



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 05:35 PM UTC

PDB ID : 4FO8 / pdb_00004fo8
Title : Pseudomonas aeruginosa MetAP with Met, in Mn form
Authors : Ye, Q.Z.; Lu, J.P.
Deposited on : 2012-06-20
Resolution : 1.90 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

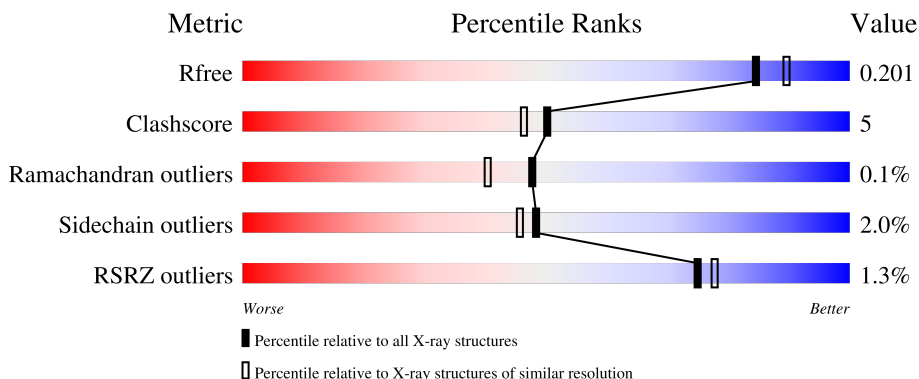
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	280	% 82% 10% • 8%
1	B	280	% 82% 10% • 7%
1	C	280	% 86% 7% • 5%
1	D	280	% 81% 10% • 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9002 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 Methionine aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	3	0
			2059	1301	357	389	12			
1	B	261	Total	C	N	O	S	0	2	0
			2059	1299	358	390	12			
1	C	266	Total	C	N	O	S	0	1	0
			2093	1322	361	398	12			
1	D	259	Total	C	N	O	S	0	3	0
			2053	1294	359	387	13			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	262	GLU	-	expression tag	UNP Q9HXY1
A	263	PHE	-	expression tag	UNP Q9HXY1
A	264	GLU	-	expression tag	UNP Q9HXY1
A	265	LEU	-	expression tag	UNP Q9HXY1
A	266	VAL	-	expression tag	UNP Q9HXY1
A	267	ASP	-	expression tag	UNP Q9HXY1
A	268	LYS	-	expression tag	UNP Q9HXY1
A	269	LEU	-	expression tag	UNP Q9HXY1
A	270	ALA	-	expression tag	UNP Q9HXY1
A	271	ALA	-	expression tag	UNP Q9HXY1
A	272	ALA	-	expression tag	UNP Q9HXY1
A	273	LEU	-	expression tag	UNP Q9HXY1
A	274	GLU	-	expression tag	UNP Q9HXY1
A	275	HIS	-	expression tag	UNP Q9HXY1
A	276	HIS	-	expression tag	UNP Q9HXY1
A	277	HIS	-	expression tag	UNP Q9HXY1
A	278	HIS	-	expression tag	UNP Q9HXY1
A	279	HIS	-	expression tag	UNP Q9HXY1
A	280	HIS	-	expression tag	UNP Q9HXY1
B	262	GLU	-	expression tag	UNP Q9HXY1
B	263	PHE	-	expression tag	UNP Q9HXY1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	264	GLU	-	expression tag	UNP Q9HXY1
B	265	LEU	-	expression tag	UNP Q9HXY1
B	266	VAL	-	expression tag	UNP Q9HXY1
B	267	ASP	-	expression tag	UNP Q9HXY1
B	268	LYS	-	expression tag	UNP Q9HXY1
B	269	LEU	-	expression tag	UNP Q9HXY1
B	270	ALA	-	expression tag	UNP Q9HXY1
B	271	ALA	-	expression tag	UNP Q9HXY1
B	272	ALA	-	expression tag	UNP Q9HXY1
B	273	LEU	-	expression tag	UNP Q9HXY1
B	274	GLU	-	expression tag	UNP Q9HXY1
B	275	HIS	-	expression tag	UNP Q9HXY1
B	276	HIS	-	expression tag	UNP Q9HXY1
B	277	HIS	-	expression tag	UNP Q9HXY1
B	278	HIS	-	expression tag	UNP Q9HXY1
B	279	HIS	-	expression tag	UNP Q9HXY1
B	280	HIS	-	expression tag	UNP Q9HXY1
C	262	GLU	-	expression tag	UNP Q9HXY1
C	263	PHE	-	expression tag	UNP Q9HXY1
C	264	GLU	-	expression tag	UNP Q9HXY1
C	265	LEU	-	expression tag	UNP Q9HXY1
C	266	VAL	-	expression tag	UNP Q9HXY1
C	267	ASP	-	expression tag	UNP Q9HXY1
C	268	LYS	-	expression tag	UNP Q9HXY1
C	269	LEU	-	expression tag	UNP Q9HXY1
C	270	ALA	-	expression tag	UNP Q9HXY1
C	271	ALA	-	expression tag	UNP Q9HXY1
C	272	ALA	-	expression tag	UNP Q9HXY1
C	273	LEU	-	expression tag	UNP Q9HXY1
C	274	GLU	-	expression tag	UNP Q9HXY1
C	275	HIS	-	expression tag	UNP Q9HXY1
C	276	HIS	-	expression tag	UNP Q9HXY1
C	277	HIS	-	expression tag	UNP Q9HXY1
C	278	HIS	-	expression tag	UNP Q9HXY1
C	279	HIS	-	expression tag	UNP Q9HXY1
C	280	HIS	-	expression tag	UNP Q9HXY1
D	262	GLU	-	expression tag	UNP Q9HXY1
D	263	PHE	-	expression tag	UNP Q9HXY1
D	264	GLU	-	expression tag	UNP Q9HXY1
D	265	LEU	-	expression tag	UNP Q9HXY1
D	266	VAL	-	expression tag	UNP Q9HXY1
D	267	ASP	-	expression tag	UNP Q9HXY1

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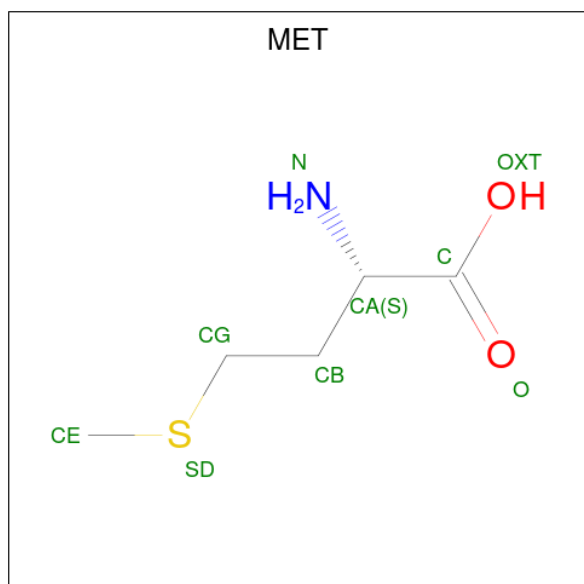
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Chain	Residue	Modelled	Actual	Comment	Reference
D	268	LYS	-	expression tag	UNP Q9HXY1
D	269	LEU	-	expression tag	UNP Q9HXY1
D	270	ALA	-	expression tag	UNP Q9HXY1
D	271	ALA	-	expression tag	UNP Q9HXY1
D	272	ALA	-	expression tag	UNP Q9HXY1
D	273	LEU	-	expression tag	UNP Q9HXY1
D	274	GLU	-	expression tag	UNP Q9HXY1
D	275	HIS	-	expression tag	UNP Q9HXY1
D	276	HIS	-	expression tag	UNP Q9HXY1
D	277	HIS	-	expression tag	UNP Q9HXY1
D	278	HIS	-	expression tag	UNP Q9HXY1
D	279	HIS	-	expression tag	UNP Q9HXY1
D	280	HIS	-	expression tag	UNP Q9HXY1

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Mn 4 4	0	0
2	B	3	Total Mn 3 3	0	0
2	C	3	Total Mn 3 3	0	0
2	D	3	Total Mn 3 3	0	0

- Molecule 3 is METHIONINE (CCD ID: MET) (formula: C₅H₁₁NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			9	5	1	2	1		
3	B	1	Total	C	N	O	S	0	0
			9	5	1	2	1		
3	C	1	Total	C	N	O	S	0	0
			9	5	1	2	1		
3	D	1	Total	C	N	O	S	0	0
			9	5	1	2	1		

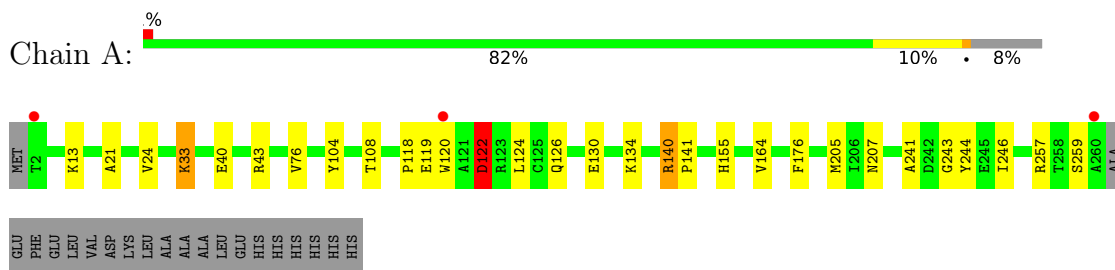
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	170	Total	O	0	0
			170	170		
4	B	188	Total	O	0	0
			188	188		
4	C	174	Total	O	0	0
			174	174		
4	D	157	Total	O	0	0
			157	157		

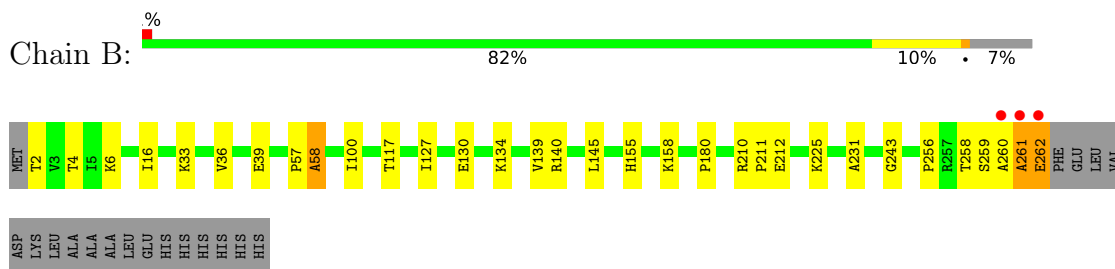
3 Residue-property plots

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.

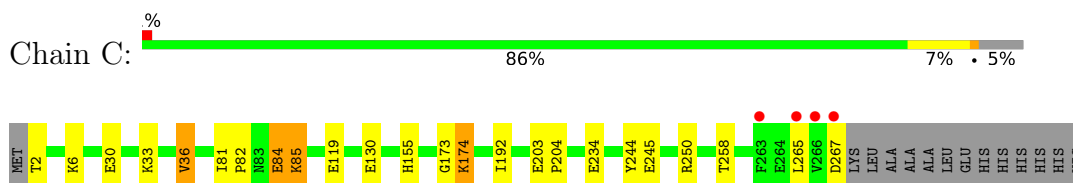
- Molecule 1: Methionine aminopeptidase



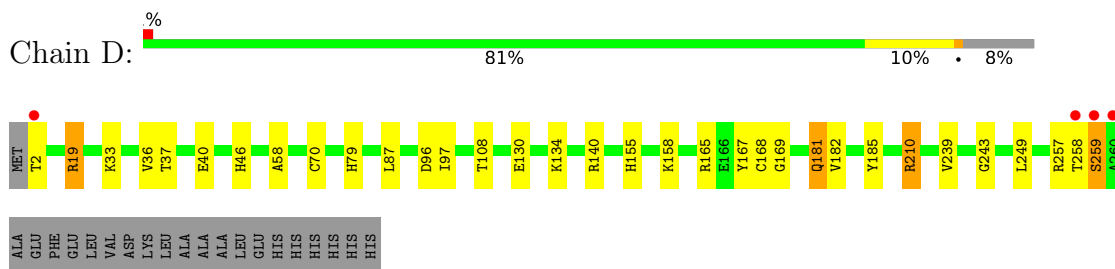
- Molecule 1: Methionine aminopeptidase



- Molecule 1: Methionine aminopeptidase



- Molecule 1: Methionine aminopeptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.65Å 105.66Å 133.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.77 – 1.90 30.77 – 1.90	Depositor EDS
% Data completeness (in resolution range)	88.3 (30.77-1.90) 88.4 (30.77-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.47 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.157 , 0.200 0.158 , 0.201	Depositor DCC
R_{free} test set	4526 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	17.6	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.1	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	0.96	EDS
Total number of atoms	9002	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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: MN

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	1.40	3/2103 (0.1%)	1.14	4/2847 (0.1%)
1	B	1.42	5/2101 (0.2%)	1.22	6/2842 (0.2%)
1	C	1.35	4/2136 (0.2%)	1.15	3/2891 (0.1%)
1	D	1.33	4/2095 (0.2%)	1.12	5/2834 (0.2%)
All	All	1.37	16/8435 (0.2%)	1.16	18/11414 (0.2%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	139	VAL	CA-CB	6.36	1.61	1.54
1	D	108	THR	CA-CB	6.16	1.64	1.53
1	B	16	ILE	CA-CB	6.07	1.61	1.54
1	C	204	PRO	CA-C	6.07	1.59	1.52
1	C	36	VAL	N-CA	5.99	1.53	1.46
1	D	58	ALA	CA-CB	5.98	1.61	1.53
1	A	24	VAL	CA-CB	5.93	1.61	1.54
1	C	81	ILE	CA-CB	5.83	1.59	1.53
1	D	97	ILE	CA-CB	5.77	1.62	1.54
1	B	231	ALA	C-O	5.72	1.31	1.23
1	C	250	ARG	CZ-NH1	5.64	1.40	1.32
1	B	36	VAL	CA-CB	5.61	1.60	1.54
1	A	124	LEU	CA-C	5.37	1.59	1.52
1	D	239	VAL	CA-C	5.34	1.59	1.52
1	A	76	VAL	CA-CB	5.31	1.60	1.54
1	B	57	PRO	N-CA	5.07	1.53	1.47

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	140	ARG	CG-CD-NE	-7.88	94.66	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	122	ASP	CB-CA-C	-7.51	98.32	110.79
1	B	33	LYS	CA-C-N	-6.98	112.59	119.78
1	B	33	LYS	C-N-CA	-6.98	112.59	119.78
1	D	181	GLN	CB-CA-C	-6.41	99.89	109.90
1	B	58	ALA	CA-C-N	-6.29	113.15	119.56
1	B	58	ALA	C-N-CA	-6.29	113.15	119.56
1	A	140	ARG	N-CA-C	-6.11	102.63	108.13
1	A	122	ASP	N-CA-CB	5.56	118.29	110.12
1	A	140	ARG	CG-CD-NE	-5.55	99.80	112.00
1	D	165	ARG	NE-CZ-NH1	-5.53	115.97	121.50
1	C	85	LYS	CA-C-N	-5.37	114.42	119.85
1	C	85	LYS	C-N-CA	-5.37	114.42	119.85
1	C	174	LYS	N-CA-C	-5.32	106.77	113.20
1	B	127	ILE	CB-CA-C	-5.23	105.00	112.22
1	D	19	ARG	N-CA-C	-5.12	105.78	111.36
1	D	185	TYR	N-CA-C	-5.04	101.42	109.07
1	D	169	GLY	N-CA-C	-5.02	104.52	112.66

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	2059	0	2046	25	0
1	B	2059	0	2055	37	0
1	C	2093	0	2082	9	1
1	D	2053	0	2048	26	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
3	A	9	0	8	1	0
3	B	9	0	8	0	0
3	C	9	0	8	0	0
3	D	9	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	170	0	0	13	0
4	B	188	0	0	1	0
4	C	174	0	0	0	0
4	D	157	0	0	2	1
All	All	9002	0	8263	88	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 5.

All (88) 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:B:6:LYS:H	1:D:181:GLN:NE2	1.51	1.08
1:B:258:THR:OG1	1:B:261:ALA:HB1	1.56	1.06
1:B:260:ALA:CA	1:B:261:ALA:HB2	1.91	1.00
1:B:260:ALA:N	1:B:261:ALA:HB2	1.78	0.98
1:B:6:LYS:H	1:D:181:GLN:HE22	0.96	0.95
1:B:260:ALA:N	1:B:261:ALA:CB	2.30	0.95
1:B:260:ALA:CB	1:B:261:ALA:HB2	2.00	0.90
4:A:567:HOH:O	1:D:158:LYS:HD2	1.71	0.89
1:B:260:ALA:HB3	1:B:261:ALA:HB2	1.52	0.88
1:A:118:PRO:O	4:A:562:HOH:O	1.92	0.88
1:A:246:ILE:O	1:A:257:ARG:NH1	2.08	0.87
1:B:6:LYS:N	1:D:181:GLN:HE22	1.74	0.86
1:A:120[B]:TRP:HB2	4:A:539:HOH:O	1.77	0.84
1:D:158:LYS:HE2	4:D:492:HOH:O	1.77	0.84
1:B:258:THR:OG1	1:B:261:ALA:CB	2.26	0.83
1:A:126:GLN:HG2	4:A:492:HOH:O	1.77	0.82
1:B:260:ALA:CA	1:B:261:ALA:CB	2.57	0.81
1:D:37:THR:OG1	1:D:40[B]:GLU:HG3	1.86	0.75
1:B:2:THR:N	1:D:79:HIS:HE2	1.84	0.75
1:B:260:ALA:N	1:B:261:ALA:HB3	2.04	0.71
1:B:258:THR:HG1	1:B:261:ALA:HB1	1.57	0.69
1:B:256:PRO:HB3	1:B:262:GLU:HA	1.74	0.68
1:A:122:ASP:CB	4:A:532:HOH:O	2.41	0.68
4:B:453:HOH:O	1:C:85:LYS:HE3	1.94	0.67
1:A:120[A]:TRP:O	4:A:539:HOH:O	2.14	0.66
1:D:46:HIS:HE1	4:D:488:HOH:O	1.77	0.66
1:B:260:ALA:H	1:B:261:ALA:HB2	1.57	0.65
1:D:243:GLY:HA3	1:D:259:SER:OG	1.97	0.65
1:A:122:ASP:HB2	4:A:532:HOH:O	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LYS:N	1:D:181:GLN:NE2	2.36	0.61
1:A:122:ASP:CG	4:A:532:HOH:O	2.44	0.60
1:C:203:GLU:HB3	1:C:234:GLU:HG3	1.84	0.59
1:A:140:ARG:NH1	4:A:564:HOH:O	2.14	0.58
1:B:155:HIS:HD2	1:B:158:LYS:NZ	2.04	0.55
1:A:140:ARG:HB3	1:A:243:GLY:HA2	1.89	0.55
1:A:13:LYS:HD3	1:A:104:TYR:CE2	2.42	0.54
1:B:134:LYS:HE3	1:B:155:HIS:CD2	2.42	0.54
1:C:84:GLU:H	1:C:84:GLU:CD	2.15	0.54
1:C:245:GLU:HG3	1:C:258:THR:HG22	1.89	0.54
1:C:6:LYS:HE3	1:C:173:GLY:HA3	1.89	0.53
1:B:2:THR:HG22	1:D:79:HIS:NE2	2.25	0.52
1:B:2:THR:HG22	1:D:79:HIS:CE1	2.44	0.52
1:D:37:THR:HG1	1:D:40[B]:GLU:HG3	1.74	0.52
1:D:130:GLU:OE1	1:D:155:HIS:HE1	1.92	0.51
1:D:140:ARG:HB3	1:D:243:GLY:HA2	1.93	0.51
1:A:130:GLU:OE1	1:A:155:HIS:HE1	1.93	0.51
1:B:212:GLU:CB	1:B:225:LYS:HD2	2.41	0.51
1:B:4:THR:HG22	1:D:167:TYR:CE1	2.46	0.50
1:B:130:GLU:OE1	1:B:155:HIS:HE1	1.94	0.50
1:A:155:HIS:HD2	4:A:533:HOH:O	1.94	0.50
1:B:261:ALA:H	1:D:210:ARG:HH22	1.58	0.49
1:C:130:GLU:OE1	1:C:155:HIS:HE1	1.97	0.48
1:B:212:GLU:HB3	1:B:225:LYS:HD2	1.96	0.48
1:C:33:LYS:O	1:C:36:VAL:HG12	2.13	0.47
1:A:207:ASN:HB3	4:A:442:HOH:O	2.15	0.47
1:A:43:ARG:HD2	4:A:510:HOH:O	2.14	0.47
1:A:120[B]:TRP:CE3	1:A:120[B]:TRP:N	2.77	0.47
1:B:260:ALA:HB3	1:B:261:ALA:CB	2.34	0.47
1:A:119:GLU:OE2	1:A:119:GLU:O	2.32	0.46
1:B:262:GLU:CD	1:B:262:GLU:H	2.24	0.45
1:D:134:LYS:HE3	1:D:155:HIS:CD2	2.52	0.45
1:B:243:GLY:HA3	1:B:259:SER:OG	2.17	0.45
1:B:58:ALA:HB2	1:B:100:ILE:CG1	2.47	0.44
1:D:158:LYS:HE3	1:D:158:LYS:HB3	1.67	0.44
1:B:258:THR:O	1:B:261:ALA:HB3	2.18	0.44
1:D:257:ARG:HG2	1:D:258:THR:HG23	2.00	0.44
1:B:145:LEU:HD11	1:B:180:PRO:HB2	1.99	0.44
1:D:19:ARG:HA	1:D:19:ARG:HD2	1.83	0.44
1:A:126:GLN:CG	4:A:492:HOH:O	2.51	0.44
1:A:164:VAL:HB	1:A:205:MET:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:ALA:H	1:B:261:ALA:CB	2.18	0.44
1:D:33:LYS:O	1:D:36:VAL:HG12	2.17	0.43
1:D:168[A]:CYS:HB2	1:D:182:VAL:O	2.18	0.43
1:C:203:GLU:HB3	1:C:234:GLU:CG	2.48	0.43
1:A:33:LYS:HB3	1:A:33:LYS:HE3	1.61	0.43
1:A:141:PRO:HG2	1:A:241:ALA:O	2.19	0.43
1:D:36:VAL:CG1	1:D:87:LEU:HD12	2.49	0.43
1:A:244:TYR:CD1	1:A:244:TYR:C	2.96	0.43
1:B:259:SER:C	1:B:261:ALA:HB3	2.44	0.43
1:A:176:PHE:CZ	3:A:305:MET:HB2	2.54	0.42
1:B:155:HIS:HD2	1:B:158:LYS:HZ2	1.68	0.42
1:A:21:ALA:HB1	1:A:108:THR:HG22	2.01	0.42
1:D:70:CYS:HB2	1:D:96:ASP:HB3	2.01	0.41
1:B:210:ARG:HB3	1:B:211:PRO:HD2	2.02	0.41
1:C:244:TYR:CD1	1:C:244:TYR:C	2.99	0.41
1:A:134:LYS:HE3	1:A:155:HIS:CD2	2.55	0.41
1:B:158:LYS:HB2	1:B:158:LYS:HE3	1.93	0.41
1:D:249:LEU:HD22	1:D:257:ARG:HB2	2.02	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:C:174:LYS:NZ	4:D:524:HOH:O[3_654]	2.13	0.07

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	260/280 (93%)	253 (97%)	7 (3%)	0	100	100
1	B	261/280 (93%)	252 (97%)	8 (3%)	1 (0%)	30	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	265/280 (95%)	258 (97%)	7 (3%)	0	100	100
1	D	260/280 (93%)	255 (98%)	5 (2%)	0	100	100
All	All	1046/1120 (93%)	1018 (97%)	27 (3%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	261	ALA

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	224/238 (94%)	219 (98%)	5 (2%)	45	42
1	B	224/238 (94%)	221 (99%)	3 (1%)	61	61
1	C	228/238 (96%)	220 (96%)	8 (4%)	32	24
1	D	224/238 (94%)	221 (99%)	3 (1%)	61	61
All	All	900/952 (94%)	881 (98%)	19 (2%)	48	44

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LYS
1	A	40[A]	GLU
1	A	40[B]	GLU
1	A	122	ASP
1	A	259	SER
1	B	39	GLU
1	B	117	THR
1	B	262	GLU
1	C	2	THR
1	C	30	GLU
1	C	82	PRO

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Mol	Chain	Res	Type
1	C	84	GLU
1	C	119	GLU
1	C	192	ILE
1	C	265	LEU
1	C	267	ASP
1	D	2	THR
1	D	210	ARG
1	D	259	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	HIS
1	A	53	GLN
1	A	126	GLN
1	A	155	HIS
1	A	159	ASN
1	A	232	GLN
1	B	46	HIS
1	B	155	HIS
1	B	159	ASN
1	C	46	HIS
1	C	51	ASN
1	C	155	HIS
1	D	46	HIS
1	D	144	HIS
1	D	155	HIS
1	D	181	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 17 ligands modelled in this entry, 13 are monoatomic - leaving 4 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
3	MET	A	305	2	7,8,8	1.13	1 (14%)	5,9,9	0.84	0
3	MET	B	304	2	7,8,8	1.14	1 (14%)	5,9,9	1.06	0
3	MET	C	304	2	7,8,8	0.76	0	5,9,9	0.64	0
3	MET	D	304	2	7,8,8	0.93	0	5,9,9	1.58	1 (20%)

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	MET	A	305	2	-	3/8/8/8	-
3	MET	B	304	2	-	4/8/8/8	-
3	MET	C	304	2	-	4/8/8/8	-
3	MET	D	304	2	-	6/8/8/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	305	MET	OXT-C	-2.62	1.22	1.30
3	B	304	MET	CB-CA	2.46	1.58	1.53

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	304	MET	OXT-C-O	-3.09	117.08	124.08

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	304	MET	O-C-CA-N
3	D	304	MET	N-CA-CB-CG
3	D	304	MET	OXT-C-CA-CB
3	B	304	MET	OXT-C-CA-CB
3	D	304	MET	C-CA-CB-CG
3	D	304	MET	OXT-C-CA-N
3	C	304	MET	OXT-C-CA-N
3	B	304	MET	O-C-CA-CB
3	A	305	MET	O-C-CA-CB
3	D	304	MET	O-C-CA-CB
3	A	305	MET	OXT-C-CA-CB
3	C	304	MET	O-C-CA-CB
3	B	304	MET	OXT-C-CA-N
3	B	304	MET	O-C-CA-N
3	A	305	MET	OXT-C-CA-N
3	C	304	MET	OXT-C-CA-CB
3	C	304	MET	O-C-CA-N

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	305	MET	1	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	259/280 (92%)	-0.56	3 (1%) 76 79	7, 15, 29, 47	3 (1%)
1	B	261/280 (93%)	-0.62	3 (1%) 78 80	7, 15, 30, 49	2 (0%)
1	C	266/280 (95%)	-0.43	4 (1%) 72 75	8, 17, 33, 66	1 (0%)
1	D	259/280 (92%)	-0.54	4 (1%) 72 75	8, 16, 33, 54	3 (1%)
All	All	1045/1120 (93%)	-0.53	14 (1%) 75 78	7, 16, 32, 66	9 (0%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	120[A]	TRP	5.0
1	A	260	ALA	4.0
1	C	265	LEU	3.4
1	C	263	PHE	3.1
1	C	266	VAL	2.7
1	B	260	ALA	2.7
1	D	259	SER	2.5
1	D	2	THR	2.5
1	A	2	THR	2.5
1	D	260	ALA	2.4
1	B	262	GLU	2.3
1	C	267	ASP	2.1
1	B	261	ALA	2.0
1	D	258	THR	2.0

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($\text{\AA}^2$)	Q<0.9
3	MET	A	305	9/9	0.97	0.06	8,13,19,22	0
3	MET	D	304	9/9	0.97	0.06	16,19,25,29	0
3	MET	C	304	9/9	0.98	0.05	14,17,21,23	0
2	MN	B	303	1/1	0.98	0.03	20,20,20,20	1
2	MN	C	303	1/1	0.99	0.05	16,16,16,16	1
2	MN	D	303	1/1	0.99	0.07	20,20,20,20	1
2	MN	A	303	1/1	0.99	0.01	19,19,19,19	0
3	MET	B	304	9/9	0.99	0.04	10,13,17,20	0
2	MN	A	304	1/1	0.99	0.04	17,17,17,17	1
2	MN	A	302	1/1	0.99	0.01	10,10,10,10	0
2	MN	D	301	1/1	1.00	0.01	13,13,13,13	0
2	MN	D	302	1/1	1.00	0.01	11,11,11,11	0
2	MN	B	302	1/1	1.00	0.01	10,10,10,10	0
2	MN	A	301	1/1	1.00	0.01	10,10,10,10	0
2	MN	C	301	1/1	1.00	0.01	14,14,14,14	0
2	MN	C	302	1/1	1.00	0.01	13,13,13,13	0
2	MN	B	301	1/1	1.00	0.01	10,10,10,10	0

6.5 Other polymers [i](#)

There are no such residues in this entry.