



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:43 AM UTC

PDB ID : 6EHR / pdb_00006ehr
Title : The crystal structure of the human LAMTOR-RagA CTD-RagC CTD complex
Authors : Scheffzek, K.; Naschberger, A.
Deposited on : 2017-09-14
Resolution : 2.90 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
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

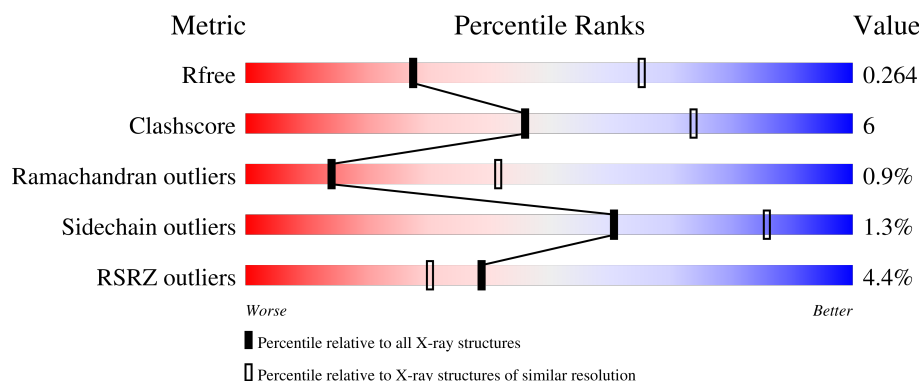
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	127	6% 83% 12% 6%
2	B	126	2% 83% 17% .
3	C	91	% 90% 10%
4	D	99	4% 84% 14% .
5	E	145	8% 64% 14% . 21%

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Mol	Chain	Length	Quality of chain
6	F	132	5% 72% 11% 17%
7	G	163	2% 62% 20% 17%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6126 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 Regulator complex protein LAMTOR3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	120	Total	C	N	O	S	0	0	0
			934	601	157	175	1			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q9UHA4
A	-1	ALA	-	expression tag	UNP Q9UHA4
A	0	HIS	-	expression tag	UNP Q9UHA4

- Molecule 2 is a protein called Regulator complex protein LAMTOR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	126	Total	C	N	O	S	0	0	0
			948	595	163	183	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP Q9Y2Q5
B	1	GLY	-	expression tag	UNP Q9Y2Q5

- Molecule 3 is a protein called Regulator complex protein LAMTOR5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	91	Total	C	N	O	S	0	0	0
			666	406	115	138	7			

- Molecule 4 is a protein called Regulator complex protein LAMTOR4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	97	Total	C	N	O	S	0	0	0
			738	460	135	140	3			

- Molecule 5 is a protein called Regulator complex protein LAMTOR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	115	Total	C	N	O	S	0	0	0
			892	560	155	175	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	17	SER	-	expression tag	UNP Q6IAA8
E	18	LEU	-	expression tag	UNP Q6IAA8
E	19	MET	-	expression tag	UNP Q6IAA8
E	20	THR	-	expression tag	UNP Q6IAA8

- Molecule 6 is a protein called Ras-related GTP-binding protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	110	Total	C	N	O	S	0	0	0
			883	565	150	162	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	182	GLY	-	expression tag	UNP Q7L523

- Molecule 7 is a protein called Ras-related GTP-binding protein C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	135	Total	C	N	O	S	0	0	0
			1065	686	165	206	8			

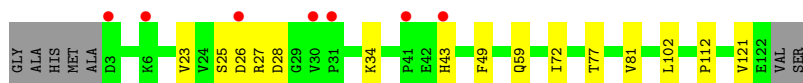
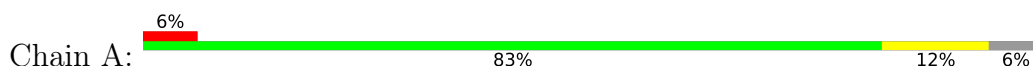
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	237	MET	-	initiating methionine	UNP Q9HB90
G	238	GLY	-	expression tag	UNP Q9HB90

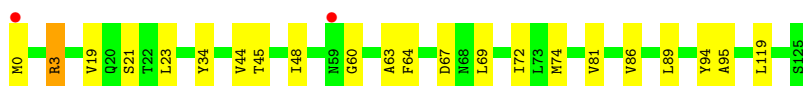
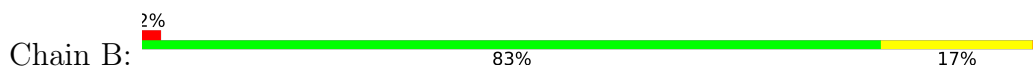
3 Residue-property plots [i](#)

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: Regulator complex protein LAMTOR3



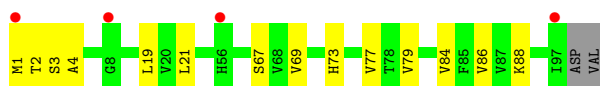
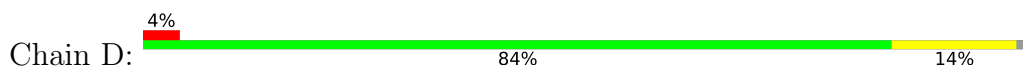
- Molecule 2: Regulator complex protein LAMTOR2



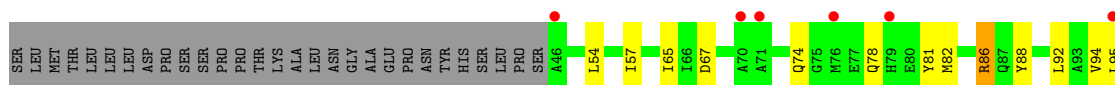
- Molecule 3: Regulator complex protein LAMTOR5



- Molecule 4: Regulator complex protein LAMTOR4

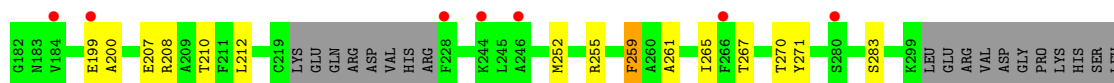


- Molecule 5: Regulator complex protein LAMTOR1





• Molecule 6: Ras-related GTP-binding protein A



LEU
MET
ARG

• Molecule 7: Ras-related GTP-binding protein C



E365
V366
V369
G370
V371
T372
SER
HIS
ARG
SER
CYS
GLY
HIS
GLN
THR
SER
ALA
SER
SER
SER
LEU
LYS
ALA
LEU
THR
HIS
ASN
GLY
THR
PRO
ARG
ASN
ALA
ILE

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.09Å 92.45Å 127.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.22 – 2.90 46.22 – 2.90	Depositor EDS
% Data completeness (in resolution range)	93.7 (46.22-2.90) 93.8 (46.22-2.90)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.18	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.216 , 0.263 0.222 , 0.264	Depositor DCC
R_{free} test set	1110 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	59.7	Xtriage
Anisotropy	0.715	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6126	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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](#)

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	0.09	0/951	0.25	0/1290
2	B	0.08	0/959	0.26	0/1298
3	C	0.07	0/672	0.23	0/911
4	D	0.10	0/747	0.31	0/1008
5	E	0.08	0/908	0.24	0/1234
6	F	0.08	0/897	0.23	0/1206
7	G	0.12	0/1082	0.36	1/1461 (0.1%)
All	All	0.09	0/6216	0.28	1/8408 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	306	SER	CB-CA-C	-5.37	108.64	116.53

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	934	0	958	12	0
2	B	948	0	958	14	0
3	C	666	0	666	6	0
4	D	738	0	753	9	0
5	E	892	0	894	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	883	0	887	9	0
7	G	1065	0	1068	23	0
All	All	6126	0	6184	71	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 6.

All (71) 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)
5:E:67:ASP:HA	7:G:253:ASN:HB2	1.67	0.75
7:G:251:ILE:HD11	7:G:259:ALA:HB2	1.76	0.67
2:B:3:ARG:NH2	5:E:152:GLU:OE1	2.30	0.64
1:A:102:LEU:HD22	3:C:47:VAL:HG21	1.78	0.63
4:D:21:LEU:HB2	4:D:84:VAL:HB	1.83	0.61
5:E:92:LEU:O	5:E:96:SER:N	2.30	0.60
3:C:68:GLU:OE2	4:D:67:SER:OG	2.16	0.59
3:C:30:ASN:ND2	3:C:39:ASP:OD1	2.34	0.59
1:A:23:VAL:HG22	1:A:34:LYS:HG3	1.85	0.59
2:B:44:VAL:HG23	2:B:45:THR:HG23	1.85	0.58
4:D:1:MET:HG2	4:D:2:THR:HG23	1.87	0.56
7:G:288:MET:HG3	7:G:318:ILE:HD12	1.87	0.55
7:G:258:LYS:NZ	7:G:275:SER:O	2.40	0.55
4:D:69:VAL:HG11	5:E:129:LEU:HD13	1.88	0.54
7:G:302:LYS:O	7:G:304:ASP:N	2.40	0.54
1:A:26:ASP:O	1:A:28:ASP:N	2.41	0.53
6:F:252:MET:HB2	7:G:318:ILE:HG12	1.91	0.53
6:F:255:ARG:NH2	6:F:283:SER:OG	2.41	0.51
4:D:79:VAL:HB	5:E:111:LEU:HG	1.93	0.51
3:C:22:LEU:HD13	3:C:45:ILE:HD12	1.93	0.51
6:F:207:GLU:HG2	6:F:212:LEU:H	1.75	0.50
4:D:19:LEU:HB3	4:D:86:VAL:HB	1.94	0.50
2:B:0:MET:N	5:E:157:GLN:HA	2.28	0.49
2:B:74:MET:HB2	2:B:81:VAL:HB	1.95	0.48
7:G:278:ASP:C	7:G:280:GLN:H	2.21	0.48
7:G:329:LYS:HG2	7:G:356:PHE:CE2	2.48	0.48
2:B:0:MET:H1	5:E:157:GLN:HA	1.79	0.47
1:A:43:HIS:HB2	2:B:63:ALA:HB2	1.97	0.47
5:E:78:GLN:HG3	5:E:81:TYR:H	1.80	0.47
6:F:208:ARG:HG3	6:F:271:TYR:HE1	1.80	0.47
7:G:256:ILE:HG21	7:G:339:CYS:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:95:LEU:O	5:E:99:LEU:HB2	2.16	0.46
2:B:21:SER:HB3	2:B:94:TYR:HB2	1.97	0.46
3:C:22:LEU:HD12	3:C:37:LEU:HB3	1.98	0.46
2:B:69:LEU:HD21	2:B:72:ILE:HD11	1.98	0.46
1:A:25:SER:OG	1:A:26:ASP:N	2.44	0.45
2:B:89:LEU:HD12	2:B:119:LEU:HD13	1.98	0.45
7:G:365:GLU:O	7:G:369:VAL:HG13	2.17	0.45
7:G:366:VAL:O	7:G:369:VAL:HG22	2.17	0.45
7:G:332:THR:HG22	7:G:335:LEU:HB2	1.99	0.44
5:E:54:LEU:HD23	5:E:57:ILE:HD12	1.99	0.44
5:E:65:ILE:HD12	7:G:249:ILE:HG22	1.99	0.44
1:A:77:THR:OG1	2:B:67:ASP:OD2	2.21	0.44
5:E:82:MET:O	5:E:86:ARG:HD2	2.18	0.43
1:A:112:PRO:HB2	5:E:102:TRP:CZ2	2.53	0.43
7:G:278:ASP:O	7:G:280:GLN:N	2.52	0.43
3:C:75:MET:HB2	5:E:132:VAL:HG21	2.00	0.43
7:G:359:PHE:CZ	7:G:363:ILE:HD11	2.54	0.43
6:F:259:PHE:CD2	7:G:300:GLY:HA2	2.54	0.43
7:G:315:MET:HG3	7:G:329:LYS:HD2	2.01	0.43
1:A:72:ILE:HG23	1:A:81:VAL:HG22	2.00	0.43
1:A:121:VAL:HG12	5:E:88:TYR:CZ	2.54	0.43
7:G:264:VAL:HG21	7:G:310:TYR:CE2	2.54	0.42
4:D:77:VAL:HG13	4:D:86:VAL:HG22	2.02	0.42
7:G:251:ILE:HD13	7:G:251:ILE:HA	1.80	0.42
2:B:19:VAL:HG22	2:B:95:ALA:HB2	2.01	0.42
6:F:267:THR:OG1	6:F:270:THR:OG1	2.24	0.42
7:G:288:MET:O	7:G:292:VAL:HG23	2.19	0.41
1:A:112:PRO:HB2	5:E:102:TRP:HZ2	1.84	0.41
6:F:207:GLU:OE2	6:F:210:THR:OG1	2.30	0.41
7:G:273:ASP:OD2	7:G:275:SER:OG	2.29	0.41
1:A:59:GLN:HB3	2:B:48:ILE:HG23	2.01	0.41
6:F:259:PHE:HE1	6:F:261:ALA:HB2	1.86	0.41
2:B:23:LEU:HG	2:B:34:TYR:HD1	1.85	0.41
4:D:2:THR:O	4:D:4:ALA:N	2.54	0.41
7:G:302:LYS:HD2	7:G:306:SER:HB3	2.02	0.41
7:G:256:ILE:HG23	7:G:341:LEU:HB3	2.02	0.41
1:A:49:PHE:CE1	2:B:60:GLY:HA2	2.56	0.41
6:F:265:ILE:HG12	6:F:271:TYR:CZ	2.56	0.41
4:D:73:HIS:CG	4:D:88:LYS:HE3	2.56	0.40
5:E:95:LEU:HB3	5:E:99:LEU:HD13	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	118/127 (93%)	111 (94%)	6 (5%)	1 (1%)	16	44
2	B	124/126 (98%)	121 (98%)	3 (2%)	0	100	100
3	C	89/91 (98%)	87 (98%)	1 (1%)	1 (1%)	11	36
4	D	95/99 (96%)	89 (94%)	5 (5%)	1 (1%)	11	36
5	E	113/145 (78%)	102 (90%)	11 (10%)	0	100	100
6	F	106/132 (80%)	94 (89%)	10 (9%)	2 (2%)	6	23
7	G	133/163 (82%)	116 (87%)	15 (11%)	2 (2%)	8	28
All	All	778/883 (88%)	720 (92%)	51 (7%)	7 (1%)	14	41

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	ARG
7	G	303	GLU
3	C	90	ALA
6	F	199	GLU
4	D	3	SER
6	F	200	ALA
7	G	371	VAL

5.3.2 Protein sidechains [i](#)

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	105/109 (96%)	105 (100%)	0	100	100
2	B	98/98 (100%)	95 (97%)	3 (3%)	35	69
3	C	77/77 (100%)	77 (100%)	0	100	100
4	D	81/83 (98%)	81 (100%)	0	100	100
5	E	99/126 (79%)	95 (96%)	4 (4%)	28	62
6	F	99/120 (82%)	98 (99%)	1 (1%)	68	89
7	G	122/145 (84%)	121 (99%)	1 (1%)	73	90
All	All	681/758 (90%)	672 (99%)	9 (1%)	61	86

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	3	ARG
2	B	64	PHE
2	B	86	VAL
5	E	74	GLN
5	E	86	ARG
5	E	94	VAL
5	E	158	PHE
6	F	259	PHE
7	G	330	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	A	68	ASN
3	C	27	GLN
3	C	73	ASN
5	E	79	HIS
5	E	117	GLN
6	F	258	ASN

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

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	120/127 (94%)	0.27	7 (5%) 29 22	45, 84, 137, 147	0
2	B	126/126 (100%)	0.10	2 (1%) 70 62	39, 58, 125, 162	0
3	C	91/91 (100%)	-0.18	1 (1%) 78 71	31, 48, 94, 115	0
4	D	97/99 (97%)	0.13	4 (4%) 41 33	41, 70, 114, 159	0
5	E	115/145 (79%)	0.59	11 (9%) 13 11	33, 74, 157, 200	0
6	F	110/132 (83%)	0.45	7 (6%) 25 20	43, 84, 136, 174	0
7	G	135/163 (82%)	0.01	3 (2%) 62 53	34, 55, 125, 150	0
All	All	794/883 (89%)	0.20	35 (4%) 39 30	31, 67, 137, 200	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	0	MET	4.0
5	E	100	THR	3.3
5	E	102	TRP	3.2
5	E	70	ALA	3.1
7	G	371	VAL	3.1
5	E	79	HIS	3.0
6	F	184	VAL	2.9
6	F	246	ALA	2.9
5	E	160	ILE	2.8
5	E	95	LEU	2.8
5	E	46	ALA	2.6
6	F	228	PHE	2.6
1	A	30	VAL	2.6
4	D	97	ILE	2.6
5	E	71	ALA	2.6
4	D	56	HIS	2.5
5	E	105	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
5	E	76	MET	2.4
1	A	6	LYS	2.4
7	G	309	ALA	2.4
1	A	26	ASP	2.4
6	F	244	LYS	2.3
1	A	3	ASP	2.3
6	F	199	GLU	2.3
4	D	1	MET	2.3
6	F	280	SER	2.3
1	A	41	PRO	2.3
3	C	91	SER	2.3
7	G	304	ASP	2.2
5	E	156	VAL	2.2
1	A	31	PRO	2.2
2	B	59	ASN	2.1
6	F	266	PHE	2.1
4	D	8	GLY	2.1
1	A	43	HIS	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.