



wwPDB X-ray Structure Validation Summary Report ⓘ

May 7, 2026 – 11:30 AM EDT

PDB ID : 4N9G / pdb_00004n9g
Title : Crystal Structure of a Computationally Designed RSV-Presenting Epitope Scaffold And Its Elicited Antibody 17HD9
Authors : Carrico, C.T.D.; Strong, R.K.
Deposited on : 2013-10-21
Resolution : 2.50 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)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

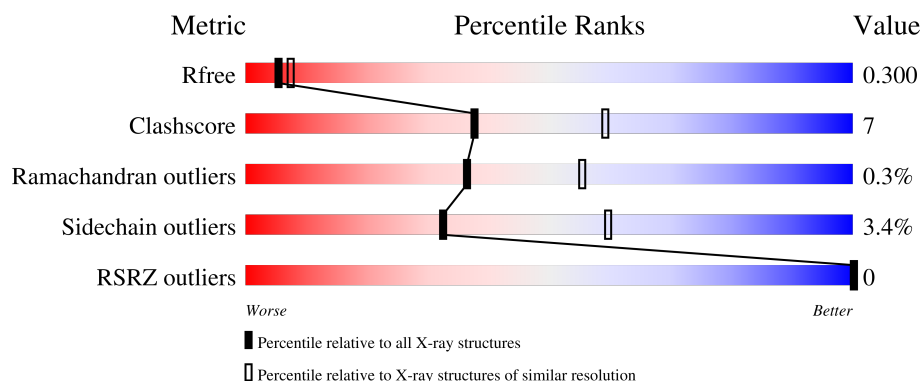
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	230	
1	E	230	
1	H	230	
1	M	230	
2	B	215	

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Mol	Chain	Length	Quality of chain
2	F	215	89%10%
2	L	215	87%11%•
2	N	215	88%10%•
3	C	123	21%7% 72%
3	D	123	21%7% 72%
3	Y	123	25%•• 71%
3	Z	123	23%5%• 71%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14304 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 17HD9, Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	1	0
			1656	1047	273	328	8			
1	E	223	Total	C	N	O	S	0	1	0
			1664	1051	277	329	7			
1	H	221	Total	C	N	O	S	0	1	0
			1650	1043	275	324	8			
1	M	223	Total	C	N	O	S	0	1	0
			1653	1043	275	327	8			

- Molecule 2 is a protein called Antibody 17HD9, Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	6	0	0
			1624	1013	271	334	6			
2	F	214	Total	C	N	O	S	8	2	0
			1645	1025	275	339	6			
2	L	214	Total	C	N	O	S	9	1	0
			1641	1023	275	337	6			
2	N	214	Total	C	N	O	S	10	0	0
			1632	1018	272	336	6			

- Molecule 3 is a protein called Epitope Scaffold rsv_lisea_FFL_001_C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	35	Total	C	N	O	S	0	0	0
			263	164	42	55	2			
3	D	35	Total	C	N	O	S	0	0	0
			268	165	45	56	2			
3	Y	36	Total	C	N	O	S	0	1	0
			281	175	46	58	2			
3	Z	36	Total	C	N	O	S	0	0	0
			268	168	43	55	2			

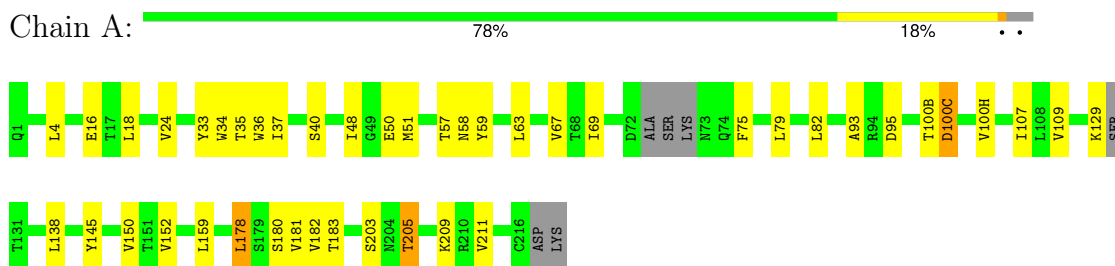
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	9	Total O 9 9	0	0
4	B	7	Total O 7 7	0	0
4	E	5	Total O 5 5	0	0
4	F	5	Total O 5 5	0	0
4	H	6	Total O 6 6	0	0
4	L	12	Total O 12 12	0	0
4	M	6	Total O 6 6	0	0
4	N	8	Total O 8 8	0	0
4	Z	1	Total O 1 1	0	0

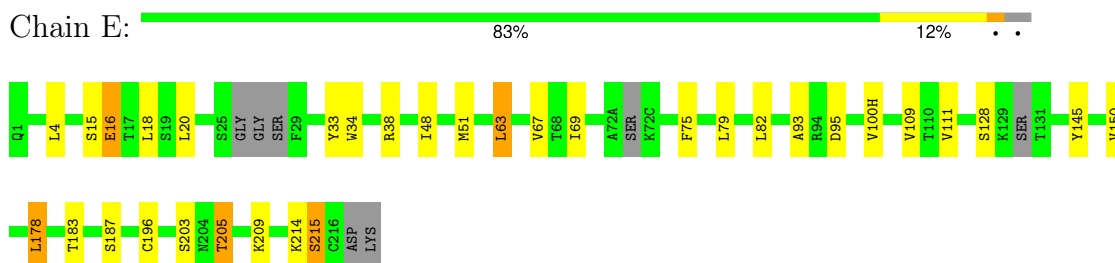
3 Residue-property plots [i](#)

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 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.

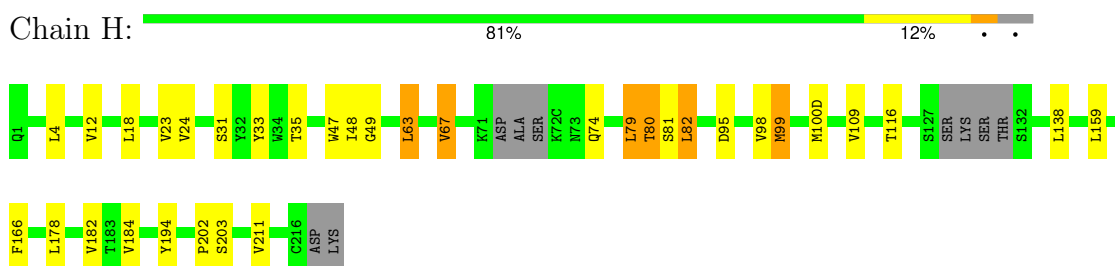
- Molecule 1: Antibody 17HD9, Heavy Chain



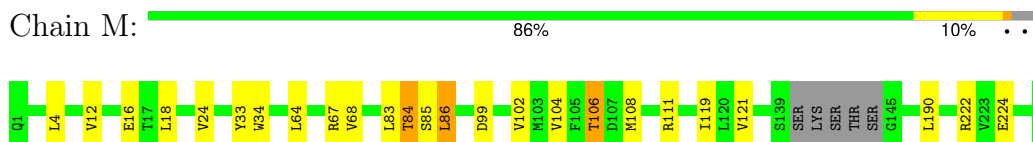
- Molecule 1: Antibody 17HD9, Heavy Chain



- Molecule 1: Antibody 17HD9, Heavy Chain



- Molecule 1: Antibody 17HD9, Heavy Chain



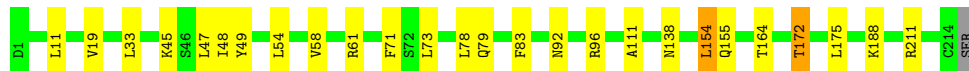
• Molecule 2: Antibody 17HD9, Light Chain

Chain B:  87% 11%

• Molecule 2: Antibody 17HD9, Light Chain

Chain F:  89% 10%

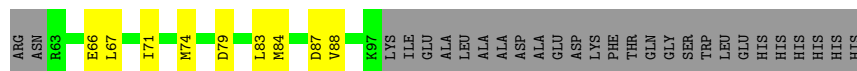
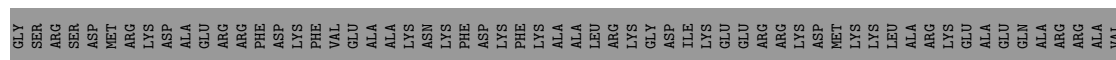
• Molecule 2: Antibody 17HD9, Light Chain

Chain L:  87% 11%

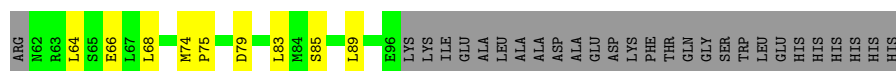
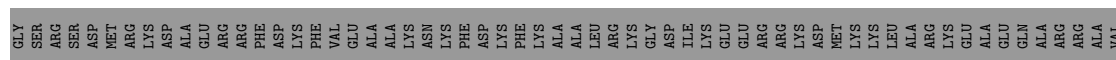
• Molecule 2: Antibody 17HD9, Light Chain

Chain N:  88% 10%

• Molecule 3: Epitope Scaffold rsv_1isea_FFL_001_C

Chain C:  21% 7% 72%

• Molecule 3: Epitope Scaffold rsv_1isea_FFL_001_C

Chain D:  21% 7% 72%

• Molecule 3: Epitope Scaffold rsv_1isea_FFL_001_C

Chain Y:  25% 71%

GLY	ARG	SER	ARG	SER	ASP	MET	ARG	LYS	ASP	ALA	GLU	ARG	ARG	PHE	ASP	LYS	PHE	VAL	GLU	ALA	ALA	LYS	ASN	LYS	PHE	ASP	LYS	PHE	GLN	GLY	LYS	ALA	ALA	LEU	ARG	LYS	GLY	ASP	ILE	LYS	GLU	ARG	LYS	LYS	ASP	ASP	MET	LYS	LEU	ALA	ARG	LYS	GLU	ALA	GLN	ALA	ARG	ALA	VAL
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ARG	R62	L68	I76	T77	Q80	L89	K97	LYS	ILE	GLU	ALA	LEU	ALA	ALA	ASP	ALA	GLU	LYS	ASP	LYS	PHE	THR	GLN	GLY	SER	TRP	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
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● Molecule 3: Epitope Scaffold rsv_1isea_FFL_001_C



GLY	SER	ARG	SER	ASP	MET	ARG	LYS	ASP	ALA	GLU	ARG	ARG	PHE	ASP	LYS	PHE	VAL	GLU	ALA	ALA	LYS	ASN	LYS	PHE	ASP	LYS	PHE	GLN	GLY	LYS	ALA	ALA	LEU	ARG	LYS	GLY	ASP	ILE	LYS	GLU	GLU	ARG	ARG	LYS	ASP	MET	LYS	LYS	LEU	ALA	ARG	LYS	GLU	ALA	GLN	ALA	ARG	ALA	VAL
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ARG	R62	L67	I71	M74	T77	N78	D79	L83	R84	K90	K97	LYS	ILE	GLU	ALA	LEU	ALA	ALA	ASP	ALA	GLU	ASP	LYS	PHE	THR	GLN	GLY	SER	TRP	LEU	GLU	HIS	HIS	HIS	HIS	HIS	HIS
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	64.21Å 89.27Å 104.30Å 89.99° 102.73° 89.91°	Depositor
Resolution (Å)	48.75 – 2.50 48.75 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.7 (48.75-2.50) 97.3 (48.75-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.59 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.263 , 0.295 0.271 , 0.300	Depositor DCC
R_{free} test set	3829 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.430 for -h,k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	14304	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.41	0/1697	0.62	0/2319
1	E	0.40	0/1701	0.60	0/2323
1	H	0.39	0/1691	0.61	0/2308
1	M	0.40	0/1695	0.61	0/2317
2	B	0.47	1/1661 (0.1%)	0.65	1/2259 (0.0%)
2	F	0.42	0/1688	0.61	0/2294
2	L	0.73	1/1681 (0.1%)	0.65	2/2284 (0.1%)
2	N	0.48	1/1669 (0.1%)	0.73	2/2268 (0.1%)
3	C	0.38	0/264	0.74	0/355
3	D	0.40	0/269	0.71	0/362
3	Y	0.45	0/285	0.79	0/382
3	Z	0.44	0/269	0.78	0/361
All	All	0.47	3/14570 (0.0%)	0.64	5/19832 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	211	ARG	CZ-NH2	-24.09	1.02	1.33
2	B	154	LEU	CG-CD1	-7.52	1.27	1.52
2	N	79	GLN	CD-NE2	5.20	1.44	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	79	GLN	OE1-CD-NE2	14.45	137.04	122.60
2	N	79	GLN	CG-CD-NE2	-9.64	101.94	116.40
2	B	154	LEU	CB-CG-CD1	7.79	134.08	110.70
2	L	45	LYS	CD-CE-NZ	7.71	136.58	111.90
2	L	211	ARG	NE-CZ-NH2	6.15	124.73	119.20

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	1656	0	1616	40	0
1	E	1664	0	1619	24	0
1	H	1650	0	1620	33	0
1	M	1653	0	1606	16	0
2	B	1624	0	1535	13	0
2	F	1645	0	1566	13	0
2	L	1641	0	1570	20	0
2	N	1632	0	1554	20	0
3	C	263	0	257	9	0
3	D	268	0	261	6	0
3	Y	281	0	282	5	0
3	Z	268	0	264	13	0
4	A	9	0	0	0	0
4	B	7	0	0	0	0
4	E	5	0	0	0	0
4	F	5	0	0	0	0
4	H	6	0	0	0	0
4	L	12	0	0	0	0
4	M	6	0	0	0	0
4	N	8	0	0	0	0
4	Z	1	0	0	0	0
All	All	14304	0	13750	196	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 7.

The worst 5 of 196 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:E:51:MET:HE2	1:E:69:ILE:HG22	1.32	1.11
1:A:51:MET:HE2	1:A:69:ILE:HG22	1.25	1.09
1:A:57[A]:THR:HG21	1:A:59:TYR:CE1	1.96	0.99
3:Z:74:MET:HE1	3:Z:84:MET:HE1	1.47	0.96
2:F:11:LEU:HD21	2:F:19:VAL:CG1	1.98	0.93

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	219/230 (95%)	212 (97%)	6 (3%)	1 (0%)	24	43
1	E	216/230 (94%)	206 (95%)	8 (4%)	2 (1%)	14	27
1	H	216/230 (94%)	209 (97%)	7 (3%)	0	100	100
1	M	220/230 (96%)	214 (97%)	6 (3%)	0	100	100
2	B	212/215 (99%)	203 (96%)	8 (4%)	1 (0%)	24	43
2	F	214/215 (100%)	204 (95%)	9 (4%)	1 (0%)	24	43
2	L	213/215 (99%)	209 (98%)	4 (2%)	0	100	100
2	N	212/215 (99%)	207 (98%)	5 (2%)	0	100	100
3	C	33/123 (27%)	32 (97%)	1 (3%)	0	100	100
3	D	33/123 (27%)	33 (100%)	0	0	100	100
3	Y	35/123 (28%)	34 (97%)	1 (3%)	0	100	100
3	Z	34/123 (28%)	34 (100%)	0	0	100	100
All	All	1857/2272 (82%)	1797 (97%)	55 (3%)	5 (0%)	36	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	16	GLU
1	E	215	SER
1	A	100(C)	ASP
2	F	138	ASN
2	B	138	ASN

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	189/198 (96%)	182 (96%)	7 (4%)	30	57
1	E	189/198 (96%)	185 (98%)	4 (2%)	47	74
1	H	189/198 (96%)	183 (97%)	6 (3%)	34	62
1	M	187/198 (94%)	180 (96%)	7 (4%)	30	57
2	B	183/190 (96%)	177 (97%)	6 (3%)	33	61
2	F	188/190 (99%)	183 (97%)	5 (3%)	39	67
2	L	188/190 (99%)	184 (98%)	4 (2%)	47	74
2	N	186/190 (98%)	181 (97%)	5 (3%)	39	67
3	C	29/104 (28%)	26 (90%)	3 (10%)	7	14
3	D	30/104 (29%)	27 (90%)	3 (10%)	7	15
3	Y	32/104 (31%)	30 (94%)	2 (6%)	16	34
3	Z	29/104 (28%)	26 (90%)	3 (10%)	7	14
All	All	1619/1968 (82%)	1564 (97%)	55 (3%)	32	60

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	63	LEU
2	L	154	LEU
3	Z	90	LYS
2	N	188	LYS
1	H	67	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	53	ASN
1	H	192	GLN
2	N	37	GLN
2	L	152	ASN

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Mol	Chain	Res	Type
1	E	73	ASN

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 [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	224/230 (97%)	-0.93	0 100 100	27, 44, 62, 78	1 (0%)
1	E	223/230 (96%)	-0.92	0 100 100	16, 43, 59, 66	1 (0%)
1	H	221/230 (96%)	-1.02	0 100 100	26, 38, 57, 70	1 (0%)
1	M	223/230 (96%)	-1.01	0 100 100	26, 39, 57, 67	1 (0%)
2	B	214/215 (99%)	-1.13	0 100 100	29, 39, 49, 61	4 (1%)
2	F	214/215 (99%)	-1.04	0 100 100	25, 40, 48, 59	7 (3%)
2	L	214/215 (99%)	-1.10	0 100 100	25, 37, 45, 61	7 (3%)
2	N	214/215 (99%)	-1.11	0 100 100	26, 37, 47, 59	7 (3%)
3	C	35/123 (28%)	-0.80	0 100 100	40, 49, 67, 75	0
3	D	35/123 (28%)	-0.78	0 100 100	39, 51, 73, 81	0
3	Y	36/123 (29%)	-0.77	0 100 100	27, 49, 69, 75	1 (2%)
3	Z	36/123 (29%)	-0.86	0 100 100	35, 45, 60, 72	0
All	All	1889/2272 (83%)	-1.01	0 100 100	16, 40, 58, 81	30 (1%)

There are no RSRZ outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.