Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 05:09 AM EDT

PDB ID	:	1O65
Title	:	Crystal structure of an hypothetical protein
Authors	:	Structural GenomiX
Deposited on	:	2003-10-23
Resolution	:	2.33 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:

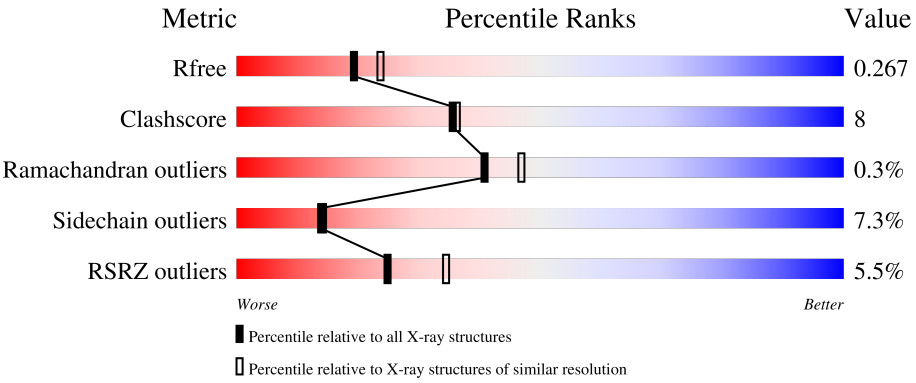
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.33 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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 <=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	246	4% 70% 16% • 11%
1	B	246	7% 67% 18% • 12%
1	C	246	3% 69% 16% • 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5360 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 Hypothetical protein yiiM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1735	1102	300	325	8			
1	B	217	Total	C	N	O	S	0	0	0
			1725	1096	297	324	8			
1	C	217	Total	C	N	O	S	0	0	0
			1717	1091	297	321	8			

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	cloning artifact	UNP P32157
A	0	SER	-	cloning artifact	UNP P32157
A	1	LEU	-	cloning artifact	UNP P32157
A	235	GLU	-	cloning artifact	UNP P32157
A	236	GLY	-	cloning artifact	UNP P32157
A	237	GLY	-	cloning artifact	UNP P32157
A	238	SER	-	cloning artifact	UNP P32157
A	239	HIS	-	cloning artifact	UNP P32157
A	240	HIS	-	cloning artifact	UNP P32157
A	241	HIS	-	cloning artifact	UNP P32157
A	242	HIS	-	cloning artifact	UNP P32157
A	243	HIS	-	cloning artifact	UNP P32157
A	244	HIS	-	cloning artifact	UNP P32157
B	-1	MET	-	cloning artifact	UNP P32157
B	0	SER	-	cloning artifact	UNP P32157
B	1	LEU	-	cloning artifact	UNP P32157
B	235	GLU	-	cloning artifact	UNP P32157
B	236	GLY	-	cloning artifact	UNP P32157
B	237	GLY	-	cloning artifact	UNP P32157
B	238	SER	-	cloning artifact	UNP P32157
B	239	HIS	-	cloning artifact	UNP P32157
B	240	HIS	-	cloning artifact	UNP P32157
B	241	HIS	-	cloning artifact	UNP P32157

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Chain	Residue	Modelled	Actual	Comment	Reference
B	242	HIS	-	cloning artifact	UNP P32157
B	243	HIS	-	cloning artifact	UNP P32157
B	244	HIS	-	cloning artifact	UNP P32157
C	-1	MET	-	cloning artifact	UNP P32157
C	0	SER	-	cloning artifact	UNP P32157
C	1	LEU	-	cloning artifact	UNP P32157
C	235	GLU	-	cloning artifact	UNP P32157
C	236	GLY	-	cloning artifact	UNP P32157
C	237	GLY	-	cloning artifact	UNP P32157
C	238	SER	-	cloning artifact	UNP P32157
C	239	HIS	-	cloning artifact	UNP P32157
C	240	HIS	-	cloning artifact	UNP P32157
C	241	HIS	-	cloning artifact	UNP P32157
C	242	HIS	-	cloning artifact	UNP P32157
C	243	HIS	-	cloning artifact	UNP P32157
C	244	HIS	-	cloning artifact	UNP P32157

- Molecule 2 is water.

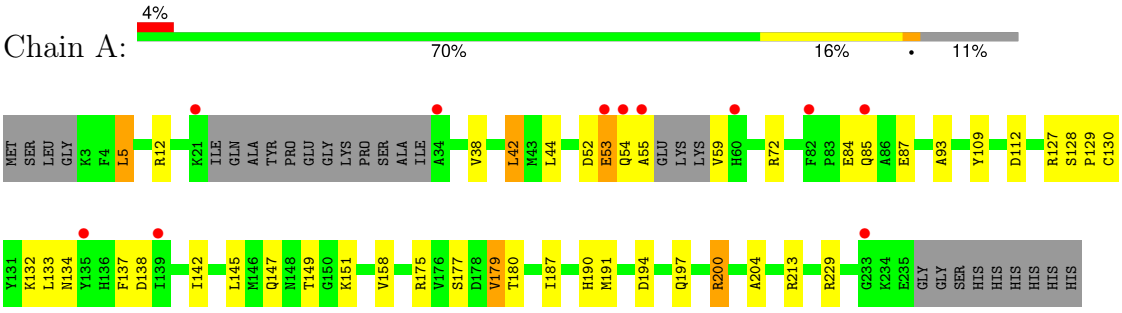
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	74	Total O 74 74	0	0
2	B	48	Total O 48 48	0	0
2	C	61	Total O 61 61	0	0

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.

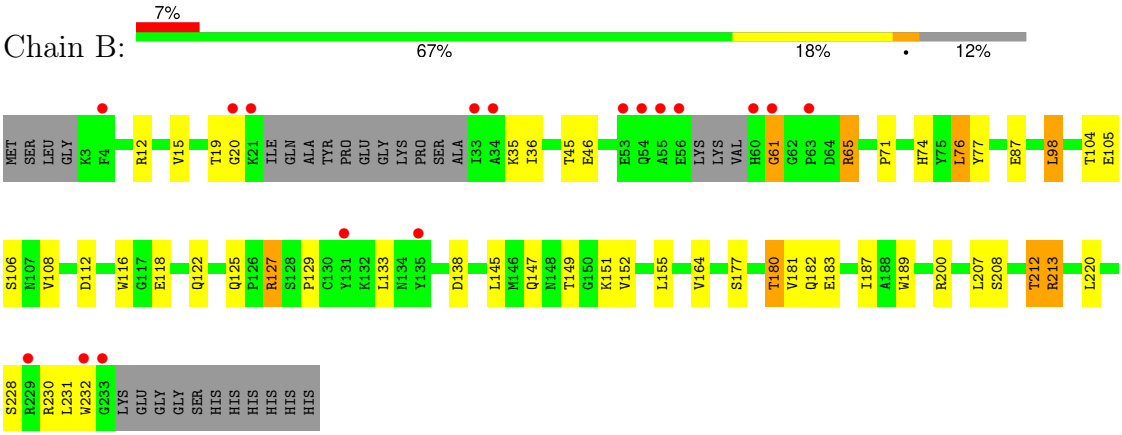
• Molecule 1: Hypothetical protein yiiM

Chain A:



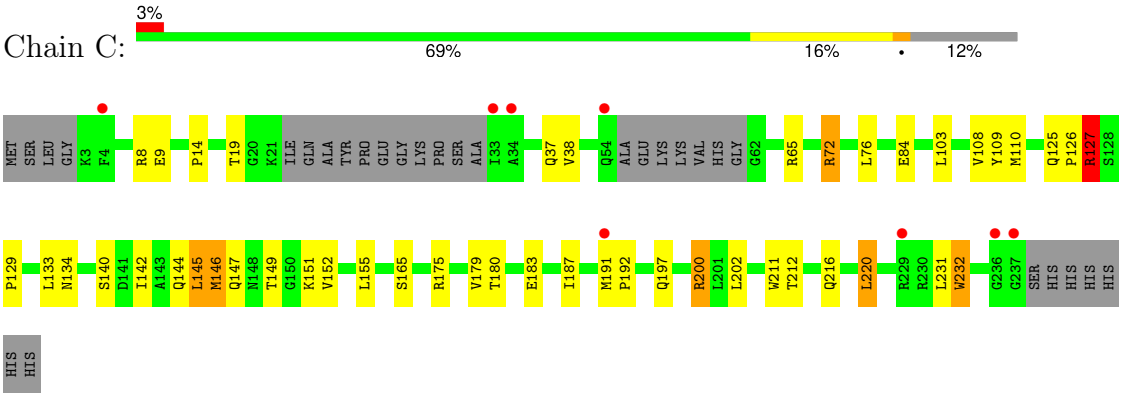
• Molecule 1: Hypothetical protein yiiM

Chain B:



• Molecule 1: Hypothetical protein yiiM

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	72.12Å 97.88Å 98.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.33 50.04 – 2.33	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.33) 99.0 (50.04-2.33)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	8.67 (at 2.34Å)	Xtriage
Refinement program	REFMAC 4.0	Depositor
R, R_{free}	0.231 , 0.308 0.207 , 0.267	Depositor DCC
R_{free} test set	1526 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	31.3	Xtriage
Anisotropy	0.252	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 48.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.016 for -h,l,k	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5360	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.56	0/1778	1.10	8/2410 (0.3%)
1	B	0.52	0/1767	1.02	6/2395 (0.3%)
1	C	0.54	0/1759	1.09	8/2383 (0.3%)
All	All	0.54	0/5304	1.07	22/7188 (0.3%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	8	ARG	NE-CZ-NH1	10.35	125.48	120.30
1	A	213	ARG	CD-NE-CZ	8.20	135.08	123.60
1	A	200	ARG	NE-CZ-NH1	-8.13	116.24	120.30
1	C	8	ARG	CD-NE-CZ	8.09	134.92	123.60
1	C	127	ARG	NE-CZ-NH1	7.93	124.27	120.30
1	C	8	ARG	NE-CZ-NH2	-7.82	116.39	120.30
1	A	72	ARG	CD-NE-CZ	7.72	134.41	123.60
1	C	175	ARG	CD-NE-CZ	7.64	134.29	123.60
1	C	127	ARG	CD-NE-CZ	7.37	133.91	123.60
1	A	175	ARG	NE-CZ-NH1	-6.48	117.06	120.30
1	A	72	ARG	NE-CZ-NH1	6.34	123.47	120.30
1	B	230	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	A	12	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	A	112	ASP	CB-CG-OD1	6.07	123.77	118.30
1	B	12	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	B	213	ARG	CD-NE-CZ	5.73	131.62	123.60
1	B	200	ARG	NE-CZ-NH2	-5.39	117.61	120.30
1	B	138	ASP	CB-CG-OD1	5.25	123.02	118.30
1	C	146	MET	CA-CB-CG	5.21	122.16	113.30
1	B	213	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	C	200	ARG	NE-CZ-NH1	-5.04	117.78	120.30
1	A	200	ARG	NH1-CZ-NH2	5.00	124.91	119.40

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	1735	0	1651	19	0
1	B	1725	0	1644	35	0
1	C	1717	0	1634	29	0
2	A	74	0	0	2	0
2	B	48	0	0	1	0
2	C	61	0	0	2	0
All	All	5360	0	4929	82	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 8.

All (82) 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:B:149:THR:HG23	1:B:151:LYS:H	1.32	0.94
1:C:127:ARG:HH11	1:C:127:ARG:HG3	1.42	0.84
1:C:149:THR:HG23	1:C:151:LYS:H	1.43	0.83
1:A:191:MET:SD	1:A:197:GLN:HG2	2.24	0.78
1:C:145:LEU:O	1:C:149:THR:HG22	1.88	0.74
1:B:180:THR:HG22	1:B:183:GLU:H	1.53	0.73
1:B:149:THR:OG1	1:B:151:LYS:HE2	1.94	0.68
1:A:191:MET:HB3	2:A:307:HOH:O	1.93	0.67
1:B:65:ARG:NH2	1:B:125:GLN:HE22	1.93	0.66
1:B:15:VAL:HG21	1:B:98:LEU:HG	1.77	0.66
1:B:129:PRO:HG2	1:B:147:GLN:HB2	1.77	0.64
1:B:145:LEU:O	1:B:149:THR:HG22	1.98	0.63
1:C:129:PRO:HG2	1:C:147:GLN:HB2	1.80	0.63
1:B:104:THR:HG22	1:B:106:SER:H	1.66	0.61
1:C:19:THR:HG22	1:C:38:VAL:HG22	1.83	0.60
1:C:65:ARG:HB2	1:C:155:LEU:HD13	1.85	0.59
1:B:104:THR:O	1:B:108:VAL:HG12	2.04	0.58
1:A:187:ILE:HG12	1:A:197:GLN:HG3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:LEU:HD22	1:C:108:VAL:HG22	1.89	0.55
1:C:72:ARG:HG2	1:C:72:ARG:HH11	1.70	0.55
1:B:45:THR:HG22	1:B:46:GLU:N	2.22	0.55
1:C:19:THR:HG21	2:C:266:HOH:O	2.07	0.55
1:B:71:PRO:HG2	1:B:74:HIS:CE1	2.42	0.54
1:B:213:ARG:HD2	2:B:289:HOH:O	2.08	0.53
1:B:149:THR:OG1	1:B:151:LYS:HG3	2.09	0.53
1:A:190:HIS:ND1	1:C:9:GLU:OE2	2.33	0.52
1:B:180:THR:CG2	1:B:182:GLN:HB3	2.39	0.52
1:C:19:THR:HG22	1:C:38:VAL:CG2	2.40	0.52
1:B:45:THR:HG22	1:B:46:GLU:H	1.75	0.52
1:C:144:GLN:OE1	1:C:231:LEU:HD13	2.11	0.51
1:C:65:ARG:CB	1:C:155:LEU:HD13	2.40	0.51
1:A:59:VAL:HA	2:A:314:HOH:O	2.12	0.50
1:B:76:LEU:HD12	1:B:77:TYR:N	2.27	0.50
1:B:108:VAL:HG13	1:B:181:VAL:CG2	2.43	0.49
1:A:44:LEU:HD11	1:A:158:VAL:HG21	1.95	0.48
1:C:216:GLN:HE21	1:C:220:LEU:HD22	1.78	0.48
1:A:194:ASP:OD2	1:A:197:GLN:HB2	2.13	0.48
1:C:134:ASN:OD1	1:C:142:ILE:HG22	2.13	0.48
1:B:77:TYR:CD2	1:B:151:LYS:HE3	2.49	0.48
1:A:52:ASP:O	1:A:53:GLU:C	2.52	0.47
1:B:208:SER:O	1:B:212:THR:HG23	2.14	0.46
1:C:109:TYR:HA	1:C:180:THR:HA	1.96	0.46
1:B:112:ASP:O	1:B:122:GLN:HA	2.15	0.46
1:C:144:GLN:OE1	1:C:232:TRP:CZ3	2.68	0.46
1:A:129:PRO:HG2	1:A:147:GLN:HB2	1.98	0.46
1:B:207:LEU:HD23	1:B:212:THR:HG22	1.97	0.46
1:B:183:GLU:O	1:B:187:ILE:HG13	2.16	0.45
1:B:77:TYR:CE2	1:B:151:LYS:HE3	2.52	0.45
1:B:20:GLY:CA	1:B:35:LYS:HG2	2.47	0.45
1:B:147:GLN:HG3	1:B:189:TRP:CD2	2.51	0.45
1:C:84:GLU:HG2	2:C:295:HOH:O	2.17	0.44
1:B:105:GLU:O	1:B:180:THR:HG23	2.17	0.44
1:A:109:TYR:HA	1:A:180:THR:HA	1.99	0.44
1:A:229:ARG:HH11	1:A:229:ARG:HG2	1.82	0.44
1:B:74:HIS:HE1	1:B:105:GLU:OE2	2.01	0.43
1:A:130:CYS:SG	1:A:132:LYS:HG2	2.58	0.43
1:B:116:TRP:O	1:B:164:VAL:HG12	2.18	0.43
1:B:127:ARG:HB3	1:B:152:VAL:O	2.19	0.43
1:A:134:ASN:HA	1:A:142:ILE:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:ALA:HB1	1:A:137:PHE:CE1	2.54	0.43
1:C:202:LEU:HD22	1:C:212:THR:HG23	2.01	0.43
1:B:65:ARG:HB3	1:B:155:LEU:HD13	2.00	0.43
1:A:179:VAL:CG1	1:A:204:ALA:HB2	2.50	0.42
1:C:183:GLU:O	1:C:187:ILE:HG13	2.20	0.42
1:C:126:PRO:HG2	1:C:211:TRP:CH2	2.55	0.42
1:B:61:GLY:HA3	1:B:65:ARG:HD2	2.00	0.42
1:C:127:ARG:HG3	1:C:127:ARG:NH1	2.16	0.42
1:C:191:MET:SD	1:C:197:GLN:HG3	2.60	0.42
1:B:20:GLY:HA3	1:B:35:LYS:HG2	2.01	0.41
1:A:5:LEU:O	1:A:5:LEU:HD12	2.20	0.41
1:B:65:ARG:CB	1:B:155:LEU:HD13	2.50	0.41
1:A:38:VAL:HG11	1:A:42:LEU:HD13	2.03	0.41
1:B:87:GLU:H	1:B:87:GLU:CD	2.23	0.41
1:A:149:THR:HB	1:A:151:LYS:HE2	2.03	0.41
1:C:110:MET:CE	1:C:125:GLN:HA	2.50	0.41
1:C:191:MET:HA	1:C:192:PRO:HD2	1.96	0.41
1:C:127:ARG:HB3	1:C:152:VAL:O	2.20	0.41
1:C:200:ARG:HG3	1:C:200:ARG:HH11	1.86	0.41
1:A:54:GLN:HB3	1:A:55:ALA:H	1.54	0.40
1:C:191:MET:HE1	1:C:197:GLN:HB2	2.03	0.40
1:B:228:SER:O	1:B:232:TRP:N	2.45	0.40
1:C:72:ARG:HG2	1:C:72:ARG:NH1	2.34	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	212/246 (86%)	204 (96%)	7 (3%)	1 (0%)	29	31
1	B	211/246 (86%)	204 (97%)	6 (3%)	1 (0%)	29	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	211/246 (86%)	205 (97%)	6 (3%)	0	100 100
All	All	634/738 (86%)	613 (97%)	19 (3%)	2 (0%)	41 47

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	GLU
1	B	61	GLY

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	179/206 (87%)	166 (93%)	13 (7%)	14 14
1	B	178/206 (86%)	165 (93%)	13 (7%)	14 14
1	C	176/206 (85%)	163 (93%)	13 (7%)	13 14
All	All	533/618 (86%)	494 (93%)	39 (7%)	14 14

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	42	LEU
1	A	84	GLU
1	A	85	GLN
1	A	87	GLU
1	A	127	ARG
1	A	128	SER
1	A	133	LEU
1	A	138	ASP
1	A	145	LEU
1	A	177	SER
1	A	179	VAL
1	A	200	ARG

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Mol	Chain	Res	Type
1	B	19	THR
1	B	36	ILE
1	B	65	ARG
1	B	76	LEU
1	B	98	LEU
1	B	118	GLU
1	B	127	ARG
1	B	133	LEU
1	B	177	SER
1	B	180	THR
1	B	212	THR
1	B	220	LEU
1	B	231	LEU
1	C	14	PRO
1	C	37	GLN
1	C	72	ARG
1	C	76	LEU
1	C	127	ARG
1	C	133	LEU
1	C	140	SER
1	C	145	LEU
1	C	146	MET
1	C	165	SER
1	C	179	VAL
1	C	220	LEU
1	C	232	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	54	GLN
1	B	74	HIS
1	B	125	GLN
1	B	144	GLN
1	B	148	ASN
1	C	37	GLN
1	C	74	HIS
1	C	182	GLN
1	C	216	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 monosaccharides 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, 95^{th} 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	218/246 (88%)	0.18	11 (5%)	28	39	16, 29, 55, 77	0
1	B	217/246 (88%)	0.34	17 (7%)	13	19	18, 32, 63, 87	0
1	C	217/246 (88%)	0.03	8 (3%)	41	52	18, 29, 55, 70	0
All	All	652/738 (88%)	0.18	36 (5%)	25	34	16, 30, 57, 87	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	55	ALA	13.6
1	B	55	ALA	10.5
1	B	232	TRP	9.8
1	C	237	GLY	7.4
1	B	33	ILE	7.0
1	A	54	GLN	6.3
1	C	33	ILE	6.3
1	B	60	HIS	6.0
1	B	61	GLY	5.7
1	B	21	LYS	5.2
1	B	54	GLN	5.2
1	C	4	PHE	4.0
1	A	233	GLY	3.3
1	A	135	TYR	3.3
1	A	139	ILE	3.2
1	B	20	GLY	3.1
1	B	4	PHE	3.1
1	B	131	TYR	3.0
1	B	34	ALA	2.9
1	C	229	ARG	2.8
1	A	34	ALA	2.7
1	B	233	GLY	2.7
1	B	53	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	63	PRO	2.6
1	B	56	GLU	2.5
1	A	82	PHE	2.4
1	A	85	GLN	2.4
1	A	60	HIS	2.4
1	C	34	ALA	2.3
1	B	229	ARG	2.2
1	A	53	GLU	2.2
1	A	21	LYS	2.1
1	C	191	MET	2.1
1	C	236	GLY	2.1
1	C	54	GLN	2.0
1	B	135	TYR	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 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.