



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 10:48 PM UTC

PDB ID : 4WJB / pdb_00004wjb
Title : X-ray crystal structure of a putative amidohydrolase/peptidase from Burkholderia cenocepacia
Authors : Lukacs, C.M.; Dranow, D.M.; Edwards, T.E.; Lorimer, D.; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2014-09-29
Resolution : 1.95 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

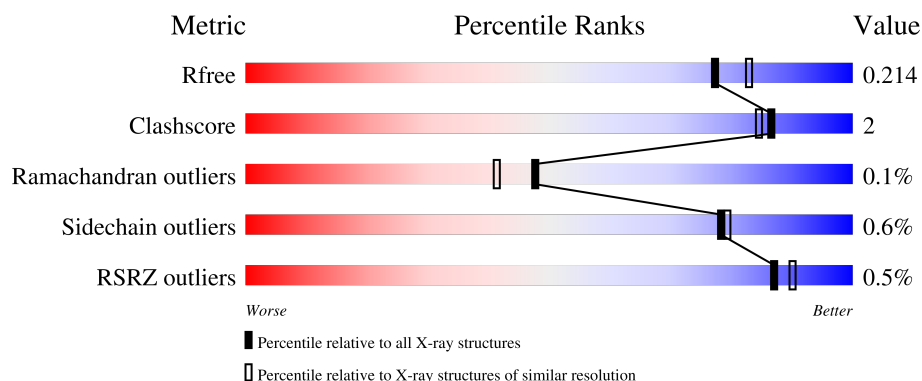
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	424	 91% 6% .
1	B	424	 91% . .
1	C	424	 92% . .
1	D	424	 90% 5% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13539 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 amidohydrolase/peptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	3	0
			3087	1917	568	586	16			
1	B	407	Total	C	N	O	S	0	1	0
			3065	1906	561	583	15			
1	C	407	Total	C	N	O	S	0	4	0
			3076	1911	567	582	16			
1	D	405	Total	C	N	O	S	0	0	0
			3030	1883	555	577	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP B4EHA1
A	-6	ALA	-	expression tag	UNP B4EHA1
A	-5	HIS	-	expression tag	UNP B4EHA1
A	-4	HIS	-	expression tag	UNP B4EHA1
A	-3	HIS	-	expression tag	UNP B4EHA1
A	-2	HIS	-	expression tag	UNP B4EHA1
A	-1	HIS	-	expression tag	UNP B4EHA1
A	0	HIS	-	expression tag	UNP B4EHA1
B	-7	MET	-	expression tag	UNP B4EHA1
B	-6	ALA	-	expression tag	UNP B4EHA1
B	-5	HIS	-	expression tag	UNP B4EHA1
B	-4	HIS	-	expression tag	UNP B4EHA1
B	-3	HIS	-	expression tag	UNP B4EHA1
B	-2	HIS	-	expression tag	UNP B4EHA1
B	-1	HIS	-	expression tag	UNP B4EHA1
B	0	HIS	-	expression tag	UNP B4EHA1
C	-7	MET	-	expression tag	UNP B4EHA1
C	-6	ALA	-	expression tag	UNP B4EHA1
C	-5	HIS	-	expression tag	UNP B4EHA1
C	-4	HIS	-	expression tag	UNP B4EHA1
C	-3	HIS	-	expression tag	UNP B4EHA1

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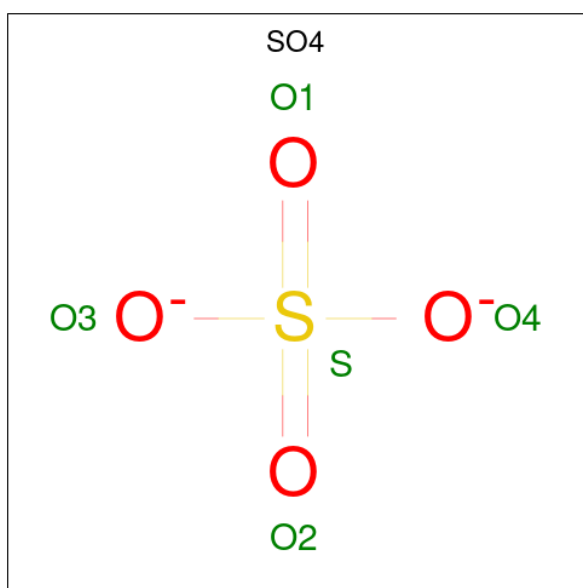
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	UNP B4EHA1
C	-1	HIS	-	expression tag	UNP B4EHA1
C	0	HIS	-	expression tag	UNP B4EHA1
D	-7	MET	-	expression tag	UNP B4EHA1
D	-6	ALA	-	expression tag	UNP B4EHA1
D	-5	HIS	-	expression tag	UNP B4EHA1
D	-4	HIS	-	expression tag	UNP B4EHA1
D	-3	HIS	-	expression tag	UNP B4EHA1
D	-2	HIS	-	expression tag	UNP B4EHA1
D	-1	HIS	-	expression tag	UNP B4EHA1
D	0	HIS	-	expression tag	UNP B4EHA1

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

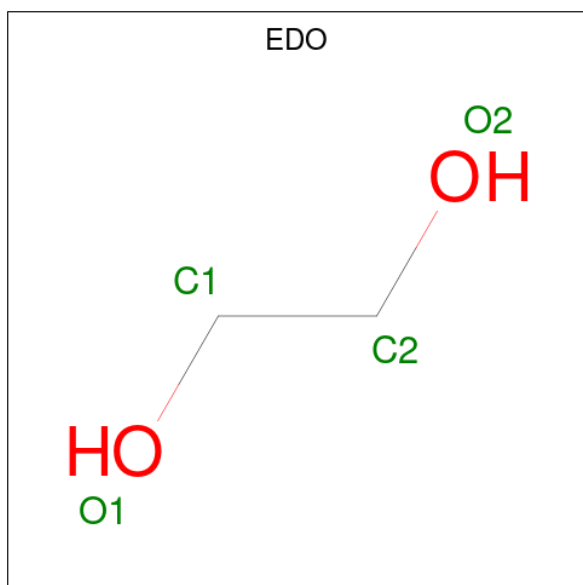
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total 2 Zn 2	0	1
2	B	1	Total 2 Zn 2	0	1
2	C	1	Total 2 Zn 2	0	1
2	D	1	Total 2 Zn 2	0	1

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0

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

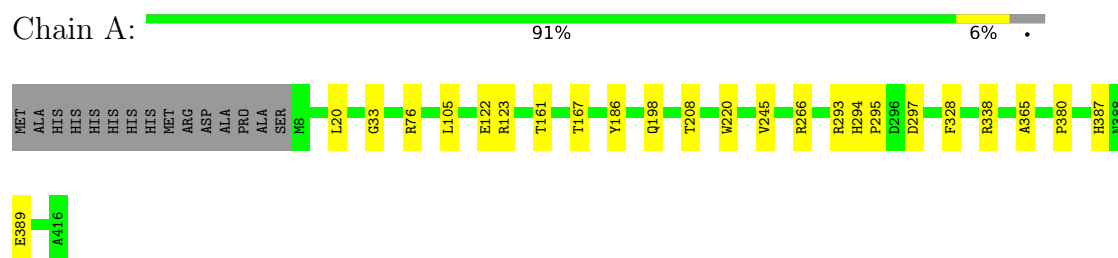
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	278	Total O 278 278	0	0
5	B	364	Total O 364 364	0	0
5	C	287	Total O 287 287	0	0
5	D	261	Total O 261 261	0	0

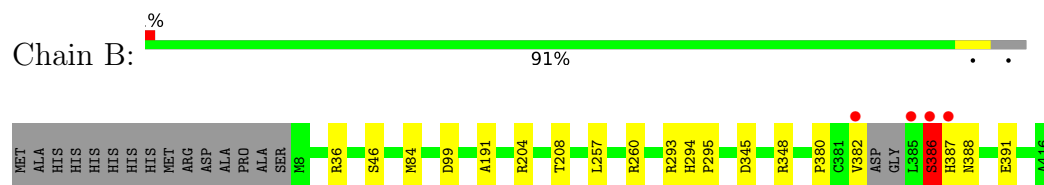
3 Residue-property plots

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.

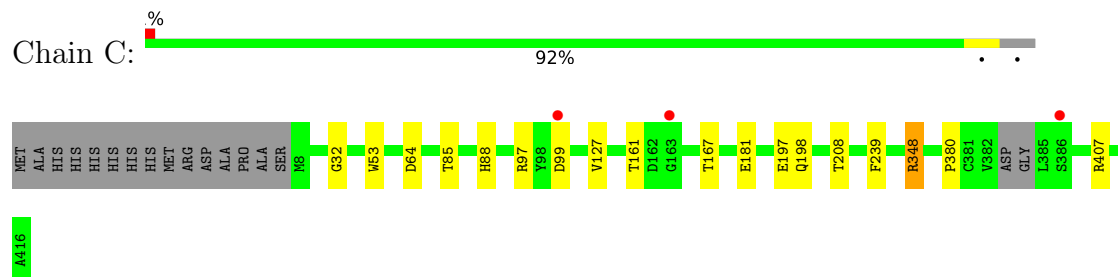
- Molecule 1: Putative amidohydrolase/peptidase



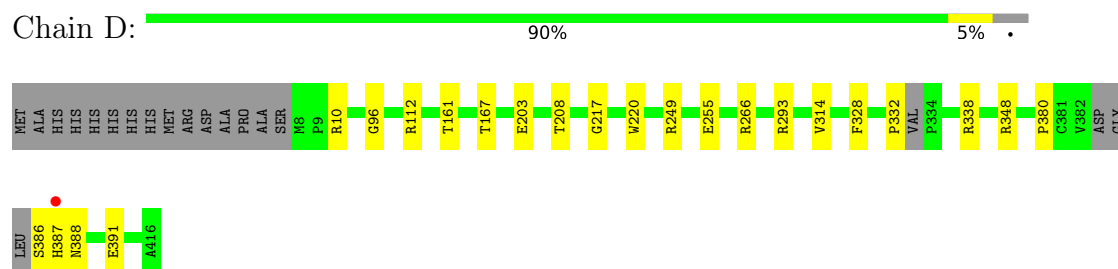
- Molecule 1: Putative amidohydrolase/peptidase



- Molecule 1: Putative amidohydrolase/peptidase



- Molecule 1: Putative amidohydrolase/peptidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.66Å 113.06Å 126.67Å 90.00° 95.50° 90.00°	Depositor
Resolution (Å)	8.72 – 1.95 8.72 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.5 (8.72-1.95) 98.4 (8.72-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1779)	Depositor
R, R_{free}	0.173 , 0.213 0.174 , 0.214	Depositor DCC
R_{free} test set	6464 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	21.4	Xtriage
Anisotropy	0.632	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.47 , 63.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13539	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.41% 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: SO4, ZN, EDO

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	0.34	0/3147	0.69	0/4278
1	B	0.36	0/3124	0.69	0/4246
1	C	0.36	0/3135	0.70	0/4261
1	D	0.34	0/3087	0.69	0/4194
All	All	0.35	0/12493	0.69	0/16979

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	3087	0	3005	14	0
1	B	3065	0	2992	11	0
1	C	3076	0	2986	11	0
1	D	3030	0	2946	16	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	25	0	0	0	0
3	C	10	0	0	1	0
3	D	10	0	0	1	0
4	A	16	0	24	4	0
4	B	8	0	12	1	0
4	C	4	0	6	1	0
5	A	278	0	0	0	0
5	B	364	0	0	1	0
5	C	287	0	0	0	0
5	D	261	0	0	4	0
All	All	13539	0	11971	50	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 2.

All (50) 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:C:88:HIS:CE1	1:C:99:ASP:OD2	2.34	0.79
1:B:99:ASP:OD2	1:B:387:HIS:CD2	2.41	0.72
1:C:88:HIS:HE1	1:C:99:ASP:OD2	1.70	0.71
1:A:161:THR:HG22	1:A:167:THR:HG22	1.78	0.66
1:B:345:ASP:OD1	1:B:348:ARG:NH2	2.30	0.64
4:A:504:EDO:H21	1:D:293:ARG:HH12	1.63	0.63
1:C:348:ARG:NE	3:C:503:SO4:O4	2.32	0.63
1:C:161:THR:HG22	1:C:167:THR:HG22	1.82	0.62
1:D:161:THR:HG22	1:D:167:THR:HG22	1.83	0.60
1:D:338:ARG:NH2	5:D:847:HOH:O	2.37	0.58
1:D:10:ARG:NH1	5:D:853:HOH:O	2.37	0.57
1:D:249:ARG:NH2	5:D:788:HOH:O	2.38	0.55
1:D:266:ARG:HB2	1:D:293:ARG:HB2	1.92	0.52
1:B:293:ARG:HH12	4:B:507:EDO:H21	1.76	0.50
1:D:348:ARG:NE	3:D:502:SO4:O1	2.41	0.49
1:A:20:LEU:HD23	1:A:105:LEU:HD12	1.94	0.49
1:D:249:ARG:HD3	1:D:314:VAL:HG22	1.94	0.49
1:A:245:VAL:HG11	1:D:255:GLU:OE1	2.13	0.49
1:A:365:ALA:HB2	4:A:506:EDO:H21	1.95	0.48
1:B:208:THR:O	1:B:380:PRO:HD3	2.13	0.48
1:B:204:ARG:HD2	1:C:239:PHE:CZ	2.48	0.47
1:A:208:THR:O	1:A:380:PRO:HD3	2.15	0.47
1:B:260:ARG:NH1	5:B:603:HOH:O	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:386:SER:HA	1:B:388:ASN:H	1.79	0.47
1:A:186:TYR:CD1	4:A:505:EDO:H11	2.50	0.46
1:A:338:ARG:HE	4:A:507:EDO:H12	1.80	0.46
1:D:112:ARG:NH1	5:D:655:HOH:O	2.45	0.46
1:D:208:THR:O	1:D:380:PRO:HD3	2.15	0.46
1:C:64:ASP:HA	1:C:181:GLU:HB2	1.98	0.46
1:B:36:ARG:HD2	1:B:46:SER:HB2	1.98	0.46
1:A:294:HIS:CG	1:A:295:PRO:HD2	2.51	0.45
1:A:198:GLN:NE2	1:A:387:HIS:NE2	2.64	0.45
1:D:96:GLY:HA3	1:D:391:GLU:CG	2.47	0.45
1:D:220:TRP:HB2	1:D:328:PHE:HB3	1.98	0.44
1:D:386:SER:OG	1:D:387:HIS:N	2.50	0.43
1:A:266:ARG:HB2	1:A:293:ARG:HB2	2.00	0.43
1:C:208:THR:O	1:C:380:PRO:HD3	2.19	0.43
1:A:33:GLY:HA3	1:A:389:GLU:HG2	2.00	0.43
1:B:294:HIS:CG	1:B:295:PRO:HD2	2.54	0.43
1:B:84:MET:O	1:B:191:ALA:HA	2.19	0.43
1:C:53:TRP:HE1	4:C:504:EDO:H21	1.84	0.43
1:D:217:GLY:CA	1:D:332:PRO:HD3	2.50	0.42
1:A:220:TRP:HB2	1:A:328:PHE:HB3	2.01	0.42
1:A:76:ARG:HE	1:A:122:GLU:CD	2.28	0.42
1:C:85:THR:O	1:C:127:VAL:HA	2.20	0.41
1:C:197:GLU:O	1:C:198:GLN:HB2	2.20	0.41
1:D:388:ASN:O	1:D:391:GLU:HG2	2.21	0.41
1:B:257:LEU:HD23	1:B:257:LEU:HA	1.94	0.41
1:A:123:ARG:NH1	3:A:502:SO4:O3	2.54	0.40
1:C:32:GLY:O	1:C:97:ARG:NH1	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	410/424 (97%)	404 (98%)	6 (2%)	0	100	100
1	B	404/424 (95%)	399 (99%)	4 (1%)	1 (0%)	43	36
1	C	407/424 (96%)	402 (99%)	5 (1%)	0	100	100
1	D	399/424 (94%)	394 (99%)	5 (1%)	0	100	100
All	All	1620/1696 (96%)	1599 (99%)	20 (1%)	1 (0%)	48	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	386	SER

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	306/318 (96%)	305 (100%)	1 (0%)	86	87
1	B	305/318 (96%)	302 (99%)	3 (1%)	68	67
1	C	303/318 (95%)	301 (99%)	2 (1%)	76	76
1	D	299/318 (94%)	298 (100%)	1 (0%)	86	87
All	All	1213/1272 (95%)	1206 (99%)	7 (1%)	78	79

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	297	ASP
1	B	382	VAL
1	B	386	SER
1	B	391	GLU
1	C	348	ARG
1	C	407	ARG
1	D	203	GLU

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	198	GLN
1	C	323	GLN
1	D	52	GLN
1	D	323	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 8 are monoatomic - leaving 18 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	SO4	B	506	-	4,4,4	0.22	0	6,6,6	0.08	0
3	SO4	D	502	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	502	-	4,4,4	0.23	0	6,6,6	0.14	0
3	SO4	B	505	-	4,4,4	0.29	0	6,6,6	0.08	0
3	SO4	B	504	-	4,4,4	0.26	0	6,6,6	0.11	0
4	EDO	A	507	-	3,3,3	0.41	0	2,2,2	0.44	0
3	SO4	C	503	-	4,4,4	0.27	0	6,6,6	0.10	0
4	EDO	A	506	-	3,3,3	0.39	0	2,2,2	0.50	0
4	EDO	B	507	-	3,3,3	0.41	0	2,2,2	0.38	0
3	SO4	A	503	-	4,4,4	0.26	0	6,6,6	0.07	0
4	EDO	A	505	-	3,3,3	0.43	0	2,2,2	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	B	508	-	3,3,3	0.39	0	2,2,2	0.54	0
3	SO4	B	503	-	4,4,4	0.25	0	6,6,6	0.09	0
3	SO4	D	503	-	4,4,4	0.26	0	6,6,6	0.07	0
3	SO4	A	502	-	4,4,4	0.23	0	6,6,6	0.11	0
3	SO4	C	502	-	4,4,4	0.28	0	6,6,6	0.05	0
4	EDO	A	504	-	3,3,3	0.44	0	2,2,2	0.36	0
4	EDO	C	504	-	3,3,3	0.44	0	2,2,2	0.34	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
4	EDO	A	507	-	-	1/1/1/1	-
4	EDO	A	506	-	-	0/1/1/1	-
4	EDO	B	507	-	-	0/1/1/1	-
4	EDO	A	505	-	-	0/1/1/1	-
4	EDO	B	508	-	-	0/1/1/1	-
4	EDO	A	504	-	-	1/1/1/1	-
4	EDO	C	504	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	507	EDO	O1-C1-C2-O2
4	A	504	EDO	O1-C1-C2-O2

There are no ring outliers.

9 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	502	SO4	1	0
4	A	507	EDO	1	0
3	C	503	SO4	1	0
4	A	506	EDO	1	0
4	B	507	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	505	EDO	1	0
3	A	502	SO4	1	0
4	A	504	EDO	1	0
4	C	504	EDO	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	409/424 (96%)	-0.45	0	100 100	10, 26, 43, 61	3 (0%)
1	B	407/424 (95%)	-0.63	4 (0%)	79 84	12, 21, 35, 63	1 (0%)
1	C	407/424 (95%)	-0.47	3 (0%)	84 88	10, 24, 44, 61	4 (0%)
1	D	405/424 (95%)	-0.47	1 (0%)	91 92	17, 25, 43, 58	0
All	All	1628/1696 (95%)	-0.51	8 (0%)	87 90	10, 24, 43, 63	8 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	387	HIS	4.1
1	B	382	VAL	3.5
1	C	163	GLY	3.0
1	B	387	HIS	2.6
1	C	386	SER	2.6
1	B	385	LEU	2.6
1	B	386	SER	2.5
1	C	99	ASP	2.5

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 ⓘ

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
3	SO4	B	505	5/5	0.54	0.17	72,72,74,74	0
4	EDO	A	507	4/4	0.75	0.10	42,43,43,45	0
3	SO4	B	506	5/5	0.81	0.15	72,72,73,73	0
4	EDO	A	505	4/4	0.82	0.08	38,41,41,42	0
4	EDO	C	504	4/4	0.84	0.08	48,48,49,49	0
3	SO4	A	503	5/5	0.85	0.11	63,65,65,66	0
4	EDO	A	504	4/4	0.86	0.10	36,38,40,41	0
4	EDO	B	508	4/4	0.87	0.07	32,32,33,34	0
3	SO4	D	503	5/5	0.87	0.13	67,67,68,68	0
2	ZN	C	501[B]	1/1	0.88	0.18	23,23,23,23	1
2	ZN	C	501[A]	1/1	0.88	0.18	71,71,71,71	1
3	SO4	B	504	5/5	0.89	0.10	47,51,52,53	0
3	SO4	C	503	5/5	0.89	0.07	60,60,62,63	0
3	SO4	B	503	5/5	0.90	0.10	61,61,61,62	0
3	SO4	D	502	5/5	0.91	0.08	67,70,71,71	0
4	EDO	B	507	4/4	0.91	0.10	30,30,33,34	0
4	EDO	A	506	4/4	0.92	0.09	34,36,36,36	0
2	ZN	B	501[A]	1/1	0.97	0.02	26,26,26,26	1
3	SO4	B	502	5/5	0.97	0.07	35,35,37,39	0
2	ZN	B	501[B]	1/1	0.97	0.02	22,22,22,22	1
3	SO4	A	502	5/5	0.97	0.06	36,38,40,43	0
2	ZN	D	501[B]	1/1	0.98	0.02	72,72,72,72	1
2	ZN	A	501[A]	1/1	0.98	0.02	30,30,30,30	1
2	ZN	A	501[B]	1/1	0.98	0.02	21,21,21,21	1
2	ZN	D	501[A]	1/1	0.98	0.02	26,26,26,26	1
3	SO4	C	502	5/5	0.98	0.06	31,31,32,33	0

6.5 Other polymers ⓘ

There are no such residues in this entry.