



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 26, 2024 – 02:10 PM JST

PDB ID : 8WKR
Title : Crystal structure of O-acetylhomoserine sulfhydrylase from *Lactobacillus plantarum* in the open form
Authors : Oda, K.; Matoba, Y.
Deposited on : 2023-09-28
Resolution : 2.05 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.002 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.2

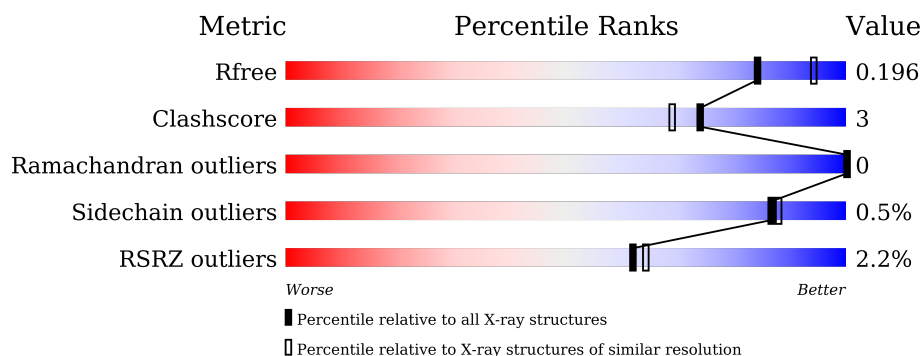
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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}	164625	2096 (2.04-2.04)
Clashscore	180529	2229 (2.04-2.04)
Ramachandran outliers	177936	2217 (2.04-2.04)
Sidechain outliers	177891	2217 (2.04-2.04)
RSRZ outliers	164620	2096 (2.04-2.04)

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	448	<div> <div>2%</div> <div>84%</div> <div>6%</div> <div>10%</div> </div>
1	B	448	<div> <div>2%</div> <div>87%</div> <div>•</div> <div>10%</div> </div>
1	C	448	<div> <div>2%</div> <div>82%</div> <div>8%</div> <div>10%</div> </div>
1	D	448	<div> <div>2%</div> <div>85%</div> <div>5%</div> <div>10%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13526 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 L-methionine gamma-lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	P	S	0	1	0
			3095	1973	519	601	1	1			
1	B	405	Total	C	N	O	P	S	0	2	0
			3103	1978	522	601	1	1			
1	C	405	Total	C	N	O	P	S	0	4	0
			3113	1985	524	602	1	1			
1	D	405	Total	C	N	O	P	S	0	2	0
			3103	1978	522	601	1	1			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A0G9F7S9
A	-18	GLY	-	expression tag	UNP A0A0G9F7S9
A	-17	SER	-	expression tag	UNP A0A0G9F7S9
A	-16	SER	-	expression tag	UNP A0A0G9F7S9
A	-15	HIS	-	expression tag	UNP A0A0G9F7S9
A	-14	HIS	-	expression tag	UNP A0A0G9F7S9
A	-13	HIS	-	expression tag	UNP A0A0G9F7S9
A	-12	HIS	-	expression tag	UNP A0A0G9F7S9
A	-11	HIS	-	expression tag	UNP A0A0G9F7S9
A	-10	HIS	-	expression tag	UNP A0A0G9F7S9
A	-9	SER	-	expression tag	UNP A0A0G9F7S9
A	-8	SER	-	expression tag	UNP A0A0G9F7S9
A	-7	GLY	-	expression tag	UNP A0A0G9F7S9
A	-6	LEU	-	expression tag	UNP A0A0G9F7S9
A	-5	VAL	-	expression tag	UNP A0A0G9F7S9
A	-4	PRO	-	expression tag	UNP A0A0G9F7S9
A	-3	ARG	-	expression tag	UNP A0A0G9F7S9
A	-2	GLY	-	expression tag	UNP A0A0G9F7S9
A	-1	SER	-	expression tag	UNP A0A0G9F7S9
A	0	HIS	-	expression tag	UNP A0A0G9F7S9
B	-19	MET	-	initiating methionine	UNP A0A0G9F7S9

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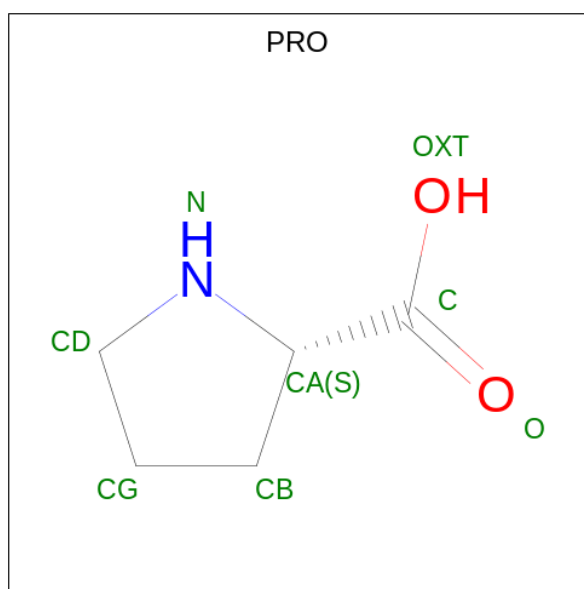
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP A0A0G9F7S9
B	-17	SER	-	expression tag	UNP A0A0G9F7S9
B	-16	SER	-	expression tag	UNP A0A0G9F7S9
B	-15	HIS	-	expression tag	UNP A0A0G9F7S9
B	-14	HIS	-	expression tag	UNP A0A0G9F7S9
B	-13	HIS	-	expression tag	UNP A0A0G9F7S9
B	-12	HIS	-	expression tag	UNP A0A0G9F7S9
B	-11	HIS	-	expression tag	UNP A0A0G9F7S9
B	-10	HIS	-	expression tag	UNP A0A0G9F7S9
B	-9	SER	-	expression tag	UNP A0A0G9F7S9
B	-8	SER	-	expression tag	UNP A0A0G9F7S9
B	-7	GLY	-	expression tag	UNP A0A0G9F7S9
B	-6	LEU	-	expression tag	UNP A0A0G9F7S9
B	-5	VAL	-	expression tag	UNP A0A0G9F7S9
B	-4	PRO	-	expression tag	UNP A0A0G9F7S9
B	-3	ARG	-	expression tag	UNP A0A0G9F7S9
B	-2	GLY	-	expression tag	UNP A0A0G9F7S9
B	-1	SER	-	expression tag	UNP A0A0G9F7S9
B	0	HIS	-	expression tag	UNP A0A0G9F7S9
C	-19	MET	-	initiating methionine	UNP A0A0G9F7S9
C	-18	GLY	-	expression tag	UNP A0A0G9F7S9
C	-17	SER	-	expression tag	UNP A0A0G9F7S9
C	-16	SER	-	expression tag	UNP A0A0G9F7S9
C	-15	HIS	-	expression tag	UNP A0A0G9F7S9
C	-14	HIS	-	expression tag	UNP A0A0G9F7S9
C	-13	HIS	-	expression tag	UNP A0A0G9F7S9
C	-12	HIS	-	expression tag	UNP A0A0G9F7S9
C	-11	HIS	-	expression tag	UNP A0A0G9F7S9
C	-10	HIS	-	expression tag	UNP A0A0G9F7S9
C	-9	SER	-	expression tag	UNP A0A0G9F7S9
C	-8	SER	-	expression tag	UNP A0A0G9F7S9
C	-7	GLY	-	expression tag	UNP A0A0G9F7S9
C	-6	LEU	-	expression tag	UNP A0A0G9F7S9
C	-5	VAL	-	expression tag	UNP A0A0G9F7S9
C	-4	PRO	-	expression tag	UNP A0A0G9F7S9
C	-3	ARG	-	expression tag	UNP A0A0G9F7S9
C	-2	GLY	-	expression tag	UNP A0A0G9F7S9
C	-1	SER	-	expression tag	UNP A0A0G9F7S9
C	0	HIS	-	expression tag	UNP A0A0G9F7S9
D	-19	MET	-	initiating methionine	UNP A0A0G9F7S9
D	-18	GLY	-	expression tag	UNP A0A0G9F7S9
D	-17	SER	-	expression tag	UNP A0A0G9F7S9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP A0A0G9F7S9
D	-15	HIS	-	expression tag	UNP A0A0G9F7S9
D	-14	HIS	-	expression tag	UNP A0A0G9F7S9
D	-13	HIS	-	expression tag	UNP A0A0G9F7S9
D	-12	HIS	-	expression tag	UNP A0A0G9F7S9
D	-11	HIS	-	expression tag	UNP A0A0G9F7S9
D	-10	HIS	-	expression tag	UNP A0A0G9F7S9
D	-9	SER	-	expression tag	UNP A0A0G9F7S9
D	-8	SER	-	expression tag	UNP A0A0G9F7S9
D	-7	GLY	-	expression tag	UNP A0A0G9F7S9
D	-6	LEU	-	expression tag	UNP A0A0G9F7S9
D	-5	VAL	-	expression tag	UNP A0A0G9F7S9
D	-4	PRO	-	expression tag	UNP A0A0G9F7S9
D	-3	ARG	-	expression tag	UNP A0A0G9F7S9
D	-2	GLY	-	expression tag	UNP A0A0G9F7S9
D	-1	SER	-	expression tag	UNP A0A0G9F7S9
D	0	HIS	-	expression tag	UNP A0A0G9F7S9

- Molecule 2 is PROLINE (three-letter code: PRO) (formula: C₅H₉NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			8	5	1	2		
2	D	1	Total	C	N	O	0	0
			8	5	1	2		

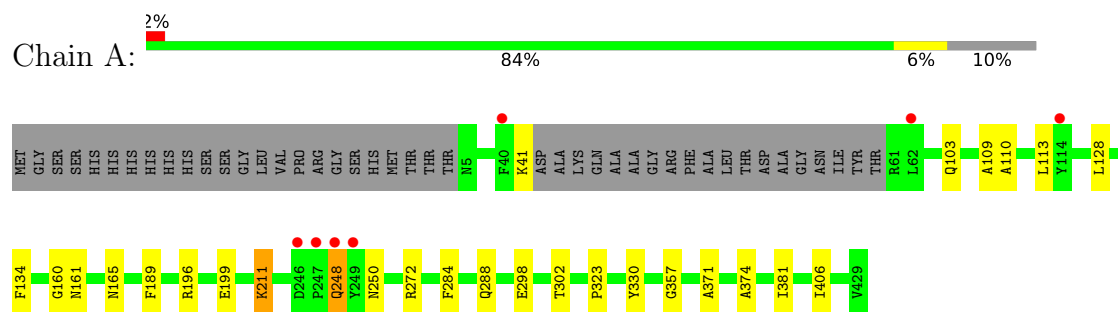
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	312	Total 312	O 312	0	0
3	B	267	Total 267	O 267	0	0
3	C	256	Total 256	O 256	0	0
3	D	261	Total 261	O 261	0	0

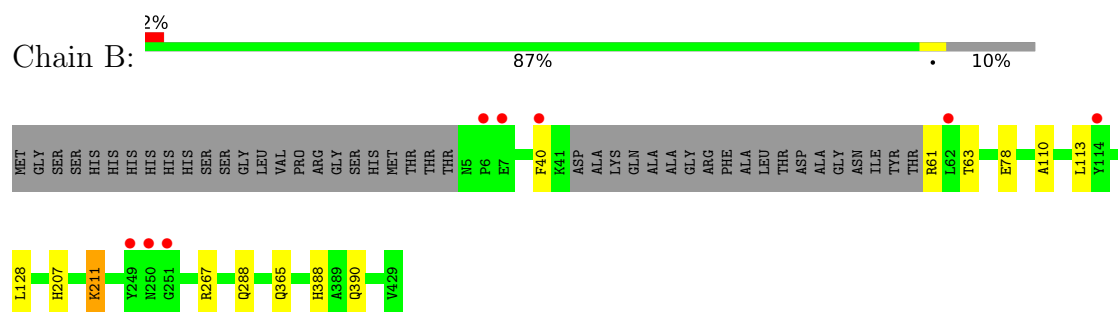
3 Residue-property plots [i](#)

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.

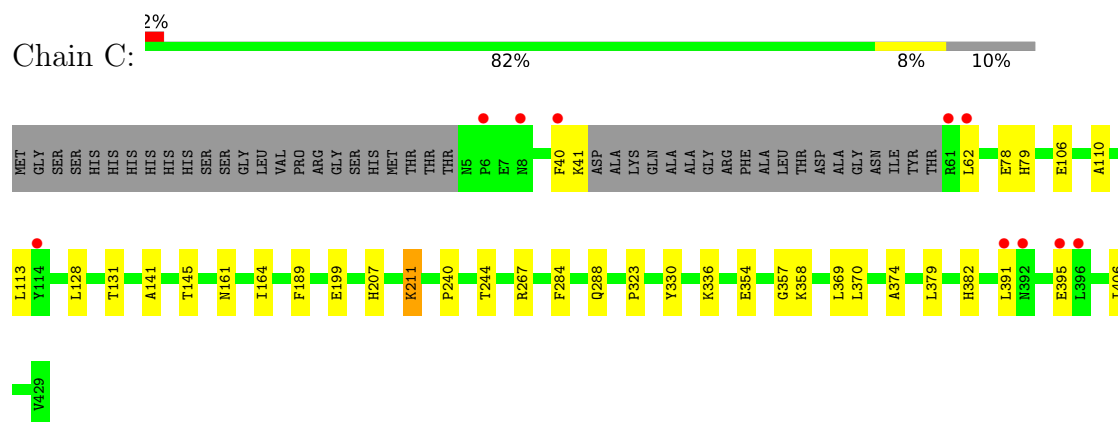
- Molecule 1: L-methionine gamma-lyase



- Molecule 1: L-methionine gamma-lyase



- Molecule 1: L-methionine gamma-lyase



- Molecule 1: L-methionine gamma-lyase

Protein	Category	Score
Met	High	0.95
Gly	High	0.92
Ser	High	0.90
Ser	High	0.88
His	High	0.85
His	High	0.82
His	High	0.80
His	High	0.78
Ser	High	0.75
Gly	High	0.72
Leu	High	0.70
Val	High	0.68
Pro	High	0.65
Arg	High	0.62
Gly	High	0.60
Ser	High	0.58
His	High	0.55
Met	High	0.52
Thr	High	0.50
Thr	High	0.48
Thr	High	0.45
N5	High	0.42
P6	High	0.40
E7	High	0.38
K41	High	0.35
ASP	High	0.32
ALA	High	0.30
LYS	High	0.28
GLN	High	0.25
ALA	High	0.22
ALA	High	0.20
Gly	High	0.18
ARG	High	0.15
PHE	High	0.12
ALA	High	0.10
ALA	High	0.08
LEU	High	0.05
THR	High	0.02
ASP	High	0.00
ALA	High	-0.02
Gly	High	-0.05
ASN	High	-0.08
Ile	High	-0.10
TVR	High	-0.12
THR	High	-0.15
R61	High	-0.18
L62	High	-0.20
T63	High	-0.22
I97	High	-0.25
Q103	High	-0.28
A110	High	-0.30
L113	High	-0.32
F121	Low	-0.35
L126	Low	-0.38
L128	Low	-0.40
N151	Low	-0.42
K211	Low	-0.45
Q288	Low	-0.48
E298	Low	-0.50
T302	Low	-0.52
K368	Low	-0.55
I361	Low	-0.58
E362	Low	-0.60
A371	Low	-0.62
I380	Low	-0.65
I381	Low	-0.68
T366	Low	-0.70
T367	Low	-0.72
Q390	Low	-0.75
L391	Low	-0.78
N392	Low	-0.80
E393	Low	-0.82
Q394	Low	-0.85
E395	Low	-0.88
L396	Low	-0.90
L397	Low	-0.92
A398	Low	-0.95
A399	Low	-0.98
G400	Low	-1.00
V429	Low	-1.02

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.28Å 114.93Å 98.91Å 90.00° 110.28° 90.00°	Depositor
Resolution (Å)	39.53 – 2.05 39.53 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.5 (39.53-2.05) 99.5 (39.53-2.05)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.05Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.153 , 0.196 0.152 , 0.196	Depositor DCC
R_{free} test set	5738 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	23.7	Xtriage
Anisotropy	0.403	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 56.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13526	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: LLP

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	0/3141	0.53	0/4287
1	B	0.37	0/3152	0.52	0/4301
1	C	0.38	0/3169	0.53	0/4324
1	D	0.37	0/3152	0.52	0/4301
All	All	0.38	0/12614	0.52	0/17213

There are no bond length outliers.

There are no bond angle outliers.

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	3095	0	3033	23	0
1	B	3103	0	3045	11	0
1	C	3113	0	3059	25	0
1	D	3103	0	3046	20	0
2	B	8	0	7	3	0
2	D	8	0	7	3	0
3	A	312	0	0	1	0
3	B	267	0	0	1	0
3	C	256	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	261	0	0	1	0
All	All	13526	0	12197	73	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 3.

The worst 5 of 73 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:248:GLN:HE22	1:A:272:ARG:NH1	1.55	1.04
1:A:248:GLN:NE2	1:A:272:ARG:HH12	1.64	0.95
1:A:248:GLN:NE2	1:A:272:ARG:NH1	2.21	0.84
1:D:391:LEU:HD13	1:D:395:GLU:HB3	1.76	0.68
1:C:391:LEU:HB3	1:C:395:GLU:HB3	1.75	0.67

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	401/448 (90%)	394 (98%)	7 (2%)	0	100	100
1	B	402/448 (90%)	393 (98%)	9 (2%)	0	100	100
1	C	404/448 (90%)	394 (98%)	10 (2%)	0	100	100
1	D	402/448 (90%)	390 (97%)	12 (3%)	0	100	100
All	All	1609/1792 (90%)	1571 (98%)	38 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	324/356 (91%)	322 (99%)	2 (1%)	84	86
1	B	325/356 (91%)	324 (100%)	1 (0%)	91	92
1	C	327/356 (92%)	326 (100%)	1 (0%)	91	92
1	D	325/356 (91%)	323 (99%)	2 (1%)	84	86
All	All	1301/1424 (91%)	1295 (100%)	6 (0%)	86	88

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	358	LYS
1	D	7	GLU
1	D	358	LYS
1	A	248	GLN
1	A	41	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	230	GLN
1	A	248	GLN
1	B	250	ASN
1	B	390	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	LLP	D	211	1	23,24,25	0.84	1 (4%)	25,32,34	1.06	2 (8%)
1	LLP	C	211	1	23,24,25	0.89	1 (4%)	25,32,34	1.03	1 (4%)
1	LLP	B	211	1	23,24,25	0.83	1 (4%)	25,32,34	1.09	2 (8%)
1	LLP	A	211	1	23,24,25	0.86	1 (4%)	25,32,34	1.97	6 (24%)

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	D	211	1	-	7/16/17/19	0/1/1/1
1	LLP	C	211	1	-	5/16/17/19	0/1/1/1
1	LLP	B	211	1	-	8/16/17/19	0/1/1/1
1	LLP	A	211	1	-	6/16/17/19	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	211	LLP	C4-C4'	2.53	1.51	1.46
1	C	211	LLP	C4-C4'	2.40	1.51	1.46
1	B	211	LLP	C4-C4'	2.11	1.50	1.46
1	D	211	LLP	C4-C4'	2.00	1.50	1.46

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	211	LLP	CE-NZ-C4'	4.55	132.88	118.90
1	A	211	LLP	C5-C4-C4'	-3.83	115.26	121.56
1	A	211	LLP	C4-C4'-NZ	3.81	141.79	124.31
1	A	211	LLP	C3-C4-C4'	3.78	127.46	120.41
1	A	211	LLP	CD-CE-NZ	-3.10	103.32	110.93

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	211	LLP	C4-C4'-NZ-CE
1	A	211	LLP	O-C-CA-CB
1	B	211	LLP	C4-C5-C5'-OP4
1	B	211	LLP	C6-C5-C5'-OP4
1	B	211	LLP	C5'-OP4-P-OP1

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	211	LLP	1	0
1	B	211	LLP	1	0
1	A	211	LLP	3	0

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$
2	PRO	D	501	-	8,8,8	1.19	1 (12%)	10,10,10	1.78	4 (40%)
2	PRO	B	501	-	8,8,8	1.18	0	10,10,10	1.88	4 (40%)

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
2	PRO	D	501	-	-	2/4/11/11	0/1/1/1
2	PRO	B	501	-	-	3/4/11/11	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	PRO	OXT-C	-2.09	1.23	1.30

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	PRO	OXT-C-O	-3.59	115.94	124.09
2	D	501	PRO	OXT-C-CA	3.02	123.43	113.40
2	B	501	PRO	OXT-C-CA	2.80	122.71	113.40
2	D	501	PRO	OXT-C-O	-2.64	118.09	124.09
2	D	501	PRO	C-CA-N	2.63	117.08	106.73

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	PRO	O-C-CA-CB
2	B	501	PRO	OXT-C-CA-CB
2	D	501	PRO	O-C-CA-CB
2	D	501	PRO	OXT-C-CA-CB
2	B	501	PRO	OXT-C-CA-N

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	501	PRO	3	0
2	B	501	PRO	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	404/448 (90%)	-0.58	7 (1%) 69 71	9, 22, 40, 69	1 (0%)
1	B	404/448 (90%)	-0.50	8 (1%) 64 68	9, 26, 44, 64	2 (0%)
1	C	404/448 (90%)	-0.39	10 (2%) 58 60	9, 26, 57, 80	4 (0%)
1	D	404/448 (90%)	-0.49	11 (2%) 56 57	9, 24, 52, 80	2 (0%)
All	All	1616/1792 (90%)	-0.49	36 (2%) 62 64	9, 24, 49, 80	9 (0%)

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	62	LEU	4.4
1	C	62	LEU	4.0
1	B	6	PRO	3.7
1	D	62	LEU	3.7
1	D	399	ALA	3.7

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	A	211	24/25	0.93	0.13	13,33,40,44	0
1	LLP	B	211	24/25	0.93	0.14	16,39,48,51	0
1	LLP	C	211	24/25	0.94	0.11	16,30,39,42	0
1	LLP	D	211	24/25	0.95	0.10	12,29,39,40	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
2	PRO	B	501	8/8	0.88	0.09	15,19,20,21	0
2	PRO	D	501	8/8	0.89	0.09	14,18,22,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.