



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:14 AM UTC

PDB ID : 5LYZ / pdb_00005lyz
Title : Real-space refinement of the structure of hen egg-white lysozyme
Authors : Diamond, R.; Phillips, D.C.; Blake, C.C.F.; North, A.C.T.
Deposited on : 1975-02-01
Resolution : 2.00 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

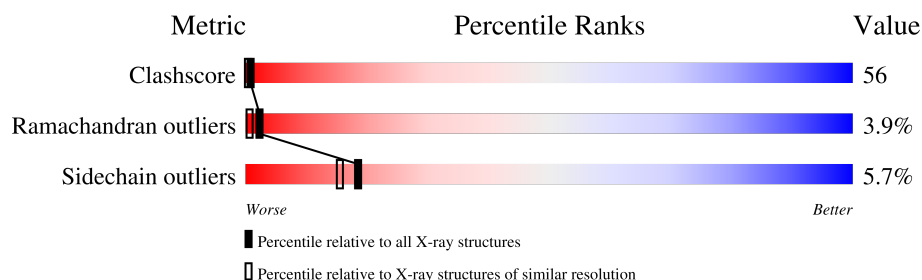
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	129	16% 50% 31% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1102 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 HEN EGG WHITE LYSOZYME.

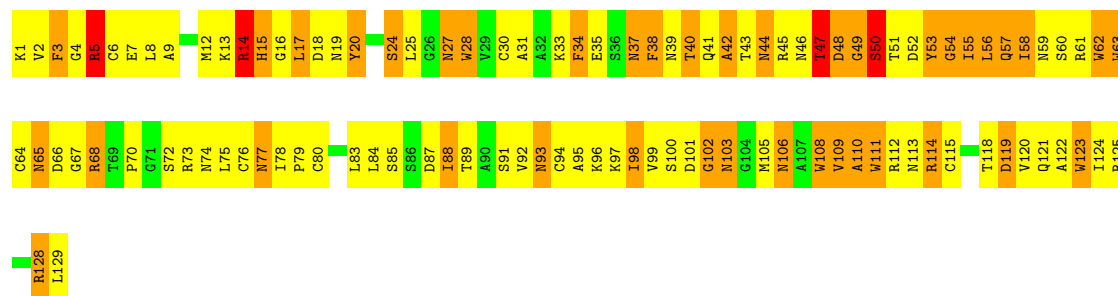
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			1001	613	193	185	10			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	101	Total	O	0	0
			101	101		

Note EDS was not executed.

Chain A: 16% 50% 31% .



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	79.10Å 79.10Å 37.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1102	wwPDB-VP
Average B, all atoms (Å ²)	6.0	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	1.61	30/1021 (2.9%)	2.55	79/1379 (5.7%)

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	3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	28	TRP	NE1-CE2	-8.64	1.27	1.37
1	A	123	TRP	NE1-CE2	-8.62	1.27	1.37
1	A	63	TRP	NE1-CE2	-8.62	1.27	1.37
1	A	62	TRP	NE1-CE2	-8.56	1.28	1.37
1	A	108	TRP	NE1-CE2	-8.56	1.28	1.37
1	A	111	TRP	NE1-CE2	-8.55	1.28	1.37
1	A	59	ASN	CG-OD1	8.35	1.39	1.23
1	A	39	ASN	CG-OD1	8.34	1.39	1.23
1	A	19	ASN	CG-OD1	8.32	1.39	1.23
1	A	37	ASN	CG-OD1	8.32	1.39	1.23
1	A	46	ASN	CG-OD1	8.32	1.39	1.23
1	A	106	ASN	CG-OD1	8.32	1.39	1.23
1	A	77	ASN	CG-OD1	8.31	1.39	1.23
1	A	93	ASN	CG-OD1	8.29	1.39	1.23
1	A	27	ASN	CG-OD1	8.28	1.39	1.23
1	A	44	ASN	CG-OD1	8.28	1.39	1.23
1	A	66	ASP	CG-OD1	7.39	1.39	1.25
1	A	48	ASP	CG-OD1	7.36	1.39	1.25
1	A	65	ASN	CG-ND2	-6.07	1.20	1.33
1	A	103	ASN	CG-ND2	-6.06	1.20	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	37	ASN	CG-ND2	-5.30	1.22	1.33
1	A	77	ASN	CG-ND2	-5.27	1.22	1.33
1	A	39	ASN	CG-ND2	-5.27	1.22	1.33
1	A	27	ASN	CG-ND2	-5.26	1.22	1.33
1	A	44	ASN	CG-ND2	-5.24	1.22	1.33
1	A	46	ASN	CG-ND2	-5.23	1.22	1.33
1	A	19	ASN	CG-ND2	-5.21	1.22	1.33
1	A	106	ASN	CG-ND2	-5.21	1.22	1.33
1	A	93	ASN	CG-ND2	-5.21	1.22	1.33
1	A	59	ASN	CG-ND2	-5.21	1.22	1.33

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	CYS	N-CA-CB	24.20	148.46	110.46
1	A	73	ARG	N-CA-C	-17.16	82.27	109.72
1	A	15	HIS	N-CA-C	14.42	129.80	113.21
1	A	47	THR	N-CA-C	14.41	130.12	112.54
1	A	72	SER	N-CA-C	14.36	131.85	110.30
1	A	110	ALA	N-CA-C	14.20	126.27	111.07
1	A	46	ASN	N-CA-C	-14.07	89.46	110.14
1	A	115	CYS	N-CA-CB	12.37	131.97	110.44
1	A	34	PHE	CA-CB-CG	-11.52	102.28	113.80
1	A	118	THR	N-CA-C	-10.86	93.19	109.81
1	A	63	TRP	N-CA-C	10.24	126.32	112.90
1	A	17	LEU	N-CA-C	10.19	125.53	112.89
1	A	60	SER	N-CA-C	9.97	125.52	113.16
1	A	62	TRP	N-CA-C	9.84	126.26	113.18
1	A	16	GLY	N-CA-C	9.59	128.11	115.36
1	A	7	GLU	N-CA-C	9.32	122.60	111.33
1	A	128	ARG	N-CA-C	-9.29	92.31	108.20
1	A	72	SER	CB-CA-C	-9.24	97.22	110.06
1	A	28	TRP	N-CA-C	9.18	122.47	111.82
1	A	114	ARG	N-CA-C	8.96	127.04	113.61
1	A	53	TYR	N-CA-C	8.54	122.98	109.50
1	A	102	GLY	N-CA-C	8.46	133.24	113.18
1	A	100	SER	N-CA-C	8.42	124.58	113.30
1	A	20	TYR	N-CA-C	-8.34	97.46	109.96
1	A	94	CYS	CB-CA-C	-8.12	95.84	110.70
1	A	48	ASP	N-CA-C	7.86	122.94	112.25
1	A	44	ASN	N-CA-C	7.56	121.13	108.13
1	A	18	ASP	N-CA-C	-7.36	98.92	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	124	ILE	N-CA-C	7.32	119.13	112.17
1	A	70	PRO	N-CA-C	7.26	127.42	112.47
1	A	20	TYR	CA-CB-CG	-7.17	100.99	113.90
1	A	123	TRP	CA-CB-CG	-7.14	100.03	113.60
1	A	67	GLY	N-CA-C	7.12	124.99	115.59
1	A	115	CYS	CB-CA-C	-7.06	98.79	110.37
1	A	124	ILE	CB-CA-C	-7.06	102.89	111.85
1	A	106	ASN	N-CA-C	-7.02	104.18	112.89
1	A	4	GLY	N-CA-C	-6.71	100.53	112.54
1	A	68	ARG	N-CA-C	6.55	121.21	112.30
1	A	27	ASN	N-CA-C	-6.43	104.19	111.07
1	A	40	THR	N-CA-C	6.38	120.32	112.54
1	A	73	ARG	CB-CA-C	6.27	121.67	109.33
1	A	114	ARG	CB-CA-C	-6.20	99.19	109.99
1	A	15	HIS	CB-CA-C	-6.04	100.03	110.72
1	A	110	ALA	N-CA-CB	-6.00	101.31	110.01
1	A	57	GLN	N-CA-C	5.99	119.45	111.30
1	A	88	ILE	CB-CA-C	-5.99	101.47	111.29
1	A	88	ILE	N-CA-C	5.91	121.62	109.34
1	A	111	TRP	N-CA-C	-5.86	104.80	111.07
1	A	55	ILE	CB-CA-C	-5.77	101.83	111.29
1	A	113	ASN	N-CA-C	5.75	117.55	111.28
1	A	63	TRP	CA-CB-CG	-5.74	102.69	113.60
1	A	49	GLY	N-CA-C	-5.74	99.59	113.18
1	A	77	ASN	CB-CG-ND2	5.68	124.93	116.40
1	A	106	ASN	CB-CG-ND2	5.66	124.88	116.40
1	A	37	ASN	CB-CG-ND2	5.65	124.88	116.40
1	A	38	PHE	CA-CB-CG	-5.65	108.15	113.80
1	A	46	ASN	CB-CG-ND2	5.65	124.87	116.40
1	A	39	ASN	CB-CG-ND2	5.64	124.87	116.40
1	A	59	ASN	CB-CG-ND2	5.63	124.85	116.40
1	A	27	ASN	CB-CG-ND2	5.62	124.84	116.40
1	A	7	GLU	CB-CA-C	-5.62	101.13	110.68
1	A	44	ASN	CB-CG-ND2	5.62	124.82	116.40
1	A	19	ASN	CB-CG-ND2	5.61	124.82	116.40
1	A	93	ASN	CB-CG-ND2	5.61	124.82	116.40
1	A	55	ILE	N-CA-C	5.56	120.91	109.34
1	A	46	ASN	CB-CA-C	5.50	120.15	110.36
1	A	48	ASP	CB-CA-C	-5.49	103.51	111.14
1	A	3	PHE	N-CA-C	5.43	117.70	110.53
1	A	54	GLY	N-CA-C	5.43	122.16	112.22
1	A	78	ILE	CA-CB-CG2	-5.19	101.68	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	ILE	CA-CB-CG2	-5.17	101.71	110.50
1	A	100	SER	CB-CA-C	-5.15	101.46	110.17
1	A	98	ILE	CA-CB-CG2	-5.14	101.75	110.50
1	A	88	ILE	CA-CB-CG2	-5.14	101.76	110.50
1	A	55	ILE	CA-CB-CG2	-5.13	101.78	110.50
1	A	124	ILE	CA-CB-CG2	-5.12	101.81	110.50
1	A	60	SER	CB-CA-C	-5.09	100.84	110.01
1	A	118	THR	CB-CA-C	5.06	119.76	110.24
1	A	68	ARG	CB-CA-C	-5.06	102.56	110.85

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	114	ARG	Sidechain
1	A	14	ARG	Sidechain
1	A	5	ARG	Sidechain

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	1001	0	955	110	4
2	A	101	0	0	18	6
All	All	1102	0	955	110	7

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 56.

All (110) 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:122:ALA:HA	1:A:125:ARG:CD	1.41	1.50
1:A:101:ASP:CB	2:A:227:HOH:O	1.71	1.30
1:A:101:ASP:HB3	2:A:227:HOH:O	1.29	1.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:ASP:OD1	2:A:228:HOH:O	1.57	1.18
1:A:101:ASP:HB3	2:A:226:HOH:O	1.42	1.18
1:A:122:ALA:HA	1:A:125:ARG:HD2	1.19	1.17
1:A:12:MET:HE2	1:A:17:LEU:CD1	1.76	1.15
1:A:12:MET:CE	1:A:17:LEU:CD1	2.32	1.07
1:A:13:LYS:NZ	1:A:129:LEU:OXT	1.88	1.05
1:A:12:MET:HE2	1:A:17:LEU:HD13	1.40	1.04
1:A:122:ALA:CA	1:A:125:ARG:CD	2.35	1.04
1:A:122:ALA:HA	1:A:125:ARG:NE	1.57	1.01
1:A:122:ALA:CA	1:A:125:ARG:NE	2.16	1.00
1:A:31:ALA:O	1:A:35:GLU:HB2	1.62	0.99
1:A:5:ARG:NH1	1:A:123:TRP:O	1.95	0.99
1:A:122:ALA:CA	1:A:125:ARG:HD2	1.93	0.98
1:A:97:LYS:O	1:A:101:ASP:OD1	1.84	0.96
1:A:12:MET:HE2	1:A:17:LEU:HD12	1.49	0.95
1:A:6:CYS:HB2	2:A:140:HOH:O	1.69	0.92
1:A:12:MET:CE	1:A:17:LEU:HD13	1.96	0.91
1:A:106:ASN:O	1:A:112:ARG:NH2	2.04	0.91
1:A:45:ARG:NH1	1:A:68:ARG:HH12	1.69	0.91
1:A:55:ILE:HG23	1:A:56:LEU:N	1.88	0.88
1:A:45:ARG:NH1	1:A:68:ARG:NH1	2.24	0.86
1:A:63:TRP:CD1	2:A:206:HOH:O	2.31	0.83
1:A:63:TRP:HD1	2:A:206:HOH:O	1.60	0.83
1:A:12:MET:HE1	1:A:28:TRP:HB3	1.60	0.82
1:A:106:ASN:HB3	1:A:112:ARG:HH21	1.41	0.82
1:A:45:ARG:CZ	1:A:68:ARG:NH1	2.43	0.81
1:A:12:MET:CE	1:A:17:LEU:HD12	2.08	0.80
1:A:103:ASN:O	1:A:106:ASN:HB2	1.81	0.79
1:A:122:ALA:HA	1:A:125:ARG:CG	2.14	0.78
1:A:101:ASP:HB2	2:A:227:HOH:O	1.48	0.77
1:A:55:ILE:CG2	1:A:56:LEU:N	2.48	0.77
1:A:24:SER:OG	2:A:153:HOH:O	1.88	0.75
1:A:12:MET:HE3	1:A:17:LEU:CD1	2.13	0.75
1:A:85:SER:HB3	2:A:182:HOH:O	1.88	0.74
1:A:121:GLN:CD	2:A:143:HOH:O	2.31	0.72
1:A:3:PHE:O	1:A:38:PHE:HB3	1.90	0.72
1:A:98:ILE:O	2:A:211:HOH:O	2.09	0.71
1:A:6:CYS:O	1:A:9:ALA:HB3	1.94	0.68
1:A:3:PHE:N	1:A:38:PHE:O	2.28	0.65
1:A:63:TRP:HH2	1:A:101:ASP:OD2	1.78	0.65
1:A:109:VAL:HG12	2:A:200:HOH:O	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:LYS:O	1:A:101:ASP:CG	2.39	0.64
1:A:12:MET:CE	1:A:28:TRP:HB3	2.29	0.62
1:A:119:ASP:CG	1:A:119:ASP:O	2.42	0.62
1:A:121:GLN:O	1:A:125:ARG:HG3	1.99	0.62
1:A:47:THR:HA	2:A:203:HOH:O	2.00	0.61
1:A:58:ILE:HD12	1:A:83:LEU:HD13	1.82	0.61
1:A:37:ASN:O	1:A:38:PHE:HB2	2.00	0.60
1:A:2:VAL:HA	1:A:38:PHE:O	2.02	0.59
1:A:25:LEU:HD23	1:A:25:LEU:O	2.02	0.59
1:A:106:ASN:CB	1:A:112:ARG:HH21	2.15	0.58
1:A:122:ALA:N	1:A:125:ARG:NE	2.53	0.56
1:A:63:TRP:CE2	1:A:98:ILE:HG12	2.40	0.56
1:A:62:TRP:O	1:A:75:LEU:HB2	2.06	0.56
1:A:40:THR:O	1:A:54:GLY:HA2	2.06	0.55
1:A:3:PHE:HB3	1:A:8:LEU:HB2	1.89	0.53
1:A:63:TRP:CH2	1:A:101:ASP:OD2	2.61	0.52
1:A:58:ILE:HD12	1:A:83:LEU:CD1	2.40	0.51
1:A:41:GLN:O	1:A:43:THR:HG23	2.11	0.51
1:A:89:THR:O	1:A:93:ASN:HB2	2.11	0.50
1:A:24:SER:O	1:A:27:ASN:HB2	2.10	0.50
1:A:62:TRP:HZ2	2:A:219:HOH:O	1.94	0.50
1:A:65:ASN:O	1:A:79:PRO:HA	2.11	0.49
1:A:105:MET:O	1:A:111:TRP:CE3	2.65	0.49
1:A:88:ILE:HD12	1:A:92:VAL:CG2	2.42	0.49
1:A:106:ASN:C	1:A:112:ARG:NH2	2.69	0.49
1:A:106:ASN:C	1:A:112:ARG:HH21	2.20	0.49
1:A:109:VAL:HG13	1:A:110:ALA:N	2.28	0.49
1:A:13:LYS:O	1:A:14:ARG:C	2.57	0.46
1:A:35:GLU:HG3	1:A:57:GLN:HB2	1.97	0.46
1:A:33:LYS:HG3	1:A:34:PHE:N	2.26	0.46
1:A:30:CYS:HB2	1:A:123:TRP:CD1	2.51	0.46
1:A:85:SER:C	1:A:87:ASP:H	2.23	0.46
1:A:96:LYS:O	1:A:99:VAL:HG12	2.16	0.46
1:A:95:ALA:HA	1:A:98:ILE:HD12	1.98	0.45
1:A:56:LEU:HD12	1:A:56:LEU:HA	1.80	0.45
1:A:61:ARG:HG2	1:A:62:TRP:CE2	2.51	0.45
1:A:120:VAL:O	1:A:123:TRP:HB2	2.16	0.45
1:A:64:CYS:O	1:A:80:CYS:SG	2.75	0.45
1:A:80:CYS:O	1:A:83:LEU:HB2	2.16	0.45
1:A:33:LYS:O	1:A:37:ASN:HA	2.15	0.45
1:A:52:ASP:HB3	1:A:57:GLN:OE1	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:MET:HA	1:A:108:TRP:HE3	1.82	0.45
1:A:74:ASN:ND2	1:A:77:ASN:N	2.65	0.44
1:A:91:SER:O	1:A:95:ALA:N	2.37	0.44
1:A:92:VAL:O	1:A:96:LYS:HG3	2.18	0.44
1:A:5:ARG:NH1	1:A:123:TRP:C	2.74	0.44
1:A:51:THR:HG22	1:A:53:TYR:CE2	2.52	0.44
1:A:35:GLU:OE2	1:A:110:ALA:HB3	2.17	0.44
1:A:48:ASP:OD1	1:A:50:SER:HB3	2.17	0.44
1:A:85:SER:HB2	2:A:181:HOH:O	2.16	0.44
1:A:31:ALA:O	1:A:35:GLU:CB	2.51	0.43
1:A:20:TYR:CD2	1:A:99:VAL:HG11	2.53	0.43
1:A:1:LYS:HG2	1:A:2:VAL:N	2.32	0.43
1:A:41:GLN:O	1:A:42:ALA:C	2.61	0.43
1:A:106:ASN:HB3	1:A:112:ARG:NH2	2.21	0.43
1:A:15:HIS:HB3	1:A:92:VAL:HG11	2.01	0.42
1:A:43:THR:HA	1:A:52:ASP:O	2.19	0.42
1:A:44:ASN:O	1:A:52:ASP:N	2.49	0.42
1:A:74:ASN:C	1:A:74:ASN:HD22	2.27	0.42
1:A:74:ASN:ND2	1:A:77:ASN:H	2.18	0.41
1:A:49:GLY:CA	2:A:214:HOH:O	2.67	0.41
1:A:65:ASN:O	1:A:80:CYS:N	2.48	0.41
1:A:40:THR:O	1:A:84:LEU:HA	2.20	0.41
1:A:63:TRP:HA	1:A:63:TRP:CE3	2.56	0.41
1:A:106:ASN:O	1:A:112:ARG:CZ	2.67	0.41
1:A:83:LEU:HA	2:A:131:HOH:O	2.21	0.40

All (7) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:193:HOH:O	2:A:213:HOH:O[6_456]	0.06	2.14
2:A:141:HOH:O	2:A:185:HOH:O[8_555]	0.13	2.07
2:A:138(A):HOH:O	2:A:220:HOH:O[4_454]	0.16	2.04
1:A:128:ARG:CD	2:A:186:HOH:O[8_555]	0.89	1.31
1:A:128:ARG:NE	2:A:186:HOH:O[8_555]	1.69	0.51
1:A:47:THR:CG2	1:A:128:ARG:NE[3_555]	2.00	0.20
1:A:128:ARG:CG	2:A:186:HOH:O[8_555]	2.19	0.01

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	127/129 (98%)	107 (84%)	15 (12%)	5 (4%)	2 1

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	50	SER
1	A	42	ALA
1	A	109	VAL
1	A	5	ARG
1	A	102	GLY

5.3.2 Protein sidechains [i](#)

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	105/105 (100%)	99 (94%)	6 (6%)	18 15

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	ARG
1	A	24	SER
1	A	47	THR
1	A	50	SER
1	A	56	LEU
1	A	119	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	65	ASN
1	A	74	ASN
1	A	77	ASN
1	A	103	ASN
1	A	121	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.