



Full wwPDB X-ray Structure Validation Report i

Feb 18, 2024 – 12:55 PM EST

PDB ID : 4F0Q
Title : MspJI Restriction Endonuclease - P21 Form
Authors : Horton, J.R.; Mabuchi, M.; Cohen-Karni, D.; Zhang, X.; Griggs, R.; Samaranayake, M.; Roberts, R.J.; Zheng, Y.; Cheng, X.
Deposited on : 2012-05-04
Resolution : 2.05 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 i 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 ①) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

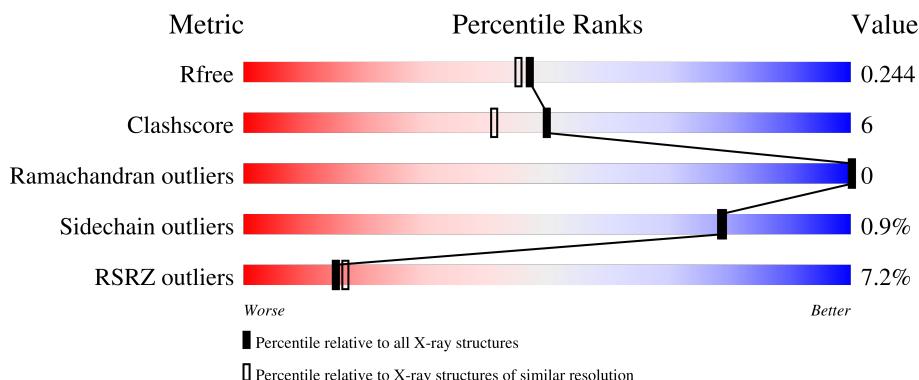
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

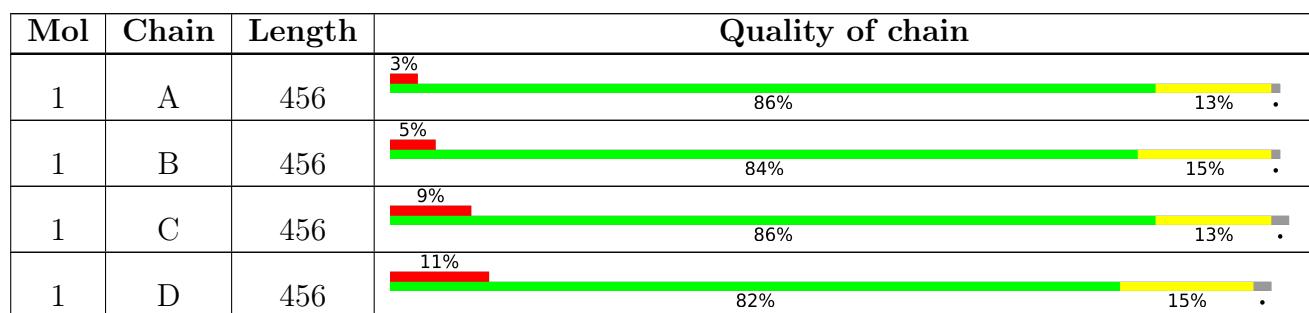
The reported resolution of this entry is 2.05 Å.

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}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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.



2 Entry composition [\(i\)](#)

There are 3 unique types of molecules in this entry. The entry contains 14351 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 Restriction endonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	452	Total	C 3440	N 2160	O 644	S 631	5	0	1	0
1	B	452	Total	C 3386	N 2124	O 630	S 627	5	0	0	0
1	C	449	Total	C 3284	N 2064	O 609	S 607	4	0	0	0
1	D	447	Total	C 3249	N 2036	O 606	S 602	5	0	1	0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg 1 1	0	0
2	B	1	Total	Mg 1 1	0	0
2	C	1	Total	Mg 1 1	0	0

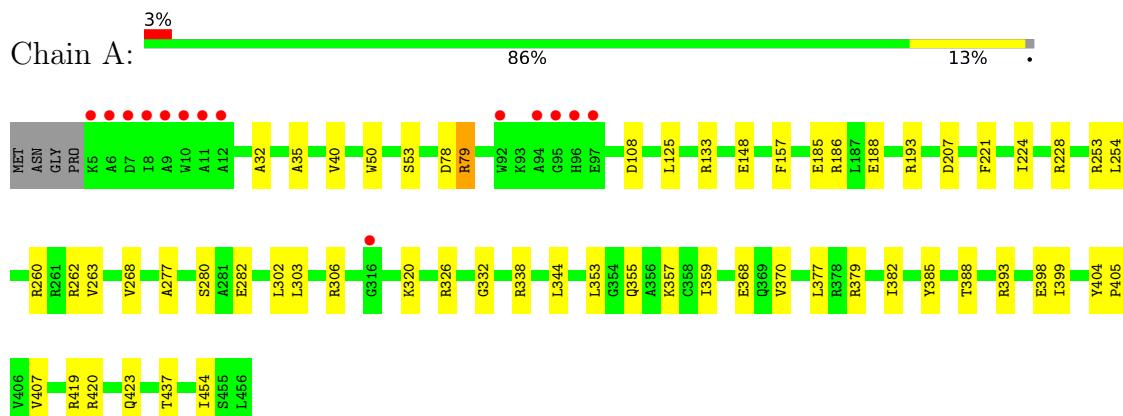
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	334	Total	O 334 334	0	0
3	B	271	Total	O 271 271	0	0
3	C	215	Total	O 215 215	0	0
3	D	169	Total	O 169 169	0	0

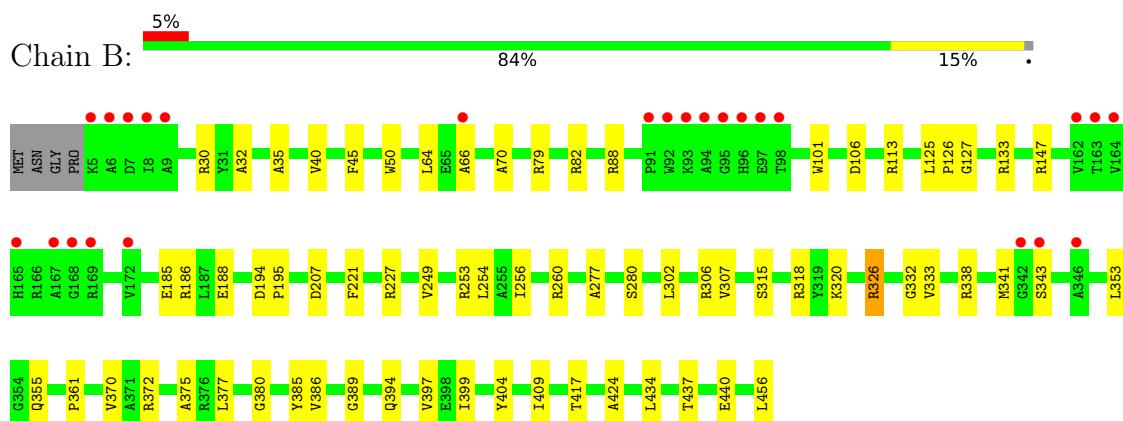
3 Residue-property plots

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 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.

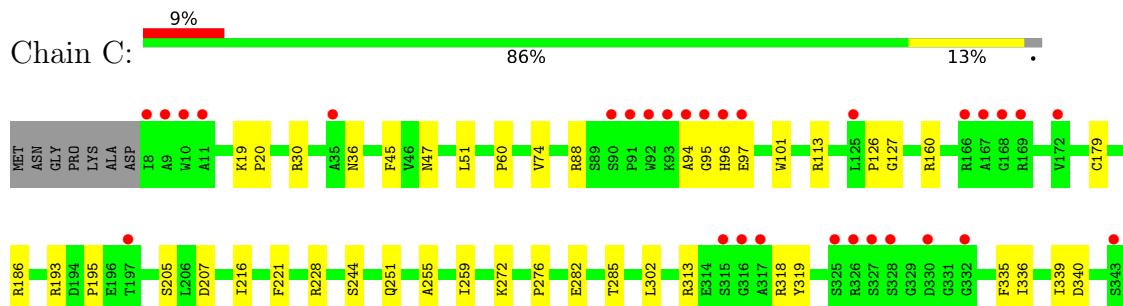
- Molecule 1: Restriction endonuclease

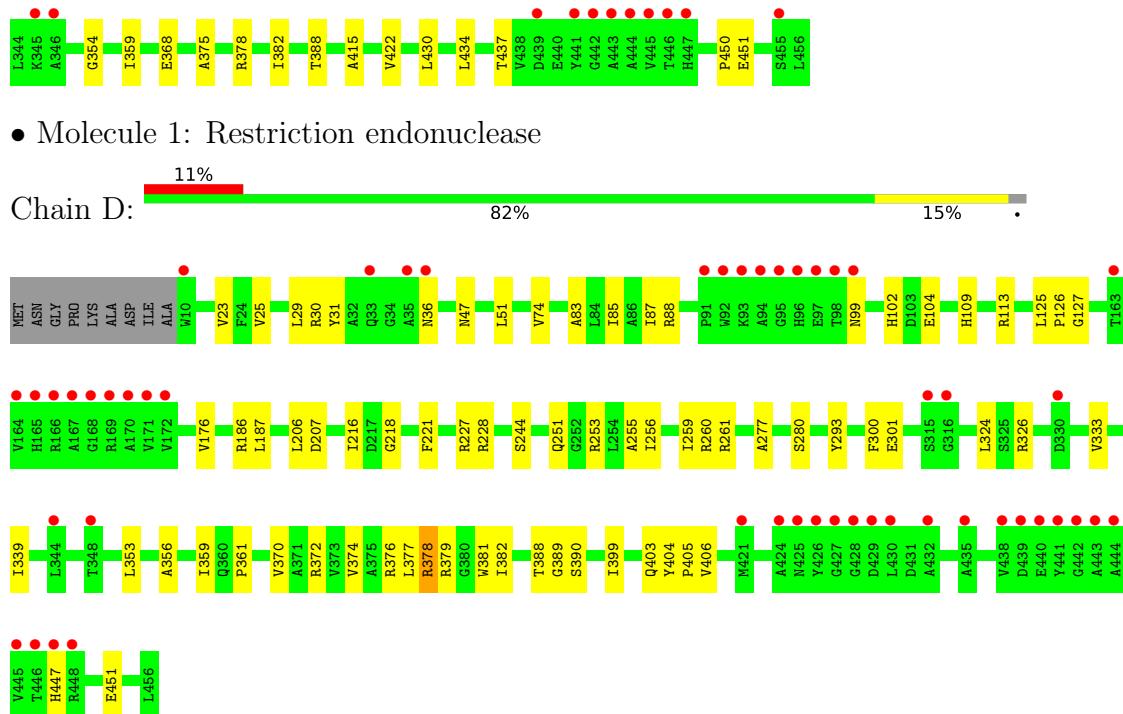


- Molecule 1: Restriction endonuclease



- Molecule 1: Restriction endonuclease





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.76 Å 144.28 Å 87.84 Å 90.00° 116.27° 90.00°	Depositor
Resolution (Å)	34.57 – 2.05 34.57 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.2 (34.57-2.05) 97.6 (34.57-2.05)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle^1$	3.18 (at 2.05 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R , R_{free}	0.210 , 0.246 0.210 , 0.244	Depositor DCC
R_{free} test set	6159 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 25.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.377 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14351	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.60% 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 [\(i\)](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.20	0/3516	0.37	0/4777
1	B	0.21	0/3455	0.38	0/4699
1	C	0.21	0/3350	0.38	0/4566
1	D	0.21	0/3318	0.39	0/4522
All	All	0.21	0/13639	0.38	0/18564

There are no bond length outliers.

There are no bond angle outliers.

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	3440	0	3393	42	0
1	B	3386	0	3300	44	0
1	C	3284	0	3138	38	0
1	D	3249	0	3064	47	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	334	0	0	3	0
3	B	271	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	215	0	0	4	0
3	D	169	0	0	4	0
All	All	14351	0	12895	152	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 6.

All (152) 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:D:125:LEU:HG	1:D:126:PRO:HD2	1.66	0.74
1:C:186:ARG:HB3	1:C:207:ASP:HB2	1.71	0.73
1:D:244:SER:HB2	1:D:259:ILE:HB	1.71	0.72
1:A:254:LEU:HD23	1:B:306:ARG:HD3	1.77	0.66
1:A:379:ARG:NH2	1:C:375:ALA:O	2.29	0.65
1:A:368:GLU:HG3	1:D:372:ARG:HD2	1.79	0.65
1:D:125:LEU:CG	1:D:126:PRO:HD2	2.26	0.65
1:D:99:ASN:O	1:D:102:HIS:ND1	2.31	0.64
1:C:113:ARG:NH1	3:C:729:HOH:O	2.31	0.63
1:B:277:ALA:HB3	1:B:280:SER:HB3	1.81	0.63
1:A:32:ALA:HB3	1:A:35:ALA:HB2	1.80	0.62
1:A:133:ARG:HG3	1:B:125:LEU:HD11	1.82	0.62
1:C:451:GLU:OE1	1:D:403:GLN:NE2	2.33	0.62
1:D:339:ILE:HD12	1:D:382:ILE:HD11	1.82	0.61
1:D:359:ILE:O	1:D:388:THR:OG1	2.19	0.60
1:A:253:ARG:NH1	3:A:908:HOH:O	2.33	0.60
1:A:382:ILE:HD13	1:B:341:MET:HE3	1.84	0.60
1:B:66:ALA:HB2	1:B:88:ARG:HH21	1.65	0.59
1:B:320:LYS:HE2	1:B:456:LEU:HB3	1.83	0.59
1:A:332:GLY:O	1:A:355:GLN:NE2	2.36	0.58
1:B:375:ALA:O	1:D:379:ARG:NH2	2.37	0.58
1:D:113:ARG:NH1	3:D:588:HOH:O	2.35	0.58
1:D:326:ARG:NH2	1:D:333:VAL:O	2.32	0.58
1:A:188:GLU:HA	1:B:188:GLU:HA	1.87	0.57
1:C:359:ILE:O	1:C:388:THR:OG1	2.22	0.57
1:D:293:TYR:HB3	1:D:300:PHE:HB2	1.87	0.57
1:A:277:ALA:HB3	1:A:280:SER:HB3	1.87	0.56
1:A:302:LEU:HD23	1:A:437:THR:HA	1.88	0.56
1:D:186:ARG:HB3	1:D:207:ASP:HB2	1.89	0.55
1:A:407:VAL:HG13	1:B:343:SER:HB2	1.88	0.55
1:D:125:LEU:CD1	1:D:126:PRO:HD2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:74:VAL:HG21	1:C:228:ARG:HA	1.89	0.55
1:C:422:VAL:HG21	1:C:430:LEU:HA	1.89	0.54
1:B:302:LEU:HD23	1:B:437:THR:HA	1.88	0.54
1:B:399:ILE:HG23	1:B:404:TYR:HB2	1.91	0.53
1:B:70:ALA:HB1	1:B:82:ARG:HD2	1.91	0.52
1:B:40:VAL:HG12	1:B:50:TRP:CE2	2.45	0.52
1:C:313:ARG:NH1	1:C:319:TYR:O	2.43	0.52
1:D:30:ARG:NH1	1:D:31:TYR:O	2.43	0.52
1:A:78:ASP:OD2	1:A:79:ARG:NH1	2.43	0.52
1:D:36:ASN:O	1:D:47:ASN:ND2	2.43	0.52
1:C:30:ARG:HG2	1:C:45:PHE:HB2	1.92	0.52
1:C:276:PRO:HB3	1:C:282:GLU:HG3	1.92	0.51
1:D:29:LEU:HB2	1:D:176:VAL:HG23	1.91	0.51
1:D:251:GLN:HB2	1:D:255:ALA:HB2	1.93	0.51
1:A:359:ILE:O	1:A:388:THR:OG1	2.28	0.51
1:B:253:ARG:HD3	1:B:256:ILE:HD12	1.93	0.51
1:A:306:ARG:HD3	1:B:254:LEU:HD13	1.92	0.50
1:C:244:SER:HB2	1:C:259:ILE:HB	1.94	0.50
1:A:379:ARG:NH1	3:A:804:HOH:O	2.39	0.50
1:D:23:VAL:HB	1:D:51:LEU:HD21	1.94	0.49
1:D:125:LEU:HD12	1:D:126:PRO:HD2	1.95	0.49
1:C:113:ARG:HE	1:C:205:SER:HG	1.59	0.49
1:B:30:ARG:HB2	1:B:45:PHE:HB2	1.95	0.48
1:D:253:ARG:HH11	1:D:256:ILE:HD12	1.77	0.48
1:D:187:LEU:HD12	1:D:206:LEU:HD11	1.95	0.48
1:A:108:ASP:OD2	1:C:193:ARG:NH1	2.47	0.48
1:B:372:ARG:HD2	1:C:368:GLU:HG3	1.96	0.48
1:D:370:VAL:HG11	1:D:399:ILE:HD11	1.94	0.48
1:C:160:ARG:NH1	1:C:179:CYS:SG	2.81	0.48
1:B:64:LEU:HG	1:B:88:ARG:HB2	1.96	0.48
1:D:374:VAL:HG22	1:D:406:VAL:HG21	1.96	0.48
1:A:357:LYS:HG2	1:A:359:ILE:HG23	1.95	0.48
1:D:88:ARG:NH2	3:D:517:HOH:O	2.46	0.48
1:D:216:ILE:HG13	1:D:218:GLY:H	1.79	0.47
1:B:82:ARG:O	1:B:227:ARG:NH2	2.43	0.47
1:B:332:GLY:O	1:B:355:GLN:NE2	2.47	0.47
1:B:306:ARG:NH2	1:B:440:GLU:OE1	2.47	0.47
1:A:399:ILE:HG23	1:A:404:TYR:HB2	1.96	0.47
1:B:260:ARG:NH1	3:B:673:HOH:O	2.44	0.47
1:B:147:ARG:HG3	1:B:249:VAL:HG12	1.97	0.46
1:C:36:ASN:O	1:C:47:ASN:ND2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ARG:NH2	1:A:148:GLU:O	2.49	0.46
1:B:186:ARG:NH1	1:B:315:SER:O	2.45	0.46
1:C:251:GLN:HB2	1:C:255:ALA:HB2	1.97	0.46
1:A:320:LYS:HG3	1:A:338:ARG:HH21	1.80	0.45
1:B:32:ALA:HB3	1:B:35:ALA:HB2	1.98	0.45
1:B:101:TRP:HZ2	1:B:424:ALA:HB2	1.81	0.45
1:B:386:VAL:HG22	1:B:409:ILE:HD12	1.98	0.45
1:C:101:TRP:HH2	1:C:195:PRO:HD3	1.82	0.45
1:C:339:ILE:HD12	1:C:382:ILE:HD11	1.99	0.45
1:D:51:LEU:HG	1:D:221:PHE:CD2	2.52	0.45
1:D:102:HIS:NE2	1:D:104:GLU:OE1	2.50	0.44
1:B:370:VAL:HG11	1:B:399:ILE:HD11	1.99	0.44
1:C:336:ILE:HD13	1:C:450:PRO:HA	1.98	0.44
1:B:394:GLN:HA	1:B:397:VAL:HG22	1.99	0.44
1:C:318:ARG:HB2	1:C:340:ASP:HB2	1.99	0.44
1:A:398:GLU:CD	1:D:376:ARG:HH22	2.20	0.44
1:A:282:GLU:HG2	1:A:419:ARG:HD3	2.00	0.44
1:C:302:LEU:HD23	1:C:437:THR:HA	1.98	0.44
1:D:74:VAL:HG21	1:D:228:ARG:HA	1.99	0.44
1:D:256:ILE:HA	1:D:259:ILE:HG12	1.98	0.44
1:A:193:ARG:NH1	1:A:423:GLN:OE1	2.49	0.44
1:C:95:GLY:HA2	1:C:96:HIS:C	2.38	0.44
1:B:353:LEU:HD22	1:B:377:LEU:HD23	1.99	0.43
1:C:51:LEU:HG	1:C:221:PHE:CD2	2.53	0.43
1:C:430:LEU:HG	1:C:434:LEU:HG	1.99	0.43
1:D:399:ILE:HG23	1:D:404:TYR:HB2	2.00	0.43
1:A:370[A]:VAL:HG11	1:A:399:ILE:HD11	2.01	0.43
1:A:405:PRO:HB3	1:B:380:GLY:HA3	2.00	0.43
1:C:94:ALA:HB2	1:D:447:HIS:HA	2.00	0.43
1:C:282:GLU:HB2	1:C:415:ALA:HB1	2.00	0.43
1:C:378:ARG:NH2	3:C:624:HOH:O	2.51	0.43
1:D:301:GLU:HG2	1:D:356:ALA:HB3	1.99	0.43
1:B:320:LYS:HB3	1:B:338:ARG:HB3	2.00	0.43
1:D:377:LEU:HD13	1:D:405:PRO:HG2	2.00	0.43
1:B:326:ARG:NH2	1:B:333:VAL:O	2.38	0.43
1:B:361:PRO:HA	1:B:389:GLY:HA2	2.01	0.43
1:B:185:GLU:OE1	1:B:260:ARG:NH1	2.52	0.43
1:A:40:VAL:HG12	1:A:50:TRP:CE2	2.53	0.43
1:C:126:PRO:HA	1:C:127:GLY:HA2	1.57	0.43
1:D:361:PRO:HA	1:D:389:GLY:HA2	2.00	0.43
1:D:370:VAL:O	1:D:374:VAL:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:PRO:HA	1:B:127:GLY:HA2	1.49	0.42
1:A:268:VAL:HG11	1:A:393:ARG:HG3	2.01	0.42
1:D:353:LEU:HD12	1:D:377:LEU:HD23	2.01	0.42
1:A:78:ASP:OD1	1:A:78:ASP:N	2.51	0.42
1:B:194:ASP:HA	1:B:195:PRO:HD3	1.89	0.42
1:B:434:LEU:O	1:B:437:THR:OG1	2.29	0.42
1:B:186:ARG:HB3	1:B:207:ASP:HB2	2.02	0.42
1:A:125:LEU:HD11	1:B:133:ARG:HG3	2.01	0.42
1:A:157:PHE:CE1	1:A:224:ILE:HD11	2.55	0.42
1:D:228:ARG:NH2	3:D:598:HOH:O	2.43	0.42
1:D:378:ARG:NH2	3:D:622:HOH:O	2.53	0.42
1:C:272:LYS:HE2	1:C:272:LYS:HB3	1.83	0.42
1:D:126:PRO:HA	1:D:127:GLY:HA2	1.35	0.42
1:B:79:ARG:NH2	3:B:680:HOH:O	2.53	0.41
1:C:19:LYS:HA	1:C:20:PRO:HD3	1.91	0.41
1:C:60:PRO:O	1:C:228:ARG:NH2	2.37	0.41
1:C:251:GLN:NE2	3:C:714:HOH:O	2.43	0.41
1:D:83:ALA:O	1:D:227:ARG:NE	2.39	0.41
1:D:381:TRP:HZ2	1:D:451:GLU:HB3	1.86	0.41
1:C:88:ARG:NH2	3:C:781:HOH:O	2.37	0.41
1:A:420:ARG:NH2	3:A:844:HOH:O	2.53	0.41
1:C:95:GLY:HA2	1:C:97:GLU:N	2.36	0.41
1:A:379:ARG:HH22	1:C:375:ALA:C	2.23	0.41
1:B:307:VAL:HG13	1:B:417:THR:HG21	2.02	0.41
1:D:109:HIS:O	1:D:260:ARG:HD3	2.20	0.41
1:A:53:SER:HB2	1:A:228:ARG:HH12	1.85	0.41
1:A:353:LEU:HD22	1:A:377:LEU:HD23	2.02	0.41
1:C:335:PHE:CE1	1:C:354:GLY:HA3	2.56	0.41
1:A:344:LEU:HD13	1:B:113:ARG:HG3	2.03	0.40
1:A:185:GLU:CD	1:A:260:ARG:HH12	2.25	0.40
1:A:303:LEU:HB2	1:A:437:THR:HG21	2.03	0.40
1:C:282:GLU:HA	1:C:285:THR:HB	2.03	0.40
1:D:25:VAL:HG11	1:D:261:ARG:NH1	2.37	0.40
1:A:186:ARG:HB3	1:A:207:ASP:HB2	2.04	0.40
1:A:262:ARG:NH1	1:A:263:VAL:O	2.54	0.40
1:A:338:ARG:NH1	1:A:454:ILE:O	2.54	0.40
1:A:344:LEU:HD21	1:B:106:ASP:HB2	2.04	0.40
1:D:85:ILE:HG22	1:D:87:ILE:HG13	2.03	0.40
1:D:277:ALA:HB3	1:D:280:SER:OG	2.22	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	451/456 (99%)	440 (98%)	11 (2%)	0	100 100
1	B	450/456 (99%)	433 (96%)	17 (4%)	0	100 100
1	C	447/456 (98%)	421 (94%)	26 (6%)	0	100 100
1	D	446/456 (98%)	427 (96%)	19 (4%)	0	100 100
All	All	1794/1824 (98%)	1721 (96%)	73 (4%)	0	100 100

There are no Ramachandran outliers to report.

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	344/358 (96%)	340 (99%)	4 (1%)	71 70
1	B	332/358 (93%)	328 (99%)	4 (1%)	71 70
1	C	308/358 (86%)	307 (100%)	1 (0%)	92 93
1	D	299/358 (84%)	296 (99%)	3 (1%)	76 75
All	All	1283/1432 (90%)	1271 (99%)	12 (1%)	78 79

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	ARG
1	A	221	PHE

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Mol	Chain	Res	Type
1	A	326	ARG
1	A	385	TYR
1	B	221	PHE
1	B	318	ARG
1	B	326	ARG
1	B	385	TYR
1	C	216	ILE
1	D	324	LEU
1	D	378	ARG
1	D	390	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [\(i\)](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	452/456 (99%)	0.09	14 (3%) 49 53	13, 22, 38, 78	0
1	B	452/456 (99%)	0.22	25 (5%) 25 27	11, 23, 51, 79	0
1	C	449/456 (98%)	0.59	41 (9%) 9 9	17, 30, 64, 105	0
1	D	447/456 (98%)	0.86	49 (10%) 5 5	16, 32, 76, 126	0
All	All	1800/1824 (98%)	0.44	129 (7%) 15 17	11, 26, 60, 126	0

All (129) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	92	TRP	24.9
1	D	92	TRP	16.9
1	D	95	GLY	16.9
1	C	446	THR	16.7
1	D	96	HIS	16.0
1	C	95	GLY	15.3
1	C	441	TYR	14.2
1	A	5	LYS	12.5
1	D	447	HIS	12.0
1	C	442	GLY	12.0
1	C	96	HIS	11.2
1	B	94	ALA	11.0
1	A	94	ALA	10.8
1	D	427	GLY	10.8
1	B	92	TRP	10.4
1	D	164	VAL	9.8
1	D	171	VAL	9.6
1	D	426	TYR	9.5
1	C	167	ALA	9.4
1	D	91	PRO	9.2
1	D	441	TYR	9.0

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Mol	Chain	Res	Type	RSRZ
1	D	94	ALA	8.9
1	D	444	ALA	8.3
1	D	168	GLY	8.1
1	D	428	GLY	8.1
1	B	168	GLY	7.7
1	D	166	ARG	7.2
1	C	166	ARG	7.1
1	A	8	ILE	7.0
1	C	447	HIS	7.0
1	C	445	VAL	6.9
1	D	170	ALA	6.8
1	D	445	VAL	6.7
1	D	35	ALA	6.4
1	D	169	ARG	6.2
1	D	98	THR	6.1
1	C	346	ALA	6.1
1	D	97	GLU	6.1
1	D	165	HIS	5.9
1	B	95	GLY	5.9
1	C	90	SER	5.9
1	C	92	TRP	5.8
1	D	10	TRP	5.7
1	A	95	GLY	5.4
1	B	96	HIS	5.4
1	C	94	ALA	5.4
1	C	443	ALA	5.3
1	C	168	GLY	5.3
1	B	342	GLY	5.2
1	C	91	PRO	5.1
1	D	443	ALA	5.0
1	D	167	ALA	4.9
1	C	8	ILE	4.9
1	B	162	VAL	4.9
1	C	316	GLY	4.9
1	B	93	LYS	4.9
1	B	346	ALA	4.7
1	B	167	ALA	4.5
1	D	442	GLY	4.5
1	B	6	ALA	4.5
1	D	440	GLU	4.5
1	D	432	ALA	4.4
1	A	96	HIS	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	164	VAL	4.4
1	B	343	SER	4.2
1	D	446	THR	4.0
1	C	9	ALA	4.0
1	C	317	ALA	4.0
1	B	98	THR	4.0
1	B	8	ILE	3.9
1	B	169	ARG	3.9
1	C	325	SER	3.8
1	C	332	GLY	3.8
1	C	315	SER	3.8
1	B	165	HIS	3.8
1	B	66	ALA	3.7
1	C	345	LYS	3.7
1	D	429	ASP	3.7
1	A	7	ASP	3.6
1	D	163	THR	3.6
1	A	6	ALA	3.5
1	A	316	GLY	3.5
1	D	36	ASN	3.4
1	C	10	TRP	3.4
1	D	438	VAL	3.4
1	B	5	LYS	3.2
1	D	344	LEU	3.1
1	B	91	PRO	3.1
1	C	169	ARG	3.1
1	B	97	GLU	3.1
1	C	444	ALA	3.1
1	C	97	GLU	3.0
1	D	330	ASP	3.0
1	D	315	SER	3.0
1	B	172	VAL	2.9
1	D	93	LYS	2.8
1	D	448	ARG	2.7
1	C	172	VAL	2.7
1	B	163	THR	2.7
1	C	93	LYS	2.7
1	D	421	MET	2.7
1	A	9	ALA	2.6
1	D	316	GLY	2.6
1	C	11	ALA	2.6
1	D	172	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	439	ASP	2.6
1	C	330	ASP	2.6
1	D	348	THR	2.5
1	C	328	SER	2.5
1	B	9	ALA	2.5
1	D	424	ALA	2.5
1	C	327	SER	2.4
1	D	435	ALA	2.4
1	D	430	LEU	2.4
1	C	326	ARG	2.4
1	D	439	ASP	2.3
1	C	35	ALA	2.3
1	D	425	ASN	2.2
1	D	99	ASN	2.2
1	C	455	SER	2.2
1	B	7	ASP	2.2
1	A	12	ALA	2.2
1	A	97	GLU	2.1
1	C	125	LEU	2.1
1	C	343	SER	2.0
1	A	10	TRP	2.0
1	D	33	GLN	2.0
1	A	11	ALA	2.0
1	C	197	THR	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 monosaccharides in this entry.

6.4 Ligands [\(i\)](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	C	501	1/1	0.95	0.07	33,33,33,33	0
2	MG	A	501	1/1	0.96	0.07	21,21,21,21	0
2	MG	B	501	1/1	0.97	0.07	19,19,19,19	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.