



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 04:08 AM UTC

PDB ID : 3IH9 / pdb_00003ih9
Title : Crystal Structure Analysis of Mglu in its tris form
Authors : Yoshimune, K.; Shirakihara, Y.
Deposited on : 2009-07-29
Resolution : 2.50 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

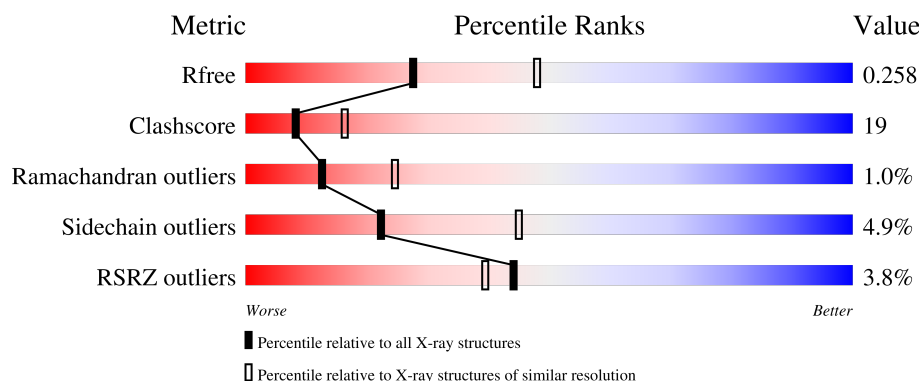
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	456	3% 61% 33% ..
1	B	456	4% 63% 31% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6950 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 Salt-tolerant glutaminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	448	Total	C	N	O	S	0	0	0
			3331	2067	611	638	15			
1	B	448	Total	C	N	O	S	0	0	0
			3331	2067	611	638	15			

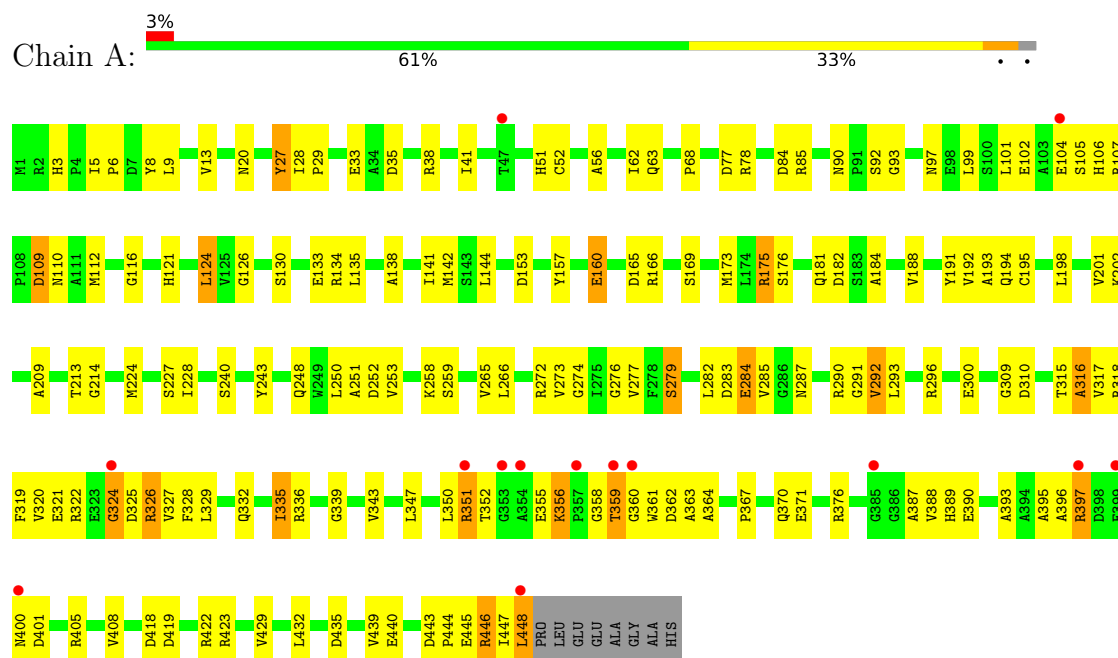
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	150	Total	O	0	0
			150	150		
2	B	138	Total	O	0	0
			138	138		

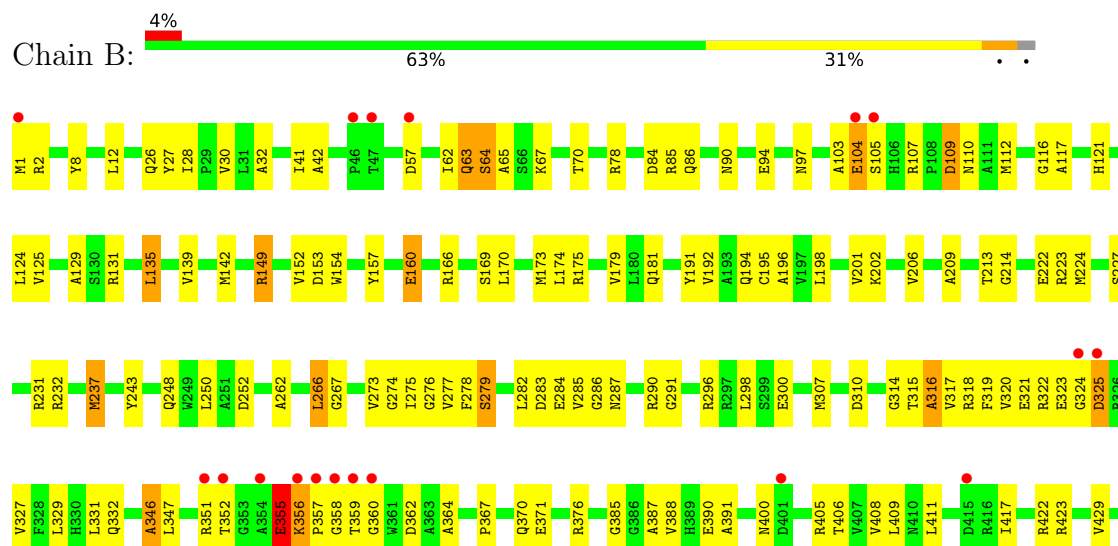
3 Residue-property plots

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: Salt-tolerant glutaminase



• Molecule 1: Salt-tolerant glutaminase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.70Å 141.39Å 75.23Å 90.00° 104.48° 90.00°	Depositor
Resolution (Å)	19.90 – 2.50 19.90 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.3 (19.90-2.50) 98.1 (19.90-2.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.41Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.217 , 0.258 0.217 , 0.258	Depositor DCC
R_{free} test set	2263 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6950	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.69% 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](#)

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	0.54	1/3384 (0.0%)	1.02	19/4594 (0.4%)
1	B	0.54	2/3384 (0.1%)	1.00	13/4594 (0.3%)
All	All	0.54	3/6768 (0.0%)	1.01	32/9188 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	57	ASP	N-CA	7.31	1.55	1.46
1	A	253	VAL	N-CA	6.71	1.52	1.46
1	B	447	ILE	C-O	6.36	1.30	1.23

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	325	ASP	N-CA-C	-8.81	102.66	113.41
1	A	124	LEU	N-CA-C	6.76	125.19	110.80
1	B	346	ALA	N-CA-C	-6.70	104.06	111.36
1	B	325	ASP	N-CA-C	-6.57	105.18	113.72
1	B	124	LEU	N-CA-C	6.53	124.70	110.80
1	B	279	SER	CA-C-N	6.52	127.99	119.84
1	B	279	SER	C-N-CA	6.52	127.99	119.84
1	A	124	LEU	CA-C-N	-6.41	116.04	122.77
1	A	124	LEU	C-N-CA	-6.41	116.04	122.77
1	A	279	SER	CA-C-N	6.34	127.77	119.84
1	A	279	SER	C-N-CA	6.34	127.77	119.84
1	A	253	VAL	N-CA-C	6.34	116.63	111.62
1	B	124	LEU	CA-C-N	-6.19	116.27	122.77
1	B	124	LEU	C-N-CA	-6.19	116.27	122.77
1	A	193	ALA	N-CA-C	-6.14	104.67	111.36
1	B	109	ASP	N-CA-C	6.08	118.41	111.11
1	B	63	GLN	CB-CA-C	-5.96	109.69	116.54
1	A	109	ASP	N-CA-C	5.83	118.38	111.33
1	A	251	ALA	N-CA-C	5.80	117.41	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	ARG	N-CA-C	5.78	120.86	113.18
1	B	252	ASP	N-CA-C	5.77	117.65	111.36
1	A	126	GLY	CA-C-N	5.65	125.32	119.05
1	A	126	GLY	C-N-CA	5.65	125.32	119.05
1	B	237	MET	N-CA-C	-5.56	105.30	111.36
1	B	243	TYR	CB-CA-C	-5.48	110.24	116.54
1	A	253	VAL	CB-CA-C	-5.41	106.24	111.05
1	A	316	ALA	N-CA-C	-5.38	105.97	112.54
1	A	335	ILE	N-CA-C	5.19	115.82	107.98
1	A	309	GLY	N-CA-C	5.14	117.37	111.36
1	A	27	TYR	N-CA-C	5.08	117.48	111.33
1	B	316	ALA	N-CA-C	-5.05	106.63	112.89
1	A	175	ARG	N-CA-C	-5.03	105.88	111.36

There are no chirality outliers.

There are no planarity outliers.

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	3331	0	3312	132	0
1	B	3331	0	3312	127	0
2	A	150	0	0	14	0
2	B	138	0	0	7	0
All	All	6950	0	6624	256	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 19.

All (256) 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:104:GLU:OE2	1:B:104:GLU:N	1.72	1.19
1:B:62:ILE:HG21	1:B:142:MET:HE1	1.46	0.97
1:B:62:ILE:HD13	1:B:142:MET:HE3	1.44	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ILE:HG21	1:A:142:MET:HE1	1.45	0.96
1:B:400:ASN:ND2	2:B:519:HOH:O	2.01	0.92
1:A:277:VAL:HG11	1:A:291:GLY:HA2	1.55	0.89
1:A:201:VAL:HG23	2:A:467:HOH:O	1.74	0.87
1:A:112:MET:HE2	1:A:258:LYS:HD3	1.58	0.86
1:B:411:LEU:HD11	1:B:448:LEU:HD12	1.57	0.85
1:A:62:ILE:HD13	1:A:142:MET:HE3	1.60	0.80
1:B:62:ILE:HD13	1:B:142:MET:CE	2.13	0.77
1:A:397:ARG:HB3	1:A:397:ARG:NH1	2.00	0.76
1:B:320:VAL:HG22	1:B:329:LEU:HD12	1.69	0.73
1:A:376:ARG:HG2	1:A:389:HIS:HB2	1.69	0.73
1:A:322:ARG:HD2	1:A:327:VAL:HG22	1.69	0.73
1:B:149:ARG:HH11	1:B:149:ARG:HB3	1.54	0.72
1:A:105:SER:O	1:A:106:HIS:HB2	1.89	0.71
1:A:446:ARG:HG3	2:A:565:HOH:O	1.91	0.71
1:B:63:GLN:HA	1:B:195:CYS:HB3	1.73	0.69
1:A:134:ARG:HG2	1:A:134:ARG:HH11	1.57	0.69
1:A:52:CYS:SG	1:A:202:LYS:HE2	2.33	0.69
1:A:284:GLU:OE1	1:A:285:VAL:HG13	1.92	0.69
1:A:279:SER:OG	1:A:290:ARG:HD2	1.93	0.69
1:B:279:SER:OG	1:B:290:ARG:HD2	1.93	0.68
1:A:445:GLU:O	1:A:447:ILE:HG13	1.94	0.68
1:A:252:ASP:OD1	2:A:492:HOH:O	2.11	0.68
1:B:110:ASN:ND2	1:B:112:MET:H	1.92	0.68
1:A:259:SER:HB2	1:A:265:VAL:HG22	1.76	0.67
1:B:160:GLU:HG2	1:B:192:VAL:HG13	1.75	0.67
1:B:356:LYS:HD3	1:B:356:LYS:O	1.94	0.67
1:B:376:ARG:HB2	1:B:376:ARG:NH1	2.10	0.67
1:B:408:VAL:HG22	1:B:440:GLU:HG3	1.75	0.67
1:A:356:LYS:O	1:A:356:LYS:HD3	1.95	0.67
1:A:397:ARG:CB	1:A:397:ARG:HH11	2.08	0.67
1:B:104:GLU:N	1:B:104:GLU:CD	2.53	0.67
1:A:324:GLY:N	2:A:465:HOH:O	2.27	0.66
1:B:376:ARG:HB2	1:B:376:ARG:HH11	1.59	0.66
1:B:231:ARG:NH2	2:B:515:HOH:O	2.27	0.66
1:B:201:VAL:HG13	1:B:276:GLY:C	2.19	0.66
1:B:423:ARG:HD3	2:B:544:HOH:O	1.95	0.66
1:B:105:SER:HB2	2:B:501:HOH:O	1.96	0.65
1:A:99:LEU:HD23	1:A:102:GLU:OE1	1.97	0.65
1:A:397:ARG:HB3	1:A:397:ARG:HH11	1.61	0.65
1:A:160:GLU:HG2	1:A:192:VAL:HG13	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:GLU:HG2	1:A:192:VAL:CG1	2.26	0.65
1:B:125:VAL:HB	1:B:129:ALA:CB	2.27	0.64
1:B:411:LEU:CD1	1:B:448:LEU:HD12	2.25	0.64
1:B:320:VAL:HB	1:B:390:GLU:HB3	1.79	0.64
1:A:296:ARG:O	1:A:300:GLU:HG3	1.97	0.64
1:A:322:ARG:CD	1:A:327:VAL:HG22	2.27	0.64
1:A:107:ARG:NH2	2:A:606:HOH:O	2.31	0.63
1:A:110:ASN:HD22	1:A:112:MET:H	1.46	0.63
1:A:277:VAL:CG1	1:A:291:GLY:HA2	2.28	0.63
1:B:160:GLU:HG2	1:B:192:VAL:CG1	2.29	0.63
1:B:103:ALA:C	1:B:105:SER:H	2.06	0.62
1:A:397:ARG:HH11	1:A:397:ARG:CA	2.13	0.62
1:B:320:VAL:HG11	1:B:391:ALA:HA	1.83	0.61
1:A:63:GLN:HA	1:A:195:CYS:HB3	1.83	0.61
1:B:70:THR:HG21	1:B:194:GLN:CD	2.25	0.61
1:B:209:ALA:O	1:B:213:THR:HG23	2.01	0.61
1:A:173:MET:O	1:A:176:SER:HB3	2.01	0.60
1:B:103:ALA:C	1:B:105:SER:N	2.59	0.60
1:A:153:ASP:HB2	1:A:198:LEU:HD11	1.83	0.60
1:B:135:LEU:O	1:B:139:VAL:HG23	2.00	0.60
1:B:296:ARG:O	1:B:300:GLU:HG3	2.01	0.60
1:A:29:PRO:O	1:A:33:GLU:HG2	2.02	0.60
1:A:408:VAL:HG22	1:A:440:GLU:HG3	1.83	0.59
1:B:406:THR:HG23	1:B:438:ARG:HB3	1.84	0.59
1:B:282:LEU:HA	1:B:287:ASN:O	2.02	0.59
1:A:317:VAL:HG21	1:A:388:VAL:HG22	1.85	0.59
1:B:27:TYR:CD1	1:B:28:ILE:HG23	2.38	0.59
1:B:28:ILE:HD12	1:B:30:VAL:HG12	1.85	0.59
1:A:121:HIS:HD2	1:A:194:GLN:OE1	1.86	0.58
1:A:62:ILE:HD13	1:A:142:MET:CE	2.30	0.58
1:B:351:ARG:HH21	1:B:351:ARG:HG3	1.69	0.58
1:B:325:ASP:OD2	1:B:405:ARG:HG3	2.04	0.58
1:B:282:LEU:HD22	1:B:286:GLY:O	2.04	0.57
1:B:67:LYS:HE2	1:B:117:ALA:HB2	1.86	0.57
1:B:351:ARG:HD2	1:B:355:GLU:HB3	1.86	0.57
1:A:27:TYR:CD1	1:A:28:ILE:HG23	2.40	0.57
1:B:223:ARG:C	1:B:224:MET:HE2	2.30	0.57
1:A:5:ILE:HB	1:A:6:PRO:HD3	1.86	0.56
1:B:352:THR:O	1:B:435:ASP:HB3	2.05	0.56
1:B:121:HIS:HD2	1:B:194:GLN:OE1	1.88	0.56
1:B:429:VAL:HG13	1:B:439:VAL:HG11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:VAL:HG13	1:A:439:VAL:HG11	1.86	0.55
1:A:110:ASN:ND2	1:A:112:MET:H	2.03	0.55
1:A:347:LEU:HD22	1:A:432:LEU:HD11	1.88	0.55
1:B:64:SER:HB2	2:B:457:HOH:O	2.06	0.55
1:A:41:ILE:HA	1:A:201:VAL:HG11	1.89	0.55
1:A:361:TRP:CZ3	1:A:370:GLN:HG2	2.40	0.55
1:B:370:GLN:HE21	1:B:370:GLN:HA	1.71	0.55
1:A:400:ASN:ND2	2:A:481:HOH:O	2.39	0.55
1:A:68:PRO:HD3	1:A:112:MET:HE1	1.90	0.54
1:B:201:VAL:HG13	1:B:276:GLY:O	2.07	0.54
1:B:355:GLU:O	1:B:355:GLU:HG3	2.07	0.54
1:B:376:ARG:HH11	1:B:376:ARG:CB	2.21	0.53
1:B:110:ASN:HD22	1:B:112:MET:H	1.55	0.53
1:A:324:GLY:CA	2:A:465:HOH:O	2.56	0.53
1:A:310:ASP:HB3	2:A:567:HOH:O	2.09	0.53
1:B:125:VAL:HB	1:B:129:ALA:HB2	1.91	0.53
1:B:222:GLU:OE1	1:B:224:MET:HE1	2.09	0.53
1:B:320:VAL:HG22	1:B:329:LEU:CD1	2.36	0.53
1:A:320:VAL:HB	1:A:390:GLU:HB3	1.90	0.53
1:A:166:ARG:O	1:A:169:SER:HB3	2.09	0.52
1:B:110:ASN:HD21	1:B:112:MET:HB2	1.74	0.52
1:A:326:ARG:HG3	2:A:465:HOH:O	2.09	0.52
1:A:85:ARG:HD3	2:A:528:HOH:O	2.10	0.52
1:A:181:GLN:CD	1:A:181:GLN:N	2.68	0.52
1:B:62:ILE:HG13	1:B:65:ALA:HB3	1.91	0.52
1:B:317:VAL:HG21	1:B:388:VAL:HG22	1.92	0.52
1:B:408:VAL:HG22	1:B:440:GLU:CG	2.40	0.52
1:B:445:GLU:O	1:B:446:ARG:C	2.52	0.51
1:A:422:ARG:CD	1:A:448:LEU:O	2.59	0.51
1:B:135:LEU:O	1:B:135:LEU:HD22	2.09	0.51
1:B:315:THR:O	1:B:315:THR:HG22	2.10	0.51
1:B:443:ASP:OD1	1:B:446:ARG:HA	2.11	0.51
1:A:355:GLU:O	1:A:355:GLU:HG3	2.11	0.51
1:B:351:ARG:HD2	1:B:355:GLU:CB	2.42	0.50
1:B:445:GLU:O	1:B:447:ILE:HG13	2.10	0.50
1:A:422:ARG:HG3	1:A:448:LEU:O	2.12	0.50
1:A:397:ARG:NH1	1:A:397:ARG:CB	2.70	0.50
1:B:370:GLN:HA	1:B:370:GLN:NE2	2.25	0.50
1:A:315:THR:HG22	1:A:315:THR:O	2.11	0.50
1:B:202:LYS:O	1:B:206:VAL:HG23	2.12	0.50
1:B:367:PRO:O	1:B:371:GLU:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:GLU:HB2	1:A:328:PHE:HB2	1.93	0.49
1:A:62:ILE:CD1	1:A:142:MET:HE3	2.38	0.49
1:A:322:ARG:HG2	1:A:322:ARG:HH21	1.77	0.49
1:A:361:TRP:HZ3	1:A:370:GLN:HG2	1.78	0.49
1:A:401:ASP:N	1:A:401:ASP:OD2	2.45	0.49
1:B:86:GLN:NE2	1:B:179:VAL:HA	2.28	0.49
1:B:322:ARG:HD3	1:B:327:VAL:HG22	1.93	0.49
1:B:214:GLY:O	1:B:227:SER:HA	2.13	0.49
1:A:84:ASP:O	1:A:107:ARG:NH1	2.46	0.49
1:A:104:GLU:OE2	1:A:104:GLU:N	2.33	0.49
1:A:445:GLU:O	1:A:446:ARG:C	2.56	0.49
1:B:325:ASP:OD1	1:B:405:ARG:HD2	2.12	0.48
1:B:411:LEU:HD11	1:B:448:LEU:CD1	2.37	0.48
1:A:339:GLY:O	1:A:343:VAL:HG23	2.13	0.48
1:A:393:ALA:O	1:A:396:ALA:HB3	2.13	0.48
1:B:78:ARG:NH2	2:B:532:HOH:O	2.45	0.48
1:B:166:ARG:O	1:B:169:SER:HB3	2.14	0.48
1:A:101:LEU:O	1:A:106:HIS:HA	2.14	0.47
1:A:134:ARG:HH11	1:A:134:ARG:CG	2.24	0.47
1:B:322:ARG:CD	1:B:327:VAL:HG22	2.44	0.47
1:A:191:TYR:O	1:A:194:GLN:HB3	2.14	0.47
1:A:201:VAL:CG1	1:A:276:GLY:O	2.62	0.47
1:B:262:ALA:HB3	2:B:465:HOH:O	2.14	0.47
1:A:184:ALA:O	1:A:188:VAL:HG23	2.14	0.47
1:A:35:ASP:OD2	1:A:38:ARG:HG3	2.15	0.47
1:A:336:ARG:HA	1:A:418:ASP:OD1	2.15	0.47
1:B:319:PHE:CD2	1:B:321:GLU:HG3	2.50	0.47
1:A:112:MET:CE	1:A:258:LYS:HD3	2.37	0.47
1:B:277:VAL:HG11	1:B:291:GLY:HA2	1.97	0.47
1:A:318:ARG:NH1	1:A:332:GLN:OE1	2.47	0.47
1:B:283:ASP:OD1	1:B:285:VAL:HG22	2.15	0.47
1:B:42:ALA:HB3	1:B:201:VAL:HG12	1.96	0.46
1:A:9:LEU:O	1:A:13:VAL:HG23	2.15	0.46
1:A:104:GLU:H	1:A:104:GLU:CD	2.18	0.46
1:B:42:ALA:CB	1:B:201:VAL:HG12	2.45	0.46
1:A:144:LEU:O	1:A:224:MET:HE2	2.16	0.46
1:A:3:HIS:O	1:A:6:PRO:HD2	2.16	0.46
1:A:284:GLU:HG2	2:A:495:HOH:O	2.15	0.46
1:A:319:PHE:CD2	1:A:321:GLU:HG2	2.51	0.46
1:B:355:GLU:C	1:B:357:PRO:HD3	2.40	0.46
1:B:152:VAL:HG13	1:B:196:ALA:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:THR:HG21	1:B:194:GLN:OE1	2.16	0.46
1:B:85:ARG:HG3	1:B:85:ARG:HH11	1.81	0.45
1:B:358:GLY:O	1:B:360:GLY:N	2.50	0.45
1:B:417:ILE:O	1:B:422:ARG:NH1	2.49	0.45
1:A:273:VAL:HG22	1:A:274:GLY:N	2.29	0.45
1:A:209:ALA:O	1:A:213:THR:HG23	2.17	0.45
1:B:110:ASN:ND2	1:B:112:MET:HB2	2.31	0.45
1:A:165:ASP:OD2	1:B:175:ARG:NH1	2.49	0.45
1:A:175:ARG:HD2	1:A:182:ASP:O	2.16	0.45
1:A:201:VAL:CG1	1:A:276:GLY:C	2.89	0.45
1:A:358:GLY:O	1:A:360:GLY:N	2.50	0.45
1:B:314:GLY:HA3	1:B:385:GLY:C	2.42	0.45
1:A:56:ALA:HA	1:A:201:VAL:CG2	2.47	0.45
1:A:432:LEU:O	1:A:435:ASP:HB2	2.16	0.45
1:B:26:GLN:HA	1:B:32:ALA:HB2	1.99	0.45
1:A:62:ILE:HG21	1:A:142:MET:CE	2.33	0.44
1:B:273:VAL:HG22	1:B:274:GLY:N	2.31	0.44
1:B:284:GLU:H	1:B:284:GLU:CD	2.26	0.44
1:A:90:ASN:O	1:A:109:ASP:HB3	2.16	0.44
1:A:362:ASP:OD1	1:A:364:ALA:N	2.48	0.44
1:B:170:LEU:O	1:B:174:LEU:HG	2.17	0.44
1:B:346:ALA:HB2	1:B:388:VAL:HG13	2.00	0.44
1:A:350:LEU:HA	1:A:395:ALA:HB2	1.99	0.44
1:B:41:ILE:HD11	1:B:298:LEU:HD11	1.99	0.44
1:B:191:TYR:O	1:B:194:GLN:HB3	2.17	0.44
1:A:282:LEU:HA	1:A:287:ASN:O	2.18	0.44
1:A:405:ARG:HG3	1:A:405:ARG:HH11	1.81	0.44
1:B:27:TYR:HD1	1:B:28:ILE:HG23	1.80	0.44
1:B:2:ARG:O	1:B:2:ARG:HG3	2.18	0.44
1:B:84:ASP:O	1:B:107:ARG:NH1	2.51	0.44
1:B:154:TRP:HA	1:B:157:TYR:HB3	1.99	0.43
1:B:323:GLU:OE1	1:B:323:GLU:HA	2.17	0.43
1:A:134:ARG:HG2	1:A:134:ARG:NH1	2.29	0.43
1:A:284:GLU:CG	2:A:495:HOH:O	2.65	0.43
1:A:20:ASN:HB2	1:A:290:ARG:NH2	2.33	0.43
1:A:240:SER:HB3	2:A:463:HOH:O	2.18	0.43
1:A:201:VAL:HG12	1:A:276:GLY:O	2.19	0.43
1:A:443:ASP:OD1	1:A:443:ASP:C	2.61	0.43
1:A:169:SER:OG	1:B:173:MET:HB2	2.19	0.43
1:A:351:ARG:HD2	1:A:355:GLU:HB3	2.01	0.43
1:A:8:TYR:CD2	1:A:8:TYR:C	2.97	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:GLY:HA2	1:A:243:TYR:HB3	2.01	0.43
1:A:110:ASN:O	1:A:116:GLY:HA3	2.18	0.43
1:A:27:TYR:CE1	1:A:28:ILE:HG12	2.53	0.43
1:B:267:GLY:HA3	1:B:275:ILE:HB	2.01	0.43
1:A:134:ARG:CG	1:A:134:ARG:NH1	2.81	0.42
1:B:316:ALA:O	1:B:331:LEU:HA	2.19	0.42
1:A:214:GLY:O	1:A:227:SER:HA	2.19	0.42
1:A:283:ASP:OD1	1:A:285:VAL:HG22	2.19	0.42
1:A:352:THR:O	1:A:435:ASP:CG	2.62	0.42
1:B:387:ALA:O	1:B:390:GLU:HB2	2.19	0.42
1:A:316:ALA:HB1	1:A:335:ILE:CD1	2.49	0.42
1:A:419:ASP:HA	1:A:422:ARG:NH1	2.35	0.42
1:B:201:VAL:HG23	1:B:278:PHE:HB2	2.02	0.42
1:B:355:GLU:C	1:B:357:PRO:CD	2.93	0.42
1:A:138:ALA:O	1:A:141:ILE:HG22	2.19	0.42
1:A:130:SER:OG	1:A:133:GLU:HG3	2.20	0.42
1:A:423:ARG:HG2	1:A:423:ARG:HH11	1.85	0.42
1:B:85:ARG:HB2	1:B:85:ARG:CZ	2.50	0.42
1:B:90:ASN:O	1:B:109:ASP:HB3	2.19	0.42
1:B:110:ASN:O	1:B:116:GLY:HA3	2.20	0.42
1:B:125:VAL:HB	1:B:129:ALA:HB1	2.01	0.42
1:A:422:ARG:NE	1:A:448:LEU:O	2.53	0.42
1:A:363:ALA:HB1	1:A:370:GLN:CD	2.45	0.41
1:B:27:TYR:CE1	1:B:28:ILE:HG12	2.55	0.41
1:B:222:GLU:HG2	1:B:224:MET:CE	2.50	0.41
1:B:347:LEU:HD22	1:B:432:LEU:HD11	2.01	0.41
1:A:317:VAL:O	1:A:387:ALA:HB3	2.21	0.41
1:B:318:ARG:NH1	1:B:332:GLN:OE1	2.53	0.41
1:A:77:ASP:OD2	1:A:124:LEU:O	2.39	0.41
1:B:318:ARG:O	1:B:319:PHE:HB3	2.21	0.41
1:B:362:ASP:OD1	1:B:364:ALA:N	2.45	0.41
1:A:258:LYS:HA	1:A:258:LYS:HD2	1.95	0.41
1:A:292:VAL:HG12	1:A:293:LEU:N	2.36	0.41
1:A:157:TYR:HD1	1:A:192:VAL:HG12	1.85	0.41
1:A:296:ARG:NH1	2:A:543:HOH:O	2.53	0.41
1:A:367:PRO:O	1:A:371:GLU:HG3	2.20	0.41
1:B:67:LYS:HE3	1:B:191:TYR:OH	2.21	0.41
1:B:232:ARG:HG2	1:B:232:ARG:NH1	2.36	0.41
1:B:237:MET:HE1	1:B:266:LEU:HD13	2.03	0.41
1:B:358:GLY:C	1:B:360:GLY:N	2.77	0.41
1:B:153:ASP:HB2	1:B:198:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:THR:C	1:A:361:TRP:H	2.28	0.40
1:B:8:TYR:CD2	1:B:8:TYR:C	3.00	0.40
1:B:322:ARG:HG2	1:B:322:ARG:HH21	1.85	0.40
1:B:443:ASP:OD1	1:B:443:ASP:C	2.64	0.40
1:A:6:PRO:HG3	1:A:51:HIS:HB3	2.03	0.40
1:A:358:GLY:C	1:A:360:GLY:N	2.77	0.40
1:A:97:ASN:ND2	1:B:97:ASN:ND2	2.69	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	446/456 (98%)	413 (93%)	29 (6%)	4 (1%)	14	27
1	B	446/456 (98%)	409 (92%)	32 (7%)	5 (1%)	11	22
All	All	892/912 (98%)	822 (92%)	61 (7%)	9 (1%)	12	24

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	446	ARG
1	A	359	THR
1	A	446	ARG
1	B	355	GLU
1	B	359	THR
1	B	310	ASP
1	A	444	PRO
1	B	324	GLY
1	A	324	GLY

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	336/341 (98%)	320 (95%)	16 (5%)	23	46
1	B	336/341 (98%)	319 (95%)	17 (5%)	21	43
All	All	672/682 (98%)	639 (95%)	33 (5%)	22	45

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

Mol	Chain	Res	Type
1	A	78	ARG
1	A	92	SER
1	A	135	LEU
1	A	160	GLU
1	A	228	ILE
1	A	248	GLN
1	A	250	LEU
1	A	266	LEU
1	A	284	GLU
1	A	292	VAL
1	A	326	ARG
1	A	329	LEU
1	A	351	ARG
1	A	356	LYS
1	A	397	ARG
1	A	448	LEU
1	B	1	MET
1	B	12	LEU
1	B	64	SER
1	B	94	GLU
1	B	104	GLU
1	B	131	ARG
1	B	135	LEU
1	B	149	ARG
1	B	160	GLU
1	B	181	GLN
1	B	248	GLN

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Mol	Chain	Res	Type
1	B	250	LEU
1	B	266	LEU
1	B	307	MET
1	B	355	GLU
1	B	356	LYS
1	B	409	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	GLN
1	A	110	ASN
1	A	121	HIS
1	A	248	GLN
1	A	433	GLN
1	B	26	GLN
1	B	51	HIS
1	B	86	GLN
1	B	110	ASN
1	B	121	HIS
1	B	181	GLN
1	B	248	GLN
1	B	370	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	448/456 (98%)	0.01	14 (3%)	51	47	24, 43, 81, 108	0
1	B	448/456 (98%)	0.11	20 (4%)	38	33	26, 45, 81, 107	0
All	All	896/912 (98%)	0.06	34 (3%)	44	39	24, 44, 81, 108	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	351	ARG	4.5
1	B	448	LEU	4.4
1	A	385	GLY	4.1
1	A	324	GLY	3.8
1	A	448	LEU	3.7
1	B	354	ALA	3.4
1	B	359	THR	3.3
1	A	357	PRO	3.2
1	A	360	GLY	3.2
1	B	360	GLY	3.2
1	B	47	THR	3.2
1	A	359	THR	3.0
1	B	325	ASP	3.0
1	B	357	PRO	2.8
1	B	351	ARG	2.8
1	A	354	ALA	2.6
1	B	57	ASP	2.6
1	B	105	SER	2.6
1	A	104	GLU	2.5
1	B	46	PRO	2.4
1	B	104	GLU	2.4
1	B	324	GLY	2.4
1	A	400	ASN	2.4
1	B	415	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	47	THR	2.3
1	A	399	GLU	2.2
1	A	353	GLY	2.2
1	B	356	LYS	2.2
1	B	358	GLY	2.2
1	B	445	GLU	2.2
1	A	397	ARG	2.2
1	B	1	MET	2.1
1	B	352	THR	2.1
1	B	401	ASP	2.1

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.