



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:25 PM UTC

PDB ID : 5T5F / pdb_00005t5f
Title : Neisseria meningitidis factor H binding protein in complex with monoclonal antibody JAR5
Authors : Malito, E.
Deposited on : 2016-08-30
Resolution : 2.98 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

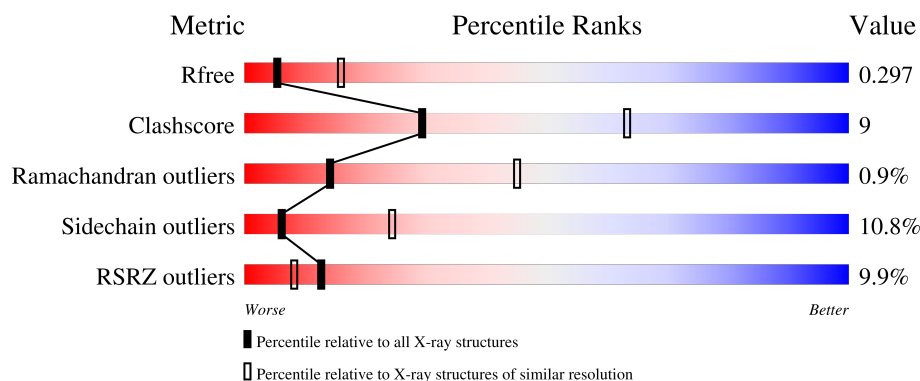
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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}	180053	3580 (3.00-2.96)
Clashscore	190562	3904 (3.00-2.96)
Ramachandran outliers	187476	3761 (3.00-2.96)
Sidechain outliers	187428	3764 (3.00-2.96)
RSRZ outliers	180081	3579 (3.00-2.96)

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	253	
2	H	212	
3	L	216	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5057 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 Factor H binding protein variant B24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1714	1064	309	340	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	256	LEU	-	expression tag	UNP Q6VRZ6

- Molecule 2 is a protein called Monoclonal antibody Jar5 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	212	Total	C	N	O	S	0	0	0
			1633	1046	265	314	8			

- Molecule 3 is a protein called Monoclonal antibody Jar5 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	216	Total	C	N	O	S	0	0	0
			1676	1049	285	334	8			

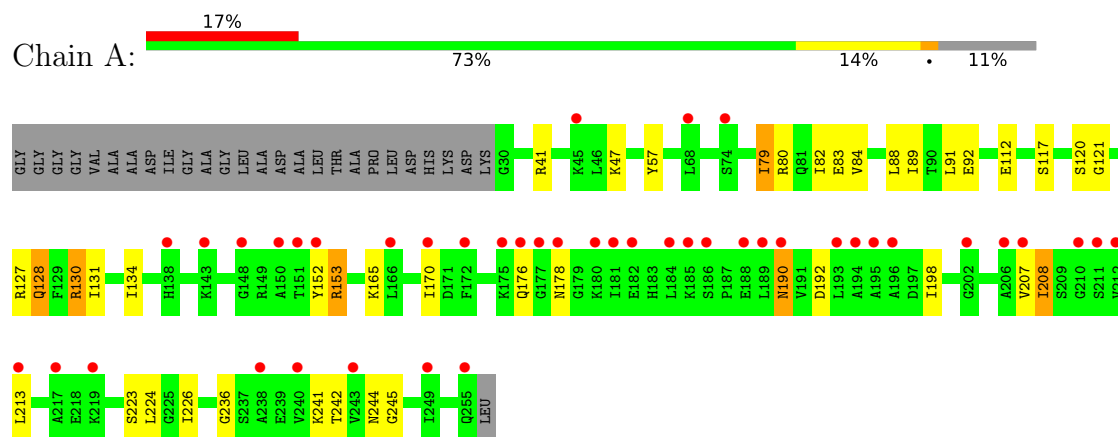
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	11	Total	O	0	0
			11	11		
4	H	12	Total	O	0	0
			12	12		
4	L	11	Total	O	0	0
			11	11		

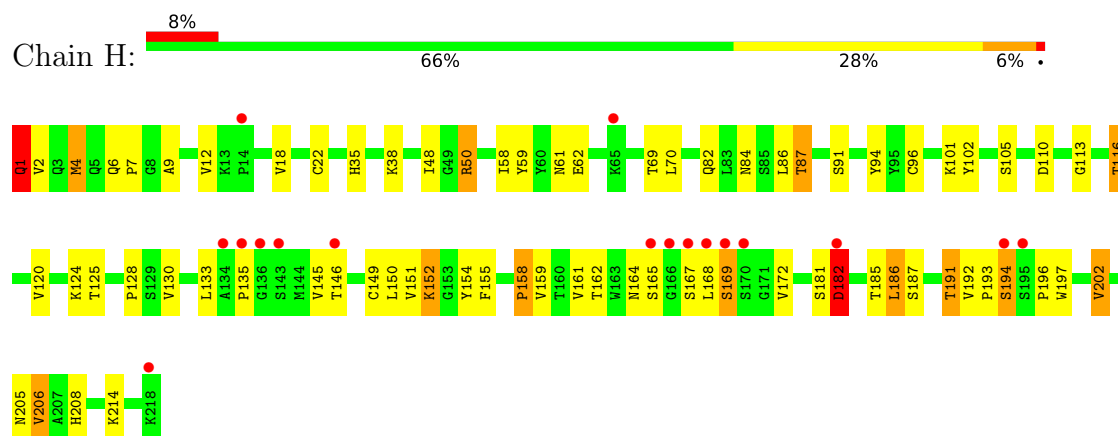
3 Residue-property plots [i](#)

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.

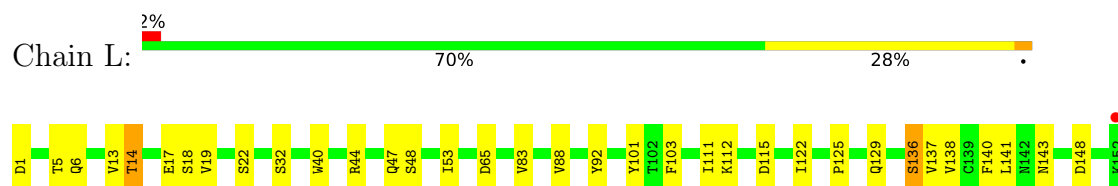
- Molecule 1: Factor H binding protein variant B24

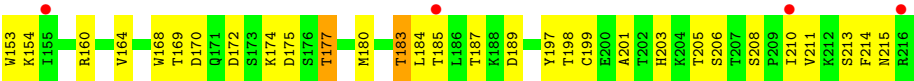


- Molecule 2: Monoclonal antibody Jar5 heavy chain



- Molecule 3: Monoclonal antibody Jar5 light chain





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	65.37Å 146.49Å 218.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.70 – 2.98 59.70 – 2.98	Depositor EDS
% Data completeness (in resolution range)	99.9 (59.70-2.98) 99.9 (59.70-2.98)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.20	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.96Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.223 , 0.273 0.243 , 0.297	Depositor DCC
R_{free} test set	1048 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	64.9	Xtriage
Anisotropy	0.286	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 70.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	5057	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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	A	0.73	1/1737 (0.1%)	1.09	6/2328 (0.3%)
2	H	0.99	1/1681 (0.1%)	1.29	7/2298 (0.3%)
3	L	0.89	0/1716	1.31	8/2330 (0.3%)
All	All	0.88	2/5134 (0.0%)	1.23	21/6956 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	120	SER	CA-C	-5.13	1.46	1.52
2	H	1	GLN	C-N	5.08	1.39	1.33

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190	ASN	CA-CB-CG	8.54	121.14	112.60
2	H	182	ASP	CA-CB-CG	7.32	119.92	112.60
1	A	117	SER	CA-C-N	7.10	130.02	120.65
1	A	117	SER	C-N-CA	7.10	130.02	120.65
2	H	110	ASP	CA-CB-CG	6.89	119.49	112.60
1	A	57	TYR	CA-C-N	6.52	128.27	122.47
1	A	57	TYR	C-N-CA	6.52	128.27	122.47
3	L	103	PHE	CA-CB-CG	5.93	119.73	113.80
2	H	202	VAL	N-CA-CB	5.56	116.78	110.72
3	L	65	ASP	CA-C-N	5.51	129.08	120.82
3	L	65	ASP	C-N-CA	5.51	129.08	120.82
3	L	206	SER	CA-C-N	5.45	127.52	120.44
3	L	206	SER	C-N-CA	5.45	127.52	120.44
3	L	1	ASP	CA-CB-CG	5.44	118.04	112.60
2	H	169	SER	CA-C-N	5.39	130.00	121.44
2	H	169	SER	C-N-CA	5.39	130.00	121.44
3	L	140	PHE	CA-CB-CG	5.35	119.15	113.80
2	H	1	GLN	CA-C-N	5.34	128.25	120.98
2	H	1	GLN	C-N-CA	5.34	128.25	120.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	101	TYR	N-CA-C	-5.24	102.11	109.96
1	A	79	ILE	N-CA-CB	5.16	119.63	111.99

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	1714	0	1704	22	0
2	H	1633	0	1599	40	0
3	L	1676	0	1617	25	0
4	A	11	0	0	0	0
4	H	12	0	0	0	0
4	L	11	0	0	0	0
All	All	5057	0	4920	85	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 (85) 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:152:TYR:HE1	1:A:170:ILE:HG22	1.26	0.99
2:H:159:VAL:HG22	2:H:186:LEU:HD21	1.50	0.93
2:H:146:THR:HG22	2:H:191:THR:HB	1.59	0.84
1:A:152:TYR:HE1	1:A:170:ILE:CG2	1.91	0.82
1:A:152:TYR:CE1	1:A:170:ILE:HG22	2.14	0.81
2:H:159:VAL:CG2	2:H:186:LEU:HD21	2.14	0.76
3:L:172:ASP:OD1	3:L:174:LYS:HG2	1.90	0.71
2:H:193:PRO:HD2	2:H:196:PRO:HG2	1.76	0.67
1:A:89:ILE:HD11	2:H:105:SER:HB3	1.75	0.67
2:H:151:VAL:HG11	2:H:159:VAL:HG21	1.78	0.66
1:A:242:THR:HG22	1:A:245:GLY:O	1.97	0.65
1:A:152:TYR:CE1	1:A:170:ILE:CG2	2.77	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:4:MET:HB3	2:H:113:GLY:HA2	1.80	0.63
2:H:7:PRO:O	2:H:116:THR:HB	2.01	0.61
3:L:129:GLN:HE22	3:L:136:SER:HB2	1.65	0.60
1:A:153:ARG:HH12	1:A:165:LYS:HB3	1.65	0.60
2:H:4:MET:HG3	2:H:22:CYS:SG	2.42	0.60
1:A:80:ARG:HE	1:A:92:GLU:HG2	1.66	0.60
2:H:38:LYS:HB2	2:H:48:ILE:HD11	1.84	0.60
2:H:159:VAL:HG22	2:H:186:LEU:CD2	2.28	0.59
1:A:170:ILE:HD13	1:A:198:ILE:HD11	1.84	0.59
1:A:242:THR:HG23	1:A:244:ASN:H	1.68	0.59
3:L:44:ARG:HB2	3:L:47:GLN:NE2	2.19	0.57
1:A:47:LYS:HB3	1:A:79:ILE:HG13	1.88	0.55
2:H:159:VAL:HG12	2:H:208:HIS:HD2	1.71	0.55
2:H:9:ALA:HB2	2:H:158:PRO:HD3	1.88	0.55
3:L:40:TRP:HB2	3:L:53:ILE:HB	1.89	0.54
2:H:205:ASN:HD21	2:H:214:LYS:HG2	1.72	0.54
1:A:82:ILE:HG12	1:A:91:LEU:HD21	1.88	0.54
3:L:6:GLN:HE22	3:L:92:TYR:HA	1.73	0.54
2:H:6:GLN:HB3	2:H:116:THR:HG22	1.90	0.53
2:H:133:LEU:HD13	3:L:138:VAL:HG11	1.90	0.53
2:H:128:PRO:HB2	2:H:151:VAL:HG13	1.91	0.53
1:A:128:GLN:HE21	1:A:130:ARG:HG2	1.74	0.51
3:L:13:VAL:HG21	3:L:83:VAL:HG21	1.93	0.51
3:L:154:LYS:HB2	3:L:198:THR:HG23	1.93	0.50
3:L:169:THR:HG22	3:L:170:ASP:O	2.12	0.50
1:A:112:GLU:OE2	1:A:127:ARG:HD2	2.12	0.50
2:H:145:VAL:HG23	2:H:194:SER:HA	1.94	0.49
3:L:198:THR:HB	3:L:213:SER:CB	2.42	0.49
3:L:198:THR:HB	3:L:213:SER:HB2	1.93	0.49
3:L:44:ARG:HB2	3:L:47:GLN:HE21	1.77	0.49
2:H:4:MET:HB3	2:H:113:GLY:CA	2.43	0.49
2:H:133:LEU:HD11	2:H:150:LEU:HB2	1.95	0.49
2:H:161:VAL:HG22	2:H:206:VAL:HB	1.94	0.49
1:A:134:ILE:HD13	1:A:236:GLY:HA2	1.94	0.48
2:H:87:THR:O	2:H:120:VAL:HG11	2.14	0.48
2:H:1:GLN:HG3	2:H:2:VAL:N	2.29	0.48
1:A:170:ILE:HD12	1:A:176:GLN:O	2.13	0.48
2:H:152:LYS:HA	2:H:185:THR:HG23	1.96	0.48
3:L:154:LYS:HB2	3:L:198:THR:CG2	2.45	0.46
2:H:151:VAL:HB	2:H:186:LEU:HG	1.96	0.46
1:A:47:LYS:HB3	1:A:79:ILE:CG1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:14:THR:O	3:L:17:GLU:HB2	2.16	0.45
3:L:175:ASP:CG	3:L:177:THR:HB	2.41	0.45
3:L:122:ILE:HD13	3:L:199:CYS:HB2	1.99	0.45
3:L:143:ASN:HA	3:L:177:THR:CG2	2.47	0.45
3:L:125:PRO:HD3	3:L:137:VAL:HG22	1.98	0.44
1:A:198:ILE:HD13	1:A:208:ILE:HB	2.00	0.44
2:H:38:LYS:HG3	2:H:94:TYR:CE2	2.53	0.44
1:A:192:ASP:HB2	1:A:213:LEU:HB2	1.99	0.44
3:L:160:ARG:HG2	3:L:184:LEU:HD21	1.99	0.44
2:H:159:VAL:HG12	2:H:208:HIS:CD2	2.50	0.44
2:H:101:LYS:HE2	2:H:102:TYR:CZ	2.52	0.43
3:L:201:ALA:HB3	3:L:210:ILE:HB	2.00	0.43
1:A:208:ILE:HG23	1:A:224:LEU:HB2	2.01	0.42
3:L:203:HIS:CD2	3:L:205:THR:HG22	2.54	0.42
1:A:47:LYS:HD2	1:A:79:ILE:HG12	2.01	0.42
3:L:153:TRP:NE1	3:L:164:VAL:HG21	2.34	0.42
3:L:138:VAL:HG23	3:L:183:THR:HG23	2.01	0.42
2:H:164:ASN:HB3	2:H:167:SER:HB2	2.02	0.42
2:H:197:TRP:HZ3	2:H:202:VAL:H	1.68	0.41
2:H:154:TYR:OH	2:H:186:LEU:HD23	2.20	0.41
2:H:35:HIS:CE1	2:H:50:ARG:HB2	2.55	0.41
2:H:61:ASN:O	2:H:62:GLU:C	2.64	0.41
2:H:130:VAL:HA	2:H:150:LEU:O	2.20	0.41
2:H:58:ILE:HG23	2:H:70:LEU:HD12	2.03	0.41
2:H:35:HIS:O	2:H:96:CYS:HA	2.20	0.41
2:H:50:ARG:HD2	2:H:59:TYR:HB2	2.02	0.41
2:H:125:THR:HA	2:H:155:PHE:O	2.21	0.41
3:L:197:TYR:HB2	3:L:214:PHE:CE1	2.56	0.41
1:A:198:ILE:HD12	1:A:226:ILE:HD11	2.01	0.40
2:H:18:VAL:O	2:H:82:GLN:HA	2.21	0.40
3:L:13:VAL:O	3:L:111:ILE:HA	2.22	0.40
2:H:86:LEU:HB3	2:H:120:VAL:HG21	2.01	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	224/253 (88%)	216 (96%)	7 (3%)	1 (0%)	30	62
2	H	208/212 (98%)	188 (90%)	16 (8%)	4 (2%)	6	27
3	L	214/216 (99%)	206 (96%)	7 (3%)	1 (0%)	24	58
All	All	646/681 (95%)	610 (94%)	30 (5%)	6 (1%)	14	45

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	GLY
2	H	181	SER
3	L	115	ASP
2	H	135	PRO
2	H	182	ASP
2	H	158	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	177/192 (92%)	163 (92%)	14 (8%)	11	37
2	H	184/184 (100%)	160 (87%)	24 (13%)	4	17
3	L	192/192 (100%)	170 (88%)	22 (12%)	5	22
All	All	553/568 (97%)	493 (89%)	60 (11%)	6	24

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ARG
1	A	83	GLU
1	A	84	VAL

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Mol	Chain	Res	Type
1	A	88	LEU
1	A	128	GLN
1	A	130	ARG
1	A	131	ILE
1	A	153	ARG
1	A	178	ASN
1	A	190	ASN
1	A	207	VAL
1	A	208	ILE
1	A	223	SER
1	A	241	LYS
2	H	1	GLN
2	H	4	MET
2	H	12	VAL
2	H	50	ARG
2	H	69	THR
2	H	84	ASN
2	H	87	THR
2	H	91	SER
2	H	116	THR
2	H	124	LYS
2	H	149	CYS
2	H	152	LYS
2	H	162	THR
2	H	165	SER
2	H	168	LEU
2	H	169	SER
2	H	172	VAL
2	H	182	ASP
2	H	186	LEU
2	H	187	SER
2	H	191	THR
2	H	192	VAL
2	H	194	SER
2	H	206	VAL
3	L	5	THR
3	L	14	THR
3	L	18	SER
3	L	19	VAL
3	L	22	SER
3	L	32	SER
3	L	48	SER

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Mol	Chain	Res	Type
3	L	88	VAL
3	L	112	LYS
3	L	136	SER
3	L	141	LEU
3	L	148	ASP
3	L	168	TRP
3	L	177	THR
3	L	180	MET
3	L	183	THR
3	L	185	THR
3	L	187	THR
3	L	189	ASP
3	L	208	SER
3	L	211	VAL
3	L	215	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	GLN
1	A	183	HIS
1	A	255	GLN
2	H	1	GLN
2	H	84	ASN
2	H	164	ASN
3	L	6	GLN
3	L	47	GLN
3	L	50	GLN
3	L	129	GLN
3	L	161	GLN
3	L	203	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	136:GLY	C	143:SER	N	14.69

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	226/253 (89%)	1.27	43 (19%) 3 2	45, 81, 117, 128	0
2	H	212/212 (100%)	0.48	17 (8%) 18 11	31, 55, 99, 116	0
3	L	216/216 (100%)	0.41	5 (2%) 61 42	33, 60, 96, 105	0
All	All	654/681 (96%)	0.73	65 (9%) 13 8	31, 65, 110, 128	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	168	LEU	6.0
1	A	211	SER	4.6
2	H	167	SER	4.3
2	H	218	LYS	4.3
1	A	184	LEU	4.0
1	A	189	LEU	3.9
2	H	165	SER	3.7
1	A	150	ALA	3.7
1	A	255	GLN	3.6
1	A	175	LYS	3.5
1	A	151	THR	3.5
2	H	14	PRO	3.3
2	H	136	GLY	3.3
1	A	206	ALA	3.3
1	A	177	GLY	3.3
2	H	143	SER	3.2
1	A	148	GLY	3.2
1	A	207	VAL	3.2
1	A	170	ILE	3.0
3	L	155	ILE	2.9
1	A	176	GLN	2.8
2	H	146	THR	2.8
1	A	178	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	190	ASN	2.8
2	H	166	GLY	2.7
1	A	217	ALA	2.7
1	A	195	ALA	2.7
1	A	180	LYS	2.7
1	A	212	VAL	2.7
1	A	249	ILE	2.6
1	A	152	TYR	2.6
1	A	186	SER	2.6
2	H	170	SER	2.6
1	A	213	LEU	2.6
1	A	238	ALA	2.6
1	A	68	LEU	2.5
1	A	243	VAL	2.5
2	H	134	ALA	2.4
1	A	202	GLY	2.4
1	A	188	GLU	2.4
1	A	185	LYS	2.3
2	H	194	SER	2.3
1	A	181	ILE	2.3
1	A	219	LYS	2.3
1	A	196	ALA	2.2
2	H	65	LYS	2.2
2	H	195	SER	2.2
2	H	135	PRO	2.2
1	A	193	LEU	2.2
1	A	172	PHE	2.2
2	H	182	ASP	2.1
3	L	185	THR	2.1
1	A	166	LEU	2.1
1	A	194	ALA	2.1
3	L	152	LYS	2.1
3	L	216	ARG	2.1
3	L	210	ILE	2.1
1	A	74	SER	2.1
1	A	45	LYS	2.0
1	A	143	LYS	2.0
2	H	169	SER	2.0
1	A	240	VAL	2.0
1	A	210	GLY	2.0
1	A	138	HIS	2.0
1	A	182	GLU	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.