



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:53 AM UTC

PDB ID : 2ZU0 / pdb_00002zu0
Title : Crystal structure of SufC-SufD complex involved in the iron-sulfur cluster biosynthesis
Authors : Wada, K.
Deposited on : 2008-10-11
Resolution : 2.20 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

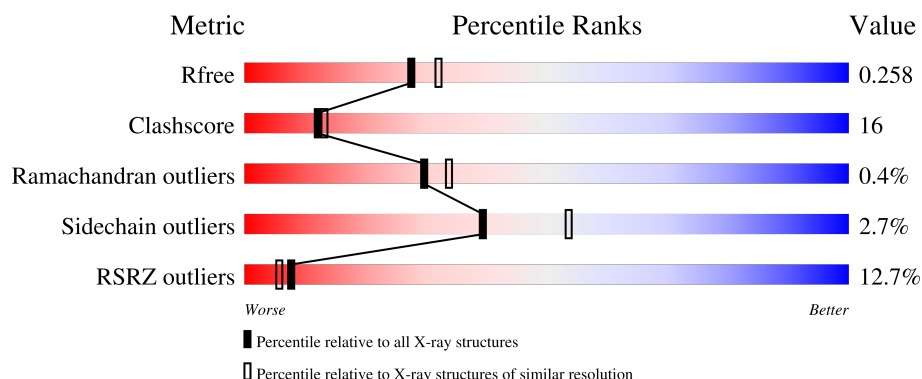
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	423	8% 73% 23% ..
1	B	423	7% 77% 20% ..
2	C	267	15% 61% 27% • 7%
2	D	267	13% 10% 6% 84%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9043 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 Protein sufD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	0	0
			3255	2028	604	615	8			
1	B	414	Total	C	N	O	S	0	0	0
			3237	2019	599	611	8			

- Molecule 2 is a protein called Probable ATP-dependent transporter sufC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	247	Total	C	N	O	S	0	0	0
			1931	1223	325	376	7			
2	D	42	Total	C	N	O	S	0	0	0
			319	205	51	62	1			

There are 38 discrepancies between the modelled and reference sequences:

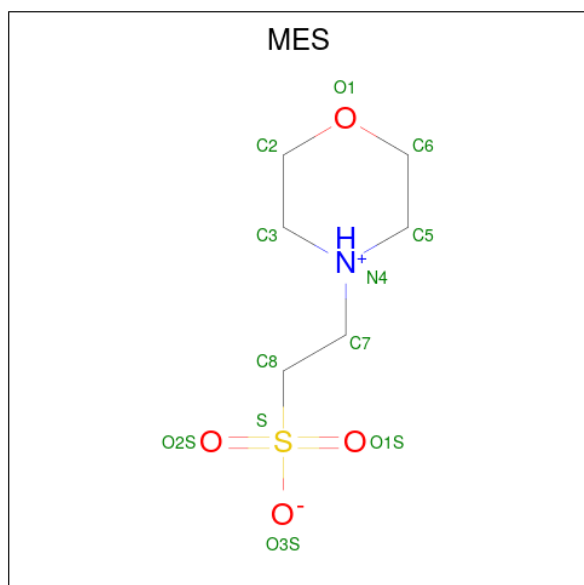
Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	MET	-	expression tag	UNP P77499
C	-17	GLY	-	expression tag	UNP P77499
C	-16	SER	-	expression tag	UNP P77499
C	-15	SER	-	expression tag	UNP P77499
C	-14	HIS	-	expression tag	UNP P77499
C	-13	HIS	-	expression tag	UNP P77499
C	-12	HIS	-	expression tag	UNP P77499
C	-11	HIS	-	expression tag	UNP P77499
C	-10	HIS	-	expression tag	UNP P77499
C	-9	SER	-	expression tag	UNP P77499
C	-8	SER	-	expression tag	UNP P77499
C	-7	GLY	-	expression tag	UNP P77499
C	-6	LEU	-	expression tag	UNP P77499
C	-5	VAL	-	expression tag	UNP P77499
C	-4	PRO	-	expression tag	UNP P77499
C	-3	ARG	-	expression tag	UNP P77499

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP P77499
C	-1	SER	-	expression tag	UNP P77499
C	0	HIS	-	expression tag	UNP P77499
D	-18	MET	-	expression tag	UNP P77499
D	-17	GLY	-	expression tag	UNP P77499
D	-16	SER	-	expression tag	UNP P77499
D	-15	SER	-	expression tag	UNP P77499
D	-14	HIS	-	expression tag	UNP P77499
D	-13	HIS	-	expression tag	UNP P77499
D	-12	HIS	-	expression tag	UNP P77499
D	-11	HIS	-	expression tag	UNP P77499
D	-10	HIS	-	expression tag	UNP P77499
D	-9	SER	-	expression tag	UNP P77499
D	-8	SER	-	expression tag	UNP P77499
D	-7	GLY	-	expression tag	UNP P77499
D	-6	LEU	-	expression tag	UNP P77499
D	-5	VAL	-	expression tag	UNP P77499
D	-4	PRO	-	expression tag	UNP P77499
D	-3	ARG	-	expression tag	UNP P77499
D	-2	GLY	-	expression tag	UNP P77499
D	-1	SER	-	expression tag	UNP P77499
D	0	HIS	-	expression tag	UNP P77499

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

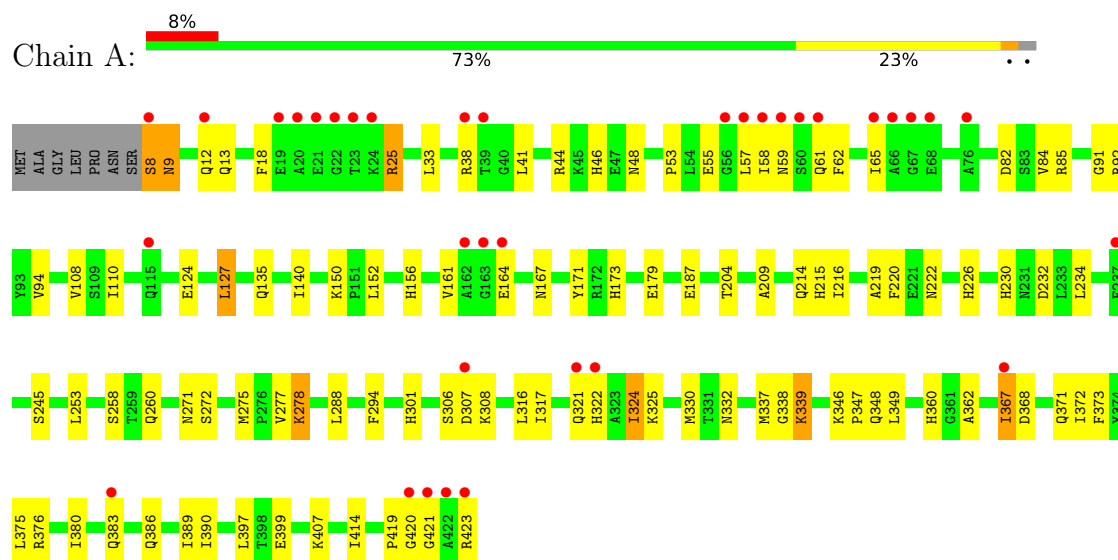
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	116	Total	O	0	0
			116	116		
4	B	126	Total	O	0	0
			126	126		
4	C	47	Total	O	0	0
			47	47		

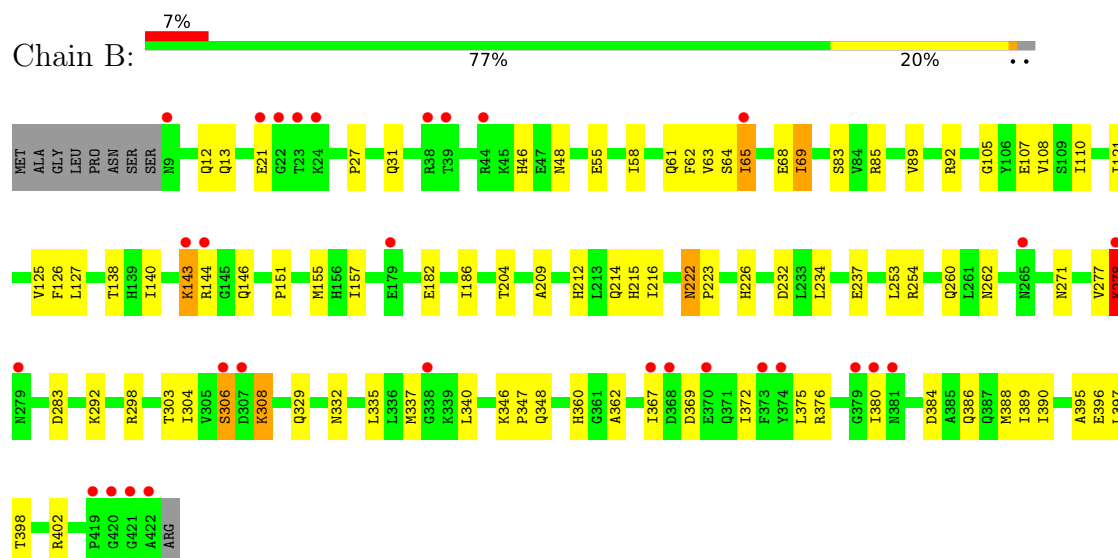
3 Residue-property plots [i](#)

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: Protein sufD

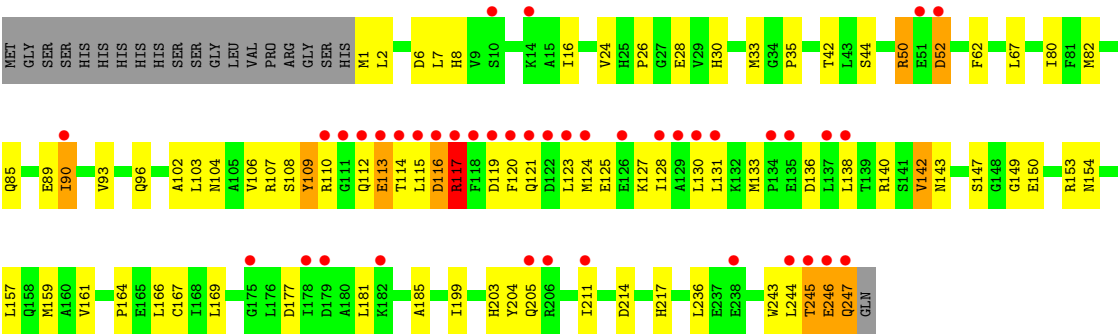


• Molecule 1: Protein sufD

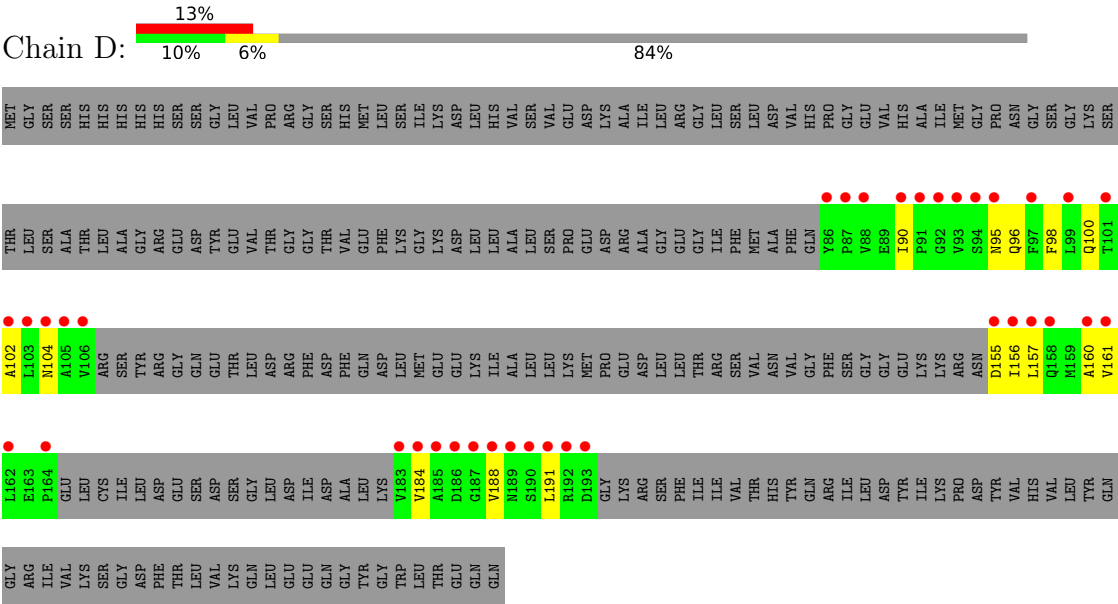


• Molecule 2: Probable ATP-dependent transporter sufC





● Molecule 2: Probable ATP-dependent transporter sufC



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.11Å 106.15Å 171.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.14 – 2.20 45.14 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (45.14-2.20) 97.2 (45.14-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.48 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.234 , 0.259 0.234 , 0.258	Depositor DCC
R_{free} test set	8973 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å ²)	29.8	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9043	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% 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

Bond lengths and bond angles in the following residue types are not validated in this section: MES

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	0.37	0/3317	0.87	8/4494 (0.2%)
1	B	0.38	0/3299	0.89	6/4472 (0.1%)
2	C	0.43	0/1963	0.98	6/2649 (0.2%)
2	D	0.35	0/322	0.77	0/438
All	All	0.39	0/8901	0.90	20/12053 (0.2%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	109	TYR	N-CA-C	-11.04	95.97	110.43
2	C	203	HIS	N-CA-C	-10.49	97.86	112.45
1	B	306	SER	N-CA-C	8.29	123.48	112.13
1	B	308	LYS	N-CA-C	-7.00	104.74	112.72
2	C	246	GLU	N-CA-C	6.98	125.66	110.80
2	C	85	GLN	N-CA-C	-6.28	104.53	111.82
2	C	205	GLN	N-CA-C	6.12	118.92	111.82
1	A	85	ARG	N-CA-C	5.94	118.42	108.73
1	A	222	ASN	CA-C-N	5.61	125.28	119.56
1	A	222	ASN	C-N-CA	5.61	125.28	119.56
1	A	84	VAL	N-CA-C	-5.56	98.43	106.88
2	C	214	ASP	N-CA-C	-5.47	105.73	112.90
1	A	108	VAL	N-CA-C	5.38	115.87	108.12
1	B	278	LYS	N-CA-C	5.30	122.09	110.80
1	A	127	LEU	N-CA-C	-5.22	105.67	111.36
1	A	94	VAL	CA-C-N	5.20	124.65	119.24
1	A	94	VAL	C-N-CA	5.20	124.65	119.24
1	B	85	ARG	N-CA-C	5.19	117.19	108.73
1	B	222	ASN	CA-C-N	5.10	124.76	119.56
1	B	222	ASN	C-N-CA	5.10	124.76	119.56

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3255	0	3202	100	0
1	B	3237	0	3184	86	0
2	C	1931	0	1928	83	0
2	D	319	0	316	13	0
3	C	12	0	13	1	0
4	A	116	0	0	1	0
4	B	126	0	0	3	0
4	C	47	0	0	0	0
All	All	9043	0	8643	272	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 16.

All (272) 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:121:ILE:HD11	1:B:234:LEU:HD21	1.36	1.07
1:B:143:LYS:H	1:B:143:LYS:HD2	1.20	1.05
1:A:65:ILE:HD12	1:A:161:VAL:HG11	1.49	0.95
1:A:367:ILE:HD13	1:A:368:ASP:N	1.84	0.93
2:C:124:MET:HG2	2:C:138:LEU:HD11	1.51	0.90
1:A:46:HIS:HD2	1:A:48:ASN:H	1.23	0.84
1:B:46:HIS:HD2	1:B:48:ASN:H	1.22	0.83
2:C:185:ALA:HA	2:C:211:ILE:HD11	1.59	0.83
1:B:13:GLN:HE22	1:B:62:PHE:H	1.27	0.82
2:C:90:ILE:N	2:C:90:ILE:HD12	1.95	0.81
2:C:90:ILE:HD13	2:C:142:VAL:CG1	2.11	0.81
1:B:13:GLN:NE2	1:B:62:PHE:H	1.77	0.81
2:C:24:VAL:HG21	2:C:199:ILE:HD11	1.64	0.78
1:A:317:ILE:HD11	1:A:330:MET:HE3	1.65	0.78
1:B:143:LYS:HD2	1:B:143:LYS:N	1.98	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:ILE:HD11	1:A:389:ILE:HG21	1.67	0.75
1:A:367:ILE:HD13	1:A:368:ASP:H	1.55	0.72
1:A:38:ARG:HH21	1:A:38:ARG:HB3	1.54	0.71
1:B:107:GLU:HG2	1:B:143:LYS:HE2	1.73	0.71
2:C:114:THR:HG22	2:C:115:LEU:N	2.06	0.71
1:B:262:ASN:C	1:B:292:LYS:HG3	2.15	0.71
2:C:1:MET:HE3	2:C:26:PRO:HA	1.73	0.70
1:A:46:HIS:CD2	1:A:48:ASN:H	2.08	0.70
1:A:383:GLN:HG2	1:A:420:GLY:O	1.91	0.70
2:C:120:PHE:CE1	2:C:124:MET:HE3	2.27	0.69
2:C:124:MET:HG3	2:C:128:ILE:HD11	1.74	0.69
2:C:90:ILE:HD13	2:C:142:VAL:HB	1.74	0.69
1:A:41:LEU:HD13	1:A:58:ILE:HG22	1.75	0.69
1:A:386:GLN:HE22	1:A:420:GLY:H	1.43	0.67
2:C:143:ASN:ND2	2:C:154:ASN:HD22	1.93	0.67
1:A:18:PHE:O	1:A:25:ARG:HD2	1.94	0.67
2:C:89:GLU:C	2:C:90:ILE:HD12	2.20	0.66
2:C:204:TYR:CE2	2:C:247:GLN:HA	2.31	0.66
1:B:55:GLU:CD	1:B:55:GLU:H	2.03	0.66
2:C:114:THR:HG22	2:C:115:LEU:H	1.59	0.66
2:C:44:SER:O	2:C:82:MET:HE1	1.96	0.66
1:A:8:SER:HB3	1:A:61:GLN:NE2	2.10	0.66
1:A:58:ILE:HD12	1:A:59:ASN:N	2.11	0.66
2:D:160:ALA:HA	2:D:191:LEU:HD21	1.78	0.65
1:B:380:ILE:HD12	1:B:380:ILE:H	1.61	0.65
1:B:105:GLY:O	1:B:143:LYS:HE3	1.97	0.65
2:C:116:ASP:O	2:C:119:ASP:N	2.30	0.64
1:A:38:ARG:HB3	1:A:38:ARG:NH2	2.13	0.64
2:C:90:ILE:HD13	2:C:142:VAL:CB	2.27	0.64
2:C:116:ASP:O	2:C:117:ARG:C	2.40	0.64
1:B:143:LYS:H	1:B:143:LYS:CD	1.90	0.63
1:B:277:VAL:HG23	1:B:278:LYS:HG2	1.80	0.63
1:A:346:LYS:HG3	1:B:348:GLN:HG2	1.81	0.63
2:D:96:GLN:HG3	2:D:100:GLN:NE2	2.14	0.63
1:A:156:HIS:HE1	1:A:173:HIS:NE2	1.97	0.62
2:C:109:TYR:O	2:C:110:ARG:CB	2.47	0.61
1:A:13:GLN:HE21	1:A:62:PHE:H	1.46	0.61
2:C:96:GLN:HB2	2:C:138:LEU:HD12	1.82	0.61
1:B:13:GLN:HE22	1:B:62:PHE:N	1.98	0.61
1:A:324:ILE:HD13	1:A:324:ILE:H	1.65	0.61
1:A:13:GLN:HE21	1:A:61:GLN:HA	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:185:ALA:CA	2:C:211:ILE:HD11	2.30	0.60
1:A:317:ILE:HB	1:A:349:LEU:HD23	1.83	0.60
1:B:121:ILE:HD11	1:B:234:LEU:CD2	2.22	0.60
2:C:90:ILE:N	2:C:90:ILE:CD1	2.65	0.60
1:A:9:ASN:C	1:A:9:ASN:HD22	2.09	0.59
1:B:64:SER:C	1:B:65:ILE:HD13	2.27	0.59
1:B:138:THR:HG22	1:B:140:ILE:HD11	1.84	0.59
1:B:386:GLN:O	1:B:390:ILE:HG12	2.01	0.59
1:B:46:HIS:CD2	1:B:48:ASN:H	2.13	0.59
1:B:214:GLN:HG2	1:B:216:ILE:HD11	1.85	0.59
1:A:9:ASN:ND2	1:A:12:GLN:H	1.99	0.59
2:C:236:LEU:HB3	2:C:244:LEU:HD11	1.85	0.59
2:C:131:LEU:HD12	2:C:157:LEU:HB2	1.85	0.58
2:C:245:THR:HG22	2:C:246:GLU:H	1.68	0.58
1:B:63:VAL:HB	1:B:65:ILE:HD11	1.84	0.58
1:B:335:LEU:HD21	1:B:367:ILE:CD1	2.33	0.58
2:C:104:ASN:OD1	2:C:114:THR:HG21	2.03	0.58
1:B:253:LEU:C	1:B:253:LEU:HD23	2.29	0.58
2:C:131:LEU:HD13	2:C:153:ARG:O	2.04	0.58
2:C:130:LEU:HD23	2:C:130:LEU:O	2.03	0.58
2:D:96:GLN:HG3	2:D:100:GLN:HE21	1.69	0.58
2:C:109:TYR:O	2:C:110:ARG:HB3	2.05	0.57
1:A:278:LYS:HG3	1:A:308:LYS:HE2	1.85	0.57
2:D:157:LEU:O	2:D:161:VAL:HG23	2.04	0.57
1:B:372:ILE:CD1	1:B:389:ILE:HD12	2.35	0.57
1:A:65:ILE:H	1:A:167:ASN:ND2	2.02	0.57
1:A:127:LEU:C	1:A:127:LEU:HD23	2.30	0.57
1:B:335:LEU:HD21	1:B:367:ILE:HD11	1.87	0.57
1:B:380:ILE:HD11	2:D:102:ALA:HB2	1.87	0.56
2:C:104:ASN:HA	2:C:114:THR:OG1	2.04	0.56
2:C:110:ARG:HG2	2:C:112:GLN:HE21	1.70	0.56
1:A:347:PRO:HG3	1:A:360:HIS:CD2	2.40	0.56
1:B:121:ILE:HD12	1:B:260:GLN:CD	2.29	0.56
2:C:124:MET:HG3	2:C:128:ILE:CD1	2.34	0.56
2:C:136:ASP:OD2	2:C:140:ARG:HD2	2.06	0.56
1:A:65:ILE:H	1:A:167:ASN:HD21	1.54	0.56
1:A:215:HIS:C	1:A:216:ILE:HD12	2.31	0.55
1:A:339:LYS:HB2	1:A:339:LYS:NZ	2.21	0.55
1:B:367:ILE:HD11	1:B:390:ILE:HD13	1.88	0.55
2:C:136:ASP:O	2:C:140:ARG:HG3	2.06	0.55
1:B:372:ILE:O	1:B:376:ARG:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:ILE:HD13	1:A:324:ILE:N	2.21	0.55
1:A:368:ASP:CG	1:A:371:GLN:HG3	2.32	0.55
1:B:340:LEU:N	1:B:340:LEU:HD22	2.22	0.55
2:C:204:TYR:CZ	2:C:246:GLU:O	2.60	0.54
2:C:30:HIS:HD2	2:C:217:HIS:NE2	2.05	0.54
1:A:275:MET:SD	1:A:414:ILE:HD12	2.47	0.54
1:A:306:SER:HA	1:A:337:MET:HB2	1.90	0.54
2:C:90:ILE:HD13	2:C:142:VAL:HG11	1.89	0.54
1:B:157:ILE:N	1:B:157:ILE:HD12	2.23	0.53
1:B:367:ILE:HD11	1:B:390:ILE:CD1	2.37	0.53
2:C:143:ASN:HD21	2:C:154:ASN:HD22	1.54	0.53
1:B:110:ILE:N	1:B:110:ILE:HD12	2.23	0.53
1:B:186:ILE:N	1:B:186:ILE:HD12	2.23	0.53
1:A:346:LYS:HE2	1:B:348:GLN:HE21	1.74	0.53
2:C:62:PHE:CD2	2:C:80:ILE:HD11	2.43	0.53
2:C:133:MET:HE2	2:C:133:MET:HA	1.90	0.53
1:B:204:THR:HG22	1:B:232:ASP:HB2	1.91	0.53
2:C:114:THR:CG2	2:C:115:LEU:N	2.72	0.53
1:B:348:GLN:NE2	4:B:548:HOH:O	2.42	0.53
2:C:106:VAL:O	2:C:109:TYR:O	2.26	0.52
1:A:216:ILE:HD12	1:A:216:ILE:N	2.25	0.52
1:B:380:ILE:HD12	1:B:380:ILE:N	2.24	0.52
1:A:399:GLU:OE1	1:A:407:LYS:HE2	2.10	0.52
1:A:321:GLN:O	1:A:322:HIS:HB2	2.08	0.52
2:C:52:ASP:OD2	2:C:52:ASP:N	2.34	0.52
2:C:107:ARG:HD2	2:C:112:GLN:HG3	1.91	0.52
1:B:303:THR:C	1:B:304:ILE:HD12	2.35	0.52
1:B:375:LEU:HD21	2:D:90:ILE:HD13	1.90	0.51
1:A:164:GLU:OE2	1:A:164:GLU:N	2.43	0.51
1:B:376:ARG:HA	1:B:380:ILE:O	2.10	0.51
2:C:33:MET:HE1	2:C:236:LEU:HD12	1.93	0.51
1:A:316:LEU:C	1:A:316:LEU:HD13	2.34	0.51
1:A:33:LEU:C	1:A:33:LEU:HD13	2.36	0.51
1:A:271:ASN:HB3	1:A:397:LEU:HD22	1.93	0.51
1:A:9:ASN:HD22	1:A:12:GLN:H	1.59	0.51
1:B:143:LYS:HD3	1:B:146:GLN:HG3	1.93	0.51
1:A:230:HIS:HE1	1:A:258:SER:OG	1.95	0.50
2:D:156:ILE:HD12	2:D:156:ILE:H	1.77	0.50
2:C:147:SER:OG	2:C:150:GLU:HG3	2.11	0.50
2:C:42:THR:N	3:C:2000:MES:O2S	2.41	0.50
1:B:83:SER:HB2	1:B:151:PRO:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:ARG:HA	1:B:283:ASP:HB3	1.92	0.50
1:B:308:LYS:HB3	1:B:308:LYS:NZ	2.26	0.50
1:A:253:LEU:HD23	1:A:253:LEU:C	2.36	0.50
1:A:324:ILE:H	1:A:324:ILE:CD1	2.24	0.50
1:B:304:ILE:HD12	1:B:304:ILE:N	2.27	0.50
2:C:113:GLU:CD	2:C:114:THR:H	2.19	0.50
2:C:16:ILE:HG21	2:C:42:THR:OG1	2.11	0.50
1:B:127:LEU:HD23	1:B:127:LEU:C	2.36	0.49
1:A:380:ILE:HD11	2:C:102:ALA:HB2	1.94	0.49
2:C:128:ILE:HG23	2:C:133:MET:HB2	1.93	0.49
1:A:380:ILE:HD12	1:A:380:ILE:N	2.27	0.49
1:B:214:GLN:HG2	1:B:216:ILE:CD1	2.43	0.49
1:A:8:SER:HB3	1:A:61:GLN:HE21	1.77	0.49
1:A:204:THR:HG22	1:A:232:ASP:HB2	1.93	0.49
1:A:278:LYS:HE3	1:A:308:LYS:HE3	1.93	0.49
2:C:123:LEU:HD12	2:C:127:LYS:HZ3	1.78	0.49
1:A:348:GLN:HG3	1:B:346:LYS:HG2	1.94	0.49
1:B:216:ILE:HD12	1:B:216:ILE:N	2.27	0.48
1:A:317:ILE:HD12	1:A:349:LEU:HD21	1.94	0.48
2:C:164:PRO:HG2	2:C:167:CYS:SG	2.53	0.48
1:A:367:ILE:HD12	1:A:372:ILE:CD1	2.42	0.48
1:B:21:GLU:OE2	1:B:21:GLU:HA	2.13	0.48
2:D:184:VAL:O	2:D:188:VAL:HG23	2.12	0.48
1:A:13:GLN:NE2	1:A:62:PHE:H	2.12	0.48
1:B:372:ILE:HD13	1:B:389:ILE:HD12	1.95	0.48
1:A:245:SER:O	1:A:272:SER:HA	2.14	0.48
2:C:67:LEU:HD11	2:C:80:ILE:HD13	1.96	0.48
2:C:103:LEU:HG	2:C:114:THR:HG23	1.96	0.48
2:C:114:THR:CG2	2:C:115:LEU:H	2.24	0.48
1:B:13:GLN:HE22	1:B:61:GLN:HA	1.78	0.48
1:A:92:ARG:HE	1:A:135:GLN:CD	2.22	0.47
1:B:271:ASN:HB3	1:B:397:LEU:HD22	1.96	0.47
1:B:27:PRO:O	1:B:31:GLN:HG3	2.14	0.47
1:A:332:ASN:O	1:A:362:ALA:HA	2.14	0.47
2:C:124:MET:C	2:C:128:ILE:HD13	2.40	0.47
1:A:110:ILE:HD12	1:A:110:ILE:N	2.29	0.47
1:A:386:GLN:HE22	1:A:420:GLY:N	2.11	0.47
1:B:138:THR:CG2	1:B:140:ILE:HD11	2.44	0.47
1:B:215:HIS:C	1:B:216:ILE:HD12	2.40	0.47
1:B:260:GLN:HE21	1:B:262:ASN:HD21	1.62	0.47
1:A:372:ILE:HG12	1:A:389:ILE:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:ARG:HD3	1:B:329:GLN:HB2	1.97	0.46
1:A:179:GLU:HG3	1:A:209:ALA:O	2.15	0.46
1:A:372:ILE:CG1	1:A:389:ILE:HD12	2.46	0.46
1:A:386:GLN:O	1:A:390:ILE:HD13	2.14	0.46
1:A:9:ASN:HB3	1:A:12:GLN:HB3	1.98	0.46
1:A:277:VAL:O	1:A:278:LYS:C	2.59	0.46
1:B:155:MET:HG2	1:B:157:ILE:HD11	1.98	0.46
1:B:58:ILE:C	1:B:58:ILE:HD12	2.41	0.46
1:A:271:ASN:HB3	1:A:397:LEU:CD2	2.46	0.46
2:C:2:LEU:HD22	2:C:166:LEU:HD21	1.97	0.46
1:A:18:PHE:CD1	1:A:25:ARG:HD3	2.52	0.45
1:B:396:GLU:HB2	4:B:543:HOH:O	2.15	0.45
1:A:55:GLU:C	1:A:57:LEU:H	2.24	0.45
1:A:275:MET:SD	1:A:414:ILE:HG23	2.57	0.45
1:B:306:SER:HA	1:B:337:MET:HB2	1.98	0.45
1:B:395:ALA:HA	1:B:398:THR:OG1	2.17	0.45
1:A:82:ASP:OD2	1:A:150:LYS:HE2	2.17	0.45
1:A:301:HIS:O	1:A:332:ASN:HA	2.15	0.45
1:A:419:PRO:C	1:A:421:GLY:H	2.24	0.45
2:C:130:LEU:HD23	2:C:130:LEU:C	2.41	0.45
1:A:18:PHE:CE1	1:A:25:ARG:HD3	2.52	0.45
1:A:234:LEU:HD23	1:A:260:GLN:HB2	1.99	0.45
1:A:44:ARG:HH21	1:A:53:PRO:HB3	1.82	0.45
1:B:182:GLU:HG2	1:B:212:HIS:HB2	1.98	0.45
1:B:125:VAL:HG13	1:B:126:PHE:CD1	2.51	0.44
1:B:384:ASP:O	1:B:388:MET:HG3	2.17	0.44
1:A:92:ARG:NE	1:A:135:GLN:OE1	2.49	0.44
1:A:226:HIS:HE1	4:A:461:HOH:O	2.01	0.44
1:B:360:HIS:HD2	1:B:360:HIS:O	2.00	0.44
2:C:159:MET:HE1	2:C:169:LEU:CD2	2.48	0.44
1:A:92:ARG:HG3	1:A:92:ARG:HH11	1.81	0.44
1:A:339:LYS:HB2	1:A:339:LYS:HZ2	1.82	0.44
2:C:30:HIS:HB2	2:C:199:ILE:HD13	1.99	0.44
2:D:157:LEU:C	2:D:157:LEU:HD23	2.43	0.44
1:A:321:GLN:O	1:A:322:HIS:CB	2.65	0.44
2:D:95:ASN:HA	2:D:98:PHE:HB3	1.99	0.44
1:B:332:ASN:O	1:B:362:ALA:HA	2.18	0.44
1:B:360:HIS:CD2	1:B:360:HIS:C	2.96	0.44
1:A:140:ILE:HD13	1:A:152:LEU:HD21	2.00	0.43
2:C:157:LEU:C	2:C:157:LEU:HD23	2.43	0.43
1:B:108:VAL:HG22	1:B:140:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:6:ASP:O	2:C:8:HIS:HD2	2.00	0.43
2:D:157:LEU:O	2:D:157:LEU:HD23	2.17	0.43
1:B:68:GLU:C	1:B:69:ILE:HD12	2.43	0.43
1:B:138:THR:HG22	1:B:140:ILE:CD1	2.47	0.43
2:C:149:GLY:O	2:C:153:ARG:HG3	2.19	0.43
2:C:28:GLU:OE1	2:C:30:HIS:HE1	2.01	0.43
2:C:113:GLU:OE1	2:C:114:THR:N	2.52	0.43
2:C:121:GLN:O	2:C:125:GLU:HG3	2.19	0.43
2:C:138:LEU:HD22	2:C:138:LEU:H	1.84	0.43
1:A:41:LEU:CD1	1:A:58:ILE:HG22	2.47	0.43
1:A:362:ALA:HB3	1:B:360:HIS:NE2	2.34	0.43
2:C:107:ARG:O	2:C:109:TYR:O	2.37	0.43
2:C:108:SER:C	2:C:109:TYR:O	2.55	0.43
1:A:91:GLY:HA2	1:A:171:TYR:CE1	2.54	0.43
1:A:307:ASP:O	1:A:308:LYS:HB2	2.19	0.43
2:D:156:ILE:HD12	2:D:156:ILE:N	2.34	0.43
1:B:335:LEU:HD21	1:B:367:ILE:HD13	2.01	0.43
1:A:219:ALA:C	1:A:220:PHE:HD2	2.27	0.42
1:A:307:ASP:OD1	1:A:338:GLY:HA3	2.19	0.42
1:A:294:PHE:CE2	1:A:325:LYS:HG3	2.54	0.42
2:C:33:MET:HE1	2:C:236:LEU:CD1	2.49	0.42
1:A:373:PHE:CZ	2:C:50:ARG:HD2	2.53	0.42
2:C:204:TYR:CD2	2:C:247:GLN:HB3	2.55	0.42
1:B:89:VAL:O	1:B:92:ARG:HD3	2.20	0.42
2:C:124:MET:O	2:C:125:GLU:C	2.63	0.42
2:D:100:GLN:O	2:D:104:ASN:ND2	2.52	0.42
1:A:13:GLN:NE2	1:A:61:GLN:HA	2.31	0.42
2:C:119:ASP:O	2:C:120:PHE:C	2.63	0.42
1:B:209:ALA:HA	1:B:237:GLU:O	2.20	0.42
2:C:35:PRO:HB3	2:C:243:TRP:CD1	2.55	0.42
1:B:144:ARG:HH21	1:B:144:ARG:HG3	1.85	0.41
1:A:347:PRO:HB3	1:A:360:HIS:CE1	2.54	0.41
1:B:402:ARG:HA	1:B:402:ARG:HD3	1.82	0.41
2:C:124:MET:O	2:C:128:ILE:HD13	2.20	0.41
1:A:373:PHE:CE1	2:C:50:ARG:HD2	2.56	0.41
1:B:253:LEU:HD23	1:B:254:ARG:N	2.34	0.41
1:A:380:ILE:HD12	1:A:380:ILE:H	1.84	0.41
2:C:116:ASP:OD2	2:C:116:ASP:N	2.53	0.41
1:A:92:ARG:HG3	1:A:92:ARG:NH1	2.36	0.41
1:A:347:PRO:HD2	1:B:347:PRO:O	2.20	0.41
2:C:128:ILE:HD12	2:C:157:LEU:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:ARG:C	1:A:423:ARG:HD3	2.45	0.41
1:B:226:HIS:HE1	4:B:449:HOH:O	2.02	0.41
2:C:93:VAL:O	2:C:142:VAL:HG23	2.20	0.41
2:C:177:ASP:O	2:C:181:LEU:HB2	2.22	0.40
1:B:143:LYS:HB2	1:B:146:GLN:HG2	2.02	0.40
1:B:222:ASN:HB2	1:B:223:PRO:CD	2.50	0.40
1:A:372:ILE:O	1:A:376:ARG:HG3	2.21	0.40
1:A:376:ARG:HA	1:A:380:ILE:O	2.22	0.40
1:B:367:ILE:HG21	1:B:372:ILE:HD11	2.02	0.40
1:A:124:GLU:OE2	1:A:230:HIS:HD2	2.04	0.40
2:C:157:LEU:O	2:C:161:VAL:HG23	2.21	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	414/423 (98%)	394 (95%)	19 (5%)	1 (0%)	43	51
1	B	412/423 (97%)	398 (97%)	13 (3%)	1 (0%)	43	51
2	C	245/267 (92%)	233 (95%)	10 (4%)	2 (1%)	16	16
2	D	36/267 (14%)	35 (97%)	1 (3%)	0	100	100
All	All	1107/1380 (80%)	1060 (96%)	43 (4%)	4 (0%)	30	34

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	117	ARG
1	B	278	LYS
2	C	142	VAL
1	A	278	LYS

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	345/350 (99%)	335 (97%)	10 (3%)	37	51
1	B	343/350 (98%)	338 (98%)	5 (2%)	57	73
2	C	211/228 (92%)	202 (96%)	9 (4%)	26	35
2	D	36/228 (16%)	35 (97%)	1 (3%)	38	52
All	All	935/1156 (81%)	910 (97%)	25 (3%)	39	53

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	SER
1	A	9	ASN
1	A	25	ARG
1	A	187	GLU
1	A	214	GLN
1	A	288	LEU
1	A	324	ILE
1	A	339	LYS
1	A	367	ILE
1	A	375	LEU
1	B	12	GLN
1	B	65	ILE
1	B	69	ILE
1	B	143	LYS
1	B	369	ASP
2	C	7	LEU
2	C	50	ARG
2	C	52	ASP
2	C	90	ILE
2	C	113	GLU
2	C	116	ASP
2	C	117	ARG
2	C	245	THR
2	C	247	GLN
2	D	155	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	13	GLN
1	A	30	GLN
1	A	46	HIS
1	A	59	ASN
1	A	61	GLN
1	A	122	GLN
1	A	156	HIS
1	A	167	ASN
1	A	212	HIS
1	A	226	HIS
1	A	230	HIS
1	A	260	GLN
1	A	265	ASN
1	A	322	HIS
1	A	329	GLN
1	A	360	HIS
1	A	371	GLN
1	A	386	GLN
1	B	13	GLN
1	B	31	GLN
1	B	46	HIS
1	B	115	GLN
1	B	122	GLN
1	B	135	GLN
1	B	206	ASN
1	B	210	ASN
1	B	226	HIS
1	B	262	ASN
1	B	265	ASN
1	B	329	GLN
1	B	348	GLN
1	B	371	GLN
1	B	386	GLN
1	B	387	GLN
1	B	416	GLN
2	C	8	HIS
2	C	30	HIS
2	C	36	ASN
2	C	95	ASN
2	C	96	GLN

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Mol	Chain	Res	Type
2	C	112	GLN
2	C	121	GLN
2	C	143	ASN
2	C	189	ASN
2	C	203	HIS
2	C	247	GLN
2	D	100	GLN
2	D	104	ASN
2	D	189	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
3	MES	C	2000	-	12,12,12	0.97	1 (8%)	15,16,16	1.02	0

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
3	MES	C	2000	-	-	0/6/14/14	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2000	MES	C8-S	3.08	1.81	1.77

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2000	MES	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

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	416/423 (98%)	0.46	35 (8%) 17 14	19, 30, 50, 83	0
1	B	414/423 (97%)	0.32	30 (7%) 21 18	17, 28, 51, 72	0
2	C	247/267 (92%)	0.75	41 (16%) 4 3	21, 35, 67, 84	0
2	D	42/267 (15%)	4.01	36 (85%) 0 0	55, 72, 92, 95	0
All	All	1119/1380 (81%)	0.61	142 (12%) 8 6	17, 31, 64, 95	0

All (142) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	422	ALA	14.2
1	A	422	ALA	11.4
2	D	183	VAL	9.9
2	D	184	VAL	9.1
2	D	185	ALA	9.1
2	C	118	PHE	8.8
2	D	86	TYR	8.1
2	D	193	ASP	7.6
2	D	106	VAL	7.6
2	C	246	GLU	6.6
1	B	22	GLY	5.8
2	D	164	PRO	5.8
1	B	421	GLY	5.6
2	C	114	THR	5.5
2	C	245	THR	5.5
2	D	188	VAL	5.5
2	D	156	ILE	5.5
2	D	157	LEU	5.2
2	D	186	ASP	5.1
2	C	247	GLN	5.1
2	D	187	GLY	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	22	GLY	5.0
1	A	423	ARG	4.8
1	A	23	THR	4.7
1	B	279	ASN	4.7
2	D	162	LEU	4.7
2	C	244	LEU	4.7
1	B	278	LYS	4.6
2	D	191	LEU	4.5
2	D	192	ARG	4.5
1	A	39	THR	4.4
2	C	119	ASP	4.2
2	D	155	ASP	4.1
1	A	421	GLY	4.1
1	A	420	GLY	4.0
2	D	87	PRO	4.0
2	D	161	VAL	3.9
2	D	160	ALA	3.9
2	C	115	LEU	3.9
2	C	120	PHE	3.9
1	B	306	SER	3.8
1	A	61	GLN	3.7
1	B	23	THR	3.7
2	C	206	ARG	3.7
1	B	21	GLU	3.6
1	A	20	ALA	3.6
2	C	117	ARG	3.6
2	C	113	GLU	3.6
2	C	112	GLN	3.5
1	A	164	GLU	3.5
2	D	88	VAL	3.4
1	A	58	ILE	3.4
1	A	322	HIS	3.3
2	D	190	SER	3.3
1	B	44	ARG	3.3
1	B	24	LYS	3.3
2	C	116	ASP	3.3
2	D	99	LEU	3.3
1	A	21	GLU	3.3
1	B	379	GLY	3.3
2	D	103	LEU	3.3
1	A	38	ARG	3.1
2	D	189	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	380	ILE	3.1
1	A	307	ASP	3.1
1	A	65	ILE	3.0
1	A	115	GLN	3.0
2	D	158	GLN	3.0
2	C	90	ILE	2.9
1	B	420	GLY	2.8
2	C	123	LEU	2.8
1	A	162	ALA	2.8
1	A	24	LYS	2.8
2	C	111	GLY	2.8
1	A	12	GLN	2.7
1	A	237	GLU	2.7
2	C	124	MET	2.7
1	A	57	LEU	2.7
2	C	52	ASP	2.7
1	B	307	ASP	2.7
1	A	367	ILE	2.7
1	A	56	GLY	2.6
2	D	105	ALA	2.6
1	A	59	ASN	2.6
2	D	90	ILE	2.6
1	A	19	GLU	2.6
1	A	383	GLN	2.6
2	C	238	GLU	2.6
1	B	39	THR	2.6
2	C	211	ILE	2.6
1	A	66	ALA	2.5
2	D	101	THR	2.5
2	C	130	LEU	2.5
2	C	178	ILE	2.5
2	C	129	ALA	2.5
2	D	95	ASN	2.5
2	C	51	GLU	2.5
2	D	97	PHE	2.5
2	C	179	ASP	2.5
2	D	91	PRO	2.5
1	B	367	ILE	2.4
1	B	9	ASN	2.4
1	A	76	ALA	2.4
1	A	60	SER	2.4
1	B	143	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
2	C	182	LYS	2.4
2	C	131	LEU	2.4
2	C	138	LEU	2.4
2	C	110	ARG	2.4
1	A	68	GLU	2.4
2	C	135	GLU	2.4
2	C	128	ILE	2.4
1	B	38	ARG	2.4
1	B	179	GLU	2.4
2	C	137	LEU	2.3
2	D	104	ASN	2.3
1	B	338	GLY	2.3
2	C	121	GLN	2.3
1	A	67	GLY	2.3
1	B	374	TYR	2.3
1	A	321	GLN	2.3
2	C	175	GLY	2.3
1	B	144	ARG	2.3
1	B	368	ASP	2.2
1	A	163	GLY	2.2
2	D	92	GLY	2.2
1	B	65	ILE	2.2
2	C	122	ASP	2.2
2	D	102	ALA	2.2
1	B	373	PHE	2.2
1	B	419	PRO	2.2
2	C	10	SER	2.2
1	B	265	ASN	2.2
2	D	93	VAL	2.1
1	B	370	GLU	2.1
2	C	126	GLU	2.1
1	A	8	SER	2.1
1	B	381	ASN	2.1
2	D	94	SER	2.1
2	C	134	PRO	2.1
2	C	14	LYS	2.0
2	C	205	GLN	2.0

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

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($\text{\AA}^2$)	Q<0.9
3	MES	C	2000	12/12	0.81	0.24	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.