



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:35 PM UTC

PDB ID : 5MQZ / pdb_00005mqz
Title : Archaeal branched-chain amino acid aminotransferase from *Archaeoglobus fulgidus*; holoform
Authors : James, P.; Isupov, M.N.; Sayer, C.; Littlechild, J.A.; Sutter, J.M.; Schmidt, M.; Schoenheit, P.
Deposited on : 2016-12-21
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

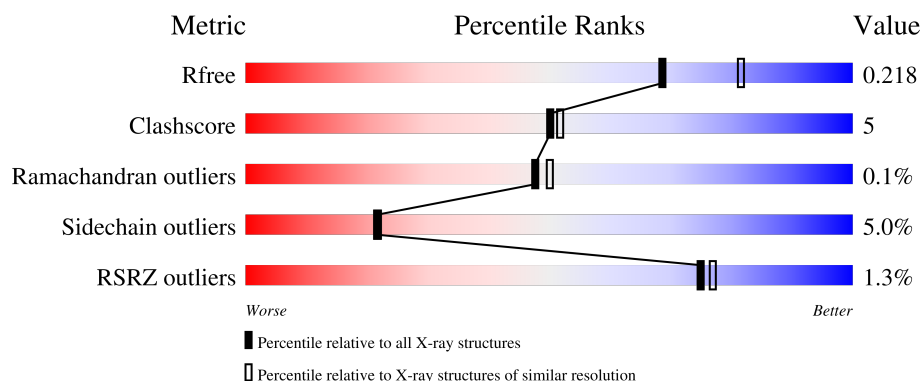
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	290	% 84% 12% ...
1	B	290	% 86% 11% ..
1	C	290	2% 86% 11% ..
1	D	290	% 88% 11% .
1	E	290	2% 84% 13% ..

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Mol	Chain	Length	Quality of chain
1	F	290	% 86% 11% ..

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15167 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.

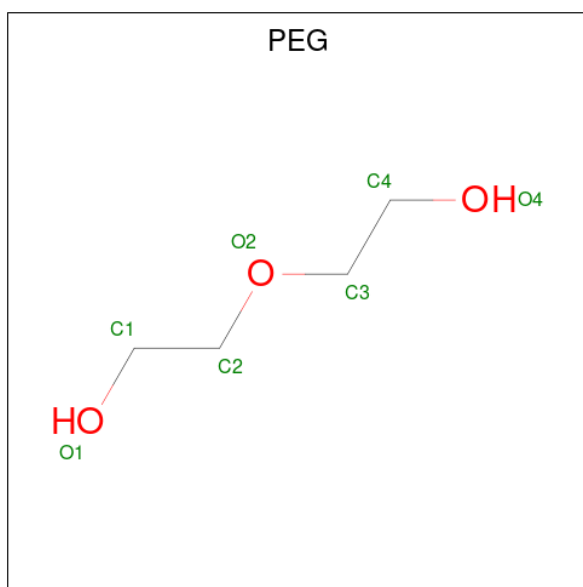
- Molecule 1 is a protein called Putative branched-chain-amino-acid aminotransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	P	S	0	30	0
			2460	1580	416	458	1	5			
1	B	286	Total	C	N	O	P	S	0	23	0
			2412	1550	409	447	1	5			
1	C	286	Total	C	N	O	P	S	0	19	0
			2395	1532	410	447	1	5			
1	D	290	Total	C	N	O	P	S	0	15	0
			2396	1534	402	454	1	5			
1	E	287	Total	C	N	O	P	S	0	22	0
			2414	1544	407	457	1	5			
1	F	287	Total	C	N	O	P	S	0	15	0
			2371	1516	399	450	1	5			

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

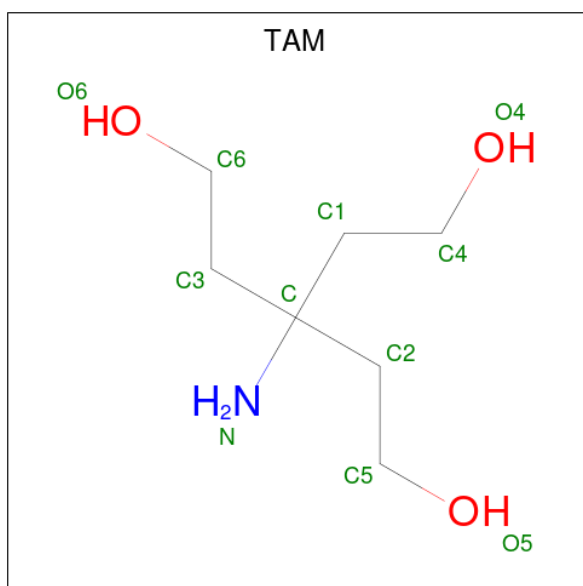
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	C	1	Total Cl 1 1	0	0
2	E	1	Total Cl 1 1	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is TRIS(HYDROXYETHYL)AMINOMETHANE (CCD ID: TAM) (formula: $C_7H_{17}NO_3$).



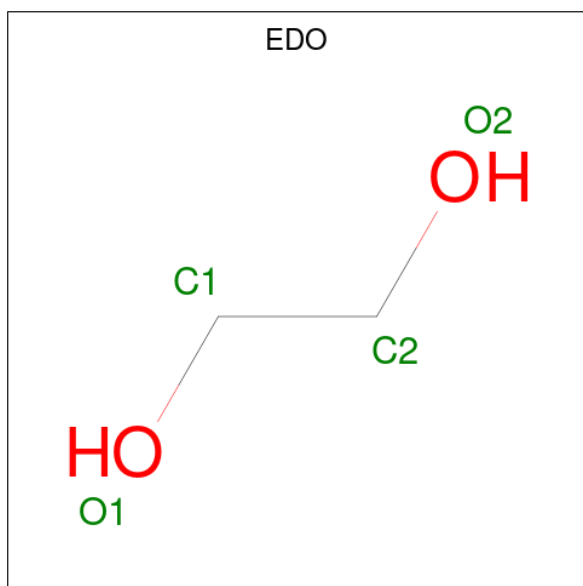
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			11	7	1	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			11	7	1	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	116	Total	O	0	0
			116	116		
6	B	118	Total	O	0	0
			118	118		
6	C	101	Total	O	0	0
			101	101		
6	D	122	Total	O	0	0
			122	122		
6	E	110	Total	O	0	0
			110	110		

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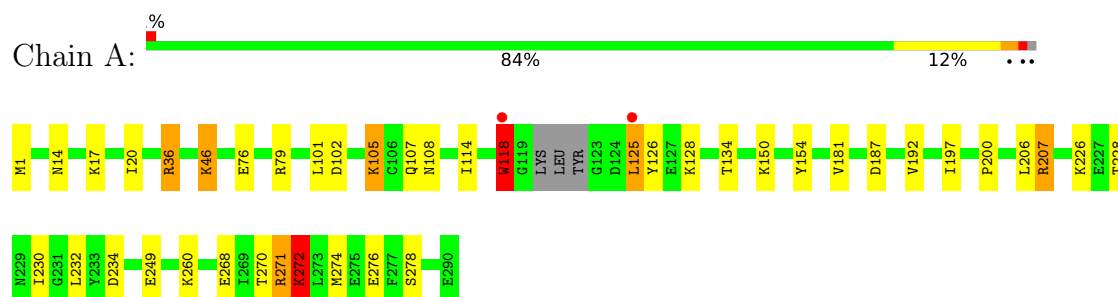
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	101	Total 101	O 101	0	0

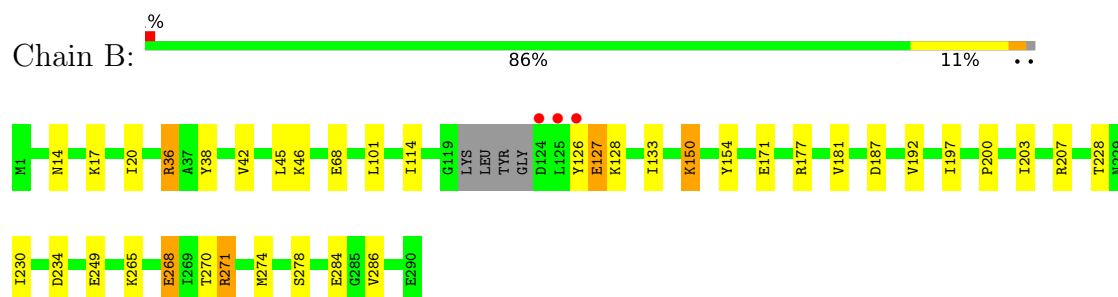
3 Residue-property plots

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.

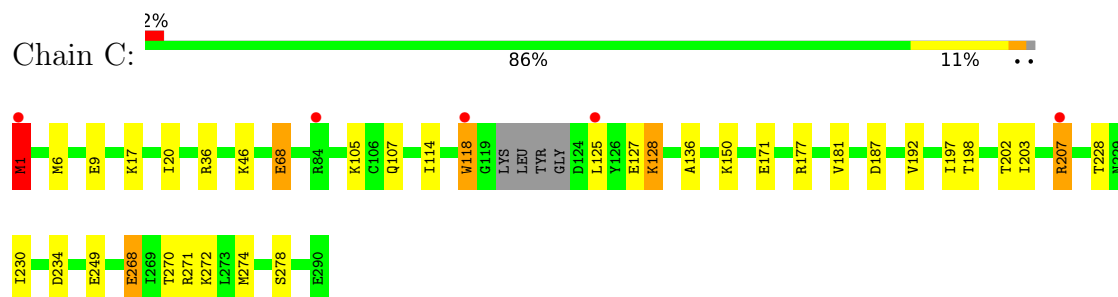
- Molecule 1: Putative branched-chain-amino-acid aminotransferase



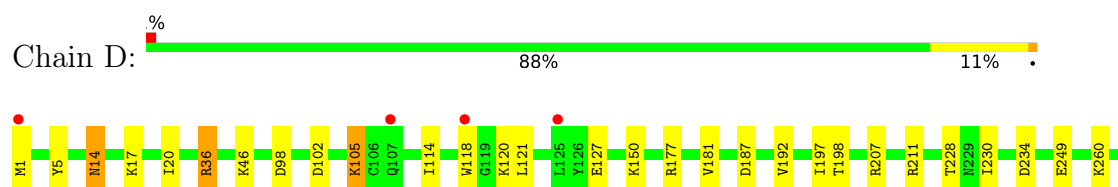
- Molecule 1: Putative branched-chain-amino-acid aminotransferase



- Molecule 1: Putative branched-chain-amino-acid aminotransferase

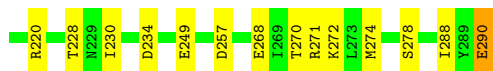
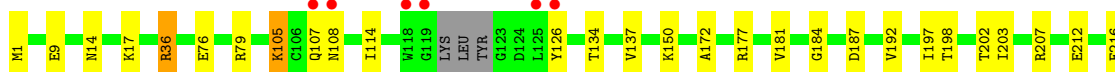
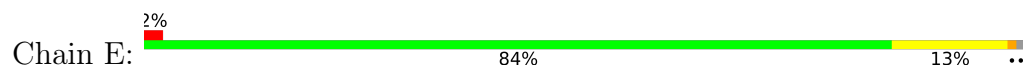


- Molecule 1: Putative branched-chain-amino-acid aminotransferase

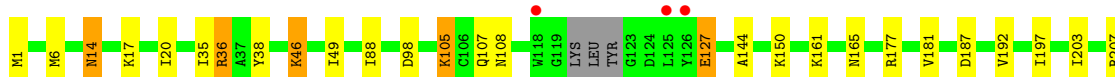
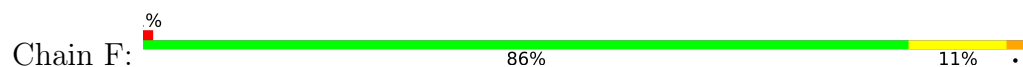




- Molecule 1: Putative branched-chain-amino-acid aminotransferase



- Molecule 1: Putative branched-chain-amino-acid aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.92Å 139.12Å 167.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.86 – 2.10 66.86 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (66.86-2.10) 99.8 (66.86-2.10)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0155, BUSTER-TNT 2.10.2	Depositor
R, R_{free}	0.181 , 0.218 0.181 , 0.218	Depositor DCC
R_{free} test set	4801 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 57.3	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	0.97	EDS
Total number of atoms	15167	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.85% 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: PEG, LLP, CL, EDO, TAM

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	0.90	1/2559 (0.0%)	1.00	2/3450 (0.1%)
1	B	0.89	1/2496 (0.0%)	0.98	1/3367 (0.0%)
1	C	0.91	0/2458	1.01	5/3317 (0.2%)
1	D	0.92	1/2452 (0.0%)	1.00	1/3315 (0.0%)
1	E	0.90	0/2486	0.97	2/3357 (0.1%)
1	F	0.88	0/2425	0.99	3/3276 (0.1%)
All	All	0.90	3/14876 (0.0%)	0.99	14/20082 (0.1%)

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	C	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	118	TRP	CA-C	-7.09	1.43	1.52
1	A	118	TRP	CA-C	-5.65	1.46	1.53
1	B	200	PRO	CA-C	5.33	1.54	1.51

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	46	LYS	CB-CG-CD	9.42	132.97	111.30
1	A	272	LYS	CB-CG-CD	9.11	132.25	111.30
1	D	46	LYS	CG-CD-CE	-7.67	93.65	111.30
1	C	268	GLU	CA-CB-CG	6.48	127.06	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	203	ILE	N-CA-C	5.83	117.27	110.62

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	68[A]	GLU	Mainchain
1	C	68[B]	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	2460	0	2569	37	0
1	B	2412	0	2514	31	0
1	C	2395	0	2471	24	0
1	D	2396	0	2449	20	0
1	E	2414	0	2479	32	0
1	F	2371	0	2419	27	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
2	E	1	0	0	0	0
3	A	7	0	10	2	0
3	D	7	0	10	1	0
4	A	11	0	17	2	0
4	B	11	0	17	1	0
5	B	8	0	12	0	0
5	D	4	0	6	0	0
6	A	116	0	0	5	0
6	B	118	0	0	4	0
6	C	101	0	0	2	0
6	D	122	0	0	2	0
6	E	110	0	0	2	0
6	F	101	0	0	3	0
All	All	15167	0	14973	156	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 5.

The worst 5 of 156 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:F:220[B]:ARG:HH11	1:F:220[B]:ARG:HG3	1.39	0.88
1:B:268[B]:GLU:HG3	1:B:271[B]:ARG:NH1	1.90	0.85
1:F:270:THR:HG22	1:F:274:MET:HE2	1.58	0.85
1:A:270:THR:HG22	1:A:274:MET:HE2	1.58	0.84
1:A:181:VAL:HB	1:A:230[A]:ILE:HG13	1.57	0.83

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	312/290 (108%)	304 (97%)	8 (3%)	0	100	100
1	B	304/290 (105%)	296 (97%)	8 (3%)	0	100	100
1	C	300/290 (103%)	292 (97%)	8 (3%)	0	100	100
1	D	302/290 (104%)	293 (97%)	9 (3%)	0	100	100
1	E	304/290 (105%)	296 (97%)	8 (3%)	0	100	100
1	F	297/290 (102%)	288 (97%)	7 (2%)	2 (1%)	18	15
All	All	1819/1740 (104%)	1769 (97%)	48 (3%)	2 (0%)	48	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	108[A]	ASN
1	F	108[B]	ASN

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	271/244 (111%)	251 (93%)	20 (7%)	13	10
1	B	264/244 (108%)	247 (94%)	17 (6%)	16	14
1	C	260/244 (107%)	245 (94%)	15 (6%)	18	16
1	D	259/244 (106%)	246 (95%)	13 (5%)	22	22
1	E	263/244 (108%)	251 (95%)	12 (5%)	24	25
1	F	256/244 (105%)	239 (93%)	17 (7%)	15	13
All	All	1573/1464 (107%)	1479 (94%)	94 (6%)	22	15

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	105	LYS
1	E	177[A]	ARG
1	D	121	LEU
1	E	1	MET
1	E	278	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	14	ASN
1	F	165	ASN
1	F	205	ASN
1	F	157	ASN
1	C	219	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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$
1	LLP	C	150	1	23,24,25	2.81	5 (21%)	25,32,34	2.01	8 (32%)
1	LLP	A	150	1	23,24,25	2.77	5 (21%)	25,32,34	2.02	9 (36%)
1	LLP	D	150	1	23,24,25	2.75	5 (21%)	25,32,34	2.00	9 (36%)
1	LLP	F	150	1	23,24,25	2.78	5 (21%)	25,32,34	1.95	9 (36%)
1	LLP	E	150	1	23,24,25	2.81	5 (21%)	25,32,34	1.98	10 (40%)
1	LLP	B	150	1	23,24,25	2.78	5 (21%)	25,32,34	1.95	9 (36%)

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
1	LLP	C	150	1	-	5/16/17/19	0/1/1/1
1	LLP	A	150	1	-	4/16/17/19	0/1/1/1
1	LLP	D	150	1	-	4/16/17/19	0/1/1/1
1	LLP	F	150	1	-	5/16/17/19	0/1/1/1
1	LLP	E	150	1	-	4/16/17/19	0/1/1/1
1	LLP	B	150	1	-	4/16/17/19	0/1/1/1

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	150	LLP	C3-C2	8.09	1.49	1.41
1	F	150	LLP	C3-C2	7.95	1.49	1.41
1	E	150	LLP	C3-C2	7.94	1.49	1.41
1	B	150	LLP	C3-C2	7.91	1.49	1.41
1	A	150	LLP	C3-C2	7.64	1.48	1.41

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	150	LLP	C4-C4'-NZ	-3.95	105.80	124.04
1	E	150	LLP	C4-C4'-NZ	-3.86	106.21	124.04
1	F	150	LLP	C4-C4'-NZ	-3.85	106.26	124.04
1	C	150	LLP	C4-C4'-NZ	-3.83	106.35	124.04
1	B	150	LLP	C4-C4'-NZ	-3.78	106.61	124.04

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	150	LLP	C4-C4'-NZ-CE
1	B	150	LLP	C4-C4'-NZ-CE
1	C	150	LLP	C4-C4'-NZ-CE
1	C	150	LLP	O-C-CA-CB
1	D	150	LLP	C4-C4'-NZ-CE

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	150	LLP	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	B	302	-	3,3,3	0.44	0	2,2,2	0.71	0
5	EDO	D	302	-	3,3,3	0.40	0	2,2,2	0.57	0
4	TAM	B	303	-	10,10,10	0.51	0	12,12,12	1.70	3 (25%)
5	EDO	B	301	-	3,3,3	0.39	0	2,2,2	0.71	0
4	TAM	A	303	-	10,10,10	0.63	0	12,12,12	0.94	0
3	PEG	D	301	-	6,6,6	0.37	0	5,5,5	0.59	0
3	PEG	A	302	-	6,6,6	0.48	0	5,5,5	0.36	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
5	EDO	B	302	-	-	0/1/1/1	-
5	EDO	D	302	-	-	0/1/1/1	-
4	TAM	B	303	-	-	4/12/12/12	-
5	EDO	B	301	-	-	1/1/1/1	-
4	TAM	A	303	-	-	6/12/12/12	-
3	PEG	D	301	-	-	2/4/4/4	-
3	PEG	A	302	-	-	3/4/4/4	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	303	TAM	C5-C2-C	-3.76	111.53	115.97
4	B	303	TAM	C4-C1-C	-2.09	113.50	115.97
4	B	303	TAM	C6-C3-C	-2.03	113.57	115.97

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	303	TAM	C2-C-C1-C4
4	A	303	TAM	N-C-C1-C4
4	A	303	TAM	C1-C-C3-C6

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Mol	Chain	Res	Type	Atoms
4	A	303	TAM	N-C-C3-C6
4	B	303	TAM	C1-C-C3-C6

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	303	TAM	1	0
4	A	303	TAM	2	0
3	D	301	PEG	1	0
3	A	302	PEG	2	0

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	286/290 (98%)	-0.12	2 (0%) 84 86	19, 38, 68, 140	30 (10%)
1	B	285/290 (98%)	-0.12	3 (1%) 78 80	17, 38, 69, 128	23 (8%)
1	C	285/290 (98%)	-0.02	5 (1%) 67 70	20, 39, 76, 118	19 (6%)
1	D	289/290 (99%)	-0.15	4 (1%) 73 75	18, 38, 78, 121	15 (5%)
1	E	286/290 (98%)	-0.16	6 (2%) 63 66	14, 37, 77, 150	22 (7%)
1	F	286/290 (98%)	-0.03	3 (1%) 79 81	18, 40, 75, 137	15 (5%)
All	All	1717/1740 (98%)	-0.10	23 (1%) 75 77	14, 38, 77, 150	124 (7%)

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	125	LEU	3.7
1	F	125	LEU	3.5
1	B	125	LEU	3.0
1	D	118	TRP	3.0
1	F	126	TYR	2.8

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LLP	C	150	24/25	0.94	0.09	30,40,56,67	0
1	LLP	A	150	24/25	0.95	0.08	31,40,52,73	0
1	LLP	E	150	24/25	0.95	0.08	31,38,54,62	0
1	LLP	F	150	24/25	0.95	0.08	30,39,52,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	LLP	B	150	24/25	0.96	0.08	28,37,54,69	0
1	LLP	D	150	24/25	0.96	0.08	29,38,52,65	0

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
5	EDO	B	302	4/4	0.83	0.16	62,68,74,78	4
5	EDO	D	302	4/4	0.84	0.20	41,44,49,56	4
5	EDO	B	301	4/4	0.85	0.16	62,70,71,76	4
3	PEG	D	301	7/7	0.87	0.21	60,67,73,81	7
4	TAM	B	303	11/11	0.92	0.18	51,59,73,83	11
4	TAM	A	303	11/11	0.92	0.17	52,63,76,76	11
3	PEG	A	302	7/7	0.93	0.15	54,62,72,78	7
2	CL	E	301	1/1	0.99	0.03	33,33,33,33	1
2	CL	C	301	1/1	0.99	0.07	32,32,32,32	1
2	CL	A	301	1/1	1.00	0.02	31,31,31,31	1

6.5 Other polymers [i](#)

There are no such residues in this entry.