



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 5, 2026 – 01:49 PM UTC

PDB ID : 2NYN / pdb_00002nyn
Title : Crystal structure of phenylalanine ammonia-lyase from *Anabaena variabilis*
Authors : Louie, G.V.; Moffitt, M.C.; Bowman, M.E.; Pence, J.; Noel, J.P.; Moore, B.S.
Deposited on : 2006-11-21
Resolution : 1.90 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)
Xtrriage (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

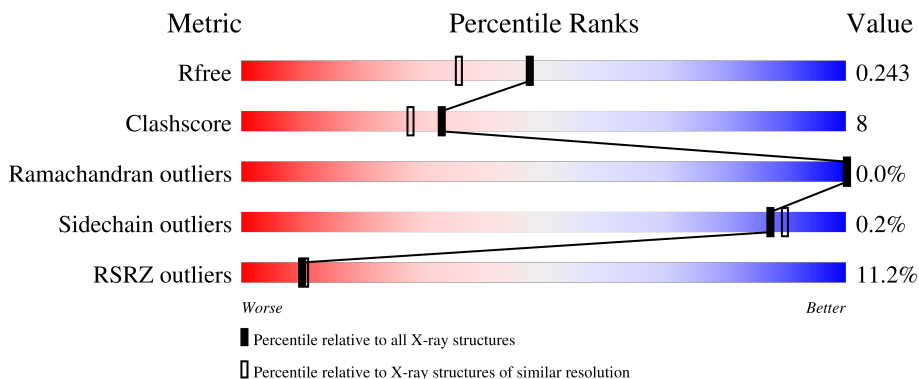
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	565	 9% 73% 17% • 9%
1	B	565	 11% 71% 18% • 9%
1	C	565	 11% 73% 17% • 9%
1	D	565	 10% 73% 17% • 9%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 16261 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 Phenylalanine/histidine ammonia-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	512	Total	C	N	O	S	0	0	0
			3930	2477	690	744	19			
1	B	512	Total	C	N	O	S	0	0	0
			3930	2477	690	744	19			
1	C	512	Total	C	N	O	S	0	0	0
			3930	2477	690	744	19			
1	D	512	Total	C	N	O	S	0	0	0
			3930	2477	690	744	19			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	167	MDO	ALA	SEE REMARK 999	UNP Q3M5Z3
A	167	MDO	SER	SEE REMARK 999	UNP Q3M5Z3
A	167	MDO	GLY	SEE REMARK 999	UNP Q3M5Z3
B	167	MDO	ALA	SEE REMARK 999	UNP Q3M5Z3
B	167	MDO	SER	SEE REMARK 999	UNP Q3M5Z3
B	167	MDO	GLY	SEE REMARK 999	UNP Q3M5Z3
C	167	MDO	ALA	SEE REMARK 999	UNP Q3M5Z3
C	167	MDO	SER	SEE REMARK 999	UNP Q3M5Z3
C	167	MDO	GLY	SEE REMARK 999	UNP Q3M5Z3
D	167	MDO	ALA	SEE REMARK 999	UNP Q3M5Z3
D	167	MDO	SER	SEE REMARK 999	UNP Q3M5Z3
D	167	MDO	GLY	SEE REMARK 999	UNP Q3M5Z3

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	142	Total	O	0	0
			142	142		
2	B	131	Total	O	0	0
			131	131		

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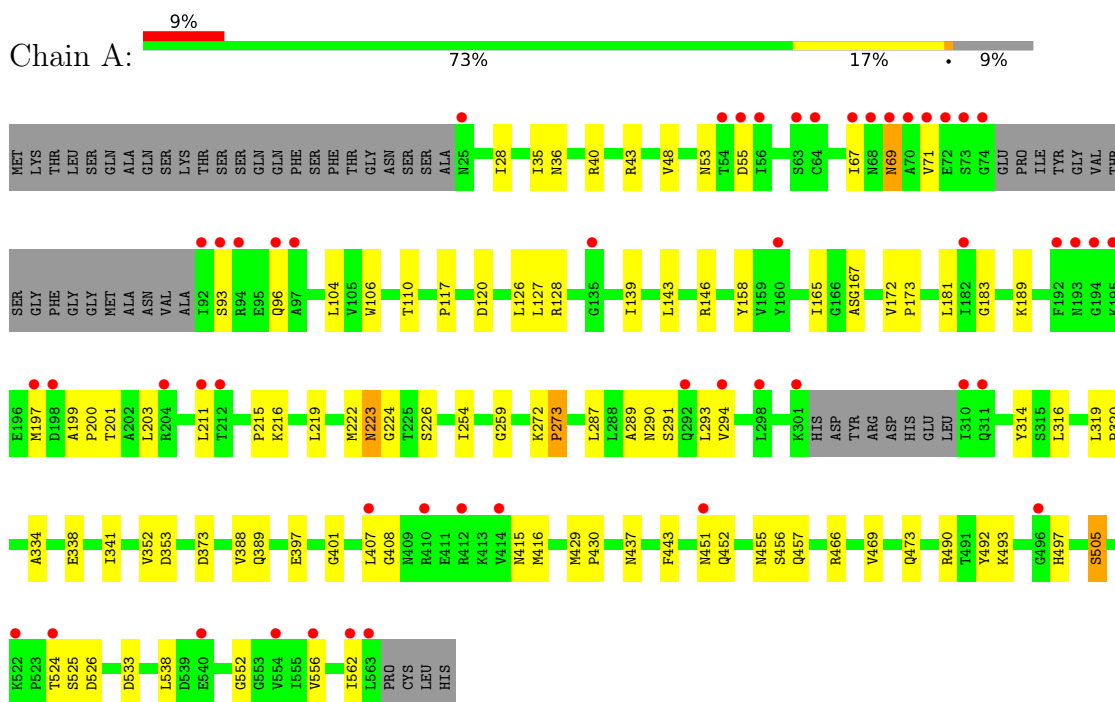
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	143	Total 143	O 143	0	0
2	D	125	Total 125	O 125	0	0

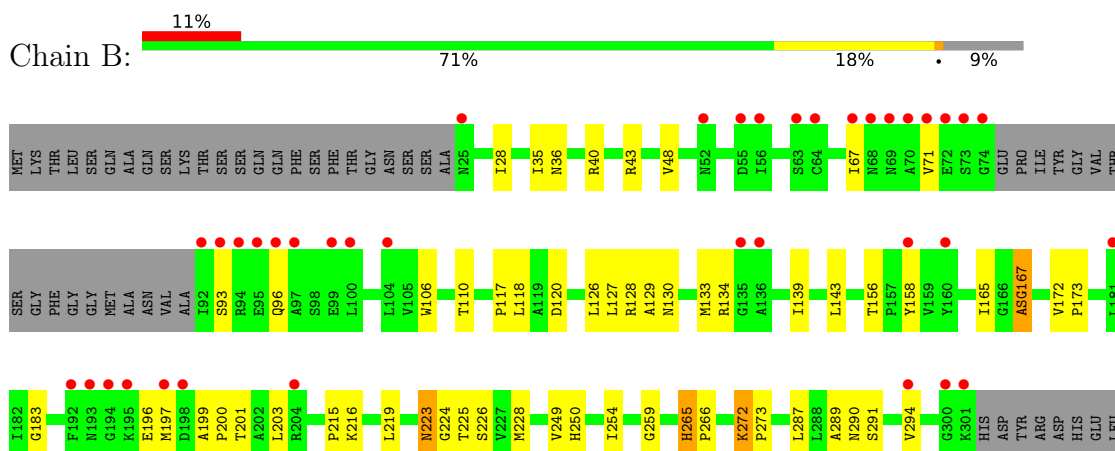
3 Residue-property plots [i](#)

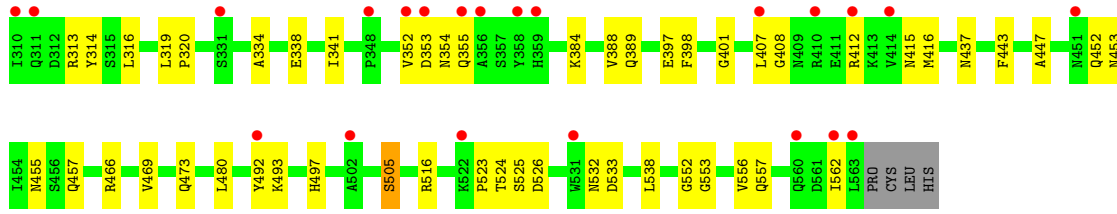
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

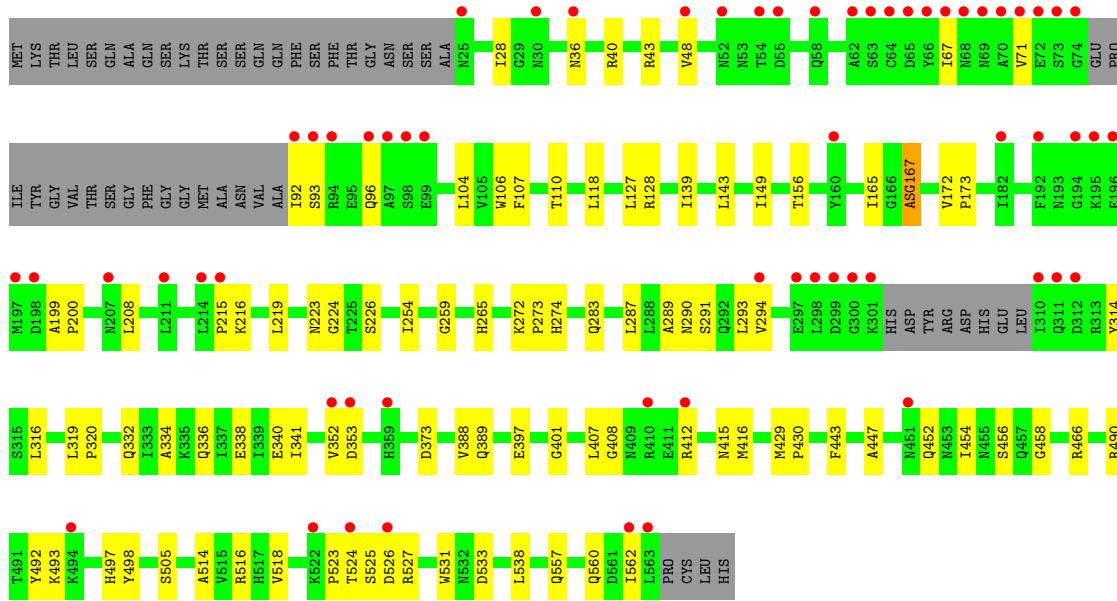
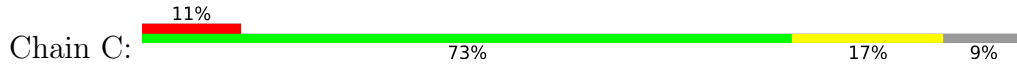


- Molecule 1: Phenylalanine/histidine ammonia-lyase

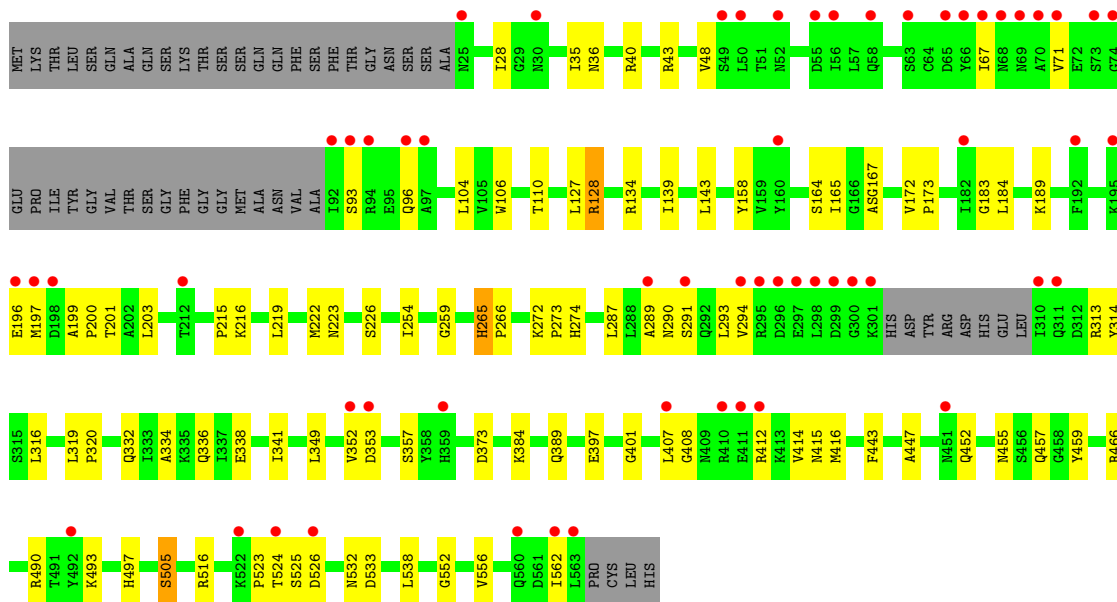
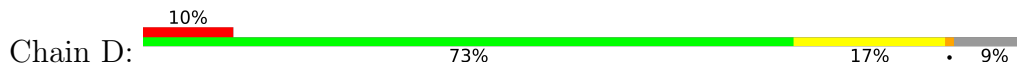




● Molecule 1: Phenylalanine/histidine ammonia-lyase



● Molecule 1: Phenylalanine/histidine ammonia-lyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	78.19Å 88.52Å 90.06Å 103.52° 97.82° 116.24°	Depositor
Resolution (Å)	100.00 – 1.90 84.20 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (100.00-1.90) 94.9 (84.20-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 1.74Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.223 , 0.242 0.223 , 0.243	Depositor DCC
R_{free} test set	7620 reflections (3.67%)	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtrriage
Anisotropy	0.488	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	16261	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.39% 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: MDO

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	0.40	0/3984	0.87	10/5406 (0.2%)
1	B	0.40	0/3984	0.85	11/5406 (0.2%)
1	C	0.41	0/3984	0.87	12/5406 (0.2%)
1	D	0.41	0/3984	0.87	13/5406 (0.2%)
All	All	0.41	0/15936	0.87	46/21624 (0.2%)

There are no bond length outliers.

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	272	LYS	CA-C-N	6.76	128.29	119.84
1	D	272	LYS	C-N-CA	6.76	128.29	119.84
1	A	106	TRP	N-CA-C	6.65	118.32	111.14
1	C	106	TRP	N-CA-C	6.37	118.02	111.14
1	D	226	SER	N-CA-C	6.19	118.82	111.33

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3930	0	3919	63	0
1	B	3930	0	3919	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3930	0	3919	65	0
1	D	3930	0	3919	62	0
2	A	142	0	0	1	0
2	B	131	0	0	5	0
2	C	143	0	0	1	0
2	D	125	0	0	5	0
All	All	16261	0	15676	244	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 8.

The worst 5 of 244 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:D:287:LEU:HD21	1:D:562:ILE:HD11	1.39	1.04
1:C:287:LEU:HD21	1:C:562:ILE:HD11	1.46	0.98
1:A:287:LEU:HD21	1:A:562:ILE:HD11	1.45	0.98
1:C:110:THR:HG22	1:D:538:LEU:HB2	1.51	0.92
1:B:287:LEU:HD21	1:B:562:ILE:HD11	1.51	0.91

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	503/565 (89%)	483 (96%)	19 (4%)	1 (0%)	43	36
1	B	503/565 (89%)	485 (96%)	18 (4%)	0	100	100
1	C	503/565 (89%)	483 (96%)	20 (4%)	0	100	100
1	D	503/565 (89%)	484 (96%)	19 (4%)	0	100	100
All	All	2012/2260 (89%)	1935 (96%)	76 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	273	PRO

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	423/468 (90%)	421 (100%)	2 (0%)	81	84
1	B	423/468 (90%)	422 (100%)	1 (0%)	87	90
1	C	423/468 (90%)	423 (100%)	0	100	100
1	D	423/468 (90%)	422 (100%)	1 (0%)	87	90
All	All	1692/1872 (90%)	1688 (100%)	4 (0%)	87	90

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	223	ASN
1	B	223	ASN
1	D	128	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	292	GLN
1	D	258	ASN
1	C	336	GLN
1	D	68	ASN
1	D	283	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 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	MDO	D	167	1	11,13,14	2.45	4 (36%)	15,18,20	2.65	5 (33%)
1	MDO	C	167	1	11,13,14	2.42	5 (45%)	15,18,20	2.65	6 (40%)
1	MDO	B	167	1	11,13,14	2.41	4 (36%)	15,18,20	2.63	5 (33%)
1	MDO	A	167	1	11,13,14	2.38	4 (36%)	15,18,20	2.61	5 (33%)

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	MDO	D	167	1	-	0/4/23/24	0/1/1/1
1	MDO	C	167	1	-	0/4/23/24	0/1/1/1
1	MDO	B	167	1	-	0/4/23/24	0/1/1/1
1	MDO	A	167	1	-	0/4/23/24	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	167	MDO	O2-C2	5.37	1.34	1.23
1	B	167	MDO	O2-C2	5.34	1.34	1.23
1	C	167	MDO	O2-C2	5.25	1.33	1.23
1	A	167	MDO	O2-C2	5.25	1.33	1.23
1	D	167	MDO	C2-N3	-3.63	1.31	1.40

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	167	MDO	CA2-C2-N3	7.01	109.39	103.50
1	D	167	MDO	CA2-C2-N3	6.94	109.33	103.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	167	MDO	CA2-C2-N3	6.84	109.25	103.50
1	B	167	MDO	CA2-C2-N3	6.84	109.24	103.50
1	C	167	MDO	O2-C2-CA2	-4.44	128.18	131.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	167	MDO	1	0
1	B	167	MDO	1	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	511/565 (90%)	0.76	50 (9%) 13 13	13, 28, 53, 88	0
1	B	511/565 (90%)	0.79	60 (11%) 9 10	13, 28, 53, 87	0
1	C	511/565 (90%)	0.79	61 (11%) 9 9	14, 28, 51, 88	0
1	D	511/565 (90%)	0.83	58 (11%) 10 10	14, 27, 53, 88	0
All	All	2044/2260 (90%)	0.79	229 (11%) 10 10	13, 28, 53, 88	0

The worst 5 of 229 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	92	ILE	8.0
1	B	310	ILE	7.4
1	A	310	ILE	7.1
1	C	92	ILE	6.9
1	A	563	LEU	6.9

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	MDO	C	167	13/14	0.86	0.10	25,27,30,32	0
1	MDO	D	167	13/14	0.86	0.10	25,28,29,30	0
1	MDO	B	167	13/14	0.87	0.10	23,26,27,29	0
1	MDO	A	167	13/14	0.88	0.10	22,27,30,31	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.