



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:19 PM UTC

PDB ID : 7F4R / pdb_00007f4r
Title : Crystal structure of MTA1
Authors : Chen, J.; Liu, L.
Deposited on : 2021-06-21
Resolution : 1.83 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)	:	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

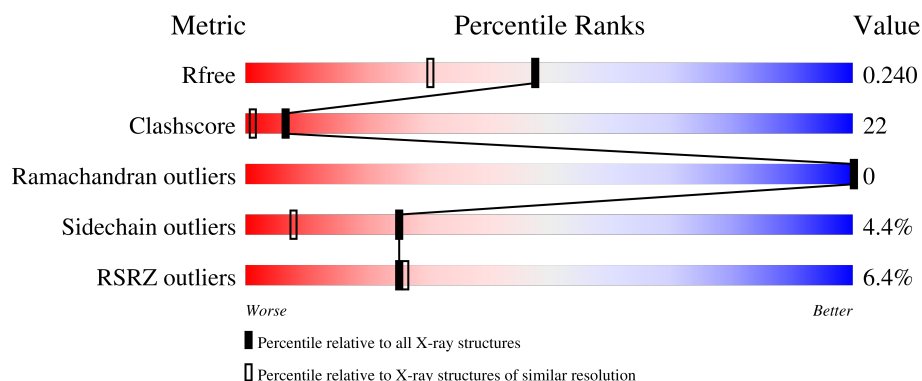
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	202	
1	B	202	
1	C	202	
1	D	202	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6260 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 MT-a70 family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	178	Total	C	N	O	S	0	0	0
			1452	927	252	265	8			
1	B	174	Total	C	N	O	S	0	0	0
			1421	908	249	256	8			
1	C	177	Total	C	N	O	S	0	0	0
			1436	917	251	260	8			
1	D	173	Total	C	N	O	S	0	0	0
			1410	901	247	254	8			

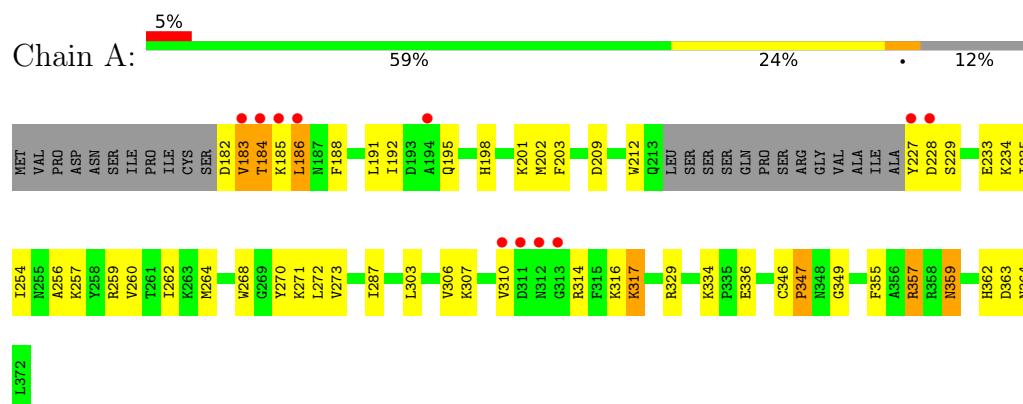
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	124	Total	O	0	0
			124	124		
2	B	133	Total	O	0	0
			133	133		
2	C	156	Total	O	0	0
			156	156		
2	D	128	Total	O	0	0
			128	128		

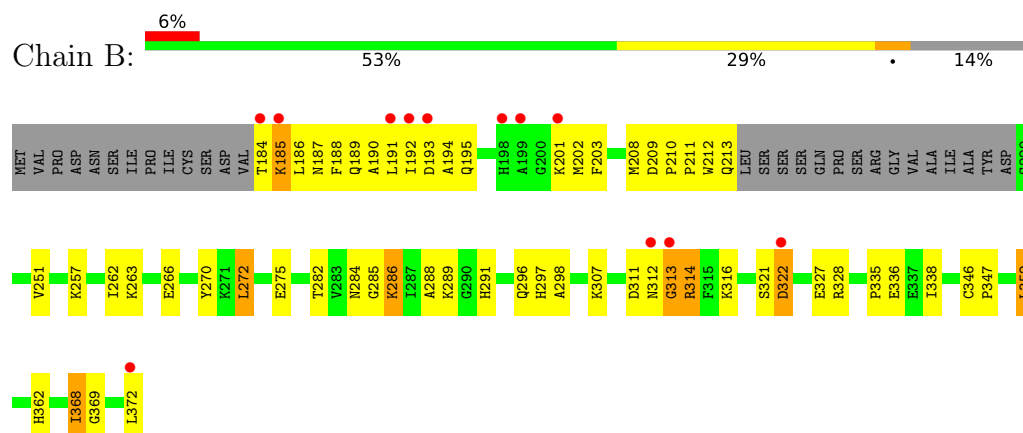
3 Residue-property plots [i](#)

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.

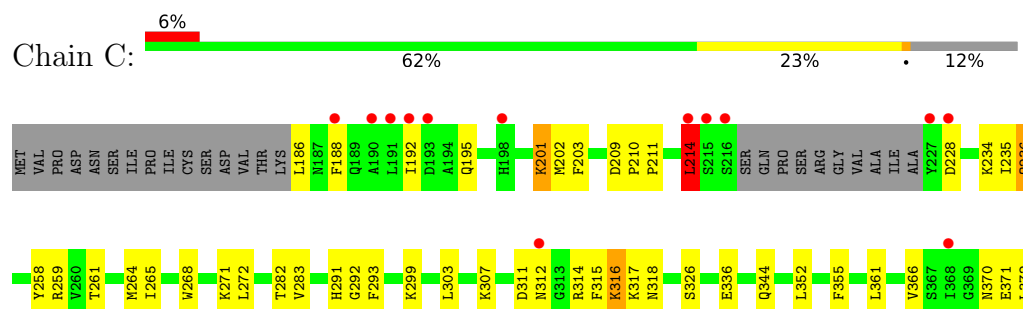
• Molecule 1: MT-a70 family protein



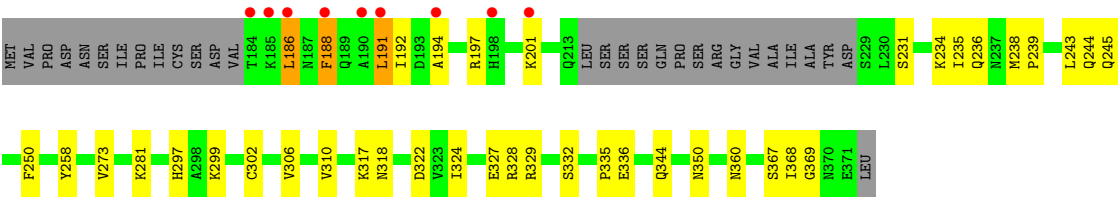
• Molecule 1: MT-a70 family protein



• Molecule 1: MT-a70 family protein



● Molecule 1: MT-a70 family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.87Å 112.95Å 81.85Å 90.00° 97.81° 90.00°	Depositor
Resolution (Å)	28.73 – 1.83 28.73 – 1.83	Depositor EDS
% Data completeness (in resolution range)	76.7 (28.73-1.83) 76.7 (28.73-1.83)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.210 , 0.241 0.210 , 0.240	Depositor DCC
R_{free} test set	2000 reflections (2.82%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6260	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.63% 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

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	0.96	3/1484 (0.2%)	0.88	6/2001 (0.3%)
1	B	0.85	4/1452 (0.3%)	0.95	12/1955 (0.6%)
1	C	0.85	5/1467 (0.3%)	0.88	7/1977 (0.4%)
1	D	0.85	1/1441 (0.1%)	0.84	2/1940 (0.1%)
All	All	0.88	13/5844 (0.2%)	0.89	27/7873 (0.3%)

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	B	0	1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	209	ASP	C-N	8.71	1.41	1.33
1	C	209	ASP	C-N	5.77	1.40	1.33
1	D	239	PRO	N-CD	5.72	1.55	1.47
1	A	346	CYS	C-N	5.54	1.40	1.33
1	C	239	PRO	N-CD	5.49	1.55	1.47
1	B	347	PRO	N-CD	5.42	1.55	1.47
1	C	210	PRO	N-CD	5.32	1.55	1.47
1	B	346	CYS	C-N	5.31	1.40	1.33
1	C	211	PRO	N-CD	5.25	1.55	1.47
1	A	347	PRO	N-CD	5.23	1.55	1.47
1	B	211	PRO	N-CD	5.22	1.55	1.47
1	C	210	PRO	C-O	-5.18	1.18	1.24
1	A	239	PRO	N-CD	5.05	1.54	1.47

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	210	PRO	O-C-N	8.71	125.31	121.31
1	B	209	ASP	CA-C-N	-8.02	113.81	119.66
1	B	209	ASP	C-N-CA	-8.02	113.81	119.66
1	C	214	LEU	N-CA-C	-7.33	99.43	110.28
1	C	371	GLU	N-CA-C	-6.46	100.34	109.96
1	B	346	CYS	CA-C-N	-6.36	113.21	119.76
1	B	346	CYS	C-N-CA	-6.36	113.21	119.76
1	C	209	ASP	CA-C-N	-6.35	113.84	120.38
1	C	209	ASP	C-N-CA	-6.35	113.84	120.38
1	B	193	ASP	CB-CA-C	-6.22	101.11	110.88
1	A	346	CYS	CA-C-N	-6.20	113.38	119.76
1	A	346	CYS	C-N-CA	-6.20	113.38	119.76
1	A	359	ASN	CA-C-N	6.12	128.48	120.28
1	A	359	ASN	C-N-CA	6.12	128.48	120.28
1	C	210	PRO	CA-C-N	-5.39	113.10	119.84
1	C	210	PRO	C-N-CA	-5.39	113.10	119.84
1	A	238	MET	CA-C-N	-5.39	113.36	120.96
1	A	238	MET	C-N-CA	-5.39	113.36	120.96
1	B	210	PRO	CA-C-N	-5.38	113.11	119.84
1	B	210	PRO	C-N-CA	-5.38	113.11	119.84
1	B	321	SER	CA-C-N	5.38	129.21	120.60
1	B	321	SER	C-N-CA	5.38	129.21	120.60
1	C	259	ARG	N-CA-C	5.34	116.91	111.14
1	B	313	GLY	N-CA-C	-5.34	108.80	114.67
1	B	210	PRO	N-CA-C	5.29	115.55	110.47
1	D	258	TYR	N-CA-C	5.22	116.66	111.07
1	D	188	PHE	N-CA-C	5.11	116.85	111.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	311	ASP	Peptide

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	1452	0	1423	100	0
1	B	1421	0	1408	82	0
1	C	1436	0	1409	57	0
1	D	1410	0	1393	35	0
2	A	124	0	0	13	0
2	B	133	0	0	14	1
2	C	156	0	0	19	0
2	D	128	0	0	6	0
All	All	6260	0	5633	246	1

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 22.

All (246) 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:186:LEU:CD2	1:B:368:ILE:HD11	1.22	1.57
1:A:186:LEU:HD22	1:B:368:ILE:CD1	1.11	1.56
1:A:209:ASP:OD2	1:A:357:ARG:CG	1.79	1.31
1:C:299:LYS:HE2	2:C:489:HOH:O	1.16	1.29
1:A:209:ASP:OD2	1:A:357:ARG:HG3	1.15	1.29
1:B:313:GLY:O	1:B:316:LYS:NZ	1.64	1.27
1:D:317:LYS:HD2	2:D:502:HOH:O	1.38	1.23
1:A:228:ASP:HB2	2:A:497:HOH:O	1.37	1.21
1:B:275:GLU:OE1	2:B:401:HOH:O	1.56	1.21
1:C:228:ASP:OD1	2:C:402:HOH:O	1.66	1.14
1:C:214:LEU:CD1	2:C:446:HOH:O	1.95	1.14
1:C:234:LYS:HE3	2:C:508:HOH:O	1.46	1.13
1:A:182:ASP:HB3	1:A:185:LYS:H	1.01	1.13
1:A:186:LEU:HD22	1:B:368:ILE:HD12	1.30	1.11
1:B:368:ILE:HD13	1:B:369:GLY:N	1.66	1.11
1:A:183:VAL:HG12	1:A:186:LEU:HD11	1.30	1.09
1:C:265:ILE:HD11	1:C:272:LEU:HD22	1.35	1.04
1:A:186:LEU:HD23	1:B:368:ILE:HD11	1.39	1.03
1:C:235:ILE:HG22	1:C:264:MET:HE1	1.44	0.98
1:C:186:LEU:N	2:C:404:HOH:O	1.97	0.97
1:A:182:ASP:HB3	1:A:185:LYS:N	1.81	0.96
1:A:186:LEU:CD2	1:B:368:ILE:CD1	1.97	0.95
1:A:271:LYS:HE2	2:A:470:HOH:O	1.66	0.95
1:C:312:ASN:HD21	1:C:314:ARG:HB2	1.30	0.95
1:B:282:THR:HG21	2:B:476:HOH:O	1.68	0.94
1:B:368:ILE:HD13	1:B:369:GLY:H	1.32	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:ASP:OD1	1:A:184:THR:OG1	1.85	0.93
1:D:194:ALA:HA	1:D:197:ARG:HD3	1.51	0.91
1:B:187:ASN:O	2:B:402:HOH:O	1.88	0.91
1:C:265:ILE:HD11	1:C:272:LEU:CD2	2.00	0.91
1:C:282:THR:HG23	2:C:497:HOH:O	1.70	0.90
1:D:186:LEU:HB2	1:D:188:PHE:HE2	1.37	0.90
1:A:191:LEU:HD12	2:A:483:HOH:O	1.71	0.90
1:C:336:GLU:OE1	2:C:403:HOH:O	1.89	0.89
1:C:228:ASP:CG	2:C:402:HOH:O	2.10	0.88
1:D:329:ARG:NH1	2:D:402:HOH:O	2.07	0.87
1:C:214:LEU:HD12	2:C:446:HOH:O	1.63	0.87
1:B:288:ALA:H	1:D:318:ASN:HD22	1.23	0.87
1:D:186:LEU:HB2	1:D:188:PHE:CE2	2.08	0.86
1:A:227:TYR:OH	1:B:372:LEU:O	1.94	0.85
1:D:344:GLN:OE1	2:D:401:HOH:O	1.95	0.84
1:B:184:THR:HG22	1:B:186:LEU:HG	1.59	0.84
1:A:182:ASP:CB	1:A:185:LYS:H	1.90	0.81
1:C:312:ASN:ND2	1:C:314:ARG:HB2	1.94	0.80
1:B:288:ALA:H	1:D:318:ASN:ND2	1.79	0.80
1:B:285:GLY:HA2	1:B:286:LYS:HE2	1.65	0.79
1:A:182:ASP:N	1:A:183:VAL:HA	1.97	0.79
1:C:336:GLU:OE2	2:C:405:HOH:O	2.02	0.76
1:B:195:GLN:HG3	1:B:203:PHE:CZ	2.20	0.76
1:D:328:ARG:NH2	2:D:403:HOH:O	2.19	0.75
2:C:405:HOH:O	1:D:328:ARG:NH1	2.19	0.74
1:B:262:ILE:HG23	1:B:272:LEU:HD13	1.69	0.74
1:C:234:LYS:CE	2:C:508:HOH:O	2.19	0.73
1:C:316:LYS:N	1:C:316:LYS:HD2	2.04	0.72
1:C:282:THR:HG22	1:C:283:VAL:N	2.03	0.72
1:A:363:ASP:O	1:A:364:ASN:HB2	1.89	0.71
1:A:262:ILE:HG23	1:A:272:LEU:CD1	2.21	0.71
1:B:263:LYS:NZ	2:B:405:HOH:O	2.16	0.70
1:B:352:LEU:HD13	1:B:352:LEU:C	2.16	0.70
1:A:183:VAL:CG1	1:A:186:LEU:HD11	2.16	0.69
1:A:254:ILE:HD13	1:A:256:ALA:H	1.55	0.69
1:A:233:GLU:O	1:A:237:ASN:OD1	2.10	0.69
1:B:266:GLU:OE2	2:B:404:HOH:O	2.10	0.69
1:A:254:ILE:HD12	1:A:257:LYS:H	1.57	0.68
1:C:312:ASN:HD21	1:C:314:ARG:CB	2.07	0.68
1:A:334:LYS:HG3	1:A:357:ARG:CD	2.24	0.68
1:B:368:ILE:CD1	1:B:369:GLY:N	2.53	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:ILE:HD11	1:B:354:ILE:HG12	1.77	0.67
1:A:257:LYS:HE3	1:A:260:VAL:HG11	1.76	0.67
1:A:363:ASP:O	2:A:401:HOH:O	2.13	0.66
1:A:334:LYS:HG3	1:A:357:ARG:HD2	1.78	0.66
1:B:188:PHE:O	1:B:191:LEU:N	2.29	0.66
1:A:317:LYS:HG3	1:C:293:PHE:CD1	2.31	0.66
1:A:254:ILE:HD12	1:A:254:ILE:C	2.19	0.66
1:B:285:GLY:HA2	1:B:286:LYS:CE	2.26	0.66
1:B:184:THR:HG22	1:B:186:LEU:CG	2.25	0.66
1:C:195:GLN:HG3	1:C:203:PHE:CZ	2.30	0.66
1:A:209:ASP:OD2	1:A:357:ARG:CD	2.42	0.66
1:C:214:LEU:C	1:C:214:LEU:HD22	2.21	0.65
1:C:214:LEU:HD13	1:C:214:LEU:O	1.94	0.65
1:A:273:VAL:CG2	1:C:291:HIS:O	2.45	0.65
1:C:344:GLN:OE1	2:C:407:HOH:O	2.14	0.65
1:B:327:GLU:CD	2:B:411:HOH:O	2.40	0.64
1:A:209:ASP:OD2	1:A:357:ARG:HG2	1.93	0.64
1:B:189:GLN:HA	1:B:192:ILE:HD12	1.79	0.64
1:B:289:LYS:HE3	2:B:412:HOH:O	1.98	0.64
1:A:366:VAL:HG23	1:B:352:LEU:HD23	1.80	0.63
1:B:312:ASN:HB3	1:B:314:ARG:HB2	1.81	0.62
1:D:231:SER:OG	1:D:234:LYS:HD2	1.99	0.61
1:B:312:ASN:N	1:B:312:ASN:HD22	1.98	0.61
1:C:282:THR:CG2	1:C:283:VAL:N	2.63	0.61
1:C:370:ASN:ND2	2:C:413:HOH:O	2.33	0.61
1:A:183:VAL:HG11	1:A:355:PHE:HE1	1.65	0.60
1:B:284:ASN:ND2	1:B:296:GLN:OE1	2.35	0.60
1:A:182:ASP:N	1:A:185:LYS:O	2.34	0.60
1:B:368:ILE:HD13	1:B:368:ILE:C	2.26	0.60
1:D:299:LYS:NZ	2:D:405:HOH:O	2.32	0.60
1:C:236:GLN:HA	1:C:264:MET:HE3	1.83	0.60
1:C:315:PHE:C	1:C:316:LYS:HD2	2.27	0.60
1:A:254:ILE:HD11	1:A:257:LYS:HG2	1.85	0.59
1:A:254:ILE:HD12	1:A:254:ILE:O	2.02	0.59
1:D:186:LEU:CB	1:D:188:PHE:CE2	2.85	0.59
1:A:227:TYR:HD1	1:A:228:ASP:H	1.45	0.59
1:D:188:PHE:HD1	1:D:243:LEU:HD21	1.68	0.58
1:A:254:ILE:CD1	1:A:257:LYS:H	2.15	0.58
1:A:186:LEU:HD22	1:B:368:ILE:HD11	0.64	0.58
1:A:195:GLN:HG3	1:A:203:PHE:CE1	2.39	0.57
1:B:312:ASN:CB	1:B:314:ARG:HB2	2.35	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:LYS:HE3	1:B:286:LYS:H	1.69	0.57
1:C:264:MET:HE2	1:C:268:TRP:CH2	2.40	0.57
1:A:201:LYS:HE2	2:A:402:HOH:O	2.03	0.57
1:B:289:LYS:CE	2:B:412:HOH:O	2.53	0.57
1:D:281:LYS:HB2	1:D:329:ARG:HG3	1.87	0.56
1:A:254:ILE:HD13	1:A:256:ALA:N	2.19	0.56
1:B:282:THR:HG23	1:B:298:ALA:HB3	1.87	0.56
1:B:188:PHE:O	1:B:192:ILE:N	2.37	0.56
1:A:262:ILE:HG23	1:A:272:LEU:HD12	1.87	0.56
1:B:270:TYR:CE2	1:B:307:LYS:HG2	2.41	0.56
1:A:303:LEU:HD12	1:A:303:LEU:N	2.21	0.55
1:A:191:LEU:CD1	2:A:483:HOH:O	2.43	0.55
1:A:316:LYS:HZ3	1:A:347:PRO:CD	2.20	0.55
1:A:254:ILE:C	1:A:254:ILE:CD1	2.80	0.55
1:A:183:VAL:HG12	1:A:186:LEU:CD1	2.20	0.54
1:B:314:ARG:HH11	1:B:314:ARG:CG	2.19	0.54
1:C:235:ILE:HG22	1:C:264:MET:CE	2.28	0.54
1:C:261:THR:HA	1:C:264:MET:HG2	1.90	0.54
1:A:306:VAL:HG21	1:A:310:VAL:HG21	1.90	0.54
1:B:213:GLN:CD	1:B:231:SER:HA	2.32	0.54
1:A:273:VAL:O	1:A:273:VAL:HG22	2.08	0.54
1:C:352:LEU:HD11	1:D:368:ILE:HG12	1.90	0.53
1:D:235:ILE:HA	1:D:238:MET:HE2	1.90	0.53
1:B:322:ASP:HB2	1:D:297:HIS:H	1.74	0.52
1:D:188:PHE:O	1:D:192:ILE:HG13	2.09	0.52
1:C:271:LYS:HE2	2:C:529:HOH:O	2.10	0.52
1:A:227:TYR:CD1	1:A:228:ASP:N	2.73	0.51
1:D:332:SER:HG	1:D:360:ASN:H	1.59	0.51
1:A:195:GLN:HG3	1:A:203:PHE:CZ	2.46	0.51
1:A:262:ILE:HG23	1:A:272:LEU:HD11	1.92	0.51
1:B:286:LYS:CD	1:B:286:LYS:N	2.73	0.51
1:B:188:PHE:O	1:B:191:LEU:HB2	2.12	0.50
1:B:291:HIS:C	2:B:419:HOH:O	2.54	0.50
1:C:235:ILE:CG2	1:C:264:MET:HE1	2.29	0.50
1:C:282:THR:CG2	1:C:283:VAL:H	2.22	0.50
1:A:317:LYS:HG2	1:C:293:PHE:HA	1.93	0.50
1:B:212:TRP:CE3	1:B:257:LYS:HE2	2.47	0.50
1:B:286:LYS:HE3	1:B:286:LYS:N	2.27	0.50
1:A:201:LYS:CE	2:A:402:HOH:O	2.58	0.50
1:C:258:TYR:CE1	1:C:303:LEU:HD11	2.47	0.50
1:B:359:ASN:HB3	1:B:362:HIS:HD2	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:PHE:O	1:A:191:LEU:HB3	2.12	0.49
1:A:235:ILE:O	1:A:238:MET:HG3	2.12	0.49
1:A:270:TYR:CE2	1:A:307:LYS:HG2	2.47	0.49
1:C:312:ASN:CG	1:C:314:ARG:H	2.20	0.49
1:D:201:LYS:HE3	1:D:350:ASN:HD22	1.76	0.49
1:A:262:ILE:HD13	1:A:303:LEU:HD23	1.95	0.49
1:A:336:GLU:OE1	1:B:359:ASN:ND2	2.33	0.49
1:A:314:ARG:HH22	1:A:349:GLY:HA2	1.77	0.49
1:B:352:LEU:CD1	1:B:354:ILE:HG13	2.43	0.49
1:B:368:ILE:CD1	1:B:368:ILE:C	2.86	0.49
1:A:212:TRP:CD2	1:A:257:LYS:HG3	2.48	0.48
1:B:213:GLN:HG3	2:B:406:HOH:O	2.14	0.48
1:B:245:GLN:OE1	1:B:245:GLN:HA	2.13	0.47
1:B:352:LEU:C	1:B:352:LEU:CD1	2.86	0.47
1:A:329:ARG:HD2	2:A:413:HOH:O	2.15	0.47
1:B:184:THR:HG21	1:B:186:LEU:HD21	1.97	0.47
1:A:209:ASP:OD2	1:A:334:LYS:NZ	2.42	0.47
1:A:212:TRP:CE3	1:A:257:LYS:HE2	2.50	0.47
1:B:190:ALA:O	1:B:194:ALA:CB	2.62	0.47
1:B:352:LEU:HD11	1:B:354:ILE:HG13	1.97	0.47
1:B:354:ILE:HG22	1:B:355:PHE:CD2	2.50	0.47
1:C:214:LEU:HD22	1:C:214:LEU:O	2.15	0.47
1:D:191:LEU:HD22	1:D:191:LEU:O	2.15	0.47
1:D:244:GLN:O	1:D:245:GLN:HG3	2.15	0.47
1:D:324:ILE:HD12	1:D:335:PRO:HG2	1.95	0.47
1:A:316:LYS:NZ	1:A:347:PRO:HD2	2.30	0.47
1:C:312:ASN:CG	1:C:314:ARG:HB2	2.40	0.47
1:A:209:ASP:OD2	1:A:357:ARG:HD2	2.14	0.47
1:A:262:ILE:HD13	1:A:272:LEU:CD1	2.45	0.47
1:D:273:VAL:O	1:D:273:VAL:HG22	2.15	0.47
1:B:184:THR:CG2	1:B:186:LEU:HD21	2.45	0.47
1:B:328:ARG:NH2	2:B:403:HOH:O	1.93	0.46
1:C:361:LEU:HD12	1:D:336:GLU:OE2	2.16	0.46
1:A:287:ILE:HD12	2:C:541:HOH:O	2.15	0.46
1:A:317:LYS:HG3	1:C:293:PHE:CE1	2.51	0.46
1:A:182:ASP:N	1:A:183:VAL:CA	2.73	0.46
1:B:270:TYR:CD2	1:B:307:LYS:HG2	2.51	0.46
1:B:232:ASP:OD2	2:B:406:HOH:O	2.20	0.45
1:B:352:LEU:HD11	1:B:354:ILE:CG1	2.46	0.45
1:A:316:LYS:NZ	1:A:347:PRO:CD	2.79	0.45
1:A:183:VAL:HG11	1:A:355:PHE:CE1	2.48	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:LYS:HG3	1:A:357:ARG:HD3	1.98	0.44
1:C:201:LYS:HG2	1:C:202:MET:O	2.17	0.44
1:A:186:LEU:CD2	1:B:368:ILE:HD13	2.28	0.44
1:A:362:HIS:HD2	2:A:506:HOH:O	2.01	0.44
1:A:262:ILE:CD1	1:A:303:LEU:HD23	2.47	0.44
1:B:352:LEU:HD13	1:B:353:GLU:N	2.33	0.44
1:A:201:LYS:NZ	2:A:402:HOH:O	2.32	0.44
1:A:314:ARG:HG2	1:A:314:ARG:HH11	1.83	0.44
1:B:195:GLN:HG2	2:B:505:HOH:O	2.18	0.44
1:C:355:PHE:HA	1:D:369:GLY:O	2.18	0.44
1:A:192:ILE:HA	1:A:202:MET:HE1	2.00	0.43
1:A:359:ASN:ND2	1:B:336:GLU:OE1	2.50	0.43
1:C:317:LYS:HG2	1:C:318:ASN:N	2.33	0.43
1:B:314:ARG:CG	1:B:314:ARG:NH1	2.75	0.43
1:C:366:VAL:HG11	1:D:191:LEU:HD21	2.01	0.43
1:A:259:ARG:NH2	2:A:409:HOH:O	2.50	0.43
1:A:347:PRO:HD2	2:A:432:HOH:O	2.19	0.43
1:D:188:PHE:CD2	1:D:188:PHE:N	2.86	0.43
1:A:212:TRP:CG	1:A:257:LYS:HG3	2.54	0.43
1:B:312:ASN:HB3	1:B:314:ARG:H	1.84	0.43
1:B:186:LEU:HB2	1:B:188:PHE:CE2	2.53	0.43
1:A:366:VAL:HG23	1:B:352:LEU:CD2	2.48	0.42
1:D:317:LYS:HE2	1:D:318:ASN:OD1	2.19	0.42
1:A:303:LEU:N	1:A:303:LEU:CD1	2.82	0.42
1:D:194:ALA:O	1:D:197:ARG:NH1	2.51	0.42
1:A:198:HIS:C	1:A:198:HIS:HD1	2.28	0.42
1:B:286:LYS:CE	1:B:286:LYS:N	2.82	0.42
1:C:214:LEU:C	1:C:214:LEU:CD2	2.88	0.42
1:B:297:HIS:H	1:D:322:ASP:HB2	1.84	0.42
1:C:326:SER:N	2:C:412:HOH:O	2.31	0.42
1:B:192:ILE:HA	1:B:202:MET:HE1	2.01	0.42
1:B:190:ALA:HB3	2:B:402:HOH:O	2.19	0.42
1:A:334:LYS:HE2	1:A:334:LYS:HB2	1.67	0.42
1:B:335:PRO:O	1:B:338:ILE:HG22	2.19	0.42
1:A:183:VAL:CG1	1:A:355:PHE:HE1	2.31	0.41
1:C:188:PHE:O	1:C:192:ILE:HG13	2.20	0.41
1:C:271:LYS:HB2	2:C:529:HOH:O	2.20	0.41
1:D:306:VAL:HG21	1:D:310:VAL:HG21	2.02	0.41
1:A:317:LYS:HD3	1:C:292:GLY:O	2.21	0.41
1:C:195:GLN:HG3	1:C:203:PHE:CE1	2.55	0.41
1:C:307:LYS:HB2	1:C:307:LYS:HE2	1.87	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:LYS:HB2	1:B:185:LYS:HE2	1.76	0.41
1:B:201:LYS:HZ2	1:B:245:GLN:HG2	1.85	0.41
1:B:208:MET:HB2	1:B:251:VAL:HG13	2.03	0.41
1:A:357:ARG:HG3	1:A:357:ARG:H	1.51	0.41
1:D:245:GLN:HG2	2:D:501:HOH:O	2.20	0.41
1:A:264:MET:HG2	1:A:268:TRP:CH2	2.55	0.41
1:A:368:ILE:HG12	1:B:191:LEU:HD11	2.04	0.40
1:C:312:ASN:HD21	1:C:314:ARG:CG	2.35	0.40
1:A:314:ARG:HG2	1:A:314:ARG:NH1	2.36	0.40
1:A:314:ARG:NH1	2:A:404:HOH:O	2.38	0.40
1:A:363:ASP:O	1:A:364:ASN:CB	2.58	0.40
1:A:273:VAL:HG22	1:C:291:HIS:O	2.19	0.40
1:A:262:ILE:HD13	1:A:272:LEU:HD11	2.03	0.40
1:C:255:ASN:HB3	2:C:420:HOH:O	2.21	0.40
1:D:250:PHE:HB3	1:D:302:CYS:SG	2.62	0.40

All (1) 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:B:434:HOH:O	2:B:506:HOH:O[1_455]	2.00	0.20

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	174/202 (86%)	169 (97%)	5 (3%)	0	100	100
1	B	170/202 (84%)	166 (98%)	4 (2%)	0	100	100
1	C	173/202 (86%)	170 (98%)	3 (2%)	0	100	100
1	D	169/202 (84%)	168 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	686/808 (85%)	673 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	156/178 (88%)	148 (95%)	8 (5%)	21	5
1	B	153/178 (86%)	146 (95%)	7 (5%)	24	7
1	C	153/178 (86%)	146 (95%)	7 (5%)	24	7
1	D	151/178 (85%)	146 (97%)	5 (3%)	33	15
All	All	613/712 (86%)	586 (96%)	27 (4%)	25	8

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	183	VAL
1	A	184	THR
1	A	186	LEU
1	A	229	SER
1	A	234	LYS
1	A	317	LYS
1	A	357	ARG
1	A	368	ILE
1	B	185	LYS
1	B	272	LEU
1	B	286	LYS
1	B	314	ARG
1	B	322	ASP
1	B	352	LEU
1	B	368	ILE
1	C	201	LYS
1	C	214	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	236	GLN
1	C	237	ASN
1	C	311	ASP
1	C	316	LYS
1	C	372	LEU
1	D	186	LEU
1	D	191	LEU
1	D	236	GLN
1	D	327	GLU
1	D	367	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	241	GLN
1	A	244	GLN
1	A	344	GLN
1	B	312	ASN
1	B	344	GLN
1	B	362	HIS
1	C	267	ASN
1	C	340	GLN
1	D	237	ASN
1	D	284	ASN
1	D	296	GLN
1	D	318	ASN
1	D	343	ASN
1	D	344	GLN
1	D	350	ASN
1	D	370	ASN

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 ⓘ

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	178/202 (88%)	0.24	11 (6%) 26 28	10, 23, 49, 80	0
1	B	174/202 (86%)	0.30	12 (6%) 23 24	11, 25, 51, 67	0
1	C	177/202 (87%)	0.21	13 (7%) 21 22	9, 21, 50, 67	0
1	D	173/202 (85%)	0.15	9 (5%) 33 34	9, 21, 54, 73	0
All	All	702/808 (86%)	0.22	45 (6%) 25 26	9, 23, 52, 80	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	184	THR	4.2
1	B	313	GLY	4.1
1	C	312	ASN	3.8
1	D	198	HIS	3.8
1	A	185	LYS	3.7
1	A	227	TYR	3.4
1	C	228	ASP	3.3
1	A	228	ASP	3.3
1	C	216	SER	3.3
1	D	190	ALA	3.2
1	C	193	ASP	3.2
1	C	214	LEU	3.2
1	C	227	TYR	3.1
1	A	183	VAL	3.0
1	B	191	LEU	2.9
1	B	201	LYS	2.9
1	C	188	PHE	2.7
1	A	311	ASP	2.6
1	D	184	THR	2.6
1	B	192	ILE	2.6
1	C	198	HIS	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	184	THR	2.6
1	C	191	LEU	2.5
1	D	191	LEU	2.5
1	C	215	SER	2.5
1	C	190	ALA	2.5
1	D	188	PHE	2.4
1	A	313	GLY	2.4
1	B	185	LYS	2.3
1	B	312	ASN	2.3
1	D	201	LYS	2.3
1	A	310	VAL	2.2
1	B	372	LEU	2.2
1	D	186	LEU	2.2
1	A	312	ASN	2.2
1	B	198	HIS	2.2
1	C	192	ILE	2.2
1	A	194	ALA	2.2
1	B	193	ASP	2.1
1	A	186	LEU	2.1
1	D	185	LYS	2.1
1	D	194	ALA	2.1
1	B	322	ASP	2.1
1	C	368	ILE	2.1
1	B	199	ALA	2.0

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.