



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:19 AM UTC

PDB ID : 4UP2 / pdb_00004up2
Title : Crystal structure of Escherichia coli tryptophanase purified from alkaline stressed bacterial culture.
Authors : Rety, S.; Deschamps, P.; Leulliot, N.
Deposited on : 2014-06-11
Resolution : 2.78 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

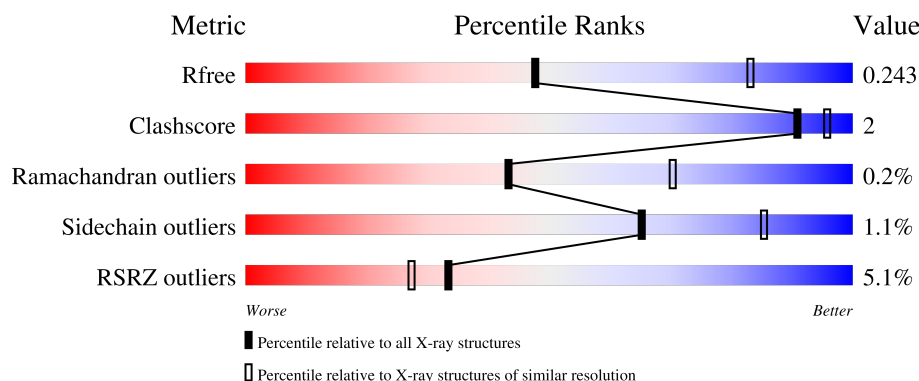
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.78 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	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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	471	5% 86% 11%
1	B	471	4% 81% 5% 13%
1	C	471	3% 82% 14%
1	D	471	6% 80% 16%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	D	1459	-	-	X	-

2 Entry composition [i](#)

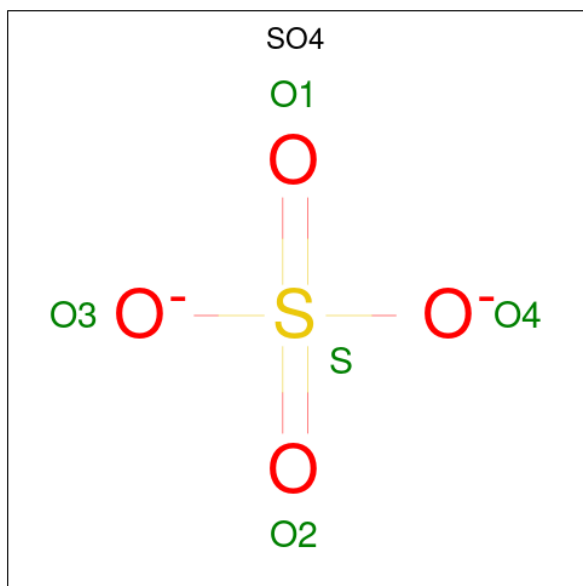
There are 4 unique types of molecules in this entry. The entry contains 25834 atoms, of which 12736 are hydrogens and 0 are deuteriums.

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 TRYPTOPHANASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	420	Total	C	H	N	O	S	0	0	0
			6612	2119	3297	558	618	20			
1	B	408	Total	C	H	N	O	S	0	0	0
			6381	2047	3171	539	605	19			
1	C	404	Total	C	H	N	O	S	0	0	0
			6336	2034	3155	534	595	18			
1	D	397	Total	C	H	N	O	S	0	0	0
			6242	2000	3107	528	589	18			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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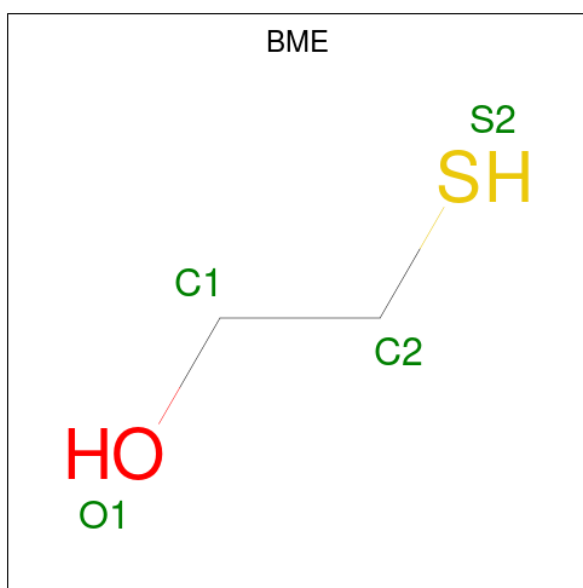
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is BETA-MERCAPTOETHANOL (CCD ID: BME) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	H	O	S	0	0
			10	2	6	1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	39	Total	O	0	0
			39	39		
4	B	32	Total	O	0	0
			32	32		
4	C	25	Total	O	0	0
			25	25		

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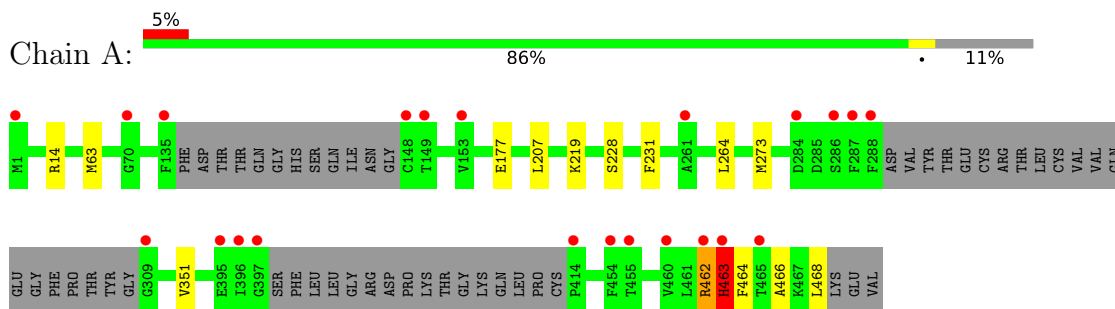
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	17	Total	O	0	0
			17	17		

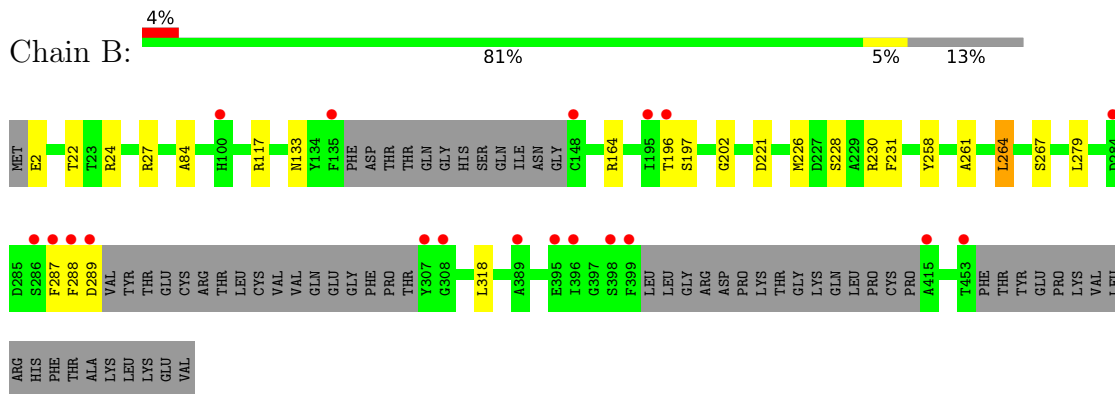
3 Residue-property plots

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.

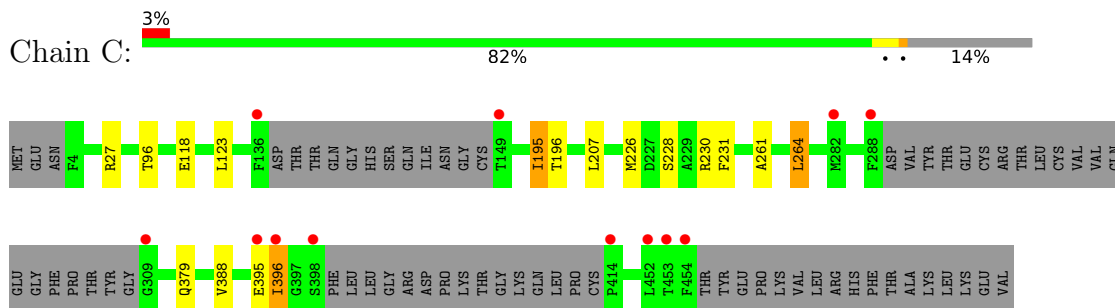
- Molecule 1: TRYPTOPHANASE



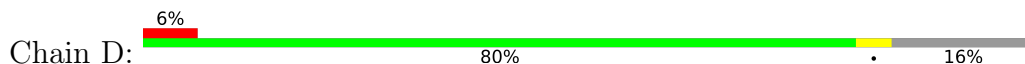
- Molecule 1: TRYPTOPHANASE

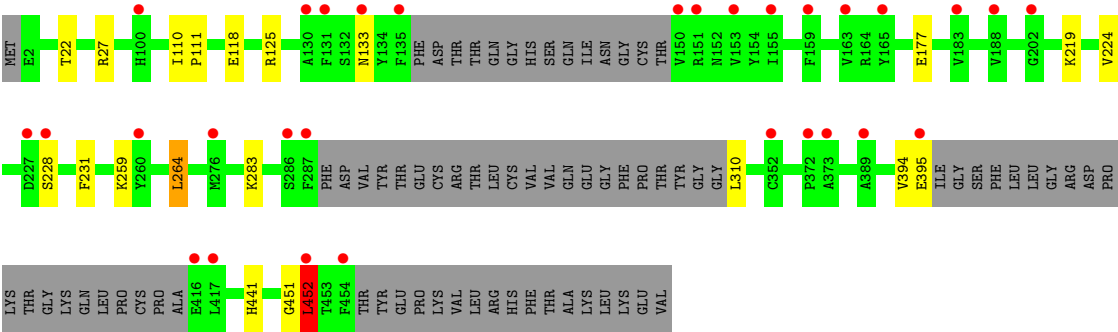


- Molecule 1: TRYPTOPHANASE



- Molecule 1: TRYPTOPHANASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	158.24Å 158.24Å 387.77Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.01 – 2.78 47.01 – 2.78	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.01-2.78) 99.8 (47.01-2.78)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.77Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.215 , 0.246 0.217 , 0.243	Depositor DCC
R_{free} test set	3672 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	56.3	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 34.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	25834	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.95% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BME, SO4

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	0.31	0/3382	0.66	0/4562
1	B	0.29	0/3273	0.65	0/4415
1	C	0.30	0/3245	0.65	0/4377
1	D	0.28	0/3196	0.65	1/4311 (0.0%)
All	All	0.29	0/13096	0.65	1/17665 (0.0%)

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	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	452	LEU	CB-CA-C	-6.82	107.67	115.79

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	462	ARG	Peptide
1	A	463	HIS	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	3315	3297	3297	7	0
1	B	3210	3171	3171	14	0
1	C	3181	3155	3155	10	0
1	D	3135	3107	3107	14	0
2	A	30	0	0	0	0
2	B	40	0	0	1	0
2	C	40	0	0	0	0
2	D	30	0	0	3	0
3	B	4	6	6	0	0
4	A	39	0	0	0	0
4	B	32	0	0	0	0
4	C	25	0	0	0	0
4	D	17	0	0	0	0
All	All	13098	12736	12736	43	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 (43) 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:310:LEU:N	2:D:1459:SO4:S	2.65	0.70
1:A:177:GLU:OE2	1:A:219:LYS:NZ	2.27	0.68
1:A:466:ALA:HB2	1:B:84:ALA:HB1	1.81	0.63
1:D:118:GLU:OE1	1:D:125:ARG:NH2	2.31	0.63
1:D:310:LEU:N	2:D:1459:SO4:O1	2.34	0.61
1:B:117:ARG:NH2	1:B:221:ASP:O	2.39	0.55
1:B:22:THR:O	1:B:27:ARG:NH1	2.40	0.55
1:A:63:MET:HE1	1:A:273:MET:O	2.08	0.54
1:C:264:LEU:C	1:C:264:LEU:HD23	2.32	0.53
1:D:264:LEU:HD23	1:D:264:LEU:C	2.33	0.53
1:D:451:GLY:C	1:D:452:LEU:HD12	2.33	0.53
1:C:27:ARG:NH2	1:C:388:VAL:O	2.42	0.53
1:B:2:GLU:OE2	1:D:441:HIS:ND1	2.42	0.53
1:B:264:LEU:C	1:B:264:LEU:HD23	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:195:ILE:HD13	1:C:226:MET:SD	2.51	0.51
1:B:279:LEU:HD21	1:B:318:LEU:HD21	1.93	0.49
1:A:228:SER:HB2	1:A:231:PHE:HB3	1.94	0.49
1:C:379:GLN:NE2	1:C:395:GLU:OE2	2.46	0.49
1:B:226:MET:HE2	1:B:261:ALA:HB2	1.94	0.48
1:C:196:THR:HG21	1:C:230:ARG:HD2	1.95	0.48
1:B:288:PHE:HA	1:B:289:ASP:C	2.40	0.47
1:D:110:ILE:HB	1:D:111:PRO:HD3	1.95	0.47
1:B:196:THR:HG21	1:B:230:ARG:HD2	1.97	0.46
1:D:133:ASN:OD1	1:D:133:ASN:N	2.48	0.46
1:C:228:SER:HB2	1:C:231:PHE:HB3	1.97	0.46
1:B:24:ARG:N	2:B:1460:SO4:O2	2.49	0.45
1:D:22:THR:O	1:D:27:ARG:NH1	2.48	0.45
1:A:462:ARG:O	1:A:463:HIS:HB2	2.16	0.44
1:A:14:ARG:NE	1:A:14:ARG:HA	2.34	0.43
1:D:394:VAL:HG22	1:D:395:GLU:N	2.34	0.42
1:C:226:MET:HE2	1:C:261:ALA:HB2	2.01	0.42
1:D:310:LEU:N	2:D:1459:SO4:O4	2.52	0.42
1:B:133:ASN:OD1	1:B:133:ASN:N	2.50	0.42
1:D:177:GLU:OE2	1:D:219:LYS:NZ	2.53	0.42
1:C:195:ILE:CG2	1:C:231:PHE:HA	2.50	0.42
1:D:228:SER:HB2	1:D:231:PHE:HB3	2.02	0.41
1:B:197:SER:O	1:B:202:GLY:HA2	2.19	0.41
1:A:264:LEU:HD12	1:A:264:LEU:C	2.45	0.41
1:B:258:TYR:CE2	1:B:264:LEU:HD12	2.55	0.41
1:C:396:ILE:O	1:C:396:ILE:HG22	2.21	0.41
1:B:228:SER:HB2	1:B:231:PHE:HB3	2.02	0.41
1:C:118:GLU:HA	1:C:123:LEU:HB3	2.02	0.41
1:D:259:LYS:O	1:D:283:LYS:NZ	2.54	0.41

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	412/471 (88%)	399 (97%)	11 (3%)	2 (0%)	24	52
1	B	400/471 (85%)	387 (97%)	13 (3%)	0	100	100
1	C	396/471 (84%)	383 (97%)	12 (3%)	1 (0%)	36	63
1	D	389/471 (83%)	376 (97%)	13 (3%)	0	100	100
All	All	1597/1884 (85%)	1545 (97%)	49 (3%)	3 (0%)	43	70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	464	PHE
1	A	463	HIS
1	C	396	ILE

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	346/391 (88%)	342 (99%)	4 (1%)	63	84
1	B	334/391 (85%)	330 (99%)	4 (1%)	63	84
1	C	331/391 (85%)	327 (99%)	4 (1%)	63	84
1	D	327/391 (84%)	324 (99%)	3 (1%)	70	87
All	All	1338/1564 (86%)	1323 (99%)	15 (1%)	65	85

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	207	LEU
1	A	351	VAL
1	A	463	HIS
1	A	468	LEU
1	B	164	ARG
1	B	264	LEU
1	B	267	SER
1	B	287	PHE

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Mol	Chain	Res	Type
1	C	96	THR
1	C	195	ILE
1	C	207	LEU
1	C	264	LEU
1	D	224	VAL
1	D	264	LEU
1	D	452	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	A	152	ASN
1	A	186	ASN
1	A	240	GLN
1	A	339	GLN
1	A	448	ASN
1	A	463	HIS
1	B	61	GLN
1	B	64	GLN
1	C	37	ASN
1	C	240	GLN
1	C	337	GLN
1	C	448	ASN
1	D	61	GLN
1	D	64	GLN
1	D	94	GLN
1	D	379	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 ⓘ

29 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	SO4	B	1455	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	B	1459	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	C	1461	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	D	1459	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	D	1455	-	4,4,4	0.24	0	6,6,6	0.08	0
3	BME	B	1461	-	3,3,3	0.30	0	2,2,2	0.09	0
2	SO4	B	1460	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	B	1456	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	A	1469	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	B	1462	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	B	1458	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	B	1454	-	4,4,4	0.24	0	6,6,6	0.10	0
2	SO4	C	1460	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	D	1456	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	C	1462	-	4,4,4	0.38	0	6,6,6	0.26	0
2	SO4	A	1470	-	4,4,4	0.26	0	6,6,6	0.07	0
2	SO4	A	1473	-	4,4,4	0.23	0	6,6,6	0.09	0
2	SO4	C	1455	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	C	1458	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	C	1459	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	A	1471	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	B	1457	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	A	1472	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	D	1458	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	D	1457	-	4,4,4	0.22	0	6,6,6	0.08	0
2	SO4	D	1460	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	C	1457	-	4,4,4	0.25	0	6,6,6	0.08	0
2	SO4	A	1474	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	C	1456	-	4,4,4	0.24	0	6,6,6	0.09	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
3	BME	B	1461	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1461	BME	O1-C1-C2-S2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1459	SO4	3	0
2	B	1460	SO4	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	420/471 (89%)	0.19	22 (5%)	33 27	30, 54, 95, 126	0
1	B	408/471 (86%)	0.17	19 (4%)	36 31	28, 57, 95, 124	0
1	C	404/471 (85%)	0.18	12 (2%)	52 45	33, 59, 99, 120	0
1	D	397/471 (84%)	0.63	30 (7%)	20 16	37, 80, 129, 140	0
All	All	1629/1884 (86%)	0.29	83 (5%)	33 27	28, 61, 109, 140	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	287	PHE	6.3
1	B	399	PHE	6.0
1	D	135	PHE	5.7
1	A	287	PHE	5.2
1	C	454	PHE	5.1
1	A	414	PRO	5.1
1	D	454	PHE	5.1
1	A	396	ILE	5.0
1	A	148	CYS	4.9
1	A	288	PHE	4.9
1	B	289	ASP	4.9
1	B	148	CYS	4.8
1	B	396	ILE	4.7
1	C	136	PHE	4.4
1	A	309	GLY	4.2
1	C	288	PHE	4.1
1	A	454	PHE	3.9
1	B	135	PHE	3.8
1	A	1	MET	3.7
1	D	130	ALA	3.6
1	C	398	SER	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	131	PHE	3.4
1	C	309	GLY	3.3
1	B	453	THR	3.3
1	D	150	VAL	3.2
1	B	288	PHE	3.2
1	A	135	PHE	3.1
1	A	397	GLY	3.1
1	B	307	TYR	3.1
1	A	465	THR	3.1
1	B	308	GLY	3.1
1	B	389	ALA	3.0
1	D	155	ILE	3.0
1	A	286	SER	2.9
1	C	149	THR	2.9
1	D	227	ASP	2.9
1	A	462	ARG	2.8
1	B	398	SER	2.8
1	C	396	ILE	2.8
1	A	284	ASP	2.8
1	D	417	LEU	2.7
1	A	463	HIS	2.7
1	D	286	SER	2.7
1	D	276	MET	2.6
1	D	165	TYR	2.6
1	A	460	VAL	2.6
1	B	284	ASP	2.6
1	B	287	PHE	2.6
1	D	395	GLU	2.5
1	D	133	ASN	2.5
1	D	228	SER	2.5
1	D	452	LEU	2.5
1	A	70	GLY	2.5
1	B	415	ALA	2.5
1	D	153	VAL	2.5
1	C	282	MET	2.5
1	C	414	PRO	2.5
1	D	159	PHE	2.5
1	D	260	TYR	2.4
1	A	153	VAL	2.4
1	D	352	CYS	2.4
1	A	395	GLU	2.4
1	D	202	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	163	VAL	2.3
1	A	261	ALA	2.3
1	D	151	ARG	2.3
1	B	195	ILE	2.3
1	C	452	LEU	2.3
1	C	453	THR	2.2
1	D	416	GLU	2.2
1	D	372	PRO	2.2
1	D	389	ALA	2.2
1	C	395	GLU	2.2
1	B	196	THR	2.1
1	D	100	HIS	2.1
1	B	395	GLU	2.1
1	B	100	HIS	2.1
1	D	188	VAL	2.1
1	A	149	THR	2.0
1	A	455	THR	2.0
1	D	183	VAL	2.0
1	D	373	ALA	2.0
1	B	286	SER	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
2	SO4	D	1460	5/5	0.36	0.20	176,177,241,283	0
2	SO4	B	1456	5/5	0.59	0.10	113,113,132,141	0
2	SO4	C	1460	5/5	0.60	0.09	121,124,129,132	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	B	1460	5/5	0.60	0.15	120,121,184,253	0
2	SO4	D	1459	5/5	0.65	0.13	93,111,116,141	0
2	SO4	C	1462	5/5	0.66	0.16	69,74,81,151	0
2	SO4	B	1459	5/5	0.69	0.27	123,132,156,271	0
2	SO4	B	1457	5/5	0.69	0.11	102,113,117,137	0
2	SO4	C	1458	5/5	0.70	0.21	83,87,110,111	0
2	SO4	A	1472	5/5	0.74	0.19	67,83,120,123	0
2	SO4	A	1473	5/5	0.76	0.26	90,92,118,129	0
2	SO4	C	1459	5/5	0.76	0.16	94,95,119,127	0
2	SO4	A	1474	5/5	0.81	0.21	91,99,111,123	0
2	SO4	C	1457	5/5	0.81	0.13	84,95,120,123	0
2	SO4	C	1461	5/5	0.82	0.32	84,88,107,125	0
2	SO4	D	1455	5/5	0.85	0.38	82,88,114,116	0
2	SO4	B	1455	5/5	0.87	0.18	61,81,97,118	0
2	SO4	D	1457	5/5	0.88	0.24	69,81,110,112	0
2	SO4	C	1455	5/5	0.89	0.26	84,86,104,110	0
2	SO4	A	1470	5/5	0.89	0.14	60,64,83,109	0
2	SO4	D	1456	5/5	0.89	0.14	69,81,105,117	0
2	SO4	B	1462	5/5	0.90	0.20	120,137,146,194	0
2	SO4	D	1458	5/5	0.90	0.13	80,92,94,99	0
2	SO4	A	1471	5/5	0.91	0.21	56,62,87,100	0
2	SO4	C	1456	5/5	0.91	0.09	57,80,88,91	0
2	SO4	B	1454	5/5	0.92	0.11	52,58,65,95	0
2	SO4	B	1458	5/5	0.93	0.09	67,79,81,85	0
3	BME	B	1461	4/4	0.93	0.10	46,60,70,74	0
2	SO4	A	1469	5/5	0.95	0.07	64,68,70,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.