



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:46 AM GMT

PDB ID : 3PZV  
Title : C2 crystal form of the endo-1,4-beta-glucanase from Bacillus subtilis 168  
Authors : Santos, C.R.; Paiva, J.H.; Akao, P.K.; Meza, A.N.; Silva, J.C.; Squina, F.M.;  
Ward, R.J.; Ruller, R.; Murakami, M.T.  
Deposited on : 2010-12-14  
Resolution : 2.87 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

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

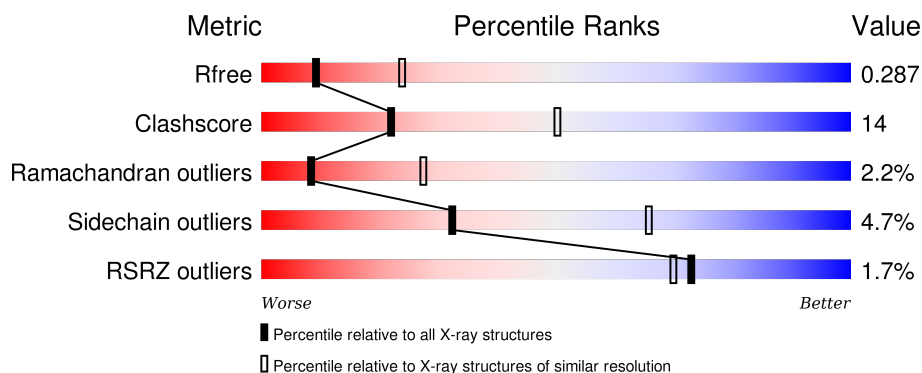
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.87 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	327	<div> <div></div> <div>71% 19% • 9%</div> </div>
1	B	327	<div> <div></div> <div>72% 18% • 9%</div> </div>
1	C	327	<div> <div>2%</div> <div>54% 31% 5% 9%</div> </div>
1	D	327	<div> <div>3%</div> <div>54% 33% • 9%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9398 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 Endoglucanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2342	1482	402	455	3			
1	B	298	Total	C	N	O	S	0	0	0
			2342	1482	402	455	3			
1	C	298	Total	C	N	O	S	0	0	0
			2342	1482	402	455	3			
1	D	298	Total	C	N	O	S	0	0	0
			2342	1482	402	455	3			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	MET	-	EXPRESSION TAG	UNP P10475
A	7	GLY	-	EXPRESSION TAG	UNP P10475
A	8	SER	-	EXPRESSION TAG	UNP P10475
A	9	SER	-	EXPRESSION TAG	UNP P10475
A	10	HIS	-	EXPRESSION TAG	UNP P10475
A	11	HIS	-	EXPRESSION TAG	UNP P10475
A	12	HIS	-	EXPRESSION TAG	UNP P10475
A	13	HIS	-	EXPRESSION TAG	UNP P10475
A	14	HIS	-	EXPRESSION TAG	UNP P10475
A	15	HIS	-	EXPRESSION TAG	UNP P10475
A	16	SER	-	EXPRESSION TAG	UNP P10475
A	17	SER	-	EXPRESSION TAG	UNP P10475
A	18	GLY	-	EXPRESSION TAG	UNP P10475
A	19	LEU	-	EXPRESSION TAG	UNP P10475
A	20	VAL	-	EXPRESSION TAG	UNP P10475
A	21	PRO	-	EXPRESSION TAG	UNP P10475
A	22	ARG	-	EXPRESSION TAG	UNP P10475
A	23	GLY	-	EXPRESSION TAG	UNP P10475
A	24	SER	-	EXPRESSION TAG	UNP P10475
A	25	HIS	-	EXPRESSION TAG	UNP P10475
A	26	MET	-	EXPRESSION TAG	UNP P10475

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Chain	Residue	Modelled	Actual	Comment	Reference
B	6	MET	-	EXPRESSION TAG	UNP P10475
B	7	GLY	-	EXPRESSION TAG	UNP P10475
B	8	SER	-	EXPRESSION TAG	UNP P10475
B	9	SER	-	EXPRESSION TAG	UNP P10475
B	10	HIS	-	EXPRESSION TAG	UNP P10475
B	11	HIS	-	EXPRESSION TAG	UNP P10475
B	12	HIS	-	EXPRESSION TAG	UNP P10475
B	13	HIS	-	EXPRESSION TAG	UNP P10475
B	14	HIS	-	EXPRESSION TAG	UNP P10475
B	15	HIS	-	EXPRESSION TAG	UNP P10475
B	16	SER	-	EXPRESSION TAG	UNP P10475
B	17	SER	-	EXPRESSION TAG	UNP P10475
B	18	GLY	-	EXPRESSION TAG	UNP P10475
B	19	LEU	-	EXPRESSION TAG	UNP P10475
B	20	VAL	-	EXPRESSION TAG	UNP P10475
B	21	PRO	-	EXPRESSION TAG	UNP P10475
B	22	ARG	-	EXPRESSION TAG	UNP P10475
B	23	GLY	-	EXPRESSION TAG	UNP P10475
B	24	SER	-	EXPRESSION TAG	UNP P10475
B	25	HIS	-	EXPRESSION TAG	UNP P10475
B	26	MET	-	EXPRESSION TAG	UNP P10475
C	6	MET	-	EXPRESSION TAG	UNP P10475
C	7	GLY	-	EXPRESSION TAG	UNP P10475
C	8	SER	-	EXPRESSION TAG	UNP P10475
C	9	SER	-	EXPRESSION TAG	UNP P10475
C	10	HIS	-	EXPRESSION TAG	UNP P10475
C	11	HIS	-	EXPRESSION TAG	UNP P10475
C	12	HIS	-	EXPRESSION TAG	UNP P10475
C	13	HIS	-	EXPRESSION TAG	UNP P10475
C	14	HIS	-	EXPRESSION TAG	UNP P10475
C	15	HIS	-	EXPRESSION TAG	UNP P10475
C	16	SER	-	EXPRESSION TAG	UNP P10475
C	17	SER	-	EXPRESSION TAG	UNP P10475
C	18	GLY	-	EXPRESSION TAG	UNP P10475
C	19	LEU	-	EXPRESSION TAG	UNP P10475
C	20	VAL	-	EXPRESSION TAG	UNP P10475
C	21	PRO	-	EXPRESSION TAG	UNP P10475
C	22	ARG	-	EXPRESSION TAG	UNP P10475
C	23	GLY	-	EXPRESSION TAG	UNP P10475
C	24	SER	-	EXPRESSION TAG	UNP P10475
C	25	HIS	-	EXPRESSION TAG	UNP P10475
C	26	MET	-	EXPRESSION TAG	UNP P10475

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Chain	Residue	Modelled	Actual	Comment	Reference
D	6	MET	-	EXPRESSION TAG	UNP P10475
D	7	GLY	-	EXPRESSION TAG	UNP P10475
D	8	SER	-	EXPRESSION TAG	UNP P10475
D	9	SER	-	EXPRESSION TAG	UNP P10475
D	10	HIS	-	EXPRESSION TAG	UNP P10475
D	11	HIS	-	EXPRESSION TAG	UNP P10475
D	12	HIS	-	EXPRESSION TAG	UNP P10475
D	13	HIS	-	EXPRESSION TAG	UNP P10475
D	14	HIS	-	EXPRESSION TAG	UNP P10475
D	15	HIS	-	EXPRESSION TAG	UNP P10475
D	16	SER	-	EXPRESSION TAG	UNP P10475
D	17	SER	-	EXPRESSION TAG	UNP P10475
D	18	GLY	-	EXPRESSION TAG	UNP P10475
D	19	LEU	-	EXPRESSION TAG	UNP P10475
D	20	VAL	-	EXPRESSION TAG	UNP P10475
D	21	PRO	-	EXPRESSION TAG	UNP P10475
D	22	ARG	-	EXPRESSION TAG	UNP P10475
D	23	GLY	-	EXPRESSION TAG	UNP P10475
D	24	SER	-	EXPRESSION TAG	UNP P10475
D	25	HIS	-	EXPRESSION TAG	UNP P10475
D	26	MET	-	EXPRESSION TAG	UNP P10475

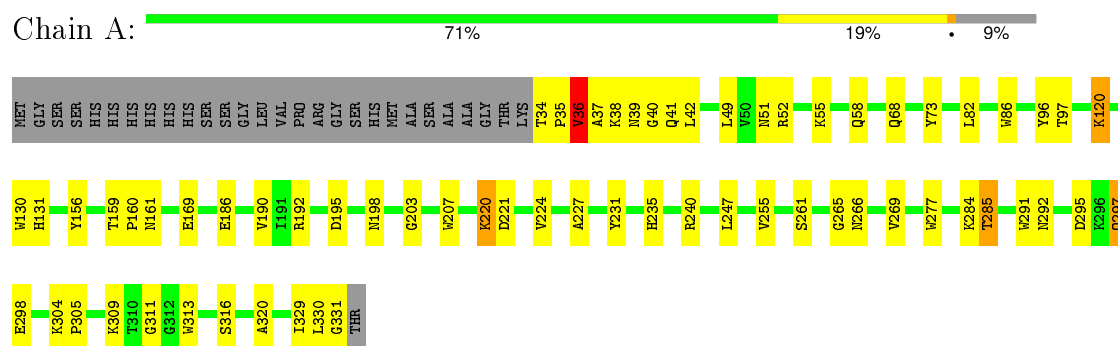
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	9	Total	O	0	0
			9	9		
2	B	11	Total	O	0	0
			11	11		
2	C	7	Total	O	0	0
			7	7		
2	D	3	Total	O	0	0
			3	3		

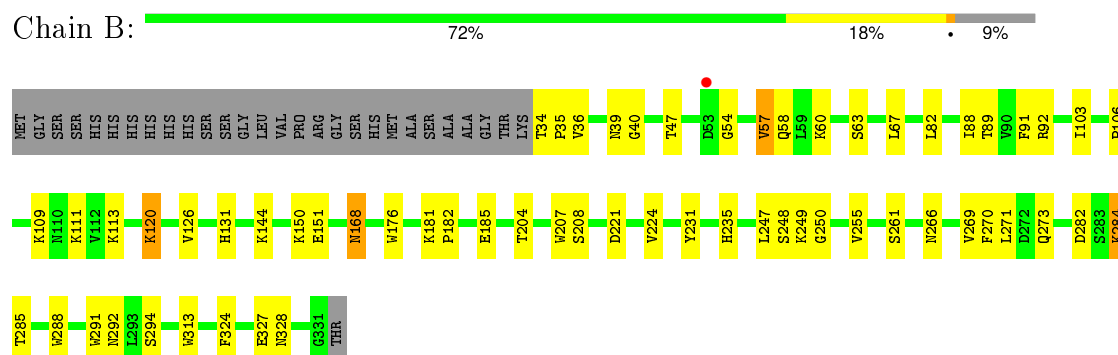
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

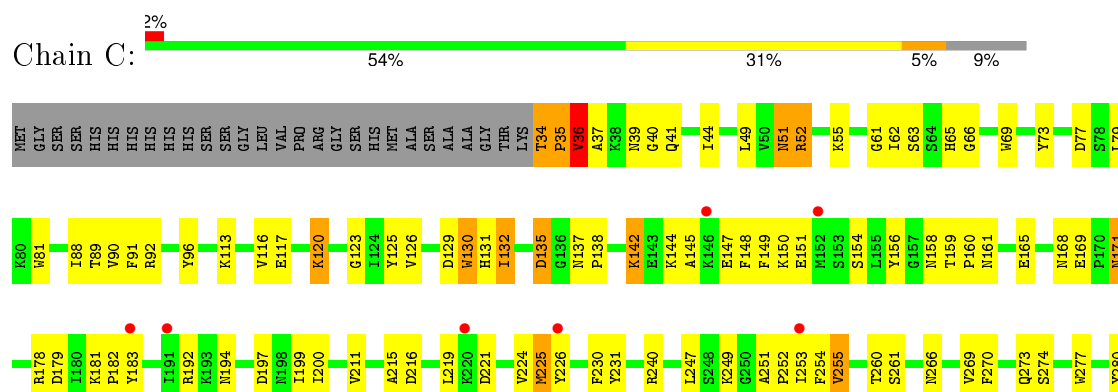
#### • Molecule 1: Endoglucanase

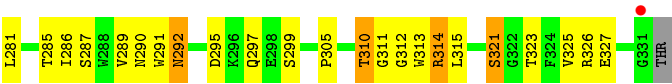


#### • Molecule 1: Endoglucanase

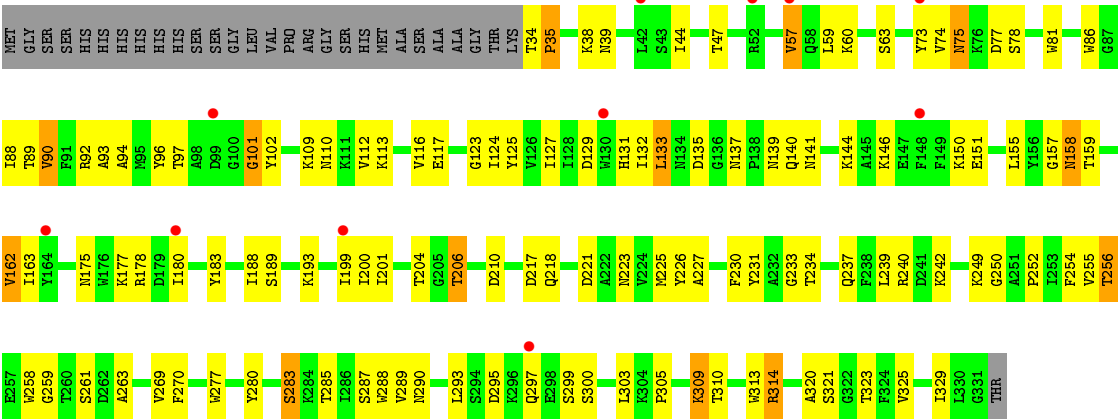


#### • Molecule 1: Endoglucanase





● Molecule 1: Endoglucanase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	155.36 Å   81.08 Å   114.27 Å 90.00°   104.29°   90.00°	Depositor
Resolution (Å)	41.46 – 2.87 41.46 – 2.87	Depositor EDS
% Data completeness (in resolution range)	89.8 (41.46-2.87) 89.3 (41.46-2.87)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 2.86 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, $R_{free}$	0.230   ,   0.296 0.220   ,   0.287	Depositor DCC
$R_{free}$ test set	1457 reflections (5.10%)	DCC
Wilson B-factor (Å <sup>2</sup> )	71.4	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29   ,   31.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 30369 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	9398	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.40	0/2396	0.72	0/3249
1	B	0.37	0/2396	0.68	1/3249 (0.0%)
1	C	0.29	0/2396	0.52	0/3249
1	D	0.26	0/2396	0.49	0/3249
All	All	0.33	0/9584	0.61	1/12996 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	54	GLY	N-CA-C	5.12	125.89	113.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2342	0	2271	48	0
1	B	2342	0	2271	43	0
1	C	2342	0	2271	92	0
1	D	2342	0	2271	75	0
2	A	9	0	0	0	0
2	B	11	0	0	0	0
2	C	7	0	0	0	0
2	D	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	9398	0	9084	256	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 (256) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:GLN:OE1	1:A:160:PRO:HA	1.60	1.00
1:C:34:THR:N	1:C:35:PRO:HD3	1.90	0.86
1:B:231:TYR:H	1:B:235:HIS:HD2	1.26	0.83
1:B:34:THR:HB	1:B:35:PRO:CD	2.09	0.83
1:C:156:TYR:O	1:C:159:THR:HB	1.79	0.82
1:C:261:SER:HB2	1:C:266:ASN:O	1.81	0.80
1:C:159:THR:HG22	1:C:161:ASN:H	1.47	0.80
1:C:144:LYS:HA	1:C:147:GLU:HB3	1.65	0.79
1:A:231:TYR:H	1:A:235:HIS:HD2	1.28	0.79
1:C:225:MET:HB3	1:C:252:PRO:HB2	1.65	0.77
1:D:280:TYR:O	1:D:283:SER:HB3	1.85	0.77
1:D:290:ASN:OD1	1:D:325:VAL:HG21	1.87	0.75
1:C:65:HIS:CD2	1:C:66:GLY:H	2.06	0.74
1:C:216:ASP:OD1	1:C:249:LYS:HE3	1.88	0.73
1:C:120:LYS:NZ	1:C:120:LYS:HB3	2.06	0.70
1:D:175:ASN:O	1:D:180:ILE:HG13	1.92	0.70
1:A:41:GLN:OE1	1:A:160:PRO:CA	2.39	0.68
1:A:231:TYR:H	1:A:235:HIS:CD2	2.09	0.68
1:C:44:ILE:HD13	1:C:49:LEU:HA	1.74	0.68
1:D:225:MET:HG2	1:D:252:PRO:HB2	1.79	0.65
1:D:231:TYR:CD2	1:D:263:ALA:HA	2.31	0.65
1:C:39:ASN:HB3	1:C:51:ASN:HB3	1.79	0.64
1:C:125:TYR:HE1	1:C:160:PRO:O	1.81	0.64
1:C:113:LYS:O	1:C:117:GLU:HG3	1.96	0.64
1:D:295:ASP:HB2	1:D:305:PRO:HA	1.79	0.64
1:B:34:THR:HB	1:B:35:PRO:HD3	1.80	0.63
1:D:35:PRO:HG2	1:D:124:ILE:HG22	1.81	0.63
1:A:221:ASP:HB3	1:A:224:VAL:HG23	1.81	0.62
1:C:221:ASP:HB3	1:C:224:VAL:HG23	1.81	0.62
1:D:39:ASN:HD21	1:D:57:VAL:HG21	1.64	0.62
1:A:120:LYS:HA	1:A:161:ASN:ND2	2.14	0.62
1:C:35:PRO:C	1:C:37:ALA:H	2.03	0.61
1:D:269:VAL:HG21	1:D:320:ALA:HB3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:230:PHE:O	1:D:258:TRP:HA	2.00	0.61
1:C:200:ILE:O	1:C:224:VAL:HG13	2.00	0.61
1:C:36:VAL:HG11	1:C:161:ASN:ND2	2.16	0.61
1:B:67:LEU:HD22	1:B:111:LYS:HG3	1.81	0.60
1:D:96:TYR:HA	1:D:131:HIS:HB3	1.83	0.60
1:D:175:ASN:ND2	1:D:178:ARG:H	2.00	0.60
1:D:321:SER:O	1:D:325:VAL:HG23	2.00	0.60
1:D:175:ASN:HD21	1:D:178:ARG:H	1.47	0.60
1:D:44:ILE:HB	1:D:223:ASN:HA	1.85	0.59
1:C:65:HIS:HD2	1:C:66:GLY:H	1.51	0.59
1:D:256:THR:O	1:D:289:VAL:HB	2.03	0.59
1:C:34:THR:N	1:C:35:PRO:CD	2.66	0.58
1:C:291:TRP:CD2	1:C:292:ASN:HB3	2.38	0.58
1:D:113:LYS:O	1:D:117:GLU:HG2	2.04	0.58
1:A:159:THR:HG22	1:A:161:ASN:H	1.68	0.58
1:D:151:GLU:O	1:D:155:LEU:HG	2.04	0.58
1:A:329:ILE:C	1:A:331:GLY:H	2.06	0.57
1:A:195:ASP:OD2	1:A:198:ASN:HB2	2.03	0.57
1:B:261:SER:OG	1:B:266:ASN:O	2.23	0.57
1:C:158:ASN:HB2	1:D:314:ARG:HD3	1.87	0.57
1:B:58:GLN:HE22	1:B:282:ASP:HA	1.68	0.57
1:B:34:THR:HB	1:B:35:PRO:HD2	1.84	0.56
1:A:34:THR:OG1	1:A:35:PRO:HD2	2.06	0.56
1:D:73:TYR:CE1	1:D:309:LYS:HA	2.41	0.56
1:B:285:THR:HG22	1:B:285:THR:O	2.05	0.56
1:C:171:ASN:N	1:C:171:ASN:HD22	2.04	0.56
1:D:34:THR:O	1:D:38:LYS:HB2	2.07	0.55
1:A:35:PRO:O	1:A:36:VAL:HG13	2.06	0.55
1:C:159:THR:CG2	1:C:161:ASN:H	2.18	0.55
1:C:270:PHE:HB3	1:C:273:GLN:OE1	2.06	0.55
1:D:254:PHE:CE2	1:D:287:SER:HB2	2.41	0.55
1:B:82:LEU:O	1:B:88:ILE:HG12	2.07	0.54
1:B:221:ASP:HB3	1:B:224:VAL:HG23	1.88	0.54
1:C:295:ASP:HB2	1:C:305:PRO:HA	1.88	0.54
1:A:68:GLN:HE22	1:A:96:TYR:HB2	1.73	0.54
1:C:51:ASN:HD21	1:C:55:LYS:HB2	1.72	0.54
1:C:225:MET:CE	1:C:254:PHE:HB2	2.38	0.54
1:C:35:PRO:C	1:C:37:ALA:N	2.61	0.53
1:D:74:VAL:O	1:D:75:ASN:HB3	2.08	0.53
1:A:156:TYR:O	1:A:159:THR:HB	2.08	0.53
1:A:190:VAL:O	1:A:190:VAL:HG23	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:SER:HA	1:B:92:ARG:HB3	1.89	0.53
1:B:231:TYR:H	1:B:235:HIS:CD2	2.16	0.53
1:C:255:VAL:HG23	1:C:286:ILE:HG21	1.89	0.53
1:D:34:THR:N	1:D:35:PRO:CD	2.72	0.53
1:A:35:PRO:O	1:A:37:ALA:N	2.37	0.53
1:A:247:LEU:HD13	1:A:284:LYS:HD3	1.91	0.53
1:C:96:TYR:HA	1:C:131:HIS:HB3	1.89	0.53
1:B:231:TYR:N	1:B:235:HIS:HD2	2.03	0.52
1:B:247:LEU:C	1:B:249:LYS:H	2.13	0.52
1:B:47:THR:CG2	1:B:250:GLY:HA2	2.39	0.52
1:B:292:ASN:ND2	1:B:294:SER:OG	2.41	0.52
1:B:204:THR:OG1	1:B:208:SER:HA	2.10	0.52
1:C:179:ASP:C	1:C:182:PRO:HD2	2.30	0.52
1:C:135:ASP:N	1:C:135:ASP:OD1	2.43	0.52
1:C:90:VAL:HA	1:C:125:TYR:O	2.10	0.51
1:C:215:ALA:HB2	1:C:251:ALA:CB	2.40	0.51
1:D:94:ALA:HB1	1:D:131:HIS:ND1	2.24	0.51
1:C:321:SER:O	1:C:325:VAL:HG23	2.11	0.51
1:B:324:PHE:O	1:B:328:ASN:ND2	2.42	0.51
1:A:295:ASP:HB2	1:A:305:PRO:HA	1.91	0.51
1:C:226:TYR:HE2	1:C:252:PRO:HD2	1.75	0.51
1:B:207:TRP:O	1:B:208:SER:HB2	2.10	0.51
1:D:60:LYS:HB3	1:D:329:ILE:HG12	1.92	0.51
1:C:252:PRO:O	1:C:253:ILE:HD13	2.10	0.51
1:B:106:PRO:O	1:B:109:LYS:HG2	2.10	0.51
1:B:91:PHE:O	1:B:126:VAL:HA	2.11	0.51
1:C:291:TRP:CG	1:C:292:ASN:HB3	2.46	0.51
1:C:129:ASP:HA	1:C:165:GLU:HB3	1.92	0.51
1:B:103:ILE:HD12	1:B:144:LYS:HD2	1.92	0.51
1:D:132:ILE:HG22	1:D:135:ASP:OD2	2.10	0.51
1:D:112:VAL:O	1:D:116:VAL:HG23	2.11	0.51
1:B:181:LYS:O	1:B:185:GLU:HG2	2.10	0.50
1:B:176:TRP:HE1	1:B:181:LYS:HD2	1.76	0.50
1:D:35:PRO:HD2	1:D:123:GLY:O	2.11	0.50
1:C:254:PHE:CE2	1:C:287:SER:HB2	2.47	0.50
1:A:297:GLN:O	1:A:297:GLN:HG3	2.12	0.50
1:C:266:ASN:HA	1:C:299:SER:HB2	1.93	0.50
1:D:188:ILE:HG12	1:D:200:ILE:HD13	1.94	0.49
1:C:178:ARG:O	1:C:182:PRO:HG2	2.11	0.49
1:C:192:ARG:C	1:C:194:ASN:H	2.14	0.49
1:D:293:LEU:HG	1:D:293:LEU:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:THR:HG21	1:A:130:TRP:CE2	2.47	0.49
1:D:92:ARG:HA	1:D:127:ILE:HB	1.93	0.49
1:C:120:LYS:HZ1	1:C:120:LYS:HB3	1.74	0.49
1:A:304:LYS:HD2	1:A:316:SER:O	2.12	0.49
1:C:62:ILE:CG1	1:C:63:SER:H	2.26	0.49
1:D:231:TYR:HD1	1:D:259:GLY:HA3	1.76	0.49
1:B:82:LEU:HD21	1:B:313:TRP:HZ3	1.77	0.49
1:C:323:THR:O	1:C:327:GLU:HB2	2.13	0.49
1:D:255:VAL:O	1:D:288:TRP:HA	2.13	0.49
1:D:269:VAL:HG21	1:D:320:ALA:CB	2.42	0.48
1:A:68:GLN:HE22	1:A:96:TYR:CB	2.25	0.48
1:D:204:THR:HB	1:D:210:ASP:O	2.13	0.48
1:C:77:ASP:HB2	1:C:310:THR:HG22	1.94	0.48
1:D:93:ALA:O	1:D:129:ASP:HB3	2.13	0.48
1:D:139:ASN:OD1	1:D:183:TYR:HB2	2.14	0.48
1:C:221:ASP:HB3	1:C:224:VAL:CG2	2.42	0.48
1:B:36:VAL:O	1:B:40:GLY:N	2.45	0.48
1:C:131:HIS:HA	1:C:168:ASN:HB2	1.95	0.48
1:C:171:ASN:ND2	1:C:171:ASN:N	2.62	0.47
1:B:47:THR:HG22	1:B:250:GLY:HA2	1.95	0.47
1:A:82:LEU:O	1:A:86:TRP:HB2	2.13	0.47
1:A:169:GLU:OE1	1:A:207:TRP:HD1	1.97	0.47
1:B:113:LYS:NZ	1:B:151:GLU:OE2	2.47	0.47
1:D:44:ILE:HD13	1:D:199:ILE:HD12	1.95	0.47
1:C:181:LYS:N	1:C:182:PRO:CD	2.78	0.47
1:D:141:ASN:HB3	1:D:144:LYS:HB2	1.97	0.47
1:B:67:LEU:HD22	1:B:111:LYS:CG	2.45	0.47
1:A:68:GLN:NE2	1:A:96:TYR:HB2	2.29	0.47
1:A:221:ASP:HB3	1:A:224:VAL:CG2	2.43	0.47
1:C:291:TRP:HA	1:C:292:ASN:HA	1.64	0.47
1:C:255:VAL:HG23	1:C:286:ILE:CG2	2.45	0.47
1:B:284:LYS:HE2	1:B:284:LYS:HB3	1.66	0.46
1:C:142:LYS:HB2	1:C:183:TYR:CD1	2.49	0.46
1:C:36:VAL:O	1:C:36:VAL:CG2	2.63	0.46
1:A:291:TRP:CG	1:A:292:ASN:HB3	2.51	0.46
1:D:110:ASN:O	1:D:113:LYS:HB2	2.14	0.46
1:A:39:ASN:O	1:A:51:ASN:HB2	2.15	0.46
1:C:314:ARG:H	1:C:314:ARG:HG2	1.51	0.46
1:C:230:PHE:C	1:C:231:TYR:CD2	2.89	0.46
1:C:35:PRO:O	1:C:37:ALA:N	2.48	0.46
1:C:61:GLY:HA3	1:C:90:VAL:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:GLY:O	1:A:298:GLU:HB2	2.16	0.45
1:C:226:TYR:CE2	1:C:252:PRO:HD2	2.51	0.45
1:A:247:LEU:CD1	1:A:284:LYS:HD3	2.46	0.45
1:D:226:TYR:N	1:D:226:TYR:CD2	2.84	0.45
1:A:120:LYS:HE3	1:A:120:LYS:HB2	1.65	0.45
1:D:201:ILE:CG2	1:D:227:ALA:HB2	2.47	0.45
1:B:60:LYS:HG2	1:B:288:TRP:CE2	2.51	0.45
1:C:148:PHE:O	1:C:150:LYS:N	2.50	0.45
1:A:58:GLN:HB2	1:A:285:THR:HG22	1.97	0.45
1:D:218:GLN:NE2	1:D:249:LYS:O	2.48	0.45
1:C:116:VAL:HA	1:C:126:VAL:HG11	1.99	0.45
1:D:146:LYS:O	1:D:150:LYS:HB2	2.16	0.45
1:C:65:HIS:HB2	1:C:292:ASN:OD1	2.17	0.45
1:A:311:GLY:HA2	1:A:313:TRP:CE2	2.52	0.45
1:D:90:VAL:HA	1:D:125:TYR:O	2.17	0.45
1:C:290:ASN:CG	1:C:291:TRP:H	2.20	0.45
1:D:63:SER:HB2	1:D:92:ARG:HB3	1.98	0.45
1:C:290:ASN:CG	1:C:291:TRP:N	2.71	0.44
1:A:51:ASN:ND2	1:A:55:LYS:HB2	2.31	0.44
1:C:199:ILE:H	1:C:199:ILE:HG12	1.59	0.44
1:A:203:GLY:HA2	1:A:227:ALA:HB3	1.98	0.44
1:A:186:GLU:O	1:A:190:VAL:HG13	2.17	0.44
1:C:260:THR:HG22	1:C:274:SER:OG	2.16	0.44
1:D:86:TRP:CD1	1:D:86:TRP:N	2.84	0.44
1:C:52:ARG:O	1:C:52:ARG:NH1	2.51	0.44
1:B:269:VAL:HG12	1:B:271:LEU:HG	1.99	0.44
1:D:127:ILE:HD13	1:D:256:THR:HG22	1.99	0.44
1:A:42:LEU:HD13	1:A:49:LEU:HD21	1.99	0.44
1:C:62:ILE:CG1	1:C:63:SER:N	2.80	0.44
1:D:102:TYR:HE1	1:D:109:LYS:HB3	1.83	0.44
1:C:225:MET:HE2	1:C:254:PHE:HB2	2.00	0.44
1:D:234:THR:OG1	1:D:263:ALA:N	2.50	0.43
1:D:261:SER:OG	1:D:300:SER:HB3	2.19	0.43
1:B:131:HIS:HA	1:B:168:ASN:HB2	2.00	0.43
1:C:39:ASN:HB3	1:C:51:ASN:CB	2.47	0.43
1:D:158:ASN:O	1:D:159:THR:C	2.56	0.43
1:D:81:TRP:HD1	1:D:313:TRP:CZ3	2.36	0.43
1:A:240:ARG:HG2	1:A:277:TRP:CZ3	2.53	0.43
1:B:35:PRO:CG	1:B:89:THR:HG22	2.49	0.43
1:A:291:TRP:CD2	1:A:292:ASN:HB3	2.54	0.43
1:C:129:ASP:OD1	1:C:129:ASP:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:ILE:HD12	1:D:90:VAL:O	2.19	0.43
1:C:73:TYR:HH	1:C:295:ASP:CG	2.22	0.43
1:B:270:PHE:HB3	1:B:273:GLN:OE1	2.19	0.43
1:D:74:VAL:O	1:D:75:ASN:CB	2.67	0.43
1:D:89:THR:O	1:D:90:VAL:HB	2.18	0.43
1:C:280:TYR:HD2	1:C:281:LEU:HD23	1.84	0.43
1:D:129:ASP:OD2	1:D:131:HIS:ND1	2.41	0.42
1:D:237:GLN:O	1:D:240:ARG:N	2.52	0.42
1:C:132:ILE:O	1:C:132:ILE:HG13	2.18	0.42
1:A:96:TYR:HA	1:A:131:HIS:HB3	2.00	0.42
1:C:91:PHE:N	1:C:125:TYR:O	2.42	0.42
1:A:329:ILE:O	1:A:331:GLY:N	2.51	0.42
1:D:59:LEU:N	1:D:287:SER:OG	2.45	0.42
1:C:151:GLU:HG3	1:D:81:TRP:CZ3	2.54	0.42
1:A:255:VAL:HG12	1:A:255:VAL:O	2.18	0.42
1:D:277:TRP:O	1:D:280:TYR:HB3	2.19	0.42
1:D:96:TYR:O	1:D:101:GLY:HA3	2.20	0.42
1:B:324:PHE:O	1:B:327:GLU:HB2	2.20	0.42
1:C:150:LYS:O	1:C:154:SER:HB2	2.20	0.42
1:D:162:VAL:C	1:D:163:ILE:HG13	2.40	0.42
1:A:73:TYR:CD1	1:A:309:LYS:HA	2.54	0.42
1:B:111:LYS:HA	1:B:111:LYS:HD3	1.72	0.42
1:C:63:SER:OG	1:C:92:ARG:HD3	2.20	0.42
1:D:75:ASN:OD1	1:D:78:SER:N	2.48	0.42
1:A:220:LYS:H	1:A:220:LYS:HD3	1.85	0.42
1:B:291:TRP:CD2	1:B:292:ASN:HB3	2.55	0.41
1:D:158:ASN:O	1:D:158:ASN:ND2	2.51	0.41
1:C:137:ASN:HA	1:C:138:PRO:HD2	1.86	0.41
1:D:227:ALA:HA	1:D:254:PHE:O	2.19	0.41
1:B:120:LYS:HE3	1:B:120:LYS:HB3	1.78	0.41
1:C:260:THR:HB	1:C:269:VAL:HG13	2.02	0.41
1:D:239:LEU:HD12	1:D:242:LYS:HD3	2.03	0.41
1:C:169:GLU:O	1:C:171:ASN:ND2	2.53	0.41
1:D:81:TRP:CD1	1:D:313:TRP:CE3	3.08	0.41
1:C:41:GLN:HB3	1:C:52:ARG:HG3	2.03	0.41
1:D:47:THR:HG22	1:D:250:GLY:O	2.20	0.41
1:B:181:LYS:HB3	1:B:182:PRO:HD3	2.02	0.41
1:C:230:PHE:O	1:C:231:TYR:CD2	2.74	0.41
1:A:40:GLY:HA3	1:A:52:ARG:HE	1.86	0.41
1:C:315:LEU:HD21	1:C:326:ARG:NH1	2.35	0.41
1:C:159:THR:HA	1:C:160:PRO:HD2	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:255:VAL:O	1:B:288:TRP:HA	2.21	0.41
1:B:39:ASN:ND2	1:B:57:VAL:HG21	2.36	0.41
1:A:41:GLN:NE2	1:A:198:ASN:OD1	2.54	0.40
1:B:34:THR:CB	1:B:35:PRO:CD	2.84	0.40
1:D:189:SER:O	1:D:193:LYS:HG3	2.20	0.40
1:A:269:VAL:HG21	1:A:320:ALA:HB3	2.02	0.40
1:C:35:PRO:HD2	1:C:123:GLY:O	2.20	0.40
1:C:254:PHE:HE1	1:C:289:VAL:HG23	1.86	0.40
1:D:206:THR:HG22	1:D:206:THR:O	2.20	0.40
1:A:192:ARG:HA	1:A:192:ARG:HD3	1.82	0.40
1:C:81:TRP:CZ2	1:C:312:GLY:HA2	2.56	0.40
1:C:130:TRP:CZ2	1:C:145:ALA:HA	2.56	0.40
1:A:261:SER:HB2	1:A:266:ASN:O	2.20	0.40
1:C:66:GLY:HA3	1:C:69:TRP:CE3	2.56	0.40
1:D:329:ILE:HG22	1:D:329:ILE:O	2.21	0.40
1:D:233:GLY:HA2	1:D:270:PHE:CD2	2.56	0.40
1:C:311:GLY:HA2	1:C:313:TRP:CE2	2.56	0.40
1:D:39:ASN:ND2	1:D:57:VAL:HG11	2.37	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	296/327 (90%)	284 (96%)	9 (3%)	3 (1%)	19	49
1	B	296/327 (90%)	277 (94%)	17 (6%)	2 (1%)	26	59
1	C	296/327 (90%)	242 (82%)	45 (15%)	9 (3%)	5	19
1	D	296/327 (90%)	244 (82%)	40 (14%)	12 (4%)	3	12
All	All	1184/1308 (90%)	1047 (88%)	111 (9%)	26 (2%)	8	27

All (26) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	330	LEU
1	C	35	PRO
1	C	40	GLY
1	D	217	ASP
1	C	51	ASN
1	C	149	PHE
1	C	297	GLN
1	D	133	LEU
1	D	157	GLY
1	D	221	ASP
1	D	283	SER
1	A	297	GLN
1	B	248	SER
1	C	130	TRP
1	C	135	ASP
1	D	75	ASN
1	A	36	VAL
1	C	255	VAL
1	D	206	THR
1	B	168	ASN
1	D	35	PRO
1	D	90	VAL
1	D	97	THR
1	D	297	GLN
1	C	36	VAL
1	D	101	GLY

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	248/270 (92%)	243 (98%)	5 (2%)	63	87
1	B	248/270 (92%)	244 (98%)	4 (2%)	70	90
1	C	248/270 (92%)	226 (91%)	22 (9%)	12	32
1	D	248/270 (92%)	232 (94%)	16 (6%)	21	49
All	All	992/1080 (92%)	945 (95%)	47 (5%)	32	66

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	VAL
1	A	38	LYS
1	A	120	LYS
1	A	220	LYS
1	A	285	THR
1	B	57	VAL
1	B	120	LYS
1	B	150	LYS
1	B	284	LYS
1	C	34	THR
1	C	36	VAL
1	C	52	ARG
1	C	79	LEU
1	C	88	ILE
1	C	89	THR
1	C	120	LYS
1	C	132	ILE
1	C	142	LYS
1	C	171	ASN
1	C	197	ASP
1	C	211	VAL
1	C	219	LEU
1	C	225	MET
1	C	240	ARG
1	C	247	LEU
1	C	277	TRP
1	C	285	THR
1	C	292	ASN
1	C	310	THR
1	C	314	ARG
1	C	321	SER
1	D	57	VAL
1	D	77	ASP
1	D	133	LEU
1	D	137	ASN
1	D	140	GLN
1	D	158	ASN
1	D	162	VAL
1	D	177	LYS
1	D	256	THR
1	D	285	THR
1	D	299	SER

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Mol	Chain	Res	Type
1	D	303	LEU
1	D	309	LYS
1	D	310	THR
1	D	314	ARG
1	D	323	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	134	ASN
1	A	140	GLN
1	A	209	GLN
1	A	235	HIS
1	A	292	ASN
1	A	297	GLN
1	B	39	ASN
1	B	134	ASN
1	B	140	GLN
1	B	235	HIS
1	B	244	ASN
1	B	292	ASN
1	C	65	HIS
1	C	140	GLN
1	C	171	ASN
1	C	209	GLN
1	C	235	HIS
1	D	39	ASN
1	D	140	GLN
1	D	141	ASN
1	D	175	ASN
1	D	194	ASN
1	D	223	ASN
1	D	235	HIS
1	D	292	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 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, 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	298/327 (91%)	-0.32	0 100 100	48, 63, 79, 90	0
1	B	298/327 (91%)	-0.27	1 (0%) 94 93	47, 68, 87, 107	0
1	C	298/327 (91%)	-0.01	8 (2%) 58 52	52, 84, 100, 115	1 (0%)
1	D	298/327 (91%)	0.30	11 (3%) 45 38	66, 103, 121, 129	1 (0%)
All	All	1192/1308 (91%)	-0.08	20 (1%) 73 70	47, 77, 114, 129	2 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	220	LYS	4.0
1	D	164	TYR	3.7
1	C	331	GLY	3.5
1	D	130	TRP	3.5
1	D	297	GLN	3.2
1	D	180	ILE	3.2
1	D	99	ASP	2.8
1	C	253	ILE	2.8
1	D	73	TYR	2.7
1	D	199	ILE	2.6
1	D	42	LEU	2.6
1	C	146	LYS	2.4
1	C	226	TYR	2.4
1	C	152	MET	2.4
1	B	53	ASP	2.4
1	C	191	ILE	2.2
1	D	148	PHE	2.2
1	D	52	ARG	2.1
1	D	57	VAL	2.1
1	C	183	TYR	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.