



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:09 PM GMT

PDB ID : 4BJN
Title : Crystal structure of the flax-rust effector AvrM-A
Authors : Ve, T.; Williams, S.J.; Kobe, B.
Deposited on : 2013-04-19
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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

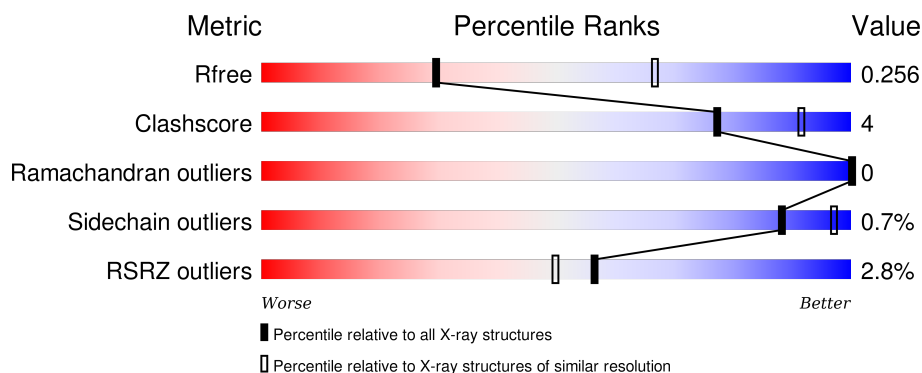
1 Overall quality at a glance

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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 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	244	<div> <div>7%</div> <div>84% 7% 9%</div> </div>
1	B	244	<div> <div>2%</div> <div>79% 11% 10%</div> </div>
1	C	244	<div> <div>%</div> <div>77% 9% 14%</div> </div>
1	D	244	<div> <div>%</div> <div>75% 8% 17%</div> </div>
1	E	244	<div> <div>%</div> <div>79% 12% 9%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	244	<div><div></div><div>3%</div><div>78%</div><div>6%</div><div>16%</div></div>
1	G	244	<div><div></div><div>2%</div><div>81%</div><div>10%</div><div>9%</div></div>
1	H	244	<div><div></div><div>3%</div><div>78%</div><div>10%</div><div>11%</div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 13996 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 AVR-M-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	0	0
			1804	1138	315	348	3			
1	B	219	Total	C	N	O	S	0	0	0
			1783	1126	313	341	3			
1	C	211	Total	C	N	O	S	0	0	0
			1717	1090	298	326	3			
1	D	203	Total	C	N	O	S	0	0	0
			1647	1042	286	316	3			
1	E	222	Total	C	N	O	S	0	0	0
			1803	1137	316	347	3			
1	F	206	Total	C	N	O	S	0	0	0
			1678	1063	293	319	3			
1	G	223	Total	C	N	O	S	0	0	0
			1809	1145	315	346	3			
1	H	216	Total	C	N	O	S	0	0	0
			1755	1108	307	337	3			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	SER	-	EXPRESSION TAG	UNP Q2MV52
A	101	ASN	-	EXPRESSION TAG	UNP Q2MV52
A	102	ALA	-	EXPRESSION TAG	UNP Q2MV52
B	100	SER	-	EXPRESSION TAG	UNP Q2MV52
B	101	ASN	-	EXPRESSION TAG	UNP Q2MV52
B	102	ALA	-	EXPRESSION TAG	UNP Q2MV52
C	100	SER	-	EXPRESSION TAG	UNP Q2MV52
C	101	ASN	-	EXPRESSION TAG	UNP Q2MV52
C	102	ALA	-	EXPRESSION TAG	UNP Q2MV52
D	100	SER	-	EXPRESSION TAG	UNP Q2MV52
D	101	ASN	-	EXPRESSION TAG	UNP Q2MV52
D	102	ALA	-	EXPRESSION TAG	UNP Q2MV52
E	100	SER	-	EXPRESSION TAG	UNP Q2MV52

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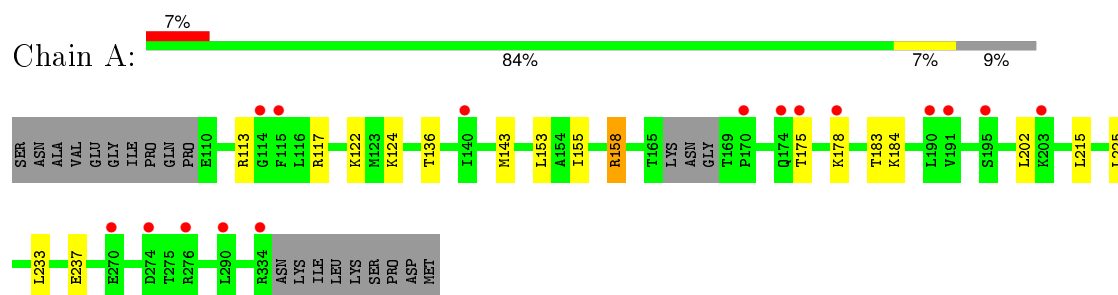
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Chain	Residue	Modelled	Actual	Comment	Reference
E	101	ASN	-	EXPRESSION TAG	UNP Q2MV52
E	102	ALA	-	EXPRESSION TAG	UNP Q2MV52
F	100	SER	-	EXPRESSION TAG	UNP Q2MV52
F	101	ASN	-	EXPRESSION TAG	UNP Q2MV52
F	102	ALA	-	EXPRESSION TAG	UNP Q2MV52
G	100	SER	-	EXPRESSION TAG	UNP Q2MV52
G	101	ASN	-	EXPRESSION TAG	UNP Q2MV52
G	102	ALA	-	EXPRESSION TAG	UNP Q2MV52
H	100	SER	-	EXPRESSION TAG	UNP Q2MV52
H	101	ASN	-	EXPRESSION TAG	UNP Q2MV52
H	102	ALA	-	EXPRESSION TAG	UNP Q2MV52

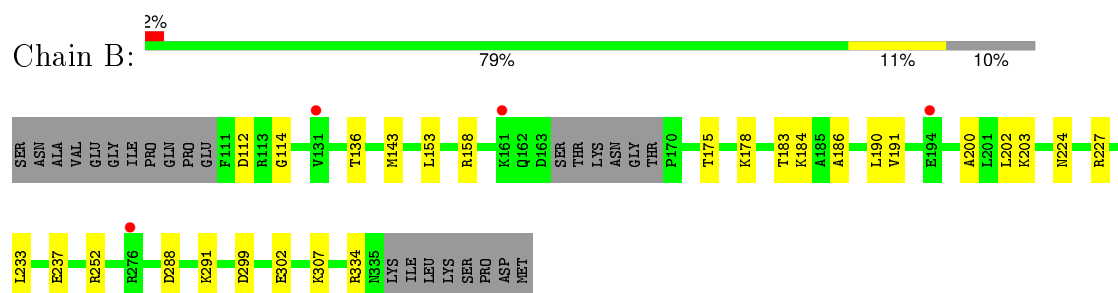
3 Residue-property plots

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.

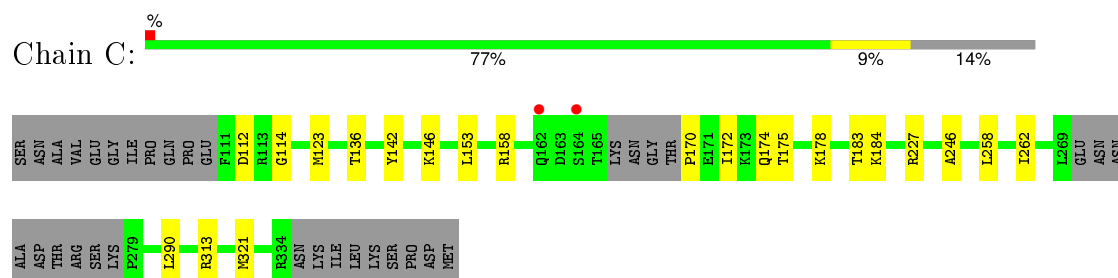
• Molecule 1: AVR-M-A



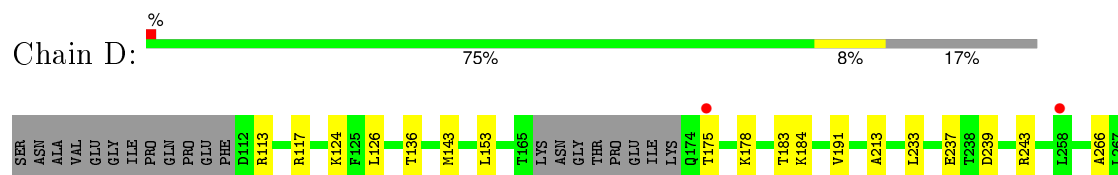
• Molecule 1: AVR-M-A

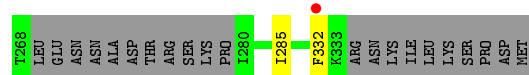


• Molecule 1: AVR-M-A

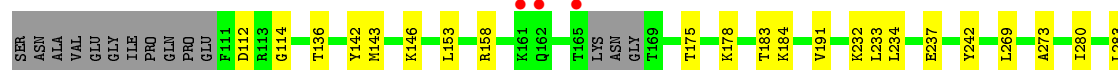
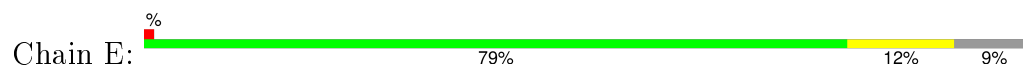


• Molecule 1: AVR-M-A

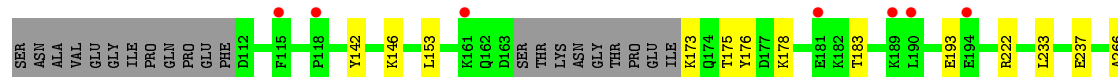
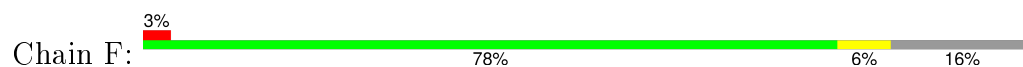




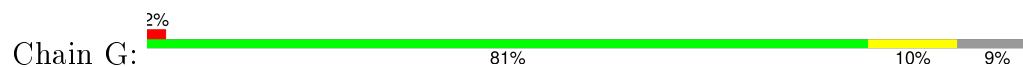
• Molecule 1: AVR-M-A



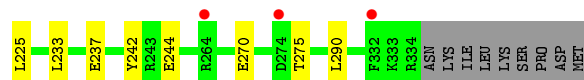
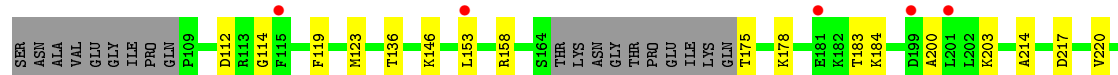
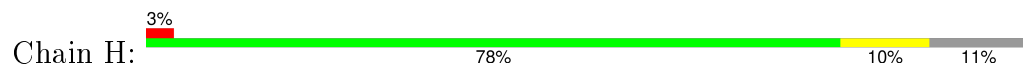
• Molecule 1: AVR-M-A



• Molecule 1: AVR-M-A



• Molecule 1: AVR-M-A



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	116.99Å 131.39Å 280.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.59 – 2.90 49.59 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.59-2.90) 99.9 (49.59-2.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.91Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.207 , 0.249 0.220 , 0.256	Depositor DCC
R_{free} test set	2438 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	74.6	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 50.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 48190 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13996	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.44	0/1826	0.59	0/2449
1	B	0.45	0/1805	0.61	0/2419
1	C	0.46	0/1738	0.60	0/2327
1	D	0.46	0/1665	0.60	0/2230
1	E	0.46	0/1825	0.58	0/2448
1	F	0.42	0/1697	0.58	0/2271
1	G	0.49	0/1832	0.64	0/2455
1	H	0.45	0/1777	0.58	0/2382
All	All	0.46	0/14165	0.60	0/18981

There are no bond length outliers.

There are no bond angle outliers.

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	1804	0	1847	14	0
1	B	1783	0	1829	18	0
1	C	1717	0	1770	13	0
1	D	1647	0	1691	10	0
1	E	1803	0	1847	22	0
1	F	1678	0	1730	9	0
1	G	1809	0	1864	16	0
1	H	1755	0	1796	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	13996	0	14374	104	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 4.

All (104) 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:G:335:ASN:HA	1:G:338:LEU:HD13	1.49	0.93
1:D:153:LEU:HB3	1:D:183:THR:HG22	1.66	0.77
1:B:153:LEU:HB3	1:B:183:THR:HG22	1.65	0.77
1:A:153:LEU:HB3	1:A:183:THR:HG22	1.67	0.77
1:F:153:LEU:HB3	1:F:183:THR:HG22	1.67	0.76
1:C:153:LEU:HB3	1:C:183:THR:HG22	1.68	0.76
1:H:153:LEU:HB3	1:H:183:THR:HG22	1.67	0.76
1:G:153:LEU:HB3	1:G:183:THR:HG22	1.67	0.75
1:E:153:LEU:HB3	1:E:183:THR:HG22	1.67	0.75
1:E:143:MET:CE	1:E:191:VAL:HG13	2.21	0.70
1:G:163:ASP:HB2	1:G:172:ILE:HG21	1.74	0.69
1:F:193:GLU:HB2	1:G:173:LYS:HE2	1.75	0.68
1:E:237:GLU:HG2	1:H:233:LEU:HD22	1.76	0.66
1:B:143:MET:CE	1:B:191:VAL:HG13	2.27	0.64
1:E:233:LEU:HD22	1:H:237:GLU:HG2	1.81	0.62
1:G:230:TYR:O	1:G:234:LEU:HB2	2.00	0.62
1:A:233:LEU:HD22	1:B:237:GLU:HG2	1.84	0.59
1:D:239:ASP:O	1:D:243:ARG:HG2	2.05	0.57
1:D:266:ALA:HA	1:D:285:ILE:HD12	1.86	0.57
1:C:258:LEU:O	1:C:262:ILE:HG12	2.07	0.55
1:A:113:ARG:HA	1:A:158:ARG:HH11	1.71	0.55
1:A:117:ARG:HH22	1:A:124:LYS:HD2	1.71	0.55
1:E:114:GLY:H	1:E:158:ARG:HD3	1.72	0.55
1:G:293:GLN:HA	1:G:296:LEU:HD12	1.90	0.54
1:G:198:ARG:HG2	1:G:334:ARG:HA	1.89	0.53
1:C:123:MET:CE	1:C:146:LYS:HD3	2.39	0.52
1:F:266:ALA:HA	1:F:285:ILE:HD12	1.92	0.52
1:F:323:GLU:HG3	1:H:275:THR:HG21	1.92	0.52
1:A:237:GLU:HG2	1:B:233:LEU:HD22	1.92	0.52
1:A:143:MET:HE1	1:A:215:LEU:HD22	1.91	0.52
1:C:123:MET:HE1	1:C:146:LYS:HD3	1.92	0.52
1:C:227:ARG:HD3	1:C:321:MET:SD	2.49	0.52
1:H:242:TYR:HA	1:H:290:LEU:HD21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:173:LYS:HA	1:F:176:TYR:HB3	1.93	0.49
1:F:233:LEU:O	1:F:237:GLU:HG3	2.13	0.49
1:C:174:GLN:HG2	1:C:178:LYS:HE3	1.94	0.48
1:H:214:ALA:HA	1:H:220:VAL:HG23	1.95	0.48
1:E:273:ALA:HB2	1:E:280:ILE:HD11	1.95	0.47
1:E:142:TYR:CZ	1:E:146:LYS:HE2	2.50	0.47
1:G:198:ARG:CB	1:G:337:ILE:HG13	2.44	0.47
1:C:170:PRO:HD2	1:C:172:ILE:HG12	1.97	0.47
1:E:293:GLN:HE21	1:H:119:PHE:HE2	1.62	0.47
1:B:224:ASN:HD21	1:B:227:ARG:HH21	1.62	0.47
1:F:222:ARG:HH12	1:H:275:THR:HA	1.80	0.47
1:H:217:ASP:HB3	1:H:220:VAL:HG22	1.97	0.47
1:C:112:ASP:O	1:C:158:ARG:HD2	2.15	0.47
1:B:186:ALA:O	1:B:190:LEU:HG	2.15	0.47
1:D:143:MET:CE	1:D:191:VAL:HG13	2.45	0.46
1:G:112:ASP:O	1:G:158:ARG:HD2	2.16	0.46
1:E:112:ASP:O	1:E:158:ARG:HD2	2.16	0.45
1:D:175:THR:HA	1:D:178:LYS:HD2	1.97	0.45
1:E:290:LEU:HD23	1:E:310:ILE:HD11	1.98	0.45
1:C:175:THR:HA	1:C:178:LYS:HD2	1.99	0.45
1:D:124:LYS:HE2	1:D:126:LEU:HD21	1.98	0.45
1:C:114:GLY:H	1:C:158:ARG:HD3	1.82	0.45
1:F:175:THR:HA	1:F:178:LYS:HD2	1.98	0.45
1:H:123:MET:CE	1:H:146:LYS:HD3	2.47	0.44
1:H:112:ASP:O	1:H:158:ARG:HD2	2.17	0.44
1:A:155:ILE:HG12	1:A:158:ARG:NH2	2.32	0.44
1:G:198:ARG:HB3	1:G:337:ILE:HG13	1.99	0.44
1:H:114:GLY:H	1:H:158:ARG:HD3	1.82	0.44
1:B:112:ASP:O	1:B:158:ARG:HD2	2.17	0.44
1:G:175:THR:HA	1:G:178:LYS:HD2	2.00	0.44
1:E:302:GLU:HA	1:H:225:LEU:HD21	2.00	0.44
1:E:269:LEU:HB3	1:E:280:ILE:HG12	2.00	0.44
1:A:175:THR:HA	1:A:178:LYS:HD2	1.99	0.44
1:F:142:TYR:CZ	1:F:146:LYS:HE2	2.52	0.44
1:B:136:THR:HG21	1:B:184:LYS:HE3	2.00	0.44
1:G:136:THR:HG21	1:G:184:LYS:HE3	1.99	0.44
1:H:175:THR:HA	1:H:178:LYS:HD2	1.99	0.43
1:E:136:THR:HG21	1:E:184:LYS:HE3	2.00	0.43
1:C:136:THR:HG21	1:C:184:LYS:HE3	2.01	0.43
1:A:122:LYS:HG3	1:B:299:ASP:HB3	2.00	0.43
1:B:175:THR:HA	1:B:178:LYS:HD2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:GLY:H	1:B:158:ARG:HD3	1.84	0.43
1:B:291:LYS:HG2	1:B:307:LYS:HG3	2.01	0.43
1:B:202:LEU:HA	1:B:334:ARG:HD2	2.00	0.42
1:D:233:LEU:O	1:D:237:GLU:HG3	2.19	0.42
1:H:136:THR:HG21	1:H:184:LYS:HE3	2.01	0.42
1:B:143:MET:HE3	1:B:191:VAL:HG13	2.01	0.42
1:G:114:GLY:H	1:G:158:ARG:HD3	1.84	0.42
1:C:142:TYR:CZ	1:C:146:LYS:HE2	2.54	0.42
1:E:232:LYS:HE2	1:H:244:GLU:OE2	2.19	0.42
1:C:246:ALA:HA	1:C:290:LEU:HD22	2.01	0.42
1:A:155:ILE:HG12	1:A:158:ARG:HH21	1.84	0.42
1:E:290:LEU:HD23	1:E:310:ILE:CD1	2.50	0.41
1:E:143:MET:HE3	1:E:191:VAL:HG13	2.01	0.41
1:D:136:THR:HG21	1:D:184:LYS:HE3	2.01	0.41
1:A:113:ARG:HD3	1:B:252:ARG:O	2.21	0.41
1:G:244:GLU:OE1	1:G:247:ARG:NH1	2.54	0.41
1:E:234:LEU:HG	1:E:283:LEU:HD11	2.01	0.41
1:E:242:TYR:HA	1:E:290:LEU:HD11	2.02	0.41
1:A:202:LEU:HD11	1:D:117:ARG:NH1	2.35	0.41
1:B:224:ASN:ND2	1:B:227:ARG:HH21	2.18	0.41
1:E:143:MET:HE2	1:E:191:VAL:HG13	2.00	0.41
1:E:302:GLU:HG3	1:H:225:LEU:HD11	2.03	0.41
1:E:175:THR:HA	1:E:178:LYS:HD2	2.02	0.41
1:A:225:LEU:HD21	1:B:302:GLU:HA	2.02	0.41
1:E:298:ALA:HB2	1:G:337:ILE:HD12	2.03	0.40
1:A:136:THR:HG21	1:A:184:LYS:HE3	2.02	0.40
1:H:200:ALA:HA	1:H:203:LYS:HD2	2.03	0.40
1:G:300:ASP:HB3	1:G:303:LEU:HB2	2.02	0.40
1:B:200:ALA:HA	1:B:203:LYS:HD2	2.03	0.40
1:D:213:ALA:HB2	1:D:332:PHE:HE2	1.86	0.40

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	218/244 (89%)	212 (97%)	6 (3%)	0	100	100
1	B	215/244 (88%)	212 (99%)	3 (1%)	0	100	100
1	C	205/244 (84%)	201 (98%)	4 (2%)	0	100	100
1	D	197/244 (81%)	194 (98%)	3 (2%)	0	100	100
1	E	218/244 (89%)	215 (99%)	3 (1%)	0	100	100
1	F	200/244 (82%)	196 (98%)	4 (2%)	0	100	100
1	G	219/244 (90%)	215 (98%)	4 (2%)	0	100	100
1	H	212/244 (87%)	207 (98%)	5 (2%)	0	100	100
All	All	1684/1952 (86%)	1652 (98%)	32 (2%)	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	190/209 (91%)	189 (100%)	1 (0%)	92	98
1	B	187/209 (90%)	186 (100%)	1 (0%)	92	98
1	C	180/209 (86%)	179 (99%)	1 (1%)	90	97
1	D	172/209 (82%)	171 (99%)	1 (1%)	90	97
1	E	190/209 (91%)	186 (98%)	4 (2%)	61	88
1	F	175/209 (84%)	175 (100%)	0	100	100
1	G	191/209 (91%)	189 (99%)	2 (1%)	82	95
1	H	184/209 (88%)	183 (100%)	1 (0%)	92	98
All	All	1469/1672 (88%)	1458 (99%)	11 (1%)	88	97

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	ARG
1	B	288	ASP
1	C	313	ARG
1	D	113	ARG
1	E	288	ASP
1	E	290	LEU
1	E	323	GLU
1	E	334	ARG
1	G	191	VAL
1	G	337	ILE
1	H	270	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	224	ASN
1	B	293	GLN
1	C	174	GLN
1	E	335	ASN

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 carbohydrates 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 ⓘ

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	222/244 (90%)	0.39	16 (7%) 18 12	54, 101, 167, 188	0
1	B	219/244 (89%)	0.01	4 (1%) 71 68	50, 93, 154, 188	0
1	C	211/244 (86%)	-0.06	2 (0%) 85 84	41, 78, 154, 185	0
1	D	203/244 (83%)	0.13	3 (1%) 76 74	45, 96, 149, 185	0
1	E	222/244 (90%)	-0.03	3 (1%) 78 76	46, 76, 125, 173	0
1	F	206/244 (84%)	0.16	7 (3%) 49 41	59, 100, 159, 203	0
1	G	223/244 (91%)	0.06	6 (2%) 58 52	48, 84, 175, 200	0
1	H	216/244 (88%)	0.30	8 (3%) 45 38	50, 95, 164, 186	0
All	All	1722/1952 (88%)	0.12	49 (2%) 56 50	41, 90, 159, 203	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	274	ASP	5.3
1	E	165	THR	4.4
1	A	334	ARG	4.3
1	H	274	ASP	4.0
1	A	140	ILE	3.6
1	C	162	GLN	3.6
1	E	162	GLN	3.4
1	G	279	PRO	3.4
1	A	191	VAL	3.3
1	G	166	LYS	3.3
1	A	170	PRO	3.3
1	H	115	PHE	3.2
1	H	181	GLU	3.1
1	G	258	LEU	3.1
1	G	167	ASN	3.0
1	D	332	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	181	GLU	2.9
1	H	201	LEU	2.8
1	A	115	PHE	2.8
1	A	190	LEU	2.7
1	A	178	LYS	2.7
1	H	199	ASP	2.6
1	G	249	PHE	2.5
1	H	153	LEU	2.5
1	A	175	THR	2.4
1	B	276	ARG	2.4
1	E	161	LYS	2.4
1	C	164	SER	2.3
1	F	189	LYS	2.3
1	A	203	LYS	2.3
1	A	270	GLU	2.3
1	B	194	GLU	2.3
1	F	194	GLU	2.3
1	B	161	LYS	2.3
1	A	114	GLY	2.2
1	F	190	LEU	2.2
1	A	195	SER	2.2
1	H	264	ARG	2.2
1	A	174	GLN	2.1
1	D	258	LEU	2.1
1	F	115	PHE	2.1
1	B	131	VAL	2.1
1	A	276	ARG	2.1
1	G	170	PRO	2.1
1	H	332	PHE	2.1
1	A	290	LEU	2.1
1	F	118	PRO	2.0
1	D	175	THR	2.0
1	F	161	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates 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.