



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 15, 2026 – 10:20 AM UTC

PDB ID : 1PV2 / pdb_00001pv2
Title : Native Form 2 E.coli Chaperone Hsp31
Authors : Quigley, P.M.; Korotkov, K.; Baneyx, F.; Hol, W.G.J.
Deposited on : 2003-06-26
Resolution : 2.71 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

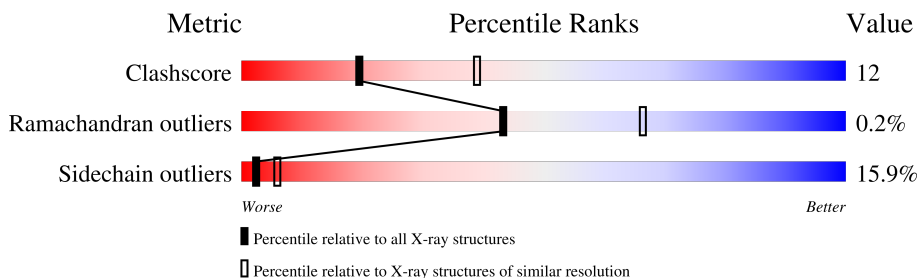
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)

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	A	283	47% 32% 5% • 15%
1	B	283	65% 20% 5% 9%
1	C	283	65% 19% • 12%
1	D	283	64% 27% • 7%
1	E	283	66% 25% • 5%
1	F	283	63% 27% • 8%
1	G	283	66% 23% • 8%
1	H	283	65% 27% 6% • •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16233 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 Chaperone protein hchA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	0	0
			1864	1203	309	344	8			
1	B	257	Total	C	N	O	S	0	0	0
			2008	1297	337	365	9			
1	C	249	Total	C	N	O	S	0	0	0
			1940	1252	323	356	9			
1	D	264	Total	C	N	O	S	0	0	0
			2048	1319	342	378	9			
1	E	270	Total	C	N	O	S	0	0	0
			2091	1341	352	389	9			
1	F	261	Total	C	N	O	S	0	0	0
			2031	1310	339	373	9			
1	G	260	Total	C	N	O	S	0	0	0
			2023	1305	338	371	9			
1	H	277	Total	C	N	O	S	0	0	0
			2156	1386	359	402	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P31658
B	1	MET	-	initiating methionine	UNP P31658
C	1	MET	-	initiating methionine	UNP P31658
D	1	MET	-	initiating methionine	UNP P31658
E	1	MET	-	initiating methionine	UNP P31658
F	1	MET	-	initiating methionine	UNP P31658
G	1	MET	-	initiating methionine	UNP P31658
H	1	MET	-	initiating methionine	UNP P31658

- Molecule 2 is water.

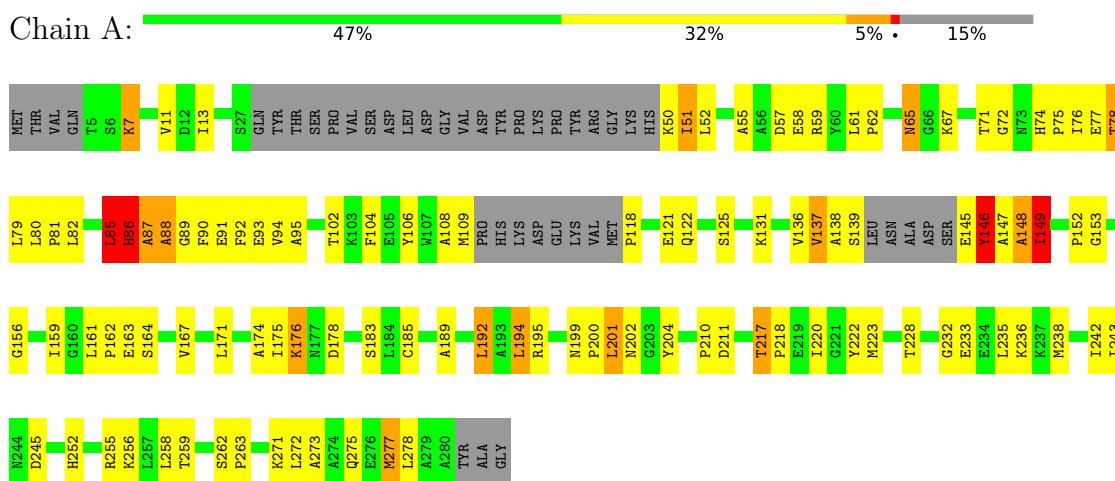
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total 7	O 7	0	0
2	B	7	Total 7	O 7	0	0
2	C	13	Total 13	O 13	0	0
2	D	7	Total 7	O 7	0	0
2	E	6	Total 6	O 6	0	0
2	F	8	Total 8	O 8	0	0
2	G	11	Total 11	O 11	0	0
2	H	13	Total 13	O 13	0	0

3 Residue-property plots

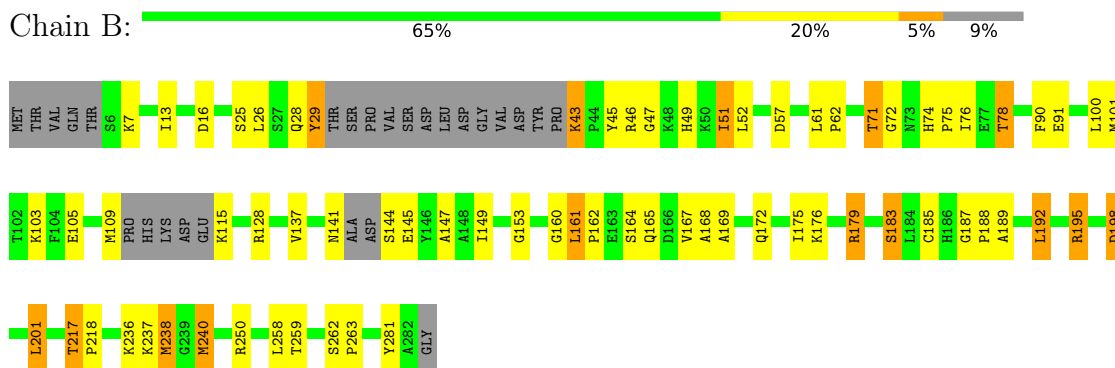
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

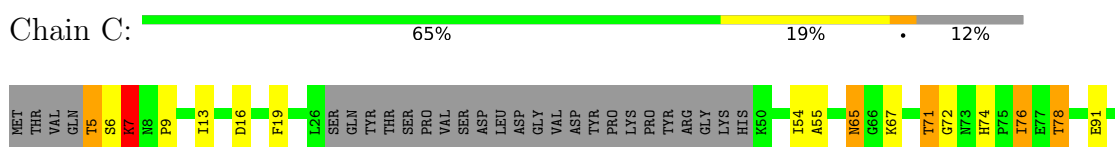
• Molecule 1: Chaperone protein hchA

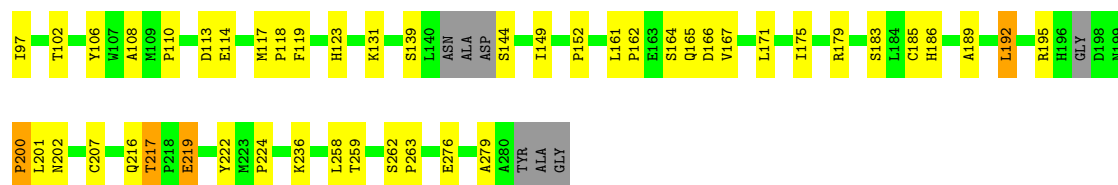


• Molecule 1: Chaperone protein hchA



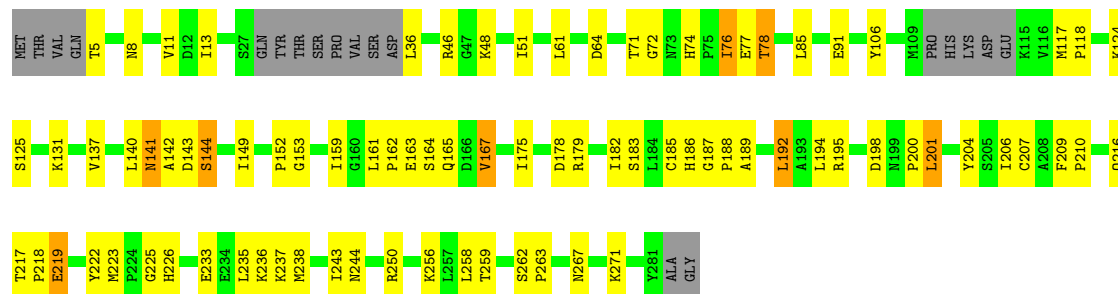
• Molecule 1: Chaperone protein hchA





• Molecule 1: Chaperone protein hchA

Chain D: 64% 27% 7%



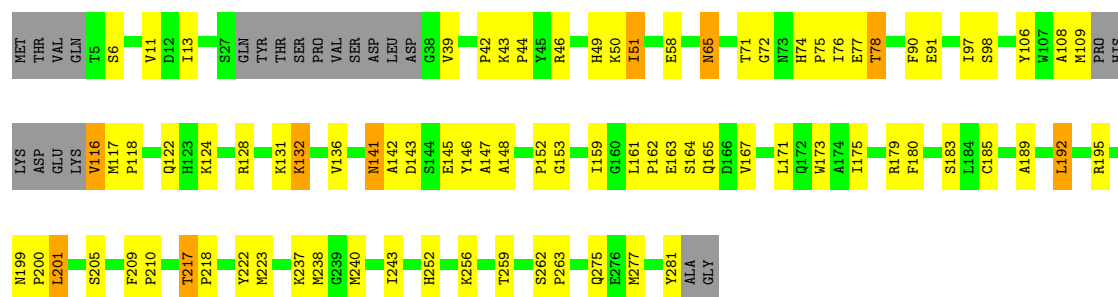
• Molecule 1: Chaperone protein hchA

Chain E: 66% 25% 5%



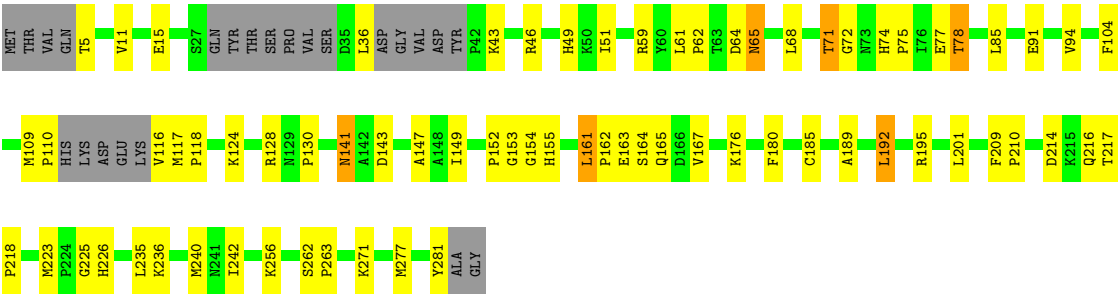
• Molecule 1: Chaperone protein hchA

Chain F: 63% 27% 8%

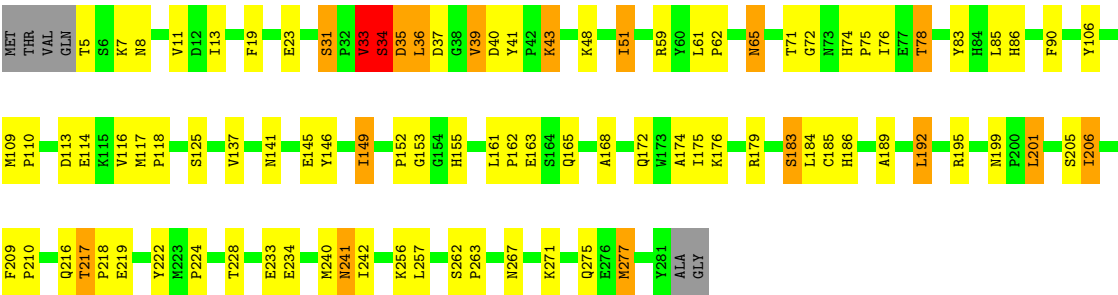


• Molecule 1: Chaperone protein hchA

Chain G: 66% 23% 8%



● Molecule 1: Chaperone protein hchA



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.49Å 99.02Å 116.80Å 102.95° 101.52° 94.19°	Depositor
Resolution (Å)	48.80 – 2.71	Depositor
% Data completeness (in resolution range)	94.0 (48.80-2.71)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.221 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16233	wwPDB-VP
Average B, all atoms (Å ²)	45.0	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	0.54	2/1912 (0.1%)	1.11	17/2591 (0.7%)
1	B	0.33	0/2062	0.77	0/2792
1	C	0.51	2/1991 (0.1%)	0.77	0/2698
1	D	0.33	0/2104	0.77	0/2853
1	E	0.43	2/2147 (0.1%)	0.84	4/2912 (0.1%)
1	F	0.34	0/2087	0.75	0/2831
1	G	0.32	0/2078	0.77	1/2817 (0.0%)
1	H	0.41	1/2218 (0.0%)	0.81	3/3014 (0.1%)
All	All	0.41	7/16599 (0.0%)	0.83	25/22508 (0.1%)

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	4
1	C	0	1
1	E	0	2
1	H	0	1
All	All	0	8

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	200	PRO	C-N	14.39	1.53	1.33
1	H	34	SER	C-N	-10.84	1.19	1.33
1	C	7	LYS	C-N	-9.69	1.10	1.33
1	A	149	ILE	N-CA	-7.18	1.37	1.46
1	A	148	ALA	C-N	-5.67	1.25	1.33

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	ALA	CA-C-N	17.63	153.70	121.97
1	A	148	ALA	C-N-CA	17.63	153.70	121.97
1	E	280	ALA	CA-C-N	10.40	140.42	121.70
1	E	280	ALA	C-N-CA	10.40	140.42	121.70
1	A	85	LEU	N-CA-C	10.06	125.59	112.72

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	146	TYR	Sidechain
1	A	148	ALA	Peptide,Mainchain
1	A	85	LEU	Peptide
1	C	7	LYS	Mainchain
1	E	280	ALA	Mainchain

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	1864	0	1818	78	0
1	B	2008	0	1965	49	0
1	C	1940	0	1898	40	0
1	D	2048	0	1987	42	0
1	E	2091	0	2035	38	0
1	F	2031	0	1979	46	0
1	G	2023	0	1976	33	0
1	H	2156	0	2088	51	0
2	A	7	0	0	1	0
2	B	7	0	0	0	0
2	C	13	0	0	1	0
2	D	7	0	0	0	0
2	E	6	0	0	0	0
2	F	8	0	0	0	0
2	G	11	0	0	0	0
2	H	13	0	0	0	0
All	All	16233	0	15746	371	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 12.

The worst 5 of 371 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:74:HIS:O	1:A:78:THR:HG22	1.59	1.00
1:A:50:LYS:N	1:A:51:ILE:HA	1.72	0.99
1:A:85:LEU:O	1:A:90:PHE:HB2	1.74	0.86
1:B:28:GLN:H	1:B:29:TYR:C	1.83	0.85
1:B:49:HIS:HB3	1:B:147:ALA:HB2	1.59	0.85

There are no symmetry-related clashes.

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	233/283 (82%)	204 (88%)	27 (12%)	2 (1%)	14	33
1	B	249/283 (88%)	232 (93%)	17 (7%)	0	100	100
1	C	241/283 (85%)	226 (94%)	14 (6%)	1 (0%)	30	52
1	D	258/283 (91%)	248 (96%)	10 (4%)	0	100	100
1	E	266/283 (94%)	251 (94%)	14 (5%)	1 (0%)	30	52
1	F	255/283 (90%)	242 (95%)	13 (5%)	0	100	100
1	G	252/283 (89%)	242 (96%)	10 (4%)	0	100	100
1	H	275/283 (97%)	256 (93%)	18 (6%)	1 (0%)	30	52
All	All	2029/2264 (90%)	1901 (94%)	123 (6%)	5 (0%)	43	66

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	36	LEU

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Mol	Chain	Res	Type
1	A	86	HIS
1	A	87	ALA
1	E	280	ALA
1	C	279	ALA

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	192/230 (84%)	160 (83%)	32 (17%)	2	5
1	B	207/230 (90%)	173 (84%)	34 (16%)	2	5
1	C	202/230 (88%)	177 (88%)	25 (12%)	4	11
1	D	211/230 (92%)	181 (86%)	30 (14%)	3	7
1	E	218/230 (95%)	176 (81%)	42 (19%)	1	3
1	F	210/230 (91%)	175 (83%)	35 (17%)	2	5
1	G	210/230 (91%)	184 (88%)	26 (12%)	4	11
1	H	225/230 (98%)	183 (81%)	42 (19%)	1	4
All	All	1675/1840 (91%)	1409 (84%)	266 (16%)	2	6

5 of 266 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	33	VAL
1	H	51	ILE
1	H	241	ASN
1	D	76	ILE
1	D	13	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	267	ASN

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Mol	Chain	Res	Type
1	G	199	ASN
1	E	199	ASN
1	G	155	HIS
1	H	196	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	H	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	34:SER	C	35:ASP	N	1.19
1	C	7:LYS	C	8:ASN	N	1.10

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.