



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 03:20 pm GMT

PDB ID : 2XPJ
Title : Crystal structure of Physalis Mottle Virus with intact ordered RNA
Authors : Sagurthi, S.R.; Rajaram, V.; Savithri, H.S.; Murthy, M.R.N.
Deposited on : 2010-08-26
Resolution : 3.40 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
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

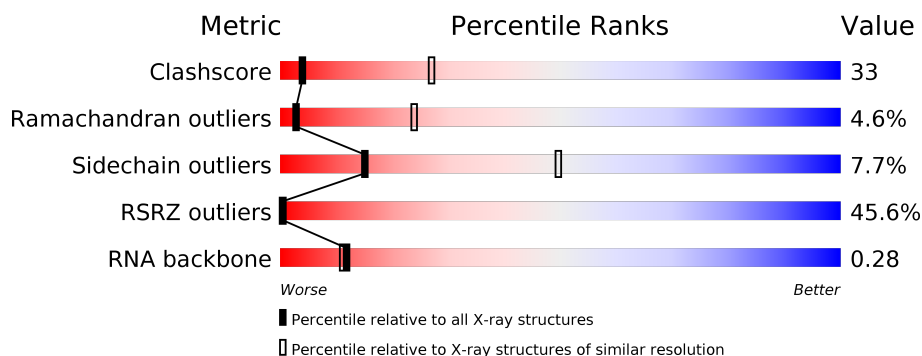
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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))
Clashscore	112137	1832 (3.50-3.30)
Ramachandran outliers	110173	1789 (3.50-3.30)
Sidechain outliers	110143	1789 (3.50-3.30)
RSRZ outliers	101464	1709 (3.50-3.30)
RNA backbone	2435	1009 (3.96-2.84)

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	188	<div> <div>38%</div> <div> <div>43%</div> <div>38%</div> <div>6%</div> <div>12%</div> </div> </div>
1	B	188	<div> <div>44%</div> <div> <div>47%</div> <div>43%</div> <div>6%</div> </div> </div>
1	C	188	<div> <div>45%</div> <div> <div>39%</div> <div>50%</div> <div>9%</div> </div> </div>
2	D	3	<div> <div>100%</div> <div> <div>67%</div> <div>33%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4001 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 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	0	0	0
			1218	777	205	233	3			
1	B	180	Total	C	N	O	S	0	0	0
			1343	859	225	256	3			
1	C	185	Total	C	N	O	S	0	0	0
			1383	882	232	266	3			

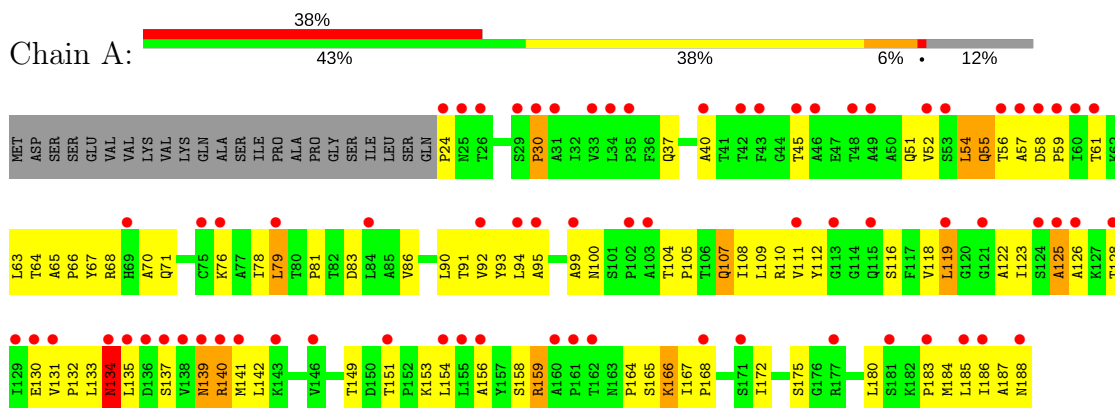
- Molecule 2 is a RNA chain called 5'-R(CP*CP*CP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	3	Total	C	N	O	P	0	0	0
			57	27	9	19	2			

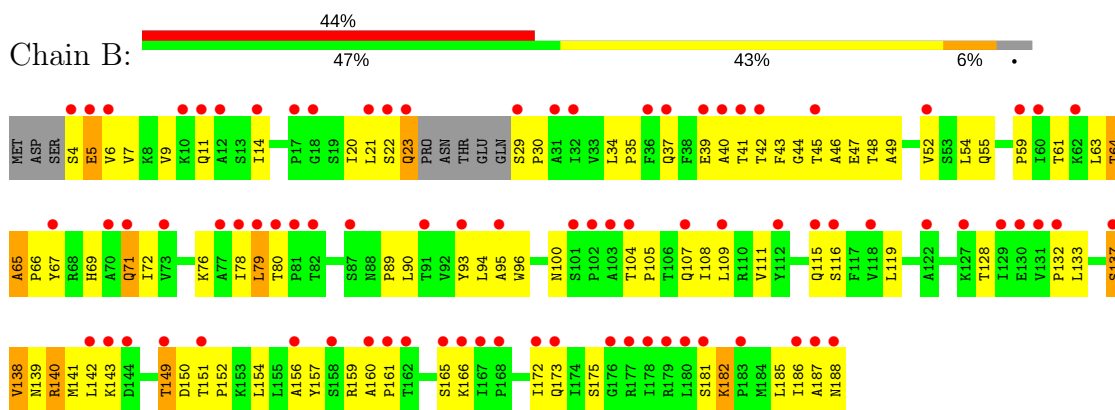
3 Residue-property plots [i](#)

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.

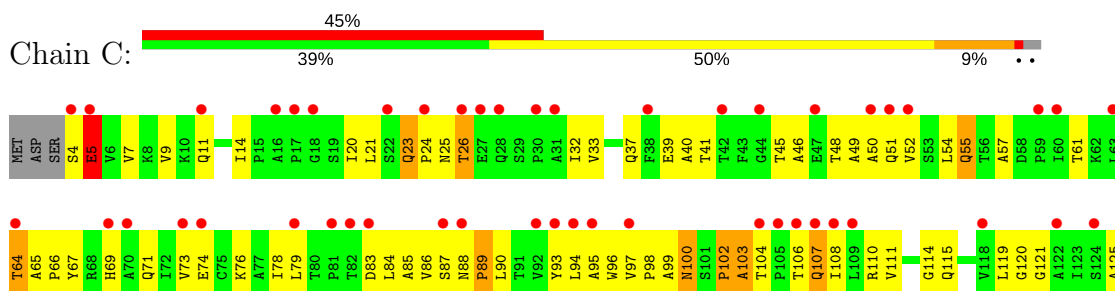
• Molecule 1: COAT PROTEIN

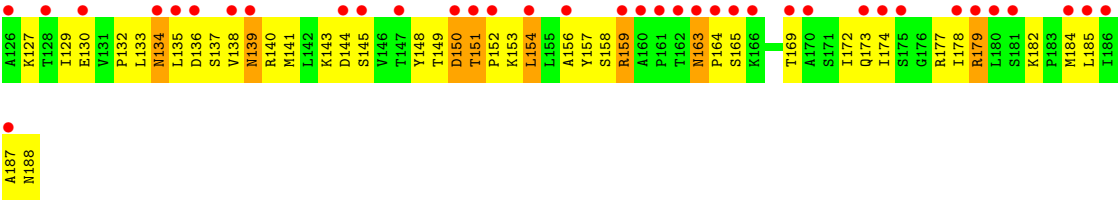


• Molecule 1: COAT PROTEIN



• Molecule 1: COAT PROTEIN





● Molecule 2: 5'-R(CP*CP*CP)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	285.40Å 288.36Å 290.61Å 62.92° 65.30° 60.85°	Depositor
Resolution (Å)	30.00 – 3.40 29.99 – 3.40	Depositor EDS
% Data completeness (in resolution range)	69.1 (30.00-3.40) 61.2 (29.99-3.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 3.39Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.308 , 0.311 (Not available) , (Not available)	Depositor DCC
R_{free} test set	NotAvailable	DCC
Wilson B-factor (Å ²)	58.5	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , -41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.000 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.17	EDS
Total number of atoms	4001	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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	0.42	0/1245	0.72	1/1710 (0.1%)
1	B	0.41	0/1370	0.69	1/1876 (0.1%)
1	C	0.40	0/1412	0.73	0/1936
2	D	0.81	0/62	0.92	0/94
All	All	0.42	0/4089	0.72	2/5616 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	137	SER	N-CA-C	-5.32	96.63	111.00
1	A	54	LEU	N-CA-C	-5.00	97.50	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	1218	0	1233	83	0
1	B	1343	0	1400	94	0
1	C	1383	0	1435	101	0
2	D	57	0	35	1	0
All	All	4001	0	4103	269	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 33.

All (269) 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:66:PRO:HA	1:A:186:ILE:HD11	1.38	1.05
1:A:81:PRO:HG3	1:A:119:LEU:HD22	1.41	0.98
1:B:11:GLN:HE22	1:B:96:TRP:H	0.98	0.96
1:A:94:LEU:HD21	1:A:172:ILE:HD13	1.49	0.95
1:B:11:GLN:NE2	1:B:96:TRP:H	1.66	0.94
1:A:186:ILE:HG22	1:A:187:ALA:H	1.28	0.93
1:C:11:GLN:HE22	1:C:96:TRP:H	1.00	0.93
1:B:140:ARG:HH11	1:B:140:ARG:HB3	1.35	0.91
1:B:64:THR:HG23	1:B:143:LYS:HD2	1.51	0.89
1:B:61:THR:HA	1:B:64:THR:HB	1.56	0.87
1:C:158:SER:O	1:C:159:ARG:HB2	1.74	0.86
1:A:186:ILE:HG22	1:A:187:ALA:N	1.92	0.85
1:B:71:GLN:HB3	1:B:141:MET:SD	2.18	0.84
1:A:90:LEU:H	1:A:90:LEU:HD23	1.42	0.83
1:B:55:GLN:HB2	1:B:151:THR:HG21	1.59	0.82
1:B:69:HIS:HB2	1:B:181:SER:HB2	1.63	0.80
1:B:137:SER:O	1:B:138:VAL:HG22	1.81	0.80
1:A:118:VAL:HB	1:A:123:ILE:CB	2.13	0.79
1:B:66:PRO:HG2	1:B:67:TYR:CE1	2.18	0.79
1:A:139:ASN:HD22	1:A:140:ARG:N	1.80	0.79
1:B:9:VAL:HG12	1:B:115:GLN:HE22	1.50	0.76
1:C:9:VAL:HG12	1:C:115:GLN:HE22	1.52	0.75
1:A:79:LEU:HD13	1:A:119:LEU:HD21	1.69	0.75
1:A:83:ASP:O	1:A:86:VAL:HG22	1.86	0.75
1:A:185:LEU:HD12	1:C:111:VAL:HG12	1.69	0.75
1:B:29:SER:HB2	1:B:30:PRO:HD2	1.67	0.74
1:A:187:ALA:O	1:A:188:ASN:HB2	1.88	0.72
1:B:40:ALA:HB1	1:B:52:VAL:HG21	1.69	0.72
1:C:102:PRO:O	1:C:103:ALA:HB3	1.88	0.72
1:B:11:GLN:HE22	1:B:96:TRP:N	1.82	0.72
1:B:139:ASN:HB2	1:B:150:ASP:CB	2.20	0.71
1:C:49:ALA:HB2	1:C:157:TYR:HD1	1.55	0.71
1:C:187:ALA:O	1:C:188:ASN:HB2	1.91	0.70
1:A:133:LEU:O	1:A:134:ASN:HB2	1.91	0.70
1:C:97:VAL:HG13	1:C:98:PRO:HD2	1.72	0.70
1:A:188:ASN:OD1	1:C:110:ARG:HD2	1.92	0.70
1:B:187:ALA:O	1:B:188:ASN:HB2	1.90	0.69
1:C:138:VAL:HG21	1:C:152:PRO:HB3	1.73	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:LEU:HD21	1:A:116:SER:HB2	1.76	0.68
1:C:11:GLN:NE2	1:C:96:TRP:H	1.84	0.68
1:B:4:SER:O	1:B:5:GLU:HG2	1.94	0.68
1:A:186:ILE:CG2	1:A:187:ALA:H	2.05	0.67
1:B:45:THR:HG22	1:B:165:SER:O	1.94	0.66
1:C:66:PRO:HG2	1:C:67:TYR:CE1	2.30	0.66
1:C:9:VAL:CG1	1:C:115:GLN:HE22	2.08	0.66
1:C:66:PRO:HG2	1:C:67:TYR:CD1	2.31	0.66
1:A:99:ALA:HB3	1:A:149:THR:O	1.95	0.66
1:C:139:ASN:HD22	1:C:140:ARG:N	1.94	0.66
1:C:98:PRO:O	1:C:99:ALA:HB3	1.95	0.66
1:C:64:THR:HG23	1:C:143:LYS:HE3	1.78	0.65
1:B:139:ASN:HB2	1:B:150:ASP:HB2	1.78	0.64
1:A:54:LEU:O	1:A:55:GLN:HB3	1.98	0.63
1:A:37:GLN:HG3	1:A:175:SER:HB3	1.80	0.63
1:A:54:LEU:HD12	1:A:54:LEU:N	2.14	0.63
1:C:134:ASN:ND2	1:C:136:ASP:H	1.97	0.63
1:A:95:ALA:HB2	1:A:108:ILE:HG23	1.79	0.63
1:B:55:GLN:CB	1:B:151:THR:HG21	2.30	0.62
1:B:64:THR:CG2	1:B:143:LYS:HD2	2.29	0.61
1:A:133:LEU:O	1:A:134:ASN:CB	2.49	0.61
1:B:138:VAL:HG21	1:B:152:PRO:HB3	1.82	0.60
1:B:37:GLN:HG3	1:B:175:SER:HB3	1.83	0.60
1:B:44:GLY:O	1:B:161:PRO:HG3	2.02	0.60
1:C:41:THR:HG21	1:C:50:ALA:HB3	1.83	0.60
1:C:103:ALA:HA	1:C:107:GLN:OE1	2.02	0.60
1:C:49:ALA:HB2	1:C:157:TYR:CD1	2.36	0.60
1:A:79:LEU:HD11	1:A:92:VAL:CG2	2.32	0.60
1:A:65:ALA:HB3	1:A:66:PRO:HD3	1.83	0.59
1:C:69:HIS:HB2	1:C:182:LYS:HD2	1.83	0.59
1:B:94:LEU:HD22	1:B:154:LEU:HD11	1.84	0.59
1:C:7:VAL:HG21	1:C:127:LYS:HE3	1.85	0.59
1:B:104:THR:O	1:B:107:GLN:HG2	2.03	0.59
1:B:139:ASN:HB2	1:B:150:ASP:HB3	1.84	0.58
1:B:49:ALA:HB2	1:B:157:TYR:HD2	1.68	0.58
1:C:135:LEU:HD22	1:C:140:ARG:HG2	1.84	0.58
1:B:105:PRO:HB2	1:B:157:TYR:HB2	1.84	0.58
1:A:93:TYR:O	1:A:156:ALA:HA	2.03	0.58
1:B:46:ALA:O	1:B:48:THR:HG23	2.03	0.57
1:C:61:THR:HG22	1:C:64:THR:HG21	1.85	0.57
1:B:55:GLN:HB2	1:B:151:THR:CG2	2.30	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:TYR:CG	1:A:180:LEU:HB3	2.40	0.57
1:A:110:ARG:HD3	1:B:188:ASN:OD1	2.05	0.57
1:B:95:ALA:HB2	1:B:108:ILE:HG23	1.87	0.57
1:C:84:LEU:HB3	1:C:169:THR:HG22	1.87	0.57
1:A:139:ASN:HD22	1:A:140:ARG:H	1.50	0.56
1:A:54:LEU:HD12	1:A:54:LEU:H	1.71	0.56
1:C:71:GLN:HB3	1:C:141:MET:SD	2.45	0.56
1:C:32:ILE:HG13	1:C:33:VAL:N	2.21	0.56
1:C:55:GLN:HG3	1:C:151:THR:HG21	1.87	0.56
1:B:61:THR:HG23	1:B:64:THR:CG2	2.35	0.56
1:A:134:ASN:HB3	1:A:137:SER:OG	2.06	0.56
1:C:11:GLN:HE22	1:C:96:TRP:N	1.85	0.56
1:A:184:MET:O	1:A:186:ILE:HG13	2.06	0.55
1:C:94:LEU:HD21	1:C:172:ILE:HD13	1.88	0.55
1:C:93:TYR:O	1:C:156:ALA:HA	2.07	0.55
1:A:94:LEU:HD21	1:A:172:ILE:CD1	2.30	0.55
1:A:104:THR:HB	1:A:107:GLN:HG3	1.87	0.55
1:A:51:GLN:HE21	1:A:153:LYS:NZ	2.05	0.55
1:A:45:THR:HG22	1:A:166:LYS:HA	1.87	0.55
1:B:100:ASN:OD1	1:B:149:THR:HB	2.06	0.55
1:C:134:ASN:HD22	1:C:135:LEU:N	2.05	0.55
1:C:102:PRO:O	1:C:103:ALA:CB	2.54	0.54
1:B:45:THR:HG22	1:B:166:LYS:HA	1.90	0.54
1:A:90:LEU:N	1:A:90:LEU:HD23	2.19	0.53
1:C:76:LYS:HD2	1:C:130:GLU:OE1	2.07	0.53
1:C:64:THR:HG23	1:C:143:LYS:CE	2.39	0.53
1:A:165:SER:C	1:A:167:ILE:H	2.11	0.53
1:C:95:ALA:HB2	1:C:108:ILE:HG23	1.89	0.53
1:A:71:GLN:HE21	1:A:140:ARG:HD3	1.73	0.53
1:B:66:PRO:HG2	1:B:67:TYR:CD1	2.43	0.53
1:B:11:GLN:NE2	1:B:96:TRP:N	2.48	0.53
1:B:21:LEU:O	1:B:23:GLN:HG3	2.09	0.53
1:C:100:ASN:HD22	1:C:100:ASN:H	1.56	0.53
1:A:54:LEU:O	1:A:55:GLN:CB	2.57	0.53
1:A:91:THR:HG23	1:A:91:THR:O	2.09	0.53
1:A:24:PRO:HD3	1:B:22:SER:HB2	1.89	0.53
1:C:139:ASN:HD22	1:C:139:ASN:C	2.10	0.53
1:C:187:ALA:O	1:C:188:ASN:CB	2.57	0.52
1:C:74:GLU:HA	1:C:135:LEU:HD11	1.91	0.52
1:A:54:LEU:CD1	1:A:54:LEU:H	2.22	0.52
1:B:4:SER:O	1:B:5:GLU:CB	2.57	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:ILE:O	1:C:172:ILE:HA	2.09	0.52
1:A:57:ALA:O	1:A:61:THR:HG23	2.10	0.52
1:C:14:ILE:HG13	1:C:14:ILE:O	2.09	0.52
1:C:20:ILE:HG22	1:C:21:LEU:O	2.09	0.51
1:C:61:THR:HA	1:C:64:THR:HB	1.90	0.51
1:B:133:LEU:HD11	1:B:152:PRO:HB2	1.92	0.51
1:C:51:GLN:HB3	1:C:153:LYS:HE2	1.92	0.51
1:A:158:SER:O	1:A:159:ARG:HG2	2.11	0.51
1:C:65:ALA:HB3	1:C:66:PRO:HD3	1.92	0.51
1:C:83:ASP:O	1:C:86:VAL:HG23	2.11	0.51
1:A:55:GLN:O	1:A:55:GLN:HG2	2.11	0.51
1:B:151:THR:HG23	1:B:152:PRO:HD2	1.93	0.51
1:B:80:THR:CG2	1:B:128:THR:HG23	2.41	0.51
1:B:64:THR:HG22	1:B:65:ALA:N	2.25	0.50
1:B:133:LEU:HD11	1:B:152:PRO:CB	2.41	0.50
1:B:49:ALA:HB1	1:B:105:PRO:CG	2.41	0.50
1:B:4:SER:O	1:B:5:GLU:CG	2.58	0.50
1:B:93:TYR:O	1:B:156:ALA:HA	2.11	0.50
1:C:90:LEU:HD21	1:C:119:LEU:HB2	1.93	0.50
1:C:98:PRO:O	1:C:99:ALA:CB	2.60	0.50
1:C:100:ASN:HB3	1:C:149:THR:O	2.12	0.49
1:C:100:ASN:HD22	1:C:100:ASN:N	2.09	0.49
1:A:37:GLN:HE21	1:A:175:SER:HB3	1.77	0.49
1:C:134:ASN:HD22	1:C:134:ASN:C	2.13	0.49
1:A:104:THR:CG2	1:A:105:PRO:HD2	2.43	0.49
1:C:178:ILE:HG22	1:C:179:ARG:N	2.28	0.48
1:B:78:ILE:O	1:B:172:ILE:HA	2.13	0.48
1:B:29:SER:HB3	1:B:182:LYS:NZ	2.29	0.48
1:B:14:ILE:HD12	1:B:14:ILE:O	2.13	0.48
1:A:58:ASP:HB2	1:A:59:PRO:HD3	1.95	0.48
1:C:41:THR:HG21	1:C:50:ALA:CB	2.42	0.48
1:B:6:VAL:HG23	1:B:128:THR:O	2.13	0.48
1:A:139:ASN:C	1:A:139:ASN:HD22	2.17	0.48
1:C:134:ASN:O	1:C:137:SER:HB3	2.14	0.48
1:C:4:SER:O	1:C:5:GLU:HB2	2.14	0.48
1:A:158:SER:C	1:A:159:ARG:HG2	2.34	0.48
1:C:52:VAL:CG1	1:C:154:LEU:HB3	2.44	0.48
1:C:97:VAL:HG12	1:C:99:ALA:H	1.79	0.48
1:C:139:ASN:ND2	1:C:141:MET:H	2.12	0.47
1:A:45:THR:HG22	1:A:166:LYS:CA	2.44	0.47
1:B:54:LEU:HD12	1:B:152:PRO:CG	2.45	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:THR:HG23	1:C:143:LYS:HD2	1.97	0.47
1:A:100:ASN:N	1:A:100:ASN:OD1	2.48	0.47
1:B:140:ARG:HB3	1:B:140:ARG:NH1	2.18	0.47
1:C:104:THR:O	1:C:107:GLN:HG3	2.15	0.47
1:C:4:SER:O	1:C:5:GLU:CB	2.62	0.47
1:C:65:ALA:HB3	1:C:66:PRO:CD	2.43	0.47
1:A:67:TYR:CD2	1:A:180:LEU:HB3	2.50	0.47
1:C:52:VAL:HG13	1:C:154:LEU:HB3	1.95	0.47
1:A:119:LEU:H	1:A:123:ILE:CB	2.28	0.47
1:A:40:ALA:HB1	1:A:52:VAL:HG21	1.97	0.47
1:B:137:SER:C	1:B:138:VAL:HG13	2.35	0.47
1:C:134:ASN:C	1:C:134:ASN:ND2	2.68	0.46
1:A:54:LEU:N	1:A:54:LEU:CD1	2.77	0.46
1:A:70:ALA:O	1:A:141:MET:O	2.34	0.46
1:A:79:LEU:HD11	1:A:92:VAL:HG22	1.95	0.46
1:C:99:ALA:HA	1:C:153:LYS:HD2	1.98	0.46
1:B:47:GLU:HB2	1:B:160:ALA:HB2	1.98	0.46
1:A:140:ARG:H	1:A:140:ARG:HG3	1.43	0.46
1:A:158:SER:O	1:A:159:ARG:O	2.34	0.46
1:A:186:ILE:CG2	1:A:187:ALA:N	2.63	0.46
1:B:39:GLU:HA	1:B:173:GLN:HA	1.98	0.46
1:A:112:TYR:HB3	1:B:185:LEU:HD22	1.98	0.46
1:A:159:ARG:HH11	1:A:159:ARG:HB3	1.81	0.46
1:B:133:LEU:HD23	1:B:133:LEU:C	2.37	0.46
1:A:159:ARG:NH1	1:A:159:ARG:HB3	2.31	0.46
1:A:67:TYR:CD1	1:A:67:TYR:N	2.84	0.46
1:C:134:ASN:HB3	1:C:137:SER:HB2	1.98	0.46
1:B:187:ALA:O	1:B:188:ASN:CB	2.61	0.45
1:B:79:LEU:CD2	1:B:119:LEU:HD11	2.46	0.45
1:B:100:ASN:OD1	1:B:149:THR:O	2.34	0.45
1:B:65:ALA:HB3	1:B:66:PRO:HD3	1.98	0.45
1:B:109:LEU:HD21	1:B:116:SER:HB2	1.99	0.45
1:C:23:GLN:NE2	1:C:23:GLN:N	2.65	0.45
1:A:183:PRO:HG2	1:C:14:ILE:HD12	1.97	0.45
1:A:68:ARG:HD3	1:C:150:ASP:HB3	1.98	0.45
1:A:111:VAL:HG12	1:A:112:TYR:N	2.31	0.45
1:A:90:LEU:CD2	1:A:90:LEU:H	2.22	0.45
1:B:186:ILE:HG12	1:B:187:ALA:N	2.32	0.45
1:C:54:LEU:HD12	1:C:152:PRO:HG2	1.99	0.45
1:C:24:PRO:HB2	1:C:26:THR:HG23	1.98	0.45
1:C:76:LYS:HA	1:C:132:PRO:HA	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:ASN:N	1:C:164:PRO:HD3	2.31	0.44
1:C:37:GLN:HA	1:C:174:ILE:O	2.17	0.44
1:A:125:ALA:O	1:A:126:ALA:HB3	2.17	0.44
1:A:76:LYS:HD2	1:A:130:GLU:OE1	2.17	0.44
1:B:140:ARG:HH11	1:B:140:ARG:CB	2.16	0.44
1:B:79:LEU:HD23	1:B:172:ILE:HG22	1.99	0.44
1:C:45:THR:HG22	1:C:165:SER:O	2.17	0.44
1:A:165:SER:O	1:A:167:ILE:N	2.51	0.44
1:A:118:VAL:O	1:A:119:LEU:O	2.36	0.44
1:A:134:ASN:O	1:A:135:LEU:HB2	2.17	0.44
1:B:41:THR:HG22	1:B:172:ILE:HG12	1.99	0.44
1:C:97:VAL:HG13	1:C:98:PRO:CD	2.46	0.44
1:A:104:THR:HG22	1:A:105:PRO:HD2	1.99	0.44
1:C:46:ALA:O	1:C:48:THR:HG23	2.18	0.44
1:A:131:VAL:HA	1:A:132:PRO:HD3	1.78	0.43
1:B:90:LEU:N	1:B:90:LEU:HD23	2.33	0.43
1:C:54:LEU:HD12	1:C:152:PRO:CG	2.48	0.43
1:B:80:THR:HG22	1:B:128:THR:HG23	1.99	0.43
1:A:55:GLN:HG3	1:A:142:LEU:O	2.19	0.43
1:B:137:SER:O	1:B:138:VAL:CG2	2.59	0.43
1:B:9:VAL:HG12	1:B:115:GLN:NE2	2.25	0.43
1:C:83:ASP:OD2	1:C:84:LEU:HD12	2.19	0.43
1:A:51:GLN:HE21	1:A:153:LYS:CE	2.31	0.43
1:B:181:SER:HB3	1:B:182:LYS:H	1.64	0.43
1:C:7:VAL:HG21	1:C:127:LYS:CE	2.48	0.43
1:C:21:LEU:HD23	1:C:148:TYR:OH	2.18	0.43
1:C:89:PRO:HG3	1:C:121:GLY:N	2.33	0.43
1:C:90:LEU:HD23	1:C:90:LEU:N	2.34	0.43
1:B:54:LEU:HD12	1:B:152:PRO:HG2	2.01	0.42
1:B:61:THR:HG23	1:B:64:THR:HG22	2.00	0.42
1:C:85:ALA:O	1:C:120:GLY:HA3	2.20	0.42
1:B:94:LEU:CD2	1:B:154:LEU:HD11	2.49	0.42
1:C:144:ASP:OD2	1:C:145:SER:N	2.44	0.42
1:C:79:LEU:HB3	1:C:129:ILE:HB	2.00	0.42
1:C:39:GLU:HG3	1:C:173:GLN:HE21	1.83	0.42
1:C:4:SER:OG	1:C:5:GLU:N	2.48	0.42
1:B:79:LEU:HD22	1:B:119:LEU:HD11	2.00	0.42
1:A:186:ILE:O	1:C:111:VAL:HA	2.20	0.42
1:B:159:ARG:HB2	1:B:159:ARG:CZ	2.50	0.42
1:B:20:ILE:C	1:C:21:LEU:HD12	2.40	0.42
1:B:59:PRO:O	1:B:63:LEU:HD13	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:PHE:HE1	1:B:172:ILE:HG23	1.85	0.42
1:B:76:LYS:HA	1:B:132:PRO:HA	2.01	0.41
1:B:6:VAL:HG22	1:B:7:VAL:N	2.35	0.41
1:C:90:LEU:CD2	1:C:119:LEU:HB2	2.49	0.41
1:B:137:SER:O	1:B:138:VAL:HG13	2.20	0.41
2:D:3:C:H3'	2:D:3:C:H6	1.85	0.41
1:A:78:ILE:O	1:A:172:ILE:HA	2.19	0.41
1:B:186:ILE:CG1	1:B:187:ALA:N	2.83	0.41
1:B:72:ILE:HD11	1:B:142:LEU:HD21	2.03	0.41
1:C:184:MET:HG3	1:C:185:LEU:N	2.35	0.41
1:B:139:ASN:O	1:B:152:PRO:HD3	2.20	0.41
1:B:54:LEU:HB2	1:B:152:PRO:HG2	2.02	0.41
1:B:34:LEU:HA	1:B:35:PRO:HD3	1.86	0.41
1:B:181:SER:O	1:B:182:LYS:C	2.58	0.41
1:C:73:VAL:HB	1:C:177:ARG:O	2.21	0.41
1:C:79:LEU:HD13	1:C:172:ILE:HG12	2.02	0.41
1:A:111:VAL:CG1	1:A:112:TYR:N	2.83	0.41
1:B:4:SER:O	1:B:5:GLU:HB3	2.20	0.40
1:C:76:LYS:HE3	1:C:78:ILE:HD11	2.02	0.40
1:A:61:THR:HA	1:A:64:THR:OG1	2.21	0.40
1:C:120:GLY:H	1:C:125:ALA:HB1	1.86	0.40
1:C:40:ALA:O	1:C:41:THR:HG23	2.22	0.40
1:A:63:LEU:O	1:A:66:PRO:HD2	2.22	0.40
1:B:111:VAL:CG1	1:C:185:LEU:HD22	2.52	0.40
1:B:61:THR:HG23	1:B:64:THR:HG21	2.03	0.40
1:C:157:TYR:CG	1:C:158:SER:N	2.89	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	163/188 (87%)	125 (77%)	26 (16%)	12 (7%)	1	12
1	B	176/188 (94%)	156 (89%)	15 (8%)	5 (3%)	6	37
1	C	183/188 (97%)	161 (88%)	15 (8%)	7 (4%)	4	29
All	All	522/564 (93%)	442 (85%)	56 (11%)	24 (5%)	3	24

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	PRO
1	A	119	LEU
1	A	159	ARG
1	B	5	GLU
1	B	138	VAL
1	C	159	ARG
1	A	134	ASN
1	C	5	GLU
1	C	114	GLY
1	A	56	THR
1	A	122	ALA
1	A	164	PRO
1	A	55	GLN
1	C	89	PRO
1	C	102	PRO
1	C	103	ALA
1	A	125	ALA
1	A	128	THR
1	B	182	LYS
1	C	57	ALA
1	A	166	LYS
1	B	65	ALA
1	B	89	PRO
1	A	168	PRO

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	132/159 (83%)	124 (94%)	8 (6%)	22	59
1	B	151/159 (95%)	144 (95%)	7 (5%)	31	68
1	C	156/159 (98%)	137 (88%)	19 (12%)	6	26
All	All	439/477 (92%)	405 (92%)	34 (8%)	15	49

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	PRO
1	A	79	LEU
1	A	107	GLN
1	A	134	ASN
1	A	139	ASN
1	A	140	ARG
1	A	151	THR
1	A	154	LEU
1	B	23	GLN
1	B	42	THR
1	B	64	THR
1	B	71	GLN
1	B	79	LEU
1	B	140	ARG
1	B	149	THR
1	C	5	GLU
1	C	23	GLN
1	C	25	ASN
1	C	26	THR
1	C	55	GLN
1	C	64	THR
1	C	87	SER
1	C	88	ASN
1	C	100	ASN
1	C	106	THR
1	C	107	GLN
1	C	133	LEU
1	C	134	ASN
1	C	139	ASN
1	C	150	ASP
1	C	151	THR
1	C	154	LEU
1	C	163	ASN
1	C	179	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	51	GLN
1	A	71	GLN
1	A	134	ASN
1	A	139	ASN
1	A	173	GLN
1	B	11	GLN
1	B	23	GLN
1	B	37	GLN
1	B	55	GLN
1	B	71	GLN
1	B	115	GLN
1	B	163	ASN
1	C	11	GLN
1	C	37	GLN
1	C	100	ASN
1	C	115	GLN
1	C	134	ASN
1	C	139	ASN
1	C	163	ASN
1	C	173	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	D	2/3 (66%)	1 (50%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	D	3	C

There are no RNA pucker outliers to report.

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 [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 [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, 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	165/188 (87%)	2.17	72 (43%) 0 0	42, 55, 96, 100	0
1	B	180/188 (95%)	2.39	83 (46%) 0 0	41, 52, 71, 96	0
1	C	185/188 (98%)	2.32	85 (45%) 0 0	39, 52, 70, 81	0
2	D	3/3 (100%)	3.28	3 (100%) 0 0	82, 82, 92, 97	0
All	All	533/567 (94%)	2.30	243 (45%) 0 0	39, 53, 82, 100	0

All (243) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	139	ASN	18.8
1	B	4	SER	11.2
1	B	22	SER	10.4
1	C	4	SER	10.1
1	C	18	GLY	9.3
1	A	24	PRO	9.1
1	B	32	ILE	8.6
1	B	129	ILE	8.2
1	B	79	LEU	7.8
1	C	26	THR	7.8
1	B	5	GLU	7.8
1	C	60	ILE	7.8
1	C	106	THR	7.7
1	B	6	VAL	7.7
1	B	132	PRO	7.7
1	A	25	ASN	7.2
1	B	52	VAL	7.1
1	C	136	ASP	7.0
1	A	69	HIS	7.0
1	C	139	ASN	6.8
1	A	119	LEU	6.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	74	GLU	6.4
1	B	37	GLN	6.4
1	B	151	THR	6.3
1	B	21	LEU	6.2
1	B	156	ALA	6.2
1	A	49	ALA	6.1
1	B	142	LEU	6.0
1	B	77	ALA	5.9
1	C	81	PRO	5.9
1	A	33	VAL	5.8
1	C	174	ILE	5.7
1	C	50	ALA	5.7
1	A	188	ASN	5.7
1	C	28	GLN	5.6
1	C	70	ALA	5.6
1	C	104	THR	5.6
1	A	140	ARG	5.4
1	A	26	THR	5.3
1	A	155	LEU	5.3
1	B	109	LEU	5.2
1	A	113	GLY	5.1
1	B	160	ALA	5.1
1	B	18	GLY	5.1
1	B	82	THR	5.0
1	C	69	HIS	5.0
1	B	81	PRO	5.0
1	C	178	ILE	4.9
1	B	130	GLU	4.9
1	A	79	LEU	4.9
1	C	38	PHE	4.9
1	C	59	PRO	4.9
1	B	103	ALA	4.8
1	C	5	GLU	4.8
1	B	161	PRO	4.8
1	B	31	ALA	4.8
1	C	184	MET	4.8
1	A	126	ALA	4.7
1	C	134	ASN	4.7
1	B	165	SER	4.6
1	A	161	PRO	4.6
1	C	180	LEU	4.5
1	A	75	CYS	4.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	70	ALA	4.5
1	C	93	TYR	4.4
1	C	135	LEU	4.4
1	A	52	VAL	4.4
1	C	17	PRO	4.4
1	B	183	PRO	4.3
1	B	71	GLN	4.3
1	C	105	PRO	4.3
1	A	115	GLN	4.3
1	B	167	ILE	4.3
1	B	177	ARG	4.2
2	D	3	C	4.2
1	C	138	VAL	4.2
1	A	95	ALA	4.1
1	C	27	GLU	4.1
1	C	124	SER	4.1
1	C	83	ASP	4.0
1	C	126	ALA	4.0
1	A	168	PRO	4.0
1	C	166	LYS	3.9
1	A	92	VAL	3.9
1	B	23	GLN	3.9
1	B	162	THR	3.9
1	A	124	SER	3.8
1	B	181	SER	3.8
1	C	109	LEU	3.8
1	A	31	ALA	3.7
1	C	24	PRO	3.7
1	B	104	THR	3.7
1	B	14	ILE	3.7
1	A	141	MET	3.7
1	B	166	LYS	3.7
1	C	11	GLN	3.7
1	C	63	LEU	3.6
1	B	10	LYS	3.6
1	C	169	THR	3.6
1	C	51	GLN	3.6
1	A	30	PRO	3.6
1	C	30	PRO	3.6
1	A	56	THR	3.5
1	A	137	SER	3.5
1	A	162	THR	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	185	LEU	3.5
1	C	151	THR	3.5
1	A	154	LEU	3.5
1	B	179	ARG	3.5
1	B	144	ASP	3.5
1	A	151	THR	3.5
1	B	107	GLN	3.5
1	C	97	VAL	3.5
1	C	44	GLY	3.5
1	A	61	THR	3.4
1	A	40	ALA	3.4
1	B	78	ILE	3.4
1	A	134	ASN	3.4
1	A	128	THR	3.4
1	C	94	LEU	3.4
1	A	183	PRO	3.3
1	C	122	ALA	3.3
1	A	185	LEU	3.3
1	B	42	THR	3.3
1	A	171	SER	3.3
1	C	165	SER	3.3
1	A	48	THR	3.3
1	B	91	THR	3.2
1	C	73	VAL	3.2
1	C	152	PRO	3.2
1	B	116	SER	3.2
1	A	129	ILE	3.2
1	A	45	THR	3.2
1	C	92	VAL	3.2
1	C	163	ASN	3.2
1	C	42	THR	3.2
1	B	137	SER	3.1
1	B	93	TYR	3.1
1	B	102	PRO	3.1
1	B	80	THR	3.1
1	C	82	THR	3.1
1	B	36	PHE	3.1
1	B	87	SER	3.1
1	A	46	ALA	3.0
1	A	58	ASP	3.0
1	B	149	THR	3.0
1	B	101	SER	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	156	ALA	3.0
1	C	175	SER	3.0
1	B	186	ILE	3.0
1	A	177	ARG	3.0
1	C	128	THR	3.0
1	B	118	VAL	2.9
1	C	87	SER	2.9
1	A	35	PRO	2.9
1	B	178	ILE	2.9
1	A	125	ALA	2.9
1	B	188	ASN	2.9
1	A	131	VAL	2.9
1	B	172	ILE	2.9
2	D	1	C	2.9
1	C	154	LEU	2.9
1	B	45	THR	2.9
1	C	173	GLN	2.9
1	B	176	GLY	2.9
1	A	111	VAL	2.8
1	A	103	ALA	2.8
1	A	181	SER	2.8
1	B	112	TYR	2.8
2	D	2	C	2.8
1	B	67	TYR	2.8
1	C	47	GLU	2.7
1	A	60	ILE	2.7
1	B	29	SER	2.7
1	B	168	PRO	2.7
1	B	39	GLU	2.7
1	A	143	LYS	2.7
1	A	94	LEU	2.7
1	C	150	ASP	2.7
1	B	187	ALA	2.6
1	B	131	VAL	2.6
1	C	162	THR	2.6
1	C	160	ALA	2.6
1	C	118	VAL	2.6
1	A	34	LEU	2.6
1	A	138	VAL	2.6
1	C	145	SER	2.6
1	B	62	LYS	2.6
1	C	187	ALA	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	31	ALA	2.6
1	C	179	ARG	2.6
1	B	59	PRO	2.6
1	C	108	ILE	2.5
1	C	181	SER	2.5
1	A	99	ALA	2.5
1	A	146	VAL	2.5
1	B	60	ILE	2.5
1	C	147	THR	2.5
1	A	186	ILE	2.5
1	A	121	GLY	2.5
1	C	64	THR	2.5
1	A	76	LYS	2.5
1	C	161	PRO	2.4
1	B	158	SER	2.4
1	A	43	PHE	2.4
1	A	160	ALA	2.4
1	B	40	ALA	2.4
1	B	115	GLN	2.4
1	A	135	LEU	2.4
1	B	11	GLN	2.4
1	A	136	ASP	2.4
1	A	102	PRO	2.4
1	A	42	THR	2.3
1	C	88	ASN	2.3
1	C	159	ARG	2.3
1	B	173	GLN	2.3
1	A	53	SER	2.3
1	C	107	GLN	2.3
1	C	164	PRO	2.3
1	B	143	LYS	2.3
1	C	52	VAL	2.2
1	B	73	VAL	2.2
1	B	122	ALA	2.2
1	C	95	ALA	2.2
1	B	41	THR	2.2
1	C	16	ALA	2.2
1	A	57	ALA	2.2
1	A	84	LEU	2.2
1	B	95	ALA	2.1
1	C	186	ILE	2.1
1	B	12	ALA	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	130	GLU	2.1
1	C	22	SER	2.1
1	C	130	GLU	2.1
1	B	180	LEU	2.1
1	B	127	LYS	2.1
1	B	17	PRO	2.1
1	C	170	ALA	2.0
1	C	144	ASP	2.0
1	A	59	PRO	2.0
1	A	156	ALA	2.0
1	C	79	LEU	2.0
1	A	29	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no 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.