



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:44 PM UTC

PDB ID : 5LOE / pdb_00005loe
Title : Structure of full length Cody from Bacillus subtilis in complex with Ile
Authors : Wilkinson, A.J.; Levnikov, V.M.; Blagova, E.V.
Deposited on : 2016-08-09
Resolution : 3.00 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

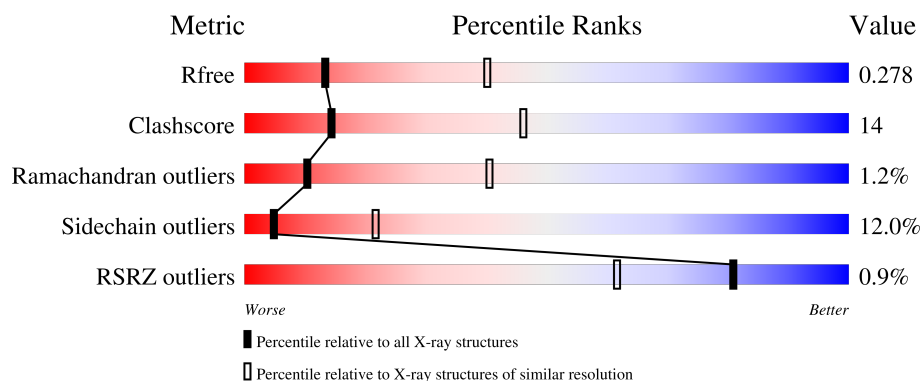
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	262	68% 26% 5% .
1	B	262	66% 27% 5% .
1	C	262	65% 30% . .
1	D	262	59% 33% 6% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8179 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.

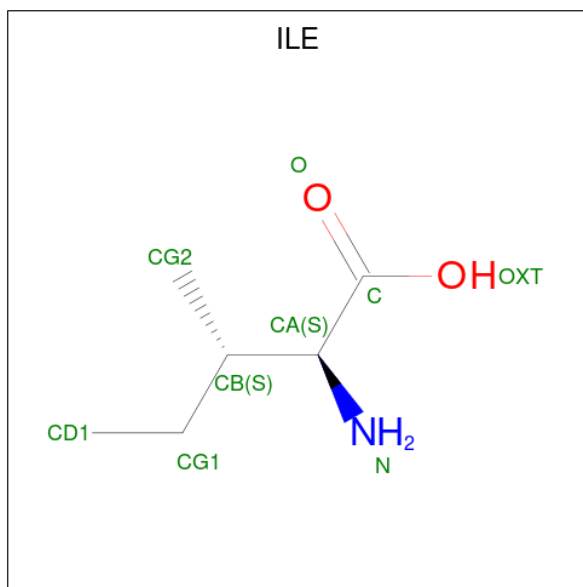
- Molecule 1 is a protein called GTP-sensing transcriptional pleiotropic repressor CodY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	5	0
			2051	1288	350	404	9			
1	B	257	Total	C	N	O	S	0	3	0
			2033	1276	346	403	8			
1	C	257	Total	C	N	O	S	0	2	0
			2025	1272	345	400	8			
1	D	257	Total	C	N	O	S	0	2	0
			2025	1272	345	400	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P39779
A	-1	SER	-	expression tag	UNP P39779
A	0	HIS	-	expression tag	UNP P39779
A	3	SER	LEU	engineered mutation	UNP P39779
B	-2	GLY	-	expression tag	UNP P39779
B	-1	SER	-	expression tag	UNP P39779
B	0	HIS	-	expression tag	UNP P39779
B	3	SER	LEU	engineered mutation	UNP P39779
C	-2	GLY	-	expression tag	UNP P39779
C	-1	SER	-	expression tag	UNP P39779
C	0	HIS	-	expression tag	UNP P39779
C	3	SER	LEU	engineered mutation	UNP P39779
D	-2	GLY	-	expression tag	UNP P39779
D	-1	SER	-	expression tag	UNP P39779
D	0	HIS	-	expression tag	UNP P39779
D	3	SER	LEU	engineered mutation	UNP P39779

- Molecule 2 is ISOLEUCINE (CCD ID: ILE) (formula: $C_6H_{13}NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			9	6	1	2		
2	B	1	Total	C	N	O	0	0
			9	6	1	2		
2	C	1	Total	C	N	O	0	0
			9	6	1	2		
2	D	1	Total	C	N	O	0	0
			9	6	1	2		

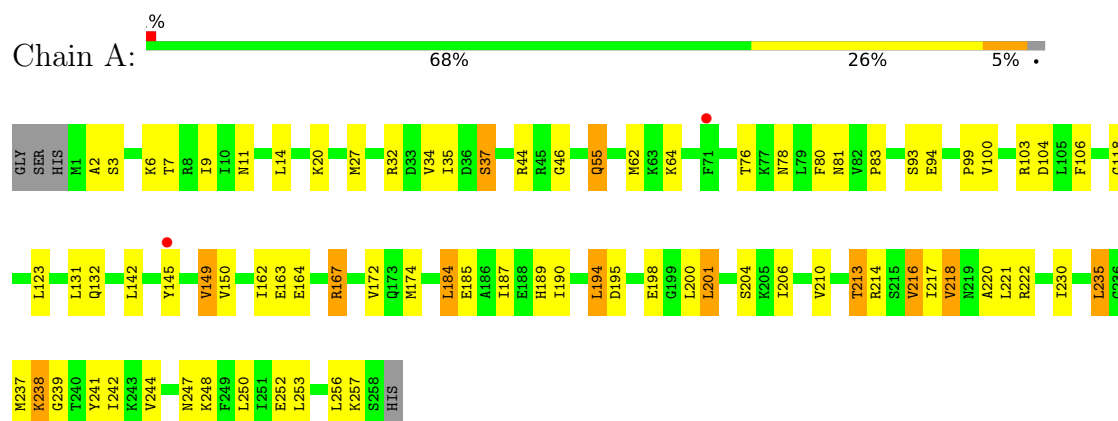
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	O	0	0
			5	5		
3	B	2	Total	O	0	0
			2	2		
3	D	2	Total	O	0	0
			2	2		

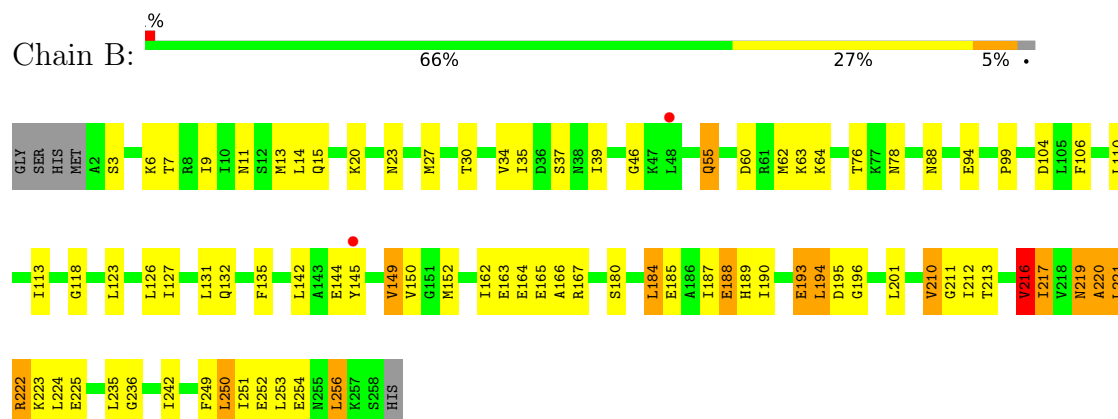
3 Residue-property plots [i](#)

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.

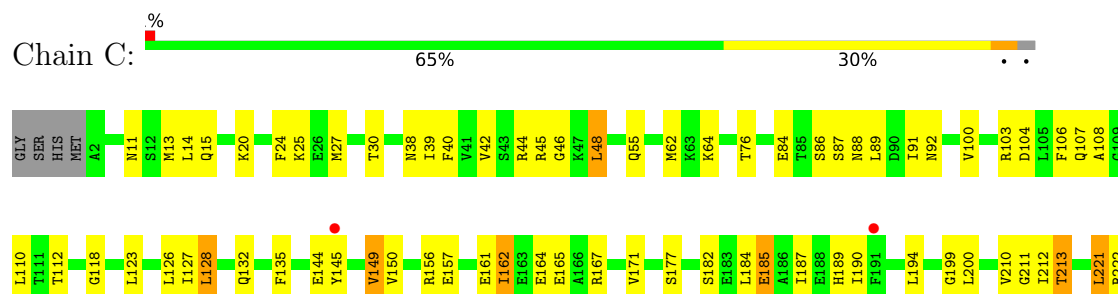
• Molecule 1: GTP-sensing transcriptional pleiotropic repressor CodY

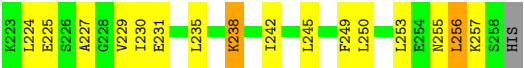


• Molecule 1: GTP-sensing transcriptional pleiotropic repressor CodY

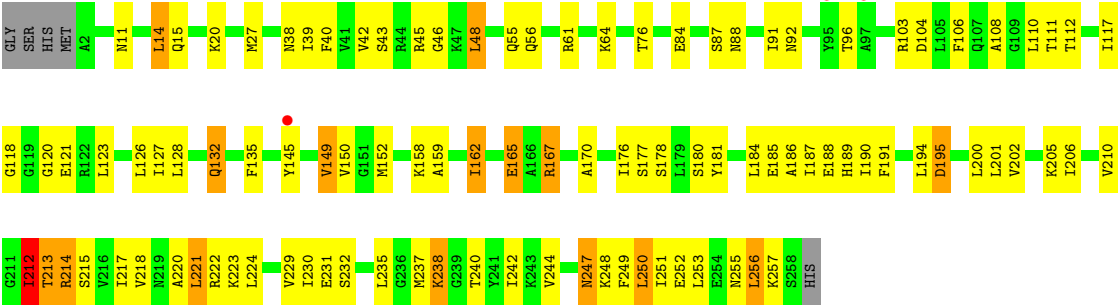


• Molecule 1: GTP-sensing transcriptional pleiotropic repressor CodY





● Molecule 1: GTP-sensing transcriptional pleiotropic repressor CodY



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	134.69Å 158.88Å 55.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.45 – 3.00 45.45 – 3.00	Depositor EDS
% Data completeness (in resolution range)	92.4 (45.45-3.00) 92.4 (45.45-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.212 , 0.302 (Not available) , 0.278	Depositor DCC
R_{free} test set	1164 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	92.1	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 81.1	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	0.95	EDS
Total number of atoms	8179	wwPDB-VP
Average B, all atoms (Å ²)	110.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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	0.94	0/2086	1.10	0/2806
1	B	0.96	0/2059	1.09	1/2771 (0.0%)
1	C	0.81	0/2051	1.02	0/2760
1	D	0.88	1/2051 (0.0%)	1.13	4/2760 (0.1%)
All	All	0.90	1/8247 (0.0%)	1.08	5/11097 (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
1	B	1	0
All	All	1	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	84	GLU	CG-CD	7.83	1.71	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	165	GLU	N-CA-C	-7.49	103.06	111.07
1	B	196	GLY	N-CA-C	-7.17	102.76	111.94
1	D	84	GLU	CB-CG-CD	7.06	124.61	112.60
1	D	212	ILE	CB-CA-C	-5.37	102.23	110.50
1	D	117	ILE	N-CA-C	5.08	115.29	108.17

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	195[B]	ASP	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	238	LYS	Peptide

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	2051	0	2103	48	0
1	B	2033	0	2071	59	0
1	C	2025	0	2068	57	0
1	D	2025	0	2068	74	0
2	A	9	0	10	1	0
2	B	9	0	10	1	0
2	C	9	0	10	1	0
2	D	9	0	10	2	0
3	A	5	0	0	0	0
3	B	2	0	0	0	0
3	D	2	0	0	0	0
All	All	8179	0	8350	233	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 14.

All (233) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:247:ASN:O	1:D:251:ILE:CD1	2.16	0.92
1:C:27[B]:MET:HE3	1:C:150:VAL:HG22	1.63	0.81
1:B:27[B]:MET:HE3	1:B:150:VAL:HG22	1.60	0.80
1:D:187:ILE:HD11	1:D:220:ALA:HB1	1.64	0.80
1:D:251:ILE:HD12	1:D:251:ILE:H	1.45	0.79
1:C:46:GLY:N	1:C:76:THR:HG21	2.01	0.76
1:A:187:ILE:HG22	1:A:253:LEU:HD11	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:11:ASN:OD1	1:B:145:TYR:OH	2.05	0.74
1:D:11:ASN:OD1	1:D:145:TYR:OH	2.05	0.73
1:B:249:PHE:CZ	1:B:253:LEU:HD11	2.23	0.73
1:D:186:ALA:O	1:D:190:ILE:HD13	1.89	0.72
1:D:178:SER:O	1:D:223:LYS:NZ	2.21	0.71
1:C:194:LEU:HD11	1:C:199:GLY:HA3	1.73	0.70
1:D:202:VAL:HG11	1:D:205:LYS:CE	2.21	0.70
1:D:213:THR:OG1	1:D:215:SER:OG	2.10	0.70
1:C:62:MET:HE1	2:C:301:ILE:HG21	1.74	0.70
1:A:27[B]:MET:HE3	1:A:150:VAL:HG22	1.73	0.69
1:A:230:ILE:HG22	1:A:244:VAL:HA	1.74	0.69
1:D:250:LEU:HG	1:D:251:ILE:HD12	1.73	0.69
1:B:27[A]:MET:HE2	1:B:150:VAL:HG22	1.73	0.69
1:D:248:LYS:HA	1:D:251:ILE:HD13	1.75	0.69
1:D:217:ILE:O	1:D:221:LEU:HD22	1.93	0.68
1:A:6:LYS:HA	1:A:9:ILE:HD12	1.77	0.67
1:B:201:LEU:HD12	1:B:242:ILE:HD12	1.76	0.67
1:D:230:ILE:HG22	1:D:244:VAL:HA	1.77	0.67
1:B:189:HIS:CE1	1:B:210:VAL:HG11	2.30	0.67
1:D:46:GLY:N	1:D:76:THR:HG21	2.10	0.66
1:D:27[A]:MET:HE2	1:D:150:VAL:HG22	1.78	0.66
1:D:202:VAL:HG11	1:D:205:LYS:HE3	1.77	0.66
1:C:229:VAL:HG11	1:C:249:PHE:CD2	2.30	0.66
1:B:201:LEU:HD12	1:B:242:ILE:CD1	2.27	0.65
1:C:187:ILE:HA	1:C:190:ILE:HD12	1.79	0.64
1:B:27[A]:MET:HE1	1:B:150:VAL:HA	1.77	0.64
1:C:187:ILE:HD12	1:C:224:LEU:HD11	1.79	0.64
1:D:27[A]:MET:HE1	1:D:150:VAL:HA	1.80	0.63
1:A:200:LEU:C	1:A:200:LEU:HD23	2.23	0.63
1:D:247:ASN:O	1:D:251:ILE:HD12	1.99	0.63
1:C:171:VAL:HG13	1:C:227:ALA:O	1.98	0.62
1:D:247:ASN:O	1:D:251:ILE:HD11	1.98	0.62
1:B:211:GLY:C	1:B:212:ILE:HD12	2.24	0.62
1:B:189:HIS:ND1	1:B:210:VAL:HG11	2.15	0.62
1:C:11:ASN:OD1	1:C:145:TYR:OH	2.16	0.61
1:C:27[A]:MET:HE2	1:C:150:VAL:HG22	1.82	0.61
1:A:189:HIS:CE1	1:A:210:VAL:HG11	2.36	0.61
1:C:187:ILE:HD13	1:C:190:ILE:HD12	1.83	0.61
1:A:241:TYR:O	1:A:242:ILE:HD12	2.01	0.60
1:B:46:GLY:N	1:B:76:THR:HG21	2.17	0.60
1:A:187:ILE:CG2	1:A:253:LEU:HD11	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:ASN:HD21	1:B:135:PHE:H	1.50	0.59
1:D:187:ILE:CD1	1:D:220:ALA:HB1	2.31	0.59
1:B:189:HIS:CG	1:B:210:VAL:HG11	2.37	0.59
1:A:46:GLY:N	1:A:76:THR:HG21	2.18	0.59
1:D:108:ALA:HB1	1:D:132:GLN:HA	1.82	0.59
1:A:241:TYR:C	1:A:242:ILE:HD12	2.27	0.59
1:C:14:LEU:HD12	1:C:149:VAL:HG22	1.83	0.59
1:D:229:VAL:HG11	1:D:249:PHE:CD2	2.38	0.58
1:B:253:LEU:HA	1:B:256:LEU:HD22	1.84	0.58
1:D:195:ASP:OD1	1:D:195:ASP:N	2.36	0.57
1:D:38:ASN:O	1:D:128:LEU:HA	2.05	0.57
1:C:212:ILE:HG22	1:C:213:THR:O	2.05	0.57
1:D:194:LEU:HB2	1:D:201:LEU:HD21	1.85	0.56
1:D:224:LEU:HD21	1:D:249:PHE:CZ	2.41	0.56
1:A:164:GLU:OE2	1:A:167:ARG:NH1	2.38	0.56
1:B:78[B]:ASN:HD21	1:B:94:GLU:CD	2.13	0.56
1:B:193:GLU:O	1:B:194:LEU:C	2.48	0.56
1:B:220:ALA:O	1:B:223:LYS:N	2.38	0.56
1:C:110:LEU:HD12	1:C:132:GLN:O	2.05	0.56
1:D:200:LEU:HD13	1:D:235:LEU:HD12	1.87	0.56
1:C:162:ILE:C	1:C:162:ILE:HD12	2.31	0.56
1:C:27[A]:MET:HE1	1:C:150:VAL:HA	1.88	0.55
1:A:62:MET:HE1	2:A:301:ILE:HG21	1.86	0.55
1:D:190:ILE:HG22	1:D:191:PHE:CD1	2.40	0.55
1:D:202:VAL:HG11	1:D:205:LYS:HE2	1.87	0.55
1:C:14:LEU:C	1:C:14:LEU:HD23	2.32	0.55
1:A:6:LYS:HD3	1:A:142:LEU:HD11	1.89	0.55
1:D:242:ILE:N	1:D:242:ILE:HD12	2.21	0.55
1:C:88:ASN:HD21	1:C:135:PHE:H	1.55	0.55
1:B:249:PHE:CE1	1:B:253:LEU:HD11	2.41	0.54
1:A:118:GLY:HA3	1:A:123:LEU:HD11	1.90	0.54
1:B:194:LEU:HD23	1:B:194:LEU:O	2.08	0.54
1:D:91:ILE:HG23	1:D:92:ASN:ND2	2.23	0.54
1:C:42:VAL:HG21	1:C:127:ILE:HD12	1.89	0.54
1:D:14:LEU:HD12	1:D:149:VAL:HG22	1.89	0.53
1:D:184:LEU:O	1:D:188:GLU:OE2	2.26	0.53
1:D:14:LEU:C	1:D:14:LEU:HD23	2.34	0.53
1:D:162:ILE:HD12	1:D:162:ILE:C	2.33	0.53
1:B:216:VAL:O	1:B:219:ASN:N	2.42	0.53
1:A:14:LEU:C	1:A:14:LEU:HD23	2.34	0.53
1:C:88:ASN:HD22	1:C:110:LEU:HD22	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:ILE:HD12	1:A:163:GLU:N	2.24	0.53
1:D:27[B]:MET:HE3	1:D:150:VAL:HG22	1.90	0.53
1:D:45:ARG:C	1:D:76:THR:HG21	2.34	0.52
1:D:214:ARG:HA	1:D:217:ILE:HD13	1.90	0.52
1:D:61:ARG:HH12	2:D:301:ILE:HD13	1.74	0.52
1:A:27[A]:MET:HE1	1:A:150:VAL:HA	1.91	0.52
1:B:189:HIS:CE1	1:B:210:VAL:CG1	2.93	0.52
1:C:128:LEU:HD12	1:C:128:LEU:N	2.25	0.52
1:D:201:LEU:HD12	1:D:242:ILE:CD1	2.39	0.52
1:A:189:HIS:ND1	1:A:210:VAL:HG11	2.25	0.52
1:D:88:ASN:HD22	1:D:110:LEU:HD22	1.75	0.52
1:B:118:GLY:HA3	1:B:123:LEU:HD11	1.92	0.51
1:A:172:VAL:HG11	1:A:252:GLU:HG3	1.93	0.51
1:C:88:ASN:ND2	1:C:110:LEU:HD13	2.26	0.51
1:C:187:ILE:CD1	1:C:224:LEU:HD11	2.41	0.50
1:D:11:ASN:O	1:D:15:GLN:HG2	2.11	0.50
1:D:247:ASN:HD22	1:D:247:ASN:N	2.09	0.50
1:C:40:PHE:HB2	1:C:127:ILE:HB	1.93	0.50
1:C:194:LEU:HD11	1:C:199:GLY:CA	2.41	0.50
1:B:220:ALA:O	1:B:221:LEU:C	2.53	0.50
1:D:167:ARG:O	1:D:170:ALA:HB3	2.12	0.49
1:A:100:VAL:HG12	1:A:103:ARG:NH1	2.27	0.49
1:A:200:LEU:HD23	1:A:201:LEU:N	2.27	0.49
1:A:14:LEU:HD12	1:A:149:VAL:HG22	1.93	0.49
1:A:204:SER:HB3	1:A:214:ARG:NH2	2.27	0.49
1:D:42:VAL:HG12	1:D:43:SER:O	2.12	0.49
1:B:6:LYS:HA	1:B:9:ILE:HD12	1.95	0.49
1:B:39:ILE:HG23	1:B:126:LEU:HD11	1.95	0.48
1:D:180:SER:O	1:D:181:TYR:C	2.55	0.48
1:A:190:ILE:HD11	1:A:217:ILE:HG23	1.94	0.48
1:C:14:LEU:HD23	1:C:15:GLN:N	2.28	0.48
1:C:38:ASN:O	1:C:128:LEU:HA	2.13	0.48
1:A:187:ILE:HD11	1:A:220:ALA:HB1	1.96	0.48
1:B:62:MET:HE1	2:B:301:ILE:HG21	1.94	0.48
1:B:187:ILE:HD11	1:B:220:ALA:HB1	1.94	0.48
1:D:40:PHE:HB2	1:D:127:ILE:HB	1.94	0.48
1:A:78[B]:ASN:HD21	1:A:94:GLU:CD	2.21	0.48
1:B:55:GLN:OE1	1:B:131:LEU:HD12	2.14	0.48
1:C:189:HIS:CG	1:C:210:VAL:HG11	2.48	0.48
1:A:3:SER:O	1:A:7:THR:HG23	2.14	0.48
1:D:61:ARG:NH1	2:D:301:ILE:HD13	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:ASN:HD21	1:D:135:PHE:H	1.60	0.48
1:B:190:ILE:HG23	1:B:201:LEU:HD13	1.95	0.48
1:B:13:MET:HE2	1:B:30:THR:HB	1.95	0.47
1:D:190:ILE:HG22	1:D:191:PHE:HD1	1.78	0.47
1:A:162:ILE:HD12	1:A:162:ILE:C	2.39	0.47
1:C:108:ALA:HB1	1:C:132:GLN:HA	1.97	0.47
1:A:14:LEU:CD1	1:A:149:VAL:HG22	2.44	0.47
1:A:34:VAL:HG23	1:A:35:ILE:HG13	1.96	0.47
1:A:55:GLN:OE1	1:A:131:LEU:HD12	2.14	0.47
1:C:200:LEU:HD12	1:C:235:LEU:HD13	1.97	0.47
1:A:216:VAL:O	1:A:217:ILE:C	2.58	0.47
1:B:3:SER:O	1:B:7:THR:HG23	2.15	0.47
1:B:187:ILE:HD12	1:B:224:LEU:HD11	1.97	0.47
1:B:190:ILE:HD13	1:B:221:LEU:HD13	1.96	0.47
1:C:48:LEU:HD23	1:C:48:LEU:HA	1.83	0.47
1:C:91:ILE:HG23	1:C:92:ASN:ND2	2.30	0.47
1:D:248:LYS:CA	1:D:251:ILE:HD13	2.44	0.47
1:A:213:THR:O	1:A:214:ARG:C	2.57	0.47
1:B:253:LEU:HA	1:B:256:LEU:CD2	2.45	0.47
1:C:230:ILE:HD12	1:C:230:ILE:C	2.40	0.47
1:A:11:ASN:OD1	1:A:145:TYR:OH	2.24	0.46
1:B:23:ASN:OD1	1:B:23:ASN:C	2.58	0.46
1:C:45:ARG:HD3	1:D:189:HIS:CE1	2.50	0.46
1:C:24:PHE:O	1:C:25:LYS:C	2.58	0.46
1:C:200:LEU:HD12	1:C:235:LEU:CD1	2.46	0.46
1:B:216:VAL:O	1:B:217:ILE:C	2.59	0.46
1:C:39:ILE:HG23	1:C:126:LEU:HD11	1.97	0.46
1:A:44:ARG:HG2	1:A:80:PHE:HZ	1.81	0.45
1:C:200:LEU:HD21	1:C:238:LYS:NZ	2.32	0.45
1:A:32:ARG:HG3	1:A:37:SER:O	2.16	0.45
1:C:161:GLU:HB3	1:D:256:LEU:CD2	2.46	0.45
1:C:184:LEU:C	1:C:184:LEU:HD23	2.42	0.45
1:D:212:ILE:HB	1:D:217:ILE:HD11	1.98	0.45
1:B:144:GLU:O	1:B:145:TYR:C	2.57	0.45
1:B:221:LEU:O	1:B:222:ARG:C	2.58	0.45
1:B:6:LYS:HB3	1:B:142:LEU:HD11	1.98	0.45
1:B:14:LEU:CD1	1:B:149:VAL:HG22	2.47	0.45
1:B:253:LEU:HD12	1:B:253:LEU:H	1.82	0.44
1:A:198:GLU:OE1	1:A:241:TYR:OH	2.32	0.44
1:D:221:LEU:O	1:D:222:ARG:C	2.60	0.44
1:D:118:GLY:O	1:D:120:GLY:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:LEU:HD23	1:A:235:LEU:O	2.18	0.44
1:D:250:LEU:HG	1:D:251:ILE:CD1	2.43	0.44
1:C:86:SER:OG	1:C:89:LEU:HD21	2.17	0.44
1:A:184:LEU:O	1:A:185:GLU:C	2.59	0.43
1:B:165:GLU:O	1:B:166:ALA:C	2.60	0.43
1:D:48:LEU:HD23	1:D:48:LEU:HA	1.88	0.43
1:B:190:ILE:HG21	1:B:221:LEU:HD11	1.99	0.43
1:A:247:ASN:OD1	1:A:247:ASN:N	2.51	0.43
1:D:38:ASN:HD21	1:D:55:GLN:HG2	1.84	0.43
1:A:190:ILE:HG23	1:A:201:LEU:CD2	2.48	0.43
1:C:253:LEU:HA	1:C:256:LEU:HD22	2.01	0.43
1:C:182:SER:OG	1:D:121:GLU:CD	2.62	0.43
1:D:201:LEU:HD12	1:D:242:ILE:HD13	2.00	0.43
1:C:221:LEU:O	1:C:222:ARG:C	2.62	0.43
1:D:110:LEU:HD12	1:D:132:GLN:O	2.19	0.43
1:C:156:ARG:O	1:C:157:GLU:C	2.60	0.43
1:C:118:GLY:HA3	1:C:123:LEU:HD11	2.01	0.42
1:C:189:HIS:ND1	1:C:210:VAL:HG11	2.34	0.42
1:D:87:SER:HA	1:D:112:THR:HG23	2.01	0.42
1:A:218:VAL:O	1:A:222[A]:ARG:HG3	2.19	0.42
1:B:14:LEU:HD23	1:B:14:LEU:C	2.44	0.42
1:B:235:LEU:HD23	1:B:236:GLY:N	2.34	0.42
1:C:100:VAL:HG12	1:C:103:ARG:NH1	2.34	0.42
1:B:152:MET:HG2	1:D:152:MET:HE3	2.01	0.42
1:D:201:LEU:HG	1:D:242:ILE:HD13	2.01	0.42
1:D:230:ILE:HD12	1:D:232:SER:N	2.35	0.42
1:B:60:ASP:O	1:B:63:LYS:HB3	2.20	0.42
1:D:39:ILE:HG23	1:D:126:LEU:HD11	2.01	0.42
1:B:11:ASN:O	1:B:15:GLN:HG2	2.20	0.42
1:A:27[A]:MET:HE2	1:A:150:VAL:HG22	2.01	0.42
1:D:118:GLY:HA3	1:D:123:LEU:HD11	2.02	0.41
1:B:162:ILE:HD12	1:B:163:GLU:N	2.36	0.41
1:C:88:ASN:HA	1:C:110:LEU:HD22	2.02	0.41
1:A:189:HIS:CE1	1:A:210:VAL:CG1	3.02	0.41
1:D:205:LYS:O	1:D:206:ILE:HD13	2.20	0.41
1:C:44:ARG:HD3	1:D:185:GLU:OE2	2.20	0.41
1:B:14:LEU:HD13	1:B:149:VAL:HG22	2.01	0.41
1:B:251:ILE:O	1:B:254:GLU:HB2	2.20	0.41
1:D:247:ASN:HA	1:D:250:LEU:HD21	2.03	0.41
1:A:44:ARG:HG3	1:A:123:LEU:O	2.21	0.41
1:C:87:SER:HA	1:C:112:THR:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:159:ALA:O	1:D:162:ILE:HG13	2.21	0.41
1:D:218:VAL:O	1:D:221:LEU:N	2.54	0.41
1:A:81:ASN:O	1:A:83:PRO:HD3	2.21	0.41
1:B:34:VAL:HG23	1:B:35:ILE:HG13	2.03	0.41
1:B:62:MET:HE3	1:B:99:PRO:HD3	2.03	0.41
1:B:184:LEU:O	1:B:188:GLU:OE2	2.38	0.41
1:B:250:LEU:HD12	1:B:251:ILE:HG13	2.03	0.41
1:A:62:MET:HE3	1:A:99:PRO:HD3	2.02	0.40
1:C:38:ASN:HD21	1:C:55:GLN:HG2	1.87	0.40
1:C:184:LEU:O	1:C:185:GLU:C	2.63	0.40
1:C:255:ASN:OD1	1:C:256:LEU:N	2.54	0.40
1:B:113:ILE:CD1	1:B:127:ILE:HG12	2.51	0.40
1:B:113:ILE:HD12	1:B:127:ILE:HG12	2.04	0.40
1:C:144:GLU:O	1:C:145:TYR:C	2.64	0.40
1:B:27[A]:MET:CE	1:B:150:VAL:HG22	2.47	0.40
1:B:110:LEU:HD12	1:B:132:GLN:O	2.21	0.40
1:C:231:GLU:HB3	1:C:245:LEU:HD11	2.03	0.40
1:D:201:LEU:HD12	1:D:242:ILE:HG12	2.03	0.40
1:C:13:MET:HE2	1:C:30:THR:HB	2.04	0.40
1:D:158:LYS:O	1:D:159:ALA:C	2.64	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	261/262 (100%)	232 (89%)	26 (10%)	3 (1%)	11	43
1	B	258/262 (98%)	230 (89%)	24 (9%)	4 (2%)	7	34
1	C	257/262 (98%)	231 (90%)	24 (9%)	2 (1%)	16	50
1	D	257/262 (98%)	229 (89%)	25 (10%)	3 (1%)	10	40
All	All	1033/1048 (99%)	922 (89%)	99 (10%)	12 (1%)	10	40

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	193	GLU
1	A	239	GLY
1	B	194	LEU
1	D	238	LYS
1	A	2	ALA
1	A	132	GLN
1	C	211	GLY
1	B	220	ALA
1	C	257	LYS
1	D	132	GLN
1	D	103	ARG
1	B	216	VAL

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	229/227 (101%)	202 (88%)	27 (12%)	5	22
1	B	220/227 (97%)	194 (88%)	26 (12%)	5	22
1	C	225/227 (99%)	203 (90%)	22 (10%)	7	30
1	D	225/227 (99%)	193 (86%)	32 (14%)	3	16
All	All	899/908 (99%)	792 (88%)	107 (12%)	5	22

All (107) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LYS
1	A	37	SER
1	A	55	GLN
1	A	64	LYS
1	A	93	SER
1	A	104	ASP
1	A	106	PHE
1	A	149	VAL

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Mol	Chain	Res	Type
1	A	167	ARG
1	A	174	MET
1	A	184	LEU
1	A	194	LEU
1	A	195[A]	ASP
1	A	195[B]	ASP
1	A	201	LEU
1	A	206	ILE
1	A	213	THR
1	A	216	VAL
1	A	218	VAL
1	A	221	LEU
1	A	235	LEU
1	A	237	MET
1	A	238	LYS
1	A	248	LYS
1	A	250	LEU
1	A	256	LEU
1	A	257	LYS
1	B	20	LYS
1	B	37	SER
1	B	55	GLN
1	B	64	LYS
1	B	104	ASP
1	B	106	PHE
1	B	149	VAL
1	B	164	GLU
1	B	167	ARG
1	B	180	SER
1	B	184	LEU
1	B	185	GLU
1	B	188	GLU
1	B	195[A]	ASP
1	B	195[B]	ASP
1	B	210	VAL
1	B	213	THR
1	B	216	VAL
1	B	217	ILE
1	B	219	ASN
1	B	221	LEU
1	B	222	ARG
1	B	225	GLU

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Mol	Chain	Res	Type
1	B	250	LEU
1	B	252	GLU
1	B	256	LEU
1	C	20	LYS
1	C	48	LEU
1	C	64	LYS
1	C	84	GLU
1	C	104	ASP
1	C	106	PHE
1	C	107	GLN
1	C	128	LEU
1	C	149	VAL
1	C	162	ILE
1	C	164	GLU
1	C	165	GLU
1	C	167	ARG
1	C	177	SER
1	C	185	GLU
1	C	213	THR
1	C	221	LEU
1	C	225	GLU
1	C	238	LYS
1	C	242	ILE
1	C	250	LEU
1	C	256	LEU
1	D	14	LEU
1	D	20	LYS
1	D	48	LEU
1	D	56	GLN
1	D	64	LYS
1	D	96	THR
1	D	104	ASP
1	D	106	PHE
1	D	111	THR
1	D	149	VAL
1	D	162	ILE
1	D	165	GLU
1	D	167	ARG
1	D	176	ILE
1	D	177	SER
1	D	195	ASP
1	D	210	VAL

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Mol	Chain	Res	Type
1	D	212	ILE
1	D	213	THR
1	D	214	ARG
1	D	221	LEU
1	D	231	GLU
1	D	237	MET
1	D	238	LYS
1	D	240	THR
1	D	247	ASN
1	D	250	LEU
1	D	252	GLU
1	D	253	LEU
1	D	255	ASN
1	D	256	LEU
1	D	257	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	A	81	ASN
1	A	107	GLN
1	A	132	GLN
1	A	255	ASN
1	B	88	ASN
1	B	107	GLN
1	B	219	ASN
1	C	56	GLN
1	C	88	ASN
1	C	92	ASN
1	C	102	ASN
1	C	219	ASN
1	D	56	GLN
1	D	88	ASN
1	D	92	ASN
1	D	189	HIS
1	D	247	ASN
1	D	255	ASN

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 ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ILE	D	301	-	8,8,8	1.00	1 (12%)	9,10,10	1.27	1 (11%)
2	ILE	B	301	-	8,8,8	0.84	1 (12%)	9,10,10	1.28	2 (22%)
2	ILE	C	301	-	8,8,8	0.92	1 (12%)	9,10,10	1.26	2 (22%)
2	ILE	A	301	-	8,8,8	1.00	1 (12%)	9,10,10	1.32	1 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ILE	D	301	-	-	6/10/10/10	-
2	ILE	B	301	-	-	3/10/10/10	-
2	ILE	C	301	-	-	0/10/10/10	-
2	ILE	A	301	-	-	0/10/10/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	ILE	OXT-C	-2.41	1.23	1.30
2	C	301	ILE	OXT-C	-2.23	1.23	1.30
2	B	301	ILE	OXT-C	-2.12	1.23	1.30
2	D	301	ILE	OXT-C	-2.01	1.24	1.30

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	ILE	OXT-C-O	-3.14	116.95	124.08
2	B	301	ILE	OXT-C-O	-3.02	117.22	124.08
2	D	301	ILE	OXT-C-O	-2.86	117.60	124.08
2	C	301	ILE	OXT-C-O	-2.63	118.12	124.08
2	C	301	ILE	OXT-C-CA	2.31	122.11	114.15
2	B	301	ILE	OXT-C-CA	2.18	121.67	114.15

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	301	ILE	N-CA-CB-CG1
2	D	301	ILE	N-CA-CB-CG2
2	D	301	ILE	C-CA-CB-CG1
2	D	301	ILE	C-CA-CB-CG2
2	B	301	ILE	CG2-CB-CG1-CD1
2	D	301	ILE	O-C-CA-CB
2	D	301	ILE	OXT-C-CA-CB
2	B	301	ILE	OXT-C-CA-N
2	B	301	ILE	O-C-CA-N

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	301	ILE	2	0
2	B	301	ILE	1	0
2	C	301	ILE	1	0
2	A	301	ILE	1	0

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	258/262 (98%)	-0.63	2 (0%)	82 64	35, 93, 149, 174	7 (2%)
1	B	257/262 (98%)	-0.68	2 (0%)	82 64	34, 88, 133, 176	5 (1%)
1	C	257/262 (98%)	-0.66	2 (0%)	82 64	36, 111, 181, 215	4 (1%)
1	D	257/262 (98%)	-0.48	3 (1%)	76 55	34, 116, 206, 262	4 (1%)
All	All	1029/1048 (98%)	-0.61	9 (0%)	81 61	34, 102, 176, 262	20 (1%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	145	TYR	6.2
1	C	145	TYR	5.5
1	D	145	TYR	4.6
1	A	71	PHE	3.3
1	B	145	TYR	2.8
1	C	191	PHE	2.7
1	D	97	ALA	2.6
1	B	48	LEU	2.2
1	D	95	TYR	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](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ILE	D	301	9/9	0.72	0.15	136,167,207,210	0
2	ILE	C	301	9/9	0.93	0.08	102,127,140,146	0
2	ILE	A	301	9/9	0.94	0.10	106,123,135,141	0
2	ILE	B	301	9/9	0.95	0.08	63,75,90,94	0

6.5 Other polymers [i](#)

There are no such residues in this entry.