



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 11:07 pm BST

PDB ID : 3UK1
Title : Crystal structure of a transketolase from Burkholderia thailandensis with an oxidized cysteinesulfonic acid in the active site
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2011-11-08
Resolution : 2.15 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 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 : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

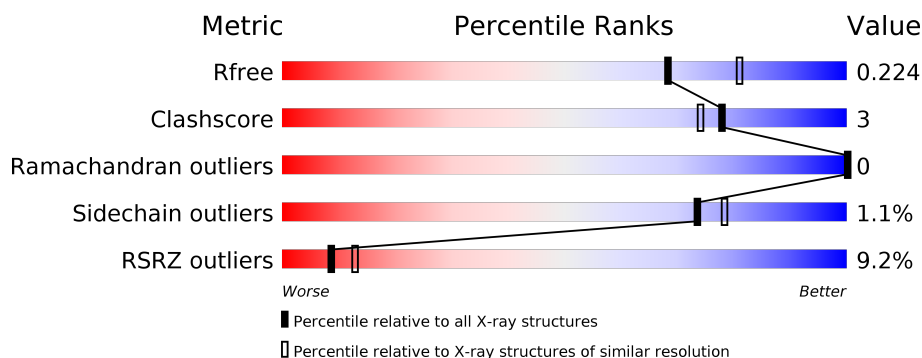
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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 on 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	711	<div> <div>9%</div> <div>85%</div> <div>6%</div> <div>8%</div> </div>
1	B	711	<div> <div>8%</div> <div>85%</div> <div>9%</div> <div>6%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10538 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 Transketolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	651	Total	C	N	O	S	0	1	0
			4894	3096	864	916	18			
1	B	669	Total	C	N	O	S	0	0	0
			4991	3150	887	936	18			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	EXPRESSION TAG	UNP Q2SZA7
A	-19	ALA	-	EXPRESSION TAG	UNP Q2SZA7
A	-18	HIS	-	EXPRESSION TAG	UNP Q2SZA7
A	-17	HIS	-	EXPRESSION TAG	UNP Q2SZA7
A	-16	HIS	-	EXPRESSION TAG	UNP Q2SZA7
A	-15	HIS	-	EXPRESSION TAG	UNP Q2SZA7
A	-14	HIS	-	EXPRESSION TAG	UNP Q2SZA7
A	-13	HIS	-	EXPRESSION TAG	UNP Q2SZA7
A	-12	MET	-	EXPRESSION TAG	UNP Q2SZA7
A	-11	GLY	-	EXPRESSION TAG	UNP Q2SZA7
A	-10	THR	-	EXPRESSION TAG	UNP Q2SZA7
A	-9	LEU	-	EXPRESSION TAG	UNP Q2SZA7
A	-8	GLU	-	EXPRESSION TAG	UNP Q2SZA7
A	-7	ALA	-	EXPRESSION TAG	UNP Q2SZA7
A	-6	GLN	-	EXPRESSION TAG	UNP Q2SZA7
A	-5	THR	-	EXPRESSION TAG	UNP Q2SZA7
A	-4	GLN	-	EXPRESSION TAG	UNP Q2SZA7
A	-3	GLY	-	EXPRESSION TAG	UNP Q2SZA7
A	-2	PRO	-	EXPRESSION TAG	UNP Q2SZA7
A	-1	GLY	-	EXPRESSION TAG	UNP Q2SZA7
A	0	SER	-	EXPRESSION TAG	UNP Q2SZA7
B	-20	MET	-	EXPRESSION TAG	UNP Q2SZA7
B	-19	ALA	-	EXPRESSION TAG	UNP Q2SZA7
B	-18	HIS	-	EXPRESSION TAG	UNP Q2SZA7
B	-17	HIS	-	EXPRESSION TAG	UNP Q2SZA7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	HIS	-	EXPRESSION TAG	UNP Q2SZA7
B	-15	HIS	-	EXPRESSION TAG	UNP Q2SZA7
B	-14	HIS	-	EXPRESSION TAG	UNP Q2SZA7
B	-13	HIS	-	EXPRESSION TAG	UNP Q2SZA7
B	-12	MET	-	EXPRESSION TAG	UNP Q2SZA7
B	-11	GLY	-	EXPRESSION TAG	UNP Q2SZA7
B	-10	THR	-	EXPRESSION TAG	UNP Q2SZA7
B	-9	LEU	-	EXPRESSION TAG	UNP Q2SZA7
B	-8	GLU	-	EXPRESSION TAG	UNP Q2SZA7
B	-7	ALA	-	EXPRESSION TAG	UNP Q2SZA7
B	-6	GLN	-	EXPRESSION TAG	UNP Q2SZA7
B	-5	THR	-	EXPRESSION TAG	UNP Q2SZA7
B	-4	GLN	-	EXPRESSION TAG	UNP Q2SZA7
B	-3	GLY	-	EXPRESSION TAG	UNP Q2SZA7
B	-2	PRO	-	EXPRESSION TAG	UNP Q2SZA7
B	-1	GLY	-	EXPRESSION TAG	UNP Q2SZA7
B	0	SER	-	EXPRESSION TAG	UNP Q2SZA7

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Cl 1	0	0

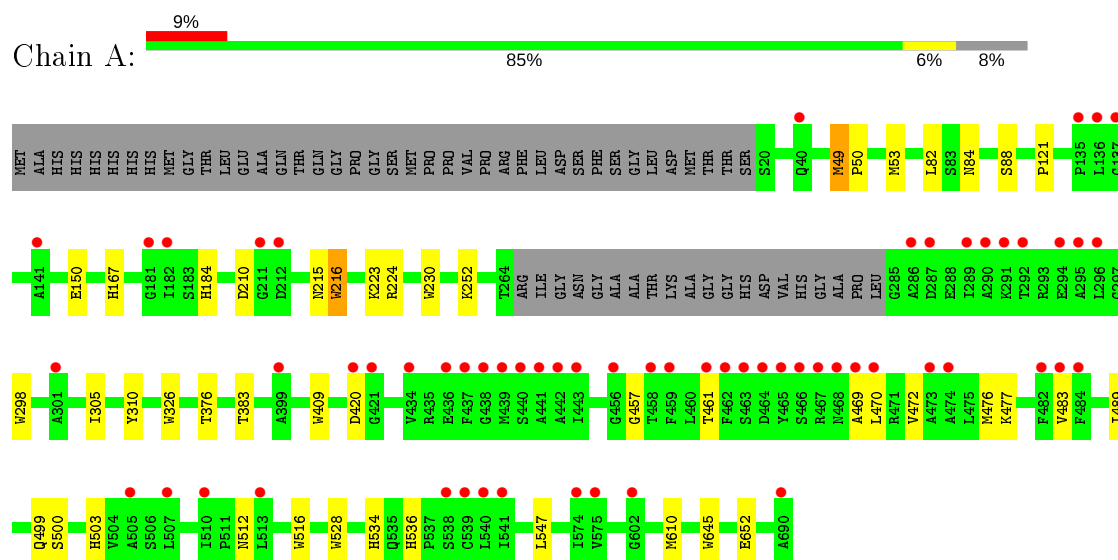
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	410	Total 410	O 410	0	0
4	B	232	Total 232	O 232	0	0

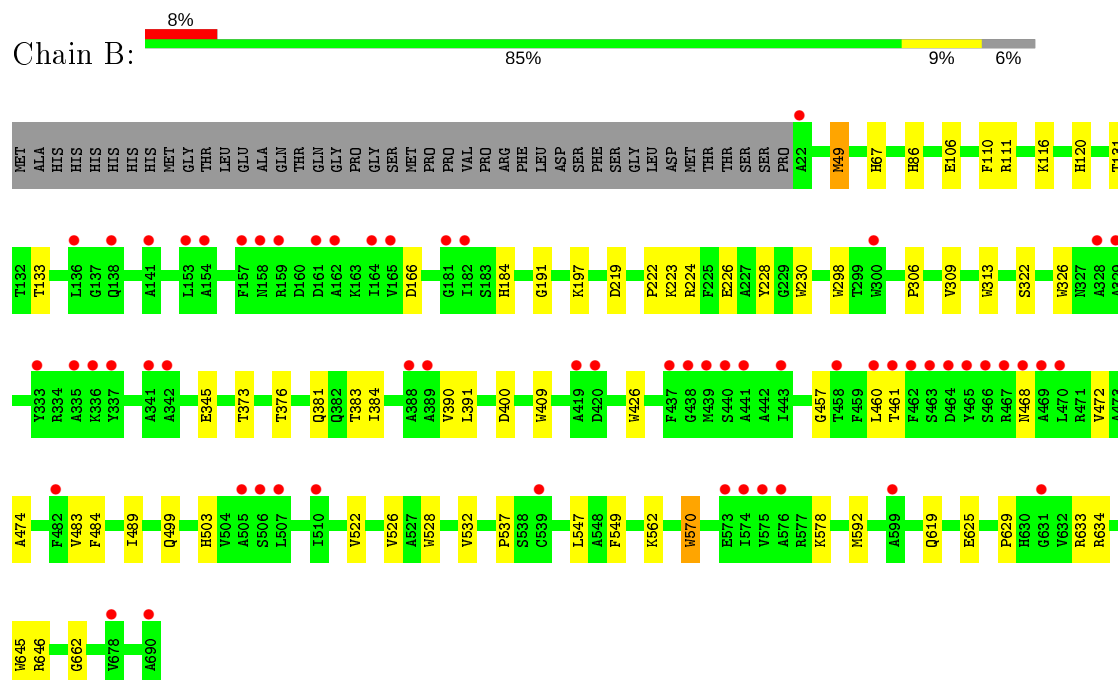
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Transketolase



• Molecule 1: Transketolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	145.35Å 145.35Å 142.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.15 47.95 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.00-2.15) 99.2 (47.95-2.15)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.48 (at 2.16Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.185 , 0.225 0.184 , 0.224	Depositor DCC
R_{free} test set	4121 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.025 for -h,-l,-k 0.024 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10538	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.87% 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: OCS, SO4, CL

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	0.77	6/5004 (0.1%)	0.76	0/6818
1	B	0.69	8/5103 (0.2%)	0.71	1/6958 (0.0%)
All	All	0.73	14/10107 (0.1%)	0.74	1/13776 (0.0%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	516	TRP	CD2-CE2	5.82	1.48	1.41
1	B	645	TRP	CD2-CE2	5.60	1.48	1.41
1	B	230	TRP	CD2-CE2	5.57	1.48	1.41
1	B	313	TRP	CD2-CE2	5.45	1.47	1.41
1	B	426	TRP	CD2-CE2	5.43	1.47	1.41
1	A	216	TRP	CD2-CE2	5.39	1.47	1.41
1	A	409	TRP	CD2-CE2	5.38	1.47	1.41
1	A	298	TRP	CD2-CE2	5.33	1.47	1.41
1	A	230	TRP	CD2-CE2	5.32	1.47	1.41
1	B	409	TRP	CD2-CE2	5.16	1.47	1.41
1	A	326	TRP	CD2-CE2	5.09	1.47	1.41
1	B	570	TRP	CD2-CE2	5.08	1.47	1.41
1	B	326	TRP	CD2-CE2	5.06	1.47	1.41
1	B	298	TRP	CD2-CE2	5.03	1.47	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	219	ASP	CB-CG-OD2	-5.16	113.65	118.30

There are no chirality outliers.

There are no planarity outliers.

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	4894	0	4713	29	0
1	B	4991	0	4769	34	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	B	1	0	0	0	0
4	A	410	0	0	3	0
4	B	232	0	0	0	0
All	All	10538	0	9482	57	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.

All (57) 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:373:THR:HG22	1:B:549:PHE:H	1.23	1.03
1:A:252:LYS:HE2	4:A:921:HOH:O	1.83	0.77
1:A:610:MET:HE1	1:A:645:TRP:HZ3	1.51	0.74
1:A:223:LYS:HE2	1:B:226:GLU:HB2	1.71	0.71
1:A:610:MET:HE1	1:A:645:TRP:CZ3	2.29	0.67
1:A:223:LYS:HE3	1:B:223:LYS:HG3	1.78	0.66
1:B:373:THR:HG22	1:B:549:PHE:N	2.06	0.62
1:B:222:PRO:O	1:B:226:GLU:HG3	2.02	0.59
1:A:150:GLU:HG3	1:A:167:HIS:CD2	2.39	0.57
1:B:376:THR:HG23	1:B:547:LEU:HD12	1.87	0.57
1:A:472:VAL:HG11	4:A:903:HOH:O	2.06	0.56
1:A:376:THR:HG23	1:A:547:LEU:HD12	1.87	0.56
1:A:652:GLU:OE1	1:A:652:GLU:N	2.25	0.55
1:A:210:ASP:HB2	1:B:400:ASP:OD1	2.09	0.53
1:A:215:ASN:HB2	1:A:216:TRP:CE3	2.43	0.53
1:A:610:MET:CE	1:A:645:TRP:CZ3	2.91	0.53
1:B:306:PRO:HG2	1:B:309:VAL:HG23	1.91	0.53
1:A:223:LYS:HG3	1:B:223:LYS:HE3	1.90	0.53
1:A:49:MET:HE3	1:A:82:LEU:HD11	1.93	0.50
1:A:469:ALA:HA	1:A:472:VAL:HG12	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:489:ILE:HA	1:A:499:GLN:HG2	1.92	0.50
1:B:49:MET:C	1:B:49:MET:SD	2.91	0.49
1:B:489:ILE:HA	1:B:499:GLN:HG2	1.93	0.49
1:A:305:ILE:HB	1:A:310:TYR:CE2	2.48	0.48
1:B:166:ASP:OD1	1:B:197:LYS:NZ	2.44	0.48
1:B:381:GLN:HA	1:B:384:ILE:HD12	1.96	0.48
1:B:570:TRP:CD2	1:B:578:LYS:HE3	2.49	0.47
1:A:534:HIS:HB2	4:A:789:HOH:O	2.15	0.47
1:A:476:MET:O	1:A:477:LYS:HB2	2.16	0.45
1:A:49:MET:C	1:A:49:MET:SD	2.95	0.45
1:A:88:SER:HB3	1:A:121:PRO:HD3	1.98	0.45
1:B:625:GLU:OE2	1:B:629:PRO:HA	2.17	0.44
1:A:184:HIS:CE1	1:B:224:ARG:CZ	3.01	0.44
1:A:512:ASN:OD1	1:A:536:HIS:ND1	2.51	0.44
1:A:461:THR:HG23	1:A:503:HIS:CE1	2.52	0.44
1:A:224:ARG:CZ	1:B:184:HIS:CE1	3.01	0.44
1:B:468:ASN:O	1:B:472:VAL:HG23	2.18	0.43
1:B:562:LYS:HA	1:B:619:GLN:NE2	2.33	0.43
1:B:461:THR:HG23	1:B:503:HIS:CE1	2.54	0.43
1:B:106:GLU:HG3	1:B:116:LYS:HD2	2.00	0.43
1:B:474:ALA:HA	1:B:537:PRO:HG3	2.01	0.42
1:B:633:ARG:C	1:B:634:ARG:HG3	2.39	0.42
1:B:391:LEU:HD11	1:B:532:VAL:HG11	2.00	0.42
1:A:49:MET:HB3	1:A:50:PRO:HD3	2.01	0.42
1:B:457:GLY:HA2	1:B:483:VAL:O	2.20	0.42
1:A:49:MET:HE1	1:A:53:MET:SD	2.60	0.42
1:B:110:PHE:CE2	1:B:111:ARG:HD2	2.55	0.41
1:B:522:VAL:O	1:B:526:VAL:HG23	2.20	0.41
1:B:646:ARG:HA	1:B:646:ARG:HD3	1.92	0.41
1:B:191:GLY:HA3	1:B:228:TYR:O	2.19	0.41
1:A:457:GLY:HA2	1:A:483:VAL:O	2.21	0.41
1:B:86:HIS:HA	1:B:120:HIS:CD2	2.55	0.41
1:B:131:THR:HG23	1:B:133:THR:HG23	2.04	0.40
1:B:499:GLN:OE1	1:B:662:GLY:HA3	2.21	0.40
1:B:460:LEU:HA	1:B:484:PHE:HB3	2.04	0.40
1:A:383:THR:HG21	1:A:528:TRP:HB2	2.03	0.40
1:B:383:THR:HG21	1:B:528:TRP:HB2	2.04	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	647/711 (91%)	631 (98%)	16 (2%)	0	100	100
1	B	666/711 (94%)	647 (97%)	19 (3%)	0	100	100
All	All	1313/1422 (92%)	1278 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	482/547 (88%)	477 (99%)	5 (1%)	76	81
1	B	486/547 (89%)	480 (99%)	6 (1%)	71	76
All	All	968/1094 (88%)	957 (99%)	11 (1%)	73	78

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	MET
1	A	84	ASN
1	A	420	ASP
1	A	470	LEU
1	A	500	SER
1	B	49	MET
1	B	67	HIS
1	B	322	SER

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Mol	Chain	Res	Type
1	B	345	GLU
1	B	390	VAL
1	B	592	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	231	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	OCS	A	177	1	7,8,9	2.09	2 (28%)	6,11,13	2.31	1 (16%)
1	OCS	B	177	1	7,8,9	2.03	2 (28%)	6,11,13	2.48	2 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OCS	A	177	1	-	0/4/7/9	-
1	OCS	B	177	1	-	0/4/7/9	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	177	OCS	OD2-SG	4.42	1.63	1.47
1	B	177	OCS	OD2-SG	3.93	1.61	1.47
1	B	177	OCS	CB-SG	-2.98	1.66	1.77
1	A	177	OCS	CB-CA	2.53	1.56	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	177	OCS	OD2-SG-CB	5.32	114.22	105.74
1	B	177	OCS	OD1-SG-CB	4.56	112.36	106.94
1	B	177	OCS	OD2-SG-CB	3.25	110.93	105.74

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z > 2$
2	SO4	A	691	-	4,4,4	0.22	0	6,6,6	1.01	0
2	SO4	B	691	-	4,4,4	0.34	0	6,6,6	0.38	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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 ⓘ

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	650/711 (91%)	0.28	61 (9%) 8 12	20, 29, 49, 70	0
1	B	668/711 (93%)	0.34	60 (8%) 9 14	25, 39, 60, 97	0
All	All	1318/1422 (92%)	0.31	121 (9%) 9 13	20, 34, 57, 97	0

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	162	ALA	6.0
1	B	575	VAL	4.7
1	A	470	LEU	4.7
1	A	437	PHE	4.6
1	A	182	ILE	4.6
1	B	182	ILE	4.5
1	B	437	PHE	4.3
1	B	470	LEU	4.2
1	A	290	ALA	3.9
1	A	465	TYR	3.9
1	A	286	ALA	3.8
1	A	482	PHE	3.8
1	A	466	SER	3.8
1	B	574	ILE	3.7
1	A	462	PHE	3.7
1	B	419	ALA	3.7
1	A	574	ILE	3.6
1	A	575	VAL	3.6
1	A	443	ILE	3.5
1	A	211	GLY	3.5
1	A	421	GLY	3.5
1	A	507	LEU	3.5
1	A	295	ALA	3.4
1	B	465	TYR	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	573	GLU	3.4
1	A	510	ILE	3.3
1	B	631	GLY	3.3
1	A	469	ALA	3.3
1	A	294	GLU	3.3
1	B	576	ALA	3.2
1	A	441	ALA	3.2
1	A	292	THR	3.2
1	A	690	ALA	3.2
1	B	153	LEU	3.1
1	A	458	THR	3.1
1	A	463	SER	3.1
1	B	154	ALA	3.1
1	A	434	VAL	3.1
1	B	420	ASP	3.0
1	B	159	ARG	3.0
1	B	181	GLY	2.9
1	B	468	ASN	2.9
1	B	505	ALA	2.9
1	A	439	MET	2.9
1	B	460	LEU	2.9
1	A	467	ARG	2.9
1	B	342	ALA	2.9
1	B	462	PHE	2.9
1	A	301	ALA	2.9
1	B	337	TYR	2.9
1	A	136	LEU	2.9
1	B	389	ALA	2.8
1	B	467	ARG	2.8
1	B	469	ALA	2.8
1	A	181	GLY	2.8
1	A	484	PHE	2.8
1	B	440	SER	2.8
1	A	420	ASP	2.7
1	B	333	TYR	2.7
1	B	164	ILE	2.7
1	A	135	PRO	2.7
1	B	461	THR	2.7
1	B	507	LEU	2.7
1	A	483	VAL	2.6
1	A	440	SER	2.6
1	A	212	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	161	ASP	2.6
1	A	399	ALA	2.6
1	B	328	ALA	2.6
1	A	539	CYS	2.6
1	A	296	LEU	2.6
1	B	136	LEU	2.6
1	B	22	ALA	2.5
1	B	466	SER	2.5
1	B	599	ALA	2.5
1	B	690	ALA	2.5
1	A	468	ASN	2.5
1	B	141	ALA	2.5
1	A	505	ALA	2.5
1	A	513	LEU	2.4
1	B	678	VAL	2.4
1	A	442	ALA	2.4
1	B	335	ALA	2.4
1	A	438	GLY	2.4
1	A	464	ASP	2.4
1	A	473	ALA	2.4
1	B	158	ASN	2.3
1	B	341	ALA	2.3
1	B	464	ASP	2.3
1	B	539	CYS	2.3
1	A	538	SER	2.3
1	A	474	ALA	2.3
1	B	439	MET	2.3
1	A	541	ILE	2.3
1	B	463	SER	2.3
1	A	40	GLN	2.3
1	A	540	LEU	2.3
1	A	141	ALA	2.2
1	A	459	PHE	2.2
1	B	157	PHE	2.2
1	A	456	GLY	2.2
1	B	300	TRP	2.2
1	A	287	ASP	2.2
1	B	388	ALA	2.2
1	B	482	PHE	2.2
1	B	441	ALA	2.2
1	A	436	GLU	2.2
1	A	289	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	438	GLY	2.2
1	B	443	ILE	2.1
1	B	336	LYS	2.1
1	A	602	GLY	2.1
1	A	461	THR	2.1
1	B	510	ILE	2.1
1	B	138	GLN	2.1
1	B	506	SER	2.1
1	B	165	VAL	2.1
1	B	458	THR	2.1
1	A	291	LYS	2.1
1	A	137	GLY	2.0
1	B	329	ALA	2.0

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	OCS	B	177	9/10	0.96	0.12	26,29,38,42	0
1	OCS	A	177	9/10	0.98	0.13	25,27,30,32	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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(Å ²)	Q<0.9
2	SO4	B	691	5/5	0.97	0.09	51,53,57,65	0
2	SO4	A	691	5/5	0.98	0.12	39,40,42,47	0
3	CL	B	692	1/1	0.98	0.26	52,52,52,52	0

6.5 Other polymers ⓘ

There are no such residues in this entry.