



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:56 PM UTC

PDB ID : 4LDX / pdb_00004ldx
Title : Crystal structure of the DNA binding domain of arabidopsis thaliana auxin response factor 1 (ARF1) in complex with protomor-like sequence ER7
Authors : Boer, D.R.; Freire-Rios, A.; van den Berg, W.M.A.; Weijers, D.; Coll, M.
Deposited on : 2013-06-25
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

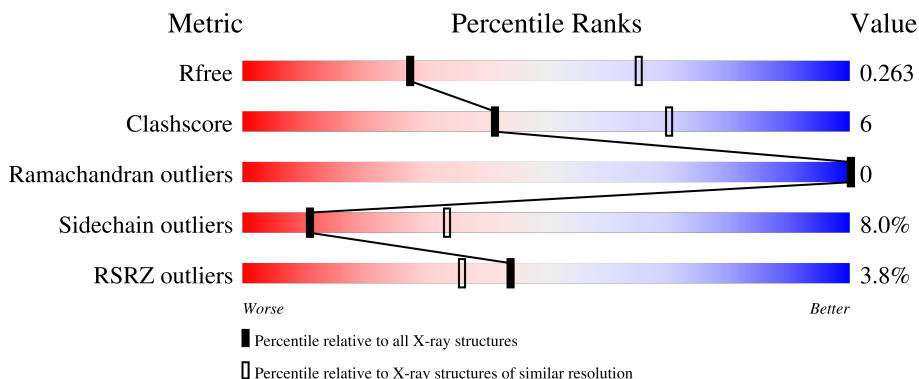
1 Overall quality at a glance

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	363	2% 73% 17% • 9%
1	B	363	5% 69% 22% • 7%
2	C	21	62% 38%
3	D	21	5% 71% 24% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6274 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 Auxin response factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	332	Total	C	N	O	S	0	0	0
			2671	1684	481	492	14			
1	B	337	Total	C	N	O	S	0	0	0
			2715	1713	487	501	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	ASN	-	expression tag	UNP Q8L7G0
A	357	SER	-	expression tag	UNP Q8L7G0
A	358	TYR	-	expression tag	UNP Q8L7G0
A	359	SER	-	expression tag	UNP Q8L7G0
A	360	GLN	-	expression tag	UNP Q8L7G0
A	361	SER	-	expression tag	UNP Q8L7G0
A	362	MET	-	expression tag	UNP Q8L7G0
A	363	CYS	-	expression tag	UNP Q8L7G0
B	356	ASN	-	expression tag	UNP Q8L7G0
B	357	SER	-	expression tag	UNP Q8L7G0
B	358	TYR	-	expression tag	UNP Q8L7G0
B	359	SER	-	expression tag	UNP Q8L7G0
B	360	GLN	-	expression tag	UNP Q8L7G0
B	361	SER	-	expression tag	UNP Q8L7G0
B	362	MET	-	expression tag	UNP Q8L7G0
B	363	CYS	-	expression tag	UNP Q8L7G0

- Molecule 2 is a DNA chain called ER7, forward sequence.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	21	Total	C	N	O	P	0	0	0
			426	205	74	127	20			

- Molecule 3 is a DNA chain called ER7, reverse sequence.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	21	Total 429	C 205	N 83	O 121	P 20	0	0	0

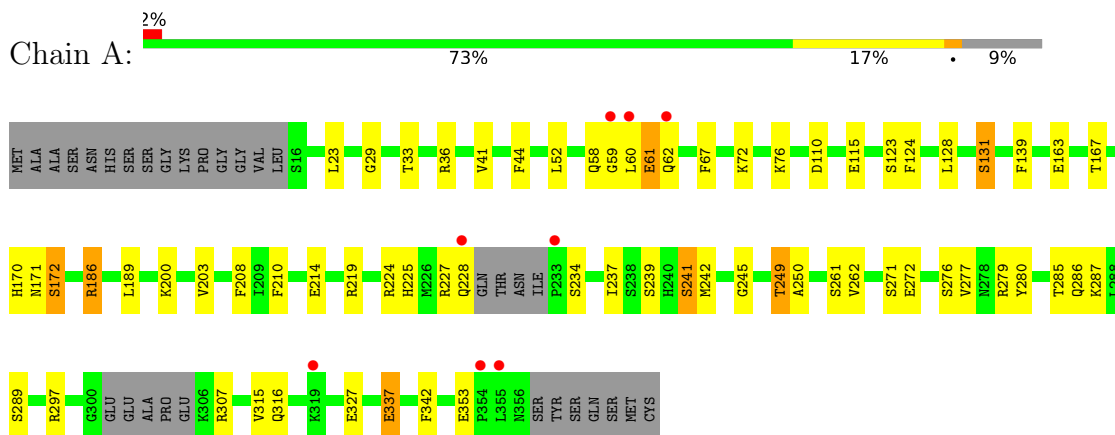
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	16	Total 16	O 16	0	0
4	B	15	Total 15	O 15	0	0
4	D	2	Total 2	O 2	0	0

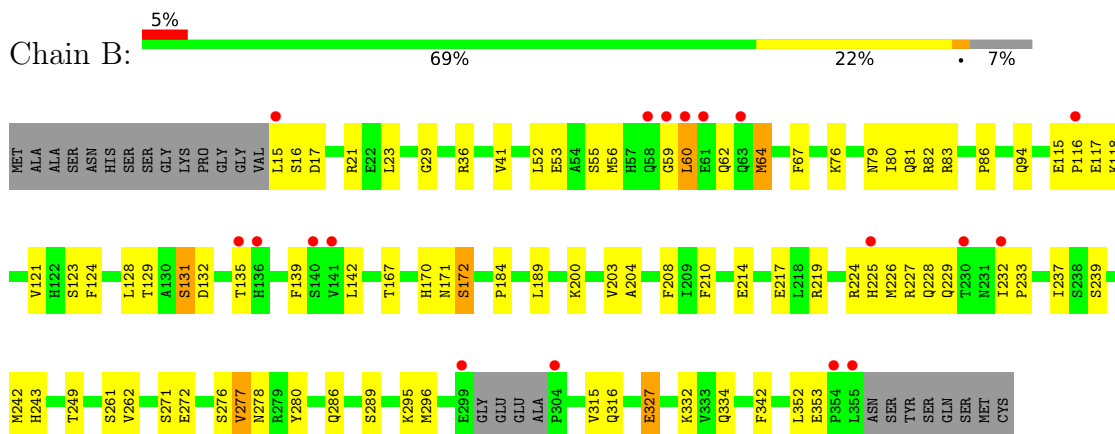
3 Residue-property plots [i](#)

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: Auxin response factor 1



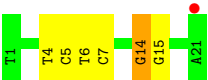
- Molecule 1: Auxin response factor 1



- Molecule 2: ER7, forward sequence



- Molecule 3: ER7, reverse sequence



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	43.52Å 105.19Å 127.91Å 90.00° 98.14° 90.00°	Depositor
Resolution (Å)	33.81 – 2.90 33.81 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.4 (33.81-2.90) 98.5 (33.81-2.90)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.214 , 0.259 0.218 , 0.263	Depositor DCC
R_{free} test set	1230 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	42.2	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6274	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.62% 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 ⓘ

5.1 Standard geometry ⓘ

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	0.85	0/2742	1.01	6/3715 (0.2%)
1	B	0.79	0/2788	1.00	8/3781 (0.2%)
2	C	0.41	0/476	0.94	1/733 (0.1%)
3	D	0.41	0/482	0.84	1/742 (0.1%)
All	All	0.77	0/6488	0.99	16/8971 (0.2%)

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
1	B	0	1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	14	DG	C4'-C3'-O3'	8.07	122.11	110.00
2	C	2	DT	C2'-C3'-O3'	-7.54	100.19	111.50
1	B	29	GLY	CA-C-N	6.32	125.94	119.56
1	B	29	GLY	C-N-CA	6.32	125.94	119.56
1	B	64	MET	CA-C-N	-6.30	113.28	119.90
1	B	64	MET	C-N-CA	-6.30	113.28	119.90
1	A	60	LEU	N-CA-C	6.15	117.98	111.28
1	B	286	GLN	N-CA-C	-6.13	102.01	110.35
1	B	67	PHE	N-CA-C	-6.09	101.51	110.52
1	A	67	PHE	N-CA-C	-5.97	100.83	110.32
1	A	110	ASP	N-CA-C	-5.75	101.97	110.48
1	A	337	GLU	N-CA-CB	5.64	116.29	109.74
1	A	29	GLY	CA-C-N	5.52	125.19	119.56
1	A	29	GLY	C-N-CA	5.52	125.19	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	277	VAL	CB-CA-C	-5.31	103.66	112.26
1	B	228	GLN	N-CA-C	-5.03	102.75	110.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	116	PRO	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	2671	0	2607	33	0
1	B	2715	0	2655	39	0
2	C	426	0	240	5	0
3	D	429	0	237	4	0
4	A	16	0	0	4	0
4	B	15	0	0	3	0
4	D	2	0	0	0	0
All	All	6274	0	5739	77	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 (77) 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:245:GLY:O	1:A:249:THR:HB	1.92	0.69
1:A:186:ARG:HH11	1:A:186:ARG:HB2	1.58	0.68
1:B:200:LYS:O	1:B:224:ARG:NH2	2.29	0.66
1:A:297:ARG:HD3	1:A:307:ARG:NH2	2.11	0.65
1:A:287:LYS:N	4:A:414:HOH:O	2.28	0.64
1:B:296:MET:CE	1:B:352:LEU:HD23	2.28	0.64
1:B:23:LEU:HD22	1:B:219:ARG:HB3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:LEU:HD22	1:A:219:ARG:HB3	1.84	0.60
1:A:241:SER:HB3	1:B:249:THR:OG1	2.02	0.60
1:B:296:MET:CE	1:B:352:LEU:CD2	2.81	0.59
1:B:227:ARG:O	1:B:229:GLN:HG2	2.04	0.57
3:D:14:DG:H4'	3:D:15:DG:OP1	2.05	0.57
1:A:170:HIS:O	1:A:171:ASN:HB2	2.04	0.55
1:A:61:GLU:O	1:A:62:GLN:C	2.50	0.55
1:B:296:MET:HE3	1:B:352:LEU:CD2	2.37	0.55
1:A:200:LYS:O	1:A:224:ARG:NH1	2.41	0.54
1:B:53:GLU:HG2	1:B:59:GLY:HA3	1.89	0.54
1:B:170:HIS:O	1:B:171:ASN:HB2	2.09	0.53
1:B:272:GLU:HG2	4:B:403:HOH:O	2.07	0.53
1:B:296:MET:HE2	1:B:352:LEU:HD23	1.92	0.52
1:A:41:VAL:HG12	1:A:276:SER:HA	1.93	0.51
1:B:128:LEU:HD11	1:B:208:PHE:HB2	1.91	0.51
1:A:131:SER:OG	3:D:4:DT:OP2	2.28	0.51
1:A:128:LEU:HD11	1:A:208:PHE:HB2	1.93	0.51
1:A:286:GLN:CA	4:A:414:HOH:O	2.59	0.50
1:A:280:TYR:OH	1:A:327:GLU:OE1	2.29	0.50
1:B:295:LYS:HD3	4:B:409:HOH:O	2.12	0.50
1:B:41:VAL:HG12	1:B:276:SER:HA	1.95	0.49
1:A:280:TYR:CE2	1:A:327:GLU:OE1	2.65	0.49
1:A:286:GLN:HB3	4:A:414:HOH:O	2.13	0.49
1:B:16:SER:HB2	1:B:217:GLU:OE1	2.14	0.48
1:B:16:SER:CB	1:B:217:GLU:OE1	2.61	0.47
1:B:237:ILE:HD11	1:B:242:MET:HG2	1.97	0.47
1:A:272:GLU:CD	1:A:279:ARG:HH22	2.22	0.46
1:B:124:PHE:CE2	1:B:210:PHE:HB3	2.51	0.46
1:B:204:ALA:O	1:B:226:MET:HG3	2.15	0.46
1:B:79:ASN:ND2	1:B:80:ILE:H	2.14	0.46
1:B:276:SER:HB3	4:B:404:HOH:O	2.16	0.45
1:A:315:VAL:O	1:A:316:GLN:C	2.59	0.45
1:A:227:ARG:O	1:A:228:GLN:HB2	2.15	0.45
1:A:124:PHE:CE2	1:A:210:PHE:HB3	2.52	0.45
1:A:36:ARG:NE	1:A:115:GLU:OE1	2.50	0.45
1:A:249:THR:CG2	1:A:250:ALA:N	2.80	0.45
1:B:225:HIS:O	1:B:226:MET:C	2.59	0.45
1:B:280:TYR:OH	1:B:327:GLU:OE1	2.29	0.45
2:C:6:DT:H2''	2:C:7:DC:OP2	2.16	0.44
3:D:6:DT:H2''	3:D:7:DC:OP2	2.16	0.44
1:A:214:GLU:N	4:A:408:HOH:O	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:ARG:HD2	1:B:117:GLU:CD	2.43	0.44
1:B:167:THR:HA	1:B:172:SER:O	2.17	0.44
1:B:56:MET:HA	1:B:233:PRO:HB3	2.00	0.44
1:B:315:VAL:O	1:B:316:GLN:C	2.60	0.44
1:B:342:PHE:CD1	1:B:342:PHE:C	2.96	0.44
1:A:225:HIS:O	1:A:227:ARG:HG2	2.17	0.44
1:B:277:VAL:HG23	1:B:278:ASN:N	2.32	0.44
1:B:123:SER:HA	1:B:210:PHE:O	2.18	0.44
1:A:237:ILE:HD11	1:A:242:MET:HG2	1.99	0.44
1:A:342:PHE:CD1	1:A:342:PHE:C	2.95	0.44
1:A:280:TYR:HE2	1:A:327:GLU:OE1	2.01	0.43
3:D:5:DC:H2''	3:D:6:DT:OP2	2.17	0.43
1:B:64:MET:HE1	1:B:243:HIS:CB	2.49	0.43
1:B:139:PHE:HB3	1:B:189:LEU:HB2	2.01	0.43
1:B:129:THR:HG22	1:B:132:ASP:CG	2.44	0.42
2:C:5:DC:H2''	2:C:6:DT:OP2	2.20	0.42
1:A:123:SER:HA	1:A:210:PHE:O	2.19	0.42
1:B:81:GLN:OE1	1:B:94:GLN:NE2	2.53	0.42
1:B:82:ARG:O	1:B:83:ARG:HG3	2.19	0.42
1:B:59:GLY:O	1:B:60:LEU:C	2.63	0.42
1:A:139:PHE:HB3	1:A:189:LEU:HB2	2.01	0.41
1:A:167:THR:HA	1:A:172:SER:O	2.20	0.41
1:A:210:PHE:CD1	1:A:210:PHE:C	2.97	0.41
1:B:86:PRO:HA	1:B:170:HIS:CE1	2.56	0.41
1:B:184:PRO:HG2	2:C:1:DT:H71	2.02	0.41
1:A:44:PHE:CE1	1:A:72:LYS:HB3	2.56	0.41
1:A:58:GLN:HG2	1:A:59:GLY:N	2.36	0.40
1:B:131:SER:OG	2:C:4:DT:OP2	2.37	0.40
2:C:13:DG:H1'	2:C:14:DG:C8	2.57	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	326/363 (90%)	313 (96%)	13 (4%)	0	100	100
1	B	333/363 (92%)	318 (96%)	15 (4%)	0	100	100
All	All	659/726 (91%)	631 (96%)	28 (4%)	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	298/323 (92%)	277 (93%)	21 (7%)	14	40
1	B	304/323 (94%)	277 (91%)	27 (9%)	9	28
All	All	602/646 (93%)	554 (92%)	48 (8%)	11	34

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	THR
1	A	52	LEU
1	A	61	GLU
1	A	76	LYS
1	A	131	SER
1	A	163	GLU
1	A	172	SER
1	A	186	ARG
1	A	203	VAL
1	A	234	SER
1	A	239	SER
1	A	241	SER
1	A	249	THR
1	A	261	SER
1	A	262	VAL
1	A	271	SER
1	A	277	VAL
1	A	285	THR

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Mol	Chain	Res	Type
1	A	289	SER
1	A	337	GLU
1	A	353	GLU
1	B	15	LEU
1	B	17	ASP
1	B	36	ARG
1	B	52	LEU
1	B	55	SER
1	B	60	LEU
1	B	62	GLN
1	B	76	LYS
1	B	115	GLU
1	B	118	LYS
1	B	121	VAL
1	B	131	SER
1	B	135	THR
1	B	142	LEU
1	B	172	SER
1	B	203	VAL
1	B	214	GLU
1	B	232	ILE
1	B	239	SER
1	B	261	SER
1	B	262	VAL
1	B	271	SER
1	B	289	SER
1	B	327	GLU
1	B	332	LYS
1	B	334	GLN
1	B	353	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	114	GLN
1	A	122	HIS
1	A	162	GLN
1	B	63	GLN
1	B	162	GLN
1	B	225	HIS
1	B	229	GLN

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](#)

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	332/363 (91%)	-0.11	8 (2%) 59 50	19, 30, 76, 120	0
1	B	337/363 (92%)	0.29	18 (5%) 32 25	21, 46, 91, 123	0
2	C	21/21 (100%)	0.22	0 100 100	35, 77, 88, 102	0
3	D	21/21 (100%)	0.29	1 (4%) 35 28	28, 68, 88, 122	0
All	All	711/768 (92%)	0.10	27 (3%) 44 36	19, 38, 88, 123	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	304	PRO	5.6
1	B	232	ILE	4.4
1	B	135	THR	4.0
1	B	15	LEU	3.6
1	A	60	LEU	3.5
1	A	228	GLN	3.3
1	A	355	LEU	3.3
1	A	354	PRO	3.2
1	B	225	HIS	3.1
1	A	62	GLN	3.0
1	B	354	PRO	2.9
1	B	230	THR	2.8
1	A	59	GLY	2.7
1	B	61	GLU	2.7
1	B	116	PRO	2.5
1	B	355	LEU	2.5
1	B	299	GLU	2.4
1	B	140	SER	2.4
1	B	63	GLN	2.4
1	A	233	PRO	2.4
1	B	141	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	59	GLY	2.3
1	B	58	GLN	2.2
1	B	136	HIS	2.1
1	B	60	LEU	2.0
3	D	21	DA	2.0
1	A	319	LYS	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.