



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:31 AM UTC

PDB ID : 1UJ3 / pdb_00001uj3
Title : Crystal structure of a humanized Fab fragment of anti-tissue-factor antibody
in complex with tissue factor
Authors : Ohto, U.; Mizutani, R.; Nakamura, M.; Adachi, H.; Satow, Y.
Deposited on : 2003-07-25
Resolution : 2.10 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

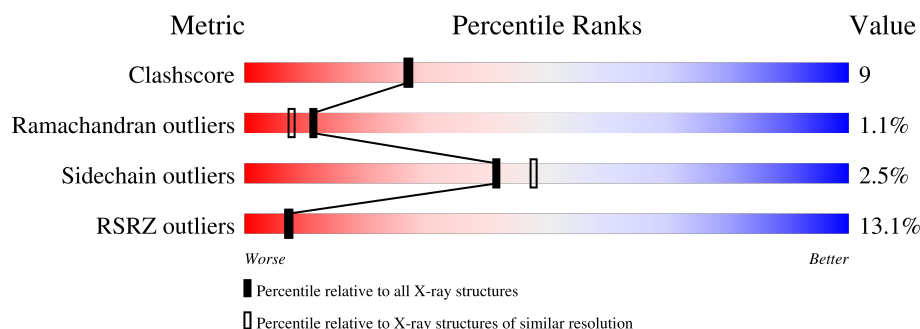
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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 ≥ 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	215	
2	B	217	
3	C	205	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5377 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 IgG Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1642	1028	270	338	6			

- Molecule 2 is a protein called IgG Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	217	Total	C	N	O	S	0	0	0
			1631	1022	274	326	9			

- Molecule 3 is a protein called tissue factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	205	Total	C	N	O	S	0	0	0
			1640	1038	266	331	5			

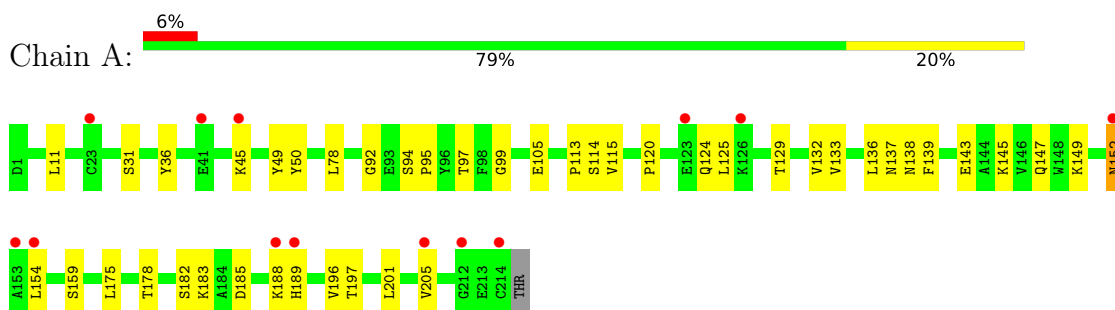
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	164	Total	O	0	0
			164	164		
4	B	216	Total	O	0	0
			216	216		
4	C	84	Total	O	0	0
			84	84		

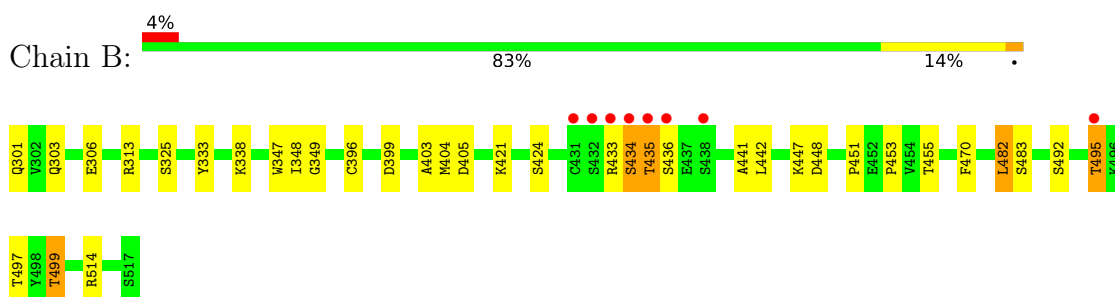
3 Residue-property plots

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.

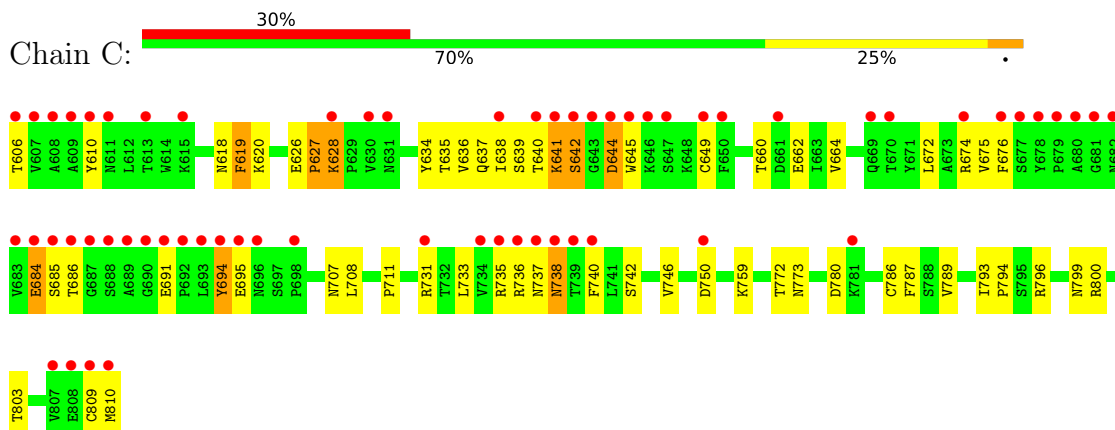
• Molecule 1: IgG Fab light chain



• Molecule 2: IgG Fab heavy chain



• Molecule 3: tissue factor



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	103.05Å 266.00Å 42.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.01 – 2.10 37.01 – 2.10	Depositor EDS
% Data completeness (in resolution range)	90.6 (37.01-2.10) 93.6 (37.01-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.19 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.196 , 0.227 0.212 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	26.5	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5377	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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	0.58	0/1678	1.04	7/2277 (0.3%)
2	B	0.62	0/1670	1.01	8/2275 (0.4%)
3	C	0.52	0/1676	1.00	7/2281 (0.3%)
All	All	0.58	0/5024	1.02	22/6833 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114	SER	N-CA-C	-7.80	96.53	109.24
3	C	772	THR	N-CA-C	-7.76	98.35	109.29
2	B	424	SER	N-CA-C	-6.87	98.50	109.76
2	B	404	MET	N-CA-C	-6.58	95.61	107.98
3	C	803	THR	N-CA-C	-6.35	101.98	110.55
1	A	92	GLY	N-CA-C	-6.31	106.84	114.66
2	B	436	SER	N-CA-C	-6.20	104.99	113.30
2	B	448	ASP	N-CA-C	6.17	119.61	111.28
3	C	628	LYS	N-CA-C	-6.16	101.99	109.57
2	B	447	LYS	N-CA-C	6.02	119.53	109.95
2	B	405	ASP	N-CA-C	5.90	118.66	111.82
3	C	642	SER	N-CA-C	-5.90	106.07	113.20
1	A	137	ASN	N-CA-C	5.82	118.72	109.24
2	B	396	CYS	N-CA-C	-5.80	100.22	109.96
3	C	620	LYS	N-CA-C	-5.65	101.28	109.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	GLY	N-CA-C	-5.55	104.02	112.51
1	A	182	SER	N-CA-C	-5.42	103.33	110.43
3	C	772	THR	N-CA-CB	5.41	115.61	108.96
2	B	470	PHE	N-CA-C	5.33	118.03	110.24
1	A	133	VAL	N-CA-C	5.33	115.57	108.11
1	A	138	ASN	N-CA-C	5.09	117.38	111.02
3	C	619	PHE	N-CA-CB	-5.07	108.39	114.17

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	36	TYR	Sidechain

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	1642	0	1587	25	0
2	B	1631	0	1581	20	0
3	C	1640	0	1592	45	0
4	A	164	0	0	2	0
4	B	216	0	0	3	0
4	C	84	0	0	1	0
All	All	5377	0	4760	89	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 9.

All (89) 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)
3:C:707:ASN:HD22	3:C:799:ASN:HD21	1.22	0.85
2:B:433:ARG:HB2	2:B:433:ARG:HH11	1.43	0.84
2:B:338:LYS:HB3	2:B:348:ILE:HD11	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:301:GLN:N	2:B:301:GLN:CD	2.41	0.78
1:A:136:LEU:HD21	1:A:196:VAL:HG21	1.66	0.75
3:C:708:LEU:HD11	3:C:793:ILE:HG12	1.68	0.74
3:C:707:ASN:ND2	3:C:799:ASN:HD21	1.87	0.72
2:B:433:ARG:HB2	2:B:433:ARG:NH1	2.08	0.67
2:B:441:ALA:O	2:B:442:LEU:HD12	1.95	0.67
1:A:136:LEU:HD21	1:A:196:VAL:CG2	2.28	0.64
2:B:421:LYS:NZ	4:B:1064:HOH:O	2.20	0.63
3:C:786:CYS:HA	3:C:809:CYS:HA	1.80	0.63
2:B:434:SER:O	2:B:435:THR:HG22	2.01	0.60
3:C:640:THR:C	3:C:642:SER:H	2.09	0.60
2:B:347:TRP:CZ2	2:B:349:GLY:HA2	2.35	0.60
3:C:737:ASN:O	3:C:738:ASN:HB2	2.00	0.60
3:C:750:ASP:O	3:C:794:PRO:HD2	2.02	0.60
3:C:676:PHE:CD2	3:C:694:TYR:HB3	2.37	0.59
1:A:188:LYS:HG3	1:A:189:HIS:CE1	2.38	0.58
1:A:143:GLU:CD	1:A:143:GLU:H	2.12	0.58
1:A:201:LEU:HD13	1:A:205:VAL:HG23	1.85	0.57
1:A:120:PRO:HD3	1:A:132:VAL:HG22	1.87	0.56
1:A:145:LYS:HB3	1:A:197:THR:HB	1.86	0.56
2:B:497:THR:HG23	2:B:514:ARG:HD2	1.88	0.55
2:B:482:LEU:HD23	2:B:482:LEU:C	2.32	0.54
3:C:645:TRP:CZ3	3:C:674:ARG:HG2	2.42	0.54
1:A:185:ASP:O	1:A:188:LYS:HG2	2.06	0.54
3:C:711:PRO:HB2	3:C:789:VAL:HG13	1.90	0.54
1:A:49:TYR:HB3	2:B:403:ALA:HB2	1.90	0.54
2:B:492:SER:O	2:B:495:THR:HG23	2.08	0.54
3:C:707:ASN:ND2	3:C:799:ASN:ND2	2.57	0.53
2:B:333:TYR:HB2	2:B:399:ASP:HB3	1.89	0.53
2:B:313:ARG:CZ	4:B:1212:HOH:O	2.55	0.53
3:C:637:GLN:HB2	3:C:674:ARG:HG3	1.91	0.53
1:A:136:LEU:CD2	1:A:196:VAL:HG21	2.37	0.52
3:C:637:GLN:HB2	3:C:674:ARG:CG	2.40	0.52
3:C:635:THR:HA	3:C:649:CYS:O	2.10	0.51
1:A:149:LYS:HG2	1:A:154:LEU:HD22	1.92	0.51
1:A:145:LYS:HE2	1:A:147:GLN:CD	2.36	0.51
1:A:124:GLN:HG2	1:A:129:THR:O	2.12	0.50
3:C:731:ARG:HA	3:C:742:SER:HA	1.93	0.50
3:C:640:THR:C	3:C:642:SER:N	2.69	0.50
3:C:708:LEU:HD21	3:C:793:ILE:HD11	1.93	0.49
3:C:606:THR:N	3:C:686:THR:HG1	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:LEU:C	1:A:175:LEU:HD23	2.39	0.48
3:C:634:TYR:HA	3:C:676:PHE:O	2.14	0.47
3:C:676:PHE:CE2	3:C:694:TYR:HB3	2.49	0.47
3:C:735:ARG:HD2	3:C:740:PHE:CE1	2.49	0.47
3:C:610:TYR:CZ	3:C:626:GLU:HB3	2.50	0.47
3:C:642:SER:HB2	3:C:644:ASP:OD1	2.15	0.47
3:C:640:THR:O	3:C:642:SER:N	2.48	0.47
1:A:143:GLU:CD	1:A:143:GLU:N	2.72	0.47
3:C:638:ILE:HG21	3:C:662:GLU:HG3	1.97	0.47
2:B:303:GLN:CG	2:B:325:SER:OG	2.63	0.46
3:C:773:ASN:HB3	4:C:1296:HOH:O	2.16	0.45
1:A:115:VAL:HG22	1:A:136:LEU:HD22	1.98	0.45
1:A:159:SER:HA	1:A:178:THR:O	2.17	0.45
1:A:94:SER:HA	1:A:95:PRO:C	2.42	0.44
2:B:499:THR:HB	2:B:514:ARG:HA	1.99	0.43
4:A:872:HOH:O	2:B:483:SER:HB2	2.18	0.43
3:C:619:PHE:CZ	3:C:746:VAL:HG11	2.53	0.43
3:C:639:SER:C	3:C:641:LYS:H	2.27	0.43
1:A:11:LEU:HD12	1:A:11:LEU:C	2.43	0.43
1:A:149:LYS:HE2	1:A:154:LEU:HD21	2.01	0.43
2:B:433:ARG:HH11	2:B:433:ARG:CB	2.22	0.43
2:B:455:THR:HG23	4:B:1092:HOH:O	2.18	0.43
3:C:636:VAL:HG22	3:C:675:VAL:HG22	2.00	0.43
3:C:674:ARG:HA	3:C:695:GLU:O	2.19	0.43
3:C:618:ASN:O	3:C:619:PHE:HB2	2.19	0.42
3:C:640:THR:HG23	3:C:642:SER:OG	2.18	0.42
3:C:736:ARG:O	3:C:737:ASN:ND2	2.52	0.42
2:B:434:SER:O	2:B:435:THR:CG2	2.67	0.42
1:A:113:PRO:HB3	1:A:139:PHE:HB3	2.01	0.42
3:C:759:LYS:NZ	3:C:780:ASP:OD2	2.41	0.42
3:C:787:PHE:HE2	3:C:810:MET:HG2	1.83	0.42
3:C:736:ARG:O	3:C:737:ASN:CG	2.63	0.42
3:C:731:ARG:HH22	3:C:733:LEU:HD23	1.85	0.42
1:A:125:LEU:O	1:A:183:LYS:HD2	2.20	0.41
3:C:660:THR:O	3:C:664:VAL:HG13	2.20	0.41
1:A:31:SER:O	1:A:50:TYR:HA	2.20	0.41
3:C:736:ARG:NH2	3:C:737:ASN:HD22	2.19	0.41
3:C:810:MET:HG3	3:C:810:MET:O	2.21	0.41
1:A:152:ASN:HD22	1:A:152:ASN:HA	1.56	0.41
1:A:45:LYS:HE2	4:A:1022:HOH:O	2.21	0.41
3:C:691:GLU:O	3:C:691:GLU:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:619:PHE:CE2	3:C:746:VAL:HG11	2.56	0.40
3:C:627:PRO:O	3:C:628:LYS:C	2.64	0.40
3:C:735:ARG:NH2	3:C:738:ASN:O	2.54	0.40
3:C:796:ARG:HB2	3:C:800:ARG:HB3	2.04	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	212/215 (99%)	206 (97%)	6 (3%)	0	100	100
2	B	215/217 (99%)	206 (96%)	7 (3%)	2 (1%)	14	10
3	C	203/205 (99%)	183 (90%)	15 (7%)	5 (2%)	4	1
All	All	630/637 (99%)	595 (94%)	28 (4%)	7 (1%)	11	8

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	434	SER
2	B	435	THR
3	C	738	ASN
3	C	684	GLU
3	C	641	LYS
3	C	644	ASP
3	C	685	SER

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	188/189 (100%)	184 (98%)	4 (2%)	47	54
2	B	185/185 (100%)	179 (97%)	6 (3%)	34	38
3	C	189/189 (100%)	185 (98%)	4 (2%)	47	54
All	All	562/563 (100%)	548 (98%)	14 (2%)	42	48

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	LEU
1	A	97	THR
1	A	105	GLU
1	A	152	ASN
2	B	306	GLU
2	B	451	PRO
2	B	453	PRO
2	B	482	LEU
2	B	495	THR
2	B	499	THR
3	C	627	PRO
3	C	672	LEU
3	C	684	GLU
3	C	694	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	152	ASN
1	A	189	HIS
2	B	351	ASN
2	B	365	GLN
3	C	682	ASN
3	C	707	ASN
3	C	718	GLN
3	C	737	ASN
3	C	784	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 oligosaccharides 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	214/215 (99%)	0.29	13 (6%) 27 29	12, 26, 49, 69	0
2	B	217/217 (100%)	0.09	8 (3%) 45 47	15, 24, 42, 76	0
3	C	205/205 (100%)	1.49	62 (30%) 1 1	15, 38, 91, 99	0
All	All	636/637 (99%)	0.61	83 (13%) 7 7	12, 27, 64, 99	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	689	ALA	7.9
3	C	688	SER	7.8
3	C	643	GLY	7.6
3	C	739	THR	7.0
3	C	687	GLY	6.6
3	C	686	THR	6.3
2	B	434	SER	5.8
3	C	809	CYS	5.3
3	C	640	THR	5.2
3	C	740	PHE	5.1
3	C	693	LEU	5.1
3	C	683	VAL	5.1
1	A	214	CYS	5.0
3	C	685	SER	4.9
3	C	607	VAL	4.9
2	B	431	CYS	4.7
3	C	737	ASN	4.6
2	B	433	ARG	4.6
3	C	682	ASN	4.5
1	A	154	LEU	4.4
3	C	642	SER	4.4
3	C	630	VAL	4.4
3	C	738	ASN	4.3

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Mol	Chain	Res	Type	RSRZ
3	C	644	ASP	4.2
3	C	679	PRO	4.1
3	C	645	TRP	4.0
3	C	690	GLY	4.0
3	C	810	MET	3.9
3	C	647	SER	3.9
3	C	731	ARG	3.8
3	C	608	ALA	3.7
3	C	694	TYR	3.6
3	C	606	THR	3.6
3	C	808	GLU	3.5
1	A	212	GLY	3.4
3	C	628	LYS	3.4
2	B	435	THR	3.4
3	C	736	ARG	3.3
3	C	641	LYS	3.2
3	C	684	GLU	3.2
3	C	681	GLY	3.1
3	C	692	PRO	3.0
3	C	670	THR	3.0
3	C	661	ASP	3.0
1	A	23	CYS	3.0
3	C	696	ASN	3.0
3	C	750	ASP	2.9
3	C	691	GLU	2.9
3	C	678	TYR	2.8
3	C	674	ARG	2.8
3	C	610	TYR	2.8
1	A	41	GLU	2.8
1	A	153	ALA	2.8
3	C	649	CYS	2.8
3	C	611	ASN	2.6
3	C	609	ALA	2.6
1	A	188	LYS	2.6
3	C	677	SER	2.6
1	A	205	VAL	2.6
2	B	432	SER	2.6
1	A	123	GLU	2.5
3	C	698	PRO	2.5
3	C	613	THR	2.4
3	C	680	ALA	2.4
3	C	734	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
3	C	807	VAL	2.4
2	B	495	THR	2.4
3	C	650	PHE	2.4
1	A	126	LYS	2.4
3	C	646	LYS	2.3
3	C	669	GLN	2.3
2	B	436	SER	2.2
3	C	638	ILE	2.2
2	B	438	SER	2.2
3	C	735	ARG	2.2
1	A	45	LYS	2.2
1	A	152	ASN	2.2
3	C	615	LYS	2.2
3	C	695	GLU	2.1
3	C	631	ASN	2.1
3	C	676	PHE	2.1
1	A	189	HIS	2.0
3	C	781	LYS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.