



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 28, 2026 – 11:01 PM UTC

PDB ID : 7ZUV / pdb_00007zuv
Title : Crystal structure of Chlamydomonas reinhardtii chloroplastic sedoheptulose-1,7-bisphosphatase in reducing conditions
Authors : Le Moigne, T.; Robert, G.Q.; Lemaire, S.D.; Henri, J.
Deposited on : 2022-05-13
Resolution : 3.11 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

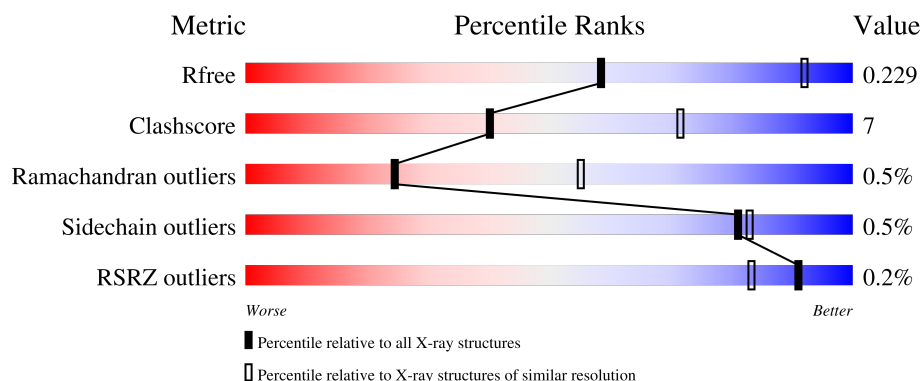
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.11 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	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)

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	331	1% 77% 16% 6%
1	B	331	80% 14% 6%
1	C	331	75% 16% 9%
1	D	331	80% 13% 6%
1	E	331	77% 13% 9%

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Mol	Chain	Length	Quality of chain
1	F	331	 82% 11% 6%
1	G	331	 79% 12% 9%
1	H	331	 76% 16% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 18714 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 FBPase domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2363	1503	391	448	21			
1	B	311	Total	C	N	O	S	0	0	0
			2372	1509	393	449	21			
1	C	302	Total	C	N	O	S	0	0	0
			2309	1471	383	435	20			
1	D	310	Total	C	N	O	S	0	0	0
			2363	1503	391	448	21			
1	E	301	Total	C	N	O	S	0	0	0
			2299	1465	381	433	20			
1	F	310	Total	C	N	O	S	0	0	0
			2363	1503	391	448	21			
1	G	301	Total	C	N	O	S	0	0	0
			2297	1464	381	431	21			
1	H	306	Total	C	N	O	S	0	0	0
			2338	1489	387	441	21			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	MET	-	initiating methionine	UNP A0A2K3DY10
A	62	HIS	-	expression tag	UNP A0A2K3DY10
A	63	HIS	-	expression tag	UNP A0A2K3DY10
A	64	HIS	-	expression tag	UNP A0A2K3DY10
A	65	HIS	-	expression tag	UNP A0A2K3DY10
A	66	HIS	-	expression tag	UNP A0A2K3DY10
A	67	HIS	-	expression tag	UNP A0A2K3DY10
A	68	HIS	-	expression tag	UNP A0A2K3DY10
A	69	MET	-	expression tag	UNP A0A2K3DY10
B	61	MET	-	initiating methionine	UNP A0A2K3DY10
B	62	HIS	-	expression tag	UNP A0A2K3DY10
B	63	HIS	-	expression tag	UNP A0A2K3DY10
B	64	HIS	-	expression tag	UNP A0A2K3DY10

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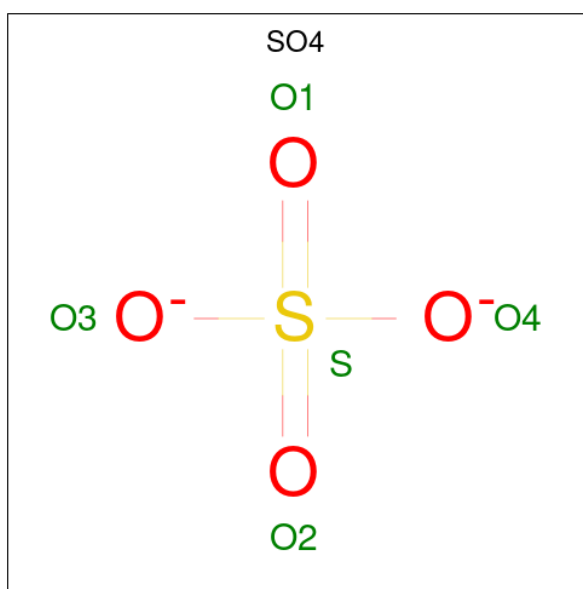
Chain	Residue	Modelled	Actual	Comment	Reference
B	65	HIS	-	expression tag	UNP A0A2K3DY10
B	66	HIS	-	expression tag	UNP A0A2K3DY10
B	67	HIS	-	expression tag	UNP A0A2K3DY10
B	68	HIS	-	expression tag	UNP A0A2K3DY10
B	69	MET	-	expression tag	UNP A0A2K3DY10
C	61	MET	-	initiating methionine	UNP A0A2K3DY10
C	62	HIS	-	expression tag	UNP A0A2K3DY10
C	63	HIS	-	expression tag	UNP A0A2K3DY10
C	64	HIS	-	expression tag	UNP A0A2K3DY10
C	65	HIS	-	expression tag	UNP A0A2K3DY10
C	66	HIS	-	expression tag	UNP A0A2K3DY10
C	67	HIS	-	expression tag	UNP A0A2K3DY10
C	68	HIS	-	expression tag	UNP A0A2K3DY10
C	69	MET	-	expression tag	UNP A0A2K3DY10
D	61	MET	-	initiating methionine	UNP A0A2K3DY10
D	62	HIS	-	expression tag	UNP A0A2K3DY10
D	63	HIS	-	expression tag	UNP A0A2K3DY10
D	64	HIS	-	expression tag	UNP A0A2K3DY10
D	65	HIS	-	expression tag	UNP A0A2K3DY10
D	66	HIS	-	expression tag	UNP A0A2K3DY10
D	67	HIS	-	expression tag	UNP A0A2K3DY10
D	68	HIS	-	expression tag	UNP A0A2K3DY10
D	69	MET	-	expression tag	UNP A0A2K3DY10
E	61	MET	-	initiating methionine	UNP A0A2K3DY10
E	62	HIS	-	expression tag	UNP A0A2K3DY10
E	63	HIS	-	expression tag	UNP A0A2K3DY10
E	64	HIS	-	expression tag	UNP A0A2K3DY10
E	65	HIS	-	expression tag	UNP A0A2K3DY10
E	66	HIS	-	expression tag	UNP A0A2K3DY10
E	67	HIS	-	expression tag	UNP A0A2K3DY10
E	68	HIS	-	expression tag	UNP A0A2K3DY10
E	69	MET	-	expression tag	UNP A0A2K3DY10
F	61	MET	-	initiating methionine	UNP A0A2K3DY10
F	62	HIS	-	expression tag	UNP A0A2K3DY10
F	63	HIS	-	expression tag	UNP A0A2K3DY10
F	64	HIS	-	expression tag	UNP A0A2K3DY10
F	65	HIS	-	expression tag	UNP A0A2K3DY10
F	66	HIS	-	expression tag	UNP A0A2K3DY10
F	67	HIS	-	expression tag	UNP A0A2K3DY10
F	68	HIS	-	expression tag	UNP A0A2K3DY10
F	69	MET	-	expression tag	UNP A0A2K3DY10
G	61	MET	-	initiating methionine	UNP A0A2K3DY10

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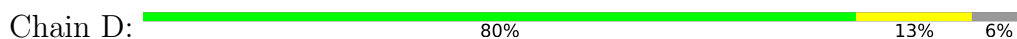
Chain	Residue	Modelled	Actual	Comment	Reference
G	62	HIS	-	expression tag	UNP A0A2K3DY10
G	63	HIS	-	expression tag	UNP A0A2K3DY10
G	64	HIS	-	expression tag	UNP A0A2K3DY10
G	65	HIS	-	expression tag	UNP A0A2K3DY10
G	66	HIS	-	expression tag	UNP A0A2K3DY10
G	67	HIS	-	expression tag	UNP A0A2K3DY10
G	68	HIS	-	expression tag	UNP A0A2K3DY10
G	69	MET	-	expression tag	UNP A0A2K3DY10
H	61	MET	-	initiating methionine	UNP A0A2K3DY10
H	62	HIS	-	expression tag	UNP A0A2K3DY10
H	63	HIS	-	expression tag	UNP A0A2K3DY10
H	64	HIS	-	expression tag	UNP A0A2K3DY10
H	65	HIS	-	expression tag	UNP A0A2K3DY10
H	66	HIS	-	expression tag	UNP A0A2K3DY10
H	67	HIS	-	expression tag	UNP A0A2K3DY10
H	68	HIS	-	expression tag	UNP A0A2K3DY10
H	69	MET	-	expression tag	UNP A0A2K3DY10

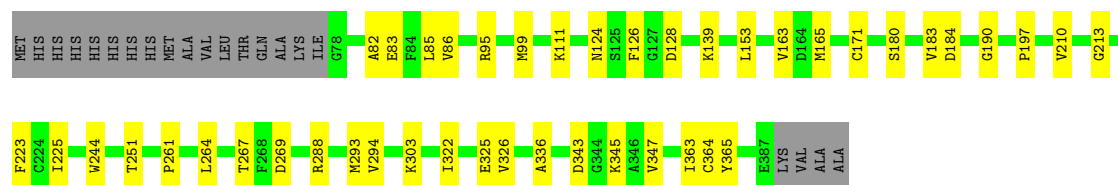
- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

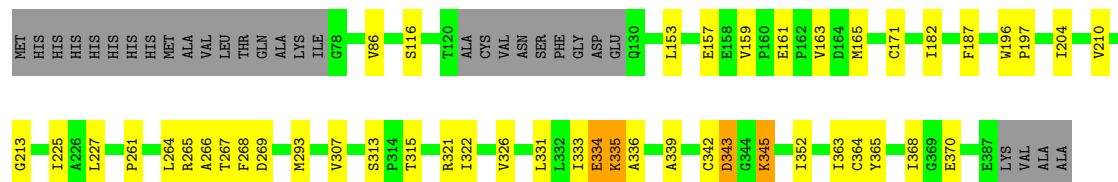
- Molecule 1: FBPase domain-containing protein





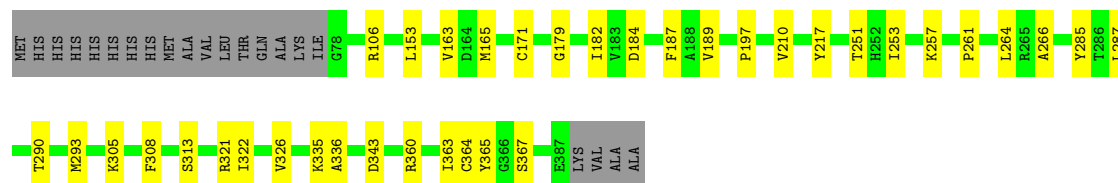
• Molecule 1: FB Pase domain-containing protein

Chain E: 77% 13% 9%



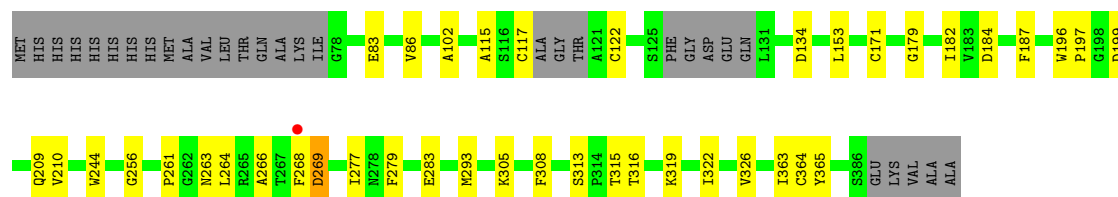
• Molecule 1: FB Pase domain-containing protein

Chain F: 82% 11% 6%



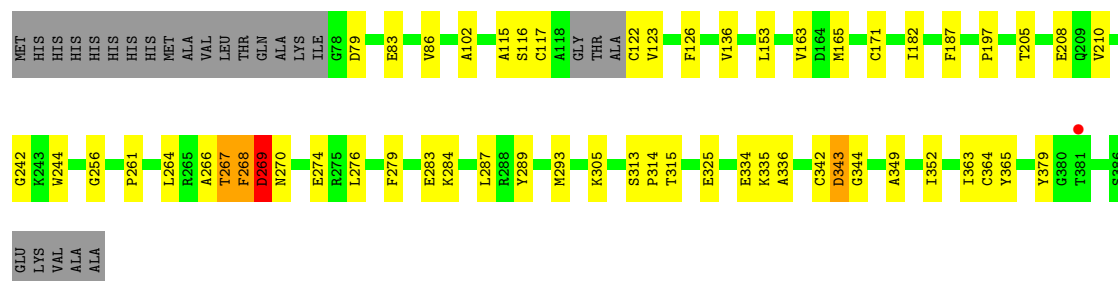
• Molecule 1: FB Pase domain-containing protein

Chain G: 79% 12% 9%



• Molecule 1: FB Pase domain-containing protein

Chain H: 76% 16% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.77Å 163.46Å 172.76Å 90.00° 91.94° 90.00°	Depositor
Resolution (Å)	48.54 – 3.11 48.54 – 3.11	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.54-3.11) 99.6 (48.54-3.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.195 , 0.231 0.197 , 0.229	Depositor DCC
R_{free} test set	1986 reflections (3.69%)	wwPDB-VP
Wilson B-factor (Å ²)	68.5	Xtriage
Anisotropy	0.432	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18714	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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

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	0.25	0/2412	0.50	1/3264 (0.0%)
1	B	0.17	0/2421	0.41	0/3275
1	C	0.20	0/2355	0.43	0/3184
1	D	0.15	0/2412	0.41	0/3264
1	E	0.24	0/2346	0.53	2/3173 (0.1%)
1	F	0.16	0/2412	0.42	0/3264
1	G	0.20	0/2343	0.45	0/3168
1	H	0.21	0/2386	0.46	0/3227
All	All	0.20	0/19087	0.45	3/25819 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	334	GLU	N-CA-C	-6.89	101.44	110.33
1	A	265	ARG	N-CA-C	-5.25	106.85	113.20
1	E	336	ALA	N-CA-C	-5.20	106.86	114.39

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	2363	0	2340	31	0
1	B	2372	0	2353	30	0
1	C	2309	0	2298	42	0
1	D	2363	0	2340	23	0
1	E	2299	0	2289	35	0
1	F	2363	0	2340	24	0
1	G	2297	0	2287	33	0
1	H	2338	0	2318	40	0
2	A	5	0	0	0	0
2	G	5	0	0	0	0
All	All	18714	0	18565	247	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 247 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:344:GLY:HA2	1:C:379:TYR:OH	1.78	0.84
1:H:293:MET:HE1	1:H:325:GLU:HB3	1.60	0.82
1:G:261:PRO:HB2	1:G:264:LEU:HD13	1.64	0.79
1:C:114:THR:HG23	1:C:124:ASN:HD21	1.46	0.79
1:E:261:PRO:HB2	1:E:264:LEU:HD13	1.64	0.79

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	308/331 (93%)	292 (95%)	14 (4%)	2 (1%)	21	50
1	B	309/331 (93%)	296 (96%)	12 (4%)	1 (0%)	36	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	296/331 (89%)	282 (95%)	13 (4%)	1 (0%)	36	65
1	D	308/331 (93%)	293 (95%)	13 (4%)	2 (1%)	21	50
1	E	297/331 (90%)	282 (95%)	14 (5%)	1 (0%)	36	65
1	F	308/331 (93%)	290 (94%)	17 (6%)	1 (0%)	36	65
1	G	295/331 (89%)	282 (96%)	12 (4%)	1 (0%)	36	65
1	H	302/331 (91%)	280 (93%)	19 (6%)	3 (1%)	12	39
All	All	2423/2648 (92%)	2297 (95%)	114 (5%)	12 (0%)	24	55

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	116	SER
1	F	343	ASP
1	H	269	ASP
1	C	179	GLY
1	G	179	GLY

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	253/270 (94%)	250 (99%)	3 (1%)	63	76
1	B	254/270 (94%)	254 (100%)	0	100	100
1	C	248/270 (92%)	248 (100%)	0	100	100
1	D	253/270 (94%)	253 (100%)	0	100	100
1	E	246/270 (91%)	242 (98%)	4 (2%)	55	73
1	F	253/270 (94%)	253 (100%)	0	100	100
1	G	247/270 (92%)	246 (100%)	1 (0%)	84	85
1	H	251/270 (93%)	248 (99%)	3 (1%)	63	76
All	All	2005/2160 (93%)	1994 (100%)	11 (0%)	81	83

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	269	ASP
1	H	267	THR
1	H	269	ASP
1	H	268	PHE
1	E	335	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	310	ASN
1	G	96	GLN
1	D	278	ASN
1	D	252	HIS
1	E	252	HIS

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](#)

2 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	A	401	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	G	401	-	4,4,4	0.23	0	6,6,6	0.09	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 [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	310/331 (93%)	-0.37	2 (0%) 85 70	30, 50, 84, 118	0
1	B	311/331 (93%)	-0.42	0 100 100	35, 49, 91, 124	0
1	C	302/331 (91%)	-0.22	0 100 100	45, 64, 88, 113	0
1	D	310/331 (93%)	-0.16	0 100 100	48, 67, 96, 126	0
1	E	301/331 (90%)	-0.21	0 100 100	49, 66, 92, 107	0
1	F	310/331 (93%)	-0.15	0 100 100	48, 71, 102, 121	0
1	G	301/331 (90%)	0.09	1 (0%) 90 80	52, 77, 104, 119	0
1	H	306/331 (92%)	0.15	1 (0%) 90 80	50, 82, 110, 134	0
All	All	2451/2648 (92%)	-0.16	4 (0%) 91 83	30, 67, 101, 134	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	120	THR	4.8
1	A	121	ALA	2.2
1	H	381	THR	2.0
1	G	268	PHE	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	A	401	5/5	0.86	0.14	79,89,92,99	0
2	SO4	G	401	5/5	0.89	0.08	85,90,106,111	0

6.5 Other polymers [i](#)

There are no such residues in this entry.