



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 11, 2017 – 02:53 PM EST

PDB ID : 5M73
Title : Structure of the human SRP S domain with SRP72 RNA-binding domain
Authors : Becker, M.M.M.; Wild, K.; Sinning, I.
Deposited on : 2016-10-26
Resolution : 3.40 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

<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

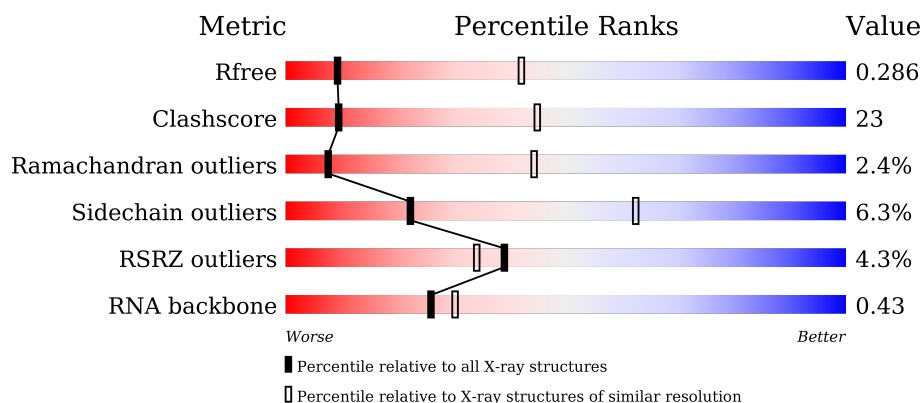
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)
RNA backbone	2183	1041 (4.00-2.80)

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. 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	145	<div> <div>16%</div> <div>57%</div> <div>21%</div> <div>6%</div> </div>
1	E	145	<div> <div>25%</div> <div>52%</div> <div>18%</div> <div>6%</div> </div>
2	B	128	<div> <div>55%</div> <div>28%</div> <div>•</div> <div>16%</div> </div>
2	F	128	<div> <div>15%</div> <div>51%</div> <div>27%</div> <div>•</div> <div>19%</div> </div>

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Mol	Chain	Length	Quality of chain
3	C	203	
3	G	203	
4	D	158	
4	H	158	

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
5	MG	A	314	-	-	-	X
5	MG	C	302	-	-	-	X
6	K	E	316	-	-	-	X
6	K	E	318	-	-	-	X
7	GOL	A	334	-	-	-	X
7	GOL	A	337	-	-	-	X
7	GOL	E	321	-	-	-	X
7	GOL	E	322	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12128 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 RNA chain called Human gene for small cytoplasmic 7SL RNA (7L30.1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	145	Total	C	N	O	P	0	0	0
			3126	1388	577	1014	147			
1	E	145	Total	C	N	O	P	0	0	0
			3117	1388	577	1007	145			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	GTP	-	additional nucleotide	GB 23924
A	249	A	-	additional nucleotide	GB 23924
E	105	GTP	-	expression tag	GB 23924
E	249	A	-	expression tag	GB 23924

- Molecule 2 is a protein called Signal recognition particle 19 kDa protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	108	Total	C	N	O	S	0	0	0
			878	553	160	159	6			
2	F	104	Total	C	N	O	S	0	0	0
			842	534	152	150	6			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP P09132
B	2	ALA	-	expression tag	UNP P09132
B	3	CYS	-	expression tag	UNP P09132
B	4	ALA	-	expression tag	UNP P09132
B	5	ALA	-	expression tag	UNP P09132
B	6	ALA	-	expression tag	UNP P09132
B	7	ARG	-	expression tag	UNP P09132
B	8	SER	-	expression tag	UNP P09132

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Chain	Residue	Modelled	Actual	Comment	Reference
B	9	PRO	-	expression tag	UNP P09132
B	10	ALA	-	expression tag	UNP P09132
B	119	THR	-	expression tag	UNP P09132
B	120	GLN	-	expression tag	UNP P09132
B	121	LEU	-	expression tag	UNP P09132
B	122	GLU	-	expression tag	UNP P09132
B	123	HIS	-	expression tag	UNP P09132
B	124	HIS	-	expression tag	UNP P09132
B	125	HIS	-	expression tag	UNP P09132
B	126	HIS	-	expression tag	UNP P09132
B	127	HIS	-	expression tag	UNP P09132
B	128	HIS	-	expression tag	UNP P09132
F	1	MET	-	initiating methionine	UNP P09132
F	2	ALA	-	expression tag	UNP P09132
F	3	CYS	-	expression tag	UNP P09132
F	4	ALA	-	expression tag	UNP P09132
F	5	ALA	-	expression tag	UNP P09132
F	6	ALA	-	expression tag	UNP P09132
F	7	ARG	-	expression tag	UNP P09132
F	8	SER	-	expression tag	UNP P09132
F	9	PRO	-	expression tag	UNP P09132
F	10	ALA	-	expression tag	UNP P09132
F	119	THR	-	expression tag	UNP P09132
F	120	GLN	-	expression tag	UNP P09132
F	121	LEU	-	expression tag	UNP P09132
F	122	GLU	-	expression tag	UNP P09132
F	123	HIS	-	expression tag	UNP P09132
F	124	HIS	-	expression tag	UNP P09132
F	125	HIS	-	expression tag	UNP P09132
F	126	HIS	-	expression tag	UNP P09132
F	127	HIS	-	expression tag	UNP P09132
F	128	HIS	-	expression tag	UNP P09132

- Molecule 3 is a protein called Signal recognition particle subunit SRP68.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	197	Total	C	N	O	S	0	0	0
			1653	1036	313	296	8			
3	G	197	Total	C	N	O	S	0	0	0
			1656	1039	316	293	8			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	52	MET	-	initiating methionine	UNP Q9UHB9
C	53	GLY	-	expression tag	UNP Q9UHB9
C	54	HIS	-	expression tag	UNP Q9UHB9
C	55	HIS	-	expression tag	UNP Q9UHB9
C	56	HIS	-	expression tag	UNP Q9UHB9
C	57	HIS	-	expression tag	UNP Q9UHB9
C	58	HIS	-	expression tag	UNP Q9UHB9
C	59	HIS	-	expression tag	UNP Q9UHB9
C	116	ASP	GLU	conflict	UNP Q9UHB9
G	52	MET	-	initiating methionine	UNP Q9UHB9
G	53	GLY	-	expression tag	UNP Q9UHB9
G	54	HIS	-	expression tag	UNP Q9UHB9
G	55	HIS	-	expression tag	UNP Q9UHB9
G	56	HIS	-	expression tag	UNP Q9UHB9
G	57	HIS	-	expression tag	UNP Q9UHB9
G	58	HIS	-	expression tag	UNP Q9UHB9
G	59	HIS	-	expression tag	UNP Q9UHB9
G	116	ASP	GLU	conflict	UNP Q9UHB9

- Molecule 4 is a protein called Signal recognition particle subunit SRP72.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	47	Total	C	N	O	S	0	0	0
			395	250	78	66	1			
4	H	41	Total	C	N	O	S	0	0	0
			352	223	71	57	1			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	511	MET	-	initiating methionine	UNP O76094
D	512	GLY	MET	conflict	UNP O76094
D	663	HIS	LYS	conflict	UNP O76094
D	664	HIS	LYS	conflict	UNP O76094
D	665	HIS	LYS	conflict	UNP O76094
D	666	HIS	GLY	conflict	UNP O76094
D	667	HIS	GLY	conflict	UNP O76094
D	668	HIS	LYS	conflict	UNP O76094
H	511	MET	-	initiating methionine	UNP O76094
H	512	GLY	MET	conflict	UNP O76094
H	663	HIS	LYS	conflict	UNP O76094
H	664	HIS	LYS	conflict	UNP O76094
H	665	HIS	LYS	conflict	UNP O76094

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Chain	Residue	Modelled	Actual	Comment	Reference
H	666	HIS	GLY	conflict	UNP O76094
H	667	HIS	GLY	conflict	UNP O76094
H	668	HIS	LYS	conflict	UNP O76094

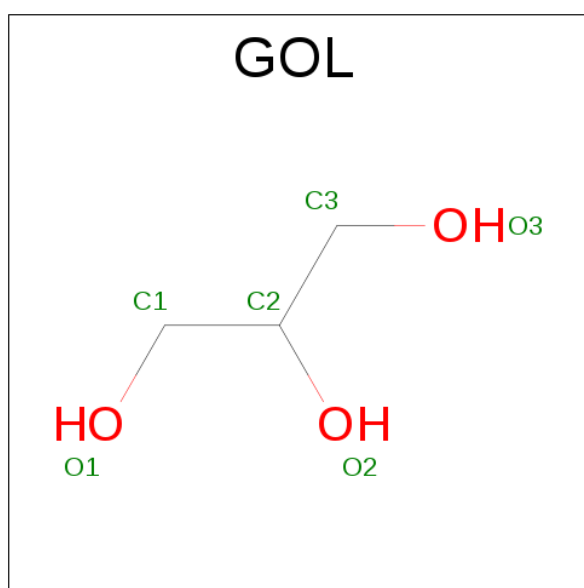
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	G	1	Total Mg 1 1	0	0
5	A	27	Total Mg 27 27	0	0
5	C	3	Total Mg 3 3	0	0
5	E	14	Total Mg 14 14	0	0

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	5	Total K 5 5	0	0
6	E	5	Total K 5 5	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total 6	C 3	O 3	0	0
7	A	1	Total 6	C 3	O 3	0	0
7	A	1	Total 6	C 3	O 3	0	0
7	A	1	Total 6	C 3	O 3	0	0
7	A	1	Total 6	C 3	O 3	0	0
7	B	1	Total 6	C 3	O 3	0	0
7	E	1	Total 6	C 3	O 3	0	0
7	E	1	Total 6	C 3	O 3	0	0
7	E	1	Total 6	C 3	O 3	0	0

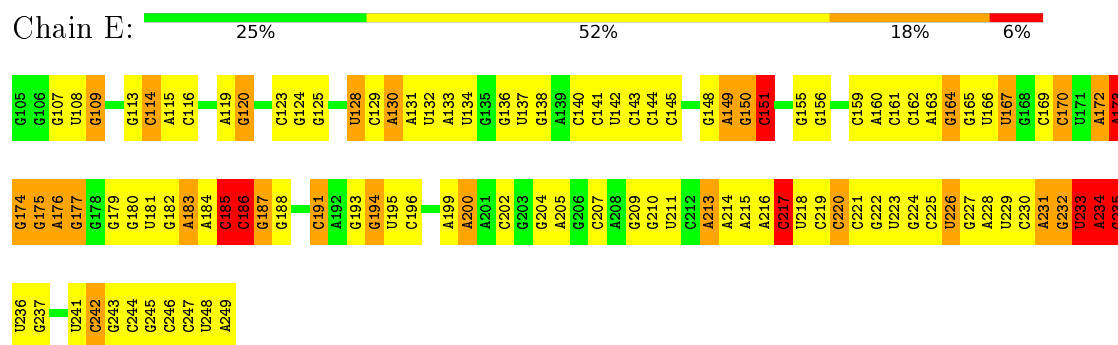
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

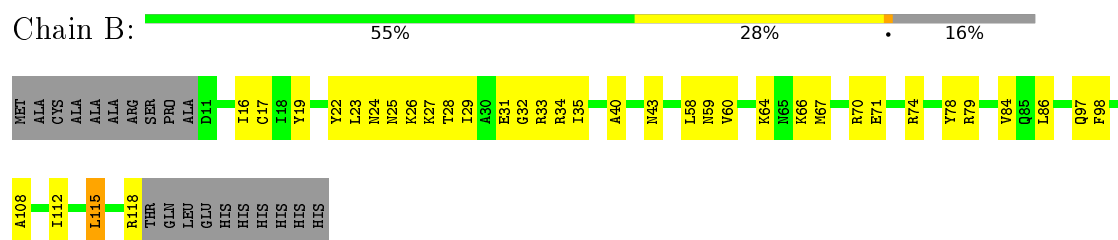
- Molecule 1: Human gene for small cytoplasmic 7SL RNA (7L30.1)



- Molecule 1: Human gene for small cytoplasmic 7SL RNA (7L30.1)



- Molecule 2: Signal recognition particle 19 kDa protein



- Molecule 2: Signal recognition particle 19 kDa protein



THR	THR	MET
VAL	PRO	GLY
ALA	ASP	SER
	P574	LEU
SER	E575	LYS
THR	R576	VAL
SER	W577	ASP
ASN	L578	VAL
ILE	P579	GLU
PRO	W580	ALA
ARG	R581	LEU
HIS	E582	GLU
GLN	R583	ASN
LYS	S584	SER
PRO	Y585	ALA
ALA	Y586	GLY
GLY	R587	ALA
ALA	G588	THR
PRO	R589	TYR
ALA	K590	ILE
ALA		ARG
ALA	K593	LYS
THR	R594	LYS
LYS	K595	GLY
LYS	D596	GLY
LYS	Q597	LYS
GLN	F598	VAL
GLN	G599	THR
LYS	K600	GLY
HIS		ASP
HIS	Q603	SER
HIS	GLY	GLN
HIS	ALA	PRO
HIS	THR	LYS
HIS	ALA	GLU
HIS	GLY	GLN
	ALA	GLY
	SER	GLN
	SER	GLY
	GLU	ASP
	LEU	LEU
	ASP	LYS
	ALA	LYS
	SER	LYS
	LYS	LYS
	THR	LYS
	VAL	K557
	SER	R558
	SER	K559
	PRO	GLY
	PRO	LYS
	THR	LEU
	SER	P563
	PRO	K564
	ARG	N565
	PRO	Y566
	GLY	D567
	SER	P568
	ALA	K569
	ALA	V570

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.57Å 139.31Å 152.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.39 – 3.40 48.39 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.39-3.40) 82.3 (48.39-3.40)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 3.40Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.237 , 0.280 0.238 , 0.286	Depositor DCC
R_{free} test set	1647 reflections (4.80%)	DCC
Wilson B-factor (Å ²)	77.1	Xtriage
Anisotropy	0.800	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.19 , 7.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.055 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12128	wwPDB-VP
Average B, all atoms (Å ²)	137.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.65% 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: GTP, GOL, K, MG

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	0.92	2/3463 (0.1%)	1.56	74/5402 (1.4%)
1	E	0.70	1/3463 (0.0%)	1.35	34/5402 (0.6%)
2	B	0.62	0/892	0.82	0/1200
2	F	0.41	0/856	0.69	1/1152 (0.1%)
3	C	0.55	1/1683 (0.1%)	0.79	1/2254 (0.0%)
3	G	0.64	1/1688 (0.1%)	0.98	5/2261 (0.2%)
4	D	1.26	1/404 (0.2%)	0.78	0/534
4	H	0.83	1/358 (0.3%)	0.63	0/466
All	All	0.75	7/12807 (0.1%)	1.24	115/18671 (0.6%)

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
3	C	0	1
4	D	0	1
4	H	0	1
All	All	0	3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	567	ASP	C-N	23.47	1.78	1.34
4	H	567	ASP	C-N	13.86	1.60	1.34
1	A	149	A	N9-C4	-9.43	1.32	1.37
1	A	205	A	N9-C4	-6.92	1.33	1.37
1	E	174	G	N9-C4	-6.15	1.33	1.38

The worst 5 of 115 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	150	G	OP1-P-O3'	-12.33	78.07	105.20
1	A	185	C	C6-N1-C2	11.19	124.78	120.30
1	A	217	C	C6-N1-C2	-10.14	116.25	120.30
1	A	123	C	C6-N1-C2	9.53	124.11	120.30
1	A	186	C	C6-N1-C2	-9.09	116.66	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	148	GLU	Peptide
4	D	569	LYS	Peptide
4	H	575	GLU	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	3126	0	1572	139	2
1	E	3117	0	1572	130	1
2	B	878	0	902	38	1
2	F	842	0	873	30	1
3	C	1653	0	1655	77	0
3	G	1656	0	1657	67	0
4	D	395	0	423	41	1
4	H	352	0	378	28	0
5	A	27	0	0	0	0
5	C	3	0	0	0	0
5	E	14	0	0	0	0
5	G	1	0	0	0	0
6	A	5	0	0	0	0
6	E	5	0	0	0	0
7	A	30	0	40	2	0
7	B	6	0	8	1	0
7	E	18	0	20	0	0
All	All	12128	0	9100	474	3

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 23.

The worst 5 of 474 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)
4:D:567:ASP:C	4:D:568:PRO:N	1.78	1.33
1:A:242:C:OP2	4:D:576:ARG:NH2	1.85	1.09
1:A:242:C:OP2	4:D:559:LYS:NZ	1.89	1.05
1:A:173:A:H5'	3:C:158:ARG:HH12	1.18	1.04
1:E:128:U:H3	1:E:222:G:H1	1.11	0.99

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:228:A:O2'	2:F:74:ARG:NH1[3_444]	2.13	0.07
1:A:124:G:O5'	2:B:79:ARG:NH2[3_554]	2.14	0.06
1:A:206:G:OP1	4:D:594:LYS:NZ[3_544]	2.15	0.05

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	
2	B	106/128 (83%)	103 (97%)	2 (2%)	1 (1%)	21	65
2	F	102/128 (80%)	99 (97%)	2 (2%)	1 (1%)	19	63
3	C	195/203 (96%)	177 (91%)	14 (7%)	4 (2%)	9	47
3	G	195/203 (96%)	177 (91%)	15 (8%)	3 (2%)	13	54
4	D	45/158 (28%)	31 (69%)	10 (22%)	4 (9%)	1	9
4	H	35/158 (22%)	22 (63%)	10 (29%)	3 (9%)	1	10
All	All	678/978 (69%)	609 (90%)	53 (8%)	16 (2%)	7	44

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	121	ASN
3	C	149	PRO
4	D	562	LEU
4	D	570	VAL
4	D	578	LEU

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	
2	B	97/112 (87%)	94 (97%)	3 (3%)	47	81
2	F	93/112 (83%)	89 (96%)	4 (4%)	35	74
3	C	173/178 (97%)	166 (96%)	7 (4%)	38	75
3	G	173/178 (97%)	169 (98%)	4 (2%)	58	85
4	D	42/129 (33%)	32 (76%)	10 (24%)	1	4
4	H	37/129 (29%)	26 (70%)	11 (30%)	0	2
All	All	615/838 (73%)	576 (94%)	39 (6%)	22	62

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	585	TYR
2	F	60	VAL
4	H	589	ARG
4	D	586	TYR
4	D	587	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	59	HIS
4	H	565	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	143/145 (98%)	38 (26%)	4 (2%)
1	E	143/145 (98%)	41 (28%)	6 (4%)
All	All	286/290 (98%)	79 (27%)	10 (3%)

5 of 79 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	109	G
1	A	113	G
1	A	120	G
1	A	128	U
1	A	130	A

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	128	U
1	E	176	A
1	E	231	A
1	A	186	C
1	E	186	C

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	GTP	A	105	1	26,34,34	0.94	1 (3%)	29,54,54	1.65	3 (10%)
1	GTP	E	105	1	18,25,34	1.06	2 (11%)	18,37,54	3.05	3 (16%)

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	GTP	A	105	1	-	0/18/38/38	0/3/3/3
1	GTP	E	105	1	-	0/3/25/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	105	GTP	C8-N7	-2.01	1.30	1.34
1	A	105	GTP	C6-N1	2.81	1.38	1.33
1	E	105	GTP	C6-N1	3.53	1.39	1.33

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	105	GTP	C5-C6-N1	-9.27	111.41	123.52
1	A	105	GTP	N3-C2-N1	-5.56	119.99	127.56
1	A	105	GTP	C5-C6-N1	-3.23	119.30	123.52
1	E	105	GTP	N3-C2-N1	-2.81	123.74	127.56
1	A	105	GTP	C6-N1-C2	3.79	120.33	115.88

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
1	A	105	GTP	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 64 ligands modelled in this entry, 55 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	$\# Z > 2$
7	GOL	A	333	-	5,5,5	0.35	0	5,5,5	0.21	0
7	GOL	A	334	-	5,5,5	0.38	0	5,5,5	0.54	0
7	GOL	A	335	6	5,5,5	0.34	0	5,5,5	0.28	0
7	GOL	A	336	6	5,5,5	0.33	0	5,5,5	0.20	0
7	GOL	A	337	-	5,5,5	0.32	0	5,5,5	0.31	0
7	GOL	B	201	-	5,5,5	0.39	0	5,5,5	0.53	0
7	GOL	E	320	6	5,5,5	0.38	0	5,5,5	0.51	0
7	GOL	E	321	6	5,5,5	0.36	0	5,5,5	0.19	0
7	GOL	E	322	6	5,5,5	0.39	0	5,5,5	0.24	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
7	GOL	A	333	-	-	0/4/4/4	0/0/0/0
7	GOL	A	334	-	-	0/4/4/4	0/0/0/0
7	GOL	A	335	6	-	0/4/4/4	0/0/0/0
7	GOL	A	336	6	-	0/4/4/4	0/0/0/0
7	GOL	A	337	-	-	0/4/4/4	0/0/0/0
7	GOL	B	201	-	-	0/4/4/4	0/0/0/0
7	GOL	E	320	6	-	0/4/4/4	0/0/0/0
7	GOL	E	321	6	-	0/4/4/4	0/0/0/0
7	GOL	E	322	6	-	0/4/4/4	0/0/0/0

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.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	334	GOL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	335	GOL	1	0
7	B	201	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	H	1
4	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	567:ASP	C	568:PRO	N	1.78
1	H	567:ASP	C	568:PRO	N	1.60

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	144/145 (99%)	-0.73	0 100 100	106, 129, 163, 205	0
1	E	144/145 (99%)	-0.79	0 100 100	105, 152, 187, 215	0
2	B	108/128 (84%)	-0.11	0 100 100	72, 108, 134, 181	0
2	F	104/128 (81%)	0.84	19 (18%) 2 2	108, 173, 223, 278	0
3	C	197/203 (97%)	-0.17	3 (1%) 76 71	84, 114, 165, 197	0
3	G	197/203 (97%)	-0.17	2 (1%) 84 79	81, 112, 155, 228	0
4	D	47/158 (29%)	0.81	6 (12%) 5 5	116, 143, 210, 233	0
4	H	41/158 (25%)	1.59	12 (29%) 1 1	131, 149, 209, 246	0
All	All	982/1268 (77%)	-0.11	42 (4%) 39 34	72, 129, 201, 278	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	H	568	PRO	12.6
4	H	569	LYS	7.4
4	H	567	ASP	7.0
4	D	572	PRO	4.5
4	D	568	PRO	4.4

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
1	GTP	A	105	32/32	0.85	0.11	-	173,207,305,306	0
1	GTP	E	105	23/32	0.82	0.12	-	213,224,235,238	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
7	GOL	A	337	6/6	0.76	0.31	10.35	101,109,111,111	0
7	GOL	E	321	6/6	0.71	0.32	7.53	126,129,138,142	0
7	GOL	E	322	6/6	0.84	0.30	7.30	102,108,112,114	0
7	GOL	A	334	6/6	0.80	0.30	6.92	117,126,129,135	0
6	K	E	318	1/1	0.94	0.23	6.82	129,129,129,129	0
6	K	E	316	1/1	0.92	0.32	5.46	113,113,113,113	0
5	MG	C	302	1/1	0.87	0.38	3.34	60,60,60,60	0
5	MG	A	314	1/1	0.87	0.34	2.63	61,61,61,61	0
7	GOL	B	201	6/6	0.87	0.21	0.18	72,90,91,95	0
6	K	E	319	1/1	0.46	0.11	-0.06	175,175,175,175	0
6	K	A	329	1/1	0.87	0.09	-0.43	172,172,172,172	0
6	K	E	315	1/1	0.89	0.11	-0.65	140,140,140,140	0
6	K	A	332	1/1	0.72	0.10	-1.40	166,166,166,166	0
5	MG	A	318	1/1	0.91	0.10	-	82,82,82,82	0
5	MG	A	324	1/1	0.80	0.13	-	81,81,81,81	0
6	K	A	331	1/1	0.68	0.78	-	173,173,173,173	0
6	K	A	330	1/1	0.71	0.47	-	156,156,156,156	0
5	MG	E	301	1/1	0.63	0.20	-	76,76,76,76	0
5	MG	A	325	1/1	0.92	0.36	-	74,74,74,74	0
5	MG	A	312	1/1	0.88	0.42	-	85,85,85,85	0
5	MG	E	302	1/1	0.65	0.18	-	74,74,74,74	0
5	MG	A	319	1/1	0.93	0.20	-	59,59,59,59	0
5	MG	A	302	1/1	0.77	0.23	-	73,73,73,73	0
5	MG	E	307	1/1	0.65	0.12	-	88,88,88,88	0
5	MG	C	303	1/1	0.90	0.35	-	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	MG	A	317	1/1	0.91	0.08	-	80,80,80,80	0
6	K	A	328	1/1	0.90	0.10	-	152,152,152,152	0
5	MG	E	304	1/1	0.89	0.32	-	72,72,72,72	0
7	GOL	A	336	6/6	0.72	0.86	-	138,150,153,156	0
5	MG	E	308	1/1	0.82	0.30	-	87,87,87,87	0
5	MG	G	301	1/1	0.86	0.30	-	73,73,73,73	0
5	MG	A	316	1/1	0.60	0.32	-	90,90,90,90	0
5	MG	C	301	1/1	0.95	0.30	-	38,38,38,38	0
5	MG	A	301	1/1	0.92	0.14	-	69,69,69,69	0
5	MG	A	320	1/1	0.75	0.52	-	69,69,69,69	0
5	MG	A	323	1/1	0.69	0.29	-	81,81,81,81	0
7	GOL	E	320	6/6	0.72	0.36	-	116,124,129,132	0
5	MG	A	315	1/1	0.91	0.47	-	88,88,88,88	0
5	MG	E	310	1/1	0.83	0.11	-	86,86,86,86	0
5	MG	E	306	1/1	0.83	0.19	-	74,74,74,74	0
5	MG	A	310	1/1	0.97	0.27	-	58,58,58,58	0
7	GOL	A	335	6/6	0.88	0.25	-	103,110,115,118	0
5	MG	E	313	1/1	0.75	0.24	-	83,83,83,83	0
5	MG	A	327	1/1	0.80	0.79	-	78,78,78,78	0
5	MG	A	313	1/1	0.53	0.81	-	73,73,73,73	0
5	MG	A	305	1/1	0.98	0.10	-	42,42,42,42	0
5	MG	E	312	1/1	0.86	0.33	-	97,97,97,97	0
5	MG	A	308	1/1	0.40	0.41	-	80,80,80,80	0
7	GOL	A	333	6/6	0.81	0.24	-	82,87,92,99	0
5	MG	E	305	1/1	0.91	0.13	-	114,114,114,114	0
5	MG	A	306	1/1	0.80	0.28	-	73,73,73,73	0
5	MG	E	309	1/1	0.91	0.08	-	84,84,84,84	0
5	MG	A	321	1/1	0.77	1.40	-	55,55,55,55	0
5	MG	E	311	1/1	0.43	0.45	-	101,101,101,101	0
5	MG	A	309	1/1	0.89	0.19	-	72,72,72,72	0
5	MG	A	326	1/1	0.75	0.56	-	74,74,74,74	0
5	MG	A	307	1/1	0.74	0.30	-	68,68,68,68	0
5	MG	A	311	1/1	0.90	0.25	-	72,72,72,72	0
5	MG	E	303	1/1	0.81	0.35	-	76,76,76,76	0
5	MG	A	322	1/1	0.88	0.24	-	78,78,78,78	0
5	MG	E	314	1/1	0.71	0.30	-	75,75,75,75	0
6	K	E	317	1/1	0.83	0.25	-	144,144,144,144	0
5	MG	A	304	1/1	0.68	0.21	-	87,87,87,87	0
5	MG	A	303	1/1	0.59	0.14	-	98,98,98,98	0

6.5 Other polymers [i](#)

There are no such residues in this entry.