



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:42 PM UTC

PDB ID : 1JTI / pdb_00001jti
Title : Loop-inserted Structure of P1-P1' Cleaved Ovalbumin Mutant R339T
Authors : Yamasaki, M.; Arai, Y.; Mikami, B.; Hirose, M.
Deposited on : 2001-08-21
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

<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

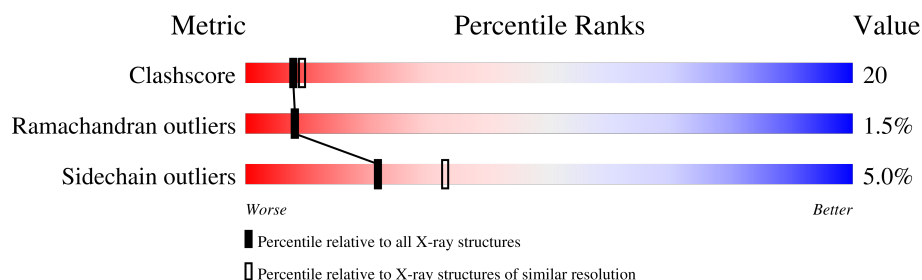
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (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 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	385	 64% 31% . .
1	B	385	 63% 32% . .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6049 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 Ovalbumin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	381	Total	C	N	O	S	0	0	0
			2969	1884	492	571	22			
1	B	381	Total	C	N	O	S	0	0	0
			2969	1884	492	571	22			

- Molecule 2 is water.

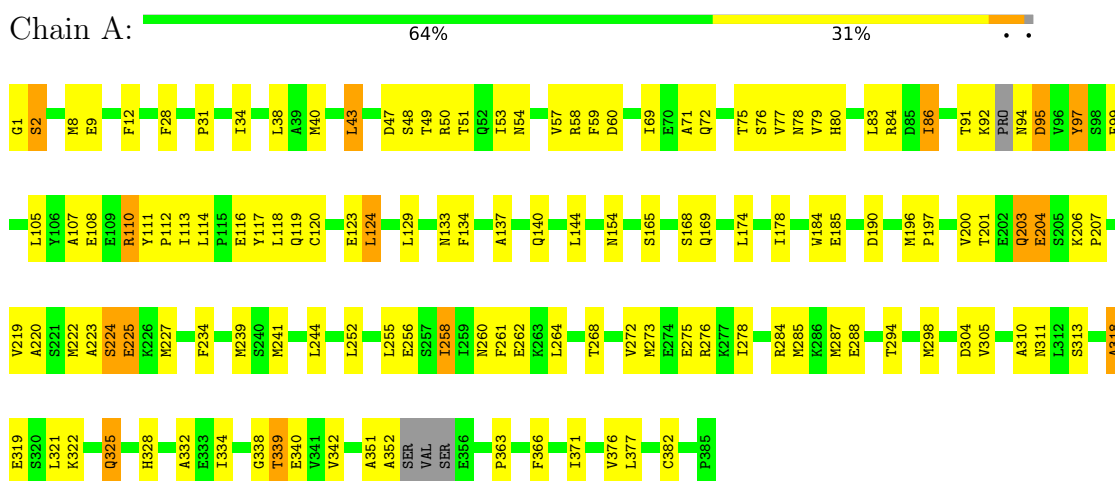
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	68	Total	O	0	0
			68	68		
2	B	43	Total	O	0	0
			43	43		

3 Residue-property plots

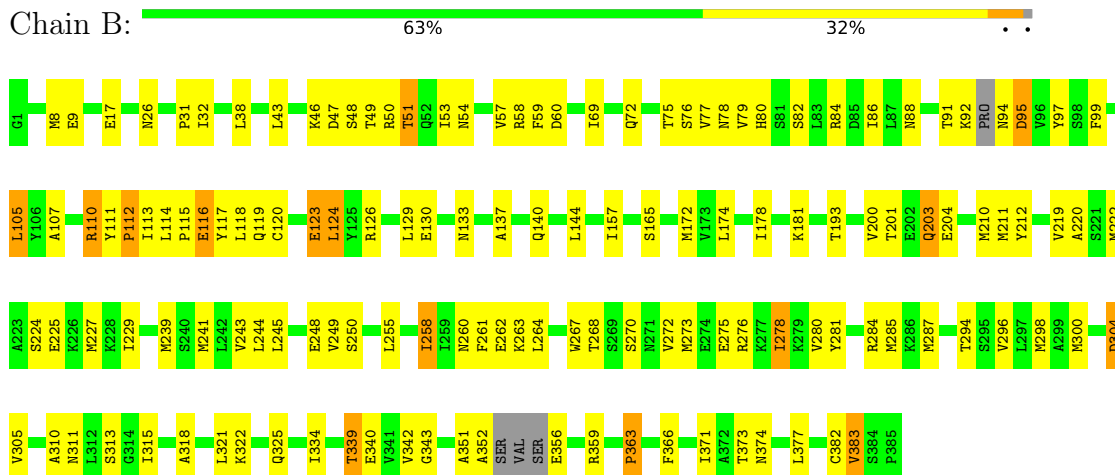
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



• Molecule 1: Ovalbumin



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	61.71Å 65.47Å 68.42Å 89.11° 63.27° 61.72°	Depositor
Resolution (Å)	15.00 – 2.30	Depositor
% Data completeness (in resolution range)	85.0 (15.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.199 , 0.252	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6049	wwPDB-VP
Average B, all atoms (Å ²)	41.0	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	0.44	0/3022	0.92	7/4080 (0.2%)
1	B	0.45	0/3022	0.94	8/4080 (0.2%)
All	All	0.44	0/6044	0.93	15/8160 (0.2%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	165	SER	N-CA-C	-9.90	101.20	113.38
1	B	371	ILE	N-CA-C	9.60	120.22	110.23
1	B	165	SER	N-CA-C	-9.30	101.94	113.38
1	A	371	ILE	N-CA-C	8.09	118.85	110.36
1	B	284	ARG	N-CA-C	-7.21	99.62	110.28
1	A	284	ARG	N-CA-C	-6.98	99.95	110.28
1	B	124	LEU	N-CA-C	6.84	118.43	110.97
1	B	304	ASP	N-CA-C	6.42	118.28	111.28
1	B	383	VAL	N-CA-C	-5.99	106.97	112.96
1	B	26	ASN	N-CA-C	-5.99	102.62	110.53
1	A	225	GLU	N-CA-C	-5.91	104.93	114.09
1	A	124	LEU	N-CA-C	5.58	118.56	111.69
1	A	185	GLU	N-CA-C	-5.13	105.60	111.14
1	A	278	ILE	N-CA-C	5.10	116.05	108.65
1	B	278	ILE	N-CA-C	5.01	116.20	108.44

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	2969	0	2953	122	0
1	B	2969	0	2953	116	0
2	A	68	0	0	3	0
2	B	43	0	0	3	0
All	All	6049	0	5906	235	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 20.

All (235) 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:B:94:ASN:ND2	1:B:95:ASP:H	1.60	0.99
1:A:239:MET:HE1	1:A:377:LEU:HD22	1.50	0.93
1:A:94:ASN:ND2	1:A:95:ASP:H	1.67	0.93
1:A:48:SER:HA	1:A:51:THR:HG22	1.52	0.90
1:B:322:LYS:HG2	1:B:352:ALA:HB2	1.55	0.85
1:B:220:ALA:HB2	1:B:273:MET:HG2	1.59	0.84
1:A:84:ARG:HD3	1:A:124:LEU:HD23	1.61	0.82
1:B:75:THR:HB	1:B:78:ASN:HD22	1.44	0.82
1:A:220:ALA:HB2	1:A:273:MET:HG2	1.63	0.80
1:A:75:THR:HB	1:A:78:ASN:ND2	1.98	0.79
1:A:322:LYS:HG2	1:A:352:ALA:HB2	1.66	0.78
1:B:75:THR:HB	1:B:78:ASN:ND2	2.00	0.76
1:B:94:ASN:HD22	1:B:95:ASP:H	1.33	0.75
1:B:75:THR:O	1:B:76:SER:HB2	1.87	0.74
1:A:75:THR:HB	1:A:78:ASN:HD22	1.51	0.74
1:A:94:ASN:HD22	1:A:95:ASP:H	1.35	0.74
1:A:75:THR:O	1:A:76:SER:HB2	1.88	0.73
1:A:92:LYS:HE3	1:A:94:ASN:HB2	1.70	0.73
1:B:239:MET:HE3	1:B:377:LEU:HD22	1.73	0.70
1:A:50:ARG:HH12	1:A:72:GLN:NE2	1.90	0.69
1:B:92:LYS:HE3	1:B:94:ASN:OD1	1.92	0.69
1:B:47:ASP:O	1:B:51:THR:HG22	1.93	0.69
1:A:48:SER:HA	1:A:51:THR:CG2	2.23	0.69
1:B:38:LEU:HD23	1:B:57:VAL:HG21	1.75	0.68
1:B:8:MET:HE3	1:B:261:PHE:HD1	1.58	0.68
1:B:58:ARG:HB2	1:B:58:ARG:NH1	2.08	0.68
1:A:9:GLU:HB2	1:A:58:ARG:NH2	2.08	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:MET:HE3	1:A:382:CYS:SG	2.34	0.68
1:B:222:MET:HG3	1:B:227:MET:HE2	1.75	0.67
1:B:80:HIS:HB3	1:B:124:LEU:HD13	1.75	0.67
1:A:58:ARG:NH1	1:A:58:ARG:HB2	2.10	0.67
1:A:92:LYS:HE3	1:A:94:ASN:CB	2.26	0.66
1:B:285:MET:HE2	1:B:287:MET:HE2	1.78	0.66
1:B:334:ILE:HG12	1:B:339:THR:HB	1.78	0.66
1:B:92:LYS:HE2	2:B:441:HOH:O	1.95	0.65
1:B:75:THR:HG22	1:B:77:VAL:H	1.61	0.65
1:A:140:GLN:O	1:A:144:LEU:HD23	1.97	0.65
1:A:8:MET:HE3	1:A:261:PHE:CD1	2.32	0.64
1:A:12:PHE:HZ	1:A:264:LEU:HD22	1.63	0.64
1:A:54:ASN:HD21	1:A:60:ASP:H	1.44	0.63
1:B:48:SER:HA	1:B:51:THR:CG2	2.28	0.63
1:A:50:ARG:HH12	1:A:72:GLN:HE22	1.47	0.63
1:A:305:VAL:HG13	2:A:408:HOH:O	1.97	0.63
1:A:94:ASN:O	1:A:95:ASP:HB3	1.98	0.63
1:A:92:LYS:HE3	1:A:94:ASN:CG	2.24	0.62
1:B:99:PHE:CE1	1:B:178:ILE:HD11	2.34	0.62
1:A:58:ARG:HB2	1:A:58:ARG:CZ	2.29	0.62
1:B:140:GLN:O	1:B:144:LEU:HD23	1.98	0.62
1:A:47:ASP:CG	1:A:48:SER:H	2.08	0.62
1:B:50:ARG:HH22	1:B:72:GLN:NE2	1.97	0.62
1:B:50:ARG:HH22	1:B:72:GLN:HE21	1.48	0.61
1:A:8:MET:HE3	1:A:261:PHE:HD1	1.64	0.61
1:B:287:MET:HE1	1:B:366:PHE:CE1	2.35	0.61
1:A:110:ARG:HE	1:A:110:ARG:HA	1.64	0.61
1:B:8:MET:HE3	1:B:261:PHE:CD1	2.35	0.61
1:A:154:ASN:ND2	1:B:82:SER:HB2	2.16	0.61
1:B:112:PRO:CB	1:B:318:ALA:HB3	2.30	0.61
1:A:285:MET:HE2	1:A:287:MET:CE	2.31	0.61
1:B:201:THR:C	1:B:203:GLN:H	2.09	0.61
1:B:54:ASN:HD21	1:B:60:ASP:H	1.49	0.59
1:B:58:ARG:HB2	1:B:58:ARG:CZ	2.31	0.59
1:B:255:LEU:HA	1:B:258:ILE:CD1	2.32	0.59
1:B:255:LEU:O	1:B:258:ILE:HD13	2.01	0.59
1:B:94:ASN:O	1:B:95:ASP:HB3	2.01	0.59
1:A:184:TRP:HH2	1:A:241:MET:HE2	1.67	0.59
1:A:268:THR:HG22	1:A:268:THR:O	2.02	0.59
1:B:133:ASN:ND2	1:B:137:ALA:HB3	2.18	0.59
1:A:239:MET:CE	1:A:377:LEU:HD22	2.28	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:SER:CA	1:A:51:THR:HG22	2.31	0.58
1:B:244:LEU:HD12	1:B:244:LEU:N	2.18	0.58
1:B:94:ASN:ND2	1:B:95:ASP:N	2.44	0.58
1:A:334:ILE:HG12	1:A:339:THR:HB	1.85	0.57
1:B:305:VAL:HG13	2:B:419:HOH:O	2.03	0.57
1:B:113:ILE:HG21	1:B:118:LEU:HD21	1.86	0.57
1:A:258:ILE:HD13	1:A:258:ILE:H	1.69	0.57
1:A:220:ALA:HB1	1:A:272:VAL:HG12	1.87	0.57
1:B:110:ARG:HE	1:B:110:ARG:HA	1.69	0.57
1:A:120:CYS:SG	1:A:124:LEU:HD12	2.46	0.56
1:B:227:MET:HE1	1:B:229:ILE:HD11	1.86	0.56
1:B:258:ILE:HD13	1:B:258:ILE:H	1.71	0.56
1:A:244:LEU:HD12	1:A:244:LEU:N	2.20	0.56
1:A:222:MET:HB2	1:A:227:MET:HG3	1.88	0.56
1:B:69:ILE:HD13	1:B:117:TYR:HA	1.87	0.56
1:A:129:LEU:HD13	1:A:129:LEU:C	2.31	0.56
1:A:113:ILE:O	1:A:114:LEU:C	2.49	0.56
1:A:285:MET:HE2	1:A:287:MET:HE2	1.87	0.56
1:A:184:TRP:CD1	1:A:338:GLY:HA2	2.41	0.56
1:B:133:ASN:HD22	1:B:137:ALA:HB3	1.71	0.55
1:B:268:THR:HG22	1:B:268:THR:O	2.07	0.55
1:B:181:LYS:HE3	1:B:340:GLU:OE1	2.07	0.54
1:A:184:TRP:CH2	1:A:241:MET:HE2	2.42	0.54
1:A:304:ASP:O	1:A:310:ALA:HB2	2.08	0.54
1:A:322:LYS:CG	1:A:352:ALA:HB2	2.37	0.54
1:B:219:VAL:HG12	1:B:220:ALA:N	2.22	0.54
1:B:105:LEU:HD11	1:B:174:LEU:HD22	1.90	0.54
1:B:48:SER:HA	1:B:51:THR:HG23	1.88	0.54
1:B:17:GLU:HG3	2:B:475:HOH:O	2.08	0.53
1:B:212:TYR:HA	1:B:280:VAL:O	2.09	0.53
1:B:222:MET:HB2	1:B:227:MET:HG3	1.90	0.53
1:B:172:MET:HE1	1:B:315:ILE:HD13	1.91	0.53
1:B:322:LYS:CG	1:B:352:ALA:HB2	2.35	0.53
1:A:107:ALA:HB1	1:A:113:ILE:HD11	1.92	0.52
1:A:86:ILE:O	1:A:86:ILE:HD13	2.09	0.52
1:B:99:PHE:CZ	1:B:178:ILE:HD11	2.44	0.52
1:A:276:ARG:NH1	1:A:276:ARG:HG2	2.24	0.52
1:B:294:THR:O	1:B:298:MET:HB2	2.09	0.52
1:A:201:THR:C	1:A:203:GLN:H	2.17	0.52
1:B:94:ASN:HD22	1:B:95:ASP:N	2.02	0.52
1:A:321:LEU:HD23	1:A:351:ALA:HA	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:296:VAL:O	1:B:300:MET:HG3	2.10	0.51
1:A:276:ARG:HG2	1:A:276:ARG:HH11	1.76	0.51
1:B:69:ILE:HD12	1:B:116:GLU:HG2	1.92	0.51
1:B:94:ASN:CG	1:B:95:ASP:H	2.14	0.51
1:A:294:THR:O	1:A:298:MET:HB2	2.11	0.51
1:A:75:THR:O	1:A:76:SER:CB	2.58	0.51
1:A:287:MET:HE1	1:A:366:PHE:CE1	2.45	0.50
1:A:113:ILE:HG21	1:A:118:LEU:HD21	1.93	0.50
1:B:285:MET:HE2	1:B:287:MET:CE	2.41	0.50
1:B:178:ILE:O	1:B:342:VAL:HA	2.12	0.50
1:B:356:GLU:O	1:B:356:GLU:HG2	2.11	0.50
1:A:340:GLU:OE1	1:B:75:THR:HG23	2.11	0.50
1:A:133:ASN:ND2	1:A:137:ALA:HB3	2.26	0.49
1:B:241:MET:HE3	1:B:243:VAL:HG22	1.94	0.49
1:A:94:ASN:HD22	1:A:95:ASP:N	2.08	0.49
1:A:252:LEU:O	1:A:256:GLU:HG3	2.13	0.49
1:A:219:VAL:HG12	1:A:220:ALA:N	2.28	0.49
1:A:203:GLN:O	1:A:204:GLU:HB2	2.13	0.49
1:B:133:ASN:ND2	1:B:137:ALA:CB	2.76	0.49
1:B:9:GLU:HB2	1:B:58:ARG:NH2	2.28	0.48
1:A:34:ILE:HD11	1:A:328:HIS:CD2	2.49	0.48
1:A:105:LEU:HD11	1:A:174:LEU:CD2	2.42	0.48
1:B:50:ARG:HH12	1:B:72:GLN:NE2	2.11	0.48
1:B:129:LEU:HD22	1:B:130:GLU:H	1.78	0.48
1:A:285:MET:HE3	1:A:382:CYS:CB	2.43	0.48
1:B:31:PRO:HD2	1:B:377:LEU:O	2.13	0.48
1:B:107:ALA:HB1	1:B:113:ILE:CD1	2.44	0.48
1:B:113:ILE:O	1:B:114:LEU:C	2.57	0.48
1:B:245:LEU:HD21	1:B:359:ARG:O	2.14	0.48
1:A:105:LEU:HG	1:A:174:LEU:HD23	1.97	0.47
1:B:8:MET:HE1	1:B:264:LEU:HD23	1.95	0.47
1:B:201:THR:OG1	1:B:204:GLU:HB3	2.13	0.47
1:B:255:LEU:HA	1:B:258:ILE:HD11	1.96	0.47
1:B:84:ARG:HH11	1:B:124:LEU:HD23	1.79	0.47
1:B:105:LEU:CD1	1:B:174:LEU:HD22	2.45	0.47
1:B:285:MET:HE3	1:B:382:CYS:SG	2.54	0.47
1:B:111:TYR:O	1:B:113:ILE:N	2.41	0.47
1:A:69:ILE:HD13	1:A:117:TYR:HA	1.97	0.47
1:A:1:GLY:O	1:A:2:SER:HB3	2.16	0.46
1:A:53:ILE:HD11	1:A:305:VAL:HG11	1.96	0.46
1:B:260:ASN:OD1	1:B:262:GLU:HB2	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:GLU:HB2	1:A:58:ARG:CZ	2.46	0.46
1:A:31:PRO:HD2	1:A:377:LEU:O	2.15	0.46
1:A:112:PRO:CB	1:A:318:ALA:HB2	2.46	0.46
1:A:260:ASN:OD1	1:A:262:GLU:HB2	2.15	0.46
1:B:91:THR:O	1:B:92:LYS:C	2.58	0.46
1:A:94:ASN:CG	1:A:95:ASP:H	2.20	0.46
1:B:50:ARG:HH12	1:B:72:GLN:HE22	1.62	0.46
1:A:111:TYR:OH	1:A:319:GLU:HB2	2.15	0.46
1:A:184:TRP:HH2	1:A:241:MET:CE	2.29	0.46
1:A:201:THR:OG1	1:A:204:GLU:HB3	2.16	0.46
1:B:129:LEU:HD22	1:B:130:GLU:N	2.31	0.46
1:B:263:LYS:HB3	1:B:267:TRP:CZ2	2.51	0.46
1:A:50:ARG:HH22	1:A:72:GLN:NE2	2.13	0.46
1:A:234:PHE:CE1	1:A:339:THR:HG23	2.51	0.46
1:A:340:GLU:OE1	1:B:75:THR:CG2	2.64	0.46
1:A:133:ASN:ND2	1:A:137:ALA:CB	2.79	0.45
1:B:115:PRO:HG2	1:B:116:GLU:H	1.81	0.45
1:B:105:LEU:HD11	1:B:174:LEU:CD2	2.45	0.45
1:B:157:ILE:CD1	1:B:343:GLY:HA2	2.46	0.45
1:B:304:ASP:O	1:B:310:ALA:HB2	2.16	0.45
1:B:201:THR:C	1:B:203:GLN:N	2.72	0.45
1:A:325:GLN:HB2	2:A:435:HOH:O	2.16	0.45
1:B:249:VAL:HG12	1:B:249:VAL:O	2.16	0.45
1:A:43:LEU:HG	1:A:80:HIS:CE1	2.52	0.45
1:B:287:MET:HE1	1:B:366:PHE:HE1	1.79	0.45
1:A:91:THR:O	1:A:92:LYS:C	2.59	0.44
1:A:311:ASN:C	1:A:311:ASN:HD22	2.25	0.44
1:B:111:TYR:C	1:B:113:ILE:H	2.26	0.44
1:B:321:LEU:HD23	1:B:351:ALA:HA	1.99	0.44
1:B:373:THR:O	1:B:374:ASN:HB2	2.18	0.44
1:A:94:ASN:O	1:A:95:ASP:CB	2.63	0.44
1:B:79:VAL:HG13	1:B:80:HIS:N	2.33	0.44
1:A:40:MET:HE2	2:A:401:HOH:O	2.17	0.44
1:A:311:ASN:ND2	1:A:313:SER:H	2.15	0.44
1:B:193:THR:HG23	1:B:210:MET:O	2.18	0.44
1:A:108:GLU:OE2	1:A:134:PHE:HB2	2.18	0.44
1:A:83:LEU:O	1:A:86:ILE:HG22	2.17	0.43
1:B:94:ASN:O	1:B:95:ASP:CB	2.65	0.43
1:A:71:ALA:O	1:A:75:THR:OG1	2.34	0.43
1:A:234:PHE:HE1	1:A:339:THR:HG23	1.84	0.43
1:A:111:TYR:OH	1:A:321:LEU:HD21	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:SER:C	1:B:272:VAL:H	2.25	0.43
1:A:49:THR:HG23	1:A:305:VAL:HG12	2.01	0.43
1:A:196:MET:HG3	1:A:197:PRO:HD2	2.01	0.43
1:B:275:GLU:C	1:B:276:ARG:HG3	2.43	0.43
1:A:50:ARG:HH22	1:A:72:GLN:HE21	1.67	0.43
1:A:80:HIS:HB3	1:A:124:LEU:HD13	2.00	0.43
1:B:311:ASN:C	1:B:311:ASN:HD22	2.26	0.43
1:A:77:VAL:HG12	1:A:77:VAL:O	2.18	0.42
1:A:255:LEU:O	1:A:258:ILE:HD13	2.18	0.42
1:B:120:CYS:SG	1:B:124:LEU:HD12	2.58	0.42
1:A:133:ASN:HD22	1:A:137:ALA:HB3	1.85	0.42
1:A:219:VAL:O	1:A:273:MET:HA	2.20	0.42
1:A:285:MET:HE3	1:A:382:CYS:HB2	2.01	0.42
1:B:248:GLU:C	1:B:250:SER:H	2.28	0.42
1:B:377:LEU:N	1:B:377:LEU:HD12	2.33	0.42
1:B:49:THR:CG2	1:B:305:VAL:HG12	2.49	0.42
1:B:129:LEU:C	1:B:129:LEU:HD13	2.45	0.42
1:A:79:VAL:HG13	1:A:80:HIS:N	2.35	0.42
1:B:75:THR:O	1:B:76:SER:CB	2.58	0.42
1:A:112:PRO:HB2	1:A:318:ALA:CB	2.50	0.42
1:A:168:SER:OG	1:A:169:GLN:NE2	2.47	0.42
1:A:178:ILE:O	1:A:342:VAL:HA	2.20	0.42
1:B:53:ILE:HD11	1:B:305:VAL:HG11	2.01	0.42
1:A:94:ASN:HA	1:A:97:TYR:O	2.20	0.41
1:A:275:GLU:C	1:A:276:ARG:HG3	2.45	0.41
1:A:99:PHE:CE1	1:A:178:ILE:HD11	2.55	0.41
1:A:196:MET:CG	1:A:197:PRO:HD2	2.50	0.41
1:A:201:THR:C	1:A:203:GLN:N	2.76	0.41
1:A:223:ALA:O	1:A:224:SER:HB3	2.21	0.41
1:B:88:ASN:HD21	1:B:126:ARG:NH2	2.18	0.41
1:A:105:LEU:CD1	1:A:174:LEU:HD23	2.50	0.41
1:B:363:PRO:HG3	1:B:383:VAL:HA	2.02	0.41
1:B:46:LYS:HD2	1:B:313:SER:OG	2.21	0.41
1:B:107:ALA:HB1	1:B:113:ILE:HD11	2.02	0.41
1:A:28:PHE:CZ	1:A:332:ALA:HB2	2.55	0.41
1:A:376:VAL:O	1:A:376:VAL:HG13	2.21	0.41
1:A:206:LYS:HA	1:A:207:PRO:HD3	1.85	0.40
1:A:258:ILE:H	1:A:258:ILE:CD1	2.34	0.40
1:A:311:ASN:C	1:A:311:ASN:ND2	2.79	0.40
1:B:211:MET:O	1:B:281:TYR:HA	2.21	0.40
1:B:219:VAL:HG21	1:B:278:ILE:HD13	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:LEU:HD23	1:A:57:VAL:HG21	2.04	0.40
1:A:285:MET:CE	1:A:382:CYS:HB2	2.51	0.40
1:B:105:LEU:CD1	1:B:174:LEU:CD2	3.00	0.40

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	375/385 (97%)	346 (92%)	23 (6%)	6 (2%)	7	7
1	B	375/385 (97%)	349 (93%)	21 (6%)	5 (1%)	9	10
All	All	750/770 (97%)	695 (93%)	44 (6%)	11 (2%)	8	8

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	SER
1	B	224	SER
1	A	204	GLU
1	B	200	VAL
1	A	95	ASP
1	A	318	ALA
1	A	2	SER
1	B	112	PRO
1	B	123	GLU
1	A	200	VAL
1	B	95	ASP

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	328/332 (99%)	312 (95%)	16 (5%)	22	34
1	B	328/332 (99%)	311 (95%)	17 (5%)	21	31
All	All	656/664 (99%)	623 (95%)	33 (5%)	22	33

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LEU
1	A	59	PHE
1	A	86	ILE
1	A	97	TYR
1	A	110	ARG
1	A	116	GLU
1	A	119	GLN
1	A	123	GLU
1	A	190	ASP
1	A	203	GLN
1	A	225	GLU
1	A	258	ILE
1	A	288	GLU
1	A	325	GLN
1	A	339	THR
1	A	363	PRO
1	B	32	ILE
1	B	43	LEU
1	B	51	THR
1	B	59	PHE
1	B	86	ILE
1	B	97	TYR
1	B	105	LEU
1	B	110	ARG
1	B	116	GLU
1	B	119	GLN
1	B	123	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	203	GLN
1	B	225	GLU
1	B	258	ILE
1	B	325	GLN
1	B	339	THR
1	B	363	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	72	GLN
1	A	88	ASN
1	A	89	GLN
1	A	133	ASN
1	A	140	GLN
1	A	152	GLN
1	A	169	GLN
1	A	311	ASN
1	A	325	GLN
1	B	54	ASN
1	B	72	GLN
1	B	88	ASN
1	B	89	GLN
1	B	94	ASN
1	B	152	GLN
1	B	169	GLN
1	B	311	ASN
1	B	325	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.