



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2024 – 11:15 AM EDT

PDB ID : 3MZ1  
Title : The crystal structure of a possible TRANSCRIPTION REGULATOR PROTEIN from Sinorhizobium meliloti 1021  
Authors : Tan, K.; Xu, X.; Cui, H.; Chin, S.; Savchenko, A.; Edwards, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2010-05-11  
Resolution : 1.88 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

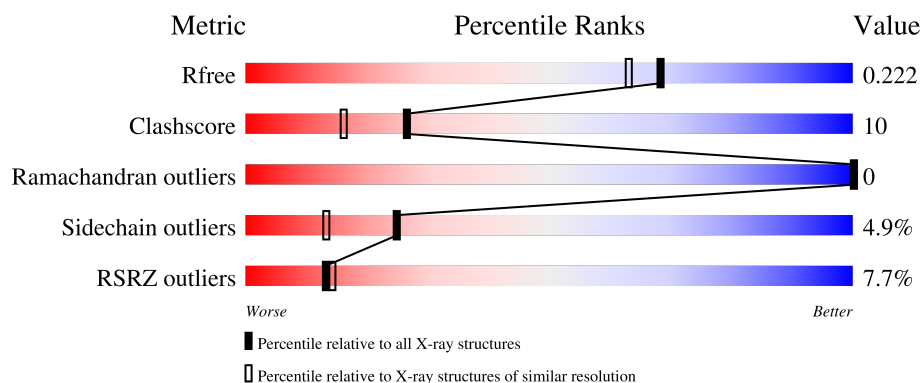
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.88 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))
$R_{free}$	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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	300	<div> <div>5%</div> <div> <div></div> <div>53%</div> <div>15%</div> <div>•</div> <div>31%</div> </div> </div>
1	B	300	<div> <div>4%</div> <div> <div></div> <div>59%</div> <div>11%</div> <div>•</div> <div>29%</div> </div> </div>
1	C	300	<div> <div>6%</div> <div> <div></div> <div>52%</div> <div>13%</div> <div>•</div> <div>32%</div> </div> </div>
1	D	300	<div> <div>5%</div> <div> <div></div> <div>55%</div> <div>15%</div> <div></div> <div>29%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7104 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 Putative transcriptional regulator.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	Se	0	3	0
			1685	1074	303	298	3	7			
1	B	212	Total	C	N	O	S	Se	0	3	0
			1704	1088	302	304	3	7			
1	C	204	Total	C	N	O	S	Se	0	2	0
			1629	1042	288	288	4	7			
1	D	212	Total	C	N	O	S	Se	0	5	0
			1722	1099	308	305	3	7			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLN	-	EXPRESSION TAG	UNP Q92SG7
A	0	GLY	-	EXPRESSION TAG	UNP Q92SG7
A	215	MSE	VAL	CLONING ARTIFACT	UNP Q92SG7
A	297	GLY	-	EXPRESSION TAG	UNP Q92SG7
A	298	SER	-	EXPRESSION TAG	UNP Q92SG7
B	-1	GLN	-	EXPRESSION TAG	UNP Q92SG7
B	0	GLY	-	EXPRESSION TAG	UNP Q92SG7
B	215	MSE	VAL	CLONING ARTIFACT	UNP Q92SG7
B	297	GLY	-	EXPRESSION TAG	UNP Q92SG7
B	298	SER	-	EXPRESSION TAG	UNP Q92SG7
C	-1	GLN	-	EXPRESSION TAG	UNP Q92SG7
C	0	GLY	-	EXPRESSION TAG	UNP Q92SG7
C	215	MSE	VAL	CLONING ARTIFACT	UNP Q92SG7
C	297	GLY	-	EXPRESSION TAG	UNP Q92SG7
C	298	SER	-	EXPRESSION TAG	UNP Q92SG7
D	-1	GLN	-	EXPRESSION TAG	UNP Q92SG7
D	0	GLY	-	EXPRESSION TAG	UNP Q92SG7
D	215	MSE	VAL	CLONING ARTIFACT	UNP Q92SG7
D	297	GLY	-	EXPRESSION TAG	UNP Q92SG7
D	298	SER	-	EXPRESSION TAG	UNP Q92SG7

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

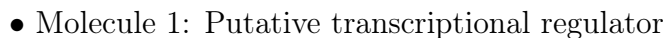
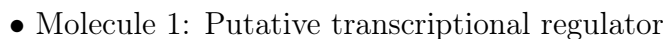
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Cl	0	0
			1	1		

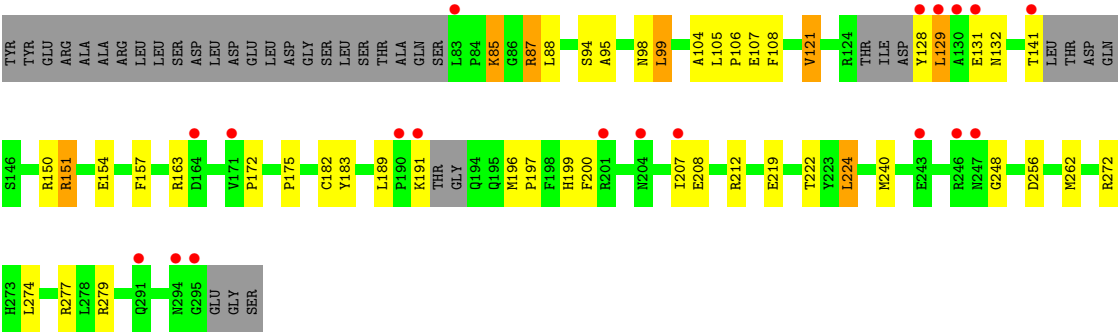
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	103	Total	O	0	0
			103	103		
3	B	90	Total	O	0	0
			90	90		
3	C	73	Total	O	0	0
			73	73		
3	D	97	Total	O	0	0
			97	97		

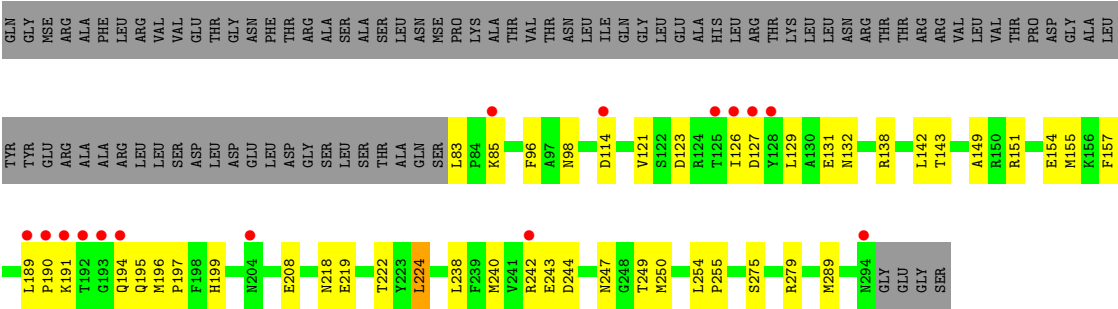


- Molecule 1: Putative transcriptional regulator





● Molecule 1: Putative transcriptional regulator



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.34Å 83.33Å 85.07Å 90.00° 91.65° 90.00°	Depositor
Resolution (Å)	36.42 – 1.88 36.42 – 1.88	Depositor EDS
% Data completeness (in resolution range)	93.8 (36.42-1.88) 99.2 (36.42-1.88)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.01 (at 1.88Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.184 , 0.224 0.184 , 0.222	Depositor DCC
$R_{free}$ test set	3817 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.4	Xtriage
Anisotropy	0.438	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 58.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.000 for -h,-l,-k 0.027 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7104	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 74.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4630e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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](#)

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

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	0.36	0/1720	0.56	0/2322
1	B	0.41	0/1747	0.57	0/2364
1	C	0.37	0/1666	0.56	0/2248
1	D	0.37	0/1768	0.58	0/2390
All	All	0.38	0/6901	0.57	0/9324

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1685	0	1690	36	0
1	B	1704	0	1720	35	0
1	C	1629	0	1631	45	0
1	D	1722	0	1744	40	0
2	D	1	0	0	0	0
3	A	103	0	0	1	0
3	B	90	0	0	1	0
3	C	73	0	0	2	0
3	D	97	0	0	1	0
All	All	7104	0	6785	139	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 10.

All (139) 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:98:ASN:HD21	1:B:222[B]:THR:HG22	1.01	1.08
1:B:272:ARG:HG2	1:B:272:ARG:HH11	1.10	1.08
1:C:98:ASN:HD21	1:D:222:THR:HG22	1.23	1.03
1:D:224:LEU:HD12	1:D:240:MSE:HE2	1.43	1.00
1:A:98:ASN:ND2	1:B:222[B]:THR:HG22	1.77	0.98
1:B:272:ARG:HH11	1:B:272:ARG:CG	1.88	0.85
1:D:151[A]:ARG:NH2	1:D:154:GLU:HG2	1.92	0.84
1:C:98:ASN:ND2	1:D:222:THR:HG22	1.91	0.84
1:C:224:LEU:HD12	1:C:240:MSE:HE2	1.56	0.84
1:D:151[A]:ARG:HH21	1:D:154:GLU:HG2	1.40	0.84
1:A:98:ASN:HD21	1:B:222[B]:THR:CG2	1.88	0.83
1:C:87:ARG:HH11	1:C:87:ARG:HB3	1.42	0.83
1:D:275:SER:O	1:D:279:ARG:HG3	1.78	0.83
1:B:272:ARG:HG2	1:B:272:ARG:NH1	1.92	0.82
1:A:146:SER:O	1:A:270:PRO:HG3	1.81	0.81
1:D:190:PRO:HG3	1:D:218:ASN:HD22	1.45	0.80
1:C:104:ALA:O	1:C:107:GLU:HG2	1.81	0.79
1:C:222:THR:HG22	1:D:98:ASN:HD21	1.51	0.74
1:B:272:ARG:O	1:B:274:LEU:HD13	1.91	0.70
1:A:121:VAL:HG21	1:B:222[B]:THR:HG21	1.72	0.70
1:C:189:LEU:HD13	1:C:191:LYS:HD3	1.74	0.69
1:D:155:MSE:HE3	1:D:157:PHE:CZ	2.29	0.68
1:C:222:THR:HG22	1:D:98:ASN:ND2	2.11	0.66
1:D:127:ASP:HB3	1:D:143:THR:OG1	1.95	0.66
1:C:98:ASN:HD21	1:D:222:THR:CG2	2.04	0.66
1:C:175:PRO:HG2	1:C:207:ILE:HD11	1.78	0.66
1:C:199:HIS:CD2	1:C:208:GLU:HB2	2.31	0.65
1:B:126:ILE:HD12	3:B:379:HOH:O	1.97	0.65
1:A:107:GLU:HG3	1:A:108:PHE:N	2.11	0.64
1:B:219:GLU:OE1	1:B:222[B]:THR:HG23	1.98	0.64
1:D:190:PRO:HG3	1:D:218:ASN:ND2	2.13	0.62
1:D:151[A]:ARG:HH21	1:D:154:GLU:CG	2.11	0.62
1:A:224:LEU:HD22	1:A:240:MSE:HE2	1.81	0.61
1:A:104:ALA:O	1:A:107:GLU:HG2	2.02	0.59
1:A:125:THR:HG22	1:A:189:LEU:HD23	1.85	0.59
1:C:87:ARG:HB3	1:C:87:ARG:NH1	2.17	0.59
1:C:172:PRO:HG3	1:C:182[A]:CYS:SG	2.43	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:SER:OG	1:B:219:GLU:OE2	2.21	0.58
1:D:189:LEU:HB2	1:D:194:GLN:HG2	1.84	0.58
1:C:212:ARG:HB3	1:C:212:ARG:NH2	2.18	0.57
1:C:85:LYS:NZ	1:C:85:LYS:HB3	2.19	0.57
1:A:222:THR:HG23	1:B:102:ILE:HD11	1.86	0.57
1:A:158:VAL:HG21	1:A:238:LEU:HD13	1.89	0.55
1:D:238:LEU:O	1:D:242[A]:ARG:HG3	2.07	0.55
1:D:224:LEU:HD11	1:D:240:MSE:HB3	1.89	0.55
1:A:189:LEU:HG	1:A:190:PRO:HD2	1.89	0.55
1:A:187:TYR:HE2	1:A:189:LEU:HD12	1.71	0.54
1:B:272:ARG:CG	1:B:272:ARG:NH1	2.56	0.54
1:C:121:VAL:HG21	1:D:222:THR:HG21	1.88	0.54
1:B:122:SER:OG	1:B:124:ARG:HG2	2.07	0.54
1:B:130:ALA:HB3	1:B:133:VAL:HG23	1.90	0.53
1:C:219:GLU:OE1	1:C:222:THR:HG23	2.08	0.53
1:D:199:HIS:HE1	1:D:208:GLU:OE1	1.91	0.53
1:C:189:LEU:HB3	1:C:191:LYS:HG3	1.91	0.53
1:C:212:ARG:HB3	1:C:212:ARG:CZ	2.40	0.52
1:D:142:LEU:HD11	1:D:149:ALA:CB	2.40	0.51
1:C:107:GLU:HG3	1:C:108:PHE:N	2.25	0.51
1:A:274:LEU:HG	1:A:279:ARG:CG	2.41	0.51
1:C:163:ARG:HG3	1:C:248:GLY:O	2.11	0.51
1:C:222:THR:HG21	1:D:121:VAL:HG11	1.93	0.50
1:A:222:THR:HG23	1:B:102:ILE:CD1	2.41	0.50
1:D:194:GLN:O	1:D:194:GLN:HG3	2.12	0.50
1:C:129:LEU:HD12	1:C:129:LEU:H	1.77	0.49
1:B:143:THR:HG23	1:B:144:ASP:OD1	2.13	0.49
1:C:222:THR:HA	1:D:98:ASN:HD21	1.77	0.49
1:A:254:LEU:N	1:A:255:PRO:HD3	2.27	0.49
1:B:172:PRO:HG3	1:B:182:CYS:SG	2.53	0.48
1:D:244:ASP:HB3	1:D:250:MSE:HG2	1.95	0.48
1:A:154:GLU:HG2	1:A:261:PRO:HB2	1.95	0.48
1:D:142:LEU:HD11	1:D:149:ALA:HB2	1.95	0.48
1:C:272:ARG:HD3	1:C:272:ARG:HA	1.69	0.47
1:D:243:GLU:HB3	3:D:333:HOH:O	2.14	0.47
1:D:199:HIS:CE1	1:D:208:GLU:OE1	2.68	0.47
1:B:155:MSE:HE2	1:B:264:ILE:HD11	1.97	0.47
1:A:111[B]:LYS:HG3	3:A:328:HOH:O	2.14	0.46
1:C:212:ARG:CZ	1:C:212:ARG:CB	2.93	0.46
1:D:155:MSE:HE3	1:D:157:PHE:HZ	1.78	0.46
1:C:151:ARG:NH1	1:C:154:GLU:HG3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:ILE:O	1:B:138:ARG:NH2	2.47	0.46
1:A:185:VAL:HB	1:A:234:ILE:HG22	1.98	0.45
1:C:189:LEU:HB3	1:C:191:LYS:CG	2.46	0.45
1:D:126:ILE:HG13	1:D:138:ARG:HB2	1.98	0.45
1:D:275:SER:O	1:D:279:ARG:CG	2.57	0.45
1:A:224:LEU:CD2	1:A:240:MSE:HE2	2.48	0.44
1:A:213:TYR:O	1:B:116:GLN:HG2	2.16	0.44
1:D:194:GLN:O	1:D:194:GLN:CG	2.66	0.44
1:A:102:ILE:HD11	1:A:119:LEU:CD2	2.47	0.44
1:B:126:ILE:O	1:B:126:ILE:HG22	2.17	0.44
1:D:85:LYS:HD2	1:D:114:ASP:HB3	1.99	0.44
1:D:247[B]:ASN:HD22	1:D:249:THR:H	1.66	0.44
1:A:137:ILE:HD12	1:A:137:ILE:N	2.33	0.43
1:C:183:TYR:HE1	1:C:212:ARG:HH22	1.57	0.43
1:B:243:GLU:HA	1:B:246:ARG:NH2	2.34	0.43
1:A:142:LEU:HD13	1:A:142:LEU:HA	1.67	0.43
1:A:196:MSE:HA	1:A:197:PRO:HD3	1.94	0.43
1:A:238:LEU:HG	1:A:242[A]:ARG:HE	1.84	0.43
1:B:132:ASN:OD1	1:B:132:ASN:N	2.52	0.43
1:C:200:PHE:HB2	1:C:207:ILE:CD1	2.49	0.43
1:D:254:LEU:N	1:D:255:PRO:HD3	2.34	0.43
1:A:158:VAL:CG2	1:A:238:LEU:HD13	2.48	0.42
1:A:85:LYS:HG2	1:A:114:ASP:HB2	2.01	0.42
1:C:189:LEU:CD1	1:C:191:LYS:HD3	2.44	0.42
1:C:274:LEU:HG	1:C:279:ARG:HG3	2.00	0.42
1:C:95:ALA:O	1:C:99:LEU:HB2	2.19	0.42
1:D:96:PHE:CD1	1:D:289:MSE:HE1	2.54	0.42
1:D:197:PRO:HB2	1:D:208:GLU:HG3	2.02	0.42
1:C:182[B]:CYS:HA	3:C:305:HOH:O	2.18	0.42
1:B:124:ARG:O	1:B:124:ARG:HG3	2.18	0.42
1:C:183:TYR:CE1	1:C:212:ARG:NH2	2.73	0.42
1:C:85:LYS:HB3	1:C:85:LYS:HZ2	1.83	0.42
1:B:126:ILE:HG21	1:B:129:LEU:HD21	2.02	0.42
1:C:222:THR:CG2	1:D:98:ASN:HD21	2.26	0.42
1:A:131:GLU:OE2	1:A:271:ASN:ND2	2.53	0.42
1:A:222:THR:CG2	1:B:102:ILE:HD11	2.49	0.42
1:B:243:GLU:HG2	1:B:247:ASN:HD21	1.84	0.42
1:B:91:GLU:OE2	1:B:120:GLY:HA3	2.20	0.41
1:B:164:ASP:OD2	1:B:168:ARG:NH1	2.53	0.41
1:D:131:GLU:O	1:D:132:ASN:HB2	2.20	0.41
1:C:94:SER:OG	1:C:219:GLU:OE2	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:105:LEU:N	1:C:106:PRO:CD	2.83	0.41
1:B:137:ILE:HD12	1:B:137:ILE:N	2.35	0.41
1:C:200:PHE:HB2	1:C:207:ILE:HD11	2.01	0.41
1:A:138:ARG:HD3	1:A:138:ARG:HA	1.84	0.41
1:A:274:LEU:HG	1:A:279:ARG:HD3	2.02	0.41
1:C:157:PHE:HE2	1:C:262:MSE:HB2	1.85	0.41
1:C:197:PRO:HB2	1:C:208:GLU:HG3	2.03	0.41
1:A:144:ASP:HB3	1:A:147:LEU:CD1	2.51	0.41
1:B:199:HIS:CE1	1:B:208:GLU:HB2	2.56	0.41
1:A:215:MSE:HE3	1:A:217:ALA:HB2	2.03	0.41
1:B:143:THR:HG23	1:B:144:ASP:N	2.36	0.41
1:D:247[B]:ASN:ND2	1:D:249:THR:H	2.19	0.41
1:A:244:ASP:HB3	1:A:250:MSE:HG2	2.02	0.40
1:B:105:LEU:N	1:B:106:PRO:CD	2.84	0.40
1:A:269:PRO:HG2	1:A:272:ARG:HH21	1.86	0.40
1:C:88:LEU:HD21	1:C:277:ARG:HG3	2.02	0.40
1:C:182[A]:CYS:HA	3:C:305:HOH:O	2.20	0.40
1:C:189:LEU:HD23	1:C:189:LEU:HA	1.72	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	205/300 (68%)	200 (98%)	5 (2%)	0	100	100
1	B	213/300 (71%)	209 (98%)	4 (2%)	0	100	100
1	C	198/300 (66%)	193 (98%)	5 (2%)	0	100	100
1	D	215/300 (72%)	212 (99%)	3 (1%)	0	100	100
All	All	831/1200 (69%)	814 (98%)	17 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	182/246 (74%)	174 (96%)	8 (4%)	28	16
1	B	186/246 (76%)	181 (97%)	5 (3%)	44	34
1	C	176/246 (72%)	162 (92%)	14 (8%)	12	4
1	D	188/246 (76%)	180 (96%)	8 (4%)	29	17
All	All	732/984 (74%)	697 (95%)	35 (5%)	25	14

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	ILE
1	A	125	THR
1	A	142	LEU
1	A	163	ARG
1	A	189	LEU
1	A	219	GLU
1	A	268	TYR
1	A	271	ASN
1	B	125	THR
1	B	138	ARG
1	B	151	ARG
1	B	272	ARG
1	B	274	LEU
1	C	85	LYS
1	C	87	ARG
1	C	99	LEU
1	C	121	VAL
1	C	128	TYR
1	C	129	LEU
1	C	131	GLU
1	C	132	ASN
1	C	141	THR
1	C	150	ARG
1	C	151	ARG

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Mol	Chain	Res	Type
1	C	196	MSE
1	C	224	LEU
1	C	256	ASP
1	D	83	LEU
1	D	123	ASP
1	D	129	LEU
1	D	191	LYS
1	D	195	GLN
1	D	196	MSE
1	D	219	GLU
1	D	224	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
1	A	145	GLN
1	A	181	ASN
1	A	271	ASN
1	B	98	ASN
1	B	247	ASN
1	B	258	GLN
1	B	293	GLN
1	C	98	ASN
1	C	194	GLN
1	D	98	ASN
1	D	116	GLN
1	D	199	HIS

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

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	201/300 (67%)	0.52	16 (7%)	12 13	16, 30, 75, 119	0
1	B	205/300 (68%)	0.37	12 (5%)	22 24	18, 31, 73, 108	0
1	C	197/300 (65%)	0.45	19 (9%)	8 8	20, 37, 81, 99	0
1	D	205/300 (68%)	0.42	15 (7%)	15 16	16, 29, 68, 104	0
All	All	808/1200 (67%)	0.44	62 (7%)	13 14	16, 32, 77, 119	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	127	ASP	9.0
1	A	189	LEU	7.3
1	C	130	ALA	6.5
1	B	128	TYR	5.6
1	C	129	LEU	5.5
1	A	274	LEU	5.2
1	A	273	HIS	5.1
1	D	189	LEU	4.8
1	D	192	THR	4.5
1	A	143	THR	4.3
1	A	125	THR	4.3
1	C	295	GLY	4.2
1	A	83	LEU	4.2
1	B	192	THR	4.2
1	B	143	THR	4.1
1	B	83	LEU	4.0
1	D	128	TYR	4.0
1	A	272	ARG	3.8
1	D	193	GLY	3.8
1	C	294	ASN	3.7
1	C	190	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	246	ARG	3.7
1	A	128	TYR	3.7
1	B	191	LYS	3.6
1	C	207	ILE	3.5
1	B	144	ASP	3.4
1	C	246	ARG	3.3
1	B	131	GLU	3.2
1	C	171	VAL	3.2
1	D	191	LYS	3.2
1	C	247	ASN	3.1
1	D	85	LYS	3.0
1	D	194	GLN	3.0
1	D	294	ASN	3.0
1	B	294	ASN	2.8
1	B	126	ILE	2.8
1	C	83	LEU	2.7
1	A	194	GLN	2.7
1	D	204	ASN	2.7
1	B	201	ARG	2.7
1	C	131	GLU	2.7
1	C	291[A]	GLN	2.6
1	A	107	GLU	2.6
1	D	125	THR	2.6
1	C	141	THR	2.6
1	D	242[A]	ARG	2.6
1	C	128	TYR	2.5
1	C	204	ASN	2.5
1	D	190	PRO	2.5
1	D	126	ILE	2.4
1	C	191	LYS	2.4
1	A	247	ASN	2.4
1	C	201	ARG	2.3
1	A	113	PRO	2.2
1	C	164	ASP	2.2
1	A	84	PRO	2.2
1	A	111[A]	LYS	2.2
1	C	243	GLU	2.1
1	A	294	ASN	2.1
1	A	243	GLU	2.1
1	B	204	ASN	2.1
1	D	114	ASP	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 monosaccharides 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, 95<sup>th</sup> 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
2	CL	D	299	1/1	0.99	0.04	24,24,24,24	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.