



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:16 AM UTC

PDB ID : 6JCO / pdb_00006jco
Title : Crystal structure of calcium free human gelsolin amyloid mutant D187N
Authors : Zorgati, H.; Robinson, R.C.
Deposited on : 2019-01-29
Resolution : 2.88 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

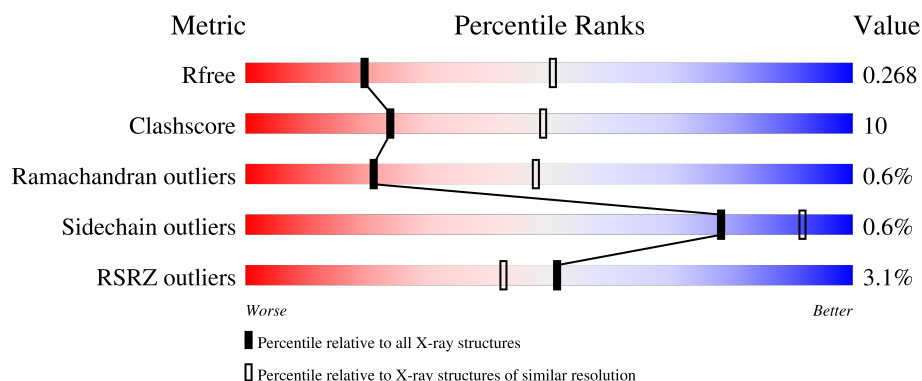
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.88 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	3557 (2.90-2.86)
Clashscore	190562	3801 (2.90-2.86)
Ramachandran outliers	187476	3699 (2.90-2.86)
Sidechain outliers	187428	3702 (2.90-2.86)
RSRZ outliers	180081	3558 (2.90-2.86)

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	727	3% 76% 20% ..
1	B	727	3% 80% 17% ..

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11022 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 Gelsolin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	701	Total	C	N	O	S	0	0	0
			5456	3440	957	1043	16			
1	B	715	Total	C	N	O	S	0	0	0
			5566	3513	975	1062	16			

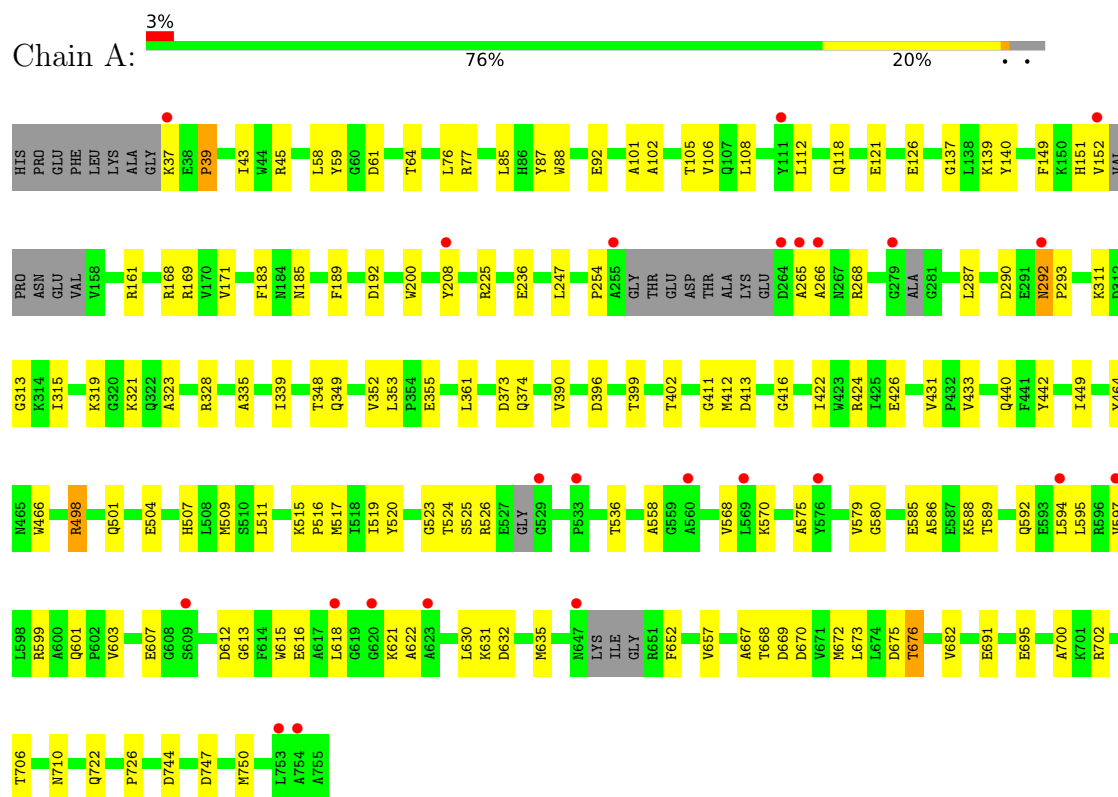
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	187	ASN	ASP	engineered mutation	UNP P06396
B	187	ASN	ASP	engineered mutation	UNP P06396

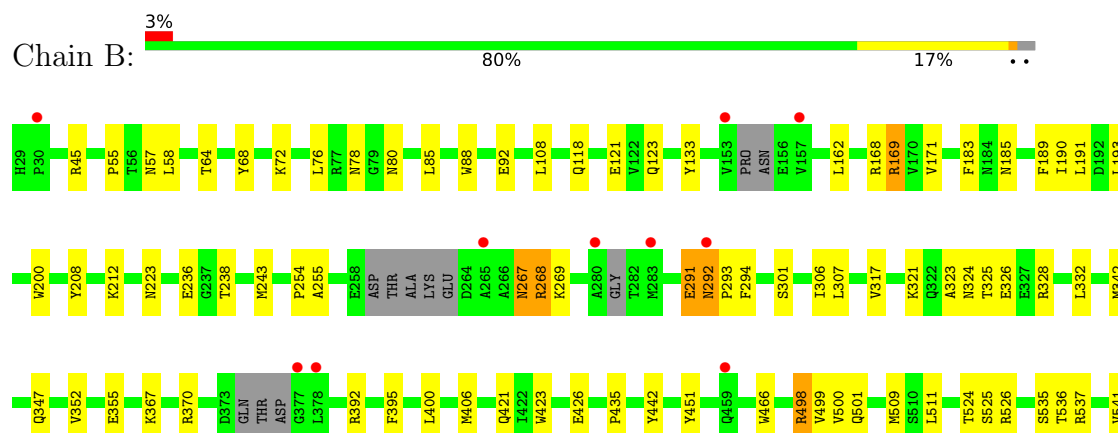
3 Residue-property plots

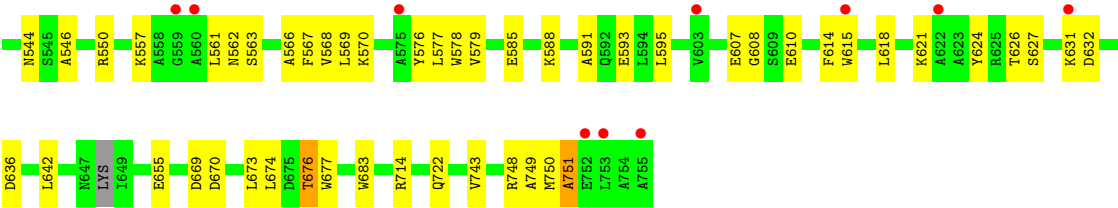
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



• Molecule 1: Gelsolin





4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	170.13Å 170.13Å 151.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.19 – 2.88 69.19 – 2.88	Depositor EDS
% Data completeness (in resolution range)	99.9 (69.19-2.88) 99.9 (69.19-2.88)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.51 (at 2.86Å)	Xtriage
Refinement program	PHENIX (1.13_2998)	Depositor
R, R_{free}	0.206 , 0.267 0.206 , 0.268	Depositor DCC
R_{free} test set	2500 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	71.8	Xtriage
Anisotropy	0.006	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11022	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% 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	0.48	1/5577 (0.0%)	0.65	3/7552 (0.0%)
1	B	0.45	0/5690	0.66	4/7702 (0.1%)
All	All	0.46	1/11267 (0.0%)	0.66	7/15254 (0.0%)

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	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	39	PRO	N-CD	-16.07	1.25	1.47

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	676	THR	CA-C-N	-7.04	106.65	121.64
1	A	676	THR	C-N-CA	-7.04	106.65	121.64
1	B	291	GLU	CA-C-N	-5.87	107.48	121.80
1	B	291	GLU	C-N-CA	-5.87	107.48	121.80
1	A	39	PRO	N-CD-CG	5.23	111.05	103.20
1	B	676	THR	CA-C-N	-5.03	110.93	121.64
1	B	676	THR	C-N-CA	-5.03	110.93	121.64

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	374	GLN	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	5456	0	5293	112	0
1	B	5566	0	5418	108	0
All	All	11022	0	10711	219	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 10.

All (219) 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:615:TRP:CE3	1:B:621:LYS:HE2	1.84	1.11
1:A:612:ASP:O	1:A:616:GLU:CD	1.97	1.07
1:A:612:ASP:O	1:A:616:GLU:OE1	1.78	1.01
1:A:524:THR:HG22	1:A:526:ARG:H	1.29	0.97
1:A:292:ASN:HB3	1:A:293:PRO:HD3	1.50	0.92
1:A:64:THR:HG22	1:A:92:GLU:HG2	1.55	0.87
1:B:169:ARG:NH2	1:B:670:ASP:OD2	2.08	0.86
1:B:631:LYS:HD2	1:B:632:ASP:H	1.41	0.85
1:A:373:ASP:HB3	1:B:435:PRO:HG2	1.60	0.84
1:B:541:VAL:HG11	1:B:591:ALA:HB2	1.59	0.82
1:B:615:TRP:CE3	1:B:621:LYS:CE	2.62	0.81
1:B:631:LYS:CD	1:B:632:ASP:H	1.97	0.78
1:A:498:ARG:HG2	1:A:498:ARG:HH11	1.51	0.76
1:A:161:ARG:NH2	1:A:192:ASP:OD2	2.20	0.74
1:B:561:LEU:HD21	1:B:578:TRP:CH2	2.22	0.74
1:A:612:ASP:O	1:A:616:GLU:OE2	2.05	0.74
1:B:118:GLN:HB2	1:B:352:VAL:HG22	1.69	0.74
1:A:168:ARG:NH2	1:A:670:ASP:OD2	2.20	0.74
1:A:424:ARG:NH1	1:A:525:SER:OG	2.20	0.73
1:A:524:THR:HG21	1:A:526:ARG:HE	1.54	0.73
1:A:673:LEU:HD23	1:A:682:VAL:HG12	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:ARG:HG2	1:A:657:VAL:HG22	1.70	0.72
1:B:563:SER:HB2	1:B:626:THR:HA	1.71	0.72
1:B:64:THR:HG22	1:B:92:GLU:HB2	1.73	0.69
1:B:615:TRP:HE3	1:B:621:LYS:CE	2.06	0.67
1:A:101:ALA:O	1:A:105:THR:HG23	1.93	0.67
1:B:615:TRP:HB3	1:B:621:LYS:NZ	2.10	0.67
1:B:524:THR:OG1	1:B:526:ARG:HG2	1.96	0.65
1:B:395:PHE:CD1	1:B:406:MET:HE3	2.30	0.65
1:B:610:GLU:HB2	1:B:615:TRP:CZ3	2.31	0.65
1:A:268:ARG:HD2	1:A:268:ARG:O	1.96	0.65
1:A:311:LYS:HE2	1:A:311:LYS:H	1.62	0.64
1:A:64:THR:CG2	1:A:92:GLU:HG2	2.26	0.64
1:A:168:ARG:HH21	1:A:667:ALA:HB1	1.62	0.64
1:B:615:TRP:CD2	1:B:621:LYS:HE2	2.33	0.64
1:A:515:LYS:NZ	1:A:516:PRO:O	2.26	0.64
1:B:631:LYS:HD2	1:B:632:ASP:N	2.12	0.64
1:A:504:GLU:HG2	1:A:517:MET:HE1	1.80	0.63
1:A:580:GLY:HA2	1:A:607:GLU:HB2	1.78	0.63
1:A:579:VAL:HG21	1:A:588:LYS:HE2	1.79	0.63
1:A:321:LYS:HG3	1:A:355:GLU:OE1	1.98	0.63
1:B:267:ASN:O	1:B:269:LYS:N	2.29	0.63
1:A:613:GLY:HA2	1:A:616:GLU:OE1	1.99	0.62
1:A:586:ALA:HA	1:A:589:THR:HG22	1.79	0.62
1:B:400:LEU:HD13	1:B:406:MET:HE2	1.80	0.62
1:B:498:ARG:HG2	1:B:498:ARG:HH11	1.65	0.61
1:B:301:SER:HB3	1:B:321:LYS:HG3	1.82	0.61
1:A:558:ALA:HB2	1:A:618:LEU:HD21	1.83	0.61
1:A:43:ILE:HD12	1:A:59:TYR:CG	2.36	0.61
1:A:524:THR:HG21	1:A:526:ARG:NE	2.16	0.60
1:B:578:TRP:CD1	1:B:614:PHE:HE1	2.20	0.59
1:A:208:TYR:HE2	1:A:667:ALA:HA	1.67	0.59
1:B:293:PRO:O	1:B:367:LYS:HE3	2.03	0.58
1:A:390:VAL:HG11	1:A:635:MET:HE1	1.86	0.57
1:B:561:LEU:HD23	1:B:562:ASN:N	2.19	0.57
1:A:87:TYR:HB3	1:A:105:THR:HG21	1.84	0.57
1:A:292:ASN:HB3	1:A:293:PRO:CD	2.26	0.57
1:B:576:TYR:CE2	1:B:614:PHE:HB2	2.41	0.56
1:B:191:LEU:HG	1:B:193:LEU:HD21	1.87	0.56
1:A:76:LEU:O	1:A:77:ARG:HB2	2.05	0.56
1:A:85:LEU:HD21	1:A:108:LEU:HD23	1.86	0.56
1:B:537:ARG:O	1:B:569:LEU:HD12	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:ALA:O	1:A:328:ARG:NH2	2.40	0.55
1:A:315:ILE:HD11	1:A:335:ALA:HB1	1.88	0.55
1:B:593:GLU:O	1:B:593:GLU:HG3	2.05	0.55
1:A:137:GLY:HA3	1:A:171:VAL:HG13	1.89	0.55
1:B:615:TRP:HB2	1:B:621:LYS:HG2	1.88	0.54
1:A:673:LEU:CD2	1:A:682:VAL:HG12	2.35	0.54
1:A:682:VAL:HG11	1:A:700:ALA:HB2	1.89	0.54
1:B:676:THR:HG22	1:B:677:TRP:H	1.73	0.54
1:A:265:ALA:HB3	1:A:652:PHE:O	2.07	0.54
1:B:168:ARG:HH12	1:B:208:TYR:HB3	1.72	0.54
1:B:168:ARG:NH2	1:B:669:ASP:OD1	2.40	0.54
1:B:185:ASN:OD1	1:B:255:ALA:HA	2.08	0.54
1:B:500:VAL:HG13	1:B:714:ARG:HB3	1.90	0.53
1:B:347:GLN:OE1	1:B:347:GLN:N	2.35	0.53
1:B:676:THR:HG22	1:B:677:TRP:N	2.23	0.53
1:A:58:LEU:HD13	1:A:151:HIS:HB3	1.90	0.53
1:B:162:LEU:HD12	1:B:190:ILE:O	2.09	0.53
1:A:498:ARG:HG2	1:A:498:ARG:NH1	2.21	0.52
1:B:615:TRP:HE3	1:B:621:LYS:HZ3	1.57	0.52
1:B:183:PHE:HA	1:B:189:PHE:CZ	2.43	0.52
1:B:200:TRP:CD1	1:B:243:MET:HE1	2.44	0.52
1:B:578:TRP:HD1	1:B:614:PHE:HE1	1.58	0.52
1:A:168:ARG:NH2	1:A:669:ASP:OD1	2.23	0.52
1:A:208:TYR:CE2	1:A:667:ALA:HA	2.45	0.52
1:A:396:ASP:OD2	1:A:399:THR:OG1	2.24	0.52
1:B:426:GLU:HA	1:B:526:ARG:HH21	1.73	0.52
1:A:524:THR:HG22	1:A:526:ARG:N	2.11	0.51
1:A:185:ASN:OD1	1:A:236:GLU:OE2	2.27	0.51
1:A:293:PRO:HG3	1:A:710:ASN:ND2	2.25	0.51
1:A:266:ALA:HB2	1:A:702:ARG:HH21	1.76	0.51
1:B:607:GLU:OE2	1:B:624:TYR:OH	2.28	0.51
1:A:45:ARG:NH2	1:A:149:PHE:O	2.39	0.51
1:A:594:LEU:HA	1:A:597:VAL:HG12	1.92	0.51
1:A:575:ALA:O	1:A:603:VAL:HG22	2.11	0.51
1:A:691:GLU:O	1:A:695:GLU:HG2	2.11	0.50
1:A:61:ASP:OD1	1:A:139:LYS:HE2	2.12	0.50
1:A:589:THR:O	1:A:592:GLN:HG3	2.12	0.49
1:B:615:TRP:HB3	1:B:621:LYS:HZ2	1.75	0.49
1:A:426:GLU:CD	1:A:431:VAL:HG21	2.37	0.49
1:B:579:VAL:HG11	1:B:588:LYS:HE3	1.94	0.49
1:A:169:ARG:CG	1:A:657:VAL:HG22	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:498:ARG:HH11	1:A:498:ARG:CG	2.22	0.49
1:B:325:THR:HG22	1:B:328:ARG:HH12	1.78	0.49
1:B:615:TRP:HE3	1:B:621:LYS:NZ	2.10	0.49
1:A:592:GLN:HA	1:A:595:LEU:HD12	1.93	0.49
1:B:291:GLU:O	1:B:294:PHE:CE1	2.66	0.48
1:A:449:ILE:HB	1:A:464:TYR:HB2	1.95	0.48
1:B:57:ASN:O	1:B:223:ASN:HB3	2.13	0.48
1:B:578:TRP:CD1	1:B:614:PHE:CE1	3.01	0.48
1:B:200:TRP:CZ2	1:B:236:GLU:HG2	2.49	0.48
1:B:743:VAL:HG13	1:B:748:ARG:NH2	2.29	0.48
1:B:749:ALA:C	1:B:751:ALA:H	2.22	0.48
1:B:292:ASN:H	1:B:293:PRO:HD2	1.78	0.48
1:A:200:TRP:CZ2	1:A:236:GLU:HG3	2.48	0.48
1:B:509:MET:SD	1:B:550:ARG:HD3	2.54	0.48
1:B:561:LEU:O	1:B:624:TYR:HB2	2.14	0.48
1:A:183:PHE:HA	1:A:189:PHE:CZ	2.49	0.48
1:B:442:TYR:CE1	1:B:525:SER:HB3	2.49	0.48
1:A:558:ALA:CB	1:A:622:ALA:H	2.27	0.47
1:B:85:LEU:HD11	1:B:108:LEU:HB3	1.97	0.47
1:B:561:LEU:HD21	1:B:578:TRP:CZ3	2.49	0.47
1:A:339:ILE:HD13	1:A:348:THR:HB	1.95	0.47
1:B:642:LEU:HD12	1:B:673:LEU:O	2.15	0.47
1:A:399:THR:O	1:A:402:THR:OG1	2.30	0.47
1:B:267:ASN:OD1	1:B:268:ARG:N	2.27	0.47
1:B:578:TRP:HD1	1:B:614:PHE:CE1	2.33	0.47
1:A:440:GLN:OE1	1:A:520:TYR:OH	2.20	0.47
1:A:616:GLU:C	1:A:618:LEU:H	2.23	0.47
1:A:558:ALA:HA	1:A:618:LEU:HD11	1.97	0.46
1:A:412:MET:HE3	1:A:412:MET:HB3	1.50	0.46
1:B:324:ASN:ND2	1:B:326:GLU:HB2	2.31	0.46
1:A:603:VAL:HG23	1:A:603:VAL:O	2.16	0.46
1:B:608:GLY:N	1:B:610:GLU:OE2	2.48	0.46
1:B:498:ARG:HH11	1:B:498:ARG:CG	2.27	0.46
1:A:313:GLY:O	1:A:349:GLN:HG3	2.15	0.46
1:A:422:ILE:O	1:A:433:VAL:HG23	2.16	0.46
1:A:517:MET:HE3	1:A:519:ILE:HD11	1.98	0.46
1:A:287:LEU:HD21	1:A:290:ASP:HB3	1.97	0.46
1:A:668:THR:HG22	1:A:722:GLN:OE1	2.16	0.46
1:B:238:THR:HG22	1:B:238:THR:O	2.16	0.46
1:B:321:LYS:HG2	1:B:355:GLU:OE2	2.15	0.46
1:A:88:TRP:HA	1:A:121:GLU:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ARG:HH22	1:A:225:ARG:NH2	2.13	0.45
1:B:118:GLN:NE2	1:B:332:LEU:HD11	2.31	0.45
1:A:319:LYS:HE2	1:A:352:VAL:HG22	1.98	0.45
1:B:76:LEU:C	1:B:78:ASN:H	2.25	0.45
1:B:683:TRP:CZ2	1:B:722:GLN:HB2	2.52	0.45
1:A:501:GLN:HE21	1:A:519:ILE:HG22	1.82	0.45
1:B:370:ARG:NH2	1:B:627:SER:HB3	2.31	0.45
1:B:370:ARG:HH11	1:B:370:ARG:HB3	1.81	0.45
1:A:85:LEU:O	1:A:118:GLN:HA	2.16	0.44
1:B:451:TYR:CE1	1:B:511:LEU:HD22	2.53	0.44
1:B:561:LEU:HA	1:B:567:PHE:CZ	2.52	0.44
1:A:87:TYR:HB3	1:A:105:THR:CG2	2.46	0.44
1:A:575:ALA:HB3	1:A:601:GLN:O	2.16	0.44
1:B:557:LYS:C	1:B:618:LEU:HD23	2.43	0.44
1:B:171:VAL:HG21	1:B:212:LYS:HB3	1.99	0.44
1:B:585:GLU:CD	1:B:585:GLU:H	2.26	0.44
1:A:168:ARG:HH21	1:A:667:ALA:CB	2.30	0.44
1:B:76:LEU:HB2	1:B:80:ASN:O	2.17	0.44
1:A:126:GLU:OE2	1:A:140:TYR:OH	2.25	0.43
1:A:411:GLY:O	1:A:507:HIS:HB2	2.18	0.43
1:B:45:ARG:HG3	1:B:68:TYR:CZ	2.53	0.43
1:B:541:VAL:HG13	1:B:566:ALA:HB3	2.00	0.43
1:B:536:THR:HA	1:B:570:LYS:O	2.18	0.43
1:B:544:ASN:O	1:B:546:ALA:N	2.51	0.43
1:A:702:ARG:O	1:A:706:THR:HG23	2.18	0.43
1:B:395:PHE:CE1	1:B:406:MET:HE3	2.54	0.43
1:B:169:ARG:HD2	1:B:655:GLU:OE1	2.19	0.43
1:A:102:ALA:O	1:A:106:VAL:HG12	2.18	0.43
1:B:76:LEU:O	1:B:78:ASN:N	2.45	0.43
1:B:88:TRP:HA	1:B:121:GLU:O	2.19	0.43
1:A:118:GLN:HB2	1:A:352:VAL:CG1	2.49	0.42
1:A:585:GLU:O	1:A:589:THR:HG22	2.19	0.42
1:B:321:LYS:HG2	1:B:355:GLU:CD	2.44	0.42
1:B:72:LYS:HG2	1:B:133:TYR:CE1	2.54	0.42
1:B:55:PRO:HG2	1:B:58:LEU:HD12	2.00	0.42
1:B:610:GLU:HB2	1:B:615:TRP:HZ3	1.80	0.42
1:A:151:HIS:O	1:A:152:VAL:HG13	2.19	0.42
1:A:352:VAL:C	1:A:353:LEU:HD23	2.44	0.42
1:B:88:TRP:CZ2	1:B:123:GLN:HB2	2.54	0.42
1:A:615:TRP:HB3	1:A:621:LYS:HG2	2.01	0.42
1:A:185:ASN:HB2	1:A:254:PRO:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:466:TRP:CZ2	1:A:501:GLN:HB2	2.55	0.42
1:B:185:ASN:ND2	1:B:254:PRO:O	2.52	0.42
1:A:247:LEU:HD23	1:A:247:LEU:HA	1.76	0.42
1:B:498:ARG:HG2	1:B:498:ARG:NH1	2.30	0.42
1:A:413:ASP:OD1	1:A:726:PRO:HB2	2.20	0.41
1:A:675:ASP:OD1	1:A:676:THR:O	2.37	0.41
1:A:536:THR:HA	1:A:570:LYS:O	2.18	0.41
1:B:400:LEU:CD1	1:B:406:MET:HE2	2.50	0.41
1:B:342:MET:HE3	1:B:342:MET:HB3	1.88	0.41
1:A:630:LEU:O	1:A:632:ASP:N	2.54	0.41
1:B:85:LEU:HD23	1:B:85:LEU:HA	1.92	0.41
1:B:306:ILE:HG12	1:B:317:VAL:HG22	2.02	0.41
1:B:332:LEU:N	1:B:332:LEU:HD12	2.35	0.41
1:B:544:ASN:C	1:B:546:ALA:H	2.27	0.41
1:B:200:TRP:CG	1:B:243:MET:HE1	2.56	0.41
1:B:579:VAL:HB	1:B:588:LYS:HZ2	1.85	0.41
1:A:43:ILE:HD12	1:A:59:TYR:CD1	2.56	0.41
1:A:108:LEU:O	1:A:112:LEU:HG	2.20	0.41
1:A:750:MET:HE3	1:A:750:MET:HB2	1.81	0.41
1:B:421:GLN:HG2	1:B:423:TRP:CZ2	2.56	0.41
1:B:466:TRP:CZ2	1:B:501:GLN:HB2	2.56	0.41
1:B:392:ARG:NH2	1:B:636:ASP:OD2	2.54	0.41
1:A:442:TYR:HB3	1:A:523:GLY:O	2.21	0.40
1:A:361:LEU:H	1:A:361:LEU:HD12	1.87	0.40
1:A:416:GLY:O	1:A:511:LEU:HA	2.22	0.40
1:A:568:VAL:HG21	1:A:594:LEU:HD23	2.03	0.40
1:A:672:MET:HE3	1:A:672:MET:HB3	1.86	0.40
1:A:744:ASP:HB3	1:A:747:ASP:HB2	2.03	0.40
1:B:323:ALA:O	1:B:328:ARG:NH2	2.55	0.40
1:B:568:VAL:CG1	1:B:595:LEU:HD11	2.51	0.40
1:A:161:ARG:HH22	1:A:225:ARG:HH22	1.67	0.40
1:A:599:ARG:HA	1:A:599:ARG:NH1	2.37	0.40
1:A:509:MET:HA	1:A:517:MET:HG3	2.03	0.40
1:B:577:LEU:C	1:B:577:LEU:HD12	2.47	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	689/727 (95%)	649 (94%)	37 (5%)	3 (0%)	30	56
1	B	703/727 (97%)	652 (93%)	45 (6%)	6 (1%)	14	38
All	All	1392/1454 (96%)	1301 (94%)	82 (6%)	9 (1%)	21	48

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	268	ARG
1	A	292	ASN
1	A	631	LYS
1	B	750	MET
1	B	751	ALA
1	A	39	PRO
1	B	267	ASN
1	B	292	ASN
1	B	535	SER

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	568/591 (96%)	566 (100%)	2 (0%)	84	94
1	B	580/591 (98%)	575 (99%)	5 (1%)	70	88
All	All	1148/1182 (97%)	1141 (99%)	7 (1%)	78	92

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LYS
1	A	498	ARG
1	B	169	ARG
1	B	307	LEU
1	B	498	ARG
1	B	499	VAL
1	B	674	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	GLN
1	A	187	ASN
1	A	204	ASN
1	A	215	GLN
1	A	292	ASN
1	A	349	GLN
1	A	364	GLN
1	A	496	GLN
1	A	647	ASN
1	A	710	ASN
1	B	118	GLN
1	B	119	HIS
1	B	198	HIS
1	B	309	HIS
1	B	389	ASN
1	B	465	ASN
1	B	467	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	701/727 (96%)	-0.04	24 (3%)	48 39	37, 63, 113, 136	0
1	B	715/727 (98%)	-0.12	20 (2%)	55 46	37, 59, 106, 128	0
All	All	1416/1454 (97%)	-0.08	44 (3%)	51 42	37, 61, 109, 136	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	529	GLY	5.4
1	A	264	ASP	4.7
1	A	753	LEU	3.9
1	B	280	ALA	3.6
1	B	157	VAL	3.6
1	A	292	ASN	3.6
1	B	292	ASN	3.5
1	B	377	GLY	3.5
1	B	753	LEU	3.3
1	B	575	ALA	3.0
1	A	111	TYR	3.0
1	B	378	LEU	3.0
1	A	279	GLY	2.9
1	A	255	ALA	2.9
1	B	755	ALA	2.9
1	A	754	ALA	2.8
1	B	622	ALA	2.8
1	A	266	ALA	2.6
1	A	623	ALA	2.6
1	A	37	LYS	2.5
1	B	752	GLU	2.5
1	A	533	PRO	2.5
1	A	597	VAL	2.5
1	B	153	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	265	ALA	2.4
1	B	265	ALA	2.4
1	B	603	VAL	2.3
1	B	30	PRO	2.3
1	A	152	VAL	2.3
1	A	560	ALA	2.3
1	A	618	LEU	2.3
1	B	559	GLY	2.3
1	B	615	TRP	2.3
1	B	283	MET	2.2
1	A	569	LEU	2.2
1	A	609	SER	2.2
1	B	459	GLN	2.2
1	A	576	TYR	2.1
1	B	560	ALA	2.1
1	A	208	TYR	2.1
1	A	647	ASN	2.1
1	B	631	LYS	2.0
1	A	594	LEU	2.0
1	A	620	GLY	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.