



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 11:33 am BST

PDB ID : 4HS6
Title : Hepatitis C envelope glycoprotein E2 fragment 412-423 with humanized and affinity-matured antibody MRCT10.v362
Authors : Eigenbrot, C.; Ultsch, M.
Deposited on : 2012-10-29
Resolution : 1.53 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

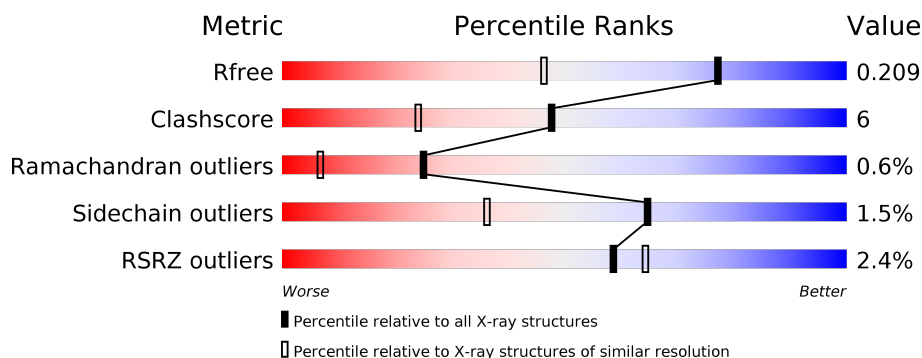
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.53 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	2556 (1.56-1.52)
Clashscore	141614	2634 (1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

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	Y	16	<div> <div>13%</div> <div> <div></div> <div>50%</div> <div>25%</div> <div>25%</div> </div> </div>
1	Z	16	<div> <div>6%</div> <div> <div></div> <div>56%</div> <div>19%</div> <div>25%</div> </div> </div>
2	A	218	<div> <div></div> <div> <div></div> <div>87%</div> <div>11%</div> <div>•</div> </div> </div>
2	L	218	<div> <div>•</div> <div> <div></div> <div>92%</div> <div>7%</div> </div> </div>
3	B	226	<div> <div>2%</div> <div> <div></div> <div>84%</div> <div>9%</div> <div>•</div> <div>5%</div> </div> </div>
3	H	226	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div>5%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7966 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 E2-peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	Z	12	Total	C	N	O	0	1	0
			105	66	21	18			
1	Y	12	Total	C	N	O	0	0	0
			98	61	19	18			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	424	GLY	-	EXPRESSION TAG	UNP Q9YK84
Z	425	SER	-	EXPRESSION TAG	UNP Q9YK84
Z	426	GLY	-	EXPRESSION TAG	UNP Q9YK84
Z	427	LYS	-	EXPRESSION TAG	UNP Q9YK84
Y	424	GLY	-	EXPRESSION TAG	UNP Q9YK84
Y	425	SER	-	EXPRESSION TAG	UNP Q9YK84
Y	426	GLY	-	EXPRESSION TAG	UNP Q9YK84
Y	427	LYS	-	EXPRESSION TAG	UNP Q9YK84

- Molecule 2 is a protein called MRCT10.v362 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	218	Total	C	N	O	S	19	7	0
			1720	1082	286	346	6			
2	L	218	Total	C	N	O	S	19	5	0
			1703	1069	284	344	6			

- Molecule 3 is a protein called MRCT10.v362 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	214	Total	C	N	O	S	0	6	0
			1639	1039	263	329	8			
3	H	215	Total	C	N	O	S	0	4	0
			1642	1036	268	330	8			

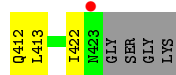
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	Z	15	Total 15	O 15	0	0
4	Y	14	Total 14	O 14	0	0
4	A	225	Total 225	O 225	0	0
4	L	252	Total 252	O 252	0	0
4	B	276	Total 276	O 276	0	0
4	H	277	Total 277	O 277	0	0

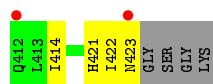
3 Residue-property plots [i](#)

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.

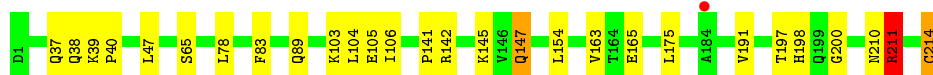
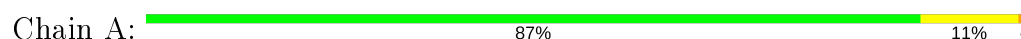
- Molecule 1: E2-peptide



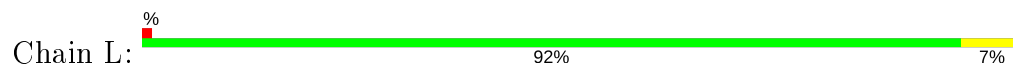
- Molecule 1: E2-peptide



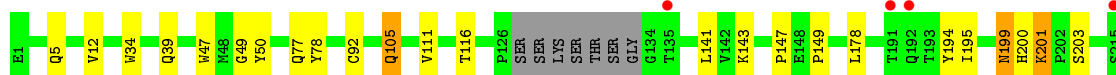
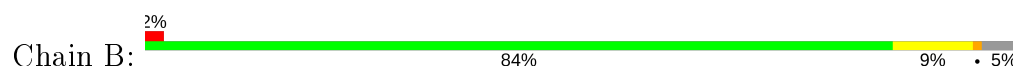
- Molecule 2: MRCT10.v362 Fab light chain

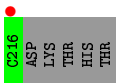


- Molecule 2: MRCT10.v362 Fab light chain

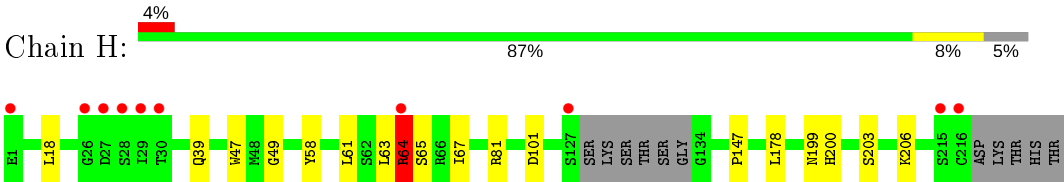


- Molecule 3: MRCT10.v362 Fab heavy chain





● Molecule 3: MRCT10.v362 Fab heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.09 Å 90.82 Å 72.68 Å 90.00° 109.35° 90.00°	Depositor
Resolution (Å)	50.00 – 1.53 37.79 – 1.53	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-1.53) 99.9 (37.79-1.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 1.53 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.175 , 0.200 0.186 , 0.209	Depositor DCC
R_{free} test set	1318 reflections (1.01%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7966	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% 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

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	Y	0.37	0/100	0.46	0/136
1	Z	0.39	0/111	0.51	0/151
2	A	0.91	2/1776 (0.1%)	0.62	0/2410
2	L	0.50	2/1756 (0.1%)	0.65	2/2384 (0.1%)
3	B	0.44	0/1696	0.63	0/2320
3	H	0.41	0/1690	0.62	0/2309
All	All	0.60	4/7129 (0.1%)	0.63	2/9710 (0.0%)

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
2	A	0	1
2	L	0	1
3	H	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	214	CYS	CB-SG	33.04	2.38	1.82
2	L	211	ARG	C-N	11.59	1.53	1.33
2	A	211	ARG	C-N	8.79	1.48	1.33
2	L	214	CYS	CB-SG	5.70	1.92	1.82

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	211	ARG	CA-C-N	-11.24	93.72	116.20
2	L	211	ARG	C-N-CA	-5.36	111.04	122.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	211	ARG	Mainchain
3	H	63	LEU	Peptide
2	L	211	ARG	Mainchain

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	Y	98	0	90	2	0
1	Z	105	0	97	3	0
2	A	1720	0	1681	22	0
2	L	1703	0	1656	24	0
3	B	1639	0	1626	21	0
3	H	1642	0	1617	15	0
4	A	225	0	0	5	0
4	B	276	0	0	3	0
4	H	277	0	0	1	0
4	L	252	0	0	0	0
4	Y	14	0	0	1	0
4	Z	15	0	0	0	0
All	All	7966	0	6767	83	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 6.

All (83) 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)
2:L:24[B]:ARG:HG2	2:L:24[B]:ARG:HH21	1.05	1.14
2:L:24[B]:ARG:CG	2:L:24[B]:ARG:HH21	1.80	0.95
2:A:38:GLN:HE22	3:B:39:GLN:HE22	1.16	0.88
2:L:24[B]:ARG:NH2	2:L:24[B]:ARG:HG2	1.87	0.82
3:B:105:GLN:CD	3:B:105:GLN:H	1.89	0.75
2:L:24[B]:ARG:NH2	2:L:24[B]:ARG:CG	2.45	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:20:THR:HG23	2:L:72[A]:THR:CG2	2.25	0.67
3:H:81[B]:ARG:NH2	4:H:316:HOH:O	2.26	0.67
2:A:83:PHE:CZ	2:A:165:GLU:HG3	2.31	0.65
2:L:198:HIS:CD2	2:L:200:GLY:H	2.14	0.65
2:L:38:GLN:HE22	3:H:39:GLN:HE22	1.45	0.64
2:L:40:PRO:HG2	2:L:165:GLU:HG3	1.80	0.63
2:A:198:HIS:CD2	2:A:200:GLY:H	2.17	0.62
3:B:199:ASN:ND2	4:B:407:HOH:O	2.19	0.62
2:A:39:LYS:NZ	4:A:383:HOH:O	2.09	0.59
3:B:194:TYR:C	3:B:195:ILE:HD12	2.22	0.59
2:A:105:GLU:OE2	4:A:463:HOH:O	2.16	0.59
2:L:40:PRO:HG2	2:L:165:GLU:CD	2.23	0.59
1:Z:413:LEU:HD23	1:Z:422:ILE:HD13	1.85	0.59
1:Z:412:GLN:OE1	1:Z:412:GLN:N	2.36	0.59
3:B:147:PRO:O	3:B:200:HIS:HE1	1.86	0.58
2:A:83:PHE:HZ	2:A:165:GLU:HG3	1.69	0.57
3:H:147:PRO:O	3:H:200:HIS:HE1	1.88	0.57
3:B:200:HIS:HD2	3:B:203:SER:OG	1.89	0.56
3:B:116[A]:THR:CG2	3:B:203:SER:HB3	2.36	0.55
2:A:78[A]:LEU:HD11	2:A:104:LEU:HD21	1.88	0.55
3:B:195:ILE:N	3:B:195:ILE:HD12	2.21	0.55
3:B:5:GLN:HA	3:B:105:GLN:OE1	2.06	0.55
2:A:191:VAL:HG22	2:A:210:ASN:ND2	2.22	0.55
3:B:12[A]:VAL:CG1	3:B:111:VAL:HG22	2.38	0.54
3:H:61:LEU:HD13	3:H:64:ARG:NE	2.22	0.54
2:L:40:PRO:HG2	2:L:165:GLU:CG	2.38	0.53
3:B:201:LYS:H	3:B:201:LYS:NZ	2.07	0.52
3:H:200:HIS:HD2	3:H:203:SER:OG	1.90	0.52
3:B:12[A]:VAL:HG13	3:B:111:VAL:HG22	1.90	0.52
2:L:38:GLN:HE22	3:H:39:GLN:NE2	2.06	0.52
2:L:110:VAL:HG21	2:L:199:GLN:NE2	2.26	0.51
2:A:103:LYS:CG	4:A:519:HOH:O	2.58	0.51
2:A:147:GLN:HE22	2:A:154:LEU:HD21	1.76	0.50
2:A:40:PRO:HG3	2:A:165:GLU:HG2	1.94	0.49
1:Z:413:LEU:CD2	1:Z:422:ILE:HD13	2.42	0.49
2:L:24[B]:ARG:HB3	2:L:24[B]:ARG:NH2	2.28	0.49
3:B:47:TRP:CZ2	3:B:49:GLY:HA2	2.48	0.48
3:H:47:TRP:CZ2	3:H:49:GLY:HA2	2.48	0.48
2:A:141:PRO:O	2:A:198:HIS:HE1	1.96	0.48
3:B:105:GLN:N	3:B:105:GLN:CD	2.65	0.48
3:B:116[A]:THR:HG22	3:B:203:SER:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:103:LYS:HG2	4:A:519:HOH:O	2.15	0.47
2:L:24[B]:ARG:HB3	2:L:24[B]:ARG:CZ	2.46	0.46
2:L:198:HIS:HD2	2:L:200:GLY:H	1.63	0.46
2:L:24[B]:ARG:CB	2:L:24[B]:ARG:NH2	2.79	0.46
2:L:20:THR:HG23	2:L:72[A]:THR:HG23	1.95	0.45
3:B:34:TRP:HB3	3:B:78:TYR:CZ	2.52	0.45
2:A:103:LYS:HG3	4:A:519:HOH:O	2.17	0.45
2:A:78[A]:LEU:HD21	2:A:104:LEU:HD21	1.97	0.45
3:B:78:TYR:OH	3:B:92:CYS:HB2	2.17	0.44
2:A:37:GLN:HB2	2:A:47:LEU:HD11	1.99	0.44
2:A:198:HIS:HD2	2:A:200:GLY:H	1.65	0.43
2:A:83:PHE:CZ	2:A:165:GLU:CG	3.01	0.43
2:L:20:THR:CG2	2:L:72[A]:THR:CG2	2.95	0.43
3:H:64:ARG:H	3:H:67:ILE:HG22	1.84	0.42
2:L:145:LYS:HB3	2:L:197:THR:HB	2.01	0.42
1:Y:422:ILE:O	1:Y:423:ASN:CB	2.67	0.42
4:Y:513:HOH:O	3:H:61:LEU:HD21	2.19	0.42
2:L:22:THR:HG22	2:L:72[B]:THR:HG22	2.02	0.42
3:B:77:GLN:NE2	4:B:335:HOH:O	2.51	0.42
3:H:199:ASN:HD22	3:H:206:LYS:HG2	1.85	0.42
2:L:141:PRO:O	2:L:198:HIS:HE1	2.02	0.41
3:H:18:LEU:HD23	3:H:18:LEU:C	2.41	0.41
2:L:78:LEU:HD11	2:L:104:LEU:HD21	2.03	0.41
2:L:38:GLN:NE2	3:H:39:GLN:HE22	2.14	0.41
2:L:20:THR:CG2	2:L:72[A]:THR:HG23	2.50	0.41
2:A:163:VAL:HG22	2:A:175:LEU:HD12	2.02	0.41
3:H:61:LEU:HD13	3:H:64:ARG:HE	1.85	0.41
3:B:141:LEU:HG	3:B:143:LYS:HG3	2.03	0.41
3:B:178:LEU:HD12	3:B:178:LEU:C	2.42	0.41
3:B:12[B]:VAL:HG22	4:B:454:HOH:O	2.21	0.40
3:H:178:LEU:HD12	3:H:178:LEU:C	2.41	0.40
1:Y:414:ILE:HG13	1:Y:421:HIS:CE1	2.57	0.40
3:H:47:TRP:CH2	3:H:58:TYR:CE2	3.10	0.40
2:A:147:GLN:HE22	2:A:154:LEU:CD2	2.34	0.40
2:A:145:LYS:HB3	2:A:197:THR:HB	2.03	0.40
2:A:78[B]:LEU:HD13	2:A:106:ILE:HD12	2.03	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	Y	10/16 (62%)	10 (100%)	0	0	100	100
1	Z	11/16 (69%)	11 (100%)	0	0	100	100
2	A	223/218 (102%)	217 (97%)	5 (2%)	1 (0%)	34	13
2	L	221/218 (101%)	216 (98%)	4 (2%)	1 (0%)	29	9
3	B	215/226 (95%)	208 (97%)	6 (3%)	1 (0%)	29	9
3	H	215/226 (95%)	209 (97%)	4 (2%)	2 (1%)	17	3
All	All	895/920 (97%)	871 (97%)	19 (2%)	5 (1%)	25	7

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	211	ARG
3	H	64	ARG
2	L	211	ARG
3	B	149	PRO
3	H	65	SER

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	Y	11/13 (85%)	11 (100%)	0	100	100
1	Z	12/13 (92%)	12 (100%)	0	100	100
2	A	199/192 (104%)	193 (97%)	6 (3%)	41	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	L	197/192 (103%)	196 (100%)	1 (0%)	88	77
3	B	192/197 (98%)	188 (98%)	4 (2%)	53	22
3	H	191/197 (97%)	189 (99%)	2 (1%)	76	55
All	All	802/804 (100%)	789 (98%)	13 (2%)	65	33

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	65	SER
2	A	89	GLN
2	A	142[A]	ARG
2	A	142[B]	ARG
2	A	147	GLN
2	A	214	CYS
2	L	214	CYS
3	B	50	TYR
3	B	105	GLN
3	B	199	ASN
3	B	201	LYS
3	H	64	ARG
3	H	101	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	Z	412	GLN
2	A	89	GLN
2	A	147	GLN
2	A	198	HIS
2	A	210	ASN
2	L	53	ASN
2	L	198	HIS
2	L	199	GLN
2	L	210	ASN
3	B	39	GLN
3	B	200	HIS
3	H	5	GLN
3	H	39	GLN
3	H	200	HIS

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	Y	12/16 (75%)	0.50	2 (16%) 1 1	17, 21, 45, 59	0
1	Z	12/16 (75%)	0.43	1 (8%) 11 12	15, 23, 37, 62	0
2	A	216/218 (99%)	-0.13	1 (0%) 91 92	12, 22, 42, 82	1 (0%)
2	L	216/218 (99%)	-0.12	2 (0%) 84 86	14, 23, 40, 82	1 (0%)
3	B	214/226 (94%)	-0.13	5 (2%) 60 66	12, 19, 39, 91	1 (0%)
3	H	215/226 (95%)	-0.04	10 (4%) 31 36	12, 18, 38, 76	2 (0%)
All	All	885/920 (96%)	-0.09	21 (2%) 59 64	12, 21, 40, 91	5 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	215	SER	8.4
3	H	216	CYS	6.7
1	Y	423	ASN	4.5
1	Z	423	ASN	4.2
3	H	215	SER	4.2
3	B	216	CYS	3.9
3	H	64	ARG	3.3
3	B	192	GLN	3.0
3	H	1	GLU	3.0
3	H	127	SER	3.0
3	H	28	SER	2.7
2	L	150	VAL	2.6
3	H	26	GLY	2.5
3	H	29	ILE	2.5
3	B	191	THR	2.4
2	A	184	ALA	2.4
3	H	27	ASP	2.3
1	Y	412	GLN	2.3
2	L	191	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
3	B	135	THR	2.2
3	H	30	THR	2.2

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.