



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 06:33 PM UTC

PDB ID : 1CDI / pdb_00001cdi
Title : STRUCTURES OF AN HIV AND MHC BINDING FRAGMENT FROM HUMAN CD4 AS REFINED IN TWO CRYSTAL LATTICES
Authors : Ryu, S.E.; Truneh, A.; Sweet, R.W.; Hendrickson, W.A.
Deposited on : 1994-01-26
Resolution : 2.90 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

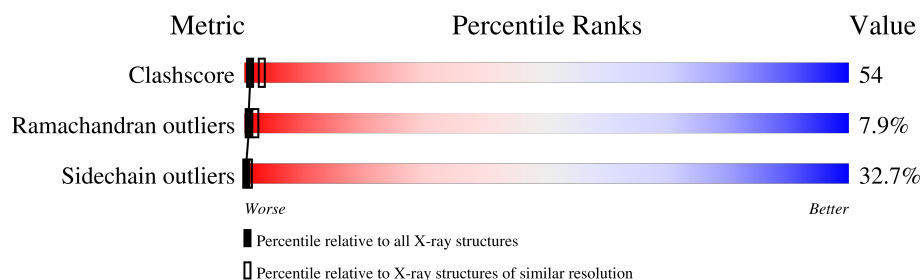
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)

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	A	179	16% 47% 26% 11%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1390 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 T CELL SURFACE GLYCOPROTEIN CD4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	0	0
			1390	869	243	274	4			

There is a discrepancy between the modelled and reference sequences:

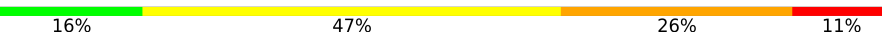
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	THR	GLY	conflict	UNP P01730

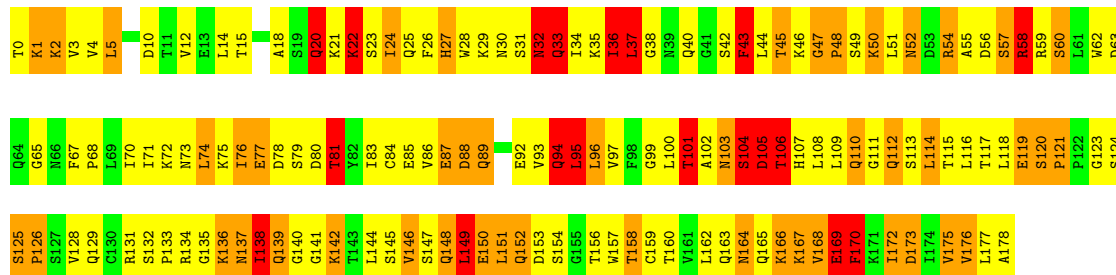
3 Residue-property plots

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: T CELL SURFACE GLYCOPROTEIN CD4

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	133.55Å 32.27Å 46.07Å 90.00° 96.12° 90.00°	Depositor
Resolution (Å)	10.00 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ, X-PLOR	Depositor
R, R_{free}	0.183 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1390	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

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	1.18	1/1409 (0.1%)	2.31	71/1901 (3.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	101	THR	CA-CB	5.42	1.61	1.53

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	134	ARG	CD-NE-CZ	11.39	140.34	124.40
1	A	20	GLN	CA-CB-CG	11.32	136.75	114.10
1	A	58	ARG	CD-NE-CZ	11.11	139.95	124.40
1	A	20	GLN	N-CA-CB	10.00	125.81	110.60
1	A	81	THR	N-CA-CB	9.79	126.38	110.43
1	A	154	SER	N-CA-C	-9.15	95.74	110.20
1	A	170	PHE	CA-CB-CG	9.02	122.82	113.80
1	A	45	THR	N-CA-CB	8.76	124.97	110.52
1	A	94	GLN	OE1-CD-NE2	8.64	131.24	122.60
1	A	10	ASP	CA-CB-CG	8.52	121.12	112.60
1	A	43	PHE	CA-CB-CG	8.48	122.28	113.80
1	A	74	LEU	N-CA-C	8.27	122.22	110.23
1	A	95	LEU	N-CA-CB	-7.91	97.54	110.43
1	A	173	ASP	CA-C-O	-7.90	112.03	120.80
1	A	121	PRO	N-CA-C	-7.64	101.38	110.70
1	A	20	GLN	N-CA-C	-7.50	99.16	109.95
1	A	176	VAL	CB-CA-C	7.39	121.63	110.62
1	A	150	GLU	CB-CG-CD	7.16	124.77	112.60
1	A	22	LYS	N-CA-C	7.14	126.02	110.80
1	A	36	ILE	N-CA-C	-6.69	106.50	112.12
1	A	25	GLN	CB-CG-CD	6.55	123.74	112.60
1	A	1	LYS	CA-CB-CG	6.35	126.79	114.10
1	A	32	ASN	CA-C-N	6.22	133.42	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	32	ASN	C-N-CA	6.22	133.42	121.54
1	A	120	SER	N-CA-C	6.13	113.53	108.07
1	A	92	GLU	CB-CG-CD	6.03	122.85	112.60
1	A	20	GLN	CA-C-O	-6.02	113.61	121.73
1	A	106	THR	N-CA-C	-5.97	106.64	114.04
1	A	42	SER	CA-C-O	5.94	126.38	120.32
1	A	81	THR	N-CA-C	-5.93	99.56	109.24
1	A	2	LYS	CA-C-O	-5.90	114.33	120.70
1	A	157	TRP	N-CA-C	-5.90	102.92	110.53
1	A	52	ASN	CA-CB-CG	-5.89	106.71	112.60
1	A	154	SER	N-CA-CB	5.85	118.89	110.06
1	A	158	THR	CA-CB-OG1	-5.85	100.83	109.60
1	A	59	ARG	N-CA-C	-5.67	105.00	111.07
1	A	25	GLN	OE1-CD-NE2	-5.67	116.93	122.60
1	A	126	PRO	CA-C-N	5.66	130.76	122.77
1	A	126	PRO	C-N-CA	5.66	130.76	122.77
1	A	137	ASN	CA-C-N	5.66	132.16	121.97
1	A	137	ASN	C-N-CA	5.66	132.16	121.97
1	A	88	ASP	N-CA-C	5.61	117.17	110.44
1	A	138	ILE	N-CA-CB	5.59	120.46	111.23
1	A	54	ARG	N-CA-C	5.56	121.48	114.31
1	A	151	LEU	N-CA-C	5.54	122.60	110.80
1	A	68	PRO	CA-C-N	5.53	130.46	122.44
1	A	68	PRO	C-N-CA	5.53	130.46	122.44
1	A	94	GLN	CB-CG-CD	-5.49	103.27	112.60
1	A	95	LEU	CB-CA-C	5.49	118.80	109.75
1	A	104	SER	CA-C-O	5.48	123.57	119.68
1	A	173	ASP	CA-CB-CG	5.47	118.07	112.60
1	A	123	GLY	N-CA-C	-5.41	107.06	114.64
1	A	154	SER	CA-C-O	-5.41	114.89	121.05
1	A	81	THR	O-C-N	5.30	129.26	123.27
1	A	37	LEU	CA-C-N	5.27	130.81	121.05
1	A	37	LEU	C-N-CA	5.27	130.81	121.05
1	A	0	THR	CA-C-N	5.23	131.53	121.54
1	A	0	THR	C-N-CA	5.23	131.53	121.54
1	A	159	CYS	N-CA-C	-5.21	102.07	110.14
1	A	120	SER	N-CA-CB	-5.20	105.93	111.29
1	A	103	ASN	CA-C-N	5.20	127.88	121.64
1	A	103	ASN	C-N-CA	5.20	127.88	121.64
1	A	149	LEU	CB-CA-C	5.19	118.37	109.80
1	A	110	GLN	N-CA-C	-5.11	103.40	110.35
1	A	169	GLU	CG-CD-OE1	-5.09	106.69	118.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	105	ASP	CA-CB-CG	5.07	117.67	112.60
1	A	168	VAL	O-C-N	5.07	128.68	123.20
1	A	5	LEU	CB-CA-C	5.07	118.48	109.72
1	A	141	GLY	N-CA-C	-5.04	101.23	113.18
1	A	138	ILE	O-C-N	5.01	128.84	122.57
1	A	33	GLN	OE1-CD-NE2	-5.00	117.60	122.60

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	1390	0	1421	151	0
All	All	1390	0	1421	151	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 54.

All (151) 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:96:LEU:HD12	1:A:121:PRO:HG3	1.28	1.09
1:A:138:ILE:HG22	1:A:144:LEU:HD23	1.40	1.02
1:A:147:SER:OG	1:A:148:GLN:HG3	1.60	1.01
1:A:100:LEU:HD23	1:A:100:LEU:O	1.65	0.95
1:A:4:VAL:HG12	1:A:95:LEU:HD23	1.47	0.94
1:A:139:GLN:HE21	1:A:140:GLY:H	1.10	0.93
1:A:40:GLN:N	1:A:43:PHE:O	2.00	0.92
1:A:14:LEU:HD23	1:A:93:VAL:CG2	1.99	0.92
1:A:111:GLY:O	1:A:148:GLN:HB3	1.73	0.89
1:A:124:SER:C	1:A:126:PRO:HD3	1.98	0.88
1:A:164:ASN:O	1:A:166:LYS:N	2.07	0.88
1:A:147:SER:OG	1:A:148:GLN:N	2.02	0.87
1:A:27:HIS:CE1	1:A:35:LYS:HD3	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:GLN:OE1	1:A:160:THR:HB	1.77	0.83
1:A:30:ASN:OD1	1:A:32:ASN:HB3	1.82	0.80
1:A:40:GLN:O	1:A:43:PHE:HD1	1.64	0.79
1:A:138:ILE:CG2	1:A:144:LEU:HD23	2.12	0.79
1:A:18:ALA:HB2	1:A:67:PHE:HE2	1.49	0.78
1:A:31:SER:C	1:A:33:GLN:H	1.89	0.77
1:A:36:ILE:O	1:A:46:LYS:HA	1.86	0.76
1:A:110:GLN:HE21	1:A:178:ALA:HB2	1.49	0.75
1:A:14:LEU:HD23	1:A:93:VAL:HG22	1.69	0.75
1:A:50:LYS:H	1:A:50:LYS:HD3	1.54	0.71
1:A:139:GLN:HE21	1:A:140:GLY:N	1.85	0.71
1:A:128:VAL:O	1:A:139:GLN:NE2	2.24	0.71
1:A:18:ALA:HB2	1:A:67:PHE:CE2	2.26	0.70
1:A:168:VAL:HG12	1:A:170:PHE:CE1	2.27	0.69
1:A:110:GLN:NE2	1:A:178:ALA:HB2	2.08	0.69
1:A:4:VAL:O	1:A:95:LEU:HA	1.93	0.69
1:A:20:GLN:O	1:A:21:LYS:C	2.36	0.68
1:A:106:THR:HG22	1:A:173:ASP:O	1.92	0.68
1:A:109:LEU:HB2	1:A:112:GLN:OE1	1.94	0.68
1:A:102:ALA:C	1:A:104:SER:H	2.02	0.67
1:A:76:ILE:HA	1:A:97:VAL:CG1	2.25	0.65
1:A:14:LEU:HD23	1:A:93:VAL:CG1	2.27	0.65
1:A:96:LEU:HD12	1:A:121:PRO:CG	2.15	0.65
1:A:44:LEU:HD13	1:A:62:TRP:CH2	2.32	0.64
1:A:36:ILE:HD12	1:A:36:ILE:N	2.12	0.63
1:A:14:LEU:HD23	1:A:93:VAL:HG21	1.78	0.63
1:A:111:GLY:O	1:A:148:GLN:CB	2.46	0.63
1:A:86:VAL:O	1:A:88:ASP:N	2.32	0.62
1:A:77:GLU:C	1:A:79:SER:H	2.08	0.62
1:A:48:PRO:O	1:A:49:SER:HB3	1.99	0.62
1:A:110:GLN:NE2	1:A:178:ALA:CB	2.63	0.62
1:A:46:LYS:O	1:A:47:GLY:O	2.17	0.61
1:A:29:LYS:HE2	1:A:85:GLU:HB2	1.82	0.61
1:A:114:LEU:HD23	1:A:115:THR:N	2.16	0.61
1:A:40:GLN:O	1:A:43:PHE:CD1	2.51	0.60
1:A:131:ARG:HH12	1:A:137:ASN:HB2	1.66	0.60
1:A:76:ILE:HD13	1:A:119:GLU:HG2	1.83	0.60
1:A:76:ILE:HG23	1:A:97:VAL:O	2.02	0.59
1:A:100:LEU:HD21	1:A:172:ILE:HD11	1.84	0.59
1:A:14:LEU:CD2	1:A:93:VAL:HG13	2.32	0.59
1:A:58:ARG:O	1:A:62:TRP:NE1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:LEU:HB3	1:A:146:VAL:HG23	1.83	0.59
1:A:139:GLN:NE2	1:A:140:GLY:H	1.93	0.57
1:A:114:LEU:HD12	1:A:149:LEU:HD21	1.86	0.57
1:A:4:VAL:CG1	1:A:95:LEU:HD23	2.29	0.57
1:A:4:VAL:HG12	1:A:95:LEU:CD2	2.28	0.57
1:A:160:THR:HG23	1:A:167:LYS:HD2	1.86	0.57
1:A:26:PHE:HA	1:A:85:GLU:O	2.05	0.56
1:A:14:LEU:CD2	1:A:93:VAL:CG1	2.83	0.56
1:A:75:LYS:C	1:A:97:VAL:HG11	2.30	0.56
1:A:27:HIS:HE1	1:A:35:LYS:HD3	1.70	0.56
1:A:28:TRP:HB2	1:A:37:LEU:HD12	1.88	0.56
1:A:104:SER:O	1:A:105:ASP:HB2	2.05	0.55
1:A:76:ILE:HA	1:A:97:VAL:HG12	1.88	0.55
1:A:100:LEU:HD23	1:A:100:LEU:C	2.32	0.55
1:A:50:LYS:H	1:A:50:LYS:CD	2.16	0.55
1:A:29:LYS:HG3	1:A:83:ILE:HB	1.88	0.55
1:A:137:ASN:CG	1:A:138:ILE:N	2.66	0.54
1:A:73:ASN:O	1:A:73:ASN:ND2	2.38	0.54
1:A:156:THR:HA	1:A:173:ASP:HA	1.90	0.54
1:A:107:HIS:HA	1:A:175:VAL:HG12	1.88	0.54
1:A:164:ASN:C	1:A:166:LYS:N	2.63	0.54
1:A:114:LEU:O	1:A:145:SER:HA	2.07	0.53
1:A:131:ARG:HA	1:A:136:LYS:O	2.08	0.53
1:A:14:LEU:HD22	1:A:93:VAL:HG13	1.89	0.53
1:A:57:SER:HB3	1:A:62:TRP:HZ2	1.73	0.53
1:A:120:SER:HB2	1:A:121:PRO:HD2	1.90	0.53
1:A:20:GLN:OE1	1:A:24:ILE:HD12	2.09	0.53
1:A:76:ILE:CD1	1:A:119:GLU:HG2	2.39	0.52
1:A:114:LEU:HB3	1:A:146:VAL:CG2	2.40	0.52
1:A:160:THR:CG2	1:A:167:LYS:HD2	2.40	0.52
1:A:124:SER:O	1:A:126:PRO:HD3	2.08	0.51
1:A:125:SER:N	1:A:126:PRO:HD3	2.24	0.51
1:A:108:LEU:HD12	1:A:149:LEU:HD11	1.93	0.51
1:A:129:GLN:CD	1:A:160:THR:HB	2.35	0.51
1:A:28:TRP:HA	1:A:83:ILE:O	2.11	0.51
1:A:101:THR:O	1:A:116:LEU:HA	2.10	0.51
1:A:114:LEU:HD21	1:A:116:LEU:CD2	2.41	0.50
1:A:77:GLU:O	1:A:79:SER:N	2.44	0.50
1:A:129:GLN:OE1	1:A:160:THR:CB	2.54	0.50
1:A:132:SER:HB2	1:A:133:PRO:CD	2.42	0.50
1:A:51:LEU:O	1:A:54:ARG:N	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:PRO:HD2	1:A:153:ASP:HB2	1.94	0.49
1:A:137:ASN:CG	1:A:138:ILE:H	2.21	0.49
1:A:102:ALA:C	1:A:104:SER:N	2.70	0.49
1:A:110:GLN:HE21	1:A:178:ALA:CB	2.19	0.49
1:A:5:LEU:HB3	1:A:168:VAL:HG23	1.95	0.48
1:A:102:ALA:O	1:A:104:SER:N	2.47	0.47
1:A:142:LYS:O	1:A:142:LYS:HE3	2.15	0.47
1:A:112:GLN:O	1:A:148:GLN:HA	2.15	0.47
1:A:150:GLU:O	1:A:152:GLN:N	2.47	0.47
1:A:137:ASN:O	1:A:138:ILE:HG13	2.15	0.47
1:A:156:THR:OG1	1:A:173:ASP:CG	2.58	0.47
1:A:14:LEU:CD2	1:A:93:VAL:HG22	2.42	0.47
1:A:77:GLU:C	1:A:79:SER:N	2.72	0.47
1:A:131:ARG:NH1	1:A:137:ASN:HB2	2.29	0.47
1:A:114:LEU:HD21	1:A:116:LEU:HD23	1.97	0.47
1:A:75:LYS:O	1:A:97:VAL:HG11	2.15	0.46
1:A:23:SER:OG	1:A:63:ASP:HA	2.16	0.46
1:A:118:LEU:HD13	1:A:118:LEU:C	2.40	0.46
1:A:96:LEU:CD1	1:A:121:PRO:HG3	2.20	0.46
1:A:158:THR:HG23	1:A:169:GLU:HG3	1.97	0.46
1:A:132:SER:HB2	1:A:133:PRO:HD2	1.98	0.46
1:A:22:LYS:HD3	1:A:22:LYS:HA	1.23	0.45
1:A:30:ASN:O	1:A:33:GLN:N	2.49	0.45
1:A:114:LEU:HD12	1:A:149:LEU:CD2	2.47	0.45
1:A:76:ILE:H	1:A:76:ILE:HG13	1.62	0.45
1:A:38:GLY:O	1:A:44:LEU:HD12	2.16	0.45
1:A:3:VAL:HG12	1:A:4:VAL:N	2.32	0.45
1:A:114:LEU:HD13	1:A:146:VAL:HG21	1.98	0.44
1:A:114:LEU:HD13	1:A:146:VAL:CG2	2.47	0.44
1:A:74:LEU:HD13	1:A:97:VAL:HG22	2.00	0.44
1:A:27:HIS:O	1:A:85:GLU:N	2.38	0.44
1:A:48:PRO:O	1:A:49:SER:CB	2.60	0.44
1:A:46:LYS:NZ	1:A:55:ALA:O	2.50	0.44
1:A:31:SER:C	1:A:33:GLN:N	2.64	0.44
1:A:76:ILE:HA	1:A:97:VAL:HB	2.00	0.43
1:A:86:VAL:HG12	1:A:89:GLN:OE1	2.18	0.43
1:A:35:LYS:C	1:A:36:ILE:HD12	2.44	0.43
1:A:58:ARG:NH1	1:A:70:ILE:HD11	2.34	0.43
1:A:114:LEU:CD2	1:A:115:THR:N	2.82	0.43
1:A:99:GLY:O	1:A:118:LEU:HD22	2.19	0.43
1:A:80:ASP:OD1	1:A:81:THR:N	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:THR:HA	1:A:94:GLN:HG3	2.00	0.42
1:A:108:LEU:CD1	1:A:149:LEU:HD11	2.49	0.42
1:A:156:THR:OG1	1:A:173:ASP:OD2	2.37	0.42
1:A:51:LEU:HD22	1:A:71:ILE:HG23	2.02	0.42
1:A:46:LYS:C	1:A:47:GLY:O	2.62	0.41
1:A:65:GLY:HA2	1:A:67:PHE:CZ	2.54	0.41
1:A:75:LYS:O	1:A:76:ILE:C	2.63	0.41
1:A:81:THR:OG1	1:A:94:GLN:HG3	2.21	0.41
1:A:5:LEU:HB3	1:A:168:VAL:CG2	2.50	0.41
1:A:28:TRP:CZ2	1:A:84:CYS:HB2	2.56	0.41
1:A:81:THR:OG1	1:A:94:GLN:CG	2.69	0.41
1:A:114:LEU:CD2	1:A:114:LEU:C	2.94	0.41
1:A:46:LYS:CB	1:A:52:ASN:OD1	2.68	0.41
1:A:29:LYS:H	1:A:29:LYS:HG2	1.70	0.40
1:A:31:SER:O	1:A:33:GLN:N	2.51	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	177/179 (99%)	140 (79%)	23 (13%)	14 (8%)	 

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	GLY
1	A	87	GLU
1	A	103	ASN
1	A	151	LEU
1	A	1	LYS
1	A	32	ASN

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Mol	Chain	Res	Type
1	A	33	GLN
1	A	78	ASP
1	A	105	ASP
1	A	135	GLY
1	A	138	ILE
1	A	165	GLN
1	A	60	SER
1	A	48	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	162/162 (100%)	109 (67%)	53 (33%)	0 1

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	12	VAL
1	A	15	THR
1	A	20	GLN
1	A	22	LYS
1	A	24	ILE
1	A	27	HIS
1	A	34	ILE
1	A	36	ILE
1	A	37	LEU
1	A	43	PHE
1	A	45	THR
1	A	50	LYS
1	A	56	ASP
1	A	57	SER
1	A	58	ARG
1	A	60	SER
1	A	72	LYS

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Mol	Chain	Res	Type
1	A	76	ILE
1	A	77	GLU
1	A	81	THR
1	A	87	GLU
1	A	89	GLN
1	A	94	GLN
1	A	95	LEU
1	A	96	LEU
1	A	101	THR
1	A	104	SER
1	A	106	THR
1	A	112	GLN
1	A	113	SER
1	A	114	LEU
1	A	117	THR
1	A	119	GLU
1	A	125	SER
1	A	136	LYS
1	A	139	GLN
1	A	142	LYS
1	A	146	VAL
1	A	148	GLN
1	A	149	LEU
1	A	152	GLN
1	A	162	LEU
1	A	163	GLN
1	A	164	ASN
1	A	166	LYS
1	A	167	LYS
1	A	169	GLU
1	A	170	PHE
1	A	172	ILE
1	A	175	VAL
1	A	176	VAL
1	A	177	LEU

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

Mol	Chain	Res	Type
1	A	103	ASN
1	A	110	GLN
1	A	139	GLN

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Mol	Chain	Res	Type
1	A	152	GLN

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.