



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:21 AM UTC

PDB ID : 1FAI / pdb_00001fai
Title : THREE-DIMENSIONAL STRUCTURE OF TWO CRYSTAL FORMS OF
FAB R19.9, FROM A MONOCLONAL ANTI-ARSONATE ANTIBODY
Authors : Lascombe, M.B.; Alzari, P.M.; Poljak, R.J.; Nisonoff, A.
Deposited on : 1992-05-27
Resolution : 2.70 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

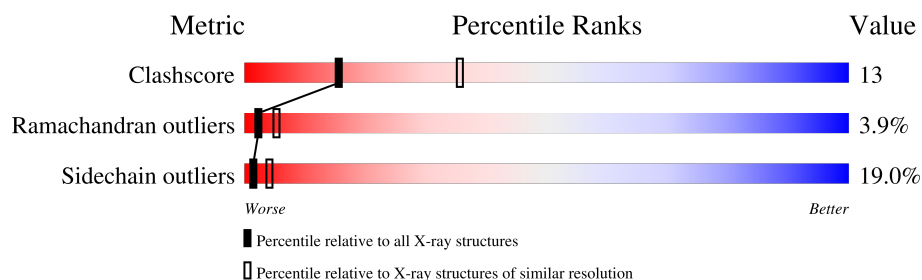
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

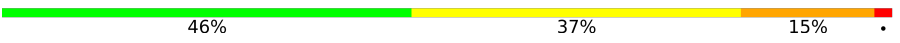
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	214	
2	H	221	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3320 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 IGG2B-KAPPA R19.9 FAB (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	214	Total	C	N	O	S	0	0	0
			1663	1027	284	345	7			

- Molecule 2 is a protein called IGG2B-KAPPA R19.9 FAB (HEAVY CHAIN).

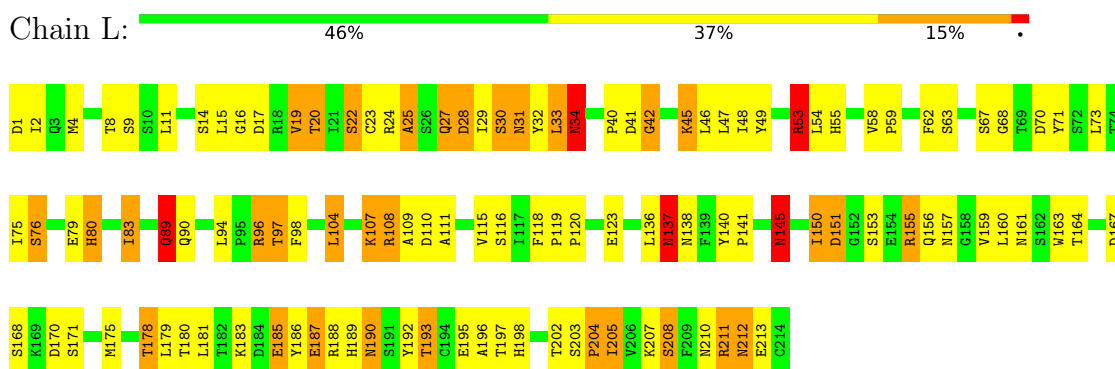
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	221	Total	C	N	O	S	0	0	0
			1657	1047	270	332	8			

3 Residue-property plots

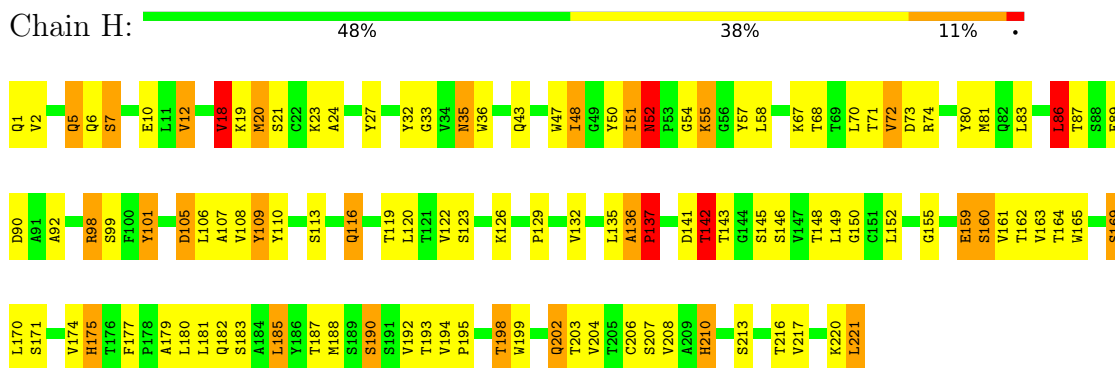
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: IGG2B-KAPPA R19.9 FAB (LIGHT CHAIN)



• Molecule 2: IGG2B-KAPPA R19.9 FAB (HEAVY CHAIN)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.00Å 80.60Å 75.20Å 90.00° 90.20° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.189 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3320	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

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	L	1.02	6/1697 (0.4%)	2.11	62/2301 (2.7%)
2	H	1.03	5/1699 (0.3%)	2.02	57/2316 (2.5%)
All	All	1.03	11/3396 (0.3%)	2.07	119/4617 (2.6%)

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	L	0	1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	55	HIS	CD2-NE2	-7.29	1.29	1.37
1	L	198	HIS	CD2-NE2	-6.55	1.30	1.37
2	H	175	HIS	CD2-NE2	-6.19	1.31	1.37
2	H	210	HIS	CD2-NE2	-6.11	1.31	1.37
1	L	189	HIS	CD2-NE2	-6.09	1.31	1.37
1	L	80	HIS	CD2-NE2	-5.62	1.31	1.37
2	H	165	TRP	CG-CD2	-5.42	1.33	1.43
1	L	198	HIS	CG-ND1	-5.33	1.32	1.38
2	H	175	HIS	CG-ND1	-5.21	1.32	1.38
2	H	210	HIS	CG-ND1	-5.14	1.32	1.38
1	L	178	THR	CA-CB	5.03	1.60	1.53

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	194	VAL	O-C-N	-11.62	114.37	121.69
1	L	145	ASN	CA-CB-CG	11.54	124.14	112.60
1	L	98	PHE	CA-CB-CG	11.05	124.85	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	28	ASP	CA-CB-CG	10.13	122.73	112.60
1	L	151	ASP	CA-CB-CG	9.98	122.58	112.60
1	L	196	ALA	N-CA-C	8.79	123.22	109.07
1	L	213	GLU	N-CA-C	-8.39	101.08	114.09
1	L	137	ASN	N-CA-C	8.39	123.29	109.95
1	L	34	ASN	OD1-CG-ND2	-8.24	114.36	122.60
2	H	141	ASP	CA-CB-CG	-8.09	104.51	112.60
1	L	212	ASN	O-C-N	7.88	133.25	123.01
2	H	105	ASP	CA-CB-CG	7.87	120.47	112.60
2	H	74	ARG	N-CA-C	7.85	122.55	112.34
2	H	203	THR	N-CA-C	7.84	122.16	108.52
1	L	212	ASN	OD1-CG-ND2	-7.79	114.81	122.60
2	H	90	ASP	CA-CB-CG	7.72	120.33	112.60
2	H	86	LEU	N-CA-C	7.67	120.20	109.15
2	H	202	GLN	N-CA-C	7.41	119.70	109.18
2	H	73	ASP	CA-CB-CG	7.19	119.79	112.60
1	L	17	ASP	CA-CB-CG	7.10	119.70	112.60
1	L	171	SER	N-CA-C	6.95	121.09	112.47
1	L	193	THR	N-CA-C	6.93	120.36	108.02
1	L	161	ASN	N-CA-C	6.91	120.44	108.76
1	L	27	GLN	O-C-N	-6.88	115.35	123.06
1	L	212	ASN	CA-C-O	6.88	128.54	120.70
1	L	83	ILE	CB-CA-C	-6.80	103.94	111.35
2	H	171	SER	N-CA-C	6.77	119.68	111.82
2	H	199	TRP	O-C-N	-6.71	116.60	121.84
1	L	211	ARG	CA-C-N	-6.68	113.25	123.14
1	L	211	ARG	C-N-CA	-6.68	113.25	123.14
1	L	118	PHE	CA-C-N	6.62	124.43	119.66
1	L	118	PHE	C-N-CA	6.62	124.43	119.66
1	L	211	ARG	CA-CB-CG	6.61	127.32	114.10
2	H	27	TYR	N-CA-C	6.54	119.10	109.69
1	L	55	HIS	CB-CG-CD2	-6.47	122.79	131.20
1	L	208	SER	N-CA-C	6.40	118.27	109.18
2	H	43	GLN	OE1-CD-NE2	-6.38	116.22	122.60
2	H	141	ASP	O-C-N	6.31	130.41	122.84
1	L	9	SER	N-CA-C	6.28	117.93	111.14
1	L	41	ASP	O-C-N	6.25	130.90	122.59
2	H	24	ALA	N-CA-C	6.25	118.91	108.73
1	L	53	ARG	NE-CZ-NH1	6.22	127.72	121.50
2	H	18	VAL	CB-CA-C	-6.21	102.68	111.38
1	L	155	ARG	N-CA-C	6.20	120.65	107.70
1	L	22	SER	N-CA-C	6.15	119.58	108.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	52	ASN	CA-CB-CG	6.13	118.73	112.60
1	L	89	GLN	N-CA-C	6.06	118.51	108.99
2	H	47	TRP	CG-CD2-CE3	6.06	139.96	133.90
1	L	153	SER	N-CA-C	6.02	118.54	108.73
1	L	27	GLN	OE1-CD-NE2	-5.92	116.68	122.60
1	L	110	ASP	N-CA-C	5.92	118.58	110.24
1	L	76	SER	CB-CA-C	-5.91	101.40	110.26
1	L	170	ASP	CA-CB-CG	5.83	118.43	112.60
1	L	167	ASP	N-CA-C	5.83	118.46	110.24
1	L	212	ASN	CA-C-N	5.82	130.69	121.44
1	L	212	ASN	C-N-CA	5.82	130.69	121.44
2	H	206	CYS	N-CA-CB	-5.79	100.99	110.43
2	H	142	THR	N-CA-C	5.77	123.09	110.80
2	H	72	VAL	N-CA-CB	-5.67	102.06	111.36
1	L	156	GLN	OE1-CD-NE2	-5.64	116.96	122.60
2	H	18	VAL	O-C-N	5.63	129.12	122.36
2	H	174	VAL	N-CA-C	5.63	116.41	108.36
2	H	52	ASN	OD1-CG-ND2	-5.63	116.97	122.60
2	H	1	GLN	OE1-CD-NE2	-5.62	116.98	122.60
1	L	168	SER	O-C-N	5.60	128.06	122.12
1	L	212	ASN	CA-CB-CG	-5.60	107.00	112.60
1	L	198	HIS	CB-CG-CD2	-5.60	123.92	131.20
1	L	150	ILE	N-CA-C	-5.59	99.54	107.98
2	H	136	ALA	CA-C-N	5.58	126.82	119.84
2	H	136	ALA	C-N-CA	5.58	126.82	119.84
2	H	72	VAL	N-CA-C	5.58	115.71	108.35
2	H	7	SER	N-CA-C	5.57	120.08	113.12
1	L	30	SER	N-CA-C	5.49	122.50	110.80
1	L	63	SER	CA-C-N	-5.43	117.26	121.82
1	L	63	SER	C-N-CA	-5.43	117.26	121.82
2	H	207	SER	N-CA-C	5.42	119.00	107.67
2	H	202	GLN	CA-C-O	5.42	127.78	121.49
2	H	165	TRP	CE2-CD2-CE3	5.41	124.21	118.80
2	H	141	ASP	CA-C-O	5.41	127.76	121.11
2	H	129	PRO	CA-C-N	5.41	125.38	120.03
2	H	129	PRO	C-N-CA	5.41	125.38	120.03
1	L	190	ASN	OD1-CG-ND2	-5.40	117.20	122.60
2	H	216	THR	CB-CA-C	-5.39	104.36	111.42
1	L	24	ARG	CB-CA-C	-5.38	102.08	110.74
1	L	70	ASP	CA-CB-CG	-5.31	107.29	112.60
1	L	210	ASN	OD1-CG-ND2	-5.31	117.29	122.60
2	H	36	TRP	CG-CD2-CE3	5.31	139.21	133.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	159	GLU	CA-CB-CG	-5.30	103.49	114.10
2	H	99	SER	O-C-N	-5.30	116.75	122.79
1	L	119	PRO	CA-C-N	5.30	126.46	119.84
1	L	119	PRO	C-N-CA	5.30	126.46	119.84
2	H	145	SER	CA-C-O	5.28	125.17	119.15
2	H	210	HIS	CA-C-N	5.28	125.34	119.32
2	H	210	HIS	C-N-CA	5.28	125.34	119.32
2	H	47	TRP	CB-CG-CD1	-5.27	119.00	126.90
2	H	51	ILE	CA-CB-CG1	-5.27	101.44	110.40
2	H	150	GLY	N-CA-C	5.26	119.96	111.38
2	H	163	VAL	N-CA-C	-5.25	100.69	108.45
2	H	210	HIS	CA-CB-CG	5.23	119.03	113.80
2	H	20	MET	CA-CB-CG	-5.18	103.75	114.10
1	L	80	HIS	CB-CG-CD2	-5.17	124.47	131.20
2	H	160	SER	CB-CA-C	-5.17	104.56	112.11
2	H	47	TRP	CE2-CD2-CG	-5.16	101.01	107.20
2	H	101	TYR	N-CA-C	5.16	121.79	110.80
1	L	14	SER	CA-C-O	-5.15	115.73	121.81
2	H	68	THR	N-CA-C	5.15	117.84	109.24
2	H	52	ASN	N-CA-CB	-5.14	100.60	110.27
2	H	202	GLN	OE1-CD-NE2	-5.13	117.47	122.60
1	L	195	GLU	N-CA-C	5.12	116.74	108.34
1	L	31	ASN	CA-C-O	5.12	127.33	120.98
2	H	199	TRP	CB-CG-CD1	-5.11	119.23	126.90
1	L	141	PRO	N-CA-C	5.09	125.34	112.10
2	H	47	TRP	CD1-CG-CD2	5.09	114.44	106.30
1	L	104	LEU	O-C-N	-5.06	116.58	122.96
2	H	137	PRO	N-CA-C	5.06	122.90	112.47
1	L	42	GLY	N-CA-C	5.05	125.15	113.18
1	L	25	ALA	N-CA-C	5.04	117.18	110.53
1	L	24	ARG	N-CA-C	5.04	116.83	108.02
1	L	202	THR	CA-C-O	5.03	125.71	119.12

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	203	SER	Peptide

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	L	1663	0	1589	46	0
2	H	1657	0	1610	45	0
All	All	3320	0	3199	87	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 13.

All (87) 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:H:149:LEU:HD13	2:H:204:VAL:HG11	1.54	0.89
1:L:53:ARG:HG2	1:L:53:ARG:HH11	1.42	0.83
1:L:190:ASN:HA	1:L:211:ARG:HB3	1.64	0.80
1:L:47:LEU:HA	1:L:58:VAL:HG21	1.63	0.79
2:H:12:VAL:HG11	2:H:86:LEU:HD23	1.70	0.72
1:L:107:LYS:HA	1:L:140:TYR:OH	1.94	0.67
2:H:146:SER:HA	2:H:195:PRO:HA	1.81	0.63
2:H:132:VAL:HB	2:H:217:VAL:HG11	1.82	0.61
1:L:137:ASN:HD21	2:H:177:PHE:HZ	1.48	0.61
2:H:18:VAL:HG22	2:H:86:LEU:HD21	1.82	0.61
1:L:183:LYS:O	1:L:187:GLU:HB2	2.00	0.60
1:L:34:ASN:ND2	2:H:110:TYR:HB3	2.17	0.59
2:H:116:GLN:H	2:H:116:GLN:NE2	2.00	0.59
2:H:51:ILE:HG13	2:H:58:LEU:HG	1.84	0.59
2:H:137:PRO:HD3	2:H:149:LEU:HD23	1.85	0.58
1:L:179:LEU:HD11	1:L:181:LEU:HD13	1.88	0.56
2:H:198:THR:O	2:H:202:GLN:HB2	2.06	0.56
1:L:45:LYS:HZ1	1:L:46:LEU:H	1.55	0.55
1:L:59:PRO:HD2	1:L:62:PHE:CE2	2.42	0.55
2:H:20:MET:O	2:H:80:TYR:HA	2.07	0.54
2:H:48:ILE:HG21	2:H:81:MET:HE3	1.89	0.54
1:L:2:ILE:HD13	1:L:29:ILE:HG22	1.90	0.54
1:L:96:ARG:HH21	2:H:109:TYR:HE1	1.56	0.54
1:L:205:ILE:HD12	1:L:205:ILE:H	1.72	0.54
1:L:33:LEU:HD22	1:L:71:TYR:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:32:TYR:CE2	2:H:101:TYR:HB2	2.44	0.53
1:L:145:ASN:HB3	1:L:197:THR:OG1	2.08	0.53
2:H:55:LYS:NZ	2:H:55:LYS:HA	2.23	0.53
1:L:155:ARG:HG2	1:L:157:ASN:HB3	1.90	0.53
2:H:175:HIS:O	2:H:190:SER:HA	2.10	0.52
1:L:159:VAL:HA	1:L:178:THR:O	2.10	0.52
1:L:19:VAL:HG23	1:L:75:ILE:HB	1.91	0.51
2:H:6:GLN:H	2:H:116:GLN:NE2	2.08	0.51
1:L:31:ASN:HD21	1:L:67:SER:HA	1.76	0.51
1:L:80:HIS:CE1	1:L:83:ILE:HD11	2.47	0.50
2:H:183:SER:O	2:H:185:LEU:HD23	2.12	0.49
1:L:28:ASP:OD1	1:L:68:GLY:HA2	2.11	0.49
2:H:33:GLY:HA3	2:H:50:TYR:CE1	2.47	0.49
1:L:53:ARG:HG2	1:L:53:ARG:NH1	2.17	0.48
2:H:19:LYS:HG2	2:H:80:TYR:HB3	1.95	0.48
2:H:136:ALA:HB2	2:H:221:LEU:HD23	1.96	0.48
1:L:108:ARG:HD3	1:L:109:ALA:O	2.14	0.48
1:L:89:GLN:HE21	1:L:89:GLN:HB2	1.55	0.48
2:H:148:THR:HG22	2:H:193:THR:OG1	2.12	0.48
1:L:181:LEU:HG	1:L:185:GLU:HB3	1.95	0.48
2:H:162:THR:O	2:H:208:VAL:HA	2.13	0.48
1:L:150:ILE:HG13	1:L:192:TYR:CE2	2.48	0.47
2:H:149:LEU:HB2	2:H:192:VAL:HG12	1.97	0.46
2:H:32:TYR:CD2	2:H:98:ARG:HD3	2.51	0.46
1:L:49:TYR:O	1:L:53:ARG:HB2	2.16	0.46
2:H:55:LYS:HA	2:H:55:LYS:HZ3	1.81	0.45
2:H:52:ASN:HD22	2:H:54:GLY:H	1.65	0.45
2:H:137:PRO:HD3	2:H:149:LEU:CD2	2.46	0.45
1:L:11:LEU:O	1:L:104:LEU:HA	2.17	0.45
1:L:175:MET:N	2:H:177:PHE:HE2	2.14	0.45
1:L:4:MET:SD	1:L:90:GLN:HB3	2.57	0.45
1:L:27:GLN:NE2	1:L:28:ASP:O	2.50	0.45
1:L:186:TYR:HA	1:L:192:TYR:OH	2.16	0.45
2:H:35:ASN:ND2	2:H:35:ASN:N	2.65	0.45
2:H:32:TYR:CZ	2:H:101:TYR:HB2	2.53	0.44
1:L:59:PRO:HD2	1:L:62:PHE:CD2	2.53	0.44
1:L:4:MET:SD	1:L:25:ALA:HB2	2.57	0.44
1:L:108:ARG:NH1	1:L:111:ALA:HB2	2.33	0.44
1:L:155:ARG:NH1	1:L:157:ASN:HD22	2.16	0.44
2:H:7:SER:HB3	2:H:21:SER:H	1.83	0.43
2:H:132:VAL:HG21	2:H:217:VAL:HB	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:5:GLN:HB2	2:H:23:LYS:HB3	2.00	0.43
1:L:179:LEU:CD1	1:L:181:LEU:HD13	2.47	0.43
2:H:161:VAL:HG22	2:H:210:HIS:HB2	2.01	0.43
1:L:4:MET:HE3	1:L:23:CYS:SG	2.59	0.43
2:H:18:VAL:HG22	2:H:86:LEU:CD2	2.49	0.43
1:L:115:VAL:HG23	1:L:136:LEU:HD13	1.99	0.43
1:L:32:TYR:O	1:L:90:GLN:HA	2.19	0.43
2:H:12:VAL:HG12	2:H:122:VAL:HG22	2.00	0.43
2:H:55:LYS:HB3	2:H:57:TYR:HD1	1.84	0.43
2:H:81:MET:HE2	2:H:83:LEU:HG	2.01	0.42
1:L:33:LEU:HD22	1:L:71:TYR:CB	2.50	0.42
2:H:135:LEU:HD11	2:H:152:LEU:HB2	2.00	0.42
1:L:20:THR:HA	1:L:73:LEU:O	2.20	0.42
1:L:90:GLN:HE21	1:L:97:THR:H	1.67	0.41
1:L:192:TYR:O	1:L:208:SER:HA	2.20	0.41
2:H:116:GLN:H	2:H:116:GLN:HE21	1.67	0.41
1:L:193:THR:HA	1:L:207:LYS:O	2.20	0.41
2:H:35:ASN:N	2:H:35:ASN:HD22	2.19	0.41
1:L:48:ILE:HD12	1:L:54:LEU:CD1	2.52	0.40
2:H:169:SER:OG	2:H:170:LEU:HG	2.21	0.40
2:H:179:ALA:HA	2:H:187:THR:O	2.21	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	L	212/214 (99%)	180 (85%)	27 (13%)	5 (2%)	4	12
2	H	219/221 (99%)	176 (80%)	31 (14%)	12 (6%)	1	2
All	All	431/435 (99%)	356 (83%)	58 (14%)	17 (4%)	2	5

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	30	SER
2	H	142	THR
2	H	155	GLY
2	H	213	SER
1	L	16	GLY
1	L	42	GLY
2	H	2	VAL
2	H	169	SER
2	H	105	ASP
2	H	108	VAL
2	H	143	THR
2	H	182	GLN
1	L	204	PRO
1	L	138	ASN
2	H	92	ALA
2	H	107	ALA
2	H	137	PRO

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	L	192/192 (100%)	157 (82%)	35 (18%)	2	5
2	H	187/187 (100%)	150 (80%)	37 (20%)	1	4
All	All	379/379 (100%)	307 (81%)	72 (19%)	1	4

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	1	ASP
1	L	8	THR
1	L	15	LEU
1	L	19	VAL
1	L	20	THR
1	L	22	SER

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Mol	Chain	Res	Type
1	L	33	LEU
1	L	34	ASN
1	L	40	PRO
1	L	45	LYS
1	L	53	ARG
1	L	76	SER
1	L	79	GLU
1	L	89	GLN
1	L	94	LEU
1	L	96	ARG
1	L	97	THR
1	L	107	LYS
1	L	108	ARG
1	L	116	SER
1	L	120	PRO
1	L	123	GLU
1	L	137	ASN
1	L	145	ASN
1	L	151	ASP
1	L	160	LEU
1	L	163	TRP
1	L	164	THR
1	L	180	THR
1	L	185	GLU
1	L	187	GLU
1	L	188	ARG
1	L	204	PRO
1	L	205	ILE
1	L	212	ASN
2	H	5	GLN
2	H	10	GLU
2	H	12	VAL
2	H	18	VAL
2	H	35	ASN
2	H	48	ILE
2	H	52	ASN
2	H	55	LYS
2	H	67	LYS
2	H	70	LEU
2	H	71	THR
2	H	72	VAL
2	H	86	LEU

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Mol	Chain	Res	Type
2	H	87	THR
2	H	89	GLU
2	H	98	ARG
2	H	106	LEU
2	H	109	TYR
2	H	113	SER
2	H	116	GLN
2	H	119	THR
2	H	120	LEU
2	H	123	SER
2	H	126	LYS
2	H	137	PRO
2	H	142	THR
2	H	159	GLU
2	H	160	SER
2	H	164	THR
2	H	180	LEU
2	H	181	LEU
2	H	185	LEU
2	H	188	MET
2	H	190	SER
2	H	198	THR
2	H	220	LYS
2	H	221	LEU

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

Mol	Chain	Res	Type
1	L	3	GLN
1	L	27	GLN
1	L	31	ASN
1	L	38	GLN
1	L	89	GLN
1	L	124	GLN
1	L	137	ASN
1	L	156	GLN
1	L	157	ASN
2	H	35	ASN
2	H	39	GLN
2	H	52	ASN
2	H	116	GLN
2	H	175	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](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.