



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:36 PM UTC

PDB ID : 1R5Z / pdb_00001r5z
Title : Crystal Structure of Subunit C of V-ATPase
Authors : Iwata, M.; Imamura, H.; Stambouli, E.; Ikeda, C.; Tamakoshi, M.; Nagata, K.; Makyio, H.; Hankamer, B.; Barber, J.; Yoshida, M.; Yokoyama, K.; Iwata, S.
Deposited on : 2003-10-14
Resolution : 1.95 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

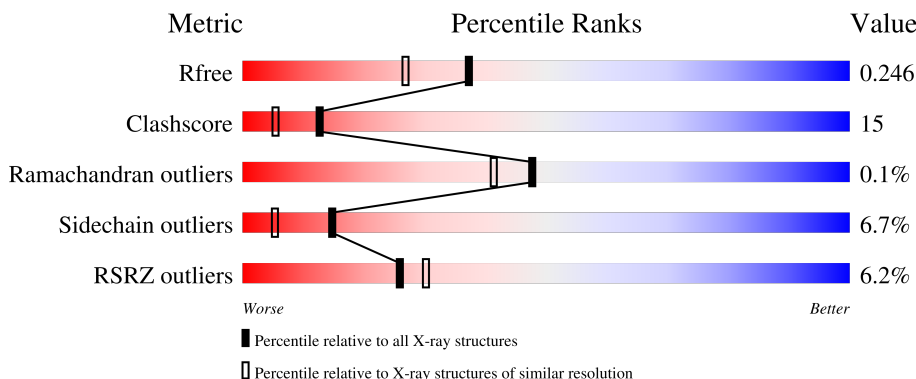
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	323	2% 77% 19% ..
1	B	323	4% 76% 18% ..
1	C	323	12% 72% 23% ...

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8179 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 V-type ATP synthase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	0	0
			2514	1599	460	451	4			
1	B	320	Total	C	N	O	S	0	0	0
			2514	1599	460	451	4			
1	C	320	Total	C	N	O	S	0	0	0
			2514	1599	460	451	4			

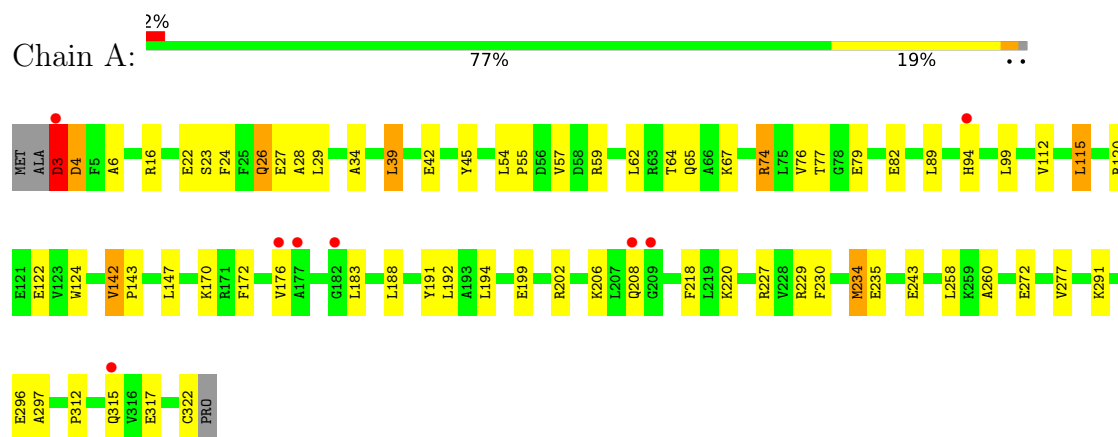
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	237	Total	O	0	0
			237	237		
2	B	217	Total	O	0	0
			217	217		
2	C	183	Total	O	0	0
			183	183		

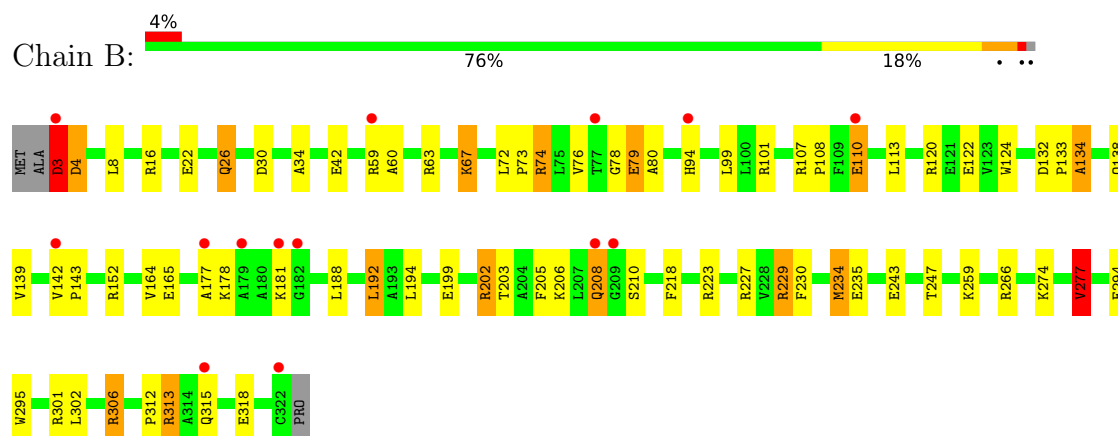
3 Residue-property plots [i](#)

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.

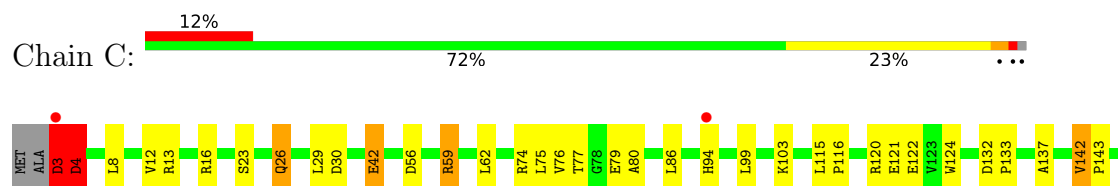
• Molecule 1: V-type ATP synthase subunit C

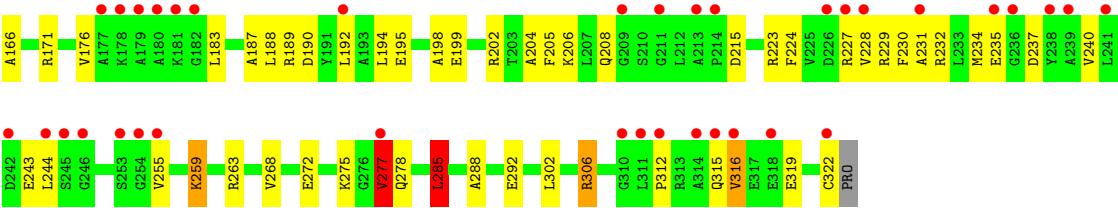


• Molecule 1: V-type ATP synthase subunit C



• Molecule 1: V-type ATP synthase subunit C





4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	118.43Å 118.43Å 152.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 1.95 40.00 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.7 (40.00-1.95) 99.3 (40.00-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.50 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.191 , 0.249 0.192 , 0.246	Depositor DCC
R_{free} test set	4353 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.029 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8179	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.91 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.2787e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	1.47	12/2553 (0.5%)	1.23	5/3447 (0.1%)
1	B	1.36	7/2553 (0.3%)	1.15	1/3447 (0.0%)
1	C	1.35	10/2553 (0.4%)	1.21	4/3447 (0.1%)
All	All	1.40	29/7659 (0.4%)	1.20	10/10341 (0.1%)

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	A	0	1
1	B	0	1
1	C	0	1
All	All	0	3

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	234	MET	SD-CE	-10.01	1.54	1.79
1	A	142	VAL	CA-CB	8.44	1.58	1.54
1	A	34	ALA	CA-CB	8.08	1.65	1.53
1	B	164	VAL	CA-CB	7.39	1.63	1.54
1	B	234	MET	SD-CE	-7.35	1.61	1.79
1	C	189	ARG	CA-C	-7.25	1.43	1.52
1	C	137	ALA	CA-CB	7.11	1.64	1.53
1	A	297	ALA	CA-CB	6.94	1.64	1.53
1	C	142	VAL	CA-CB	6.62	1.57	1.54
1	B	34	ALA	CA-CB	6.52	1.63	1.53
1	C	198	ALA	CA-CB	6.48	1.63	1.53
1	C	187	ALA	C-O	-6.39	1.16	1.24
1	C	12	VAL	CA-CB	6.22	1.62	1.54
1	B	60	ALA	CA-CB	6.09	1.62	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	268	VAL	CA-CB	6.09	1.61	1.54
1	B	134	ALA	CA-CB	5.98	1.62	1.53
1	C	166	ALA	CA-CB	5.85	1.62	1.53
1	B	247	THR	N-CA	5.80	1.50	1.46
1	A	260	ALA	CA-CB	-5.68	1.44	1.53
1	A	6	ALA	CA-CB	5.65	1.62	1.53
1	C	316	VAL	CA-CB	5.58	1.61	1.54
1	A	28	ALA	CA-CB	5.30	1.62	1.53
1	A	115	LEU	C-O	5.24	1.30	1.23
1	A	170	LYS	CA-C	-5.18	1.46	1.52
1	A	112	VAL	CA-C	5.13	1.58	1.52
1	A	147	LEU	C-O	-5.09	1.17	1.24
1	C	285	LEU	CA-C	5.08	1.59	1.52
1	B	203	THR	C-O	5.03	1.29	1.24
1	A	39	LEU	CA-C	5.02	1.59	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	ASP	CB-CA-C	7.26	122.64	110.43
1	C	4	ASP	CB-CA-C	6.97	122.02	110.03
1	A	142	VAL	N-CA-CB	6.73	115.03	110.52
1	C	142	VAL	N-CA-CB	6.27	114.72	110.52
1	C	277	VAL	CB-CA-C	-6.21	102.54	112.16
1	A	277	VAL	CB-CA-C	-6.06	102.77	112.16
1	C	30	ASP	N-CA-C	5.29	119.04	112.59
1	A	57	VAL	N-CA-C	-5.22	105.62	110.53
1	B	277	VAL	CB-CA-C	-5.09	105.37	112.04
1	A	89	LEU	N-CA-C	5.01	116.74	111.28

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	ASP	Peptide
1	B	3	ASP	Peptide
1	C	3	ASP	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	2514	0	2587	72	0
1	B	2514	0	2587	73	0
1	C	2514	0	2587	87	0
2	A	237	0	0	25	0
2	B	217	0	0	22	0
2	C	183	0	0	22	0
All	All	8179	0	7761	232	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 15.

All (232) 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:229:ARG:NH1	1:A:243:GLU:OE1	1.77	1.17
1:B:142:VAL:HG23	1:B:143:PRO:CD	1.75	1.14
1:B:142:VAL:HG23	1:B:143:PRO:HD3	1.11	1.09
1:A:94:HIS:HB2	2:A:529:HOH:O	1.51	1.08
1:B:165:GLU:HG2	2:B:523:HOH:O	1.51	1.08
1:B:110:GLU:H	1:B:110:GLU:CD	1.65	1.04
1:C:120:ARG:NH1	1:C:122:GLU:OE2	1.94	1.00
1:B:142:VAL:HG21	2:B:467:HOH:O	1.61	0.99
1:C:188:LEU:O	1:C:192:LEU:HD13	1.66	0.94
1:C:278:GLN:HG2	2:C:473:HOH:O	1.67	0.92
1:A:172:PHE:CE2	1:A:176:VAL:HG21	2.06	0.90
1:B:94:HIS:HB2	2:B:477:HOH:O	1.73	0.89
1:B:59:ARG:HG2	2:B:524:HOH:O	1.74	0.88
1:B:3:ASP:OD1	1:B:79:GLU:HG2	1.73	0.87
1:A:99:LEU:HB3	2:A:547:HOH:O	1.76	0.86
1:A:142:VAL:CG2	2:A:514:HOH:O	2.24	0.86
1:A:322:CYS:HB2	2:A:546:HOH:O	1.76	0.85
1:A:188:LEU:O	1:A:192:LEU:HD13	1.78	0.84
1:A:23:SER:O	1:A:27:GLU:HG3	1.77	0.84
1:B:120:ARG:HD2	1:B:122:GLU:OE2	1.78	0.83
1:A:3:ASP:HB2	1:A:79:GLU:HB3	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:VAL:HG23	1:A:143:PRO:HD3	1.59	0.82
1:C:259:LYS:HE3	1:C:319:GLU:OE2	1.78	0.82
1:A:322:CYS:SG	2:A:546:HOH:O	2.37	0.82
1:C:275:LYS:HD2	2:C:493:HOH:O	1.79	0.82
1:B:108:PRO:HB2	1:B:110:GLU:OE1	1.79	0.82
1:C:302:LEU:HG	2:C:395:HOH:O	1.79	0.82
1:B:110:GLU:OE1	1:B:110:GLU:N	2.13	0.81
1:B:313:ARG:HH11	1:B:313:ARG:HG3	1.44	0.81
1:C:171:ARG:HD3	2:C:487:HOH:O	1.80	0.81
1:C:188:LEU:CD1	1:C:192:LEU:HD11	2.10	0.81
1:A:23:SER:HA	1:A:26:GLN:HG3	1.63	0.81
1:A:322:CYS:C	2:A:545:HOH:O	2.23	0.80
1:A:23:SER:HA	1:A:26:GLN:CG	2.12	0.80
1:C:259:LYS:CE	1:C:319:GLU:OE2	2.30	0.79
1:C:120:ARG:HH12	1:C:122:GLU:HG3	1.50	0.77
1:A:322:CYS:CB	2:A:546:HOH:O	2.32	0.76
1:B:99:LEU:CD1	1:B:124:TRP:CE3	2.68	0.76
1:C:42:GLU:HG3	2:C:355:HOH:O	1.87	0.75
1:B:63:ARG:HD3	2:B:432:HOH:O	1.87	0.73
1:B:142:VAL:CG2	2:B:467:HOH:O	2.26	0.73
1:A:77:THR:HG23	2:A:479:HOH:O	1.88	0.73
1:B:142:VAL:CG2	1:B:143:PRO:CD	2.62	0.73
1:C:142:VAL:CG2	1:C:143:PRO:HD3	2.18	0.72
1:C:142:VAL:HG23	1:C:143:PRO:HD3	1.71	0.72
1:C:205:PHE:O	1:C:208:GLN:HG2	1.88	0.72
1:C:59:ARG:HD3	2:C:426:HOH:O	1.88	0.72
1:B:294:GLU:OE1	2:B:508:HOH:O	2.07	0.72
1:B:218:PHE:CE2	1:B:227:ARG:HG2	2.25	0.71
1:C:229:ARG:NH1	1:C:243:GLU:OE1	2.23	0.71
1:A:59:ARG:NH1	2:A:399:HOH:O	2.24	0.70
1:B:188:LEU:HG	1:B:192:LEU:HD22	1.73	0.70
1:B:139:VAL:O	1:B:142:VAL:HG22	1.91	0.70
1:C:120:ARG:NH1	1:C:122:GLU:CG	2.55	0.69
1:C:3:ASP:OD2	1:C:4:ASP:HA	1.92	0.69
1:A:291:LYS:NZ	2:A:421:HOH:O	2.26	0.69
1:C:120:ARG:NH1	1:C:122:GLU:HG3	2.08	0.68
1:B:313:ARG:HG3	1:B:313:ARG:NH1	2.03	0.67
1:A:172:PHE:CZ	1:A:176:VAL:HG21	2.30	0.66
1:C:3:ASP:HB2	1:C:80:ALA:H	1.60	0.65
1:C:99:LEU:CD1	1:C:124:TRP:CE3	2.80	0.65
1:C:94:HIS:ND1	2:C:370:HOH:O	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:223:ARG:HD2	2:C:407:HOH:O	1.96	0.65
1:B:22:GLU:O	1:B:26:GLN:HG3	1.97	0.64
1:A:312:PRO:HG2	1:A:315:GLN:HB2	1.80	0.64
1:A:229:ARG:HH11	1:A:229:ARG:HG2	1.63	0.63
1:B:63:ARG:O	1:B:67:LYS:HG2	1.98	0.62
1:C:120:ARG:NH1	1:C:122:GLU:CD	2.58	0.62
1:B:3:ASP:OD2	1:B:3:ASP:C	2.43	0.61
1:A:208:GLN:HG3	2:A:555:HOH:O	2.00	0.61
1:C:275:LYS:CD	2:C:493:HOH:O	2.45	0.61
1:C:312:PRO:HD2	1:C:315:GLN:OE1	2.00	0.61
1:A:120:ARG:NH1	1:A:122:GLU:HG3	2.16	0.61
1:B:99:LEU:CD1	1:B:124:TRP:HE3	2.13	0.60
1:A:227:ARG:NH1	2:A:515:HOH:O	2.28	0.60
1:B:122:GLU:HB2	2:B:479:HOH:O	1.99	0.60
1:B:229:ARG:CG	1:B:229:ARG:HH11	2.13	0.60
1:A:172:PHE:CE2	1:A:176:VAL:CG2	2.85	0.59
1:C:3:ASP:HB2	1:C:80:ALA:N	2.17	0.59
1:C:263:ARG:NE	1:C:319:GLU:OE1	2.33	0.59
1:B:229:ARG:HH11	1:B:229:ARG:HG2	1.68	0.59
1:A:142:VAL:CG2	1:A:143:PRO:HD3	2.29	0.58
1:C:188:LEU:O	1:C:192:LEU:CD1	2.46	0.58
1:A:99:LEU:HD22	2:A:547:HOH:O	2.04	0.58
1:A:79:GLU:HG3	1:A:183:LEU:HD22	1.85	0.58
1:A:27:GLU:HB3	2:A:530:HOH:O	2.04	0.58
1:B:230:PHE:CZ	1:B:234:MET:HE3	2.38	0.58
1:C:188:LEU:HG	1:C:192:LEU:CD1	2.33	0.58
1:A:172:PHE:CZ	1:A:176:VAL:CG2	2.86	0.57
1:C:142:VAL:CG2	2:C:345:HOH:O	2.52	0.57
1:C:199:GLU:OE1	1:C:202:ARG:NH1	2.37	0.57
1:B:229:ARG:NH1	1:B:243:GLU:OE1	2.37	0.57
1:C:13:ARG:HD2	2:C:457:HOH:O	2.04	0.57
1:C:188:LEU:CD1	1:C:192:LEU:CD1	2.81	0.57
1:C:322:CYS:C	2:C:483:HOH:O	2.47	0.56
1:A:3:ASP:CB	1:A:79:GLU:HB3	2.34	0.56
1:B:3:ASP:OD2	1:B:4:ASP:HA	2.05	0.56
1:C:237:ASP:O	1:C:240:VAL:HG23	2.06	0.56
1:B:99:LEU:HD13	1:B:124:TRP:HE3	1.71	0.55
1:C:3:ASP:OD2	1:C:4:ASP:CA	2.54	0.55
1:C:120:ARG:HH11	1:C:122:GLU:CD	2.05	0.55
1:A:79:GLU:HB2	2:A:533:HOH:O	2.06	0.55
1:B:3:ASP:HB2	1:B:80:ALA:H	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:59:ARG:CZ	2:C:359:HOH:O	2.53	0.55
1:A:59:ARG:NH1	2:A:523:HOH:O	2.39	0.55
1:B:208:GLN:HG3	2:B:525:HOH:O	2.07	0.55
1:C:142:VAL:HG22	2:C:345:HOH:O	2.06	0.55
1:C:194:LEU:HD12	1:C:272:GLU:CG	2.37	0.55
1:C:223:ARG:HD3	1:C:224:PHE:CZ	2.43	0.54
1:C:29:LEU:O	1:C:306:ARG:NH1	2.40	0.54
1:C:115:LEU:HB3	1:C:116:PRO:HD2	1.89	0.54
1:A:120:ARG:HH11	1:A:122:GLU:CG	2.21	0.54
1:B:59:ARG:HD3	2:B:524:HOH:O	2.07	0.54
1:A:94:HIS:CG	1:A:115:LEU:HD12	2.42	0.53
1:B:78:GLY:C	2:B:533:HOH:O	2.51	0.53
1:C:188:LEU:HD11	1:C:192:LEU:HD11	1.85	0.53
1:B:230:PHE:CZ	1:B:234:MET:CE	2.91	0.53
1:C:188:LEU:HG	1:C:192:LEU:HD11	1.91	0.53
1:B:266:ARG:HD2	1:B:295:TRP:CZ3	2.44	0.53
1:C:194:LEU:HD12	1:C:272:GLU:CD	2.33	0.53
1:C:272:GLU:OE1	2:C:492:HOH:O	2.19	0.52
1:A:99:LEU:CB	2:A:547:HOH:O	2.47	0.52
1:B:8:LEU:HD11	1:B:72:LEU:HD22	1.90	0.52
1:C:288:ALA:O	1:C:292:GLU:HG3	2.10	0.52
1:A:99:LEU:CD1	1:A:124:TRP:CE3	2.93	0.51
1:C:188:LEU:HD12	1:C:192:LEU:CD1	2.40	0.51
1:C:79:GLU:HG3	1:C:183:LEU:HD22	1.91	0.51
1:C:99:LEU:CD1	1:C:124:TRP:HE3	2.23	0.51
1:C:142:VAL:HG22	1:C:143:PRO:HD3	1.91	0.51
1:C:188:LEU:CG	1:C:192:LEU:HD11	2.40	0.51
1:A:120:ARG:NH1	1:A:122:GLU:CG	2.73	0.51
1:A:220:LYS:CD	1:A:227:ARG:HH22	2.23	0.50
1:B:266:ARG:HD3	2:B:509:HOH:O	2.09	0.50
1:C:204:ALA:HB2	1:C:230:PHE:CD1	2.45	0.50
1:A:23:SER:O	1:A:27:GLU:CG	2.56	0.50
1:C:59:ARG:NE	2:C:359:HOH:O	2.43	0.50
1:C:8:LEU:HD13	1:C:75:LEU:HB2	1.93	0.50
1:C:79:GLU:HB2	2:C:484:HOH:O	2.10	0.50
1:C:132:ASP:HB2	1:C:133:PRO:HD2	1.94	0.50
1:A:220:LYS:HD2	1:A:227:ARG:HH22	1.76	0.50
1:C:16:ARG:HD3	2:C:474:HOH:O	2.11	0.49
1:B:74:ARG:O	1:B:74:ARG:HG3	2.10	0.49
1:C:94:HIS:CE1	2:C:370:HOH:O	2.66	0.49
1:B:3:ASP:HB3	2:B:419:HOH:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:GLU:CD	1:B:110:GLU:N	2.45	0.48
1:B:134:ALA:O	1:B:138:GLN:HG3	2.13	0.48
1:A:230:PHE:CZ	1:A:234:MET:HE1	2.48	0.48
1:C:59:ARG:NH1	2:C:360:HOH:O	2.45	0.48
1:A:54:LEU:HB3	1:A:55:PRO:HD3	1.94	0.48
1:C:215:ASP:HB2	2:C:444:HOH:O	2.13	0.48
1:C:142:VAL:CG2	1:C:143:PRO:CD	2.90	0.48
1:A:22:GLU:O	1:A:26:GLN:HG2	2.13	0.48
1:A:29:LEU:HD11	1:A:317:GLU:HG3	1.96	0.47
1:B:142:VAL:HG23	1:B:143:PRO:HD2	1.84	0.47
1:A:42:GLU:CG	2:A:371:HOH:O	2.61	0.47
1:C:3:ASP:OD2	1:C:3:ASP:C	2.58	0.47
1:A:59:ARG:CZ	2:A:523:HOH:O	2.61	0.47
1:B:113:LEU:HD13	1:B:301:ARG:HD3	1.95	0.47
1:A:312:PRO:HD2	1:A:315:GLN:OE1	2.14	0.47
1:B:72:LEU:N	1:B:73:PRO:CD	2.78	0.47
1:C:277:VAL:O	1:C:285:LEU:HD13	2.16	0.46
1:A:94:HIS:CD2	1:A:115:LEU:HD12	2.50	0.46
1:B:205:PHE:O	1:B:208:GLN:NE2	2.49	0.46
1:A:82:GLU:HG2	2:A:548:HOH:O	2.15	0.46
1:A:208:GLN:HA	1:A:234:MET:O	2.16	0.46
1:B:79:GLU:N	2:B:533:HOH:O	2.47	0.46
1:B:306:ARG:HD3	2:B:337:HOH:O	2.16	0.46
1:B:63:ARG:HD2	2:B:502:HOH:O	2.15	0.46
1:C:23:SER:HA	1:C:26:GLN:CG	2.46	0.45
1:B:274:LYS:O	1:B:277:VAL:HG22	2.16	0.45
1:C:223:ARG:HD3	1:C:224:PHE:CE2	2.50	0.45
1:A:191:TYR:OH	2:A:472:HOH:O	2.19	0.45
1:B:313:ARG:HH11	1:B:313:ARG:CG	2.17	0.45
1:C:208:GLN:HA	1:C:234:MET:O	2.16	0.45
1:B:30:ASP:OD1	1:B:313:ARG:NE	2.39	0.45
1:B:229:ARG:CG	1:B:229:ARG:NH1	2.79	0.45
1:C:188:LEU:C	1:C:192:LEU:HD13	2.38	0.45
1:A:229:ARG:HH11	1:A:229:ARG:CG	2.27	0.45
1:C:23:SER:HA	1:C:26:GLN:HG2	1.99	0.45
1:B:113:LEU:HD23	2:B:538:HOH:O	2.17	0.44
1:C:103:LYS:NZ	2:C:448:HOH:O	2.51	0.44
1:A:3:ASP:C	1:A:3:ASP:OD2	2.61	0.44
1:B:223:ARG:NH1	2:B:438:HOH:O	2.51	0.44
1:B:312:PRO:HG2	1:B:315:GLN:HB2	2.00	0.44
1:C:194:LEU:HD12	1:C:272:GLU:HG2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:VAL:HG21	2:A:514:HOH:O	2.04	0.43
1:C:99:LEU:HD12	1:C:124:TRP:CE3	2.53	0.43
1:C:204:ALA:HB2	1:C:230:PHE:CE1	2.53	0.43
1:C:259:LYS:HE2	1:C:263:ARG:HH21	1.83	0.43
1:B:72:LEU:N	1:B:73:PRO:HD3	2.34	0.43
1:C:56:ASP:HA	1:C:59:ARG:NH1	2.33	0.43
1:B:3:ASP:O	1:B:4:ASP:HB3	2.19	0.43
1:B:142:VAL:CG2	1:B:143:PRO:HD2	2.46	0.43
1:A:188:LEU:CD1	1:A:192:LEU:HD11	2.49	0.43
1:B:206:LYS:HD3	2:B:472:HOH:O	2.18	0.43
1:C:188:LEU:CG	1:C:192:LEU:CD1	2.97	0.43
1:C:188:LEU:HG	1:C:192:LEU:HD13	1.99	0.43
1:C:230:PHE:CZ	1:C:234:MET:HE3	2.53	0.43
1:B:132:ASP:HB2	1:B:133:PRO:HD2	2.01	0.43
1:B:16:ARG:HH11	1:B:16:ARG:HD3	1.67	0.42
1:C:312:PRO:CD	1:C:315:GLN:OE1	2.67	0.42
1:C:231:ALA:O	1:C:235:GLU:HG2	2.19	0.42
1:A:229:ARG:NH1	1:A:229:ARG:HG2	2.34	0.42
1:A:194:LEU:HD12	1:A:272:GLU:CG	2.50	0.42
1:A:24:PHE:CE1	1:A:39:LEU:HG	2.55	0.42
1:A:235:GLU:HG3	2:A:527:HOH:O	2.20	0.42
1:B:101:ARG:NE	1:B:165:GLU:OE2	2.50	0.42
1:C:86:LEU:HD22	1:C:176:VAL:HG22	2.01	0.42
1:C:244:LEU:HD23	1:C:244:LEU:HA	1.82	0.42
1:A:227:ARG:HG3	2:A:409:HOH:O	2.18	0.42
1:A:199:GLU:OE1	1:A:202:ARG:NH1	2.53	0.41
1:B:59:ARG:CD	2:B:524:HOH:O	2.67	0.41
1:B:199:GLU:OE1	1:B:202:ARG:NH1	2.51	0.41
1:A:39:LEU:O	1:A:42:GLU:HG2	2.20	0.41
1:C:132:ASP:HB2	1:C:133:PRO:CD	2.50	0.41
1:A:16:ARG:HH11	1:A:16:ARG:HD3	1.63	0.41
1:B:107:ARG:HA	1:B:108:PRO:HD3	1.93	0.41
1:B:177:ALA:HB3	2:B:520:HOH:O	2.20	0.41
1:B:205:PHE:O	1:B:208:GLN:CD	2.64	0.41
1:C:228:VAL:O	1:C:232:ARG:HG3	2.21	0.41
1:B:315:GLN:C	2:B:365:HOH:O	2.63	0.41
1:C:142:VAL:HG23	1:C:143:PRO:CD	2.46	0.41
1:A:208:GLN:HB2	2:A:555:HOH:O	2.20	0.41
1:A:230:PHE:CZ	1:A:234:MET:CE	3.03	0.41
1:A:23:SER:HA	1:A:26:GLN:HG2	1.97	0.41
1:A:45:TYR:OH	1:A:296:GLU:OE1	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:ARG:O	1:A:74:ARG:HG3	2.20	0.40
1:A:206:LYS:HE3	1:A:258:LEU:HD21	2.03	0.40
1:B:192:LEU:HD12	1:B:192:LEU:HA	1.82	0.40
1:B:99:LEU:HD11	1:B:124:TRP:CE3	2.55	0.40
1:A:218:PHE:CE2	1:A:227:ARG:HG2	2.56	0.40
1:A:64:THR:HA	1:A:67:LYS:HD3	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	318/323 (98%)	314 (99%)	4 (1%)	0	100	100
1	B	318/323 (98%)	312 (98%)	5 (2%)	1 (0%)	36	28
1	C	318/323 (98%)	311 (98%)	7 (2%)	0	100	100
All	All	954/969 (98%)	937 (98%)	16 (2%)	1 (0%)	48	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	210	SER

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	254/256 (99%)	247 (97%)	7 (3%)	38	30
1	B	254/256 (99%)	230 (91%)	24 (9%)	8	2
1	C	254/256 (99%)	234 (92%)	20 (8%)	11	3
All	All	762/768 (99%)	711 (93%)	51 (7%)	15	5

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASP
1	A	4	ASP
1	A	26	GLN
1	A	62	LEU
1	A	65	GLN
1	A	74	ARG
1	A	76	VAL
1	B	3	ASP
1	B	4	ASP
1	B	26	GLN
1	B	42	GLU
1	B	67	LYS
1	B	74	ARG
1	B	76	VAL
1	B	79	GLU
1	B	110	GLU
1	B	152	ARG
1	B	178	LYS
1	B	181	LYS
1	B	192	LEU
1	B	194	LEU
1	B	202	ARG
1	B	208	GLN
1	B	229	ARG
1	B	235	GLU
1	B	259	LYS
1	B	277	VAL
1	B	302	LEU
1	B	306	ARG
1	B	313	ARG
1	B	318	GLU
1	C	3	ASP
1	C	4	ASP
1	C	26	GLN

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Mol	Chain	Res	Type
1	C	42	GLU
1	C	59	ARG
1	C	62	LEU
1	C	74	ARG
1	C	76	VAL
1	C	77	THR
1	C	121	GLU
1	C	190	ASP
1	C	195	GLU
1	C	206	LYS
1	C	227	ARG
1	C	255	VAL
1	C	259	LYS
1	C	277	VAL
1	C	285	LEU
1	C	306	ARG
1	C	316	VAL

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	94	HIS
1	B	26	GLN
1	B	94	HIS
1	B	138	GLN
1	B	208	GLN
1	C	65	GLN
1	C	208	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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	320/323 (99%)	0.21	8 (2%) 58 65	18, 28, 47, 57	0
1	B	320/323 (99%)	0.32	14 (4%) 39 45	22, 32, 51, 65	0
1	C	320/323 (99%)	0.65	38 (11%) 9 10	22, 34, 61, 70	0
All	All	960/969 (99%)	0.39	60 (6%) 26 30	18, 31, 56, 70	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	322	CYS	4.0
1	C	209	GLY	3.9
1	A	209	GLY	3.8
1	C	177	ALA	3.5
1	B	3	ASP	3.3
1	B	315	GLN	3.3
1	C	228	VAL	3.2
1	C	315	GLN	3.2
1	C	235	GLU	3.2
1	C	245	SER	3.2
1	C	310	GLY	3.1
1	C	181	LYS	3.1
1	C	211	GLY	3.0
1	B	209	GLY	3.0
1	B	177	ALA	3.0
1	C	239	ALA	3.0
1	C	3	ASP	2.9
1	A	3	ASP	2.9
1	B	77	THR	2.8
1	A	315	GLN	2.8
1	C	312	PRO	2.8
1	C	180	ALA	2.7
1	C	314	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	236	GLY	2.7
1	C	254	GLY	2.7
1	C	178	LYS	2.6
1	B	142	VAL	2.6
1	B	208	GLN	2.6
1	A	176	VAL	2.6
1	C	311	LEU	2.6
1	B	94	HIS	2.5
1	B	322	CYS	2.4
1	C	238	TYR	2.4
1	C	192	LEU	2.4
1	C	253	SER	2.4
1	C	226	ASP	2.3
1	C	227	ARG	2.3
1	C	94	HIS	2.3
1	C	246	GLY	2.3
1	C	241	LEU	2.3
1	B	182	GLY	2.3
1	C	244	LEU	2.3
1	C	231	ALA	2.3
1	A	208	GLN	2.3
1	A	177	ALA	2.2
1	A	182	GLY	2.2
1	C	242	ASP	2.2
1	C	179	ALA	2.2
1	C	213	ALA	2.2
1	A	94	HIS	2.2
1	C	214	PRO	2.2
1	C	318	GLU	2.1
1	C	277	VAL	2.1
1	B	181	LYS	2.1
1	B	110	GLU	2.1
1	C	182	GLY	2.1
1	B	59	ARG	2.1
1	B	179	ALA	2.0
1	C	255	VAL	2.0
1	C	316	VAL	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 [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.