



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:48 PM UTC

PDB ID : 1NBY / pdb_00001nby
Title : Crystal Structure of HyHEL-63 complexed with HEL mutant K96A
Authors : Mariuzza, R.A.; Li, Y.; Urrutia, M.; Smith-Gill, S.J.
Deposited on : 2002-12-04
Resolution : 1.80 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

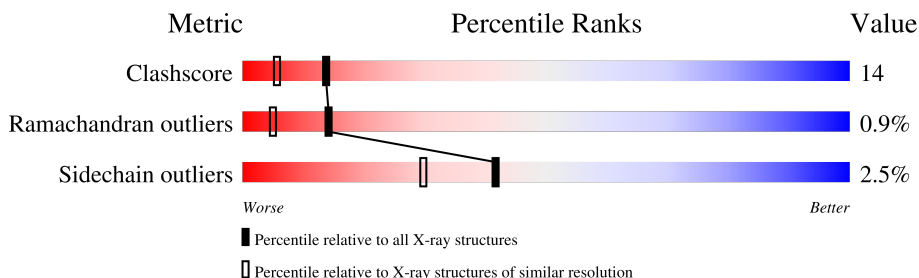
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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	214	 83% 14% .
2	B	210	 78% 18% .
3	C	129	 73% 26% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4911 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 antibody kappa light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1657	1027	280	343	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ASP	GLU	cloning artifact	UNP P01837
A	2	ILE	LEU	cloning artifact	UNP P01837
A	4	LEU	MET	cloning artifact	UNP P01837

- Molecule 2 is a protein called immunoglobulin gamma 1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	210	Total	C	N	O	S	0	0	0
			1587	1002	253	326	6			

- Molecule 3 is a protein called Lysozyme C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	129	Total	C	N	O	S	0	0	0
			997	610	192	185	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	696	ALA	LYS	engineered mutation	UNP P00698

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	279	Total	O	0	0
			279	279		

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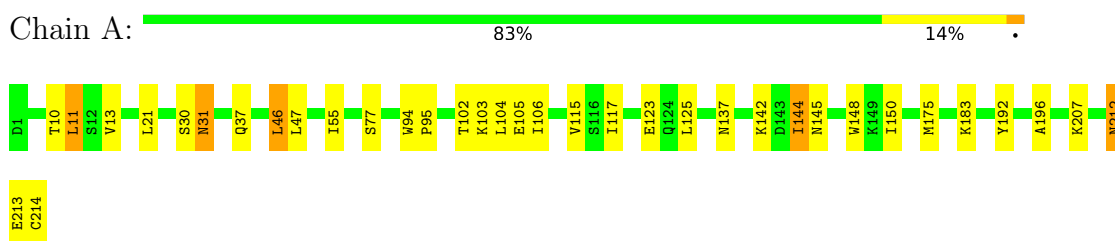
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	281	Total 281	O 281	0	0
4	C	110	Total 110	O 110	0	0

3 Residue-property plots

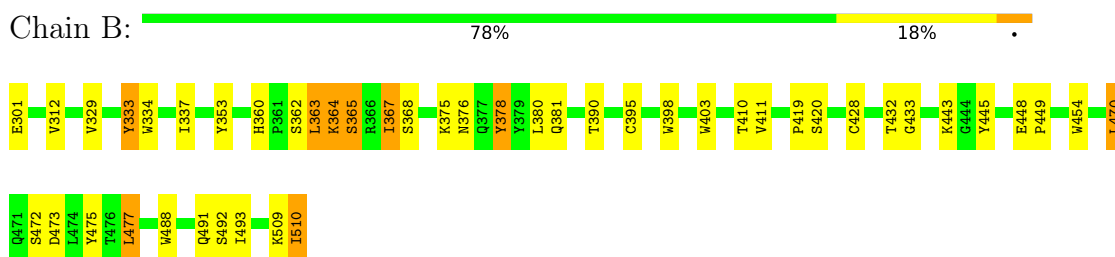
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

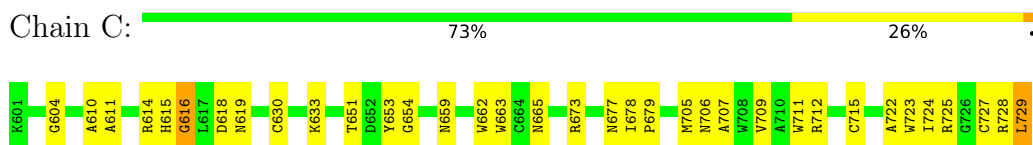
- Molecule 1: antibody kappa light chain



- Molecule 2: immunoglobulin gamma 1 chain



- Molecule 3: Lysozyme C



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 4 ₂ 21 2	Depositor
Cell constants a, b, c, α , β , γ	90.87 Å 90.87 Å 151.94 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 1.80	Depositor
% Data completeness (in resolution range)	97.0 (19.89-1.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.216 , 0.250	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4911	wwPDB-VP
Average B, all atoms (Å ²)	21.0	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	0.45	0/1695	0.94	2/2300 (0.1%)
2	B	0.48	0/1629	0.95	7/2233 (0.3%)
3	C	0.41	0/1017	0.98	5/1375 (0.4%)
All	All	0.45	0/4341	0.96	14/5908 (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
2	B	0	1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	663	TRP	N-CA-C	8.56	124.12	112.90
3	C	604	GLY	N-CA-C	-7.92	100.43	113.02
2	B	420	SER	N-CA-C	-7.17	98.01	109.76
3	C	616	GLY	N-CA-C	6.12	124.51	115.08
1	A	137	ASN	N-CA-C	6.03	119.54	109.95
2	B	367	ILE	N-CA-C	5.84	117.76	108.89
3	C	654	GLY	N-CA-C	5.75	123.37	112.62
2	B	448	GLU	N-CA-C	-5.62	102.11	110.20
2	B	395	CYS	N-CA-C	-5.59	101.06	109.95
1	A	142	LYS	N-CA-C	5.46	118.15	111.82
3	C	659	ASN	N-CA-C	5.44	118.33	110.28
2	B	333	TYR	N-CA-C	-5.37	100.95	109.76
2	B	443	LYS	N-CA-C	5.10	117.76	109.24
2	B	353	TYR	N-CA-C	5.03	117.41	111.33

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	378	TYR	Sidechain

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	1657	0	1575	38	0
2	B	1587	0	1536	49	0
3	C	997	0	954	31	0
4	A	279	0	0	4	0
4	B	281	0	0	1	0
4	C	110	0	0	5	0
All	All	4911	0	4065	113	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 14.

All (113) 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:B:488:TRP:HD1	2:B:493:ILE:HD13	1.24	1.01
2:B:367:ILE:HD11	2:B:380:LEU:HD12	1.44	0.97
2:B:329:VAL:H	2:B:376:ASN:HD21	1.12	0.92
2:B:493:ILE:O	2:B:510:ILE:HD13	1.74	0.88
2:B:367:ILE:HD11	2:B:380:LEU:CD1	2.05	0.87
2:B:329:VAL:H	2:B:376:ASN:ND2	1.75	0.84
1:A:144:ILE:HD13	1:A:145:ASN:N	1.92	0.83
2:B:488:TRP:CD1	2:B:493:ILE:HD13	2.13	0.81
2:B:329:VAL:N	2:B:376:ASN:HD21	1.79	0.80
1:A:30:SER:OG	3:C:616:GLY:HA2	1.86	0.76
2:B:367:ILE:HD12	2:B:381:GLN:O	1.87	0.74
2:B:492:SER:C	2:B:493:ILE:HD12	2.13	0.73
2:B:367:ILE:CD1	2:B:380:LEU:CD1	2.66	0.73
1:A:212:ASN:HD22	1:A:212:ASN:C	1.95	0.73
2:B:334:TRP:HB3	2:B:378:TYR:CZ	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:360:HIS:HD2	2:B:362:SER:H	1.37	0.71
2:B:367:ILE:CD1	2:B:380:LEU:HD12	2.19	0.71
3:C:677:ASN:HB3	4:C:779:HOH:O	1.93	0.69
2:B:364:LYS:O	2:B:365:SER:HB2	1.92	0.67
1:A:150:ILE:HD12	1:A:192:TYR:CD2	2.29	0.67
3:C:709:VAL:HG22	4:C:764:HOH:O	1.94	0.66
1:A:11:LEU:HD13	1:A:11:LEU:O	1.96	0.66
1:A:214:CYS:HB2	2:B:428:CYS:SG	2.36	0.65
3:C:662:TRP:CZ3	3:C:673:ARG:NH2	2.65	0.64
1:A:46:LEU:HD13	1:A:55:ILE:HD13	1.80	0.63
2:B:493:ILE:O	2:B:510:ILE:CD1	2.46	0.63
1:A:103:LYS:HG2	1:A:105:GLU:HG3	1.80	0.63
3:C:727:CYS:HB2	3:C:729:LEU:HD22	1.81	0.63
3:C:615:HIS:HD2	4:C:823:HOH:O	1.82	0.62
2:B:367:ILE:HD12	2:B:368:SER:H	1.64	0.62
2:B:492:SER:HB2	2:B:509:LYS:HE2	1.80	0.62
2:B:510:ILE:N	2:B:510:ILE:HD12	2.16	0.61
2:B:367:ILE:HD13	2:B:380:LEU:HD11	1.83	0.60
3:C:729:LEU:H	3:C:729:LEU:HD23	1.66	0.60
2:B:419:PRO:HB3	2:B:445:TYR:HB3	1.84	0.59
1:A:144:ILE:HD13	1:A:145:ASN:H	1.64	0.59
1:A:214:CYS:SG	2:B:428:CYS:SG	3.01	0.59
1:A:11:LEU:HD13	1:A:104:LEU:HA	1.85	0.59
1:A:46:LEU:HD13	1:A:55:ILE:CD1	2.33	0.59
1:A:212:ASN:C	1:A:212:ASN:ND2	2.60	0.58
1:A:37:GLN:HB2	1:A:47:LEU:HD11	1.86	0.58
2:B:367:ILE:CD1	2:B:380:LEU:HD11	2.32	0.58
2:B:493:ILE:C	2:B:510:ILE:HD13	2.29	0.57
3:C:722:ALA:HA	3:C:725:ARG:HH21	1.70	0.57
2:B:364:LYS:O	2:B:365:SER:CB	2.54	0.56
2:B:363:LEU:O	2:B:364:LYS:C	2.50	0.55
1:A:31:ASN:ND2	3:C:616:GLY:HA3	2.21	0.55
1:A:94:TRP:CD2	1:A:95:PRO:HA	2.42	0.54
2:B:470:LEU:HD13	2:B:475:TYR:CE1	2.43	0.53
1:A:212:ASN:HD22	1:A:213:GLU:N	2.07	0.53
3:C:728:ARG:HG3	3:C:728:ARG:HH11	1.74	0.53
1:A:117:ILE:HD11	1:A:148:TRP:CH2	2.43	0.53
3:C:662:TRP:HZ3	3:C:673:ARG:NH2	2.07	0.52
3:C:651:THR:HB	3:C:653:TYR:CE1	2.44	0.52
3:C:727:CYS:CB	3:C:729:LEU:HD22	2.40	0.52
2:B:375:LYS:HE3	4:B:759:HOH:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:THR:HG22	4:A:405:HOH:O	2.11	0.51
1:A:31:ASN:H	1:A:31:ASN:HD22	1.59	0.50
2:B:491:GLN:O	2:B:493:ILE:CD1	2.60	0.50
3:C:610:ALA:O	3:C:614:ARG:HG3	2.11	0.50
1:A:103:LYS:HG2	1:A:105:GLU:CG	2.41	0.50
2:B:301:GLU:HG2	2:B:301:GLU:O	2.13	0.49
3:C:633:LYS:HD3	3:C:633:LYS:C	2.37	0.49
1:A:115:VAL:O	1:A:207:LYS:HE3	2.13	0.49
1:A:11:LEU:CD1	1:A:104:LEU:HA	2.43	0.48
1:A:123:GLU:CD	4:A:471:HOH:O	2.55	0.48
1:A:11:LEU:HD11	1:A:104:LEU:HD13	1.96	0.48
2:B:333:TYR:HB2	2:B:398:TRP:CB	2.43	0.47
2:B:329:VAL:N	2:B:376:ASN:ND2	2.48	0.47
2:B:477:LEU:C	2:B:477:LEU:HD23	2.40	0.47
1:A:11:LEU:HD22	1:A:13:VAL:HG13	1.95	0.47
2:B:492:SER:O	2:B:493:ILE:HD12	2.14	0.47
3:C:665:ASN:HA	4:C:811:HOH:O	2.15	0.47
3:C:724:ILE:C	3:C:724:ILE:HD12	2.40	0.47
3:C:633:LYS:HG3	3:C:723:TRP:CZ3	2.50	0.47
3:C:729:LEU:HB2	4:C:817:HOH:O	2.15	0.46
3:C:630:CYS:HB2	3:C:723:TRP:CD1	2.50	0.46
2:B:454:TRP:HZ3	2:B:510:ILE:HD11	1.81	0.46
2:B:510:ILE:CD1	2:B:510:ILE:N	2.78	0.46
1:A:106:ILE:HD12	4:A:490:HOH:O	2.16	0.46
1:A:214:CYS:SG	1:A:214:CYS:OXT	2.74	0.46
1:A:150:ILE:HD12	1:A:192:TYR:CE2	2.51	0.46
2:B:334:TRP:HB3	2:B:378:TYR:CE1	2.51	0.46
1:A:10:THR:HG22	1:A:11:LEU:N	2.31	0.45
1:A:106:ILE:HD12	1:A:106:ILE:H	1.81	0.45
3:C:709:VAL:HG12	3:C:712:ARG:HH22	1.80	0.45
1:A:21:LEU:HD22	1:A:102:THR:HG21	1.99	0.45
1:A:214:CYS:CB	2:B:428:CYS:SG	3.04	0.45
2:B:312:VAL:O	2:B:411:VAL:HA	2.17	0.45
1:A:125:LEU:O	1:A:183:LYS:HD2	2.16	0.45
2:B:337:ILE:HD12	2:B:403:TRP:CH2	2.52	0.44
3:C:711:TRP:CD1	3:C:715:CYS:HB2	2.51	0.44
1:A:214:CYS:HB3	4:A:362:HOH:O	2.16	0.44
3:C:678:ILE:CD1	3:C:679:PRO:HD2	2.47	0.44
3:C:678:ILE:HD12	3:C:679:PRO:HD2	1.99	0.44
2:B:493:ILE:HG22	2:B:510:ILE:HD13	1.99	0.43
2:B:390:THR:HG23	2:B:410:THR:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:618:ASP:O	3:C:619:ASN:HB3	2.19	0.43
1:A:144:ILE:HD11	1:A:196:ALA:HB1	2.01	0.43
2:B:363:LEU:O	2:B:364:LYS:O	2.37	0.42
3:C:678:ILE:HG13	3:C:679:PRO:HD2	2.01	0.42
2:B:367:ILE:HD12	2:B:368:SER:N	2.31	0.42
3:C:633:LYS:HG3	3:C:723:TRP:CH2	2.54	0.42
1:A:106:ILE:HD12	1:A:106:ILE:N	2.34	0.41
3:C:728:ARG:HG3	3:C:728:ARG:NH1	2.35	0.41
3:C:611:ALA:HA	3:C:614:ARG:NH1	2.35	0.41
1:A:31:ASN:ND2	1:A:31:ASN:C	2.77	0.41
2:B:472:SER:O	2:B:473:ASP:HB2	2.21	0.41
3:C:705:MET:C	3:C:707:ALA:H	2.29	0.41
2:B:333:TYR:HB2	2:B:398:TRP:HB2	2.02	0.41
2:B:492:SER:CB	2:B:509:LYS:HE2	2.50	0.41
3:C:706:ASN:HB3	3:C:712:ARG:HD3	2.03	0.41
2:B:510:ILE:HD12	2:B:510:ILE:H	1.85	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	212/214 (99%)	205 (97%)	6 (3%)	1 (0%)	24	14
2	B	208/210 (99%)	200 (96%)	4 (2%)	4 (2%)	6	1
3	C	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
All	All	547/553 (99%)	527 (96%)	15 (3%)	5 (1%)	14	5

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	365	SER

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Mol	Chain	Res	Type
1	A	77	SER
2	B	364	LYS
2	B	433	GLY
2	B	432	THR

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	193/193 (100%)	187 (97%)	6 (3%)	35	23
2	B	186/186 (100%)	181 (97%)	5 (3%)	39	27
3	C	104/104 (100%)	103 (99%)	1 (1%)	68	64
All	All	483/483 (100%)	471 (98%)	12 (2%)	42	30

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	31	ASN
1	A	46	LEU
1	A	144	ILE
1	A	175	MET
1	A	212	ASN
2	B	363	LEU
2	B	449	PRO
2	B	470	LEU
2	B	477	LEU
2	B	510	ILE
3	C	729	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN

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Mol	Chain	Res	Type
1	A	53	GLN
1	A	137	ASN
1	A	156	GLN
1	A	189	HIS
1	A	212	ASN
2	B	343	ASN
2	B	360	HIS
2	B	376	ASN
2	B	377	GLN
2	B	471	GLN
3	C	615	HIS
3	C	641	GLN
3	C	657	GLN
3	C	693	ASN
3	C	713	ASN
3	C	721	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 ⓘ

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.