



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:26 AM UTC

PDB ID : 1BDF / pdb\_00001bdf  
Title : STRUCTURE OF ESCHERICHIA COLI RNA POLYMERASE ALPHA  
SUBUNIT N-TERMINAL DOMAIN  
Authors : Zhang, G.; Darst, S.A.  
Deposited on : 1998-05-08  
Resolution : 2.50 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

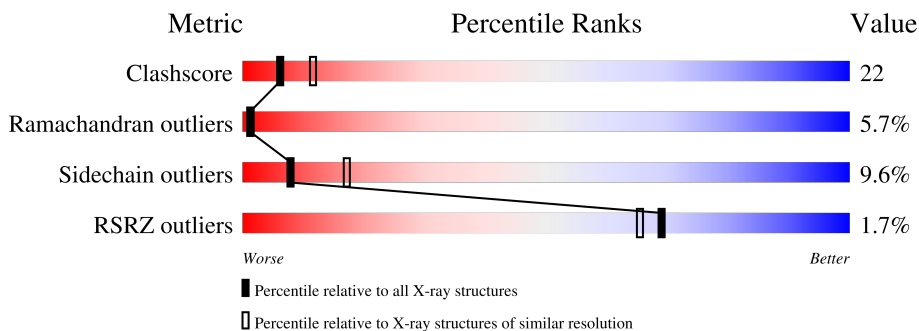
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


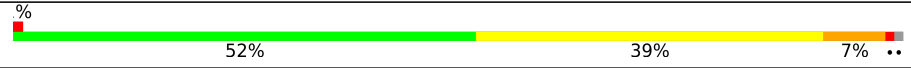

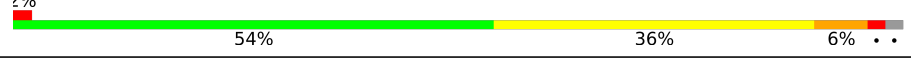
The reported resolution of this entry is 2.50 Å.

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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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  $\geq 3$ , 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	235	
1	B	235	
1	C	235	
1	D	235	

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7179 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 RNA POLYMERASE ALPHA SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	226	Total 1710	C 1069	N 299	O 336	S 6	7	0	0
1	B	232	Total 1762	C 1098	N 310	O 347	S 7	0	0	0
1	C	228	Total 1721	C 1074	N 300	O 340	S 7	16	0	0
1	D	231	Total 1747	C 1092	N 304	O 344	S 7	24	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	45	ALA	ARG	engineered mutation	UNP P0A7Z4
B	45	ALA	ARG	engineered mutation	UNP P0A7Z4
C	45	ALA	ARG	engineered mutation	UNP P0A7Z4
D	45	ALA	ARG	engineered mutation	UNP P0A7Z4

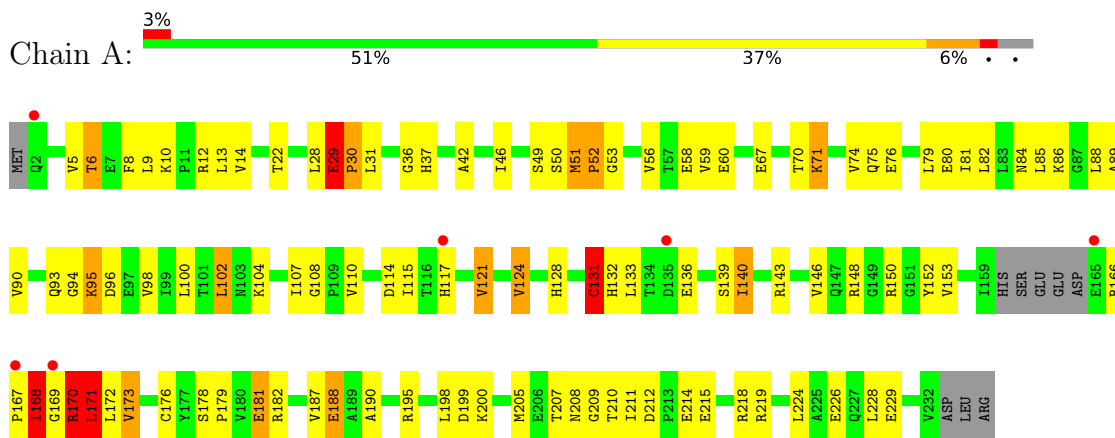
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	63	Total 63	O 63	0	0
2	B	61	Total 61	O 61	0	0
2	C	49	Total 49	O 49	0	0
2	D	66	Total 66	O 66	0	0

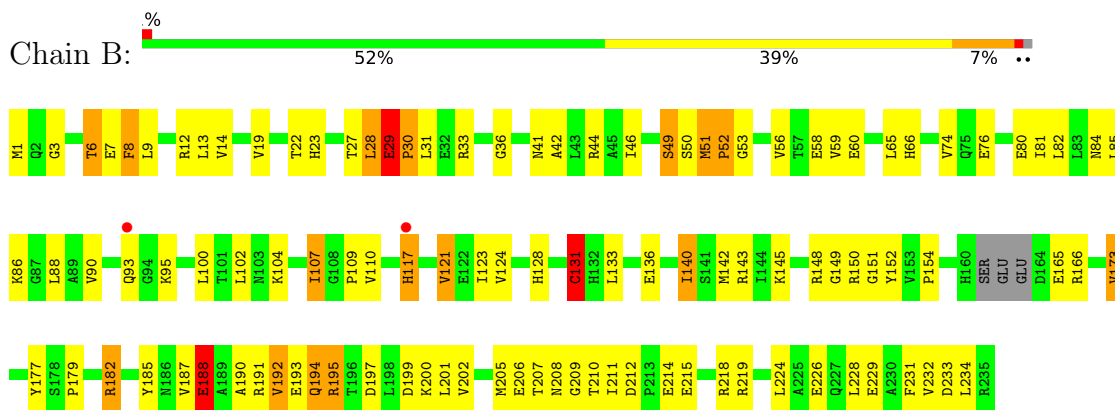
### 3 Residue-property plots [i](#)

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.

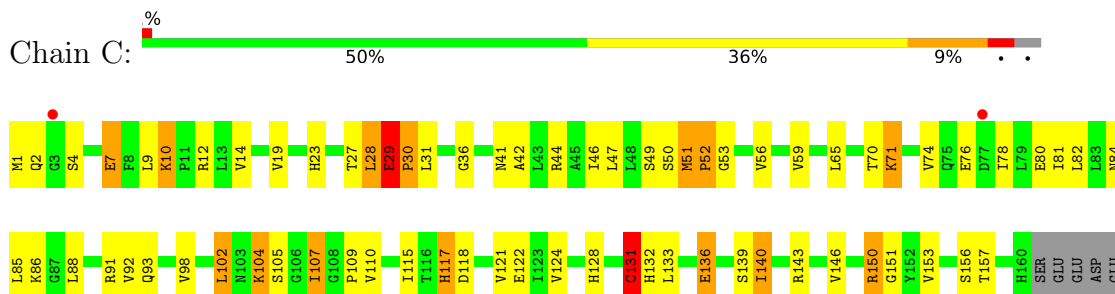
#### • Molecule 1: RNA POLYMERASE ALPHA SUBUNIT



#### • Molecule 1: RNA POLYMERASE ALPHA SUBUNIT

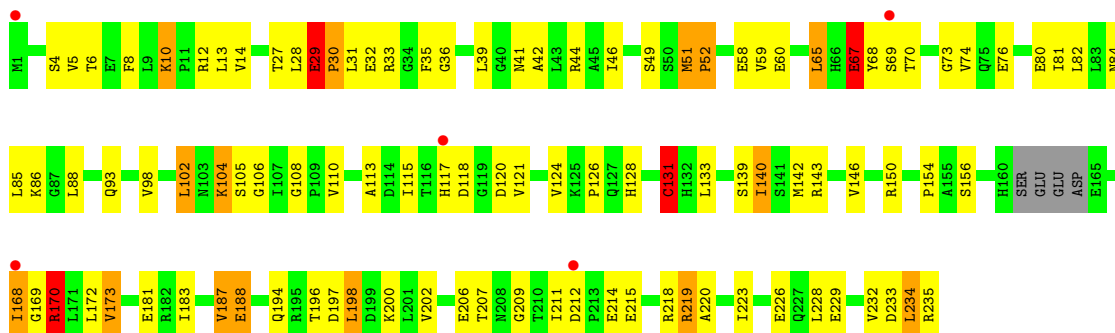


#### • Molecule 1: RNA POLYMERASE ALPHA SUBUNIT





● Molecule 1: RNA POLYMERASE ALPHA SUBUNIT



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	117.20Å 117.20Å 350.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 2.50 6.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	78.4 (6.00-2.50) 78.0 (6.00-2.50)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.98 (at 2.51Å)	Xtrriage
Refinement program	X-PLOR 3.8	Depositor
R, $R_{free}$	0.225 , 0.308 0.237 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.6	Xtrriage
Anisotropy	0.489	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 109.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	7179	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 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	0.53	0/1729	1.11	16/2345 (0.7%)
1	B	0.55	0/1781	1.05	10/2413 (0.4%)
1	C	0.57	0/1740	1.09	11/2358 (0.5%)
1	D	0.57	1/1767 (0.1%)	1.08	13/2396 (0.5%)
All	All	0.56	1/7017 (0.0%)	1.08	50/9512 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	51	MET	SD-CE	-5.95	1.64	1.79

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	219	ARG	NE-CZ-NH2	-9.79	110.39	119.20
1	C	219	ARG	CD-NE-CZ	8.84	136.78	124.40
1	C	53	GLY	N-CA-C	8.71	122.04	112.29
1	C	219	ARG	NE-CZ-NH1	8.37	129.87	121.50
1	A	29	GLU	N-CA-C	7.62	126.65	109.81
1	B	29	GLU	N-CA-C	7.58	126.57	109.81
1	D	29	GLU	N-CA-C	7.58	126.56	109.81
1	C	29	GLU	N-CA-C	7.44	126.25	109.81
1	A	171	LEU	N-CA-C	6.98	125.67	110.80
1	A	153	VAL	CA-C-N	6.94	128.52	119.84
1	A	153	VAL	C-N-CA	6.94	128.52	119.84
1	A	70	THR	N-CA-C	-6.93	98.78	109.52
1	D	124	VAL	N-CA-C	6.79	116.94	110.42
1	B	124	VAL	N-CA-C	6.75	116.91	110.42
1	A	167	PRO	N-CA-CB	6.66	110.37	102.85
1	A	124	VAL	N-CA-C	6.48	116.64	110.42
1	A	71	LYS	N-CA-C	6.47	119.94	109.40
1	A	170	ARG	N-CA-C	6.23	117.76	107.73
1	D	187	VAL	N-CA-C	6.03	117.97	111.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	124	VAL	N-CA-C	5.96	116.14	110.42
1	C	51	MET	CA-C-N	5.89	127.20	119.84
1	C	51	MET	C-N-CA	5.89	127.20	119.84
1	D	68	TYR	N-CA-C	5.88	118.35	107.99
1	A	28	LEU	N-CA-C	-5.88	99.65	109.24
1	B	3	GLY	N-CA-C	-5.83	107.10	114.16
1	D	170	ARG	N-CA-C	5.77	117.26	110.97
1	A	51	MET	CA-C-N	5.71	126.97	119.84
1	A	51	MET	C-N-CA	5.71	126.97	119.84
1	A	108	GLY	CA-C-N	5.60	125.36	119.76
1	A	108	GLY	C-N-CA	5.60	125.36	119.76
1	A	131	CYS	N-CA-C	5.47	116.28	108.74
1	D	131	CYS	N-CA-C	5.45	116.26	108.74
1	B	131	CYS	N-CA-C	5.41	116.21	108.74
1	D	51	MET	CA-C-N	5.41	126.60	119.84
1	D	51	MET	C-N-CA	5.41	126.60	119.84
1	C	131	CYS	N-CA-C	5.36	116.14	108.74
1	C	151	GLY	N-CA-C	5.36	120.05	110.95
1	C	28	LEU	N-CA-C	-5.34	100.53	109.24
1	B	28	LEU	N-CA-C	-5.28	100.64	109.24
1	B	51	MET	CA-C-N	5.22	126.36	119.84
1	B	51	MET	C-N-CA	5.22	126.36	119.84
1	B	188	GLU	N-CA-C	5.21	121.90	110.80
1	D	6	THR	CB-CA-C	-5.21	109.57	117.07
1	B	193	GLU	N-CA-C	5.20	117.62	111.33
1	D	219	ARG	N-CA-C	-5.15	107.13	113.41
1	A	121	VAL	N-CA-C	5.14	116.31	109.37
1	B	121	VAL	N-CA-C	5.14	117.24	109.12
1	D	108	GLY	CA-C-N	5.12	124.88	119.76
1	D	108	GLY	C-N-CA	5.12	124.88	119.76
1	D	28	LEU	N-CA-C	-5.05	101.01	109.24

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	1710	0	1721	80	0
1	B	1762	0	1779	83	0
1	C	1721	0	1725	92	0
1	D	1747	0	1758	76	0
2	A	63	0	0	1	0
2	B	61	0	0	3	0
2	C	49	0	0	3	0
2	D	66	0	0	1	0
All	All	7179	0	6983	310	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 (310) 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:59:VAL:HG21	1:C:85:LEU:HD13	1.38	1.00
1:C:110:VAL:HG21	1:C:140:ILE:HD11	1.43	0.98
1:A:59:VAL:HG21	1:A:85:LEU:HD13	1.50	0.94
1:B:110:VAL:HG21	1:B:140:ILE:HD11	1.48	0.92
1:A:110:VAL:HG21	1:A:140:ILE:HD11	1.57	0.86
1:D:10:LYS:H	1:D:10:LYS:HD3	1.46	0.80
1:D:110:VAL:HG21	1:D:140:ILE:HD11	1.65	0.78
1:C:233:ASP:HB2	1:D:218:ARG:NH1	1.99	0.78
1:B:152:TYR:CZ	1:B:154:PRO:HG3	2.20	0.77
1:B:59:VAL:HG21	1:B:85:LEU:HD13	1.68	0.75
1:A:100:LEU:HD21	1:A:121:VAL:HG21	1.70	0.73
1:C:50:SER:O	1:C:150:ARG:HD3	1.90	0.72
1:D:110:VAL:HB	1:D:131:CYS:HB2	1.72	0.71
1:A:95:LYS:HA	1:A:95:LYS:HE2	1.72	0.71
1:B:110:VAL:HB	1:B:131:CYS:HB2	1.73	0.71
1:A:53:GLY:HA3	1:A:179:PRO:HG3	1.73	0.70
1:A:168:ILE:HD12	1:A:168:ILE:H	1.55	0.70
1:D:86:LYS:HG2	1:D:173:VAL:CG2	2.22	0.70
1:D:59:VAL:HG21	1:D:85:LEU:HD13	1.74	0.70
1:C:1:MET:HG2	1:C:2:GLN:H	1.57	0.69
1:C:191:ARG:HH11	1:C:191:ARG:HB3	1.56	0.69
1:A:86:LYS:HG2	1:A:173:VAL:CG2	2.23	0.69
1:C:190:ALA:HB2	1:C:200:LYS:HB3	1.76	0.68
1:B:131:CYS:SG	1:B:140:ILE:HD13	2.34	0.68
1:C:153:VAL:HG22	1:C:177:TYR:HE2	1.59	0.68
1:B:51:MET:HE1	1:B:219:ARG:HB3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:HIS:NE2	1:C:12:ARG:NH2	2.42	0.67
1:A:107:ILE:HG13	1:A:136:GLU:HG3	1.75	0.67
1:C:51:MET:HE1	1:C:219:ARG:HB3	1.78	0.65
1:A:86:LYS:HG2	1:A:173:VAL:HG23	1.77	0.65
1:D:8:PHE:HD1	1:D:32:GLU:HG3	1.62	0.65
1:C:195:ARG:O	1:C:196:THR:HG23	1.97	0.64
1:C:191:ARG:HB3	1:C:191:ARG:NH1	2.13	0.63
1:B:152:TYR:CE2	1:B:154:PRO:HG3	2.33	0.63
1:C:10:LYS:HD2	1:C:10:LYS:O	1.99	0.62
1:C:182:ARG:HB3	1:C:206:GLU:HB3	1.82	0.62
1:B:100:LEU:HD21	1:B:121:VAL:HG21	1.82	0.62
1:D:229:GLU:HG2	1:D:234:LEU:HD13	1.80	0.62
1:C:107:ILE:HD12	1:C:107:ILE:N	2.15	0.61
1:C:110:VAL:HB	1:C:131:CYS:HB2	1.80	0.61
1:B:107:ILE:HG13	1:B:136:GLU:HG2	1.82	0.61
1:C:136:GLU:CD	1:C:136:GLU:H	2.08	0.61
1:C:235:ARG:HD2	2:C:252:HOH:O	2.01	0.61
1:B:107:ILE:CG1	1:B:136:GLU:HG2	2.30	0.60
1:C:153:VAL:HG22	1:C:177:TYR:CE2	2.37	0.60
1:D:234:LEU:HD12	1:D:234:LEU:H	1.65	0.60
1:B:56:VAL:HG12	1:B:173:VAL:HG11	1.83	0.60
1:A:60:GLU:HA	1:A:170:ARG:CG	2.32	0.59
1:A:53:GLY:CA	1:A:179:PRO:HG3	2.33	0.59
1:A:131:CYS:SG	1:A:140:ILE:HD13	2.42	0.59
1:A:22:THR:HB	1:A:207:THR:O	2.03	0.59
1:D:46:ILE:HG21	1:D:220:ALA:HA	1.85	0.59
1:D:8:PHE:CD1	1:D:32:GLU:HG3	2.38	0.58
1:B:82:LEU:O	1:B:86:LYS:HG3	2.02	0.58
1:B:226:GLU:HA	1:B:229:GLU:HG3	1.85	0.58
1:D:131:CYS:SG	1:D:140:ILE:HD13	2.44	0.58
1:A:110:VAL:HB	1:A:131:CYS:HB2	1.85	0.58
1:A:150:ARG:HE	1:B:7:GLU:HB2	1.69	0.58
1:B:12:ARG:NH2	1:C:117:HIS:NE2	2.51	0.58
1:B:31:LEU:HD13	1:B:36:GLY:HA2	1.86	0.58
1:C:233:ASP:HB2	1:D:218:ARG:HH11	1.64	0.58
1:B:33:ARG:HG2	1:B:197:ASP:O	2.04	0.58
1:C:226:GLU:HA	1:C:229:GLU:HG3	1.86	0.58
1:A:74:VAL:HG22	1:A:133:LEU:HD23	1.86	0.57
1:D:86:LYS:HG2	1:D:173:VAL:HG21	1.86	0.57
1:A:95:LYS:NZ	1:A:96:ASP:H	2.02	0.57
1:A:31:LEU:HD13	1:A:36:GLY:HA2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:ARG:NH2	1:B:6:THR:O	2.38	0.57
1:B:49:SER:HB3	2:B:240:HOH:O	2.05	0.57
1:D:31:LEU:HD13	1:D:36:GLY:HA2	1.86	0.57
1:C:31:LEU:HD13	1:C:36:GLY:HA2	1.87	0.56
1:C:82:LEU:O	1:C:86:LYS:HG3	2.05	0.56
1:C:7:GLU:HG2	1:D:150:ARG:HE	1.69	0.56
1:C:23:HIS:HB2	2:C:249:HOH:O	2.05	0.56
1:D:226:GLU:HA	1:D:229:GLU:HG3	1.86	0.56
1:A:226:GLU:HA	1:A:229:GLU:HG3	1.87	0.56
1:A:51:MET:HE1	1:A:219:ARG:HB3	1.87	0.55
1:B:50:SER:O	1:B:150:ARG:HD2	2.06	0.55
1:C:10:LYS:H	1:C:10:LYS:CD	2.17	0.55
1:A:82:LEU:O	1:A:86:LYS:HG3	2.07	0.55
1:D:106:GLY:O	1:D:133:LEU:HB2	2.07	0.55
1:B:182:ARG:HG3	1:B:206:GLU:HB3	1.88	0.55
1:A:94:GLY:O	1:A:95:LYS:HG2	2.07	0.55
1:C:232:VAL:HG13	1:D:218:ARG:HH22	1.71	0.55
1:D:82:LEU:O	1:D:86:LYS:HG3	2.06	0.55
1:B:190:ALA:H	1:B:199:ASP:HA	1.71	0.54
1:C:29:GLU:O	1:C:199:ASP:O	2.24	0.54
1:A:124:VAL:HG21	1:A:210:THR:HA	1.89	0.54
1:C:107:ILE:HD11	1:C:136:GLU:HB3	1.89	0.54
1:C:51:MET:O	1:C:150:ARG:HG2	2.08	0.54
1:C:71:LYS:HG3	1:C:78:ILE:HD11	1.90	0.54
1:A:74:VAL:HG11	1:A:81:ILE:HD11	1.90	0.54
1:A:228:LEU:HD11	1:B:224:LEU:HD23	1.90	0.54
1:C:56:VAL:HG12	1:C:173:VAL:HG11	1.90	0.53
1:D:74:VAL:HG22	1:D:133:LEU:HD23	1.90	0.53
1:A:90:VAL:CG1	1:A:121:VAL:HG13	2.39	0.53
1:A:89:ALA:HB1	1:A:210:THR:HG23	1.91	0.53
1:B:123:ILE:HG23	2:B:293:HOH:O	2.08	0.53
1:A:84:ASN:O	1:A:128:HIS:HE1	1.92	0.53
1:C:7:GLU:HG2	1:D:150:ARG:HH21	1.74	0.53
1:C:118:ASP:HB3	1:C:121:VAL:HB	1.90	0.53
1:A:60:GLU:HA	1:A:170:ARG:HG2	1.91	0.52
1:B:179:PRO:HB3	1:B:210:THR:OG1	2.09	0.52
1:A:52:PRO:O	1:A:179:PRO:HD3	2.08	0.52
1:C:227:GLN:HG3	1:D:35:PHE:CE1	2.44	0.52
1:D:27:THR:HG22	1:D:202:VAL:HG22	1.91	0.52
1:A:102:LEU:HG	1:A:115:ILE:HG12	1.92	0.52
1:B:6:THR:HA	1:B:8:PHE:CZ	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:ALA:H	1:A:199:ASP:HA	1.74	0.52
1:B:95:LYS:H	1:B:148:ARG:HH21	1.56	0.52
1:A:37:HIS:CE1	1:A:187:VAL:HG21	2.45	0.52
1:D:84:ASN:O	1:D:128:HIS:HE1	1.93	0.52
1:C:207:THR:OG1	1:C:211:ILE:HG22	2.10	0.52
1:B:207:THR:OG1	1:B:211:ILE:HG22	2.09	0.51
1:D:86:LYS:HE2	1:D:173:VAL:HG23	1.91	0.51
1:B:143:ARG:HD2	1:B:143:ARG:N	2.26	0.51
1:B:187:VAL:O	1:B:200:LYS:O	2.28	0.51
1:D:65:LEU:N	1:D:65:LEU:HD23	2.26	0.51
1:A:133:LEU:HD21	1:A:140:ILE:HG12	1.93	0.51
1:D:105:SER:HB3	1:D:139:SER:HB3	1.93	0.51
1:B:151:GLY:O	1:B:177:TYR:HB2	2.11	0.51
1:C:29:GLU:HG3	1:C:200:LYS:HB3	1.92	0.51
1:B:109:PRO:HA	1:B:131:CYS:O	2.11	0.50
1:D:74:VAL:HG11	1:D:81:ILE:HD11	1.92	0.50
1:A:143:ARG:N	1:A:143:ARG:HD2	2.27	0.50
1:D:58:GLU:HG2	1:D:172:LEU:CD2	2.41	0.50
1:A:89:ALA:HB1	1:A:210:THR:CG2	2.41	0.50
1:D:207:THR:OG1	1:D:211:ILE:HG22	2.11	0.50
1:B:194:GLN:N	1:B:194:GLN:CD	2.70	0.50
1:C:28:LEU:HD12	1:C:201:LEU:HD23	1.94	0.50
1:C:92:VAL:HG22	1:C:121:VAL:HG22	1.94	0.50
1:D:143:ARG:HD2	1:D:143:ARG:N	2.26	0.50
1:B:29:GLU:O	1:B:31:LEU:N	2.45	0.50
1:C:74:VAL:HG11	1:C:81:ILE:HD11	1.94	0.50
1:B:74:VAL:HG11	1:B:81:ILE:HD11	1.92	0.50
1:C:7:GLU:HG2	1:D:150:ARG:NE	2.27	0.50
1:C:228:LEU:HD21	1:D:39:LEU:HD22	1.93	0.50
1:C:27:THR:HA	1:C:201:LEU:O	2.12	0.49
1:C:224:LEU:HD23	1:D:228:LEU:HD11	1.93	0.49
1:D:76:GLU:HB2	1:D:80:GLU:HB2	1.94	0.49
1:D:110:VAL:HB	1:D:131:CYS:CB	2.39	0.49
1:A:170:ARG:HB2	1:A:171:LEU:HG	1.93	0.49
1:A:152:TYR:CD1	1:A:176:CYS:HA	2.47	0.49
1:A:56:VAL:HG12	1:A:173:VAL:HG11	1.93	0.49
1:D:33:ARG:HG2	1:D:197:ASP:OD2	2.12	0.49
1:A:187:VAL:O	1:A:188:GLU:O	2.30	0.49
1:D:29:GLU:HG3	1:D:200:LYS:HB3	1.94	0.49
1:D:170:ARG:HE	1:D:170:ARG:HA	1.78	0.49
1:B:229:GLU:HA	1:B:232:VAL:HG22	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:143:ARG:N	1:C:143:ARG:HD2	2.27	0.49
1:A:207:THR:OG1	1:A:211:ILE:HG22	2.13	0.49
1:C:76:GLU:HB2	1:C:80:GLU:HB2	1.95	0.49
1:D:197:ASP:O	1:D:198:LEU:O	2.29	0.49
1:B:86:LYS:HD3	2:B:241:HOH:O	2.13	0.49
1:C:187:VAL:O	1:C:188:GLU:O	2.30	0.49
1:C:27:THR:HG22	1:C:202:VAL:HG22	1.94	0.48
1:D:51:MET:O	1:D:150:ARG:HG2	2.13	0.48
1:A:67:GLU:HB2	1:A:79:LEU:HD21	1.96	0.48
1:B:107:ILE:HB	1:C:193:GLU:OE1	2.13	0.48
1:B:90:VAL:HG13	1:B:121:VAL:HG13	1.96	0.48
1:A:71:LYS:NZ	1:A:139:SER:O	2.47	0.48
1:D:187:VAL:O	1:D:188:GLU:O	2.31	0.48
1:B:29:GLU:O	1:B:199:ASP:O	2.32	0.48
1:A:9:LEU:HD12	1:A:198:LEU:HD21	1.95	0.48
1:B:27:THR:HG22	1:B:202:VAL:HG22	1.96	0.47
1:C:98:VAL:HG12	1:C:146:VAL:HB	1.95	0.47
1:B:23:HIS:HA	1:B:205:MET:O	2.14	0.47
1:D:76:GLU:CD	1:D:76:GLU:H	2.23	0.47
1:C:29:GLU:O	1:C:31:LEU:N	2.46	0.47
1:D:181:GLU:HB2	1:D:206:GLU:O	2.15	0.47
1:A:187:VAL:O	1:A:200:LYS:O	2.31	0.47
1:A:214:GLU:O	1:A:218:ARG:HG3	2.15	0.47
1:B:53:GLY:HA3	1:B:179:PRO:HD3	1.97	0.47
1:C:107:ILE:HD11	1:C:136:GLU:CB	2.44	0.47
1:B:212:ASP:HB2	1:B:215:GLU:HG2	1.97	0.47
1:A:90:VAL:HG13	1:A:121:VAL:HG13	1.95	0.47
1:C:190:ALA:H	1:C:199:ASP:HA	1.78	0.47
1:D:214:GLU:O	1:D:218:ARG:HG3	2.15	0.47
1:D:44:ARG:HG3	1:D:183:ILE:HB	1.96	0.47
1:C:105:SER:HB3	1:C:139:SER:HB3	1.97	0.47
1:C:110:VAL:HB	1:C:131:CYS:CB	2.45	0.47
1:D:29:GLU:O	1:D:31:LEU:N	2.48	0.46
1:D:29:GLU:HB3	1:D:30:PRO:HD3	1.97	0.46
1:C:86:LYS:HG2	1:C:173:VAL:HG23	1.95	0.46
1:A:212:ASP:HB2	1:A:215:GLU:HG2	1.97	0.46
1:A:152:TYR:CE1	1:A:178:SER:HB3	2.51	0.46
1:B:52:PRO:HA	1:B:149:GLY:O	2.15	0.46
1:C:74:VAL:HG22	1:C:133:LEU:HD23	1.96	0.46
1:C:153:VAL:HG23	1:C:153:VAL:O	2.15	0.46
1:A:98:VAL:HG12	1:A:146:VAL:HB	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ILE:HG22	1:A:169:GLY:H	1.80	0.46
1:C:190:ALA:HB2	1:C:200:LYS:CB	2.44	0.46
1:C:214:GLU:O	1:C:218:ARG:HG3	2.15	0.46
1:C:233:ASP:N	1:D:218:ARG:HH12	2.14	0.46
1:B:84:ASN:O	1:B:128:HIS:HE1	1.99	0.46
1:B:228:LEU:O	1:B:232:VAL:HG13	2.15	0.46
1:D:102:LEU:HG	1:D:115:ILE:HG12	1.97	0.46
1:B:28:LEU:HD12	1:B:201:LEU:HD23	1.98	0.46
1:C:175:ALA:HA	2:C:241:HOH:O	2.16	0.46
1:D:212:ASP:HB2	1:D:215:GLU:HG2	1.98	0.46
1:D:228:LEU:O	1:D:232:VAL:HG23	2.16	0.46
1:A:80:GLU:HB3	2:A:294:HOH:O	2.15	0.45
1:C:42:ALA:O	1:C:46:ILE:HG12	2.16	0.45
1:C:109:PRO:HA	1:C:131:CYS:O	2.16	0.45
1:B:29:GLU:HB3	1:B:30:PRO:HD3	1.98	0.45
1:C:76:GLU:CD	1:C:76:GLU:H	2.25	0.45
1:B:149:GLY:HA3	1:B:177:TYR:CD1	2.52	0.45
1:D:187:VAL:O	1:D:200:LYS:O	2.35	0.45
1:A:181:GLU:OE2	1:A:208:ASN:HB3	2.17	0.45
1:C:212:ASP:HB2	1:C:215:GLU:HG2	1.99	0.45
1:A:58:GLU:HG2	1:A:172:LEU:CD2	2.47	0.45
1:B:76:GLU:HB2	1:B:80:GLU:HB2	1.99	0.45
1:C:131:CYS:SG	1:C:140:ILE:HD13	2.56	0.45
1:D:51:MET:HA	1:D:52:PRO:HD3	1.77	0.45
1:D:154:PRO:C	1:D:156:SER:H	2.25	0.45
1:B:42:ALA:O	1:B:46:ILE:HG12	2.16	0.45
1:A:29:GLU:O	1:A:31:LEU:N	2.50	0.45
1:C:133:LEU:HD21	1:C:140:ILE:HG12	1.99	0.45
1:D:42:ALA:O	1:D:46:ILE:HG12	2.17	0.45
1:A:42:ALA:O	1:A:46:ILE:HG12	2.17	0.45
1:C:10:LYS:CD	1:C:10:LYS:N	2.80	0.45
1:C:65:LEU:O	1:C:169:GLY:HA2	2.17	0.45
1:A:76:GLU:H	1:A:76:GLU:CD	2.25	0.44
1:B:53:GLY:HA3	1:B:177:TYR:O	2.17	0.44
1:A:10:LYS:N	1:A:10:LYS:HD2	2.33	0.44
1:B:22:THR:HB	1:B:207:THR:O	2.17	0.44
1:B:190:ALA:HB2	1:B:200:LYS:HB3	1.98	0.44
1:C:7:GLU:HG2	1:D:150:ARG:NH2	2.32	0.44
1:C:205:MET:HE3	1:C:205:MET:HB2	1.83	0.44
1:A:205:MET:HE3	1:A:205:MET:HB2	1.78	0.44
1:B:182:ARG:HG3	1:B:206:GLU:CB	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:LEU:CD1	1:A:198:LEU:HD11	2.48	0.44
1:B:27:THR:HA	1:B:201:LEU:O	2.16	0.44
1:B:187:VAL:O	1:B:188:GLU:O	2.36	0.44
1:B:194:GLN:HG2	1:B:195:ARG:H	1.81	0.44
1:B:76:GLU:CD	1:B:76:GLU:H	2.25	0.44
1:B:166:ARG:O	1:B:166:ARG:HG3	2.17	0.44
1:C:190:ALA:O	1:C:192:VAL:N	2.50	0.44
1:B:65:LEU:HG	1:B:66:HIS:H	1.83	0.44
1:A:224:LEU:HD23	1:B:228:LEU:HD11	1.99	0.43
1:A:56:VAL:HG12	1:A:173:VAL:CG1	2.48	0.43
1:A:76:GLU:HB2	1:A:80:GLU:HB2	2.00	0.43
1:B:65:LEU:HD23	1:B:65:LEU:H	1.82	0.43
1:D:98:VAL:HG12	1:D:146:VAL:HB	2.00	0.43
1:A:12:ARG:HA	1:B:231:PHE:CE1	2.53	0.43
1:B:29:GLU:O	1:B:30:PRO:C	2.60	0.43
1:C:102:LEU:HG	1:C:115:ILE:HG12	2.01	0.43
1:A:29:GLU:HB3	1:A:30:PRO:HD3	1.99	0.43
1:A:84:ASN:O	1:A:128:HIS:CE1	2.70	0.43
1:B:207:THR:HG23	1:B:209:GLY:H	1.84	0.43
1:A:171:LEU:H	1:A:171:LEU:HD23	1.84	0.43
1:C:46:ILE:HG21	1:C:220:ALA:HA	2.01	0.43
1:D:73:GLY:O	1:D:133:LEU:HA	2.18	0.43
1:B:6:THR:OG1	1:B:7:GLU:N	2.51	0.43
1:B:214:GLU:O	1:B:218:ARG:HG3	2.19	0.43
1:A:8:PHE:O	1:A:10:LYS:HD2	2.18	0.42
1:D:10:LYS:HD3	1:D:10:LYS:N	2.22	0.42
1:D:67:GLU:CD	1:D:67:GLU:H	2.27	0.42
1:C:109:PRO:HB3	1:C:132:HIS:NE2	2.34	0.42
1:A:86:LYS:CG	1:A:173:VAL:HG23	2.45	0.42
1:D:51:MET:HE1	1:D:219:ARG:HB3	2.01	0.42
1:C:91:ARG:HB3	1:C:122:GLU:HB3	2.01	0.42
1:D:46:ILE:CG2	1:D:223:ILE:HD12	2.49	0.42
1:D:168:ILE:HG22	1:D:169:GLY:N	2.35	0.42
1:B:41:ASN:ND2	1:B:44:ARG:NH2	2.68	0.42
1:B:208:ASN:OD1	1:B:208:ASN:C	2.62	0.42
1:A:102:LEU:HD21	1:A:114:ASP:HB2	2.01	0.42
1:A:190:ALA:HB2	1:A:200:LYS:HB3	2.02	0.42
1:C:51:MET:HA	1:C:52:PRO:HD3	1.76	0.42
1:D:113:ALA:HB2	1:D:126:PRO:HB2	2.02	0.42
1:C:231:PHE:CE1	1:D:12:ARG:HA	2.54	0.42
1:D:168:ILE:HG21	1:D:170:ARG:NH2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ILE:HD12	1:A:168:ILE:N	2.31	0.41
1:C:84:ASN:O	1:C:128:HIS:HE1	2.03	0.41
1:A:51:MET:HA	1:A:52:PRO:HD3	1.75	0.41
1:C:207:THR:HG23	1:C:209:GLY:H	1.86	0.41
1:D:104:LYS:O	1:D:139:SER:HA	2.21	0.41
1:C:47:LEU:HD21	1:C:216:ALA:O	2.21	0.41
1:B:74:VAL:HG22	1:B:133:LEU:HD23	2.01	0.41
1:C:19:VAL:HB	1:C:23:HIS:ND1	2.35	0.41
1:C:104:LYS:O	1:C:139:SER:HA	2.20	0.41
1:B:56:VAL:HG12	1:B:173:VAL:CG1	2.50	0.41
1:B:190:ALA:O	1:B:192:VAL:N	2.52	0.41
1:D:41:ASN:ND2	1:D:44:ARG:NH2	2.68	0.41
1:A:207:THR:HG23	1:A:209:GLY:H	1.86	0.41
1:B:194:GLN:NE2	1:C:107:ILE:HD13	2.35	0.41
1:B:131:CYS:SG	1:B:140:ILE:CD1	3.05	0.41
1:C:29:GLU:O	1:C:30:PRO:C	2.62	0.41
1:D:118:ASP:HB3	1:D:121:VAL:HB	2.03	0.41
1:D:234:LEU:HD12	1:D:234:LEU:N	2.35	0.41
1:A:50:SER:O	1:A:150:ARG:NH1	2.54	0.41
1:A:181:GLU:C	1:A:182:ARG:HG2	2.45	0.41
1:C:107:ILE:HD12	1:C:107:ILE:H	1.83	0.41
1:B:58:GLU:OE1	1:B:145:LYS:HD2	2.21	0.40
1:D:229:GLU:HB3	1:D:234:LEU:O	2.21	0.40
1:A:75:GLN:HB3	1:A:132:HIS:HB2	2.03	0.40
1:B:19:VAL:HB	1:B:23:HIS:ND1	2.36	0.40
1:B:185:TYR:HA	1:B:202:VAL:O	2.22	0.40
1:C:31:LEU:HD11	1:C:201:LEU:HB2	2.04	0.40
1:C:187:VAL:O	1:C:200:LYS:O	2.39	0.40
1:A:67:GLU:HB2	1:A:79:LEU:CD2	2.50	0.40
1:B:60:GLU:O	1:B:142:MET:HA	2.22	0.40
1:B:194:GLN:CD	1:B:194:GLN:H	2.30	0.40
1:D:30:PRO:HG2	2:D:291:HOH:O	2.22	0.40
1:A:95:LYS:O	1:A:148:ARG:NH2	2.54	0.40
1:C:41:ASN:ND2	1:C:44:ARG:NH2	2.69	0.40
1:B:133:LEU:HD21	1:B:140:ILE:HG12	2.04	0.40
1:C:91:ARG:NH2	1:C:209:GLY:O	2.54	0.40
1:D:60:GLU:O	1:D:142:MET:HA	2.21	0.40
1:D:207:THR:HG23	1:D:209:GLY:H	1.87	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	222/235 (94%)	192 (86%)	19 (9%)	11 (5%)	1	2
1	B	228/235 (97%)	196 (86%)	22 (10%)	10 (4%)	2	2
1	C	224/235 (95%)	192 (86%)	17 (8%)	15 (7%)	1	1
1	D	227/235 (97%)	192 (85%)	20 (9%)	15 (7%)	1	1
All	All	901/940 (96%)	772 (86%)	78 (9%)	51 (6%)	1	1

All (51) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	6	THR
1	A	52	PRO
1	A	93	GLN
1	A	171	LEU
1	A	188	GLU
1	B	52	PRO
1	B	93	GLN
1	B	188	GLU
1	C	52	PRO
1	C	188	GLU
1	C	191	ARG
1	D	52	PRO
1	D	69	SER
1	D	188	GLU
1	D	194	GLN
1	D	198	LEU
1	A	5	VAL
1	A	168	ILE
1	B	6	THR
1	B	191	ARG
1	C	93	GLN
1	C	157	THR

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Mol	Chain	Res	Type
1	C	194	GLN
1	C	196	THR
1	C	233	ASP
1	D	4	SER
1	D	233	ASP
1	A	166	ARG
1	D	67	GLU
1	D	93	GLN
1	A	29	GLU
1	B	29	GLU
1	B	49	SER
1	B	195	ARG
1	B	233	ASP
1	C	29	GLU
1	C	49	SER
1	D	5	VAL
1	D	29	GLU
1	D	49	SER
1	D	168	ILE
1	A	49	SER
1	C	156	SER
1	C	195	ARG
1	C	232	VAL
1	A	30	PRO
1	C	4	SER
1	D	30	PRO
1	D	70	THR
1	B	30	PRO
1	C	30	PRO

### 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	185/201 (92%)	170 (92%)	15 (8%)	<b>11</b> <b>23</b>
1	B	191/201 (95%)	173 (91%)	18 (9%)	<b>8</b> <b>18</b>

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	185/201 (92%)	163 (88%)	22 (12%)	5	11
1	D	189/201 (94%)	172 (91%)	17 (9%)	9	19
All	All	750/804 (93%)	678 (90%)	72 (10%)	8	17

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	THR
1	A	13	LEU
1	A	14	VAL
1	A	88	LEU
1	A	95	LYS
1	A	102	LEU
1	A	104	LYS
1	A	117	HIS
1	A	131	CYS
1	A	140	ILE
1	A	168	ILE
1	A	170	ARG
1	A	173	VAL
1	A	181	GLU
1	A	195	ARG
1	B	1	MET
1	B	8	PHE
1	B	9	LEU
1	B	13	LEU
1	B	14	VAL
1	B	88	LEU
1	B	102	LEU
1	B	104	LYS
1	B	107	ILE
1	B	117	HIS
1	B	131	CYS
1	B	140	ILE
1	B	165	GLU
1	B	173	VAL
1	B	182	ARG
1	B	192	VAL
1	B	194	GLN
1	B	234	LEU
1	C	7	GLU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	9	LEU
1	C	10	LYS
1	C	14	VAL
1	C	70	THR
1	C	71	LYS
1	C	88	LEU
1	C	102	LEU
1	C	104	LYS
1	C	107	ILE
1	C	117	HIS
1	C	131	CYS
1	C	136	GLU
1	C	140	ILE
1	C	150	ARG
1	C	173	VAL
1	C	191	ARG
1	C	193	GLU
1	C	196	THR
1	C	219	ARG
1	C	232	VAL
1	C	235	ARG
1	D	10	LYS
1	D	13	LEU
1	D	14	VAL
1	D	65	LEU
1	D	67	GLU
1	D	88	LEU
1	D	102	LEU
1	D	104	LYS
1	D	117	HIS
1	D	120	ASP
1	D	131	CYS
1	D	140	ILE
1	D	170	ARG
1	D	173	VAL
1	D	196	THR
1	D	234	LEU
1	D	235	ARG

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	128	HIS
1	A	137	ASN
1	A	194	GLN
1	B	2	GLN
1	B	75	GLN
1	B	128	HIS
1	B	186	ASN
1	C	37	HIS
1	C	41	ASN
1	C	66	HIS
1	C	75	GLN
1	C	103	ASN
1	C	128	HIS
1	C	132	HIS
1	D	37	HIS
1	D	41	ASN
1	D	75	GLN
1	D	128	HIS
1	D	147	GLN

### 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](#)

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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	225/235 (95%)	-0.18	6 (2%) 56 51	4, 23, 59, 76	0
1	B	232/235 (98%)	-0.16	2 (0%) 81 78	3, 23, 55, 73	0
1	C	225/235 (95%)	-0.22	2 (0%) 81 78	3, 20, 49, 59	1 (0%)
1	D	227/235 (96%)	-0.15	5 (2%) 62 58	6, 21, 57, 70	1 (0%)
All	All	909/940 (96%)	-0.18	15 (1%) 69 65	3, 22, 55, 76	2 (0%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	169	GLY	6.6
1	A	2	GLN	3.5
1	D	1	MET	2.8
1	D	212	ASP	2.5
1	B	93	GLN	2.3
1	A	167	PRO	2.3
1	D	69	SER	2.2
1	C	3	GLY	2.2
1	A	165	GLU	2.2
1	B	117	HIS	2.1
1	D	117	HIS	2.1
1	C	77	ASP	2.1
1	D	168	ILE	2.0
1	A	117	HIS	2.0
1	A	135	ASP	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.