



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:49 PM UTC

PDB ID : 3NOC / pdb_00003noc
Title : Designed ankyrin repeat protein (DARPin) binders to AcrB: Plasticity of the Interface
Authors : Monroe, N.; Briand, C.; Gruetter, M.G.
Deposited on : 2010-06-25
Resolution : 2.70 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

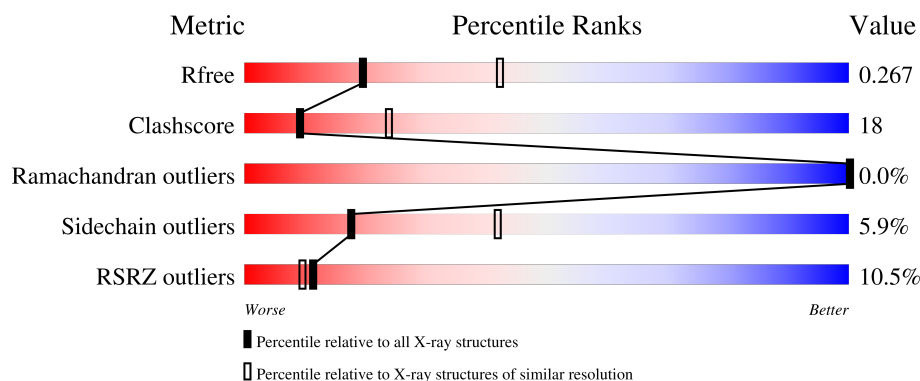
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	1049	12% 66% 29% ..
1	B	1049	9% 69% 27% ..
1	C	1049	8% 69% 26% ..
2	D	169	9% 60% 21% 9% . 9%
2	E	169	26% 39% 38% 11% . 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25558 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 Acriflavine resistance protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1028	Total	C	N	O	S	5	0	0
			7569	4878	1234	1417	40			
1	B	1026	Total	C	N	O	S	2	0	0
			7632	4916	1248	1426	42			
1	C	1034	Total	C	N	O	S	0	0	0
			7690	4957	1264	1426	43			

- Molecule 2 is a protein called Designed ankyrin repeat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	154	Total	C	N	O	S	0	0	0
			1128	708	208	211	1			
2	E	152	Total	C	N	O		11	0	0
			1101	691	205	205				

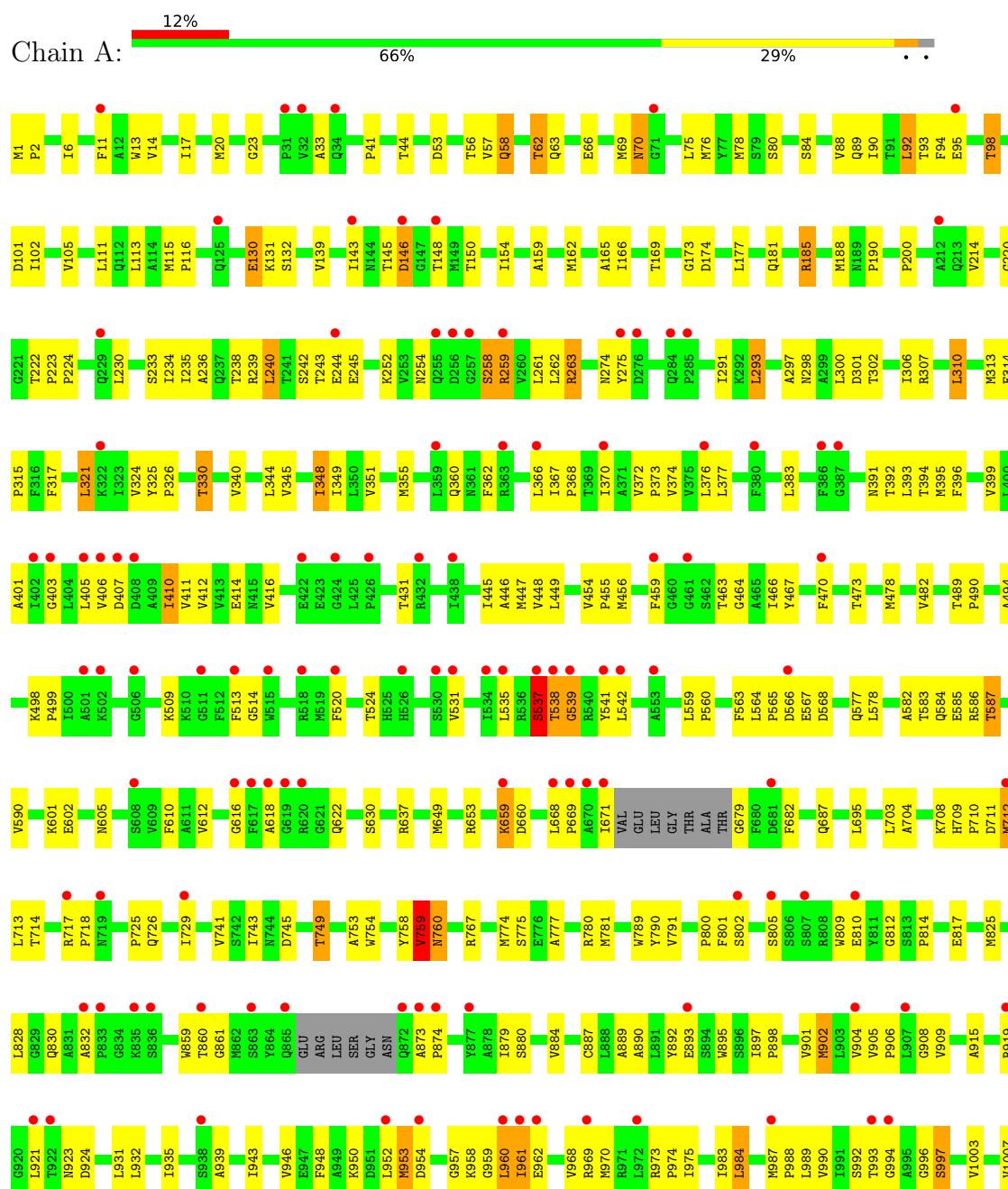
- Molecule 3 is water.

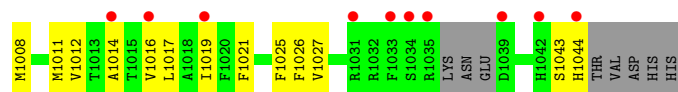
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	133	Total	O	0	0
			133	133		
3	B	132	Total	O	0	0
			132	132		
3	C	151	Total	O	0	0
			151	151		
3	D	17	Total	O	0	0
			17	17		
3	E	5	Total	O	0	0
			5	5		

3 Residue-property plots

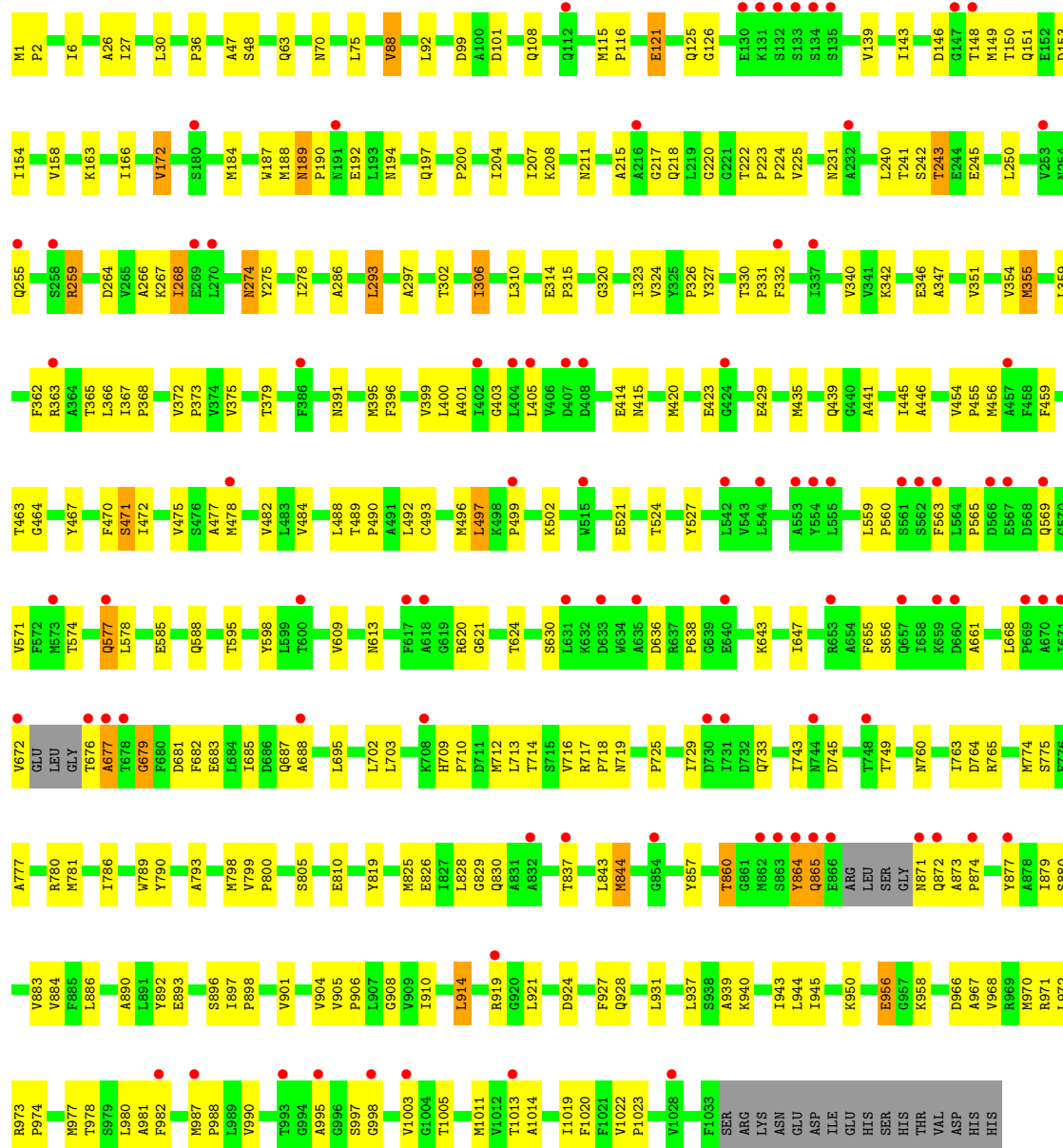
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Acriflavine resistance protein B

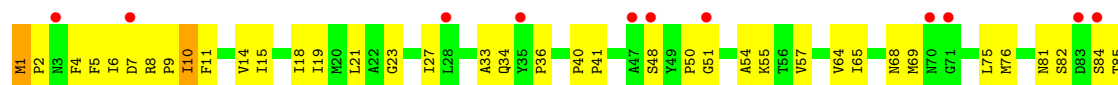


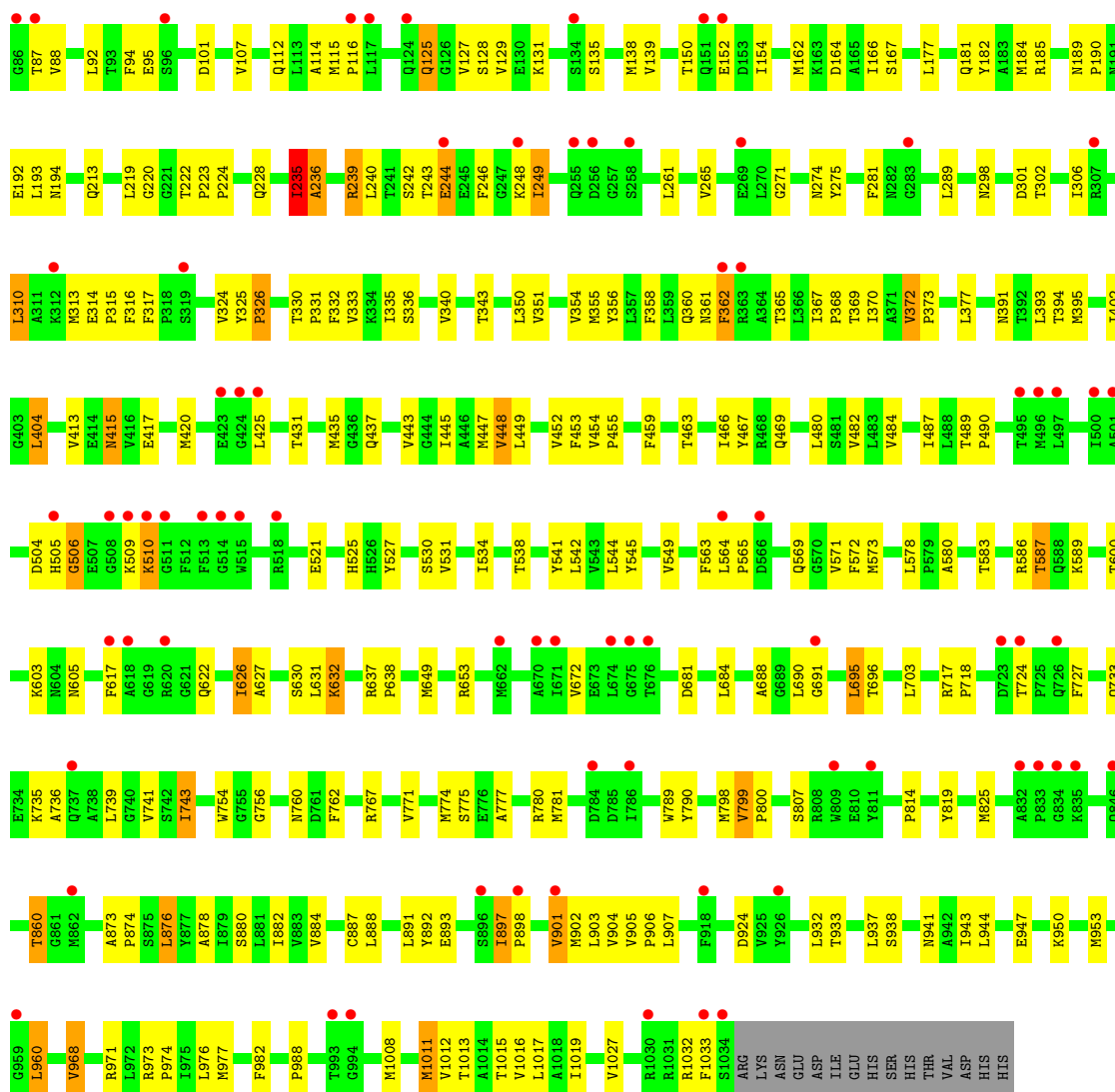


• Molecule 1: Acriflavine resistance protein B

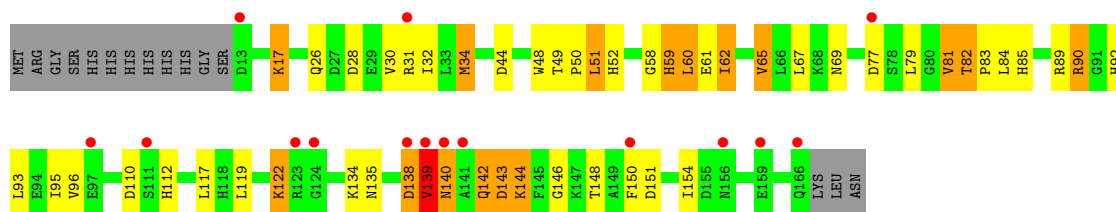


• Molecule 1: Acriflavine resistance protein B

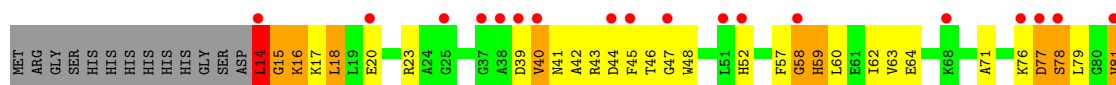


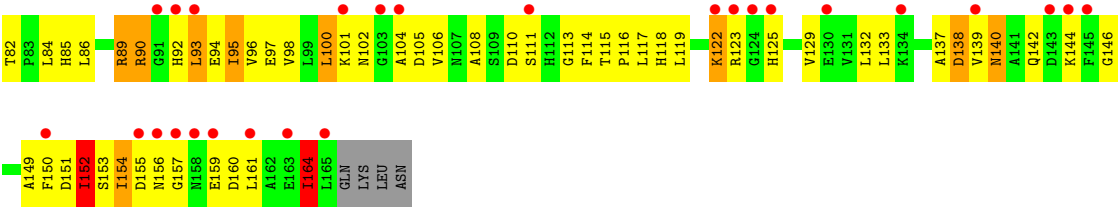


• Molecule 2: Designed ankyrin repeat protein



• Molecule 2: Designed ankyrin repeat protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	145.85Å 158.92Å 245.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.21 – 2.70 49.21 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.21-2.70) 99.0 (49.21-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.6.2_432	Depositor
R, R_{free}	0.242 , 0.268 0.240 , 0.267	Depositor DCC
R_{free} test set	1548 reflections (1.00%)	wwPDB-VP
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.495	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	25558	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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: FME

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	0.55	2/7702 (0.0%)	0.80	10/10496 (0.1%)
1	B	0.55	3/7768 (0.0%)	0.76	10/10581 (0.1%)
1	C	0.48	3/7828 (0.0%)	0.76	8/10661 (0.1%)
2	D	1.25	3/1145 (0.3%)	1.14	16/1554 (1.0%)
2	E	1.16	1/1117 (0.1%)	1.25	12/1519 (0.8%)
All	All	0.62	12/25560 (0.0%)	0.82	56/34811 (0.2%)

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	C	0	1
All	All	0	2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	236	ALA	CA-CB	-7.11	1.42	1.53
1	A	410	ILE	CA-CB	-6.33	1.46	1.54
2	D	139	VAL	CA-CB	-6.24	1.46	1.54
2	D	82	THR	C-O	-6.22	1.18	1.24
1	C	760	ASN	C-O	-6.00	1.18	1.24

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	15	GLY	N-CA-C	-17.97	91.16	112.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	506	GLY	N-CA-C	-9.48	97.44	112.61
2	D	90	ARG	N-CA-C	-9.46	97.30	110.35
1	B	865	GLN	N-CA-C	-8.55	99.55	111.52
1	B	864	TYR	N-CA-C	-8.17	96.94	109.85

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	759	VAL	Peptide
1	C	235	ILE	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	7569	0	7466	287	0
1	B	7632	0	7566	227	0
1	C	7690	0	7693	259	0
2	D	1128	0	1096	57	0
2	E	1101	0	1067	130	0
3	A	133	0	0	18	0
3	B	132	0	0	13	0
3	C	151	0	0	13	0
3	D	17	0	0	2	0
3	E	5	0	0	1	0
All	All	25558	0	24888	910	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 18.

The worst 5 of 910 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:960:LEU:HD12	1:A:961:ILE:N	1.40	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:960:LEU:HD12	1:A:960:LEU:C	1.53	1.29
2:E:18:LEU:O	2:E:18:LEU:HD13	1.35	1.24
1:C:509:LYS:O	1:C:510:LYS:HE3	1.37	1.18
1:A:259:ARG:HD3	1:A:259:ARG:N	1.44	1.15

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	1020/1049 (97%)	981 (96%)	39 (4%)	0	100	100
1	B	1020/1049 (97%)	985 (97%)	34 (3%)	1 (0%)	48	73
1	C	1032/1049 (98%)	993 (96%)	39 (4%)	0	100	100
2	D	152/169 (90%)	150 (99%)	2 (1%)	0	100	100
2	E	150/169 (89%)	141 (94%)	9 (6%)	0	100	100
All	All	3374/3485 (97%)	3250 (96%)	123 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	677	ALA

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	766/854 (90%)	721 (94%)	45 (6%)	18	42
1	B	780/854 (91%)	746 (96%)	34 (4%)	25	53
1	C	792/854 (93%)	753 (95%)	39 (5%)	22	49
2	D	108/133 (81%)	95 (88%)	13 (12%)	5	12
2	E	104/133 (78%)	85 (82%)	19 (18%)	2	5
All	All	2550/2828 (90%)	2400 (94%)	150 (6%)	18	42

5 of 150 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	968	VAL
2	E	100	LEU
2	D	26	GLN
2	D	140	ASN
1	B	163	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	360	GLN
2	D	59	HIS
1	C	517	ASN
1	C	744	ASN
2	D	142	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 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	FME	A	1	1	8,9,10	0.36	0	8,9,11	11.89	2 (25%)
1	FME	C	1	1	8,9,10	0.35	0	8,9,11	1.09	1 (12%)
1	FME	B	1	1	8,9,10	0.35	0	8,9,11	8.31	2 (25%)

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	FME	A	1	1	-	1/7/9/11	-
1	FME	C	1	1	-	1/7/9/11	-
1	FME	B	1	1	-	1/7/9/11	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	FME	CA-N-CN	27.93	165.77	122.82
1	A	1	FME	O1-CN-N	18.64	173.45	125.32
1	B	1	FME	CA-N-CN	17.80	150.20	122.82
1	B	1	FME	O1-CN-N	15.23	164.66	125.32
1	C	1	FME	C-CA-N	2.02	113.41	109.50

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1	FME	O1-CN-N-CA
1	B	1	FME	O1-CN-N-CA
1	C	1	FME	O1-CN-N-CA

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	1	FME	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	1026/1049 (97%)	0.79	122 (11%)	9 7	26, 61, 114, 188	0
1	B	1025/1049 (97%)	0.61	90 (8%)	15 13	22, 56, 89, 154	1 (0%)
1	C	1033/1049 (98%)	0.51	86 (8%)	17 14	27, 53, 88, 168	0
2	D	154/169 (91%)	0.63	15 (9%)	13 11	33, 64, 104, 162	0
2	E	152/169 (89%)	1.56	44 (28%)	1 1	14, 97, 140, 200	2 (1%)
All	All	3390/3485 (97%)	0.68	357 (10%)	11 9	14, 57, 107, 200	3 (0%)

The worst 5 of 357 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	672	VAL	12.5
1	B	676	THR	8.1
2	E	14	LEU	7.8
2	E	38	ALA	7.1
1	B	562	SER	7.0

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	FME	A	1	10/11	0.62	0.25	47,80,97,110	0
1	FME	B	1	10/11	0.82	0.16	42,74,88,109	0
1	FME	C	1	10/11	0.85	0.18	65,71,86,87	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.