



Full wwPDB X-ray Structure Validation Report i

May 13, 2020 – 11:34 am BST

PDB ID : 6N9N
Title : Crystal structure of murine GSDMD
Authors : Liu, Z.; Wang, C.; Yang, J.; Xiao, T.S.
Deposited on : 2018-12-03
Resolution : 3.30 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 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 : 2.11
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) : 2.11

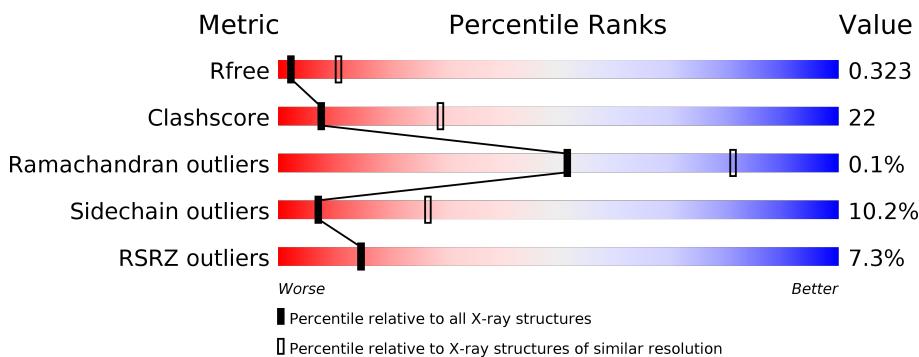
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

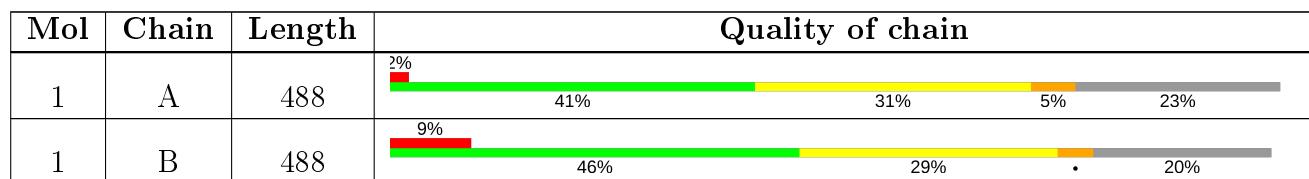
The reported resolution of this entry is 3.30 Å.

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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 on 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 is only 1 type of molecule in this entry. The entry contains 5954 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 Gasdermin-D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	378	Total	C 2945	N 1869	O 493	S 568	15	0	0
1	B	388	Total	C 3009	N 1906	O 503	S 585	15	0	0

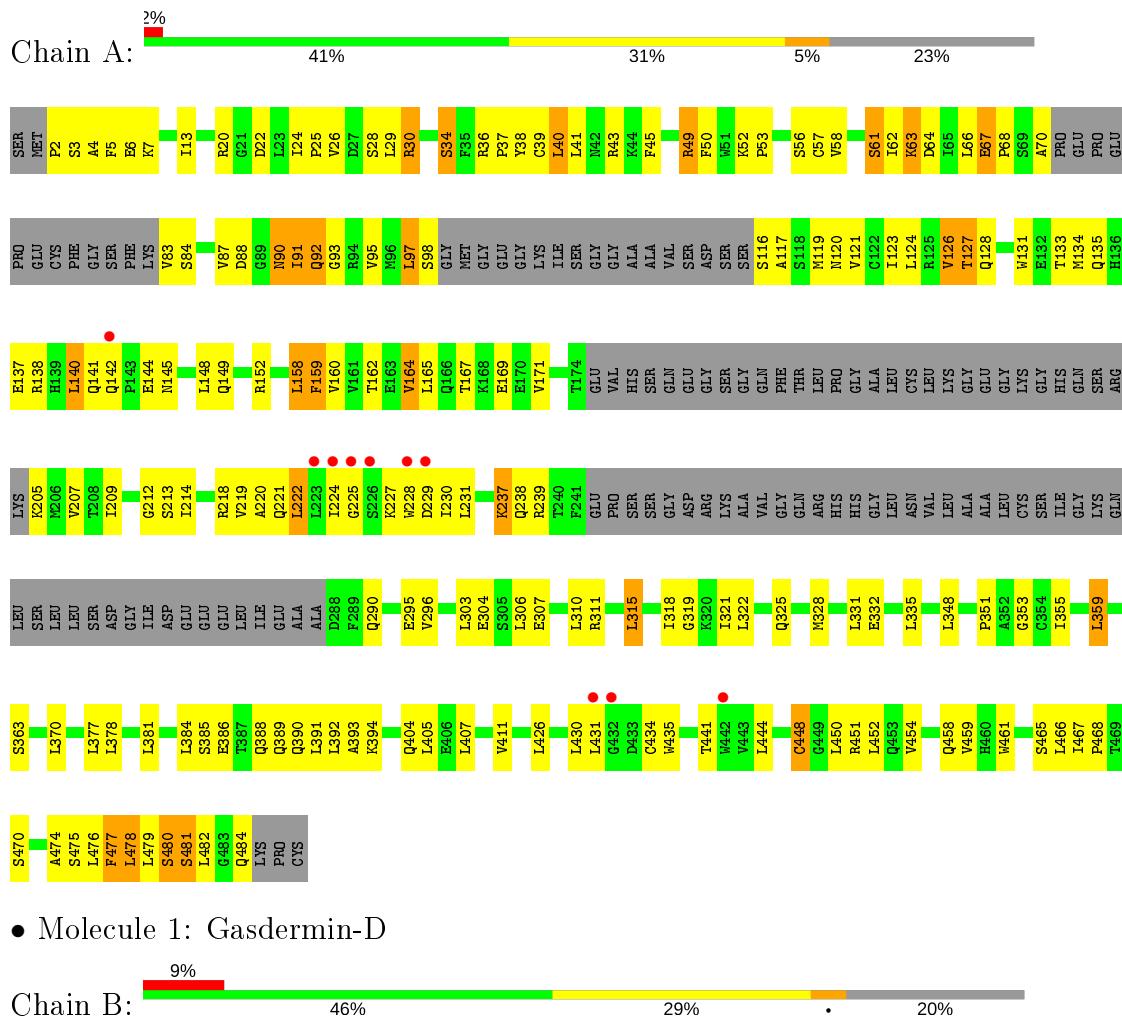
There are 2 discrepancies between the modelled and reference sequences:

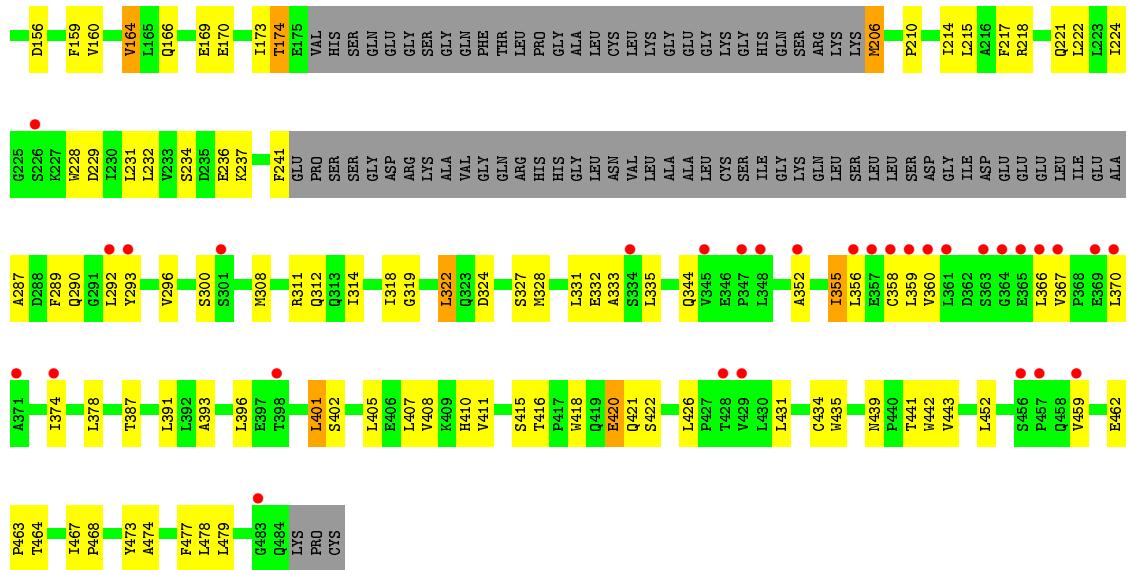
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q9D8T2
B	0	SER	-	expression tag	UNP Q9D8T2

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Gasdermin-D





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.42 Å 86.84 Å 83.54 Å 90.00° 95.27° 90.00°	Depositor
Resolution (Å)	46.01 – 3.30 46.01 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (46.01-3.30) 99.6 (46.01-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ ¹	1.44 (at 3.32 Å)	Xtriage
Refinement program	PHENIX (1.15.2_3472: ???)	Depositor
R , R_{free}	0.261 , 0.321 0.266 , 0.323	Depositor DCC
R_{free} test set	697 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	139.8	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 120.6	EDS
L-test for twinning ²	$< L > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5954	wwPDB-VP
Average B, all atoms (Å ²)	152.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $< |L| >$, $< L^2 >$ 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	0.55	0/2991	0.76	0/4053
1	B	0.47	0/3054	0.67	0/4136
All	All	0.51	0/6045	0.72	0/8189

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	2945	0	2998	147	0
1	B	3009	0	3051	120	0
All	All	5954	0	6049	263	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 22.

All (263) 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:319:GLY:HA2	1:A:322:LEU:HD12	1.21	1.16
1:A:67:GLU:CB	1:A:68:PRO:HD3	1.75	1.13

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:ILE:O	1:A:322:LEU:HG	1.48	1.10
1:A:319:GLY:HA2	1:A:322:LEU:CD1	1.87	1.03
1:A:67:GLU:HB2	1:A:68:PRO:HD3	1.40	1.00
1:A:67:GLU:CB	1:A:68:PRO:CD	2.43	0.97
1:A:335:LEU:HD12	1:A:378:LEU:HD12	1.44	0.96
1:A:67:GLU:HB3	1:A:68:PRO:HD3	1.47	0.96
1:A:67:GLU:HB2	1:A:68:PRO:CD	1.96	0.95
1:A:335:LEU:CD1	1:A:378:LEU:HD12	2.00	0.91
1:B:12:VAL:HG13	1:B:95:VAL:HG21	1.55	0.87
1:A:407:LEU:HD11	1:A:431:LEU:HD21	1.58	0.86
1:A:144:GLU:HG3	1:A:148:LEU:HB2	1.60	0.82
1:A:335:LEU:HD12	1:A:378:LEU:CD1	2.09	0.82
1:A:39:CYS:SG	1:A:40:LEU:N	2.56	0.79
1:A:66:LEU:CD2	1:A:140:LEU:HA	2.16	0.76
1:A:123:ILE:HG22	1:A:165:LEU:HG	1.67	0.74
1:A:66:LEU:O	1:A:141:GLN:HB2	1.86	0.74
1:A:40:LEU:HD23	1:A:158:LEU:HD21	1.70	0.74
1:A:407:LEU:HD12	1:A:441:THR:HG21	1.70	0.73
1:A:124:LEU:HB2	1:A:164:VAL:HG12	1.71	0.72
1:B:43:ARG:HG3	1:B:53:PRO:HG2	1.72	0.72
1:B:159:PHE:HD1	1:B:221:GLN:HA	1.56	0.70
1:B:332:GLU:HA	1:B:335:LEU:HD12	1.74	0.70
1:B:152:ARG:NH2	1:B:241:PHE:O	2.25	0.70
1:A:237:LYS:HE3	1:A:238:GLN:HG3	1.74	0.70
1:B:332:GLU:HB3	1:B:378:LEU:HD23	1.73	0.70
1:B:367:VAL:HB	1:B:370:LEU:HB2	1.73	0.68
1:A:303:LEU:HD23	1:A:482:LEU:HD21	1.74	0.68
1:B:166:GLN:HB3	1:B:214:ILE:HD13	1.75	0.68
1:A:62:ILE:HG22	1:A:83:VAL:HG21	1.77	0.66
1:A:221:GLN:O	1:A:231:LEU:HB2	1.95	0.65
1:A:2:PRO:O	1:A:7:LYS:HE2	1.96	0.65
1:A:452:LEU:HD22	1:A:459:VAL:HG12	1.79	0.65
1:A:474:ALA:O	1:A:478:LEU:HD22	1.97	0.64
1:A:222:LEU:H	1:A:222:LEU:HD12	1.62	0.64
1:A:296:VAL:HG11	1:A:474:ALA:HA	1.80	0.64
1:A:66:LEU:HD23	1:A:140:LEU:HA	1.78	0.64
1:A:87:VAL:HG11	1:A:127:THR:HG22	1.81	0.62
1:A:66:LEU:HD22	1:A:140:LEU:HA	1.80	0.62
1:A:34:SER:HB3	1:A:57:CYS:SG	2.41	0.61
1:A:306:LEU:HB3	1:A:310:LEU:HD23	1.82	0.61
1:A:133:THR:O	1:A:137:GLU:N	2.31	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:314:ILE:HG12	1:B:355:ILE:HG22	1.82	0.61
1:A:97:LEU:HD22	1:A:98:SER:H	1.64	0.61
1:A:315:LEU:HD11	1:A:482:LEU:HB2	1.83	0.60
1:A:83:VAL:HG12	1:A:84:SER:H	1.66	0.60
1:A:45:PHE:HE1	1:A:239:ARG:NE	1.99	0.60
1:A:224:ILE:HG22	1:A:225:GLY:H	1.66	0.60
1:A:335:LEU:CD1	1:A:378:LEU:CD1	2.73	0.60
1:A:171:VAL:HG22	1:A:209:ILE:HB	1.82	0.59
1:A:135:GLN:HA	1:A:228:TRP:CZ2	2.37	0.59
1:A:148:LEU:O	1:A:152:ARG:HG2	2.01	0.59
1:A:386:GLU:O	1:A:390:GLN:HG2	2.03	0.59
1:A:405:LEU:HD12	1:A:477:PHE:HA	1.83	0.59
1:B:86:VAL:HG13	1:B:125:ARG:O	2.02	0.59
1:A:90:ASN:HB3	1:B:93:GLY:H	1.66	0.59
1:A:116:SER:OG	1:A:117:ALA:N	2.25	0.59
1:B:40:LEU:HD11	1:B:62:ILE:HD12	1.83	0.59
1:A:322:LEU:HD13	1:A:393:ALA:HA	1.85	0.59
1:A:332:GLU:HG2	1:A:378:LEU:HB3	1.83	0.59
1:B:314:ILE:HA	1:B:355:ILE:HG22	1.85	0.58
1:B:61:SER:OG	1:B:62:ILE:N	2.36	0.58
1:A:88:ASP:OD1	1:B:94:ARG:HG3	2.04	0.58
1:A:70:ALA:HB2	1:A:138:ARG:HH12	1.69	0.57
1:B:411:VAL:O	1:B:415:SER:N	2.37	0.57
1:A:381:LEU:HA	1:A:384:LEU:HD13	1.87	0.57
1:A:392:LEU:HD21	1:A:479:LEU:HD12	1.87	0.56
1:A:41:LEU:HD23	1:A:57:CYS:HA	1.87	0.56
1:B:86:VAL:HG22	1:B:126:VAL:HG13	1.85	0.56
1:B:435:TRP:NE1	1:B:442:TRP:HE3	2.04	0.56
1:A:467:ILE:HB	1:A:468:PRO:HD3	1.86	0.55
1:A:43:ARG:HG3	1:A:53:PRO:O	2.05	0.55
1:B:435:TRP:CH2	1:B:441:THR:HB	2.41	0.55
1:B:41:LEU:HD12	1:B:55:TYR:HB3	1.88	0.55
1:B:50:PHE:O	1:B:51:TRP:HD1	1.88	0.55
1:A:450:LEU:HD22	1:A:461:TRP:HA	1.88	0.54
1:A:311:ARG:HH21	1:A:482:LEU:HD23	1.73	0.54
1:B:63:LYS:HD3	1:B:82:LYS:HB3	1.89	0.54
1:A:315:LEU:HD21	1:A:482:LEU:O	2.08	0.54
1:A:377:LEU:HD13	1:A:478:LEU:HB2	1.90	0.54
1:B:40:LEU:HD12	1:B:61:SER:O	2.08	0.54
1:A:13:ILE:HD13	1:A:25:PRO:HB3	1.89	0.54
1:A:37:PRO:O	1:A:38:TYR:HB2	2.08	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:402:SER:O	1:B:405:LEU:HB3	2.09	0.53
1:A:24:ILE:HD12	1:A:219:VAL:HG13	1.91	0.53
1:A:158:LEU:O	1:A:222:LEU:HD12	2.08	0.53
1:A:359:LEU:HD12	1:A:370:LEU:HG	1.91	0.53
1:B:319:GLY:HA3	1:B:396:LEU:HD22	1.89	0.53
1:A:160:VAL:HG23	1:A:222:LEU:HG	1.91	0.53
1:A:435:TRP:CH2	1:A:458:GLN:HB3	2.43	0.53
1:B:408:VAL:HA	1:B:411:VAL:HG12	1.89	0.53
1:A:135:GLN:NE2	1:A:229:ASP:HB3	2.23	0.52
1:B:467:ILE:HB	1:B:468:PRO:HD3	1.90	0.52
1:A:384:LEU:HG	1:A:388:GLN:HE21	1.75	0.52
1:A:466:LEU:O	1:A:470:SER:HB2	2.09	0.52
1:A:5:PHE:CE1	1:A:29:LEU:HD12	2.45	0.52
1:B:43:ARG:NH2	1:B:52:LYS:HG3	2.23	0.52
1:A:2:PRO:HA	1:A:6:GLU:HB2	1.91	0.52
1:B:387:THR:O	1:B:391:LEU:HG	2.09	0.52
1:B:19:SER:H	1:B:218:ARG:HH22	1.56	0.51
1:B:435:TRP:HE1	1:B:442:TRP:HE3	1.58	0.51
1:A:391:LEU:HD23	1:A:444:LEU:HD21	1.92	0.51
1:A:392:LEU:HD23	1:A:392:LEU:O	2.10	0.51
1:A:404:GLN:HB3	1:A:476:LEU:HD13	1.92	0.51
1:B:45:PHE:HD2	1:B:47:SER:HG	1.58	0.51
1:A:43:ARG:HD3	1:A:53:PRO:HD2	1.92	0.51
1:B:229:ASP:N	1:B:229:ASP:OD1	2.44	0.51
1:B:356:LEU:O	1:B:360:VAL:HG23	2.10	0.51
1:A:126:VAL:HG13	1:A:131:TRP:HE1	1.74	0.51
1:B:164:VAL:HG12	1:B:217:PHE:HB3	1.93	0.51
1:A:142:GLN:O	1:A:144:GLU:N	2.40	0.51
1:B:236:GLU:CD	1:B:236:GLU:H	2.15	0.51
1:A:355:ILE:O	1:A:359:LEU:HD22	2.11	0.50
1:B:174:THR:HA	1:B:206:MET:HA	1.93	0.50
1:B:148:LEU:HD11	1:B:224:ILE:HD12	1.93	0.50
1:B:415:SER:OG	1:B:418:TRP:NE1	2.31	0.50
1:B:435:TRP:CD1	1:B:442:TRP:HE3	2.30	0.50
1:A:475:SER:O	1:A:479:LEU:HG	2.12	0.49
1:B:442:TRP:CZ2	1:B:452:LEU:HB2	2.47	0.49
1:A:134:MET:HA	1:A:137:GLU:HB3	1.95	0.49
1:A:28:SER:OG	1:A:30:ARG:HG3	2.12	0.49
1:B:97:LEU:HD11	1:B:119:MET:HE2	1.94	0.49
1:A:164:VAL:HG21	1:A:214:ILE:HD13	1.92	0.49
1:B:150:GLN:O	1:B:153:SER:HB3	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:LYS:HD3	1:B:332:GLU:HG3	1.95	0.49
1:B:44:LYS:HA	1:B:156:ASP:CG	2.33	0.49
1:B:462:GLU:HB3	1:B:464:THR:HG22	1.94	0.49
1:A:40:LEU:HD23	1:A:158:LEU:CD2	2.41	0.49
1:A:478:LEU:HA	1:A:481:SER:HB3	1.95	0.49
1:B:308:MET:HG3	1:B:311:ARG:NH2	2.27	0.49
1:A:290:GLN:OE1	1:A:290:GLN:N	2.45	0.49
1:B:311:ARG:HH12	1:B:312:GLN:NE2	2.11	0.49
1:B:405:LEU:HD22	1:B:477:PHE:HA	1.95	0.49
1:A:90:ASN:HB3	1:B:93:GLY:N	2.27	0.49
1:B:147:ILE:HD12	1:B:148:LEU:H	1.77	0.49
1:B:145:ASN:HB2	1:B:149:GLN:HB2	1.94	0.49
1:B:327:SER:HB3	1:B:352:ALA:HB2	1.94	0.49
1:A:205:LYS:HE2	1:A:207:VAL:HG13	1.95	0.49
1:A:3:SER:OG	1:A:4:ALA:N	2.45	0.48
1:A:49:ARG:HG3	1:A:50:PHE:CE1	2.47	0.48
1:A:87:VAL:HG22	1:A:88:ASP:H	1.79	0.48
1:B:407:LEU:O	1:B:410:HIS:HB3	2.13	0.48
1:A:325:GLN:NE2	1:A:389:GLN:OE1	2.46	0.48
1:A:64:ASP:OD1	1:A:64:ASP:N	2.35	0.48
1:B:45:PHE:O	1:B:46:SER:OG	2.25	0.48
1:B:46:SER:HB3	1:B:53:PRO:HG3	1.95	0.47
1:B:314:ILE:HD11	1:B:358:CYS:HB2	1.95	0.47
1:A:148:LEU:HA	1:A:148:LEU:HD13	1.67	0.47
1:A:29:LEU:HD23	1:A:29:LEU:O	2.15	0.47
1:B:452:LEU:HD22	1:B:459:VAL:HG22	1.95	0.47
1:B:146:LYS:HB2	1:B:146:LYS:HE2	1.47	0.47
1:B:140:LEU:H	1:B:140:LEU:HG	1.46	0.47
1:A:321:ILE:HG23	1:A:351:PRO:HB2	1.97	0.47
1:A:36:ARG:O	1:A:39:CYS:HB3	2.15	0.47
1:A:40:LEU:HD13	1:A:61:SER:O	2.14	0.47
1:A:83:VAL:HG12	1:A:84:SER:N	2.29	0.47
1:A:91:ILE:O	1:B:91:ILE:O	2.32	0.47
1:B:84:SER:O	1:B:85:ASP:HB2	2.15	0.47
1:B:415:SER:HG	1:B:418:TRP:HE1	1.58	0.46
1:A:63:LYS:HG3	1:A:63:LYS:H	1.54	0.46
1:B:84:SER:OG	1:B:85:ASP:N	2.47	0.46
1:B:322:LEU:HB3	1:B:393:ALA:HB2	1.98	0.46
1:B:135:GLN:HA	1:B:228:TRP:CZ2	2.51	0.46
1:A:167:THR:HG22	1:A:213:SER:O	2.15	0.46
1:B:5:PHE:CD1	1:B:5:PHE:C	2.89	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:LYS:HA	1:B:156:ASP:OD1	2.16	0.46
1:B:23:LEU:HD12	1:B:23:LEU:HA	1.54	0.46
1:A:444:LEU:O	1:A:448:CYS:HB2	2.16	0.46
1:A:222:LEU:N	1:A:222:LEU:HD12	2.29	0.46
1:A:325:GLN:O	1:A:328:MET:N	2.48	0.46
1:A:128:GLN:O	1:A:128:GLN:HG2	2.15	0.46
1:A:435:TRP:HZ3	1:A:454:VAL:HA	1.80	0.46
1:B:290:GLN:OE1	1:B:290:GLN:N	2.48	0.45
1:A:38:TYR:HB3	1:A:83:VAL:HG21	1.98	0.45
1:A:451:ARG:HD2	1:A:452:LEU:H	1.81	0.45
1:A:465:SER:HA	1:A:468:PRO:HD2	1.98	0.45
1:A:220:ALA:HB1	1:A:230:ILE:HG22	1.97	0.45
1:A:67:GLU:HB3	1:A:68:PRO:CD	2.29	0.45
1:B:296:VAL:HG21	1:B:474:ALA:HA	1.98	0.45
1:A:224:ILE:HG22	1:A:225:GLY:N	2.31	0.45
1:A:304:GLU:OE2	1:A:484:GLN:NE2	2.49	0.45
1:A:296:VAL:HG12	1:A:477:PHE:HD2	1.81	0.45
1:B:105:ILE:HD13	1:B:173:ILE:HD11	1.99	0.45
1:B:405:LEU:HD11	1:B:477:PHE:HD1	1.80	0.45
1:A:322:LEU:CD1	1:A:393:ALA:HA	2.47	0.45
1:B:142:GLN:O	1:B:144:GLU:N	2.41	0.45
1:B:296:VAL:HG11	1:B:473:TYR:CE2	2.51	0.45
1:B:401:LEU:HD13	1:B:479:LEU:HD12	1.99	0.45
1:A:348:LEU:O	1:A:353:GLY:HA3	2.17	0.45
1:B:231:LEU:HD23	1:B:231:LEU:HA	1.71	0.45
1:B:29:LEU:HG	1:B:30:ARG:NH1	2.33	0.44
1:A:311:ARG:HE	1:A:482:LEU:HA	1.83	0.44
1:B:10:LYS:O	1:B:13:ILE:HG13	2.16	0.44
1:A:303:LEU:HD23	1:A:482:LEU:HD11	1.99	0.44
1:B:160:VAL:HG12	1:B:222:LEU:HD22	1.99	0.44
1:B:224:ILE:HD11	1:B:241:PHE:CE1	2.53	0.44
1:A:311:ARG:NH2	1:A:482:LEU:HD23	2.32	0.44
1:B:420:GLU:OE1	1:B:422:SER:HB3	2.18	0.44
1:A:476:LEU:O	1:A:480:SER:HB3	2.18	0.44
1:B:156:ASP:O	1:B:241:PHE:HE2	2.01	0.44
1:B:120:ASN:HB2	1:B:169:GLU:HG2	1.99	0.43
1:B:308:MET:O	1:B:312:GLN:HG2	2.18	0.43
1:A:167:THR:O	1:A:212:GLY:N	2.47	0.43
1:A:385:SER:O	1:A:389:GLN:HG2	2.18	0.43
1:B:29:LEU:CD1	1:B:30:ARG:HD3	2.48	0.43
1:B:41:LEU:HA	1:B:58:VAL:HG23	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:ARG:NH1	1:A:52:LYS:HD2	2.33	0.43
1:A:49:ARG:HG2	1:A:295:GLU:OE2	2.18	0.43
1:B:314:ILE:O	1:B:318:ILE:HG12	2.18	0.43
1:B:328:MET:HB3	1:B:378:LEU:HD11	2.00	0.43
1:A:405:LEU:HD11	1:A:477:PHE:CD1	2.53	0.43
1:A:145:ASN:O	1:A:149:GLN:HB3	2.19	0.43
1:B:431:LEU:HB3	1:B:435:TRP:CE3	2.53	0.43
1:A:307:GLU:O	1:A:311:ARG:HG3	2.19	0.43
1:B:431:LEU:O	1:B:435:TRP:HE3	2.02	0.43
1:A:331:LEU:HD12	1:A:331:LEU:HA	1.73	0.43
1:B:141:GLN:O	1:B:144:GLU:HB3	2.19	0.43
1:A:95:VAL:HG22	1:A:119:MET:O	2.18	0.42
1:A:92:GLN:HB3	1:A:121:VAL:HG23	2.00	0.42
1:A:411:VAL:HG22	1:A:426:LEU:HD21	2.02	0.42
1:B:58:VAL:HG12	1:B:60:LEU:HD23	2.01	0.42
1:A:378:LEU:HA	1:A:378:LEU:HD23	1.93	0.42
1:B:145:ASN:HA	1:B:149:GLN:HB2	2.01	0.42
1:B:435:TRP:HH2	1:B:441:THR:HB	1.84	0.42
1:B:50:PHE:CZ	1:B:287:ALA:HA	2.55	0.42
1:B:81:PHE:HB2	1:B:83:VAL:O	2.20	0.42
1:A:22:ASP:O	1:A:218:ARG:HG3	2.19	0.42
1:A:159:PHE:HD1	1:A:221:GLN:HB2	1.85	0.42
1:B:439:ASN:O	1:B:443:VAL:HG23	2.20	0.42
1:B:170:GLU:HG3	1:B:210:PRO:HA	2.01	0.42
1:B:324:ASP:OD2	1:B:327:SER:OG	2.33	0.42
1:B:360:VAL:HG22	1:B:366:LEU:HD21	2.00	0.42
1:A:87:VAL:HG22	1:A:88:ASP:N	2.34	0.42
1:B:289:PHE:CD2	1:B:292:LEU:HD23	2.55	0.42
1:B:318:ILE:HA	1:B:318:ILE:HD13	1.77	0.42
1:B:401:LEU:HG	1:B:402:SER:N	2.35	0.42
1:B:159:PHE:HD1	1:B:221:GLN:CA	2.30	0.42
1:A:169:GLU:O	1:A:171:VAL:HG13	2.20	0.41
1:B:322:LEU:HD12	1:B:322:LEU:HA	1.84	0.41
1:B:421:GLN:HG2	1:B:463:PRO:HD3	2.01	0.41
1:B:43:ARG:CG	1:B:53:PRO:HG2	2.47	0.41
1:A:435:TRP:CZ3	1:A:454:VAL:HA	2.55	0.41
1:B:148:LEU:CD1	1:B:224:ILE:HD12	2.51	0.41
1:A:67:GLU:HB2	1:A:68:PRO:HD2	1.92	0.41
1:A:58:VAL:HG12	1:A:58:VAL:O	2.20	0.41
1:A:92:GLN:O	1:A:93:GLY:C	2.59	0.41
1:B:151:LEU:HA	1:B:151:LEU:HD23	1.83	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331:LEU:HD12	1:B:331:LEU:HA	1.71	0.41
1:B:355:ILE:H	1:B:355:ILE:HG12	1.68	0.41
1:A:450:LEU:HD21	1:A:465:SER:HB2	2.03	0.41
1:B:300:SER:HB3	1:B:478:LEU:CD2	2.51	0.41
1:B:426:LEU:HD12	1:B:431:LEU:HD11	2.03	0.41
1:A:435:TRP:CZ3	1:A:458:GLN:HG2	2.55	0.40
1:B:66:LEU:O	1:B:67:GLU:HB3	2.21	0.40
1:A:126:VAL:HG12	1:A:162:THR:O	2.21	0.40
1:B:135:GLN:HA	1:B:228:TRP:H2	1.86	0.40
1:B:359:LEU:HD13	1:B:374:ILE:HD13	2.02	0.40
1:B:92:GLN:HB2	1:B:121:VAL:HG22	2.03	0.40
1:A:92:GLN:HB3	1:A:121:VAL:CG2	2.51	0.40
1:A:49:ARG:HG3	1:A:50:PHE:CD1	2.57	0.40
1:B:332:GLU:HG2	1:B:333:ALA:N	2.36	0.40
1:B:43:ARG:HH22	1:B:52:LYS:HE3	1.85	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	368/488 (75%)	337 (92%)	30 (8%)	1 (0%)	41 71
1	B	378/488 (78%)	345 (91%)	33 (9%)	0	100 100
All	All	746/976 (76%)	682 (91%)	63 (8%)	1 (0%)	51 81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	GLU

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	339/424 (80%)	305 (90%)	34 (10%)	7 27
1	B	345/424 (81%)	309 (90%)	36 (10%)	7 25
All	All	684/848 (81%)	614 (90%)	70 (10%)	7 27

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ARG
1	A	26	VAL
1	A	30	ARG
1	A	34	SER
1	A	40	LEU
1	A	49	ARG
1	A	56	SER
1	A	61	SER
1	A	63	LYS
1	A	90	ASN
1	A	91	ILE
1	A	92	GLN
1	A	97	LEU
1	A	120	ASN
1	A	126	VAL
1	A	127	THR
1	A	140	LEU
1	A	158	LEU
1	A	159	PHE
1	A	164	VAL
1	A	222	LEU
1	A	227	LYS
1	A	237	LYS
1	A	315	LEU
1	A	359	LEU
1	A	363	SER
1	A	394	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	430	LEU
1	A	434	CYS
1	A	448	CYS
1	A	477	PHE
1	A	478	LEU
1	A	480	SER
1	A	481	SER
1	B	5	PHE
1	B	9	VAL
1	B	30	ARG
1	B	41	LEU
1	B	57	CYS
1	B	60	LEU
1	B	63	LYS
1	B	90	ASN
1	B	91	ILE
1	B	92	GLN
1	B	94	ARG
1	B	95	VAL
1	B	127	THR
1	B	134	MET
1	B	136	HIS
1	B	139	HIS
1	B	140	LEU
1	B	141	GLN
1	B	146	LYS
1	B	147	ILE
1	B	148	LEU
1	B	164	VAL
1	B	174	THR
1	B	206	MET
1	B	215	LEU
1	B	232	LEU
1	B	234	SER
1	B	237	LYS
1	B	293	TYR
1	B	322	LEU
1	B	344	GLN
1	B	355	ILE
1	B	401	LEU
1	B	416	THR
1	B	420	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	434	CYS

Some 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 carbohydrates 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 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	378/488 (77%)	0.28	10 (2%) 56 53	92, 133, 176, 195	0
1	B	388/488 (79%)	0.63	46 (11%) 4 4	95, 174, 212, 222	0
All	All	766/976 (78%)	0.46	56 (7%) 15 15	92, 150, 207, 222	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	360	VAL	7.0
1	B	361	LEU	6.0
1	B	111	VAL	5.5
1	B	18	GLY	5.1
1	B	369	GLU	4.5
1	B	356	LEU	4.5
1	B	359	LEU	4.4
1	B	457	PRO	4.4
1	B	348	LEU	4.3
1	B	352	ALA	4.3
1	B	110	ALA	4.2
1	B	371	ALA	4.1
1	A	228	TRP	4.1
1	B	121	VAL	3.9
1	B	364	GLY	3.8
1	B	347	PRO	3.6
1	B	456	SER	3.4
1	B	357	GLU	3.3
1	A	224	ILE	3.3
1	B	366	LEU	3.2
1	B	109	ALA	3.2
1	B	105	ILE	3.2
1	A	223	LEU	3.1
1	B	49	ARG	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	112	SER	3.0
1	B	429	VAL	2.9
1	B	120	ASN	2.9
1	B	334	SER	2.9
1	A	225	GLY	2.8
1	B	483	GLY	2.8
1	B	118	SER	2.7
1	A	432	GLY	2.7
1	B	116	SER	2.7
1	B	358	CYS	2.7
1	B	374	ILE	2.7
1	A	442	TRP	2.6
1	A	229	ASP	2.6
1	B	365	GLU	2.5
1	B	370	LEU	2.5
1	B	292	LEU	2.5
1	B	79	GLY	2.4
1	B	293	TYR	2.3
1	B	301	SER	2.3
1	B	345	VAL	2.3
1	A	226	SER	2.3
1	A	431	LEU	2.3
1	B	94	ARG	2.2
1	B	459	VAL	2.2
1	B	398	THR	2.2
1	B	226	SER	2.2
1	B	428	THR	2.1
1	B	367	VAL	2.1
1	B	80	SER	2.1
1	B	363	SER	2.1
1	A	142	GLN	2.0
1	B	19	SER	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 carbohydrates 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.