



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:09 AM UTC

PDB ID : 3RC8 / pdb_00003rc8
Title : Human Mitochondrial Helicase Suv3 in Complex with Short RNA Fragment
Authors : Dauter, Z.; Jedrzejczak, R.; Dauter, M.; Wang, J.; Szczesny, R.; Stepień, P.
Deposited on : 2011-03-30
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

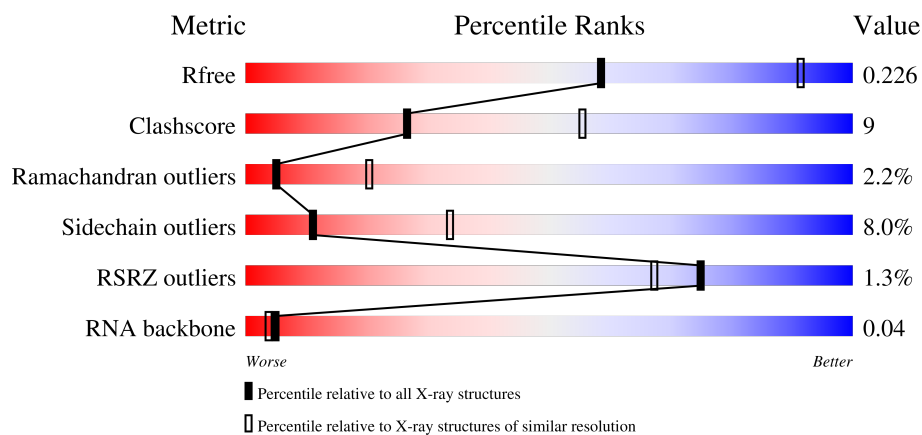
1 Overall quality at a glance

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)
RNA backbone	3983	1120 (3.10-2.70)

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	677	67% 19% • 10%
2	E	6	17% 33% 17% 33%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4975 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 ATP-dependent RNA helicase SUPV3L1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	610	Total	C	N	O	S	0	0	0
			4868	3126	830	884	28			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	GLY	-	expression tag	UNP Q8IYB8

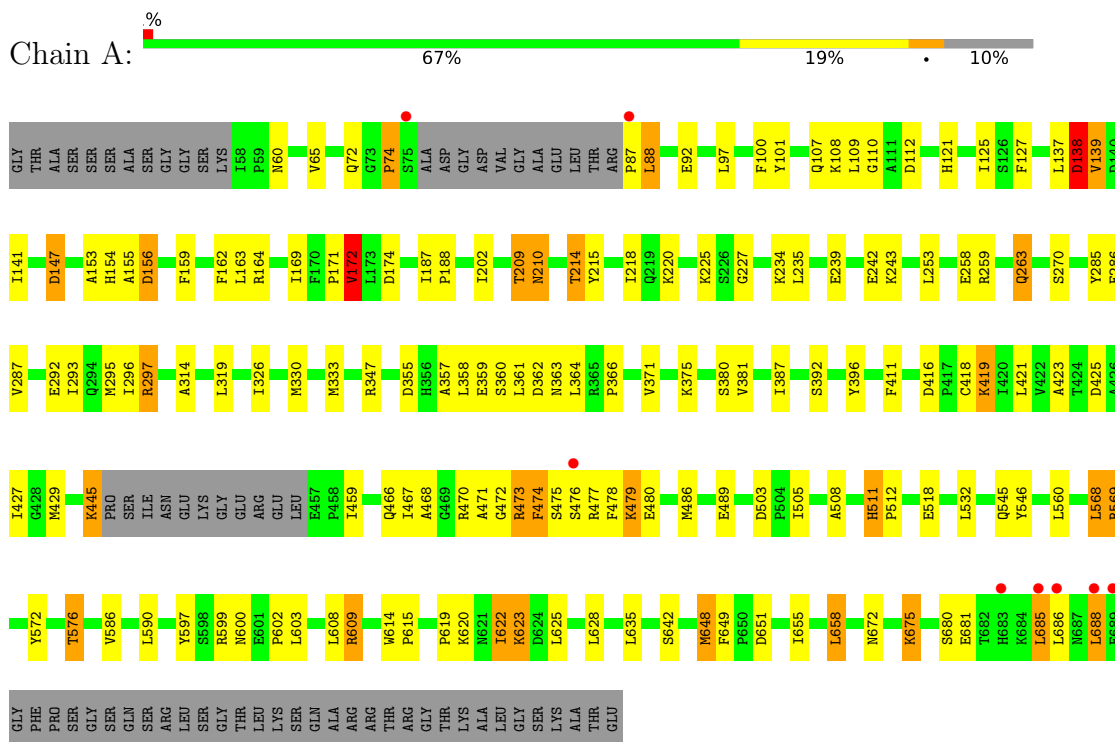
- Molecule 2 is a RNA chain called RNA fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	6	Total	C	N	O	P	0	0	0
			107	46	17	38	6			

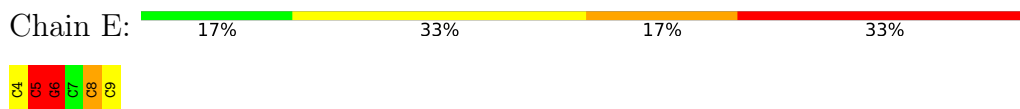
3 Residue-property plots

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: ATP-dependent RNA helicase SUPV3L1, mitochondrial



- Molecule 2: RNA fragment



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	94.43Å 94.43Å 88.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.90 30.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-2.90) 99.9 (30.00-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.85 (at 2.90Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.177 , 0.238 0.172 , 0.226	Depositor DCC
R_{free} test set	991 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	61.8	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l 0.056 for h,-h-k,-l 0.033 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4975	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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	0.94	0/4980	1.11	16/6747 (0.2%)
2	E	1.39	4/117 (3.4%)	1.72	5/180 (2.8%)
All	All	0.95	4/5097 (0.1%)	1.13	21/6927 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	9	C	P-OP1	5.97	1.60	1.48
2	E	5	C	C1'-N1	5.70	1.57	1.48
2	E	9	C	P-O5'	-5.52	1.49	1.60
2	E	4	C	C1'-N1	5.43	1.56	1.48

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	PRO	N-CA-CB	6.86	110.45	103.25
1	A	416	ASP	CA-C-N	6.85	126.55	119.56
1	A	416	ASP	C-N-CA	6.85	126.55	119.56
1	A	169	ILE	CB-CA-C	-6.30	103.79	112.24
1	A	139	VAL	N-CA-C	6.21	116.96	110.62
1	A	263	GLN	N-CA-C	6.10	117.07	109.57
1	A	392	SER	N-CA-C	5.96	118.24	109.24
1	A	479	LYS	N-CA-C	-5.86	102.26	110.35
1	A	159	PHE	CA-C-N	-5.78	112.92	119.28
1	A	159	PHE	C-N-CA	-5.78	112.92	119.28
2	E	5	C	O4'-C4'-C3'	-5.71	98.29	104.00
2	E	6	G	O4'-C4'-C3'	-5.65	98.35	104.00
1	A	65	VAL	CA-C-N	5.59	125.60	119.90
1	A	65	VAL	C-N-CA	5.59	125.60	119.90
2	E	8	C	P-O5'-C5'	5.42	129.03	120.90
2	E	5	C	O4'-C1'-N1	5.37	116.55	108.50
1	A	172	VAL	CB-CA-C	-5.32	102.56	111.29
2	E	6	G	C5'-C4'-O4'	5.08	117.42	109.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	622	ILE	N-CA-C	5.08	115.69	110.36
1	A	586	VAL	N-CA-C	-5.04	105.79	110.53
1	A	511	HIS	N-CA-C	5.04	114.09	108.25

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	4868	0	4897	91	1
2	E	107	0	55	4	0
All	All	4975	0	4952	92	1

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 9.

All (92) 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:A:473:ARG:O	1:A:474:PHE:HB2	1.60	0.99
1:A:292:GLU:HG3	1:A:429:MET:HE2	1.59	0.82
1:A:209:THR:HG21	1:A:466:GLN:HA	1.73	0.71
1:A:608:LEU:HD23	1:A:655:ILE:HD12	1.73	0.71
1:A:473:ARG:O	1:A:474:PHE:CB	2.40	0.68
1:A:87:PRO:O	1:A:88:LEU:HG	1.94	0.67
1:A:361:LEU:C	1:A:363:ASN:H	2.06	0.64
1:A:285:TYR:O	1:A:314:ALA:HA	1.99	0.63
1:A:380:SER:HB2	1:A:688:LEU:CB	2.30	0.62
1:A:188:PRO:HG2	1:A:546:TYR:CZ	2.35	0.61
1:A:225:LYS:HB2	1:A:286:GLU:OE1	2.01	0.61
1:A:572:TYR:O	1:A:576:THR:HG23	2.00	0.61
1:A:293:ILE:O	1:A:293:ILE:HG13	1.99	0.61
1:A:227:GLY:HA2	1:A:287:VAL:O	2.00	0.61
1:A:672:ASN:HB3	1:A:675:LYS:HD2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:467:ILE:O	1:A:470:ARG:HG2	2.02	0.59
1:A:609:ARG:HG2	1:A:614:TRP:HB3	1.83	0.58
1:A:121:HIS:CE1	1:A:125:ILE:HD11	2.38	0.58
1:A:380:SER:HB2	1:A:688:LEU:HB3	1.86	0.57
1:A:445:LYS:HE2	2:E:5:C:H6	1.68	0.56
1:A:418:CYS:O	1:A:419:LYS:HD2	2.04	0.56
1:A:614:TRP:CG	1:A:615:PRO:HA	2.40	0.55
1:A:658:LEU:HD12	1:A:658:LEU:O	2.06	0.55
1:A:602:PRO:HG3	1:A:648:MET:HE2	1.88	0.54
1:A:292:GLU:CG	1:A:429:MET:HE2	2.36	0.52
1:A:479:LYS:O	1:A:480:GLU:HB2	2.10	0.51
1:A:380:SER:HB2	1:A:688:LEU:HB2	1.92	0.51
1:A:599:ARG:O	1:A:600:ASN:C	2.52	0.51
1:A:60:ASN:OD1	1:A:60:ASN:C	2.53	0.51
1:A:425:ASP:OD1	1:A:425:ASP:N	2.39	0.50
1:A:635:LEU:HD22	1:A:655:ILE:HG23	1.92	0.50
1:A:608:LEU:CD2	1:A:655:ILE:HD12	2.42	0.50
1:A:101:TYR:O	1:A:107:GLN:NE2	2.46	0.49
1:A:467:ILE:O	1:A:468:ALA:C	2.55	0.49
1:A:109:LEU:O	1:A:110:GLY:C	2.55	0.49
1:A:164:ARG:CB	1:A:164:ARG:HH11	2.26	0.48
1:A:97:LEU:O	1:A:100:PHE:HB3	2.13	0.48
2:E:5:C:H2'	2:E:6:G:H5'	1.95	0.48
1:A:371:VAL:HA	1:A:423:ALA:O	2.12	0.48
1:A:188:PRO:HG2	1:A:546:TYR:CE1	2.49	0.48
1:A:326:ILE:O	1:A:330:MET:HG2	2.14	0.48
1:A:347:ARG:NH2	1:A:471:ALA:O	2.47	0.47
1:A:375:LYS:HE3	1:A:396:TYR:CD1	2.49	0.47
1:A:511:HIS:HB2	1:A:512:PRO:HD2	1.96	0.47
1:A:295:MET:C	1:A:297:ARG:H	2.22	0.47
1:A:164:ARG:HH11	1:A:164:ARG:HB3	1.80	0.47
1:A:171:PRO:O	1:A:172:VAL:C	2.57	0.47
1:A:476:SER:C	1:A:478:PHE:H	2.22	0.47
1:A:202:ILE:HD12	1:A:202:ILE:N	2.31	0.46
1:A:259:ARG:HE	1:A:259:ARG:HB2	1.60	0.46
1:A:518:GLU:HA	1:A:568:LEU:HD22	1.96	0.46
1:A:361:LEU:HD22	1:A:364:LEU:HD11	1.98	0.46
1:A:427:ILE:C	1:A:429:MET:H	2.24	0.46
1:A:138:ASP:O	1:A:141:ILE:HG22	2.16	0.45
1:A:137:LEU:O	1:A:138:ASP:C	2.59	0.45
1:A:253:LEU:HD23	1:A:258:GLU:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:LYS:HB2	2:E:5:C:OP1	2.17	0.45
1:A:569:ARG:HD2	1:A:569:ARG:HA	1.76	0.45
1:A:239:GLU:HG2	1:A:243:LYS:HE3	1.98	0.45
1:A:295:MET:C	1:A:297:ARG:N	2.73	0.44
1:A:622:ILE:O	1:A:623:LYS:C	2.58	0.44
1:A:147:ASP:HB3	1:A:153:ALA:HB2	2.00	0.44
1:A:411:PHE:CD1	1:A:421:LEU:HB2	2.53	0.44
1:A:127:PHE:CD2	1:A:162:PHE:HD1	2.36	0.43
1:A:214:THR:HG23	1:A:218:ILE:HG12	1.99	0.43
1:A:608:LEU:HD21	1:A:635:LEU:CD2	2.49	0.43
1:A:642:SER:HA	1:A:649:PHE:HB2	2.01	0.43
1:A:560:LEU:HD23	1:A:590:LEU:HD23	1.99	0.43
1:A:635:LEU:HD23	1:A:635:LEU:HA	1.81	0.43
1:A:518:GLU:HA	1:A:568:LEU:CD2	2.49	0.43
1:A:614:TRP:CD2	1:A:615:PRO:HA	2.54	0.43
1:A:597:TYR:O	1:A:600:ASN:N	2.52	0.42
1:A:532:LEU:HD23	1:A:532:LEU:HA	1.90	0.42
1:A:681:GLU:C	1:A:685:LEU:HA	2.45	0.42
1:A:375:LYS:HE3	1:A:396:TYR:CG	2.55	0.42
1:A:154:HIS:O	1:A:155:ALA:C	2.62	0.42
1:A:597:TYR:C	1:A:597:TYR:CD1	2.98	0.42
1:A:366:PRO:HA	1:A:419:LYS:HB3	2.02	0.41
1:A:361:LEU:O	1:A:363:ASN:N	2.53	0.41
1:A:121:HIS:O	1:A:125:ILE:HG12	2.20	0.41
1:A:209:THR:O	1:A:210:ASN:CB	2.69	0.41
1:A:358:LEU:O	1:A:360:SER:N	2.48	0.41
1:A:109:LEU:O	1:A:112:ASP:N	2.53	0.41
1:A:651:ASP:O	1:A:655:ILE:HG12	2.21	0.41
1:A:296:ILE:HG12	1:A:508:ALA:HB1	2.02	0.41
1:A:333:MET:HA	1:A:333:MET:HE2	2.03	0.41
1:A:427:ILE:C	1:A:429:MET:N	2.77	0.41
1:A:680:SER:O	1:A:685:LEU:N	2.54	0.41
1:A:459:ILE:O	1:A:459:ILE:HG13	2.19	0.41
1:A:445:LYS:HE2	2:E:5:C:C6	2.52	0.40
1:A:163:LEU:HD12	1:A:163:LEU:HA	1.81	0.40
1:A:619:PRO:HG3	1:A:628:LEU:HD12	2.03	0.40

All (1) 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:A:92:GLU:OE2	1:A:215:TYR:OH[1_455]	2.16	0.04

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	604/677 (89%)	548 (91%)	43 (7%)	13 (2%)	5	20

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	LEU
1	A	362	ASP
1	A	474	PHE
1	A	475	SER
1	A	685	LEU
1	A	156	ASP
1	A	357	ALA
1	A	686	LEU
1	A	138	ASP
1	A	210	ASN
1	A	472	GLY
1	A	477	ARG
1	A	74	PRO

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	538/589 (91%)	495 (92%)	43 (8%)	11	34

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	108	LYS
1	A	138	ASP
1	A	139	VAL
1	A	147	ASP
1	A	156	ASP
1	A	172	VAL
1	A	174	ASP
1	A	187	ILE
1	A	209	THR
1	A	214	THR
1	A	220	LYS
1	A	234	LYS
1	A	235	LEU
1	A	242	GLU
1	A	263	GLN
1	A	270	SER
1	A	297	ARG
1	A	319	LEU
1	A	355	ASP
1	A	359	GLU
1	A	381	VAL
1	A	387	ILE
1	A	419	LYS
1	A	445	LYS
1	A	473	ARG
1	A	486	MET
1	A	489	GLU
1	A	503	ASP
1	A	505	ILE
1	A	545	GLN
1	A	568	LEU
1	A	569	ARG
1	A	576	THR
1	A	603	LEU
1	A	609	ARG
1	A	620	LYS
1	A	623	LYS

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Mol	Chain	Res	Type
1	A	625	LEU
1	A	648	MET
1	A	658	LEU
1	A	675	LYS
1	A	688	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	129	ASN
1	A	135	HIS
1	A	165	HIS
1	A	263	GLN
1	A	268	GLN
1	A	466	GLN
1	A	545	GLN
1	A	667	GLN
1	A	671	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	4/6 (66%)	2 (50%)	1 (25%)

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	5	C
2	E	8	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	E	6	G

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](#)

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 [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	610/677 (90%)	-0.46	8 (1%) 75 67	31, 61, 99, 146	0
2	E	6/6 (100%)	-0.62	0 100 100	68, 79, 88, 104	0
All	All	616/683 (90%)	-0.46	8 (1%) 75 67	31, 61, 99, 146	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	686	LEU	8.2
1	A	87	PRO	3.7
1	A	75	SER	2.8
1	A	476	SER	2.7
1	A	685	LEU	2.6
1	A	683	HIS	2.2
1	A	689	GLU	2.1
1	A	688	LEU	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.