



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 23, 2026 – 06:59 AM UTC

PDB ID : 7DLV / pdb_00007dlv
Title : shrimp dUTPase in complex with Stl
Authors : Ma, Q.; Wang, F.
Deposited on : 2020-11-30
Resolution : 2.52 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 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

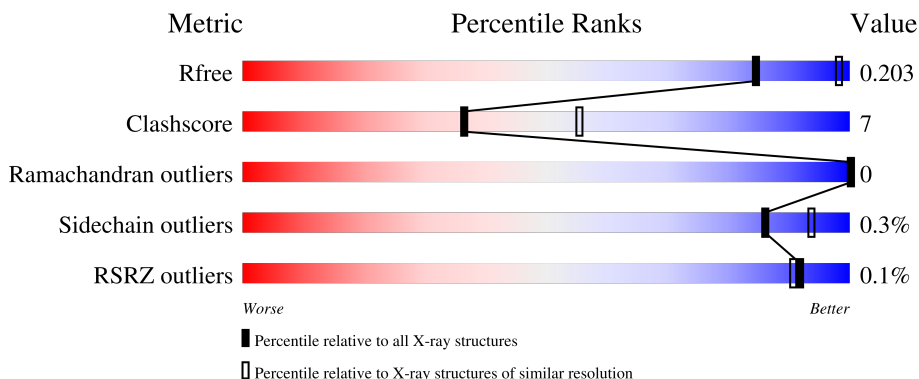
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

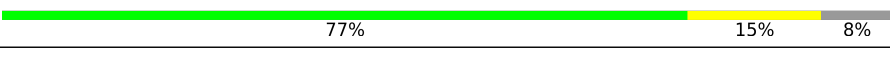
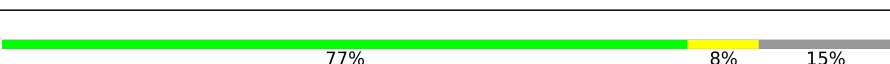
The reported resolution of this entry is 2.52 Å.

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	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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	149	 77% 11% 12%
1	B	149	 77% 15% 8%
1	C	149	 74% 17% 9%
1	G	149	 73% 17% 9%
1	H	149	 77% 8% 15%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	I	149	 70%21%9%
2	D	157	 75%17%8%
2	E	157	 73%17%10%
2	F	157	 75%16%9%
2	J	157	 82%11%7%
2	K	157	 78%13%8%
2	L	157	 72%19%9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13439 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 shrimp dUTPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	131	Total	C	N	O	S	0	0	0
			1029	657	178	190	4			
1	B	137	Total	C	N	O	S	0	0	0
			1065	679	184	198	4			
1	C	136	Total	C	N	O	S	0	0	0
			1061	677	183	197	4			
1	G	136	Total	C	N	O	S	0	0	0
			1061	677	183	197	4			
1	H	127	Total	C	N	O	S	0	0	0
			993	637	171	181	4			
1	I	136	Total	C	N	O	S	0	0	0
			1061	677	183	197	4			

- Molecule 2 is a protein called Orf20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	144	Total	C	N	O	S	0	0	0
			1191	766	191	232	2			
2	E	141	Total	C	N	O	S	0	0	0
			1169	751	188	228	2			
2	F	143	Total	C	N	O	S	0	0	0
			1183	760	190	231	2			
2	J	146	Total	C	N	O	S	0	0	0
			1205	774	193	236	2			
2	K	144	Total	C	N	O	S	0	0	0
			1191	766	191	232	2			
2	L	143	Total	C	N	O	S	0	0	0
			1183	760	190	231	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	GLY	-	expression tag	UNP Q9F0J8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	ALA	-	expression tag	UNP Q9F0J8
E	-1	GLY	-	expression tag	UNP Q9F0J8
E	0	ALA	-	expression tag	UNP Q9F0J8
F	-1	GLY	-	expression tag	UNP Q9F0J8
F	0	ALA	-	expression tag	UNP Q9F0J8
J	-1	GLY	-	expression tag	UNP Q9F0J8
J	0	ALA	-	expression tag	UNP Q9F0J8
K	-1	GLY	-	expression tag	UNP Q9F0J8
K	0	ALA	-	expression tag	UNP Q9F0J8
L	-1	GLY	-	expression tag	UNP Q9F0J8
L	0	ALA	-	expression tag	UNP Q9F0J8

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



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

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		

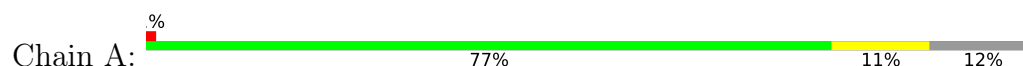
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	H	1	Total	Ca	0	0
			1	1		

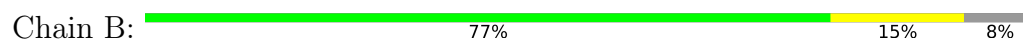
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

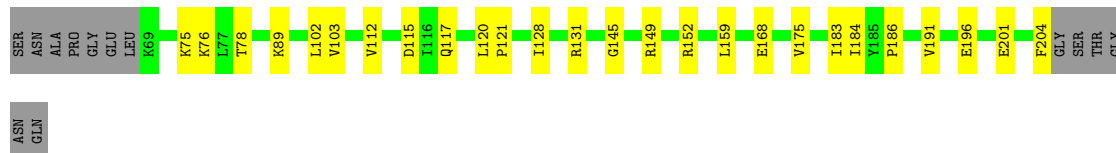
- Molecule 1: shrimp dUTPase



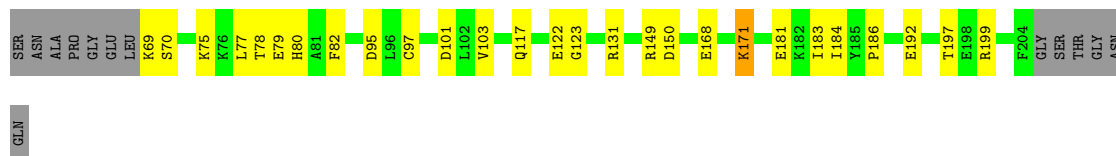
- Molecule 1: shrimp dUTPase



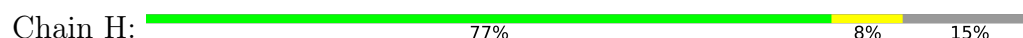
- Molecule 1: shrimp dUTPase



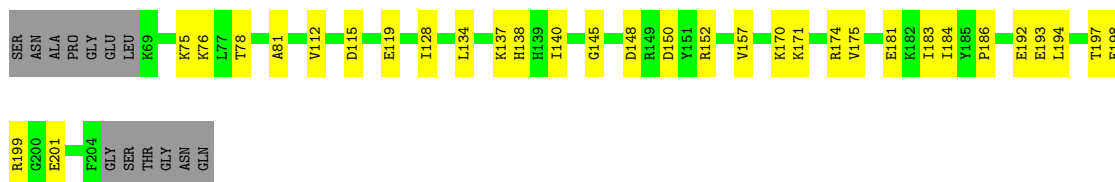
- Molecule 1: shrimp dUTPase



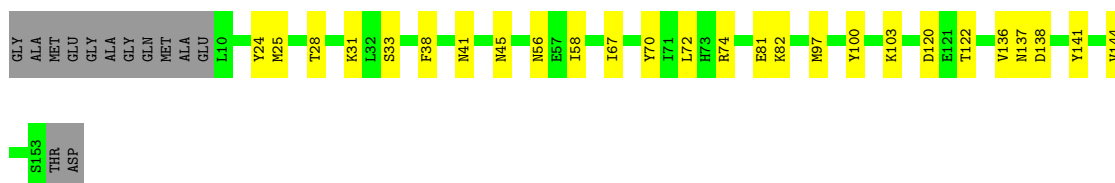
- Molecule 1: shrimp dUTPase



- Molecule 1: shrimp dUTPase



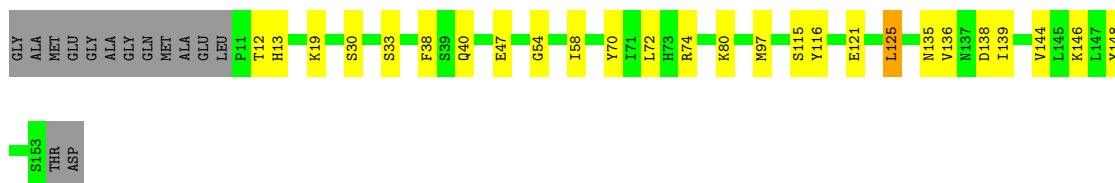
- Molecule 2: Orf20



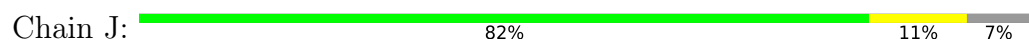
- Molecule 2: Orf20



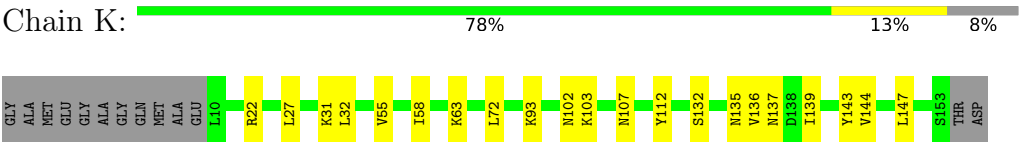
- Molecule 2: Orf20



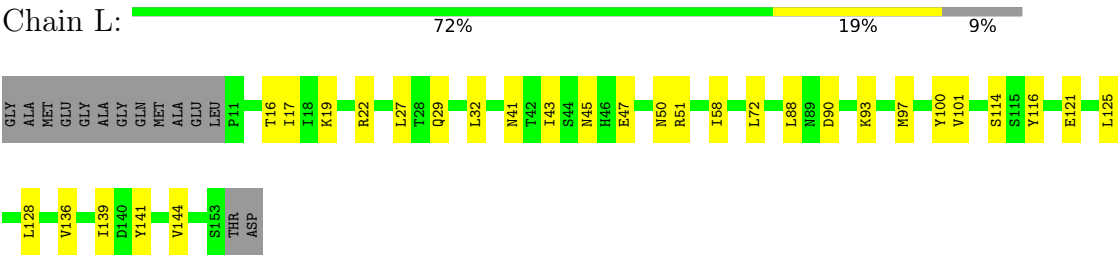
- Molecule 2: Orf20



● Molecule 2: Orf20



● Molecule 2: Orf20



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.70Å 135.88Å 135.63Å 90.00° 105.79° 90.00°	Depositor
Resolution (Å)	94.13 – 2.52 94.13 – 2.52	Depositor EDS
% Data completeness (in resolution range)	98.8 (94.13-2.52) 97.9 (94.13-2.52)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.172 , 0.201 0.173 , 0.203	Depositor DCC
R_{free} test set	4411 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	58.7	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.449 for h,-k,-h-l	Xtriage
Reported twinning fraction	0.480 for -h,-k,h+l	Depositor
Outliers	0 of 86385 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13439	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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, CA

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	0.15	0/1049	0.40	0/1414
1	B	0.12	0/1086	0.32	0/1462
1	C	0.13	0/1082	0.35	0/1457
1	G	0.14	0/1082	0.32	0/1457
1	H	0.11	0/1013	0.31	0/1366
1	I	0.16	0/1082	0.37	0/1457
2	D	0.13	0/1216	0.34	0/1638
2	E	0.17	0/1193	0.45	0/1605
2	F	0.11	0/1208	0.31	0/1626
2	J	0.11	0/1230	0.31	0/1657
2	K	0.17	0/1216	0.35	0/1638
2	L	0.21	0/1208	0.45	2/1626 (0.1%)
All	All	0.15	0/13665	0.36	2/18403 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	51	ARG	CA-C-N	-6.07	109.83	122.03
2	L	51	ARG	C-N-CA	-6.07	109.83	122.03

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	1029	0	1041	13	0
1	B	1065	0	1068	17	0
1	C	1061	0	1065	19	0
1	G	1061	0	1065	27	0
1	H	993	0	1009	10	0
1	I	1061	0	1065	33	0
2	D	1191	0	1176	19	0
2	E	1169	0	1151	22	0
2	F	1183	0	1166	17	0
2	J	1205	0	1187	11	0
2	K	1191	0	1176	17	0
2	L	1183	0	1166	21	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	1	0
3	F	5	0	0	0	0
3	G	5	0	0	0	0
3	H	10	0	0	0	0
3	J	5	0	0	0	0
3	K	5	0	0	0	0
4	A	1	0	0	0	0
4	H	1	0	0	0	0
All	All	13439	0	13335	192	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 7.

The worst 5 of 192 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)
2:L:97:MET:HE2	2:L:125:LEU:HD23	1.52	0.91
1:G:199:ARG:NH1	2:K:102:ASN:OD1	2.11	0.84
1:G:192:GLU:O	1:I:75:LYS:NZ	2.10	0.83
2:L:121:GLU:O	2:L:125:LEU:HD13	1.79	0.82
1:G:192:GLU:C	1:I:75:LYS:HZ1	1.86	0.82

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	129/149 (87%)	125 (97%)	4 (3%)	0	100	100
1	B	135/149 (91%)	129 (96%)	6 (4%)	0	100	100
1	C	134/149 (90%)	128 (96%)	6 (4%)	0	100	100
1	G	134/149 (90%)	130 (97%)	4 (3%)	0	100	100
1	H	125/149 (84%)	121 (97%)	4 (3%)	0	100	100
1	I	134/149 (90%)	129 (96%)	5 (4%)	0	100	100
2	D	142/157 (90%)	137 (96%)	5 (4%)	0	100	100
2	E	139/157 (88%)	134 (96%)	5 (4%)	0	100	100
2	F	141/157 (90%)	135 (96%)	6 (4%)	0	100	100
2	J	144/157 (92%)	141 (98%)	3 (2%)	0	100	100
2	K	142/157 (90%)	138 (97%)	4 (3%)	0	100	100
2	L	141/157 (90%)	138 (98%)	3 (2%)	0	100	100
All	All	1640/1836 (89%)	1585 (97%)	55 (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	110/121 (91%)	109 (99%)	1 (1%)	70	86
1	B	112/121 (93%)	112 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	112/121 (93%)	112 (100%)	0	100	100
1	G	112/121 (93%)	111 (99%)	1 (1%)	70	86
1	H	106/121 (88%)	106 (100%)	0	100	100
1	I	112/121 (93%)	111 (99%)	1 (1%)	70	86
2	D	133/140 (95%)	133 (100%)	0	100	100
2	E	130/140 (93%)	130 (100%)	0	100	100
2	F	132/140 (94%)	130 (98%)	2 (2%)	57	79
2	J	134/140 (96%)	134 (100%)	0	100	100
2	K	133/140 (95%)	133 (100%)	0	100	100
2	L	132/140 (94%)	132 (100%)	0	100	100
All	All	1458/1566 (93%)	1453 (100%)	5 (0%)	86	94

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	149	ARG
2	F	125	LEU
2	F	146	LYS
1	G	171	LYS
1	I	150	ASP

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

Mol	Chain	Res	Type
2	D	137	ASN
2	F	40	GLN
2	F	50	ASN
2	K	48	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	H	301	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	F	201	-	4,4,4	0.24	0	6,6,6	0.06	0
3	SO4	J	201	-	4,4,4	0.25	0	6,6,6	0.09	0
3	SO4	H	302	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	K	201	-	4,4,4	0.24	0	6,6,6	0.09	0
3	SO4	A	301	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	B	301	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	C	301	-	4,4,4	0.23	0	6,6,6	0.10	0
3	SO4	G	301	-	4,4,4	0.23	0	6,6,6	0.08	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	301	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	131/149 (87%)	-0.46	1 (0%) 82 80	35, 52, 81, 124	0
1	B	137/149 (91%)	-0.48	0 100 100	43, 59, 84, 127	0
1	C	136/149 (91%)	-0.50	0 100 100	37, 57, 90, 125	0
1	G	136/149 (91%)	-0.51	0 100 100	38, 59, 91, 116	0
1	H	127/149 (85%)	-0.53	0 100 100	35, 50, 71, 92	0
1	I	136/149 (91%)	-0.48	0 100 100	36, 57, 85, 117	0
2	D	144/157 (91%)	-0.47	0 100 100	44, 62, 94, 114	0
2	E	141/157 (89%)	-0.21	0 100 100	53, 86, 115, 150	0
2	F	143/157 (91%)	-0.55	0 100 100	39, 51, 79, 101	0
2	J	146/157 (92%)	-0.45	0 100 100	39, 57, 78, 102	0
2	K	144/157 (91%)	-0.53	0 100 100	40, 60, 98, 117	0
2	L	143/157 (91%)	-0.19	0 100 100	58, 82, 120, 155	0
All	All	1664/1836 (90%)	-0.45	1 (0%) 92 91	35, 60, 102, 155	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	123	GLY	2.3

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(Å ²)	Q<0.9
3	SO4	H	302	5/5	0.95	0.08	93,101,101,103	0
3	SO4	J	201	5/5	0.95	0.10	57,60,63,69	0
3	SO4	B	301	5/5	0.97	0.07	68,74,77,77	0
3	SO4	G	301	5/5	0.97	0.08	63,65,69,71	0
3	SO4	A	301	5/5	0.98	0.06	50,56,58,59	0
3	SO4	H	301	5/5	0.98	0.09	74,79,82,83	0
3	SO4	C	301	5/5	0.98	0.06	78,85,87,93	0
3	SO4	F	201	5/5	0.98	0.05	66,68,70,72	0
3	SO4	K	201	5/5	0.99	0.07	65,71,73,78	0
4	CA	A	302	1/1	0.99	0.04	75,75,75,75	0
4	CA	H	303	1/1	0.99	0.04	67,67,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.