



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:39 AM GMT

PDB ID : 3MPO
Title : The crystal structure of a hydrolase from *Lactobacillus brevis*
Authors : Zhang, Z.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center
for Structural Genomics (NYSGXRC)
Deposited on : 2010-04-27
Resolution : 2.90 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

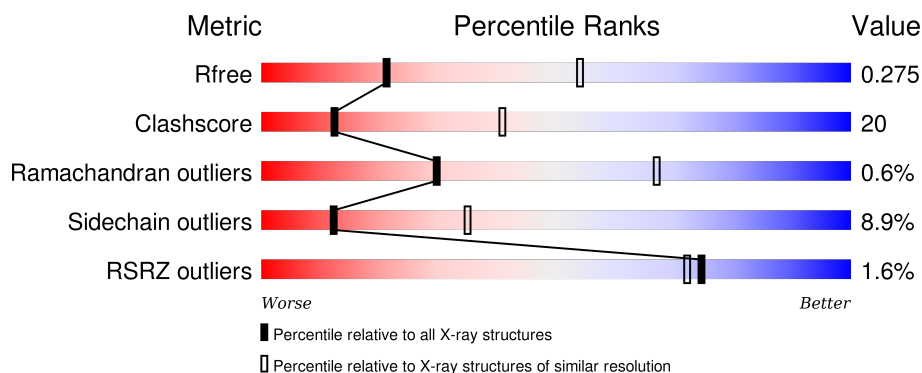
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	279	 48% 33% 5% 14%
1	B	279	 57% 35% • 5%
1	C	279	 55% 34% • 8%
1	D	279	 53% 27% • 16%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7803 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 Predicted hydrolase of the HAD superfamily.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	Se	0	0	0
			1856	1176	308	363	1	8			
1	B	266	Total	C	N	O	S	Se	0	0	0
			2049	1291	341	408	1	8			
1	C	257	Total	C	N	O	S	Se	0	0	0
			1976	1248	329	390	1	8			
1	D	233	Total	C	N	O	S	Se	0	0	0
			1807	1145	297	356	1	8			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	EXPRESSION TAG	UNP Q03T33
A	0	SER	-	EXPRESSION TAG	UNP Q03T33
A	1	LEU	-	EXPRESSION TAG	UNP Q03T33
A	271	GLY	-	EXPRESSION TAG	UNP Q03T33
A	272	HIS	-	EXPRESSION TAG	UNP Q03T33
A	273	HIS	-	EXPRESSION TAG	UNP Q03T33
A	274	HIS	-	EXPRESSION TAG	UNP Q03T33
A	275	HIS	-	EXPRESSION TAG	UNP Q03T33
A	276	HIS	-	EXPRESSION TAG	UNP Q03T33
A	277	HIS	-	EXPRESSION TAG	UNP Q03T33
B	-1	MSE	-	EXPRESSION TAG	UNP Q03T33
B	0	SER	-	EXPRESSION TAG	UNP Q03T33
B	1	LEU	-	EXPRESSION TAG	UNP Q03T33
B	271	GLY	-	EXPRESSION TAG	UNP Q03T33
B	272	HIS	-	EXPRESSION TAG	UNP Q03T33
B	273	HIS	-	EXPRESSION TAG	UNP Q03T33
B	274	HIS	-	EXPRESSION TAG	UNP Q03T33
B	275	HIS	-	EXPRESSION TAG	UNP Q03T33
B	276	HIS	-	EXPRESSION TAG	UNP Q03T33
B	277	HIS	-	EXPRESSION TAG	UNP Q03T33
C	-1	MSE	-	EXPRESSION TAG	UNP Q03T33

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	SER	-	EXPRESSION TAG	UNP Q03T33
C	1	LEU	-	EXPRESSION TAG	UNP Q03T33
C	271	GLY	-	EXPRESSION TAG	UNP Q03T33
C	272	HIS	-	EXPRESSION TAG	UNP Q03T33
C	273	HIS	-	EXPRESSION TAG	UNP Q03T33
C	274	HIS	-	EXPRESSION TAG	UNP Q03T33
C	275	HIS	-	EXPRESSION TAG	UNP Q03T33
C	276	HIS	-	EXPRESSION TAG	UNP Q03T33
C	277	HIS	-	EXPRESSION TAG	UNP Q03T33
D	-1	MSE	-	EXPRESSION TAG	UNP Q03T33
D	0	SER	-	EXPRESSION TAG	UNP Q03T33
D	1	LEU	-	EXPRESSION TAG	UNP Q03T33
D	271	GLY	-	EXPRESSION TAG	UNP Q03T33
D	272	HIS	-	EXPRESSION TAG	UNP Q03T33
D	273	HIS	-	EXPRESSION TAG	UNP Q03T33
D	274	HIS	-	EXPRESSION TAG	UNP Q03T33
D	275	HIS	-	EXPRESSION TAG	UNP Q03T33
D	276	HIS	-	EXPRESSION TAG	UNP Q03T33
D	277	HIS	-	EXPRESSION TAG	UNP Q03T33

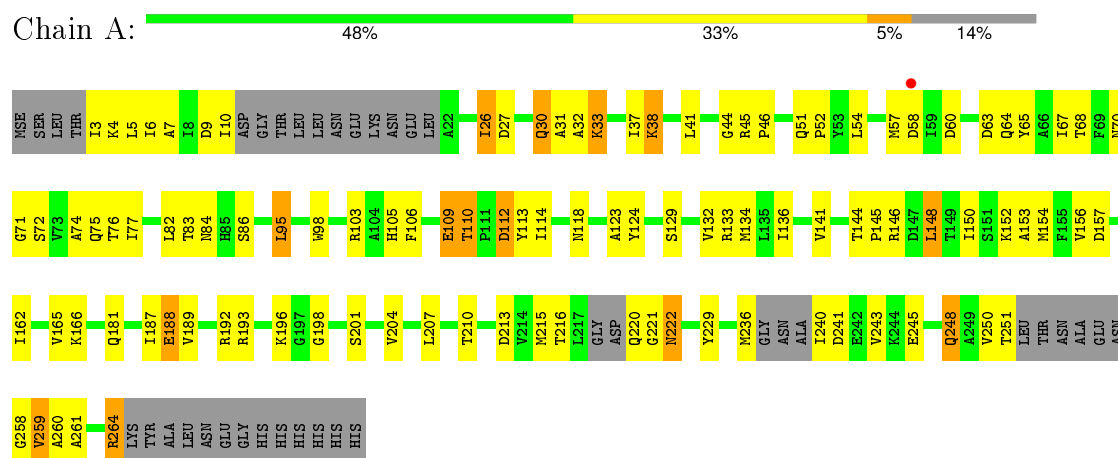
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	26	Total O 26 26	0	0
2	B	31	Total O 31 31	0	0
2	C	31	Total O 31 31	0	0
2	D	27	Total O 27 27	0	0

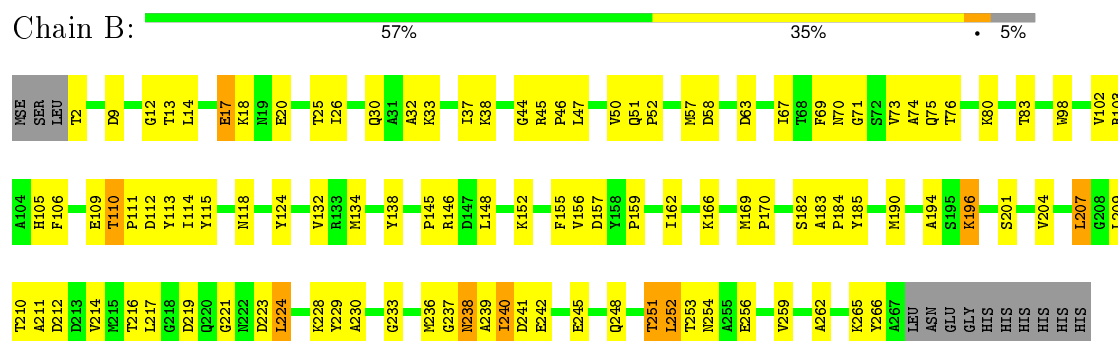
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

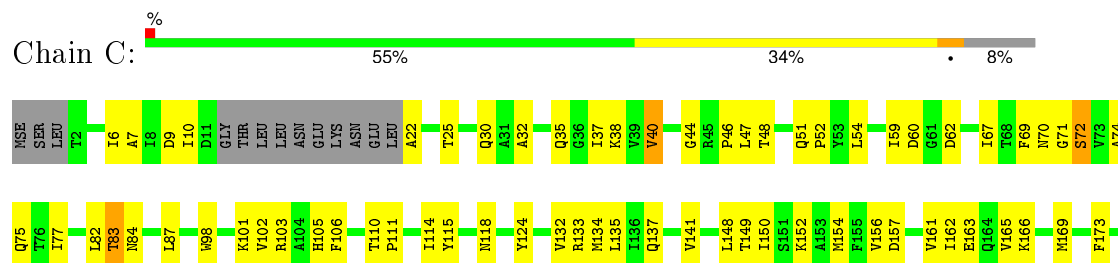
- Molecule 1: Predicted hydrolase of the HAD superfamily



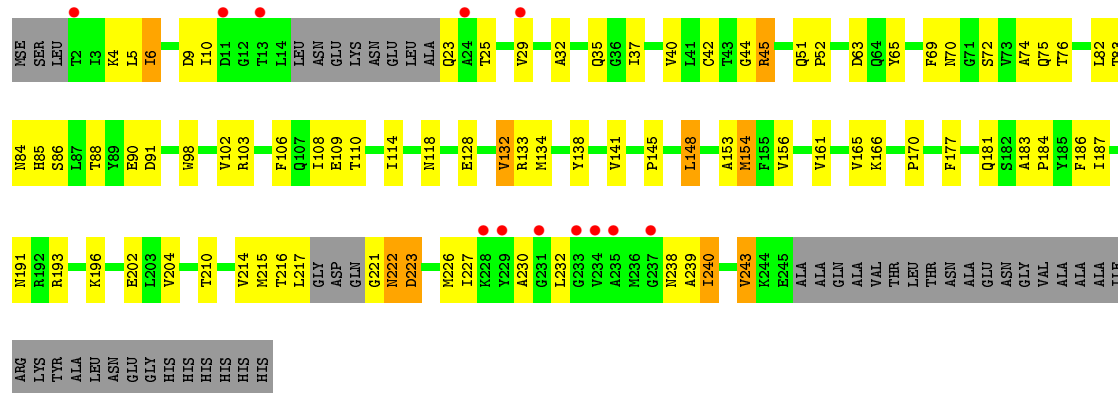
- Molecule 1: Predicted hydrolase of the HAD superfamily



- Molecule 1: Predicted hydrolase of the HAD superfamily



- Molecule 1: Predicted hydrolase of the HAD superfamily



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.25Å 108.25Å 130.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.13 – 2.90 54.13 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (54.13-2.90) 99.9 (54.13-2.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.76 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.226 , 0.283 0.215 , 0.275	Depositor DCC
R_{free} test set	1458 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	40.9	Xtriage
Anisotropy	0.535	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 30.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 28717 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7803	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.80% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.34	0/1872	0.51	0/2522
1	B	0.34	0/2070	0.50	0/2797
1	C	0.33	0/1996	0.52	0/2696
1	D	0.34	0/1825	0.52	0/2461
All	All	0.34	0/7763	0.51	0/10476

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	1856	0	1860	78	0
1	B	2049	0	2044	81	0
1	C	1976	0	1972	82	0
1	D	1807	0	1803	66	0
2	A	26	0	0	2	0
2	B	31	0	0	0	0
2	C	31	0	0	0	0
2	D	27	0	0	0	0
All	All	7803	0	7679	301	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 20.

All (301) 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:C:106:PHE:H	1:C:118:ASN:HD21	1.11	0.97
1:B:238:ASN:N	1:B:238:ASN:HD22	1.59	0.96
1:C:264:ARG:HH11	1:C:264:ARG:HG3	1.28	0.96
1:B:110:THR:HG22	1:B:112:ASP:H	1.31	0.95
1:D:106:PHE:H	1:D:118:ASN:HD21	1.08	0.95
1:C:169:MSE:HE1	1:C:173:PHE:HB2	1.50	0.94
1:B:238:ASN:HD21	1:B:253:THR:HA	1.31	0.94
1:A:110:THR:HG22	1:A:112:ASP:H	1.34	0.92
1:B:240:ILE:HD11	1:B:242:GLU:HB2	1.55	0.88
1:A:106:PHE:H	1:A:118:ASN:HD21	1.19	0.85
1:B:252:LEU:HB3	1:B:256:GLU:HG3	1.59	0.84
1:B:106:PHE:H	1:B:118:ASN:HD21	1.29	0.81
1:B:238:ASN:N	1:B:238:ASN:ND2	2.24	0.81
1:A:220:GLN:HG2	1:A:221:GLY:H	1.46	0.79
1:D:70:ASN:HD22	1:D:196:LYS:HE3	1.48	0.78
1:C:106:PHE:H	1:C:118:ASN:ND2	1.83	0.76
1:B:114:ILE:HG13	1:B:134:MSE:CE	2.17	0.74
1:C:264:ARG:HH11	1:C:264:ARG:CG	2.01	0.73
1:D:74:ALA:HB3	1:D:83:THR:HG22	1.70	0.73
1:B:233:GLY:H	1:B:248:GLN:HE21	1.37	0.73
1:D:45:ARG:CG	1:D:45:ARG:HH21	2.02	0.73
1:A:74:ALA:HB3	1:A:83:THR:HG22	1.71	0.72
1:C:215:MSE:HG3	1:C:232:LEU:HG	1.71	0.72
1:D:114:ILE:HG13	1:D:134:MSE:HE3	1.70	0.72
1:A:60:ASP:HA	1:A:77:ILE:HG21	1.71	0.71
1:B:238:ASN:ND2	1:B:253:THR:HA	2.04	0.71
1:D:106:PHE:H	1:D:118:ASN:ND2	1.86	0.71
1:A:145:PRO:HB2	1:A:148:LEU:HD13	1.73	0.70
1:B:251:THR:HG22	1:B:252:LEU:H	1.56	0.70
1:B:114:ILE:HG13	1:B:134:MSE:HE2	1.72	0.70
1:D:145:PRO:HB2	1:D:148:LEU:HD13	1.74	0.70
1:B:47:LEU:HD22	1:B:75:GLN:NE2	2.08	0.69
1:C:105:HIS:HB2	1:C:156:VAL:O	1.92	0.69
1:A:9:ASP:C	1:A:10:ILE:HG13	2.13	0.68
1:A:6:ILE:HG12	1:A:215:MSE:HG2	1.75	0.68
1:D:6:ILE:HG23	1:D:215:MSE:HB3	1.76	0.68
1:C:106:PHE:N	1:C:118:ASN:HD21	1.86	0.67
1:A:109:GLU:OE2	1:A:154:MSE:SE	2.63	0.67
1:C:241:ASP:O	1:C:245:GLU:HG2	1.95	0.66
1:C:252:LEU:HB2	1:C:258:GLY:HA2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:GLY:H	1:C:248:GLN:HE21	1.43	0.66
1:B:26:ILE:O	1:B:30:GLN:HG3	1.95	0.66
1:A:75:GLN:HA	1:A:82:LEU:HG	1.78	0.66
1:A:103:ARG:NH2	1:B:146:ARG:HD2	2.11	0.65
1:B:13:THR:HA	1:B:236:MSE:HE2	1.78	0.65
1:D:216:THR:HG23	1:D:230:ALA:HB2	1.78	0.64
1:B:17:GLU:HG2	1:B:18:LYS:N	2.11	0.64
1:A:236:MSE:HE1	1:A:259:VAL:HG22	1.79	0.64
1:C:169:MSE:HE1	1:C:173:PHE:CB	2.24	0.64
1:B:210:THR:HG22	1:B:212:ASP:H	1.63	0.64
1:C:114:ILE:HG13	1:C:134:MSE:HE3	1.80	0.64
1:C:233:GLY:H	1:C:248:GLN:NE2	1.96	0.63
1:C:9:ASP:OD1	1:C:10:ILE:N	2.31	0.63
1:B:14:LEU:HD11	1:B:57:MSE:HE1	1.80	0.63
1:D:114:ILE:CG1	1:D:134:MSE:HE3	2.29	0.62
1:D:240:ILE:HG12	1:D:243:VAL:HB	1.82	0.61
1:D:98:TRP:CZ2	1:D:170:PRO:HD3	2.34	0.61
1:B:238:ASN:H	1:B:238:ASN:ND2	1.98	0.61
1:A:76:THR:HG23	1:A:82:LEU:HD21	1.83	0.61
1:A:114:ILE:HG13	1:A:134:MSE:HG2	1.83	0.61
1:C:238:ASN:ND2	1:C:254:ASN:H	1.98	0.60
1:B:110:THR:HG23	1:B:111:PRO:HD2	1.84	0.60
1:D:45:ARG:HG2	1:D:45:ARG:HH21	1.67	0.60
1:A:110:THR:CG2	1:A:112:ASP:H	2.12	0.59
1:B:162:ILE:HG13	1:B:185:TYR:HA	1.84	0.59
1:D:84:ASN:ND2	1:D:86:SER:OG	2.35	0.59
1:B:216:THR:HG23	1:B:230:ALA:HB2	1.83	0.59
1:D:110:THR:HG21	1:D:148:LEU:HG	1.84	0.59
1:D:216:THR:O	1:D:217:LEU:HD23	2.03	0.59
1:A:105:HIS:HB2	1:A:156:VAL:O	2.02	0.59
1:D:221:GLY:HA2	1:D:240:ILE:HD13	1.85	0.58
1:A:222:ASN:HD22	1:A:222:ASN:C	2.07	0.58
1:C:238:ASN:HD21	1:C:254:ASN:H	1.51	0.58
1:D:239:ALA:HB1	1:D:243:VAL:HG12	1.86	0.58
1:C:215:MSE:HE1	1:C:267:ALA:HB2	1.86	0.58
1:A:110:THR:HG22	1:A:112:ASP:N	2.13	0.57
1:B:240:ILE:HD11	1:B:242:GLU:CB	2.31	0.57
1:A:220:GLN:HG2	1:A:221:GLY:N	2.19	0.57
1:A:44:GLY:HA2	1:A:70:ASN:ND2	2.19	0.57
1:C:35:GLN:O	1:C:35:GLN:HG2	2.05	0.57
1:B:109:GLU:HG2	1:B:134:MSE:CE	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:ILE:HG13	1:B:134:MSE:HE3	1.87	0.56
1:A:7:ALA:HB3	1:A:216:THR:HG22	1.87	0.56
1:C:240:ILE:HG13	1:C:243:VAL:HG23	1.85	0.56
1:C:87:LEU:HD12	1:C:150:ILE:HG22	1.86	0.56
1:D:32:ALA:O	1:D:37:ILE:HB	2.04	0.56
1:B:38:LYS:HE3	1:B:63:ASP:O	2.04	0.56
1:C:264:ARG:NH1	1:C:264:ARG:HG3	2.08	0.56
1:B:33:LYS:HE2	1:B:58:ASP:HB2	1.87	0.56
1:D:70:ASN:ND2	1:D:196:LYS:HE3	2.20	0.56
1:B:238:ASN:ND2	1:B:253:THR:HG23	2.20	0.55
1:A:124:TYR:HB2	1:A:156:VAL:CG2	2.36	0.55
1:D:45:ARG:HG2	1:D:45:ARG:NH2	2.21	0.55
1:B:217:LEU:HD13	1:B:259:VAL:HG13	1.87	0.55
1:D:4:LYS:O	1:D:37:ILE:HG23	2.07	0.55
1:A:123:ALA:HB2	1:C:135:LEU:HD21	1.87	0.55
1:A:32:ALA:O	1:A:37:ILE:HB	2.06	0.55
1:B:240:ILE:HG13	1:B:242:GLU:H	1.72	0.55
1:C:253:THR:HG22	1:C:256:GLU:HG3	1.89	0.54
1:C:124:TYR:HB2	1:C:156:VAL:CG2	2.38	0.54
1:A:41:LEU:HD22	1:A:54:LEU:HD21	1.90	0.54
1:B:138:TYR:CE2	1:D:138:TYR:CE2	2.95	0.54
1:A:251:THR:HG21	1:A:258:GLY:O	2.07	0.54
1:C:46:PRO:HG2	1:C:132:VAL:HG11	1.90	0.54
1:B:110:THR:HG22	1:B:112:ASP:N	2.11	0.54
1:D:5:LEU:HD23	1:D:5:LEU:C	2.28	0.54
1:A:146:ARG:NH2	1:B:103:ARG:HD3	2.24	0.53
1:D:10:ILE:HG12	1:D:42:CYS:O	2.08	0.53
1:C:162:ILE:HG13	1:C:185:TYR:HA	1.90	0.53
1:C:40:VAL:O	1:C:40:VAL:HG23	2.08	0.53
1:B:98:TRP:CZ2	1:B:102:VAL:HG21	2.44	0.53
1:A:67:ILE:HG23	1:A:71:GLY:HA2	1.90	0.53
1:B:240:ILE:HG13	1:B:242:GLU:N	2.24	0.53
1:B:224:LEU:CD1	1:B:228:LYS:HE3	2.38	0.53
1:A:166:LYS:HD2	1:A:181:GLN:HE22	1.74	0.53
1:A:67:ILE:CG2	1:A:71:GLY:HA2	2.39	0.52
1:C:252:LEU:O	1:C:258:GLY:HA3	2.09	0.52
1:A:193:ARG:CG	1:A:193:ARG:O	2.57	0.52
1:A:192:ARG:HG3	2:A:294:HOH:O	2.09	0.52
1:C:74:ALA:HB3	1:C:83:THR:HG22	1.91	0.52
1:B:105:HIS:HB2	1:B:156:VAL:O	2.09	0.52
1:C:267:ALA:O	1:C:268:LEU:HD23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:ILE:HG23	1:C:215:MSE:HB3	1.92	0.52
1:C:54:LEU:HD13	1:C:77:ILE:HG23	1.92	0.52
1:A:45:ARG:HB3	1:A:46:PRO:CD	2.41	0.51
1:B:51:GLN:HB3	1:B:52:PRO:HD3	1.91	0.51
1:C:152:LYS:HD2	1:C:188:GLU:OE2	2.11	0.51
1:C:110:THR:HG21	1:C:148:LEU:HD22	1.93	0.51
1:A:5:LEU:HD12	1:A:38:LYS:O	2.09	0.51
1:B:45:ARG:HB3	1:B:46:PRO:CD	2.40	0.51
1:D:222:ASN:H	1:D:222:ASN:ND2	2.08	0.51
1:D:166:LYS:HD2	1:D:181:GLN:NE2	2.26	0.51
1:A:103:ARG:CZ	1:B:146:ARG:HD2	2.40	0.51
1:D:45:ARG:CG	1:D:45:ARG:NH2	2.67	0.51
1:A:41:LEU:HD22	1:A:54:LEU:CD2	2.40	0.51
1:C:238:ASN:HD21	1:C:254:ASN:HB3	1.76	0.50
1:C:22:ALA:HB3	1:C:25:THR:OG1	2.11	0.50
1:C:44:GLY:HA2	1:C:70:ASN:H	1.75	0.50
1:C:162:ILE:HG23	1:C:187:ILE:HG13	1.93	0.50
1:A:60:ASP:HA	1:A:77:ILE:CG2	2.41	0.50
1:C:82:LEU:HB3	1:C:206:GLN:NE2	2.27	0.50
1:A:260:ALA:O	1:A:264:ARG:HG3	2.11	0.50
1:A:9:ASP:O	1:A:10:ILE:HG13	2.11	0.50
1:C:40:VAL:O	1:C:40:VAL:CG2	2.59	0.50
1:D:222:ASN:HD22	1:D:222:ASN:N	2.09	0.50
1:A:220:GLN:CG	1:A:221:GLY:H	2.21	0.50
1:C:252:LEU:HB3	1:C:256:GLU:HB2	1.94	0.50
1:A:57:MSE:O	1:A:58:ASP:HB3	2.10	0.50
1:C:70:ASN:HD22	1:C:196:LYS:HE3	1.76	0.49
1:C:250:VAL:HG12	1:C:251:THR:N	2.26	0.49
1:C:264:ARG:CG	1:C:264:ARG:NH1	2.66	0.49
1:B:114:ILE:N	1:B:134:MSE:HE3	2.28	0.49
1:B:245:GLU:O	1:B:245:GLU:HG2	2.12	0.49
1:D:40:VAL:HG23	1:D:40:VAL:O	2.12	0.49
1:A:65:TYR:CZ	1:A:207:LEU:HD21	2.48	0.48
1:D:109:GLU:HG2	1:D:134:MSE:CE	2.43	0.48
1:D:98:TRP:CZ2	1:D:102:VAL:HG21	2.48	0.48
1:D:74:ALA:HB3	1:D:83:THR:CG2	2.41	0.48
1:C:101:LYS:HG2	1:D:90:GLU:HG3	1.95	0.48
1:A:33:LYS:NZ	1:A:33:LYS:HB3	2.28	0.48
1:A:45:ARG:HB3	1:A:46:PRO:HD2	1.95	0.48
1:A:240:ILE:HG13	1:A:241:ASP:N	2.29	0.48
1:A:250:VAL:HG12	1:A:251:THR:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:GLN:HA	1:A:30:GLN:HE21	1.79	0.47
1:C:67:ILE:HG23	1:C:71:GLY:HA2	1.95	0.47
1:B:98:TRP:CZ2	1:B:170:PRO:HD3	2.50	0.47
1:C:215:MSE:CE	1:C:267:ALA:HB2	2.43	0.47
1:C:157:ASP:HB3	1:C:161:VAL:HB	1.97	0.47
1:B:74:ALA:HB3	1:B:83:THR:HB	1.95	0.47
1:D:215:MSE:HG3	1:D:232:LEU:HD23	1.97	0.46
1:A:63:ASP:HB2	2:A:287:HOH:O	2.15	0.46
1:D:161:VAL:O	1:D:165:VAL:HG23	2.16	0.46
1:D:222:ASN:ND2	1:D:222:ASN:N	2.63	0.46
1:B:110:THR:HG23	1:B:111:PRO:CD	2.45	0.46
1:B:9:ASP:OD2	1:B:223:ASP:OD2	2.33	0.46
1:A:86:SER:HB3	1:A:150:ILE:O	2.16	0.46
1:D:23:GLN:C	1:D:25:THR:H	2.18	0.46
1:D:128:GLU:O	1:D:132:VAL:HB	2.14	0.46
1:D:88:THR:O	1:D:91:ASP:HB2	2.15	0.46
1:A:106:PHE:N	1:A:118:ASN:HD21	2.00	0.46
1:B:17:GLU:HG2	1:B:18:LYS:HG2	1.97	0.46
1:A:153:ALA:O	1:A:189:VAL:N	2.40	0.46
1:D:63:ASP:O	1:D:65:TYR:CE2	2.68	0.46
1:B:12:GLY:O	1:B:254:ASN:HB3	2.16	0.46
1:B:219:ASP:O	1:B:239:ALA:HA	2.16	0.46
1:D:102:VAL:HG12	1:D:102:VAL:O	2.16	0.46
1:B:204:VAL:HG13	1:B:209:LEU:HB2	1.99	0.46
1:D:45:ARG:HH21	1:D:45:ARG:HG3	1.79	0.45
1:C:60:ASP:HA	1:C:77:ILE:HB	1.97	0.45
1:B:70:ASN:HD22	1:B:196:LYS:CE	2.29	0.45
1:A:193:ARG:O	1:A:193:ARG:HG3	2.16	0.45
1:A:45:ARG:HG2	1:A:132:VAL:HG22	1.98	0.45
1:C:238:ASN:HD21	1:C:254:ASN:CB	2.30	0.45
1:C:166:LYS:HD2	1:C:181:GLN:HE22	1.81	0.45
1:A:152:LYS:HD2	1:A:188:GLU:OE1	2.17	0.45
1:B:113:TYR:C	1:B:134:MSE:HE3	2.37	0.45
1:B:190:MSE:HE3	1:B:194:ALA:HB3	1.99	0.45
1:D:85:HIS:HE1	1:D:202:GLU:OE1	1.99	0.45
1:D:148:LEU:HA	1:D:148:LEU:HD12	1.84	0.45
1:A:51:GLN:N	1:A:52:PRO:CD	2.80	0.45
1:D:154:MSE:HE2	1:D:186:PHE:CE1	2.52	0.45
1:B:67:ILE:HG23	1:B:71:GLY:HA2	1.99	0.44
1:B:253:THR:H	1:B:256:GLU:HG3	1.81	0.44
1:B:45:ARG:HB3	1:B:46:PRO:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:44:GLY:HA2	1:C:70:ASN:N	2.33	0.44
1:C:74:ALA:HB3	1:C:83:THR:CG2	2.48	0.44
1:D:109:GLU:HG2	1:D:114:ILE:HG12	1.98	0.44
1:B:18:LYS:HB2	1:B:20:GLU:OE1	2.17	0.44
1:B:33:LYS:HE2	1:B:57:MSE:O	2.16	0.44
1:B:115:TYR:CE1	1:B:148:LEU:HD21	2.52	0.44
1:B:110:THR:CG2	1:B:112:ASP:H	2.15	0.44
1:A:4:LYS:HG2	1:A:213:ASP:HB3	2.00	0.44
1:B:155:PHE:CE2	1:B:169:MSE:HE1	2.53	0.44
1:C:124:TYR:HB2	1:C:156:VAL:HG23	2.00	0.44
1:A:124:TYR:HB2	1:A:156:VAL:HG22	1.99	0.44
1:B:265:LYS:HD3	1:B:266:TYR:CE2	2.53	0.44
1:A:112:ASP:HB2	1:A:113:TYR:CD1	2.53	0.44
1:B:46:PRO:HG3	1:B:69:PHE:CE1	2.53	0.44
1:C:250:VAL:CG1	1:C:251:THR:N	2.80	0.44
1:C:98:TRP:CZ3	1:C:165:VAL:HG13	2.53	0.44
1:D:108:ILE:HG22	1:D:153:ALA:HA	2.00	0.44
1:C:72:SER:O	1:C:84:ASN:HA	2.18	0.44
1:B:251:THR:OG1	1:B:262:ALA:HB2	2.18	0.44
1:D:23:GLN:C	1:D:25:THR:N	2.71	0.44
1:A:5:LEU:HD13	1:A:38:LYS:HB3	2.00	0.43
1:B:159:PRO:HA	1:B:184:PRO:O	2.19	0.43
1:B:237:GLY:C	1:B:238:ASN:HD22	2.15	0.43
1:A:144:THR:HA	1:A:145:PRO:HD3	1.88	0.43
1:A:33:LYS:HE2	1:A:58:ASP:HB3	2.01	0.43
1:D:166:LYS:HG3	1:D:187:ILE:HD11	2.00	0.43
1:C:7:ALA:HB3	1:C:216:THR:HG22	2.00	0.43
1:C:220:GLN:O	1:C:223:ASP:HB2	2.19	0.43
1:B:210:THR:HG22	1:B:211:ALA:N	2.33	0.43
1:D:223:ASP:O	1:D:226:MSE:HB2	2.18	0.43
1:A:132:VAL:O	1:A:133:ARG:HB2	2.17	0.43
1:A:98:TRP:CZ3	1:A:165:VAL:HG13	2.54	0.43
1:C:84:ASN:HD22	1:C:149:THR:HG23	1.84	0.43
1:A:64:GLN:C	1:A:77:ILE:HG12	2.40	0.43
1:A:51:GLN:HB3	1:A:52:PRO:HD3	2.00	0.43
1:C:10:ILE:HD13	1:C:10:ILE:HA	1.84	0.42
1:C:75:GLN:HA	1:C:82:LEU:HG	2.01	0.42
1:B:145:PRO:HD2	1:B:148:LEU:HD22	2.01	0.42
1:B:207:LEU:HD12	1:B:207:LEU:HA	1.72	0.42
1:B:124:TYR:HB2	1:B:156:VAL:CG2	2.49	0.42
1:C:163:GLU:OE1	1:C:166:LYS:HD3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:5:LEU:HD23	1:D:6:ILE:N	2.35	0.42
1:A:204:VAL:HG11	1:A:229:TYR:OH	2.19	0.42
1:D:75:GLN:HG3	1:D:76:THR:O	2.19	0.42
1:A:222:ASN:ND2	1:A:222:ASN:C	2.71	0.42
1:D:156:VAL:O	1:D:156:VAL:HG13	2.19	0.42
1:B:69:PHE:HD1	1:B:152:LYS:HD2	1.84	0.42
1:D:166:LYS:HD2	1:D:181:GLN:HE22	1.85	0.42
1:C:161:VAL:O	1:C:165:VAL:HG23	2.19	0.42
1:C:51:GLN:N	1:C:52:PRO:CD	2.83	0.42
1:D:132:VAL:O	1:D:133:ARG:HB2	2.20	0.42
1:C:235:ALA:HB2	1:C:247:ALA:HB2	2.02	0.42
1:B:240:ILE:HG13	1:B:241:ASP:N	2.31	0.41
1:C:30:GLN:HE21	1:C:30:GLN:HB3	1.70	0.41
1:C:59:ILE:O	1:C:60:ASP:HB3	2.20	0.41
1:B:32:ALA:HB1	1:B:37:ILE:HB	2.02	0.41
1:D:9:ASP:OD2	1:D:223:ASP:OD2	2.37	0.41
1:A:26:ILE:HG22	1:A:27:ASP:N	2.35	0.41
1:D:191:ASN:OD1	1:D:193:ARG:HG2	2.20	0.41
1:B:201:SER:HA	1:B:229:TYR:CZ	2.56	0.41
1:C:32:ALA:O	1:C:37:ILE:HB	2.20	0.41
1:A:251:THR:HG21	1:A:261:ALA:HB3	2.01	0.41
1:C:181:GLN:HG3	1:C:183:ALA:O	2.21	0.41
1:A:129:SER:HB2	1:A:136:ILE:HD11	2.03	0.41
1:B:76:THR:OG1	1:B:80:LYS:HB3	2.20	0.41
1:C:231:GLY:O	1:C:232:LEU:HB3	2.20	0.41
1:D:40:VAL:O	1:D:40:VAL:CG2	2.69	0.41
1:B:148:LEU:HD12	1:B:148:LEU:HA	1.94	0.41
1:C:233:GLY:N	1:C:248:GLN:HE21	2.13	0.41
1:D:69:PHE:HB2	1:D:72:SER:HB3	2.03	0.41
1:C:231:GLY:O	1:C:232:LEU:CB	2.68	0.41
1:D:109:GLU:CG	1:D:134:MSE:HE1	2.51	0.41
1:C:110:THR:HB	1:C:111:PRO:HD2	2.03	0.41
1:C:223:ASP:OD1	1:C:226:MSE:HE2	2.20	0.41
1:B:57:MSE:O	1:B:58:ASP:HB2	2.21	0.41
1:C:38:LYS:HA	1:C:38:LYS:HD2	1.84	0.41
1:B:221:GLY:O	1:B:224:LEU:HB2	2.21	0.40
1:A:45:ARG:O	1:A:68:THR:HB	2.22	0.40
1:B:44:GLY:HA2	1:B:70:ASN:H	1.86	0.40
1:D:223:ASP:O	1:D:227:ILE:HG12	2.20	0.40
1:C:115:TYR:CZ	1:C:137:GLN:OE1	2.75	0.40
1:C:232:LEU:O	1:C:232:LEU:HG	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:LEU:HB2	1:C:258:GLY:CA	2.50	0.40
1:A:95:LEU:HD12	1:A:95:LEU:HA	1.94	0.40
1:D:183:ALA:HB1	1:D:184:PRO:HD2	2.03	0.40
1:A:162:ILE:HG23	1:A:187:ILE:HG13	2.04	0.40
1:A:46:PRO:HD2	1:A:132:VAL:CG1	2.52	0.40
1:D:82:LEU:HA	1:D:82:LEU:HD23	1.84	0.40
1:A:110:THR:HG22	1:A:113:TYR:H	1.86	0.40
1:C:114:ILE:CG1	1:C:134:MSE:HE3	2.50	0.40
1:A:198:GLY:O	1:A:201:SER:HB3	2.21	0.40
1:A:248:GLN:HE21	1:A:248:GLN:N	2.19	0.40
1:D:51:GLN:N	1:D:52:PRO:CD	2.85	0.40
1:D:44:GLY:HA2	1:D:70:ASN:H	1.85	0.40
1:A:70:ASN:HD22	1:A:196:LYS:HE2	1.86	0.40
1:C:69:PHE:O	1:C:72:SER:HB2	2.22	0.40
1:B:183:ALA:HB1	1:B:184:PRO:CD	2.51	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	230/279 (82%)	215 (94%)	13 (6%)	2 (1%)	21	57
1	B	264/279 (95%)	247 (94%)	16 (6%)	1 (0%)	39	74
1	C	253/279 (91%)	231 (91%)	19 (8%)	3 (1%)	16	48
1	D	227/279 (81%)	217 (96%)	10 (4%)	0	100	100
All	All	974/1116 (87%)	910 (93%)	58 (6%)	6 (1%)	30	67

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	245	GLU
1	C	232	LEU
1	A	31	ALA
1	B	252	LEU
1	C	212	ASP
1	C	231	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	198/221 (90%)	177 (89%)	21 (11%)	8	25
1	B	218/221 (99%)	201 (92%)	17 (8%)	16	41
1	C	209/221 (95%)	192 (92%)	17 (8%)	15	39
1	D	195/221 (88%)	177 (91%)	18 (9%)	11	33
All	All	820/884 (93%)	747 (91%)	73 (9%)	12	35

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ILE
1	A	26	ILE
1	A	30	GLN
1	A	33	LYS
1	A	38	LYS
1	A	72	SER
1	A	84	ASN
1	A	95	LEU
1	A	109	GLU
1	A	110	THR
1	A	112	ASP
1	A	141	VAL
1	A	148	LEU
1	A	157	ASP
1	A	188	GLU
1	A	210	THR

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Mol	Chain	Res	Type
1	A	222	ASN
1	A	243	VAL
1	A	248	GLN
1	A	259	VAL
1	A	264	ARG
1	B	2	THR
1	B	17	GLU
1	B	25	THR
1	B	50	VAL
1	B	73	VAL
1	B	110	THR
1	B	132	VAL
1	B	157	ASP
1	B	166	LYS
1	B	182	SER
1	B	196	LYS
1	B	207	LEU
1	B	214	VAL
1	B	224	LEU
1	B	238	ASN
1	B	240	ILE
1	B	251	THR
1	C	40	VAL
1	C	47	LEU
1	C	48	THR
1	C	62	ASP
1	C	72	SER
1	C	83	THR
1	C	102	VAL
1	C	103	ARG
1	C	133	ARG
1	C	141	VAL
1	C	154	MSE
1	C	193	ARG
1	C	210	THR
1	C	224	LEU
1	C	226	MSE
1	C	238	ASN
1	C	264	ARG
1	D	6	ILE
1	D	29	VAL
1	D	35	GLN

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Mol	Chain	Res	Type
1	D	45	ARG
1	D	103	ARG
1	D	132	VAL
1	D	141	VAL
1	D	148	LEU
1	D	154	MSE
1	D	177	PHE
1	D	204	VAL
1	D	210	THR
1	D	214	VAL
1	D	222	ASN
1	D	223	ASP
1	D	238	ASN
1	D	240	ILE
1	D	243	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	70	ASN
1	A	84	ASN
1	A	85	HIS
1	A	118	ASN
1	A	168	ASN
1	A	181	GLN
1	A	206	GLN
1	A	220	GLN
1	A	222	ASN
1	A	248	GLN
1	B	23	GLN
1	B	70	ASN
1	B	118	ASN
1	B	181	GLN
1	B	238	ASN
1	B	248	GLN
1	C	30	GLN
1	C	70	ASN
1	C	118	ASN
1	C	181	GLN
1	C	206	GLN
1	C	238	ASN

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Mol	Chain	Res	Type
1	C	248	GLN
1	C	254	ASN
1	D	30	GLN
1	D	70	ASN
1	D	75	GLN
1	D	84	ASN
1	D	85	HIS
1	D	118	ASN
1	D	181	GLN
1	D	222	ASN
1	D	238	ASN

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	232/279 (83%)	-0.08	1 (0%) 93 92	19, 35, 62, 75	0
1	B	258/279 (92%)	-0.16	0 100 100	18, 33, 61, 68	0
1	C	249/279 (89%)	-0.12	2 (0%) 87 86	19, 38, 60, 69	0
1	D	225/279 (80%)	0.12	12 (5%) 30 23	20, 36, 64, 76	0
All	All	964/1116 (86%)	-0.06	15 (1%) 74 72	18, 36, 62, 76	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	13	THR	3.9
1	D	235	ALA	3.7
1	D	2	THR	3.3
1	D	234	VAL	3.1
1	D	11	ASP	3.0
1	C	218	GLY	2.9
1	A	58	ASP	2.4
1	C	217	LEU	2.4
1	D	24	ALA	2.3
1	D	233	GLY	2.2
1	D	228	LYS	2.2
1	D	237	GLY	2.2
1	D	29	VAL	2.2
1	D	229	TYR	2.1
1	D	231	GLY	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 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.