



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2021 – 04:03 PM EDT

PDB ID : 1C1A  
Title : CRYSTAL STRUCTURE OF RSV TWO-DOMAIN INTEGRASE  
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Deposited on : 1999-07-21  
Resolution : 3.10 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](mailto: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.

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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	:	2.23.2
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)	:	2.23.2

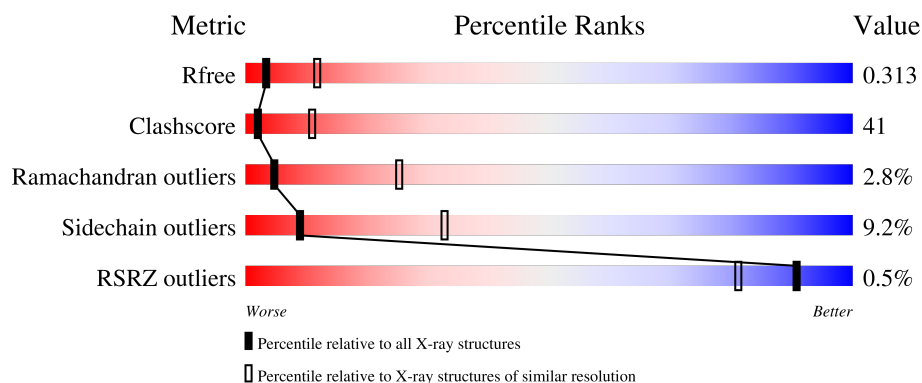
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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  $\geq 3$ , 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	238	
1	B	238	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3397 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 RSV INTEGRASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1746	1104	330	307	5			
1	B	209	Total	C	N	O	S	0	0	0
			1651	1048	311	287	5			

There are 2 discrepancies between the modelled and reference sequences:

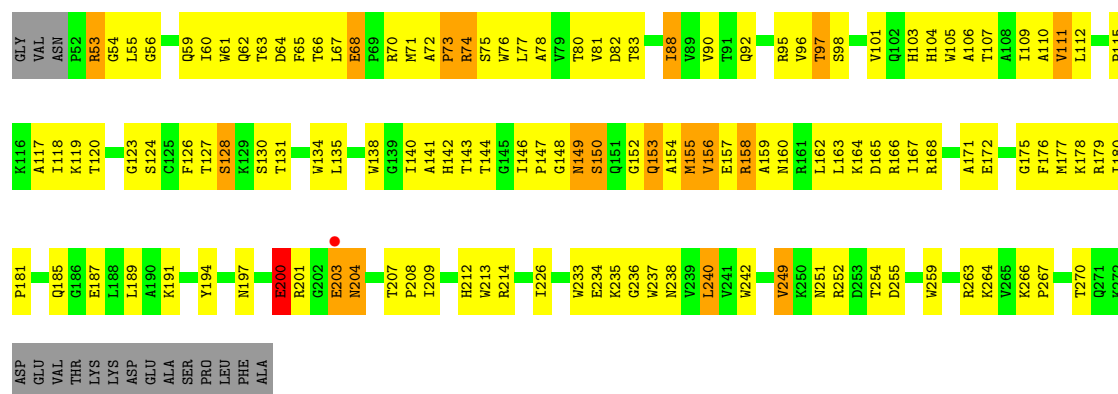
Chain	Residue	Modelled	Actual	Comment	Reference
A	199	LYS	PHE	engineered mutation	UNP P03354
B	199	LYS	PHE	engineered mutation	UNP P03354

### 3 Residue-property plots

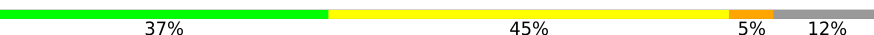
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

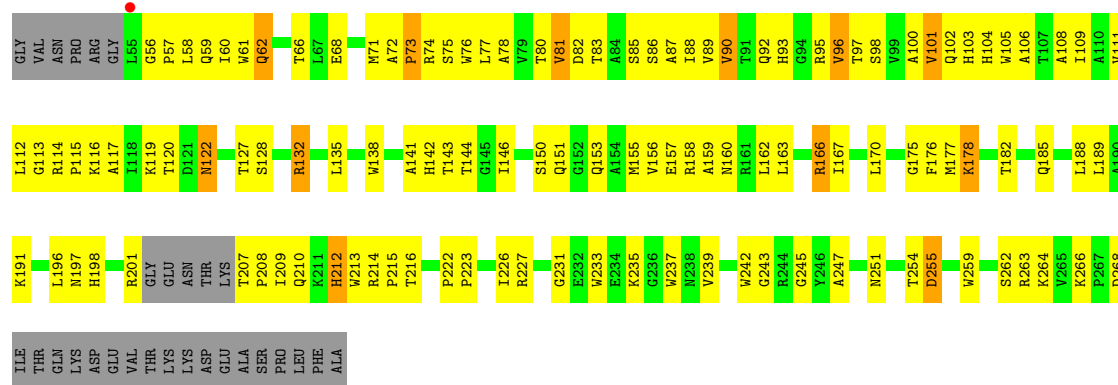
#### • Molecule 1: RSV INTEGRASE

Chain A: 



#### • Molecule 1: RSV INTEGRASE

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.24Å 46.34Å 94.31Å 90.00° 101.76° 90.00°	Depositor
Resolution (Å)	15.00 – 3.10 14.88 – 3.10	Depositor EDS
% Data completeness (in resolution range)	5.1 (15.00-3.10) 11.9 (14.88-3.10)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.74 (at 3.12Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.256 , 0.337 0.222 , 0.313	Depositor DCC
$R_{free}$ test set	71 reflections (5.79%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.9	Xtriage
Anisotropy	0.324	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 30.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3397	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	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 58.44 % 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 2.0452e-05.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.50	0/1789	0.70	0/2428
1	B	0.48	0/1692	0.67	0/2298
All	All	0.49	0/3481	0.68	0/4726

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

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	1746	0	1784	150	0
1	B	1651	0	1683	141	0
All	All	3397	0	3467	280	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 41.

All (280) 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:158:ARG:HH21	1:A:158:ARG:HB2	1.05	1.10
1:B:71:MET:HG3	1:B:92:GLN:HE21	1.24	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:ARG:HB2	1:A:158:ARG:NH2	1.76	1.01
1:B:132:ARG:HH11	1:B:132:ARG:HB2	1.23	1.00
1:B:71:MET:HG3	1:B:92:GLN:NE2	1.86	0.91
1:A:234:GLU:HG2	1:A:237:TRP:HZ3	1.37	0.89
1:B:85:SER:CB	1:B:212:HIS:HB3	2.01	0.89
1:B:92:GLN:HE22	1:B:185:GLN:HE21	1.22	0.88
1:B:85:SER:HB3	1:B:212:HIS:CB	2.04	0.86
1:A:53:ARG:HG3	1:A:53:ARG:HH11	1.37	0.86
1:B:114:ARG:HG2	1:B:114:ARG:HH11	1.41	0.86
1:A:235:LYS:NZ	1:A:270:THR:HG21	1.91	0.84
1:A:233:TRP:CE3	1:A:266:LYS:HD2	2.13	0.83
1:B:132:ARG:HB2	1:B:132:ARG:NH1	1.94	0.82
1:B:71:MET:CG	1:B:92:GLN:HE21	1.93	0.81
1:B:66:THR:HB	1:B:160:ASN:ND2	1.95	0.80
1:B:92:GLN:NE2	1:B:185:GLN:HE21	1.80	0.79
1:B:207:THR:HG22	1:B:210:GLN:H	1.48	0.78
1:A:238:ASN:HD21	1:A:252:ARG:HE	1.28	0.78
1:B:207:THR:HB	1:B:210:GLN:HB3	1.66	0.76
1:A:123:GLY:O	1:A:127:THR:HG23	1.85	0.76
1:B:85:SER:HB3	1:B:212:HIS:HB2	1.67	0.76
1:B:119:LYS:HG2	1:B:143:THR:HB	1.68	0.76
1:B:92:GLN:HE22	1:B:185:GLN:NE2	1.84	0.75
1:A:158:ARG:HH21	1:A:158:ARG:CB	1.94	0.74
1:A:61:TRP:HB2	1:A:118:ILE:HG13	1.67	0.74
1:A:111:VAL:HG13	1:A:112:LEU:HD22	1.70	0.73
1:B:85:SER:HB3	1:B:212:HIS:HB3	1.66	0.73
1:B:209:ILE:O	1:B:213:TRP:HB2	1.88	0.73
1:B:61:TRP:CE3	1:B:115:PRO:HG3	2.22	0.73
1:B:66:THR:HB	1:B:160:ASN:HD22	1.52	0.73
1:B:117:ALA:HB2	1:B:141:ALA:HB3	1.69	0.73
1:B:92:GLN:HE22	1:B:185:GLN:HG2	1.52	0.73
1:A:53:ARG:HG3	1:A:53:ARG:NH1	2.05	0.72
1:B:85:SER:HB2	1:B:212:HIS:HB3	1.70	0.72
1:A:158:ARG:O	1:A:162:LEU:HG	1.91	0.71
1:A:88:ILE:HD12	1:A:88:ILE:N	2.06	0.70
1:A:234:GLU:HG2	1:A:237:TRP:CZ3	2.25	0.70
1:B:95:ARG:HG2	1:B:95:ARG:HH11	1.55	0.70
1:B:122:ASN:C	1:B:122:ASN:HD22	1.95	0.70
1:A:105:TRP:CZ3	1:A:135:LEU:HD21	2.27	0.70
1:A:135:LEU:HD13	1:A:142:HIS:HB2	1.74	0.70
1:A:191:LYS:HE3	1:B:138:TRP:HZ2	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:GLN:OE1	1:A:153:GLN:HA	1.92	0.69
1:A:62:GLN:HE22	1:A:155:MET:HB2	1.56	0.69
1:A:235:LYS:HZ1	1:A:270:THR:HG21	1.55	0.68
1:B:209:ILE:HB	1:B:213:TRP:HD1	1.59	0.68
1:A:153:GLN:O	1:A:153:GLN:HG2	1.93	0.67
1:A:234:GLU:CG	1:A:237:TRP:HZ3	2.06	0.67
1:A:55:LEU:HG	1:A:59:GLN:HE22	1.60	0.67
1:A:163:LEU:O	1:A:167:ILE:HG13	1.95	0.67
1:B:85:SER:O	1:B:86:SER:HB3	1.94	0.66
1:A:162:LEU:O	1:A:166:ARG:HB2	1.95	0.66
1:A:68:GLU:OE1	1:A:70:ARG:HB2	1.95	0.66
1:B:61:TRP:CZ3	1:B:115:PRO:HG3	2.31	0.66
1:B:85:SER:CB	1:B:212:HIS:CB	2.70	0.66
1:B:81:VAL:HG23	1:B:88:ILE:HG13	1.79	0.65
1:A:179:ARG:HD2	1:A:180:ILE:N	2.13	0.64
1:A:146:ILE:HB	1:A:150:SER:HB2	1.80	0.64
1:A:62:GLN:NE2	1:A:155:MET:HB2	2.13	0.63
1:A:152:GLY:C	1:A:154:ALA:H	2.00	0.63
1:B:105:TRP:O	1:B:109:ILE:HG13	1.99	0.63
1:B:58:LEU:HD11	1:B:212:HIS:CE1	2.34	0.63
1:A:237:TRP:C	1:A:238:ASN:HD22	2.02	0.63
1:A:73:PRO:O	1:A:75:SER:N	2.32	0.62
1:A:65:PHE:CD1	1:A:96:VAL:HG12	2.34	0.62
1:B:62:GLN:NE2	1:B:153:GLN:HA	2.14	0.62
1:A:187:GLU:HG3	1:A:191:LYS:NZ	2.14	0.62
1:A:200:GLU:N	1:A:207:THR:HG22	2.16	0.61
1:A:66:THR:HG22	1:A:67:LEU:N	2.16	0.61
1:A:105:TRP:O	1:A:109:ILE:HG13	2.01	0.61
1:B:146:ILE:HG12	1:B:150:SER:HB2	1.82	0.61
1:B:132:ARG:HH11	1:B:132:ARG:CB	2.04	0.60
1:A:62:GLN:NE2	1:A:156:VAL:HG12	2.15	0.60
1:B:73:PRO:O	1:B:75:SER:N	2.34	0.60
1:B:235:LYS:NZ	1:B:268:ASP:CB	2.64	0.60
1:B:226:ILE:O	1:B:226:ILE:HD12	2.01	0.60
1:B:227:ARG:HE	1:B:231:GLY:HA2	1.67	0.60
1:B:114:ARG:HG2	1:B:114:ARG:NH1	2.13	0.60
1:A:111:VAL:HG13	1:A:112:LEU:CD2	2.31	0.59
1:A:180:ILE:HG22	1:A:185:GLN:HG3	1.83	0.59
1:A:92:GLN:HG3	1:A:189:LEU:HD22	1.83	0.59
1:A:213:TRP:O	1:B:215:PRO:HA	2.02	0.59
1:A:68:GLU:HG2	1:A:164:LYS:HD2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:GLU:O	1:A:204:ASN:HB2	2.02	0.58
1:A:194:TYR:OH	1:B:114:ARG:HB2	2.04	0.58
1:A:112:LEU:HD22	1:A:112:LEU:N	2.19	0.57
1:B:72:ALA:HA	1:B:73:PRO:C	2.25	0.57
1:B:92:GLN:NE2	1:B:185:GLN:HG2	2.19	0.57
1:B:106:ALA:HA	1:B:109:ILE:HD12	1.86	0.57
1:A:197:ASN:O	1:A:208:PRO:HD2	2.04	0.57
1:B:117:ALA:CB	1:B:141:ALA:HB3	2.35	0.57
1:B:158:ARG:CZ	1:B:158:ARG:HB3	2.35	0.57
1:A:149:ASN:OD1	1:A:157:GLU:HG2	2.05	0.56
1:A:95:ARG:O	1:A:97:THR:HG22	2.04	0.56
1:A:120:THR:O	1:A:144:THR:HA	2.04	0.56
1:A:237:TRP:CD1	1:A:249:VAL:HG13	2.41	0.56
1:B:90:VAL:HG21	1:B:189:LEU:HD11	1.88	0.56
1:B:92:GLN:HE22	1:B:185:GLN:CG	2.18	0.56
1:A:233:TRP:CZ3	1:A:266:LYS:HD2	2.41	0.56
1:A:73:PRO:HG2	1:A:74:ARG:H	1.69	0.56
1:A:117:ALA:HB2	1:A:141:ALA:HB3	1.88	0.56
1:A:201:ARG:HH11	1:A:201:ARG:HG3	1.71	0.56
1:A:72:ALA:HA	1:A:73:PRO:C	2.27	0.55
1:A:118:ILE:HD13	1:A:140:ILE:HG21	1.89	0.55
1:B:61:TRP:CH2	1:B:115:PRO:HD3	2.41	0.55
1:A:234:GLU:OE2	1:A:237:TRP:CH2	2.59	0.55
1:B:66:THR:CB	1:B:160:ASN:HD22	2.20	0.55
1:B:114:ARG:HH11	1:B:114:ARG:CG	2.18	0.55
1:B:95:ARG:HG2	1:B:95:ARG:NH1	2.19	0.55
1:A:156:VAL:O	1:A:159:ALA:HB3	2.05	0.55
1:A:146:ILE:HG22	1:A:148:GLY:H	1.72	0.54
1:A:97:THR:OG1	1:A:98:SER:N	2.41	0.54
1:B:254:THR:O	1:B:255:ASP:HB2	2.06	0.54
1:B:112:LEU:HB3	1:B:212:HIS:HE1	1.73	0.54
1:B:95:ARG:O	1:B:97:THR:HG23	2.07	0.54
1:A:65:PHE:HE2	1:A:101:VAL:HG22	1.73	0.54
1:A:56:GLY:O	1:A:59:GLN:HG3	2.08	0.53
1:A:53:ARG:HD3	1:A:54:GLY:O	2.08	0.53
1:B:105:TRP:CZ3	1:B:135:LEU:HD21	2.44	0.53
1:A:88:ILE:HD12	1:A:88:ILE:H	1.72	0.53
1:A:55:LEU:H	1:A:59:GLN:NE2	2.06	0.53
1:B:227:ARG:HH11	1:B:264:LYS:NZ	2.07	0.53
1:B:57:PRO:HB3	1:B:212:HIS:HB2	1.91	0.53
1:A:62:GLN:CD	1:A:153:GLN:HA	2.30	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:PHE:HA	1:A:131:THR:HG21	1.91	0.52
1:A:118:ILE:CD1	1:A:140:ILE:HG21	2.39	0.52
1:A:149:ASN:O	1:A:150:SER:C	2.48	0.52
1:B:235:LYS:HZ1	1:B:268:ASP:CB	2.21	0.52
1:A:64:ASP:HB3	1:A:156:VAL:HG21	1.91	0.52
1:B:98:SER:O	1:B:102:GLN:HG3	2.09	0.52
1:A:101:VAL:O	1:A:104:HIS:HB3	2.10	0.52
1:A:235:LYS:HZ3	1:A:270:THR:HG21	1.74	0.52
1:A:149:ASN:ND2	1:A:157:GLU:OE1	2.43	0.52
1:A:236:GLY:HA2	1:A:252:ARG:NH1	2.25	0.51
1:B:87:ALA:HA	1:B:208:PRO:HB3	1.91	0.51
1:A:142:HIS:CD2	1:A:143:THR:H	2.27	0.51
1:A:187:GLU:HG3	1:A:191:LYS:HZ2	1.73	0.51
1:B:170:LEU:HD21	1:B:191:LYS:HD2	1.92	0.51
1:A:78:ALA:O	1:A:90:VAL:HA	2.09	0.51
1:A:110:ALA:O	1:B:198:HIS:HE1	1.94	0.51
1:B:72:ALA:HB2	1:B:75:SER:HB3	1.93	0.51
1:A:59:GLN:O	1:A:60:ILE:HG13	2.10	0.50
1:B:162:LEU:O	1:B:166:ARG:HB2	2.11	0.50
1:A:179:ARG:HD2	1:A:180:ILE:H	1.77	0.50
1:A:194:TYR:CE1	1:B:109:ILE:HG22	2.46	0.50
1:A:172:GLU:HA	1:A:177:MET:CE	2.41	0.50
1:B:227:ARG:O	1:B:227:ARG:HD3	2.12	0.50
1:A:70:ARG:HG3	1:A:70:ARG:HH11	1.76	0.50
1:B:59:GLN:HA	1:B:116:LYS:HB2	1.93	0.50
1:B:112:LEU:HB3	1:B:212:HIS:CE1	2.47	0.50
1:A:149:ASN:N	1:A:149:ASN:HD22	2.09	0.50
1:A:81:VAL:HG11	1:A:159:ALA:HB2	1.94	0.50
1:A:187:GLU:O	1:A:191:LYS:HG3	2.12	0.50
1:A:65:PHE:CE2	1:A:101:VAL:HG22	2.47	0.50
1:B:98:SER:O	1:B:101:VAL:HG13	2.12	0.50
1:B:61:TRP:NE1	1:B:82:ASP:OD1	2.42	0.49
1:B:178:LYS:C	1:B:178:LYS:HD3	2.33	0.49
1:A:201:ARG:HG3	1:A:201:ARG:NH1	2.27	0.49
1:B:159:ALA:O	1:B:163:LEU:HB2	2.13	0.49
1:B:58:LEU:HD21	1:B:113:GLY:HA3	1.95	0.49
1:B:62:GLN:CD	1:B:153:GLN:HA	2.33	0.49
1:B:156:VAL:HG13	1:B:157:GLU:N	2.27	0.49
1:B:78:ALA:O	1:B:90:VAL:HA	2.13	0.49
1:A:59:GLN:C	1:A:60:ILE:HG13	2.33	0.49
1:B:122:ASN:C	1:B:122:ASN:ND2	2.65	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:201:ARG:HG3	1:B:201:ARG:HH11	1.78	0.49
1:B:198:HIS:CD2	1:B:209:ILE:CD1	2.96	0.48
1:A:153:GLN:O	1:A:153:GLN:CG	2.58	0.48
1:A:172:GLU:HA	1:A:177:MET:HE2	1.95	0.48
1:A:214:ARG:HE	1:B:216:THR:HG22	1.78	0.48
1:A:62:GLN:HE21	1:A:156:VAL:HG12	1.77	0.48
1:A:119:LYS:HG2	1:A:143:THR:O	2.13	0.48
1:A:72:ALA:HB2	1:A:75:SER:HB3	1.96	0.48
1:B:175:GLY:O	1:B:177:MET:N	2.47	0.48
1:A:80:THR:HG1	1:A:104:HIS:CD2	2.30	0.47
1:B:227:ARG:NH1	1:B:264:LYS:NZ	2.62	0.47
1:B:150:SER:O	1:B:151:GLN:HB2	2.15	0.47
1:B:213:TRP:O	1:B:214:ARG:HB2	2.14	0.47
1:A:70:ARG:HB3	1:A:180:ILE:HD13	1.96	0.47
1:A:160:ASN:O	1:A:164:LYS:HG3	2.15	0.47
1:A:207:THR:OG1	1:A:209:ILE:HG22	2.15	0.47
1:B:61:TRP:CE2	1:B:115:PRO:HB3	2.50	0.47
1:A:267:PRO:HB3	1:B:259:TRP:CD2	2.50	0.47
1:B:251:ASN:HD22	1:B:254:THR:H	1.63	0.46
1:A:180:ILE:CG2	1:A:185:GLN:HG3	2.45	0.46
1:B:142:HIS:CD2	1:B:143:THR:H	2.34	0.46
1:B:150:SER:O	1:B:151:GLN:CB	2.63	0.46
1:A:70:ARG:O	1:A:180:ILE:HB	2.14	0.46
1:A:175:GLY:O	1:A:177:MET:N	2.48	0.46
1:A:66:THR:HG22	1:A:67:LEU:H	1.79	0.46
1:A:234:GLU:OE2	1:A:237:TRP:CZ3	2.69	0.46
1:A:263:ARG:HG2	1:A:263:ARG:HH11	1.81	0.46
1:B:96:VAL:O	1:B:96:VAL:CG2	2.63	0.46
1:A:178:LYS:HB3	1:A:179:ARG:H	1.52	0.46
1:B:142:HIS:HD2	1:B:143:THR:H	1.64	0.46
1:A:167:ILE:O	1:A:171:ALA:HB2	2.16	0.46
1:A:226:ILE:HA	1:A:264:LYS:O	2.15	0.46
1:A:254:THR:O	1:A:255:ASP:HB2	2.16	0.46
1:A:242:TRP:CZ3	1:B:243:GLY:HA3	2.50	0.45
1:A:153:GLN:O	1:A:156:VAL:HG13	2.16	0.45
1:A:214:ARG:NE	1:B:216:THR:CG2	2.80	0.45
1:A:55:LEU:H	1:A:59:GLN:HE22	1.62	0.45
1:A:147:PRO:C	1:A:149:ASN:H	2.20	0.45
1:B:98:SER:C	1:B:102:GLN:HE21	2.20	0.45
1:A:61:TRP:CD1	1:A:82:ASP:HA	2.52	0.45
1:A:175:GLY:HA2	1:A:177:MET:HE3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:ARG:NH2	1:B:216:THR:HG21	2.32	0.45
1:A:124:SER:O	1:A:128:SER:HB2	2.17	0.45
1:B:226:ILE:HA	1:B:264:LYS:O	2.17	0.45
1:A:53:ARG:HD2	1:A:259:TRP:CH2	2.51	0.45
1:B:242:TRP:CZ3	1:B:247:ALA:HB2	2.51	0.45
1:A:240:LEU:HD12	1:A:240:LEU:HA	1.78	0.45
1:A:263:ARG:HG3	1:A:264:LYS:HG2	1.99	0.45
1:A:105:TRP:O	1:A:106:ALA:C	2.54	0.45
1:A:146:ILE:HG23	1:A:147:PRO:HD2	1.98	0.45
1:A:200:GLU:H	1:A:207:THR:HG22	1.80	0.45
1:B:60:ILE:HA	1:B:117:ALA:O	2.16	0.45
1:B:188:LEU:HD23	1:B:188:LEU:C	2.38	0.44
1:B:233:TRP:CZ3	1:B:266:LYS:HG2	2.53	0.44
1:B:100:ALA:O	1:B:103:HIS:HB3	2.16	0.44
1:B:61:TRP:CD1	1:B:82:ASP:HA	2.53	0.44
1:A:237:TRP:C	1:A:238:ASN:ND2	2.71	0.44
1:B:227:ARG:HH11	1:B:264:LYS:CE	2.30	0.44
1:B:245:GLY:O	1:B:262:SER:HB3	2.17	0.44
1:B:163:LEU:O	1:B:167:ILE:HG13	2.18	0.44
1:A:180:ILE:HA	1:A:181:PRO:HD2	1.80	0.44
1:B:201:ARG:HG3	1:B:201:ARG:NH1	2.32	0.44
1:A:234:GLU:OE2	1:A:237:TRP:HH2	2.00	0.43
1:B:66:THR:CG2	1:B:77:LEU:HB2	2.49	0.43
1:B:226:ILE:HG13	1:B:237:TRP:CD1	2.53	0.43
1:B:239:VAL:O	1:B:239:VAL:HG13	2.18	0.43
1:B:66:THR:CB	1:B:160:ASN:ND2	2.75	0.43
1:B:92:GLN:NE2	1:B:185:GLN:NE2	2.52	0.43
1:B:222:PRO:HA	1:B:223:PRO:HD3	1.74	0.43
1:B:89:VAL:HG11	1:B:108:ALA:HA	2.01	0.43
1:B:197:ASN:O	1:B:207:THR:HG23	2.18	0.43
1:B:226:ILE:HD12	1:B:226:ILE:C	2.39	0.43
1:A:134:TRP:CZ2	1:A:138:TRP:NE1	2.87	0.43
1:A:175:GLY:O	1:A:177:MET:HE3	2.18	0.43
1:B:80:THR:HG1	1:B:104:HIS:CD2	2.36	0.43
1:A:53:ARG:HG2	1:A:83:THR:HB	2.01	0.42
1:A:187:GLU:CG	1:A:191:LYS:HZ3	2.32	0.42
1:A:214:ARG:HE	1:B:216:THR:CG2	2.31	0.42
1:A:152:GLY:C	1:A:154:ALA:N	2.68	0.42
1:A:152:GLY:O	1:A:154:ALA:N	2.52	0.42
1:A:165:ASP:O	1:A:168:ARG:HB3	2.18	0.42
1:A:251:ASN:HD22	1:A:254:THR:H	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:GLU:HB2	1:A:77:LEU:CD1	2.50	0.42
1:A:112:LEU:HB3	1:A:212:HIS:NE2	2.34	0.42
1:B:87:ALA:CA	1:B:208:PRO:HB3	2.49	0.42
1:B:153:GLN:O	1:B:156:VAL:HG12	2.19	0.42
1:B:188:LEU:HD23	1:B:188:LEU:O	2.19	0.42
1:A:76:TRP:CE3	1:A:96:VAL:HG13	2.54	0.42
1:B:87:ALA:C	1:B:88:ILE:HD12	2.38	0.42
1:B:251:ASN:ND2	1:B:254:THR:H	2.17	0.42
1:B:120:THR:O	1:B:144:THR:HA	2.20	0.42
1:B:66:THR:HG23	1:B:77:LEU:HB2	2.01	0.42
1:B:82:ASP:HB3	1:B:85:SER:OG	2.19	0.42
1:B:198:HIS:CD2	1:B:209:ILE:HD13	2.55	0.42
1:A:251:ASN:ND2	1:A:254:THR:H	2.18	0.41
1:B:93:HIS:HE1	1:B:103:HIS:HD2	1.68	0.41
1:A:101:VAL:HG12	1:A:105:TRP:CE3	2.56	0.41
1:A:115:PRO:HG3	1:A:118:ILE:HD11	2.01	0.41
1:B:68:GLU:HB3	1:B:77:LEU:HD11	2.02	0.41
1:B:56:GLY:HA2	1:B:57:PRO:HD3	1.81	0.41
1:B:60:ILE:HG22	1:B:83:THR:HG21	2.03	0.41
1:B:71:MET:O	1:B:185:GLN:NE2	2.53	0.41
1:B:114:ARG:NH1	1:B:114:ARG:CG	2.76	0.41
1:A:55:LEU:HD12	1:A:55:LEU:O	2.21	0.41
1:A:107:THR:O	1:A:111:VAL:HG12	2.19	0.41
1:A:63:THR:HG22	1:A:64:ASP:N	2.35	0.41
1:A:88:ILE:N	1:A:88:ILE:CD1	2.73	0.40
1:B:71:MET:CG	1:B:92:GLN:NE2	2.64	0.40
1:B:175:GLY:O	1:B:177:MET:HG2	2.21	0.40
1:A:66:THR:CG2	1:A:67:LEU:N	2.82	0.40
1:B:207:THR:CB	1:B:210:GLN:HB3	2.45	0.40
1:B:76:TRP:CD1	1:B:95:ARG:HA	2.56	0.40
1:B:105:TRP:O	1:B:106:ALA:C	2.58	0.40
1:B:207:THR:HB	1:B:210:GLN:CB	2.43	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	219/238 (92%)	188 (86%)	23 (10%)	8 (4%)	3	19
1	B	205/238 (86%)	173 (84%)	28 (14%)	4 (2%)	7	31
All	All	424/476 (89%)	361 (85%)	51 (12%)	12 (3%)	5	25

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	SER
1	B	73	PRO
1	B	128	SER
1	A	73	PRO
1	A	74	ARG
1	A	150	SER
1	A	176	PHE
1	B	74	ARG
1	B	176	PHE
1	A	153	GLN
1	A	200	GLU
1	A	204	ASN

### 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	184/198 (93%)	168 (91%)	16 (9%)	10	36
1	B	173/198 (87%)	156 (90%)	17 (10%)	8	29
All	All	357/396 (90%)	324 (91%)	33 (9%)	9	33

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ARG
1	A	68	GLU
1	A	71	MET
1	A	88	ILE
1	A	97	THR
1	A	103	HIS
1	A	111	VAL
1	A	130	SER
1	A	149	ASN
1	A	155	MET
1	A	156	VAL
1	A	158	ARG
1	A	200	GLU
1	A	203	GLU
1	A	240	LEU
1	A	249	VAL
1	B	62	GLN
1	B	81	VAL
1	B	90	VAL
1	B	96	VAL
1	B	101	VAL
1	B	111	VAL
1	B	122	ASN
1	B	127	THR
1	B	132	ARG
1	B	155	MET
1	B	166	ARG
1	B	178	LYS
1	B	182	THR
1	B	196	LEU
1	B	212	HIS
1	B	255	ASP
1	B	263	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	62	GLN
1	A	92	GLN
1	A	102	GLN
1	A	238	ASN
1	A	251	ASN

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Mol	Chain	Res	Type
1	B	92	GLN
1	B	102	GLN
1	B	103	HIS
1	B	122	ASN
1	B	153	GLN
1	B	160	ASN
1	B	198	HIS
1	B	210	GLN
1	B	212	HIS
1	B	251	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 monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	221/238 (92%)	-0.80	1 (0%) 91 81	20, 43, 65, 86	0
1	B	209/238 (87%)	-0.75	1 (0%) 91 81	19, 52, 64, 77	0
All	All	430/476 (90%)	-0.78	2 (0%) 91 81	19, 48, 65, 86	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	203	GLU	2.3
1	B	55	LEU	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 monosaccharides 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.