



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2026 – 09:53 AM UTC

PDB ID : 3F9V / pdb_00003f9v
Title : Crystal Structure Of A Near Full-Length Archaeal MCM: Functional Insights For An AAA+ Hexameric Helicase
Authors : Chen, X.J.; Brewster, A.S.; Wang, G.G.; Yu, X.; Greenleaf, W.; Tjajadi, M.; Klein, M.
Deposited on : 2008-11-14
Resolution : 4.35 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

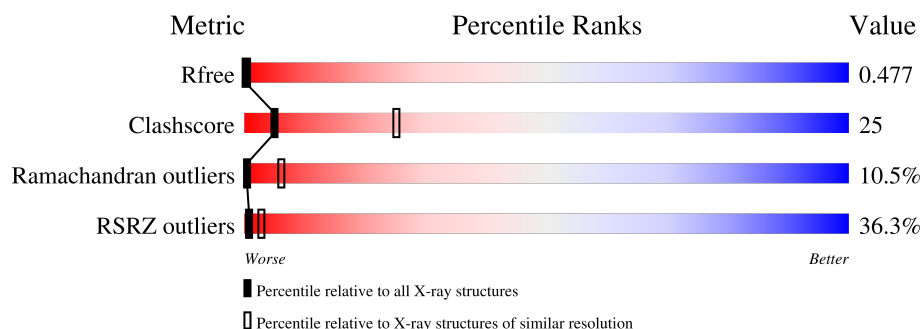
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.35 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	1059 (4.76-3.90)
Clashscore	190562	1105 (4.76-3.90)
Ramachandran outliers	187476	1007 (4.76-3.90)
RSRZ outliers	180081	1056 (4.76-3.90)

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	595	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2944 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.

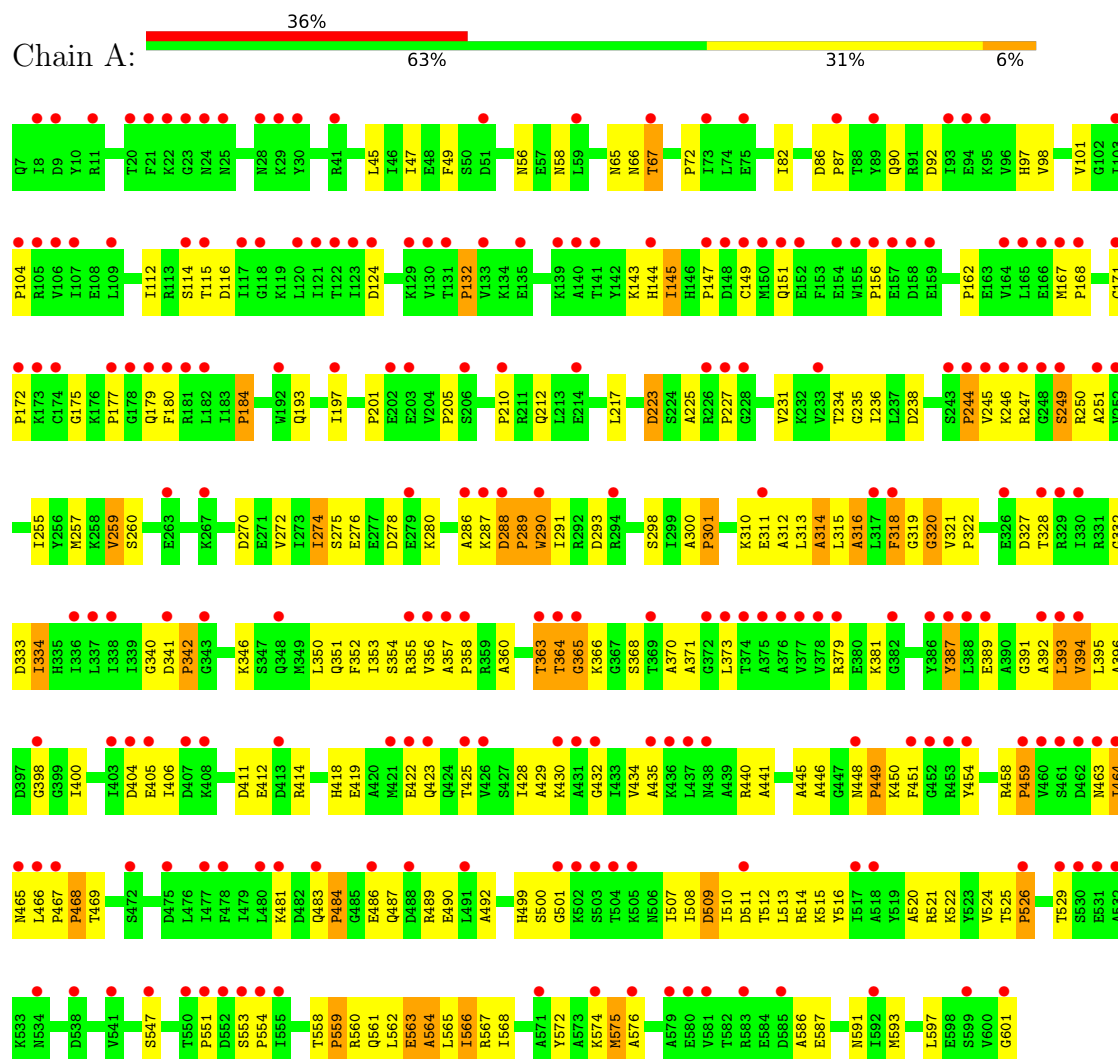
- Molecule 1 is a protein called Minichromosome maintenance protein MCM.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	0	0	0
			2944	1754	595	595			

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: Minichromosome maintenance protein MCM



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	202.53Å 202.53Å 128.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 4.35 30.00 – 4.35	Depositor EDS
% Data completeness (in resolution range)	82.1 (30.00-4.35) 81.7 (30.00-4.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.68 (at 4.42Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.412 , 0.481 0.410 , 0.477	Depositor DCC
R_{free} test set	343 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	183.4	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.62 , 999.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	2944	wwPDB-VP
Average B, all atoms (Å ²)	185.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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	0.67	0/2943	1.25	42/4100 (1.0%)

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

There are no bond length outliers.

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	168	PRO	N-CA-CB	11.30	110.80	103.23
1	A	481	LYS	N-CA-C	9.28	116.39	108.78
1	A	210	PRO	N-CA-CB	8.31	110.58	103.35
1	A	526	PRO	N-CA-CB	8.00	110.31	103.35
1	A	205	PRO	N-CA-CB	7.96	110.39	103.31
1	A	227	PRO	N-CA-CB	7.94	110.38	103.31
1	A	551	PRO	N-CA-CB	7.93	110.84	103.15
1	A	366	LYS	N-CA-C	-7.76	102.46	112.23
1	A	563	GLU	N-CA-C	-7.70	105.85	114.62
1	A	289	PRO	N-CA-CB	7.45	111.07	103.25
1	A	554	PRO	N-CA-CB	7.22	110.84	103.25
1	A	559	PRO	N-CA-CB	7.19	111.14	103.52
1	A	322	PRO	N-CA-CB	7.18	110.79	103.25
1	A	72	PRO	N-CA-CB	7.06	110.66	103.25
1	A	244	PRO	N-CA-CB	7.04	110.64	103.25
1	A	484	PRO	N-CA-CB	6.94	110.54	103.25
1	A	301	PRO	N-CA-CB	6.93	110.53	103.25
1	A	104	PRO	N-CA-CB	6.92	110.16	103.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	PRO	N-CA-CB	6.83	110.42	103.25
1	A	156	PRO	N-CA-CB	6.83	110.42	103.25
1	A	184	PRO	N-CA-CB	6.72	110.31	103.25
1	A	177	PRO	N-CA-CB	6.68	110.27	103.25
1	A	358	PRO	N-CA-CB	6.65	110.74	103.30
1	A	87	PRO	N-CA-CB	6.64	110.56	103.52
1	A	201	PRO	N-CA-CB	6.58	110.50	103.39
1	A	459	PRO	N-CA-CB	6.48	110.06	103.25
1	A	172	PRO	N-CA-CB	6.46	110.62	103.26
1	A	468	PRO	N-CA-CB	6.38	109.94	103.25
1	A	467	PRO	N-CA-CB	6.29	109.18	103.08
1	A	147	PRO	N-CA-CB	6.22	110.27	103.30
1	A	342	PRO	N-CA-CB	6.05	109.60	103.25
1	A	449	PRO	N-CA-CB	5.86	109.40	103.25
1	A	320	GLY	N-CA-C	-5.68	108.03	115.47
1	A	167	MET	N-CA-C	5.49	118.25	110.24
1	A	481	LYS	CA-C-O	5.39	121.07	117.94
1	A	464	ILE	N-CA-C	-5.36	106.58	111.67
1	A	469	THR	N-CA-C	-5.34	107.31	113.88
1	A	270	ASP	N-CA-C	5.27	117.33	110.53
1	A	49	PHE	N-CA-C	5.24	117.07	111.36
1	A	162	PRO	N-CA-CB	5.17	110.24	103.42
1	A	445	ALA	N-CA-C	5.16	117.48	108.76
1	A	387	TYR	N-CA-C	5.16	116.57	109.15

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	363	THR	Peptide
1	A	364	THR	Peptide
1	A	365	GLY	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	2944	0	1322	107	0
All	All	2944	0	1322	107	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 25.

All (107) 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:370:ALA:HB1	1:A:389:GLU:CB	1.88	1.03
1:A:398:GLY:HA2	1:A:440:ARG:O	1.70	0.90
1:A:313:LEU:C	1:A:315:LEU:H	1.90	0.78
1:A:320:GLY:HA2	1:A:572:TYR:CB	2.15	0.76
1:A:574:LYS:C	1:A:576:ALA:H	1.97	0.71
1:A:363:THR:C	1:A:365:GLY:N	2.48	0.69
1:A:274:ILE:O	1:A:276:GLU:N	2.26	0.69
1:A:236:ILE:O	1:A:257:MET:HA	1.94	0.66
1:A:171:CYS:O	1:A:175:GLY:N	2.29	0.64
1:A:398:GLY:CA	1:A:440:ARG:O	2.42	0.64
1:A:286:ALA:O	1:A:289:PRO:N	2.31	0.64
1:A:591:ASN:C	1:A:593:MET:H	2.06	0.64
1:A:313:LEU:C	1:A:315:LEU:N	2.54	0.63
1:A:360:ALA:HA	1:A:400:ILE:O	2.02	0.60
1:A:489:ARG:O	1:A:492:ALA:HB3	2.02	0.60
1:A:371:ALA:O	1:A:392:ALA:N	2.34	0.60
1:A:507:ILE:C	1:A:509:ASP:H	2.10	0.60
1:A:404:ASP:HA	1:A:446:ALA:HB3	1.84	0.59
1:A:354:SER:C	1:A:356:VAL:H	2.10	0.59
1:A:47:ILE:O	1:A:101:VAL:N	2.35	0.59
1:A:124:ASP:HA	1:A:231:VAL:O	2.02	0.59
1:A:572:TYR:HA	1:A:575:MET:CB	2.32	0.59
1:A:332:GLY:C	1:A:334:ILE:H	2.10	0.57
1:A:193:GLN:N	1:A:217:LEU:O	2.37	0.57
1:A:354:SER:C	1:A:356:VAL:N	2.63	0.57
1:A:368:SER:O	1:A:371:ALA:HB3	2.04	0.56
1:A:591:ASN:C	1:A:593:MET:N	2.62	0.56
1:A:516:TYR:O	1:A:520:ALA:N	2.38	0.56
1:A:512:THR:HA	1:A:515:LYS:CB	2.36	0.56
1:A:464:ILE:C	1:A:466:LEU:H	2.14	0.56
1:A:363:THR:CB	1:A:365:GLY:HA3	2.37	0.55
1:A:574:LYS:C	1:A:576:ALA:N	2.62	0.55
1:A:274:ILE:C	1:A:276:GLU:H	2.15	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:ASP:C	1:A:290:TRP:N	2.65	0.54
1:A:310:LYS:O	1:A:314:ALA:N	2.23	0.54
1:A:350:LEU:O	1:A:351:GLN:C	2.51	0.54
1:A:574:LYS:O	1:A:576:ALA:N	2.33	0.54
1:A:313:LEU:O	1:A:315:LEU:N	2.42	0.53
1:A:311:GLU:HA	1:A:314:ALA:HB3	1.89	0.53
1:A:90:GLN:C	1:A:92:ASP:H	2.16	0.53
1:A:346:LYS:O	1:A:350:LEU:N	2.42	0.53
1:A:564:ALA:O	1:A:565:LEU:C	2.51	0.53
1:A:82:ILE:O	1:A:86:ASP:N	2.36	0.52
1:A:286:ALA:O	1:A:287:LYS:C	2.52	0.52
1:A:313:LEU:HA	1:A:316:ALA:HB3	1.92	0.52
1:A:561:GLN:C	1:A:563:GLU:H	2.18	0.52
1:A:561:GLN:O	1:A:563:GLU:N	2.32	0.52
1:A:311:GLU:O	1:A:315:LEU:N	2.43	0.52
1:A:565:LEU:O	1:A:566:ILE:C	2.53	0.51
1:A:354:SER:O	1:A:357:ALA:N	2.37	0.51
1:A:428:ILE:O	1:A:435:ALA:N	2.44	0.51
1:A:291:ILE:C	1:A:293:ASP:H	2.19	0.51
1:A:510:ILE:O	1:A:514:ARG:N	2.42	0.51
1:A:332:GLY:C	1:A:334:ILE:N	2.69	0.50
1:A:145:ILE:N	1:A:179:GLN:O	2.44	0.50
1:A:450:LYS:CB	1:A:463:ASN:HA	2.41	0.49
1:A:507:ILE:O	1:A:509:ASP:N	2.45	0.49
1:A:418:HIS:O	1:A:419:GLU:C	2.54	0.49
1:A:143:LYS:O	1:A:180:PHE:HA	2.12	0.49
1:A:381:LYS:CB	1:A:387:TYR:H	2.26	0.49
1:A:507:ILE:C	1:A:509:ASP:N	2.71	0.48
1:A:56:ASN:C	1:A:58:ASN:H	2.21	0.48
1:A:398:GLY:H	1:A:441:ALA:HB2	1.77	0.48
1:A:234:THR:O	1:A:260:SER:N	2.47	0.48
1:A:524:VAL:O	1:A:526:PRO:N	2.47	0.47
1:A:45:LEU:CB	1:A:98:VAL:HA	2.44	0.47
1:A:197:ILE:O	1:A:212:GLN:HA	2.13	0.47
1:A:429:ALA:HA	1:A:434:VAL:HA	1.96	0.47
1:A:499:HIS:O	1:A:501:GLY:N	2.47	0.47
1:A:311:GLU:O	1:A:312:ALA:C	2.58	0.47
1:A:318:PHE:C	1:A:320:GLY:H	2.24	0.46
1:A:423:GLN:O	1:A:425:THR:N	2.48	0.46
1:A:235:GLY:HA3	1:A:259:VAL:HA	1.98	0.46
1:A:249:SER:O	1:A:251:ALA:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:VAL:O	1:A:357:ALA:C	2.59	0.45
1:A:114:SER:C	1:A:116:ASP:H	2.24	0.45
1:A:393:LEU:O	1:A:394:VAL:C	2.59	0.45
1:A:586:ALA:O	1:A:587:GLU:C	2.60	0.45
1:A:278:ASP:C	1:A:280:LYS:N	2.74	0.44
1:A:521:ARG:O	1:A:522:LYS:C	2.61	0.44
1:A:395:LEU:O	1:A:396:ALA:C	2.61	0.43
1:A:567:ARG:O	1:A:568:ILE:C	2.59	0.43
1:A:559:PRO:O	1:A:560:ARG:C	2.61	0.43
1:A:423:GLN:C	1:A:425:THR:H	2.27	0.43
1:A:298:SER:C	1:A:300:ALA:N	2.77	0.43
1:A:340:GLY:C	1:A:449:PRO:CB	2.92	0.43
1:A:511:ASP:C	1:A:513:LEU:H	2.27	0.43
1:A:354:SER:O	1:A:356:VAL:N	2.52	0.42
1:A:319:GLY:C	1:A:321:VAL:N	2.76	0.42
1:A:490:GLU:C	1:A:492:ALA:N	2.78	0.42
1:A:391:GLY:O	1:A:392:ALA:C	2.63	0.42
1:A:448:ASN:O	1:A:450:LYS:N	2.45	0.42
1:A:405:GLU:O	1:A:406:ILE:C	2.63	0.42
1:A:486:GLU:O	1:A:487:GLN:C	2.62	0.42
1:A:66:ASN:O	1:A:67:THR:C	2.62	0.41
1:A:597:LEU:O	1:A:601:GLY:N	2.53	0.41
1:A:65:ASN:C	1:A:67:THR:H	2.28	0.41
1:A:223:ASP:C	1:A:225:ALA:N	2.78	0.41
1:A:412:GLU:C	1:A:414:ARG:N	2.77	0.41
1:A:149:CYS:C	1:A:151:GLN:N	2.77	0.41
1:A:490:GLU:C	1:A:492:ALA:H	2.28	0.41
1:A:149:CYS:C	1:A:151:GLN:H	2.28	0.41
1:A:320:GLY:O	1:A:321:VAL:C	2.63	0.41
1:A:418:HIS:O	1:A:422:GLU:N	2.50	0.41
1:A:223:ASP:C	1:A:225:ALA:H	2.28	0.40
1:A:244:PRO:C	1:A:246:LYS:H	2.29	0.40
1:A:223:ASP:O	1:A:225:ALA:N	2.55	0.40

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	593/595 (100%)	390 (66%)	141 (24%)	62 (10%)	0 6

All (62) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	272	VAL
1	A	275	SER
1	A	316	ALA
1	A	334	ILE
1	A	342	PRO
1	A	373	LEU
1	A	411	ASP
1	A	454	TYR
1	A	458	ARG
1	A	468	PRO
1	A	483	GLN
1	A	484	PRO
1	A	508	ILE
1	A	525	THR
1	A	553	SER
1	A	97	HIS
1	A	145	ILE
1	A	247	ARG
1	A	249	SER
1	A	250	ARG
1	A	274	ILE
1	A	314	ALA
1	A	318	PHE
1	A	352	PHE
1	A	353	ILE
1	A	364	THR
1	A	379	ARG
1	A	394	VAL

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Mol	Chain	Res	Type
1	A	430	LYS
1	A	459	PRO
1	A	500	SER
1	A	529	THR
1	A	562	LEU
1	A	564	ALA
1	A	575	MET
1	A	115	THR
1	A	144	HIS
1	A	223	ASP
1	A	259	VAL
1	A	355	ARG
1	A	451	PHE
1	A	509	ASP
1	A	547	SER
1	A	184	PRO
1	A	290	TRP
1	A	328	THR
1	A	333	ASP
1	A	393	LEU
1	A	465	ASN
1	A	67	THR
1	A	132	PRO
1	A	238	ASP
1	A	245	VAL
1	A	255	ILE
1	A	288	ASP
1	A	327	ASP
1	A	341	ASP
1	A	112	ILE
1	A	301	PRO
1	A	432	GLY
1	A	558	THR
1	A	566	ILE

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

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 ⓘ

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	595/595 (100%)	1.99	216 (36%) ⓘ ⓘ	182, 185, 188, 191	0

All (216) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	157	GLU	14.2
1	A	149	CYS	13.4
1	A	248	GLY	12.2
1	A	480	LEU	11.3
1	A	247	ARG	11.0
1	A	180	PHE	11.0
1	A	167	MET	10.7
1	A	554	PRO	10.6
1	A	328	THR	10.3
1	A	93	ILE	10.1
1	A	503	SER	9.9
1	A	463	ASN	9.9
1	A	358	PRO	9.7
1	A	181	ARG	9.6
1	A	174	CYS	9.5
1	A	356	VAL	9.2
1	A	148	ASP	8.4
1	A	453	ARG	8.2
1	A	105	ARG	7.9
1	A	288	ASP	7.8
1	A	462	ASP	7.7
1	A	553	SER	7.3
1	A	168	PRO	7.3
1	A	95	LYS	7.3
1	A	460	VAL	7.0
1	A	122	THR	6.5
1	A	502	LYS	6.5

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Mol	Chain	Res	Type	RSRZ
1	A	114	SER	6.4
1	A	422	GLU	6.2
1	A	287	LYS	6.2
1	A	158	ASP	6.1
1	A	375	ALA	6.0
1	A	466	LEU	5.9
1	A	29	LYS	5.9
1	A	154	GLU	5.9
1	A	94	GLU	5.9
1	A	576	ALA	5.8
1	A	501	GLY	5.8
1	A	244	PRO	5.7
1	A	121	ILE	5.6
1	A	376	ALA	5.5
1	A	579	ALA	5.5
1	A	252	VAL	5.4
1	A	166	GLU	5.4
1	A	21	PHE	5.4
1	A	555	ILE	5.4
1	A	374	THR	5.3
1	A	249	SER	5.2
1	A	317	LEU	5.2
1	A	436	LYS	5.2
1	A	263	GLU	4.9
1	A	451	PHE	4.9
1	A	404	ASP	4.7
1	A	159	GLU	4.7
1	A	531	GLU	4.6
1	A	435	ALA	4.5
1	A	452	GLY	4.5
1	A	481	LYS	4.5
1	A	124	ASP	4.4
1	A	243	SER	4.4
1	A	386	TYR	4.4
1	A	365	GLY	4.4
1	A	144	HIS	4.3
1	A	133	VAL	4.3
1	A	173	LYS	4.3
1	A	369	THR	4.2
1	A	24	ASN	4.1
1	A	461	SER	4.1
1	A	131	THR	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	206	SER	4.1
1	A	326	GLU	4.0
1	A	580	GLU	4.0
1	A	227	PRO	4.0
1	A	343	GLY	3.9
1	A	551	PRO	3.9
1	A	155	TRP	3.8
1	A	279	GLU	3.8
1	A	171	CYS	3.8
1	A	245	VAL	3.8
1	A	246	LYS	3.8
1	A	574	LYS	3.7
1	A	22	LYS	3.7
1	A	532	ALA	3.6
1	A	192	TRP	3.6
1	A	156	PRO	3.6
1	A	394	VAL	3.5
1	A	348	GLN	3.5
1	A	431	ALA	3.5
1	A	177	PRO	3.5
1	A	210	PRO	3.5
1	A	9	ASP	3.4
1	A	477	ILE	3.4
1	A	472	SER	3.3
1	A	464	ILE	3.3
1	A	172	PRO	3.3
1	A	547	SER	3.3
1	A	139	LYS	3.2
1	A	398	GLY	3.2
1	A	106	VAL	3.2
1	A	20	THR	3.2
1	A	150	MET	3.2
1	A	140	ALA	3.2
1	A	120	LEU	3.1
1	A	341	ASP	3.1
1	A	389	GLU	3.1
1	A	51	ASP	3.1
1	A	585	ASP	3.1
1	A	107	ILE	3.1
1	A	202	GLU	3.1
1	A	387	TYR	3.1
1	A	421	MET	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	318	PHE	3.1
1	A	103	ILE	3.1
1	A	179	GLN	3.0
1	A	518	ALA	3.0
1	A	135	GLU	3.0
1	A	8	ILE	3.0
1	A	437	LEU	3.0
1	A	115	THR	3.0
1	A	337	LEU	3.0
1	A	226	ARG	3.0
1	A	330	ILE	3.0
1	A	164	VAL	2.9
1	A	151	GLN	2.9
1	A	123	ILE	2.9
1	A	59	LEU	2.9
1	A	403	ILE	2.9
1	A	552	ASP	2.9
1	A	30	TYR	2.8
1	A	89	TYR	2.8
1	A	530	SER	2.8
1	A	109	LEU	2.8
1	A	329	ARG	2.8
1	A	488	ASP	2.8
1	A	599	SER	2.8
1	A	465	ASN	2.7
1	A	373	LEU	2.7
1	A	475	ASP	2.7
1	A	251	ALA	2.7
1	A	486	GLU	2.7
1	A	432	GLY	2.7
1	A	438	ASN	2.7
1	A	550	THR	2.7
1	A	454	TYR	2.6
1	A	511	ASP	2.6
1	A	392	ALA	2.6
1	A	290	TRP	2.6
1	A	355	ARG	2.6
1	A	104	PRO	2.6
1	A	311	GLU	2.6
1	A	165	LEU	2.6
1	A	182	LEU	2.6
1	A	388	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	117	ILE	2.6
1	A	118	GLY	2.5
1	A	11	ARG	2.5
1	A	377	VAL	2.5
1	A	147	PRO	2.5
1	A	357	ALA	2.5
1	A	571	ALA	2.5
1	A	129	LYS	2.5
1	A	197	ILE	2.5
1	A	25	ASN	2.5
1	A	372	GLY	2.5
1	A	505	LYS	2.5
1	A	152	GLU	2.4
1	A	379	ARG	2.4
1	A	382	GLY	2.4
1	A	413	ASP	2.4
1	A	504	THR	2.4
1	A	73	ILE	2.4
1	A	448	ASN	2.4
1	A	592	ILE	2.4
1	A	130	VAL	2.4
1	A	467	PRO	2.4
1	A	363	THR	2.4
1	A	336	ILE	2.4
1	A	529	THR	2.3
1	A	364	THR	2.3
1	A	581	VAL	2.3
1	A	178	GLY	2.3
1	A	338	ILE	2.3
1	A	405	GLU	2.3
1	A	426	VAL	2.3
1	A	294	ARG	2.3
1	A	526	PRO	2.3
1	A	423	GLN	2.2
1	A	517	ILE	2.2
1	A	67	THR	2.2
1	A	425	THR	2.2
1	A	228	GLY	2.2
1	A	491	LEU	2.2
1	A	214	GLU	2.2
1	A	408	LYS	2.2
1	A	41	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	87	PRO	2.2
1	A	407	ASP	2.2
1	A	141	THR	2.2
1	A	267	LYS	2.2
1	A	393	LEU	2.2
1	A	378	VAL	2.1
1	A	483	GLN	2.1
1	A	286	ALA	2.1
1	A	601	GLY	2.1
1	A	23	GLY	2.1
1	A	541	VAL	2.1
1	A	534	ASN	2.1
1	A	430	LYS	2.1
1	A	478	PHE	2.1
1	A	459	PRO	2.1
1	A	233	VAL	2.1
1	A	583	ARG	2.1
1	A	75	GLU	2.1
1	A	538	ASP	2.0
1	A	28	ASN	2.0
1	A	203	GLU	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.