Full wwPDB X-ray Structure Validation Report

Jan 31, 2016 – 06:45 PM GMT

PDB ID	:	1CDH
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	:	2.30 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

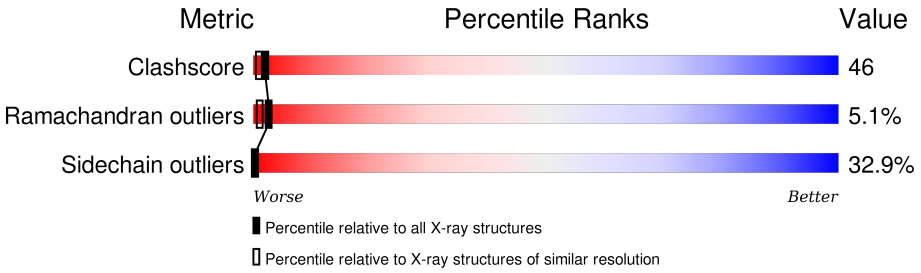
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.30 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	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	178	29% 40% 25% 6%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1469 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	178	Total	C	N	O	S	0	0	0
			1383	865	242	272	4			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	86	Total	O	0	0
			86	86		

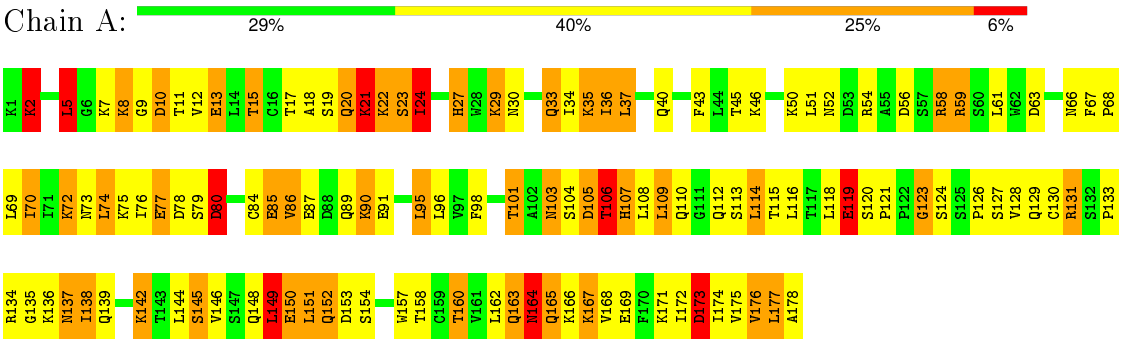
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

- Molecule 1: T CELL SURFACE GLYCOPROTEIN CD4

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	83.71Å 30.01Å 87.54Å 90.00° 117.28° 90.00°	Depositor
Resolution (Å)	10.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ, X-PLOR	Depositor
R, R_{free}	0.193 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1469	wwPDB-VP
Average B, all atoms (Å^2)	29.0	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	A	0.99	0/1402	2.01	38/1891 (2.0%)

There are no bond length outliers.

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	131	ARG	CD-NE-CZ	16.09	146.13	123.60
1	A	54	ARG	NE-CZ-NH1	-13.85	113.37	120.30
1	A	43	PHE	CA-CB-CG	10.05	138.01	113.90
1	A	54	ARG	NE-CZ-NH2	9.97	125.28	120.30
1	A	58	ARG	CD-NE-CZ	8.86	136.00	123.60
1	A	59	ARG	NE-CZ-NH1	-8.68	115.96	120.30
1	A	87	GLU	OE1-CD-OE2	8.66	133.69	123.30
1	A	131	ARG	NE-CZ-NH2	8.53	124.56	120.30
1	A	78	ASP	CB-CG-OD1	7.40	124.96	118.30
1	A	13	GLU	OE1-CD-OE2	7.34	132.11	123.30
1	A	2	LYS	CA-CB-CG	7.12	129.06	113.40
1	A	173	ASP	CB-CG-OD2	-7.09	111.92	118.30
1	A	8	LYS	C-N-CA	6.99	136.97	122.30
1	A	37	LEU	CA-CB-CG	6.93	131.24	115.30
1	A	5	LEU	CA-CB-CG	6.87	131.10	115.30
1	A	58	ARG	NE-CZ-NH2	6.83	123.71	120.30
1	A	106	THR	CB-CA-C	6.48	129.09	111.60
1	A	29	LYS	CA-CB-CG	6.47	127.64	113.40
1	A	56	ASP	CB-CG-OD1	6.45	124.10	118.30
1	A	74	LEU	CA-CB-CG	6.06	129.24	115.30
1	A	173	ASP	O-C-N	5.89	132.13	122.70
1	A	56	ASP	CB-CG-OD2	-5.74	113.14	118.30
1	A	77	GLU	CG-CD-OE1	-5.68	106.93	118.30
1	A	105	ASP	N-CA-C	-5.62	95.82	111.00
1	A	37	LEU	CB-CA-C	5.62	120.88	110.20
1	A	80	ASP	N-CA-CB	-5.62	100.49	110.60
1	A	105	ASP	N-CA-CB	5.47	120.45	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	86	VAL	CA-CB-CG2	5.45	119.07	110.90
1	A	17	THR	CA-CB-CG2	5.42	119.98	112.40
1	A	105	ASP	CB-CG-OD1	5.39	123.15	118.30
1	A	21	LYS	N-CA-CB	5.38	120.28	110.60
1	A	59	ARG	NE-CZ-NH2	5.24	122.92	120.30
1	A	87	GLU	CG-CD-OE2	-5.18	107.94	118.30
1	A	36	ILE	O-C-N	5.10	130.85	122.70
1	A	128	VAL	CB-CA-C	5.08	121.05	111.40
1	A	149	LEU	CA-CB-CG	5.03	126.87	115.30
1	A	119	GLU	CG-CD-OE2	-5.03	108.25	118.30
1	A	24	ILE	CA-C-N	5.01	128.23	117.20

There are no chirality outliers.

There are no planarity outliers.

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	1383	0	1414	128	0
2	A	86	0	0	8	0
All	All	1469	0	1414	128	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 46.

All (128) 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:131:ARG:HH11	1:A:137:ASN:HB3	1.07	1.11
1:A:20:GLN:HE22	1:A:86:VAL:HG12	0.93	1.08
1:A:20:GLN:NE2	1:A:86:VAL:HG12	1.69	1.06
1:A:103:ASN:HD21	1:A:115:THR:HB	1.17	1.05
1:A:136:LYS:HD2	1:A:137:ASN:H	1.26	0.99
1:A:30:ASN:HD21	1:A:34:ILE:HD12	1.29	0.95
1:A:20:GLN:HE22	1:A:86:VAL:CG1	1.79	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:GLN:HE21	1:A:45:THR:HG21	1.33	0.92
1:A:106:THR:HG22	1:A:174:ILE:HD13	1.50	0.91
1:A:131:ARG:NH1	1:A:137:ASN:HB3	1.87	0.89
1:A:79:SER:O	1:A:80:ASP:HB2	1.73	0.88
1:A:10:ASP:O	1:A:74:LEU:HB2	1.76	0.84
1:A:104:SER:HB2	1:A:108:LEU:HD21	1.60	0.83
1:A:22:LYS:HB3	1:A:63:ASP:O	1.80	0.82
1:A:114:LEU:HD12	1:A:149:LEU:HD21	1.59	0.82
1:A:106:THR:O	1:A:175:VAL:N	2.13	0.82
1:A:106:THR:HG22	1:A:174:ILE:CD1	2.11	0.80
1:A:30:ASN:HD21	1:A:34:ILE:CD1	1.94	0.80
1:A:133:PRO:HG2	1:A:154:SER:O	1.81	0.80
1:A:114:LEU:HD23	1:A:116:LEU:HD21	1.64	0.79
1:A:20:GLN:HG2	2:A:183:HOH:O	1.83	0.79
1:A:136:LYS:HD2	1:A:137:ASN:N	1.97	0.78
1:A:101:THR:O	1:A:116:LEU:HA	1.82	0.78
1:A:5:LEU:HD22	1:A:166:LYS:HB3	1.66	0.77
1:A:20:GLN:NE2	1:A:86:VAL:CG1	2.43	0.77
1:A:131:ARG:HH11	1:A:137:ASN:CB	1.94	0.77
1:A:118:LEU:HD21	1:A:126:PRO:HG2	1.65	0.77
1:A:23:SER:OG	1:A:23:SER:O	1.97	0.76
1:A:114:LEU:CD2	1:A:116:LEU:HD21	2.14	0.76
1:A:30:ASN:ND2	1:A:34:ILE:HD12	1.99	0.76
1:A:103:ASN:ND2	1:A:115:THR:HB	1.98	0.75
1:A:138:ILE:HD13	1:A:146:VAL:HG22	1.69	0.73
1:A:40:GLN:NE2	1:A:45:THR:HG21	2.04	0.71
1:A:114:LEU:O	1:A:145:SER:HA	1.91	0.71
1:A:163:GLN:O	1:A:165:GLN:N	2.24	0.71
1:A:109:LEU:HD12	1:A:177:LEU:HB3	1.72	0.70
1:A:104:SER:CB	1:A:108:LEU:HD21	2.21	0.69
1:A:67:PHE:CE1	1:A:86:VAL:HG11	2.30	0.67
1:A:163:GLN:O	1:A:164:ASN:C	2.32	0.66
1:A:20:GLN:OE1	1:A:24:ILE:HG13	1.96	0.66
1:A:160:THR:HG23	1:A:169:GLU:HG3	1.78	0.65
1:A:106:THR:HB	1:A:173:ASP:O	1.98	0.64
1:A:134:ARG:HG3	1:A:152:GLN:HB3	1.78	0.63
1:A:107:HIS:HA	1:A:175:VAL:O	1.99	0.62
1:A:84:CYS:O	1:A:90:LYS:HA	2.01	0.61
1:A:119:GLU:HG2	2:A:197:HOH:O	2.00	0.60
1:A:79:SER:HA	1:A:95:LEU:O	2.01	0.60
1:A:152:GLN:O	1:A:153:ASP:OD1	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:VAL:HG12	1:A:176:VAL:O	2.02	0.59
1:A:120:SER:HB2	1:A:121:PRO:HD2	1.85	0.58
1:A:58:ARG:HD2	1:A:61:LEU:HD12	1.85	0.57
1:A:33:GLN:N	1:A:33:GLN:HE21	2.00	0.57
1:A:114:LEU:HD23	1:A:116:LEU:CD2	2.33	0.57
1:A:8:LYS:HD3	1:A:9:GLY:N	2.20	0.57
1:A:167:LYS:O	1:A:167:LYS:HG3	2.03	0.56
1:A:40:GLN:NE2	1:A:45:THR:CG2	2.70	0.55
1:A:108:LEU:HD13	1:A:114:LEU:HD12	1.89	0.55
1:A:20:GLN:HB3	2:A:247:HOH:O	2.07	0.54
1:A:107:HIS:HA	1:A:175:VAL:HB	1.89	0.54
1:A:27:HIS:CE1	1:A:85:GLU:HB2	2.43	0.54
1:A:116:LEU:N	1:A:116:LEU:HD23	2.22	0.54
1:A:107:HIS:ND1	1:A:107:HIS:N	2.56	0.54
1:A:164:ASN:O	1:A:166:LYS:N	2.31	0.53
1:A:115:THR:C	1:A:116:LEU:HD23	2.30	0.52
1:A:59:ARG:HB2	1:A:59:ARG:HH11	1.75	0.51
1:A:163:GLN:CG	1:A:164:ASN:H	2.24	0.51
1:A:7:LYS:HG2	1:A:168:VAL:HG11	1.93	0.50
1:A:59:ARG:O	1:A:59:ARG:CG	2.60	0.50
1:A:151:LEU:HD21	1:A:178:ALA:HB2	1.92	0.50
1:A:8:LYS:C	1:A:8:LYS:CD	2.80	0.50
1:A:58:ARG:HG3	2:A:185:HOH:O	2.11	0.50
1:A:130:CYS:HA	1:A:158:THR:O	2.12	0.49
1:A:144:LEU:O	1:A:145:SER:HB2	2.12	0.49
1:A:157:TRP:CD1	1:A:174:ILE:HG12	2.48	0.48
1:A:164:ASN:C	1:A:166:LYS:H	2.12	0.48
1:A:109:LEU:CD1	1:A:177:LEU:HB3	2.42	0.48
1:A:85:GLU:HG3	1:A:90:LYS:HB2	1.96	0.48
1:A:124:SER:HB2	1:A:163:GLN:HE22	1.79	0.48
1:A:70:ILE:HG21	1:A:72:LYS:HZ3	1.78	0.48
1:A:112:GLN:O	1:A:149:LEU:HD22	2.14	0.47
1:A:5:LEU:HB3	1:A:168:VAL:HG22	1.96	0.47
1:A:133:PRO:CG	1:A:154:SER:O	2.56	0.47
1:A:15:THR:CG2	2:A:258:HOH:O	2.61	0.47
1:A:23:SER:C	1:A:24:ILE:HG12	2.34	0.47
1:A:130:CYS:SG	1:A:144:LEU:CD2	3.03	0.47
1:A:121:PRO:O	1:A:123:GLY:N	2.48	0.47
1:A:127:SER:O	1:A:162:LEU:HD12	2.15	0.47
1:A:103:ASN:HD21	1:A:115:THR:CB	2.07	0.46
1:A:108:LEU:C	1:A:109:LEU:HD13	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:SER:CB	1:A:163:GLN:HE22	2.28	0.46
1:A:36:ILE:HD13	1:A:51:LEU:HD13	1.98	0.46
1:A:149:LEU:HB3	1:A:176:VAL:HG21	1.98	0.45
1:A:22:LYS:O	1:A:23:SER:HB3	2.16	0.45
1:A:151:LEU:HA	1:A:176:VAL:CG1	2.45	0.45
1:A:12:VAL:HG23	2:A:245:HOH:O	2.17	0.45
1:A:8:LYS:C	1:A:8:LYS:HD2	2.37	0.45
1:A:150:GLU:O	1:A:176:VAL:HG11	2.18	0.44
1:A:30:ASN:C	1:A:30:ASN:OD1	2.55	0.44
1:A:70:ILE:CG2	1:A:72:LYS:HZ3	2.31	0.44
1:A:11:THR:HG23	1:A:72:LYS:HA	1.99	0.44
1:A:157:TRP:O	1:A:171:LYS:HA	2.17	0.44
1:A:59:ARG:HH11	1:A:59:ARG:CB	2.30	0.44
1:A:101:THR:O	1:A:116:LEU:CA	2.60	0.43
1:A:136:LYS:HA	1:A:136:LYS:HD3	1.77	0.43
1:A:104:SER:HA	2:A:262:HOH:O	2.18	0.43
1:A:98:PHE:HZ	1:A:163:GLN:OE1	2.01	0.43
1:A:22:LYS:HE3	1:A:63:ASP:O	2.19	0.43
1:A:2:LYS:HZ1	1:A:15:THR:HB	1.83	0.42
1:A:108:LEU:HD23	1:A:112:GLN:OE1	2.19	0.42
1:A:2:LYS:NZ	1:A:15:THR:HG22	2.34	0.42
1:A:18:ALA:HB2	1:A:86:VAL:HG21	2.02	0.42
1:A:104:SER:C	1:A:105:ASP:O	2.57	0.42
1:A:7:LYS:O	1:A:8:LYS:C	2.58	0.42
1:A:163:GLN:HG2	1:A:164:ASN:OD1	2.20	0.42
1:A:35:LYS:HB2	2:A:182:HOH:O	2.20	0.42
1:A:134:ARG:CG	1:A:152:GLN:HB3	2.49	0.42
1:A:138:ILE:CD1	1:A:146:VAL:HG22	2.43	0.41
1:A:59:ARG:NH1	1:A:59:ARG:CB	2.84	0.41
1:A:68:PRO:HB2	1:A:70:ILE:CD1	2.50	0.41
1:A:75:LYS:HB3	1:A:77:GLU:OE2	2.21	0.41
1:A:164:ASN:C	1:A:166:LYS:N	2.73	0.41
1:A:13:GLU:HG3	1:A:70:ILE:HD12	2.03	0.41
1:A:46:LYS:HE3	1:A:52:ASN:O	2.20	0.41
1:A:27:HIS:HD1	1:A:27:HIS:C	2.22	0.41
1:A:85:GLU:HG3	1:A:90:LYS:CB	2.51	0.41
1:A:21:LYS:O	1:A:22:LYS:C	2.60	0.40
1:A:29:LYS:HA	1:A:34:ILE:O	2.22	0.40
1:A:7:LYS:O	1:A:10:ASP:HB2	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	A	176/178 (99%)	149 (85%)	18 (10%)	9 (5%)	2 1

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	165	GLN
1	A	22	LYS
1	A	80	ASP
1	A	142	LYS
1	A	164	ASN
1	A	21	LYS
1	A	145	SER
1	A	135	GLY
1	A	123	GLY

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	161/161 (100%)	108 (67%)	53 (33%)	0 0

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

Mol	Chain	Res	Type
1	A	2	LYS
1	A	5	LEU

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Mol	Chain	Res	Type
1	A	10	ASP
1	A	15	THR
1	A	19	SER
1	A	20	GLN
1	A	21	LYS
1	A	23	SER
1	A	24	ILE
1	A	27	HIS
1	A	33	GLN
1	A	35	LYS
1	A	37	LEU
1	A	50	LYS
1	A	66	ASN
1	A	69	LEU
1	A	70	ILE
1	A	72	LYS
1	A	73	ASN
1	A	76	ILE
1	A	85	GLU
1	A	89	GLN
1	A	90	LYS
1	A	91	GLU
1	A	95	LEU
1	A	96	LEU
1	A	101	THR
1	A	103	ASN
1	A	106	THR
1	A	107	HIS
1	A	109	LEU
1	A	110	GLN
1	A	113	SER
1	A	114	LEU
1	A	119	GLU
1	A	129	GLN
1	A	137	ASN
1	A	138	ILE
1	A	139	GLN
1	A	142	LYS
1	A	148	GLN
1	A	149	LEU
1	A	150	GLU
1	A	151	LEU

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Mol	Chain	Res	Type
1	A	152	GLN
1	A	160	THR
1	A	163	GLN
1	A	164	ASN
1	A	167	LYS
1	A	172	ILE
1	A	173	ASP
1	A	176	VAL
1	A	177	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	33	GLN
1	A	40	GLN
1	A	73	ASN
1	A	103	ASN
1	A	129	GLN
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 carbohydrates in this entry.

5.6 Ligand geometry (i)

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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.