



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 01:14 am BST

PDB ID : 5WCO
Title : Matrix Protein (M1) of Infectious Salmon Anaemia Virus
Authors : Zhang, W.; Zheng, W.; Toh, Y.; Betancourt, M.A.; Tu, J.; Fan, Y.; Vakharia, V.; Liu, J.; McNew, J.A.; Jin, M.; Tao, Y.J.
Deposited on : 2017-07-01
Resolution : 2.60 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

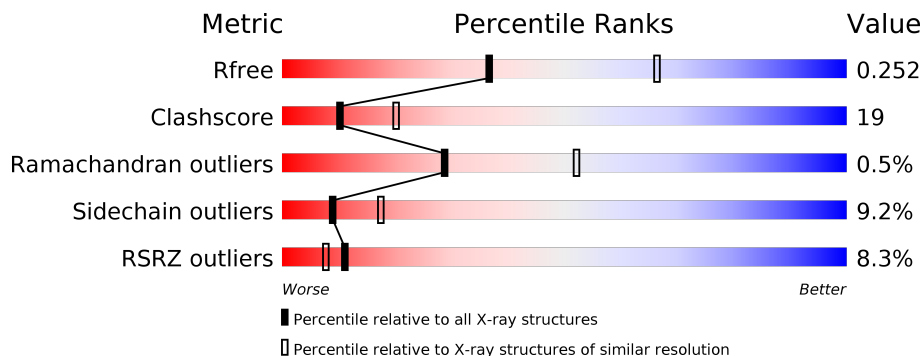
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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	216	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 63%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 25%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">4% 63% 25% • 9%</p>
1	B	216	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 59%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 25%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">8% 59% 25% 6% 9%</p>
1	C	216	<div style="display: flex; align-items: center;"> <div style="width: 11%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 62%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 26%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: grey;"></div> </div> <p style="font-size: small; margin-top: 5px;">11% 62% 26% •• 9%</p>

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 4584 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 NS2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	196	1524	961	266	277	20	0	0	0
1	B	196	1524	961	266	277	20	0	0	0
1	C	196	1521	958	266	277	20	0	0	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q910W0
A	-18	GLY	-	expression tag	UNP Q910W0
A	-17	SER	-	expression tag	UNP Q910W0
A	-16	SER	-	expression tag	UNP Q910W0
A	-15	HIS	-	expression tag	UNP Q910W0
A	-14	HIS	-	expression tag	UNP Q910W0
A	-13	HIS	-	expression tag	UNP Q910W0
A	-12	HIS	-	expression tag	UNP Q910W0
A	-11	HIS	-	expression tag	UNP Q910W0
A	-10	HIS	-	expression tag	UNP Q910W0
A	-9	SER	-	expression tag	UNP Q910W0
A	-8	SER	-	expression tag	UNP Q910W0
A	-7	GLY	-	expression tag	UNP Q910W0
A	-6	LEU	-	expression tag	UNP Q910W0
A	-5	VAL	-	expression tag	UNP Q910W0
A	-4	PRO	-	expression tag	UNP Q910W0
A	-3	ARG	-	expression tag	UNP Q910W0
A	-2	GLY	-	expression tag	UNP Q910W0
A	-1	SER	-	expression tag	UNP Q910W0
A	0	HIS	-	expression tag	UNP Q910W0
B	-19	MET	-	expression tag	UNP Q910W0
B	-18	GLY	-	expression tag	UNP Q910W0
B	-17	SER	-	expression tag	UNP Q910W0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	SER	-	expression tag	UNP Q910W0
B	-15	HIS	-	expression tag	UNP Q910W0
B	-14	HIS	-	expression tag	UNP Q910W0
B	-13	HIS	-	expression tag	UNP Q910W0
B	-12	HIS	-	expression tag	UNP Q910W0
B	-11	HIS	-	expression tag	UNP Q910W0
B	-10	HIS	-	expression tag	UNP Q910W0
B	-9	SER	-	expression tag	UNP Q910W0
B	-8	SER	-	expression tag	UNP Q910W0
B	-7	GLY	-	expression tag	UNP Q910W0
B	-6	LEU	-	expression tag	UNP Q910W0
B	-5	VAL	-	expression tag	UNP Q910W0
B	-4	PRO	-	expression tag	UNP Q910W0
B	-3	ARG	-	expression tag	UNP Q910W0
B	-2	GLY	-	expression tag	UNP Q910W0
B	-1	SER	-	expression tag	UNP Q910W0
B	0	HIS	-	expression tag	UNP Q910W0
C	-19	MET	-	expression tag	UNP Q910W0
C	-18	GLY	-	expression tag	UNP Q910W0
C	-17	SER	-	expression tag	UNP Q910W0
C	-16	SER	-	expression tag	UNP Q910W0
C	-15	HIS	-	expression tag	UNP Q910W0
C	-14	HIS	-	expression tag	UNP Q910W0
C	-13	HIS	-	expression tag	UNP Q910W0
C	-12	HIS	-	expression tag	UNP Q910W0
C	-11	HIS	-	expression tag	UNP Q910W0
C	-10	HIS	-	expression tag	UNP Q910W0
C	-9	SER	-	expression tag	UNP Q910W0
C	-8	SER	-	expression tag	UNP Q910W0
C	-7	GLY	-	expression tag	UNP Q910W0
C	-6	LEU	-	expression tag	UNP Q910W0
C	-5	VAL	-	expression tag	UNP Q910W0
C	-4	PRO	-	expression tag	UNP Q910W0
C	-3	ARG	-	expression tag	UNP Q910W0
C	-2	GLY	-	expression tag	UNP Q910W0
C	-1	SER	-	expression tag	UNP Q910W0
C	0	HIS	-	expression tag	UNP Q910W0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	6	Total O 6 6	0	0

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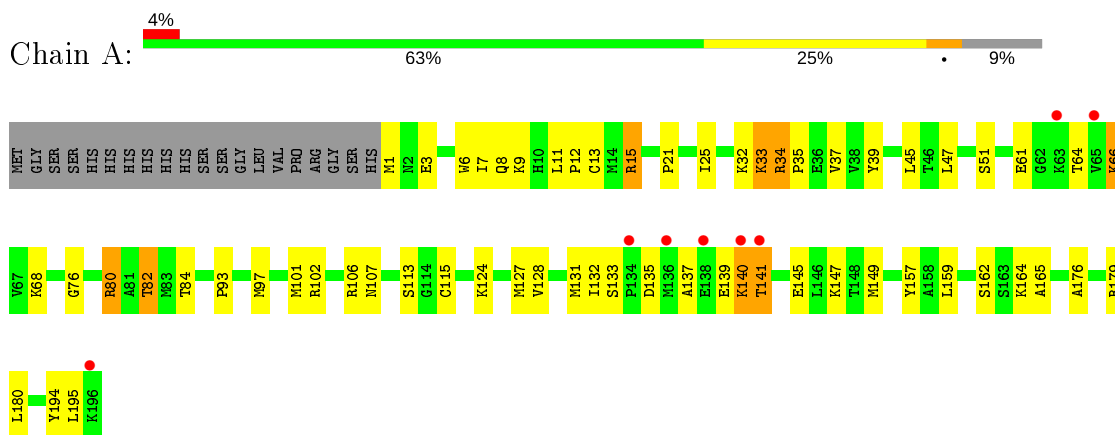
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	7	Total O 7 7	0	0
2	C	2	Total O 2 2	0	0

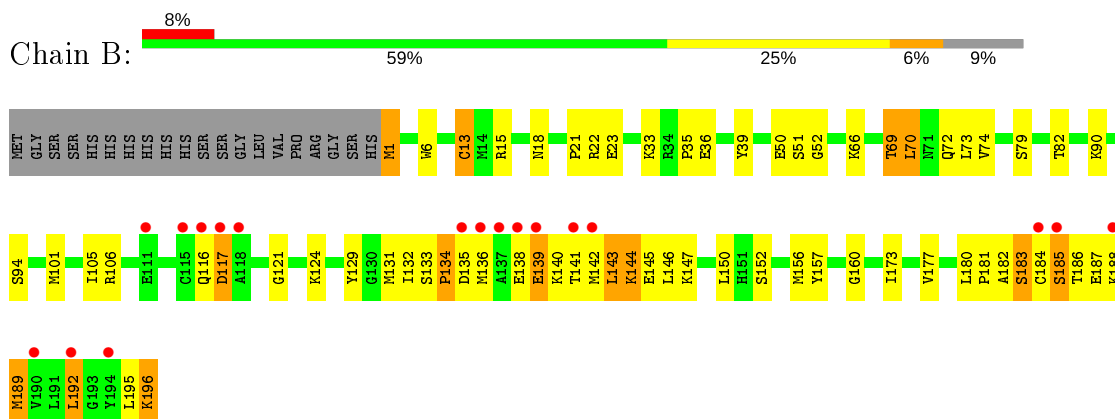
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

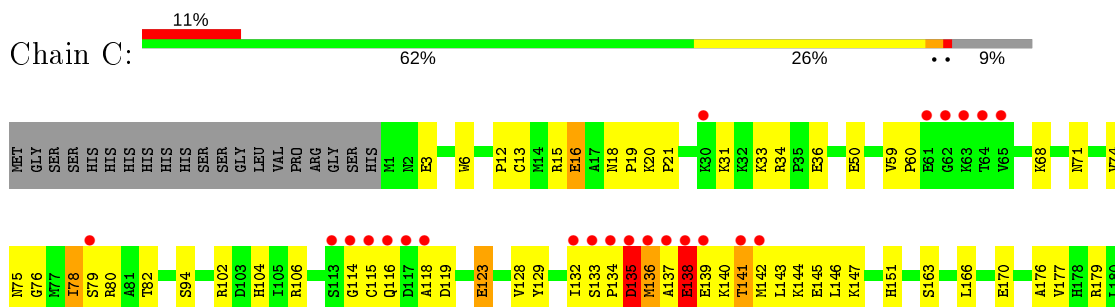
- Molecule 1: NS2



- Molecule 1: NS2



- Molecule 1: NS2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	38.80Å 95.89Å 85.41Å 90.00° 93.03° 90.00°	Depositor
Resolution (Å)	28.05 – 2.60 28.05 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.3 (28.05-2.60) 98.3 (28.05-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.61Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.203 , 0.253 0.202 , 0.252	Depositor DCC
R_{free} test set	921 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	56.3	Xtrriage
Anisotropy	0.168	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4584	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.01% 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	0.52	0/1550	0.70	2/2082 (0.1%)
1	B	0.50	0/1550	0.78	6/2082 (0.3%)
1	C	0.47	0/1547	0.73	1/2078 (0.0%)
All	All	0.50	0/4647	0.74	9/6242 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	195	LEU	N-CA-C	-8.02	89.35	111.00
1	C	135	ASP	N-CA-C	-7.48	90.81	111.00
1	A	141	THR	N-CA-CB	7.44	124.43	110.30
1	B	185	SER	N-CA-C	7.22	130.50	111.00
1	A	140	LYS	N-CA-C	-7.02	92.04	111.00
1	B	52	GLY	N-CA-C	-6.21	97.58	113.10
1	B	196	LYS	N-CA-CB	-5.68	100.37	110.60
1	B	184	CYS	N-CA-C	-5.50	96.14	111.00
1	B	183	SER	N-CA-C	-5.21	96.92	111.00

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	1524	0	1583	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1524	0	1583	56	0
1	C	1521	0	1572	74	0
2	A	6	0	0	1	0
2	B	7	0	0	0	0
2	C	2	0	0	0	0
All	All	4584	0	4738	175	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 19.

All (175) 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:139:GLU:OE2	1:A:141:THR:CG2	1.66	1.44
1:C:132:ILE:O	1:C:147:LYS:HD2	1.44	1.18
1:C:133:SER:HB3	1:C:134:PRO:HD2	1.17	1.16
1:C:133:SER:O	1:C:135:ASP:OD2	1.70	1.09
1:B:13:CYS:SG	1:B:33:LYS:NZ	2.26	1.08
1:A:139:GLU:HG3	1:A:141:THR:OG1	1.53	1.06
1:A:139:GLU:CD	1:A:141:THR:HG21	1.77	1.04
1:C:141:THR:O	1:C:145:GLU:OE1	1.77	1.02
1:A:33:LYS:NZ	1:A:115:CYS:SG	2.35	0.97
1:A:140:LYS:O	1:A:141:THR:HG23	1.64	0.97
1:C:136:MET:SD	1:C:138:GLU:HA	2.06	0.96
1:C:133:SER:HB3	1:C:134:PRO:CD	1.98	0.90
1:A:139:GLU:CG	1:A:141:THR:OG1	2.18	0.90
1:A:139:GLU:OE2	1:A:141:THR:HG21	0.72	0.89
1:A:76:GLY:HA3	1:A:84:THR:HG21	1.57	0.86
1:C:13:CYS:SG	1:C:33:LYS:NZ	2.49	0.85
1:B:140:LYS:HE2	1:B:144:LYS:HB3	1.60	0.82
1:C:132:ILE:O	1:C:147:LYS:CD	2.27	0.81
1:C:133:SER:CB	1:C:134:PRO:HD2	2.08	0.80
1:C:142:MET:O	1:C:146:LEU:N	2.13	0.80
1:C:33:LYS:NZ	1:C:115:CYS:SG	2.55	0.79
1:B:135:ASP:HB3	1:B:138:GLU:H	1.49	0.78
1:A:13:CYS:SG	1:A:33:LYS:NZ	2.57	0.78
1:C:76:GLY:HA2	1:C:80:ARG:NH1	1.99	0.77
1:B:1:MET:N	1:B:1:MET:SD	2.58	0.77
1:B:142:MET:HA	1:B:145:GLU:HB3	1.67	0.76
1:A:34:ARG:NH1	2:A:201:HOH:O	2.20	0.75
1:A:139:GLU:CD	1:A:141:THR:CG2	2.44	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:137:ALA:HB1	1:C:144:LYS:N	2.03	0.74
1:C:136:MET:HG3	1:C:138:GLU:N	2.04	0.72
1:C:136:MET:SD	1:C:136:MET:O	2.48	0.72
1:C:137:ALA:HB1	1:C:143:LEU:C	2.11	0.71
1:C:142:MET:O	1:C:146:LEU:HB2	1.93	0.69
1:B:124:LYS:NZ	1:B:196:LYS:HE2	2.09	0.68
1:C:75:ASN:O	1:C:78:ILE:HG23	1.96	0.66
1:C:142:MET:HE2	1:C:179:ARG:NE	2.10	0.66
1:A:139:GLU:HG3	1:A:141:THR:HG1	1.61	0.65
1:B:135:ASP:O	1:B:138:GLU:N	2.29	0.65
1:A:139:GLU:O	1:A:139:GLU:HG3	1.95	0.65
1:A:140:LYS:O	1:A:141:THR:CG2	2.42	0.64
1:C:139:GLU:OE2	1:C:181:PRO:HD3	1.98	0.63
1:A:76:GLY:CA	1:A:84:THR:HG21	2.29	0.62
1:C:141:THR:O	1:C:145:GLU:CD	2.37	0.62
1:B:133:SER:H	1:B:134:PRO:HD2	1.64	0.61
1:B:66:LYS:NZ	1:B:90:LYS:NZ	2.48	0.61
1:B:133:SER:N	1:B:134:PRO:HD2	2.15	0.61
1:C:136:MET:HE2	1:C:136:MET:O	2.00	0.60
1:C:76:GLY:HA2	1:C:80:ARG:HH11	1.64	0.59
1:A:176:ALA:HA	1:A:179:ARG:HG2	1.84	0.59
1:A:139:GLU:HG3	1:A:141:THR:CB	2.33	0.59
1:B:146:LEU:HD21	1:B:177:VAL:HG22	1.85	0.59
1:B:124:LYS:HZ2	1:B:196:LYS:HE2	1.67	0.58
1:B:66:LYS:HZ2	1:B:90:LYS:HZ3	1.52	0.57
1:B:157:TYR:CZ	1:C:15:ARG:HD3	2.39	0.57
1:B:186:THR:O	1:B:189:MET:N	2.24	0.57
1:A:8:GLN:O	1:A:15:ARG:HD3	2.04	0.57
1:C:136:MET:HG3	1:C:138:GLU:H	1.68	0.56
1:C:142:MET:HE2	1:C:179:ARG:CZ	2.35	0.56
1:A:132:ILE:O	1:A:137:ALA:HB2	2.05	0.56
1:A:12:PRO:O	1:A:15:ARG:HG3	2.05	0.55
1:B:140:LYS:HG3	1:B:144:LYS:H	1.71	0.55
1:B:142:MET:O	1:B:146:LEU:N	2.29	0.54
1:C:142:MET:O	1:C:146:LEU:CB	2.55	0.54
1:B:181:PRO:C	1:B:183:SER:H	2.11	0.54
1:C:139:GLU:OE2	1:C:181:PRO:CD	2.56	0.54
1:B:66:LYS:HZ3	1:B:90:LYS:NZ	2.06	0.53
1:C:135:ASP:N	1:C:135:ASP:OD2	2.42	0.53
1:B:188:LYS:O	1:B:192:LEU:HB2	2.09	0.53
1:C:136:MET:CE	1:C:136:MET:O	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:TRP:CE2	1:C:106:ARG:HG2	2.44	0.53
1:A:139:GLU:HG3	1:A:141:THR:CG2	2.38	0.52
1:B:129:TYR:HB2	1:B:150:LEU:HB3	1.92	0.52
1:A:139:GLU:CG	1:A:141:THR:CG2	2.87	0.52
1:C:166:LEU:O	1:C:170:GLU:HG3	2.11	0.51
1:A:139:GLU:O	1:A:141:THR:OG1	2.16	0.51
1:B:140:LYS:HE2	1:B:144:LYS:HD2	1.92	0.51
1:C:137:ALA:C	1:C:139:GLU:N	2.61	0.51
1:A:128:VAL:HG21	1:A:195:LEU:HD11	1.93	0.50
1:B:18:ASN:HB3	1:B:23:GLU:HG3	1.94	0.50
1:B:101:MET:O	1:B:105:ILE:HG12	2.12	0.50
1:C:137:ALA:O	1:C:138:GLU:C	2.48	0.50
1:C:18:ASN:ND2	1:C:19:PRO:HD2	2.27	0.50
1:A:37:VAL:HG22	1:A:113:SER:HB2	1.94	0.50
1:B:21:PRO:HG2	1:B:50:GLU:HG3	1.94	0.49
1:B:66:LYS:HZ3	1:B:90:LYS:HZ1	1.60	0.49
1:C:142:MET:HE2	1:C:179:ARG:HE	1.77	0.49
1:C:12:PRO:HG2	1:C:118:ALA:HB2	1.95	0.49
1:C:16:GLU:CD	1:C:16:GLU:H	2.16	0.49
1:A:3:GLU:O	1:A:7:ILE:HG13	2.12	0.49
1:C:128:VAL:HG21	1:C:195:LEU:HD21	1.94	0.49
1:B:142:MET:O	1:B:146:LEU:HB2	2.13	0.49
1:B:70:LEU:HD22	1:B:74:VAL:HG23	1.95	0.48
1:C:142:MET:CE	1:C:179:ARG:HE	2.26	0.48
1:A:145:GLU:O	1:A:149:MET:HG3	2.14	0.48
1:B:135:ASP:HB3	1:B:138:GLU:N	2.22	0.48
1:C:33:LYS:HZ1	1:C:115:CYS:CB	2.26	0.48
1:B:150:LEU:HD23	1:B:173:ILE:HD13	1.96	0.48
1:A:68:LYS:O	1:A:97:MET:HG2	2.13	0.48
1:C:123:GLU:H	1:C:123:GLU:CD	2.17	0.48
1:B:142:MET:HE3	1:B:180:LEU:HD23	1.94	0.47
1:A:93:PRO:HG3	1:A:101:MET:SD	2.54	0.47
1:A:139:GLU:O	1:A:141:THR:N	2.48	0.47
1:B:185:SER:O	1:B:186:THR:C	2.49	0.47
1:C:146:LEU:HD21	1:C:177:VAL:HG22	1.95	0.47
1:C:21:PRO:HG2	1:C:50:GLU:HG3	1.96	0.47
1:A:133:SER:N	1:A:147:LYS:HE3	2.29	0.47
1:C:134:PRO:C	1:C:136:MET:H	2.05	0.47
1:C:13:CYS:HB2	1:C:31:LYS:HE2	1.95	0.47
1:C:114:GLY:O	1:C:116:GLN:HG3	2.14	0.47
1:A:34:ARG:HG3	1:A:37:VAL:HG23	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3:GLU:OE2	1:C:102:ARG:HD2	2.15	0.46
1:A:6:TRP:CZ2	1:A:106:ARG:HG3	2.51	0.46
1:B:69:THR:CG2	1:B:72:GLN:H	2.28	0.46
1:C:133:SER:HA	1:C:147:LYS:HE3	1.97	0.46
1:B:66:LYS:NZ	1:B:90:LYS:HZ3	2.13	0.46
1:A:162:SER:OG	1:A:164:LYS:HG3	2.16	0.46
1:C:129:TYR:CE1	1:C:151:HIS:HB2	2.49	0.46
1:B:116:GLN:O	1:B:117:ASP:C	2.53	0.46
1:A:39:TYR:CD1	1:A:82:THR:HG22	2.51	0.45
1:B:180:LEU:HA	1:B:180:LEU:HD23	1.77	0.45
1:C:137:ALA:HB1	1:C:143:LEU:HB3	1.98	0.45
1:B:73:LEU:HD21	1:B:105:ILE:HD11	1.99	0.45
1:A:139:GLU:OE2	1:A:141:THR:CB	2.57	0.45
1:A:33:LYS:HB3	1:A:33:LYS:HE2	1.51	0.45
1:B:160:GLY:O	1:C:118:ALA:HB1	2.16	0.45
1:C:142:MET:HG2	1:C:176:ALA:HB1	1.98	0.45
1:C:136:MET:HG3	1:C:138:GLU:CA	2.45	0.45
1:C:12:PRO:O	1:C:15:ARG:HG3	2.17	0.45
1:A:80:ARG:O	1:A:84:THR:HG23	2.17	0.45
1:C:132:ILE:O	1:C:147:LYS:CE	2.65	0.45
1:C:137:ALA:O	1:C:139:GLU:N	2.50	0.44
1:C:139:GLU:O	1:C:143:LEU:HB2	2.17	0.44
1:C:74:VAL:HG22	1:C:104:HIS:CE1	2.52	0.44
1:B:121:GLY:O	1:B:124:LYS:HB3	2.18	0.44
1:C:136:MET:HE3	1:C:136:MET:HB2	1.79	0.44
1:A:47:LEU:O	1:A:102:ARG:NH2	2.35	0.44
1:B:138:GLU:HG3	1:B:139:GLU:HG2	2.00	0.44
1:B:141:THR:OG1	1:B:181:PRO:HG2	2.18	0.44
1:B:6:TRP:CZ2	1:B:106:ARG:HG2	2.53	0.44
1:A:66:LYS:N	1:A:66:LYS:HD2	2.33	0.43
1:C:142:MET:HE2	1:C:179:ARG:NH2	2.33	0.43
1:C:136:MET:CG	1:C:138:GLU:HA	2.49	0.43
1:B:152:SER:O	1:B:156:MET:HG3	2.18	0.43
1:C:137:ALA:CB	1:C:143:LEU:C	2.86	0.43
1:A:139:GLU:HG2	1:A:141:THR:OG1	2.14	0.43
1:A:157:TYR:CE1	1:B:15:ARG:HD3	2.53	0.43
1:B:180:LEU:O	1:B:181:PRO:C	2.58	0.43
1:C:116:GLN:H	1:C:116:GLN:HG3	1.64	0.43
1:B:36:GLU:HG3	1:B:82:THR:HG22	2.01	0.42
1:C:136:MET:SD	1:C:138:GLU:CA	2.92	0.42
1:C:76:GLY:HA2	1:C:80:ARG:HH12	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:135:ASP:O	1:B:138:GLU:HB3	2.20	0.42
1:A:21:PRO:O	1:A:25:ILE:HG12	2.19	0.42
1:A:34:ARG:HA	1:A:35:PRO:HD2	1.75	0.42
1:B:135:ASP:O	1:B:136:MET:C	2.56	0.42
1:B:35:PRO:O	1:B:39:TYR:HD1	2.02	0.42
1:B:132:ILE:O	1:B:147:LYS:NZ	2.43	0.42
1:A:124:LYS:HD2	1:A:194:TYR:O	2.20	0.42
1:B:82:THR:HG23	1:C:94:SER:OG	2.20	0.42
1:C:143:LEU:HD12	1:C:143:LEU:HA	1.69	0.41
1:C:6:TRP:CD1	1:C:6:TRP:C	2.92	0.41
1:B:13:CYS:CB	1:B:33:LYS:NZ	2.82	0.41
1:C:136:MET:CG	1:C:138:GLU:CA	2.99	0.41
1:A:127:MET:O	1:A:131:MET:HG3	2.20	0.41
1:B:143:LEU:HA	1:B:143:LEU:HD12	1.85	0.41
1:A:164:LYS:HG3	1:A:165:ALA:H	1.84	0.41
1:C:20:LYS:HA	1:C:21:PRO:HD3	1.94	0.41
1:A:135:ASP:O	1:A:137:ALA:N	2.54	0.41
1:A:32:LYS:HZ2	1:B:51:SER:HG	1.64	0.41
1:B:124:LYS:HZ1	1:B:196:LYS:HE2	1.86	0.40
1:C:13:CYS:O	1:C:16:GLU:OE2	2.40	0.40
1:A:25:ILE:HD11	1:A:45:LEU:HD12	2.03	0.40
1:B:157:TYR:CE1	1:C:15:ARG:HD3	2.56	0.40
1:C:59:VAL:HA	1:C:60:PRO:HD3	1.92	0.40
1:A:139:GLU:O	1:A:140:LYS:C	2.59	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	194/216 (90%)	178 (92%)	16 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	194/216 (90%)	173 (89%)	19 (10%)	2 (1%)	15	32
1	C	194/216 (90%)	174 (90%)	19 (10%)	1 (0%)	29	52
All	All	582/648 (90%)	525 (90%)	54 (9%)	3 (0%)	29	52

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	138	GLU
1	B	134	PRO
1	B	182	ALA

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	167/185 (90%)	152 (91%)	15 (9%)	9	18
1	B	167/185 (90%)	152 (91%)	15 (9%)	9	18
1	C	166/185 (90%)	150 (90%)	16 (10%)	8	16
All	All	500/555 (90%)	454 (91%)	46 (9%)	9	17

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	9	LYS
1	A	11	LEU
1	A	15	ARG
1	A	33	LYS
1	A	34	ARG
1	A	51	SER
1	A	61	GLU
1	A	64	THR
1	A	66	LYS
1	A	80	ARG

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Mol	Chain	Res	Type
1	A	82	THR
1	A	107	ASN
1	A	159	LEU
1	A	180	LEU
1	B	1	MET
1	B	13	CYS
1	B	22	ARG
1	B	69	THR
1	B	70	LEU
1	B	79	SER
1	B	94	SER
1	B	117	ASP
1	B	131	MET
1	B	139	GLU
1	B	143	LEU
1	B	144	LYS
1	B	187	GLU
1	B	189	MET
1	B	192	LEU
1	C	16	GLU
1	C	34	ARG
1	C	36	GLU
1	C	68	LYS
1	C	71	ASN
1	C	78	ILE
1	C	79	SER
1	C	82	THR
1	C	119	ASP
1	C	123	GLU
1	C	135	ASP
1	C	136	MET
1	C	138	GLU
1	C	140	LYS
1	C	141	THR
1	C	163	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 [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	196/216 (90%)	0.07	8 (4%) 37 30	42, 60, 95, 118	0
1	B	196/216 (90%)	0.31	18 (9%) 9 6	37, 58, 107, 130	0
1	C	196/216 (90%)	0.51	23 (11%) 4 3	42, 64, 105, 117	0
All	All	588/648 (90%)	0.30	49 (8%) 11 8	37, 61, 106, 130	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	118	ALA	8.4
1	B	117	ASP	8.3
1	C	141	THR	8.2
1	A	134	PRO	7.4
1	C	117	ASP	6.4
1	C	115	CYS	6.2
1	B	135	ASP	5.9
1	C	133	SER	5.8
1	C	137	ALA	5.4
1	A	140	LYS	5.4
1	B	138	GLU	5.2
1	C	142	MET	5.0
1	C	134	PRO	4.9
1	B	136	MET	4.8
1	C	138	GLU	4.6
1	C	116	GLN	4.2
1	C	139	GLU	3.9
1	C	62	GLY	3.9
1	B	118	ALA	3.7
1	B	116	GLN	3.7
1	B	137	ALA	3.7
1	B	190	VAL	3.6
1	C	136	MET	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	115	CYS	3.5
1	A	196	LYS	3.4
1	A	138	GLU	3.3
1	C	132	ILE	3.2
1	C	30	LYS	3.2
1	C	61	GLU	3.2
1	A	136	MET	3.1
1	C	64	THR	3.1
1	B	184	CYS	2.9
1	C	135	ASP	2.9
1	B	141	THR	2.9
1	B	111	GLU	2.7
1	C	114	GLY	2.6
1	A	65	VAL	2.6
1	B	142	MET	2.6
1	B	139	GLU	2.6
1	A	141	THR	2.5
1	C	63	LYS	2.5
1	C	113	SER	2.5
1	B	192	LEU	2.4
1	A	63	LYS	2.4
1	B	194	TYR	2.3
1	B	185	SER	2.3
1	B	188	LYS	2.2
1	C	65	VAL	2.2
1	C	79	SER	2.1

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 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.