Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 12:24 pm BST

PDB ID	:	5XRQ
Title	:	Crystal structure of human monoclonal antibody H3v-47
Authors	:	Zhang, H.; Willson, I.A.
Deposited on	:	2017-06-09
Resolution	:	2.60 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:

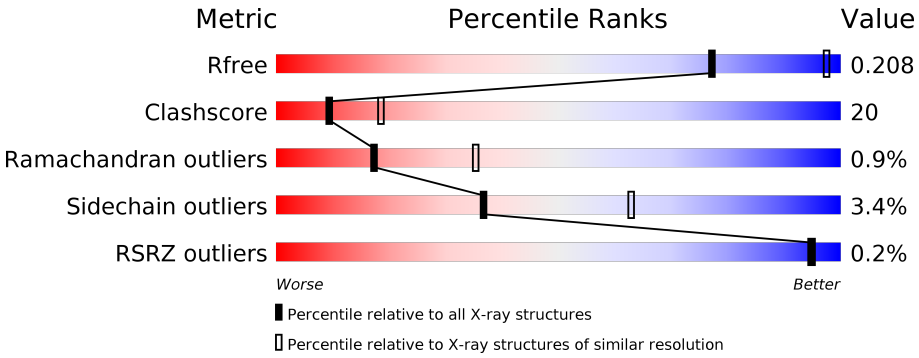
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 <=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	236	56% 32% 5% 7%
1	H	236	58% 32% • 7%
2	B	214	66% 30% ••
2	L	214	74% 23% ••

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6639 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 Fab H3v-47 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	220	Total	C	N	O	S	0	0	0
			1647	1039	275	326	7			
1	A	219	Total	C	N	O	S	0	0	0
			1638	1034	273	324	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	217	HIS	-	expression tag	UNP Q6N089
H	218	HIS	-	expression tag	UNP Q6N089
H	219	HIS	-	expression tag	UNP Q6N089
H	220	HIS	-	expression tag	UNP Q6N089
H	221	HIS	-	expression tag	UNP Q6N089
H	222	HIS	-	expression tag	UNP Q6N089
A	217	HIS	-	expression tag	UNP Q6N089
A	218	HIS	-	expression tag	UNP Q6N089
A	219	HIS	-	expression tag	UNP Q6N089
A	220	HIS	-	expression tag	UNP Q6N089
A	221	HIS	-	expression tag	UNP Q6N089
A	222	HIS	-	expression tag	UNP Q6N089

- Molecule 2 is a protein called Fab H3v-47 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	213	Total	C	N	O	S	0	1	0
			1629	1009	282	333	5			
2	B	212	Total	C	N	O	S	0	1	0
			1619	1003	280	331	5			

- Molecule 3 is water.

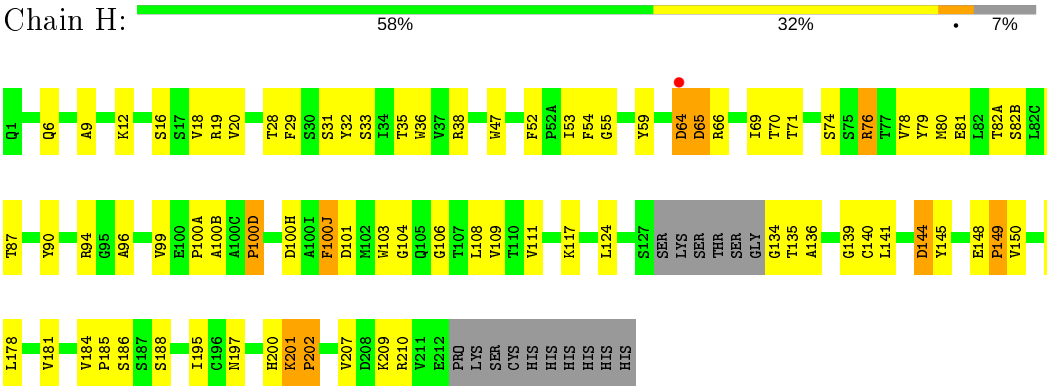
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	17	Total O 17 17	0	0
3	L	30	Total O 30 30	0	0
3	A	19	Total O 19 19	0	0
3	B	40	Total O 40 40	0	0

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.

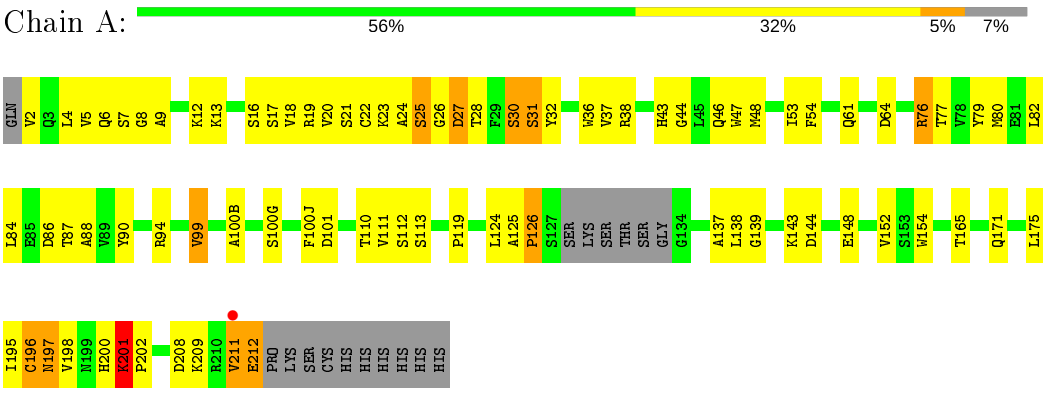
- Molecule 1: Fab H3v-47 heavy chain

Chain H:



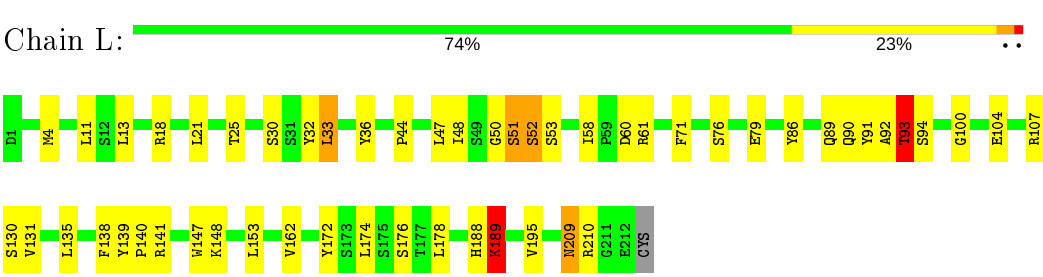
- Molecule 1: Fab H3v-47 heavy chain

Chain A:



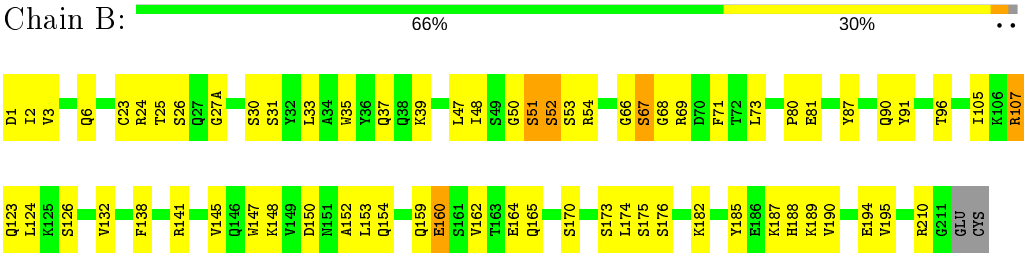
- Molecule 2: Fab H3v-47 light chain

Chain L:



• Molecule 2: Fab H3v-47 light chain

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	135.13Å 135.13Å 78.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.92 – 2.60 46.92 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.5 (46.92-2.60) 98.3 (46.92-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	1.60 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.180 , 0.214 0.183 , 0.208	Depositor DCC
R_{free} test set	2456 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	50.9	Xtriage
Anisotropy	0.631	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 39.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l 0.468 for h,-h-k,-l 0.027 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6639	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% 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	0.51	1/1677 (0.1%)	0.77	2/2287 (0.1%)
1	H	0.53	1/1686 (0.1%)	0.74	3/2299 (0.1%)
2	B	0.46	0/1656	0.74	4/2247 (0.2%)
2	L	0.47	0/1668	0.78	5/2263 (0.2%)
All	All	0.49	2/6687 (0.0%)	0.76	14/9096 (0.2%)

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	2
1	H	0	1
2	L	0	1
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	202	PRO	N-CD	-9.35	1.34	1.47
1	A	76	ARG	CZ-NH1	-6.13	1.25	1.33

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	211	VAL	N-CA-C	-9.82	84.47	111.00
2	L	93	THR	N-CA-C	8.96	135.21	111.00
1	A	212	GLU	N-CA-C	8.89	134.99	111.00
2	B	52	SER	N-CA-CB	-8.84	97.25	110.50
1	H	65	ASP	N-CA-CB	-8.49	95.32	110.60
2	L	52	SER	N-CA-CB	-7.93	98.61	110.50
1	H	145	TYR	N-CA-CB	-6.76	98.42	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	144	ASP	N-CA-C	6.10	127.46	111.00
2	L	209	ASN	CB-CA-C	-6.02	98.35	110.40
2	B	52	SER	CB-CA-C	5.97	121.44	110.10
2	B	51	SER	CB-CA-C	5.88	121.26	110.10
2	L	189	LYS	CB-CA-C	-5.46	99.47	110.40
2	L	33	LEU	CA-CB-CG	-5.13	103.49	115.30
2	B	107	ARG	CG-CD-NE	-5.04	101.21	111.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	100(J)	PHE	Peptide
1	A	201	LYS	Mainchain
1	H	100(J)	PHE	Peptide
2	L	93	THR	Peptide

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	1638	0	1598	90	0
1	H	1647	0	1609	72	0
2	B	1619	0	1575	55	1
2	L	1629	0	1586	43	1
3	A	19	0	0	3	0
3	B	40	0	0	4	1
3	H	17	0	0	2	1
3	L	30	0	0	2	0
All	All	6639	0	6368	254	2

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 20.

All (254) 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:8:GLY:CA	1:A:201:LYS:NZ	1.80	1.44
1:A:8:GLY:HA3	1:A:201:LYS:NZ	1.33	1.42
1:H:201:LYS:HG3	1:H:202:PRO:HD3	1.09	1.07
1:A:8:GLY:HA2	1:A:201:LYS:NZ	1.69	1.04
1:A:100(G):SER:OG	2:B:91:TYR:O	1.79	0.99
1:A:8:GLY:CA	1:A:201:LYS:HZ2	1.57	0.97
1:H:207:VAL:CG1	1:H:209:LYS:HE2	2.01	0.90
1:H:135:THR:HA	1:H:185:PRO:HA	1.50	0.90
1:A:8:GLY:HA3	1:A:201:LYS:HZ2	0.94	0.89
1:A:201:LYS:HG3	1:A:202:PRO:HD3	1.55	0.88
2:B:150:ASP:OD2	2:B:188:HIS:ND1	2.05	0.88
1:A:8:GLY:CA	1:A:201:LYS:HZ1	1.78	0.87
1:A:8:GLY:HA3	1:A:201:LYS:HZ3	1.31	0.86
2:B:123:GLN:O	2:B:126:SER:OG	1.95	0.85
1:H:65:ASP:N	1:H:65:ASP:OD1	2.11	0.84
2:B:150:ASP:HA	2:B:190:VAL:HG23	1.59	0.83
2:B:148:LYS:NZ	2:B:194:GLU:OE1	2.12	0.83
2:B:189:LYS:NZ	2:B:210:ARG:O	2.12	0.82
1:A:126:PRO:HD3	1:A:211:VAL:CG1	2.10	0.82
1:A:26:GLY:O	1:A:27:ASP:HB2	1.79	0.82
1:H:9:ALA:HB3	1:H:201:LYS:HZ2	1.43	0.81
1:H:117:LYS:HD3	1:H:144:ASP:O	1.82	0.80
1:A:9:ALA:N	1:A:201:LYS:NZ	2.30	0.79
1:A:9:ALA:H	1:A:201:LYS:NZ	1.81	0.79
1:H:201:LYS:HG3	1:H:202:PRO:CD	2.04	0.79
1:A:8:GLY:CA	1:A:201:LYS:HZ3	1.82	0.77
1:A:201:LYS:CG	1:A:202:PRO:HD3	2.14	0.77
1:H:201:LYS:CG	1:H:202:PRO:HD3	2.03	0.77
1:H:207:VAL:HG13	1:H:209:LYS:HE2	1.66	0.76
2:L:93:THR:OG1	2:L:94:SER:N	2.18	0.76
2:L:209:ASN:O	2:L:210:ARG:HB2	1.86	0.75
1:H:195:ILE:HG12	1:H:210:ARG:HG2	1.68	0.75
1:A:201:LYS:HG3	1:A:202:PRO:CD	2.17	0.74
1:A:8:GLY:HA2	1:A:201:LYS:HZ1	1.34	0.73
1:A:2:VAL:HG13	1:A:25:SER:HB3	1.69	0.73
1:H:207:VAL:HG12	1:H:209:LYS:HG2	1.71	0.73
1:H:66:ARG:NH2	1:H:86:ASP:OD2	2.19	0.73
1:A:8:GLY:C	1:A:201:LYS:NZ	2.42	0.72
2:B:96:THR:OG1	3:B:301:HOH:O	2.07	0.72
1:A:138:LEU:HD13	1:A:211:VAL:HG21	1.71	0.71
1:A:82(B):SER:O	3:A:301:HOH:O	2.08	0.71
1:H:207:VAL:HG11	1:H:209:LYS:HE2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:THR:HG1	1:A:180:SER:HG	1.30	0.71
1:A:8:GLY:C	1:A:201:LYS:HZ2	1.94	0.70
2:B:80:PRO:O	3:B:302:HOH:O	2.09	0.70
1:A:94:ARG:NH1	1:A:101:ASP:OD2	2.22	0.70
1:H:9:ALA:HB1	1:H:108:LEU:O	1.91	0.70
2:L:48:ILE:HG21	2:L:51:SER:O	1.90	0.69
1:H:19:ARG:HB2	1:H:81:GLU:HG3	1.75	0.69
1:H:35:THR:CG2	1:H:47:TRP:HE1	2.06	0.69
1:H:85:GLU:N	1:H:85:GLU:OE1	2.22	0.68
2:L:188:HIS:O	2:L:210:ARG:NH1	2.26	0.68
1:H:103:TRP:O	3:H:301:HOH:O	2.12	0.67
2:L:90:GLN:NE2	2:L:93:THR:H	1.93	0.67
1:A:7:SER:OG	1:A:20:VAL:HG23	1.94	0.66
1:A:9:ALA:N	1:A:201:LYS:HZ1	1.92	0.66
1:A:61:GLN:HA	1:A:64:ASP:OD1	1.96	0.66
1:H:31:SER:O	1:H:99:VAL:HG13	1.95	0.66
2:B:37:GLN:HB2	2:B:47:LEU:HD21	1.76	0.66
2:B:147:TRP:HB2	2:B:154:GLN:HB2	1.79	0.65
2:L:90:GLN:HE21	2:L:92:ALA:N	1.95	0.65
1:H:134:GLY:O	1:H:186:SER:N	2.27	0.64
1:A:9:ALA:H	1:A:201:LYS:HZ1	1.44	0.64
2:B:150:ASP:HA	2:B:190:VAL:CG2	2.26	0.63
1:H:35:THR:HG23	1:H:47:TRP:HE1	1.63	0.63
1:A:38:ARG:HH22	1:A:86:ASP:HA	1.63	0.63
2:B:2:ILE:O	3:B:301:HOH:O	2.16	0.62
2:L:119:PRO:HD3	2:L:131:VAL:HG22	1.79	0.62
1:A:13:LYS:O	1:A:16:SER:OG	2.17	0.61
2:B:141:ARG:NH2	2:B:162:VAL:HG21	2.15	0.61
1:A:126:PRO:HD3	1:A:211:VAL:HG13	1.81	0.61
1:A:200:HIS:CD2	1:A:202:PRO:HD2	2.35	0.61
1:A:31:SER:O	1:A:99:VAL:HG23	2.02	0.59
1:A:125:ALA:HA	1:A:211:VAL:HG13	1.84	0.59
2:B:23:CYS:HB2	2:B:35:TRP:CH2	2.37	0.59
2:L:48:ILE:CG2	2:L:51:SER:O	2.50	0.59
2:L:107:ARG:NH1	2:L:108:THR:O	2.35	0.59
2:B:50:GLY:O	2:B:52:SER:N	2.34	0.59
1:A:119:PRO:HD3	1:A:200:HIS:ND1	2.18	0.58
1:A:126:PRO:HB3	1:A:137:ALA:O	2.03	0.58
1:H:117:LYS:CD	1:H:144:ASP:O	2.52	0.58
1:A:84:LEU:O	3:A:302:HOH:O	2.17	0.57
1:H:136:ALA:N	1:H:184:VAL:O	2.31	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:47:LEU:HD23	2:L:58:ILE:HD12	1.86	0.57
2:B:39:LYS:HE2	2:B:81:GLU:O	2.05	0.57
2:L:209:ASN:O	2:L:210:ARG:CB	2.51	0.56
2:L:104:GLU:OE2	2:L:172:TYR:OH	2.23	0.56
1:A:124:LEU:HB3	2:B:117:PHE:CD2	2.41	0.55
2:B:105:ILE:O	2:B:165:GLN:NE2	2.32	0.55
1:H:9:ALA:HB3	1:H:201:LYS:NZ	2.18	0.55
1:A:26:GLY:O	1:A:27:ASP:CB	2.54	0.55
2:B:148:LYS:HA	2:B:152:ALA:O	2.06	0.55
2:L:189:LYS:O	2:L:189:LYS:HG3	2.06	0.55
1:H:35:THR:CG2	1:H:47:TRP:NE1	2.68	0.55
1:H:207:VAL:CG1	1:H:209:LYS:HG2	2.36	0.55
2:B:124:LEU:HD21	2:B:185:TYR:HD2	1.70	0.55
1:A:195:ILE:HA	1:A:209:LYS:O	2.06	0.55
1:A:38:ARG:HB2	1:A:88:ALA:HB1	1.88	0.55
2:L:50:GLY:O	2:L:52:SER:N	2.39	0.54
1:A:165:THR:OG1	1:A:180:SER:OG	2.07	0.54
2:B:141:ARG:NH1	2:B:141:ARG:O	2.39	0.54
1:H:33:SER:HB3	1:H:52:PHE:CE1	2.43	0.54
1:A:139:GLY:HA3	1:A:181:VAL:HG12	1.89	0.54
1:A:21:SER:HB3	1:A:79:TYR:CE2	2.43	0.53
2:B:3:VAL:N	2:B:26:SER:OG	2.35	0.53
1:A:38:ARG:NH2	1:A:86:ASP:HA	2.23	0.53
1:H:35:THR:HG23	1:H:47:TRP:NE1	2.23	0.53
1:A:37:VAL:HG22	1:A:47:TRP:HA	1.90	0.53
1:A:53:ILE:HG23	1:A:54:PHE:CD1	2.45	0.52
2:B:145:VAL:HG22	2:B:195:VAL:HG22	1.92	0.52
2:B:30:SER:O	2:B:51:SER:HB3	2.10	0.52
1:H:33:SER:HB3	1:H:52:PHE:CZ	2.45	0.52
1:A:36:TRP:HB3	1:A:48:MET:HE3	1.90	0.51
1:H:66:ARG:O	1:H:82(A):THR:N	2.43	0.51
1:H:100(A):PRO:HA	1:A:54:PHE:CZ	2.45	0.51
1:A:9:ALA:N	1:A:201:LYS:HZ2	2.02	0.51
1:H:100(J):PHE:O	1:H:103:TRP:NE1	2.40	0.51
1:A:195:ILE:HG23	1:A:208:ASP:HB3	1.91	0.51
1:A:48:MET:HE1	1:A:90:TYR:HD2	1.76	0.51
1:H:6:GLN:HE21	1:H:104:GLY:HA3	1.76	0.51
1:H:28:THR:HG23	1:H:94:ARG:HD3	1.92	0.50
1:H:71:THR:HG22	1:H:78:VAL:HG22	1.92	0.50
2:B:35:TRP:CD2	2:B:73:LEU:HB2	2.46	0.50
2:B:141:ARG:CZ	2:B:162:VAL:HG21	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:90:GLN:HE21	2:L:92:ALA:H	1.58	0.50
1:A:211:VAL:HG12	1:A:212:GLU:N	2.26	0.50
2:L:30:SER:O	2:L:51:SER:HB3	2.11	0.50
1:A:12:LYS:HE2	1:A:17:SER:O	2.12	0.50
2:B:162:VAL:HG13	2:B:173:SER:O	2.12	0.49
1:A:112:SER:OG	1:A:113:SER:N	2.43	0.49
1:A:18:VAL:HG13	1:A:82(C):LEU:HD11	1.94	0.49
2:L:135:LEU:HD21	2:L:195:VAL:HG13	1.94	0.49
2:B:123:GLN:HA	2:B:126:SER:OG	2.12	0.49
1:A:139:GLY:HA2	1:A:154:TRP:CH2	2.47	0.49
2:L:32:TYR:HA	2:L:91:TYR:CE1	2.48	0.49
2:B:112:PRO:HB3	2:B:138:PHE:HB3	1.95	0.49
1:A:197:ASN:ND2	1:A:208:ASP:OD1	2.29	0.48
1:A:23:LYS:HB2	1:A:77:THR:HG22	1.95	0.48
2:L:4:MET:HE1	2:L:25:THR:HG22	1.95	0.48
2:L:36:TYR:OH	2:L:89:GLN:OE1	2.12	0.48
2:B:132:VAL:HA	2:B:176:SER:O	2.14	0.48
1:H:53:ILE:HG23	1:H:54:PHE:CD1	2.49	0.48
1:H:38:ARG:HD3	1:H:90:TYR:CE2	2.49	0.48
1:H:6:GLN:NE2	1:H:106:GLY:H	2.12	0.48
1:H:70:THR:O	1:H:79:TYR:N	2.42	0.48
2:B:107:ARG:HG2	2:B:107:ARG:NH1	2.28	0.47
2:L:147:TRP:CD2	2:L:178:LEU:HB2	2.49	0.47
2:B:2:ILE:HB	3:B:301:HOH:O	2.14	0.47
1:A:171:GLN:HA	2:B:159:GLN:HE22	1.80	0.47
2:B:124:LEU:HD22	2:B:182:LYS:HG3	1.96	0.47
2:B:48:ILE:HG23	2:B:52:SER:O	2.14	0.47
2:L:107:ARG:HG2	2:L:108:THR:O	2.14	0.47
1:A:171:GLN:HE21	1:A:175:LEU:C	2.12	0.47
1:A:13:LYS:HA	1:A:112:SER:O	2.15	0.47
1:A:9:ALA:H	1:A:201:LYS:CE	2.26	0.47
1:A:37:VAL:HG13	1:A:46:GLN:C	2.36	0.47
2:B:185:TYR:CZ	2:B:210:ARG:HD3	2.50	0.47
1:A:5:VAL:O	1:A:22:CYS:HA	2.14	0.46
1:H:87:THR:HA	1:H:109:VAL:O	2.15	0.46
1:H:103:TRP:CE3	2:L:44:PRO:HD2	2.50	0.46
1:H:100(B):ALA:HA	1:A:100(B):ALA:HA	1.97	0.46
1:H:35:THR:HG21	1:H:47:TRP:HE1	1.77	0.46
1:H:35:THR:HG21	1:H:47:TRP:NE1	2.30	0.46
1:H:20:VAL:HB	1:H:80:MET:SD	2.56	0.46
1:A:12:LYS:HG3	1:A:18:VAL:CG1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:164:HIS:HB2	1:H:181:VAL:HG22	1.98	0.46
2:B:37:GLN:OE1	2:B:39:LYS:HE3	2.16	0.46
1:A:201:LYS:HG3	1:A:202:PRO:N	2.29	0.46
1:H:20:VAL:HB	1:H:80:MET:HG2	1.99	0.45
1:H:52:PHE:CE2	1:H:100(D):PRO:HB2	2.51	0.45
1:A:12:LYS:HG3	1:A:18:VAL:HG12	1.97	0.45
1:A:83:ARG:O	1:A:111:VAL:HG11	2.15	0.45
1:H:83:ARG:O	1:H:111:VAL:HG11	2.16	0.45
2:L:148:LYS:HG2	2:L:153:LEU:HD23	1.97	0.45
2:L:162:VAL:HG22	2:L:174:LEU:HB2	1.99	0.45
1:A:171:GLN:NE2	1:A:175:LEU:O	2.30	0.45
2:L:21:LEU:HB3	3:L:309:HOH:O	2.16	0.45
1:A:87:THR:HG23	1:A:110:THR:HA	1.99	0.45
2:L:148:LYS:HG2	2:L:153:LEU:CD2	2.46	0.45
1:H:29:PHE:CG	1:H:76:ARG:HB3	2.52	0.45
2:L:33:LEU:O	2:L:50:GLY:N	2.50	0.45
1:A:28:THR:O	1:A:32:TYR:HB2	2.16	0.45
2:B:30:SER:O	2:B:51:SER:CB	2.64	0.45
2:L:51:SER:OG	2:L:52:SER:N	2.50	0.45
2:B:187:LYS:HG2	2:B:188:HIS:CD2	2.51	0.45
1:H:35:THR:HG22	1:H:36:TRP:N	2.32	0.45
2:B:25:THR:O	2:B:69:ARG:HD2	2.17	0.44
1:A:21:SER:HB3	1:A:79:TYR:CD2	2.53	0.44
1:H:96:ALA:N	1:H:100(H):ASP:OD2	2.51	0.44
1:A:4:LEU:HD21	1:A:28:THR:HG21	2.00	0.44
1:A:84:LEU:HD23	1:A:84:LEU:HA	1.84	0.44
2:B:27(A):GLY:HA2	2:B:69:ARG:HG2	2.00	0.44
2:L:89:GLN:NE2	2:L:91:TYR:HB3	2.33	0.44
2:B:152:ALA:O	2:B:154:GLN:NE2	2.44	0.44
2:L:33:LEU:HD13	2:L:71:PHE:CG	2.52	0.44
1:H:207:VAL:HG11	1:H:209:LYS:CE	2.46	0.44
2:L:11:LEU:HG	2:L:13:LEU:HD11	1.98	0.44
1:A:152:VAL:HG22	1:A:198:VAL:HG22	1.99	0.44
2:B:165:GLN:HG2	2:B:170:SER:HA	2.00	0.44
2:L:135:LEU:HB3	2:L:138:PHE:CE2	2.53	0.44
2:L:4:MET:SD	2:L:25:THR:HG22	2.58	0.43
1:A:201:LYS:N	1:A:202:PRO:CD	2.81	0.43
2:L:141:ARG:NH1	2:L:162:VAL:HG21	2.33	0.43
1:H:32:TYR:CG	1:H:94:ARG:HD2	2.53	0.43
1:A:26:GLY:HA3	1:A:76:ARG:CZ	2.49	0.43
2:B:67:SER:OG	2:B:68:GLY:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:LEU:CD2	1:A:24:ALA:HA	2.49	0.43
2:B:48:ILE:HD13	2:B:54:ARG:HA	2.00	0.43
1:H:35:THR:HG21	1:H:47:TRP:CD1	2.54	0.43
1:H:12:LYS:HG3	1:H:18:VAL:HB	1.99	0.43
1:H:150:VAL:HG12	1:H:200:HIS:HB2	1.99	0.43
2:B:107:ARG:HG2	2:B:107:ARG:HH11	1.83	0.43
2:B:124:LEU:HA	2:B:124:LEU:HD23	1.90	0.43
1:H:148:GLU:HA	1:H:149:PRO:HA	1.75	0.43
1:H:59:TYR:HB2	1:H:64:ASP:OD1	2.18	0.43
1:A:6:GLN:HA	1:A:21:SER:O	2.19	0.42
1:H:141:LEU:HD12	1:H:178:LEU:O	2.20	0.42
2:B:160:GLU:HB3	2:B:174:LEU:HD21	2.01	0.42
1:H:185:PRO:O	1:H:188:SER:OG	2.35	0.42
1:H:19:ARG:HA	1:H:80:MET:O	2.19	0.42
2:B:66:GLY:HA3	2:B:71:PHE:HA	2.01	0.42
1:H:150:VAL:HG22	1:H:178:LEU:HD13	2.02	0.42
1:H:69:ILE:HA	1:H:79:TYR:O	2.19	0.42
1:A:196:CYS:O	1:A:208:ASP:HA	2.20	0.42
1:H:164:HIS:HB2	1:H:181:VAL:CG2	2.49	0.42
2:L:18:ARG:HG3	2:L:76:SER:HA	2.02	0.42
1:H:52:PHE:O	1:H:55:GLY:N	2.53	0.42
2:L:61:ARG:CZ	2:L:79:GLU:HG3	2.50	0.41
1:H:139:GLY:HA2	1:H:154:TRP:CZ2	2.55	0.41
1:H:9:ALA:HB2	3:H:311:HOH:O	2.19	0.41
2:L:139:TYR:CG	2:L:140:PRO:HA	2.54	0.41
1:A:19:ARG:HA	1:A:80:MET:O	2.20	0.41
1:A:18:VAL:CG2	1:A:82:LEU:HB3	2.51	0.41
2:B:124:LEU:HD21	2:B:185:TYR:CD2	2.53	0.41
2:L:33:LEU:C	2:L:33:LEU:HD23	2.40	0.41
1:A:148:GLU:O	3:A:303:HOH:O	2.22	0.41
2:B:165:GLN:NE2	2:B:170:SER:HB3	2.35	0.41
1:A:211:VAL:HG12	1:A:212:GLU:H	1.86	0.41
1:A:30:SER:O	1:A:53:ILE:HD13	2.21	0.41
1:A:88:ALA:HB3	1:A:90:TYR:CE1	2.56	0.41
2:B:153:LEU:HD23	2:B:154:GLN:O	2.21	0.41
2:B:124:LEU:HD11	2:B:185:TYR:HE2	1.85	0.41
2:B:6:GLN:OE1	2:B:87:TYR:HA	2.21	0.41
2:L:141:ARG:CZ	2:L:162:VAL:HG21	2.50	0.41
2:L:176:SER:OG	3:L:301:HOH:O	2.22	0.41
1:H:195:ILE:HG23	1:H:209:LYS:C	2.41	0.41
2:L:33:LEU:HD13	2:L:71:PHE:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:86:TYR:O	2:L:100:GLY:HA2	2.21	0.41
1:A:143:LYS:O	1:A:144:ASP:HB2	2.20	0.40
1:A:38:ARG:HB3	1:A:90:TYR:CD2	2.56	0.40
1:H:124:LEU:HD12	1:H:140:CYS:N	2.37	0.40
1:H:29:PHE:CZ	1:H:76:ARG:HA	2.56	0.40
2:B:2:ILE:HD12	2:B:90:GLN:OE1	2.21	0.40
1:H:82(A):THR:HG22	1:H:82(B):SER:N	2.37	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:164:GLU:OE1	3:B:303:HOH:O[3_454]	2.06	0.14
2:L:107:ARG:NH2	3:H:305:HOH:O[3_564]	2.14	0.06

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	215/236 (91%)	197 (92%)	15 (7%)	3 (1%)	11 22
1	H	216/236 (92%)	196 (91%)	16 (7%)	4 (2%)	8 15
2	B	211/214 (99%)	196 (93%)	15 (7%)	0	100 100
2	L	212/214 (99%)	203 (96%)	8 (4%)	1 (0%)	29 52
All	All	854/900 (95%)	792 (93%)	54 (6%)	8 (1%)	17 35

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	101	ASP
1	A	27	ASP

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Mol	Chain	Res	Type
1	A	44	GLY
1	H	64	ASP
1	H	100(D)	PRO
2	L	51	SER
1	H	149	PRO
1	A	126	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	184/200 (92%)	176 (96%)	8 (4%)	29	54
1	H	185/200 (92%)	180 (97%)	5 (3%)	44	71
2	B	185/186 (100%)	177 (96%)	8 (4%)	29	54
2	L	186/186 (100%)	182 (98%)	4 (2%)	52	76
All	All	740/772 (96%)	715 (97%)	25 (3%)	37	63

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	16	SER
1	H	74	SER
1	H	76	ARG
1	H	197	ASN
1	H	201	LYS
2	L	53	SER
2	L	60	ASP
2	L	130	SER
2	L	189	LYS
1	A	25	SER
1	A	30	SER
1	A	31	SER
1	A	43	HIS
1	A	99	VAL
1	A	196	CYS

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Mol	Chain	Res	Type
1	A	197	ASN
1	A	201	LYS
2	B	1	ASP
2	B	24	ARG
2	B	31	SER
2	B	33	LEU
2	B	53	SER
2	B	67	SER
2	B	160	GLU
2	B	175	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	6	GLN
2	L	90	GLN
2	B	38	GLN
2	B	159	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 carbohydrates 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	219/236 (92%)	-0.28	1 (0%)	91	89	37, 64, 99, 117	0
1	H	220/236 (93%)	-0.21	1 (0%)	91	89	39, 65, 98, 171	0
2	B	212/214 (99%)	-0.30	0	100	100	29, 52, 81, 117	0
2	L	213/214 (99%)	-0.24	0	100	100	37, 57, 84, 102	0
All	All	864/900 (96%)	-0.26	2 (0%)	95	95	29, 60, 91, 171	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	64	ASP	4.6
1	A	211	VAL	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.