1:A:280:LYS:HB3	1:A:283[B]:HIS:CE1	2.55	0.42
1:A:112:LYS:HB2	1:A:112:LYS:HE2	1.30	0.41
1:A:295:LEU:HD23	1:A:295:LEU:HA	1.89	0.41
1:A:47:LEU:C	1:A:47:LEU:HD23	2.46	0.41
1:A:56:GLN:HE22	1:A:99:LYS:N	2.18	0.41
1:A:175:LYS:HE2	4:A:534:HOH:O	2.21	0.41
1:A:308:GLU:O	1:A:309:HIS:CG	2.74	0.41
1:A:5:GLU:OE1	4:A:516:HOH:O	2.22	0.40

All (1) 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)
1:A:27:ASP:OD2	4:A:432:HOH:O[3_554]	2.14	0.06

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	310/314 (99%)	304 (98%)	4 (1%)	2 (1%)	21 23

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	280	LYS
1	A	185	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	274/276 (99%)	239 (87%)	35 (13%)	4 4

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18[A]	GLU
1	A	18[B]	GLU
1	A	26	LYS
1	A	28	GLU
1	A	29	LYS
1	A	74	ASN
1	A	79	LEU
1	A	84	LYS
1	A	87	ASP
1	A	112	LYS
1	A	139	ARG
1	A	140	GLU
1	A	149	VAL
1	A	175	LYS
1	A	179	LEU
1	A	186	LYS
1	A	202	GLU
1	A	207	SER
1	A	220	GLU
1	A	228	LYS
1	A	237	GLU
1	A	249	LEU
1	A	250	GLU
1	A	254	THR
1	A	256	LYS
1	A	257	ARG
1	A	267	VAL
1	A	271	GLU
1	A	279	ASN
1	A	284	PRO

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Mol	Chain	Res	Type
1	A	287	LEU
1	A	295	LEU
1	A	297	LYS
1	A	304	LYS
1	A	305	ARG

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	48	GLN
1	A	56	GLN
1	A	74	ASN
1	A	193	ASN
1	A	279	ASN
1	A	309	HIS

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](#)

2 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	BME	A	401	-	3,3,3	1.01	0	2,2,2	1.08	0
2	TFQ	A	400	-	16,17,17	1.41	3 (18%)	19,24,24	2.47	3 (15%)

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	BME	A	401	-	-	1/1/1/1	-
2	TFQ	A	400	-	-	5/13/13/13	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	400	TFQ	C5-C6	3.11	1.43	1.38
2	A	400	TFQ	C13-C14	2.89	1.56	1.48
2	A	400	TFQ	C7-C4	2.27	1.56	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	400	TFQ	F16-C14-C13	-9.06	105.98	112.74
2	A	400	TFQ	F17-C14-C13	3.41	115.29	112.74
2	A	400	TFQ	C6-C5-C4	2.24	123.95	121.00

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	BME	O1-C1-C2-S2
2	A	400	TFQ	O11-C10-C8-C7
2	A	400	TFQ	O12-C10-C8-C7
2	A	400	TFQ	C5-C4-C7-C8
2	A	400	TFQ	C3-C4-C7-C8
2	A	400	TFQ	O11-C10-C8-N9

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	308/314 (98%)	-0.08	1 (0%) 90 88	27, 55, 75, 98	4 (1%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	285[A]	MET	2.1

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(Å ²)	Q<0.9
3	BME	A	401	4/4	0.77	0.26	71,74,74,81	0
2	TFQ	A	400	17/17	0.92	0.10	49,50,66,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.