



# Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 09:58 pm BST

PDB ID : 2GZX  
Title : Crystal Structure of the TatD deoxyribonuclease MW0446 from *Staphylococcus aureus*. Northeast Structural Genomics Consortium Target ZR237.  
Authors : Vorobiev, S.M.; Neely, H.; Seetharaman, J.; Wang, D.; Fang, Y.; Xiao, R.; Acton, T.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)  
Deposited on : 2006-05-12  
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](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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

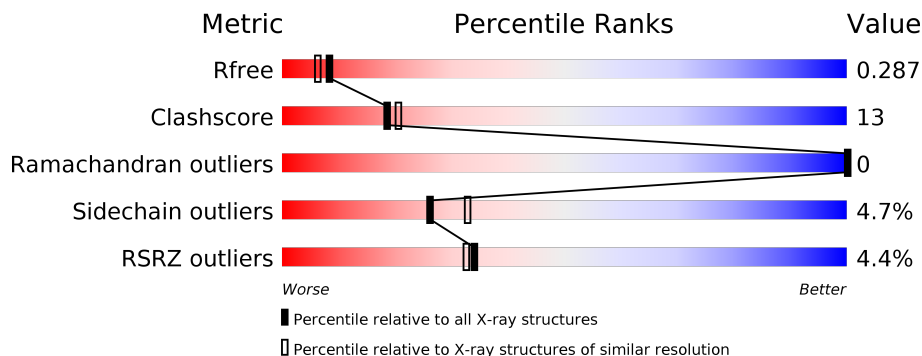
# 1 Overall quality at a glance

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))
$R_{free}$	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 on 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	265	 3% 73% 21% 5% 5%
1	B	265	 5% 66% 24% 5% 5%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 4104 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 TatD related DNase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	253	2015	1283	343	382	2	5	0	0	0
1	B	253	2004	1276	341	380	2	5	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
A	33	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
A	47	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
A	93	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
A	152	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
A	196	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
A	258	LEU	-	EXPRESSION TAG	UNP Q1Y6Z0
A	259	GLU	-	EXPRESSION TAG	UNP Q1Y6Z0
A	260	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
A	261	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
A	262	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
A	263	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
A	264	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
A	265	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
B	33	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
B	47	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
B	93	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
B	152	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
B	196	MSE	MET	MODIFIED RESIDUE	UNP Q1Y6Z0
B	258	LEU	-	EXPRESSION TAG	UNP Q1Y6Z0
B	259	GLU	-	EXPRESSION TAG	UNP Q1Y6Z0
B	260	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
B	261	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
B	262	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	263	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
B	264	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0
B	265	HIS	-	EXPRESSION TAG	UNP Q1Y6Z0

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Ni 2 2	0	0
2	A	2	Total Ni 2 2	0	0

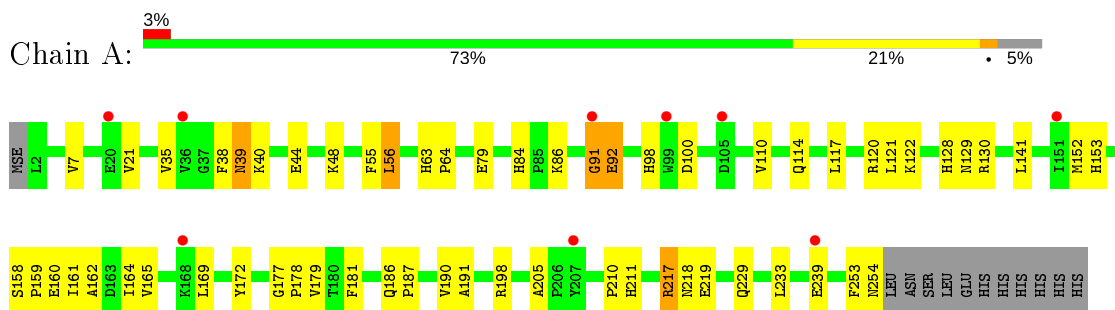
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	41	Total O 41 41	0	0
3	B	40	Total O 40 40	0	0

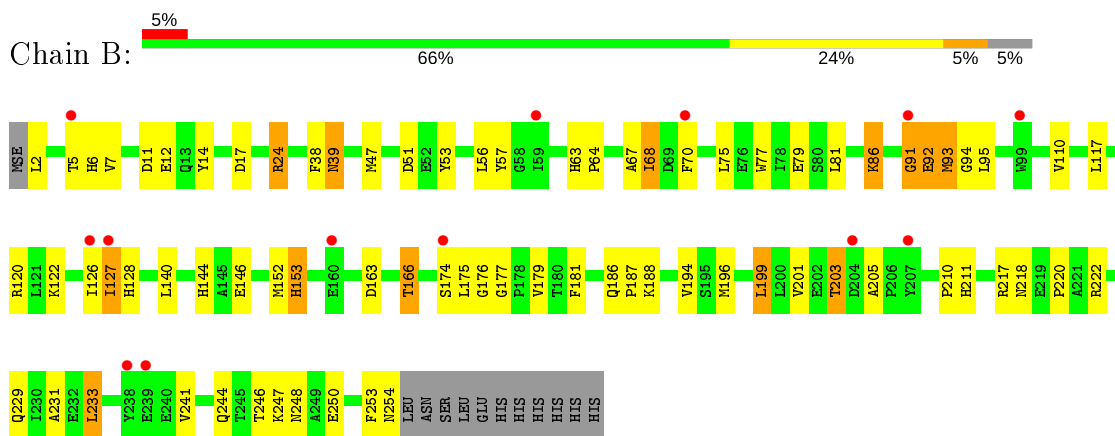
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: putative TatD related DNase



- Molecule 1: putative TatD related DNase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.68Å 77.32Å 76.13Å 90.00° 98.01° 90.00°	Depositor
Resolution (Å)	26.79 – 2.20 29.66 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.9 (26.79-2.20) 98.3 (29.66-2.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.06 (at 2.20Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.258 , 0.286 0.262 , 0.287	Depositor DCC
$R_{free}$ test set	2103 reflections (3.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.4	Xtrriage
Anisotropy	0.294	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 34.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	4104	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.95% 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](#)

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

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	0.59	2/2054 (0.1%)	0.77	7/2774 (0.3%)
1	B	0.52	2/2043 (0.1%)	0.74	7/2762 (0.3%)
All	All	0.56	4/4097 (0.1%)	0.75	14/5536 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	92	GLU	CB-CG	-15.30	1.23	1.52
1	B	92	GLU	CB-CG	-9.33	1.34	1.52
1	B	93	MSE	SE-CE	-6.25	1.58	1.95
1	A	91	GLY	CA-C	-5.98	1.42	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	GLU	CA-CB-CG	-11.83	87.38	113.40
1	A	91	GLY	CA-C-N	-10.38	94.38	117.20
1	B	91	GLY	CA-C-N	-10.17	94.83	117.20
1	A	92	GLU	N-CA-CB	9.59	127.86	110.60
1	B	92	GLU	CA-CB-CG	-8.90	93.82	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	91	GLY	C-N-CA	8.72	143.51	121.70
1	B	92	GLU	N-CA-CB	8.28	125.50	110.60
1	B	91	GLY	C-N-CA	7.27	139.88	121.70
1	A	91	GLY	O-C-N	7.22	134.25	122.70
1	A	92	GLU	CB-CG-CD	-6.12	97.69	114.20
1	A	92	GLU	N-CA-C	-6.08	94.59	111.00
1	B	203	THR	N-CA-C	-6.04	94.71	111.00
1	B	91	GLY	O-C-N	5.26	131.12	122.70
1	B	92	GLU	N-CA-C	-5.03	97.41	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	91	GLY	Mainchain
1	B	91	GLY	Mainchain

## 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	2015	0	1977	43	0
1	B	2004	0	1953	63	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	41	0	0	3	0
3	B	40	0	0	2	0
All	All	4104	0	3930	105	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 13.

All (105) 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:24:ARG:HG2	1:B:24:ARG:HH11	1.32	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:MSE:HE2	1:B:81:LEU:HD12	1.55	0.89
1:A:229:GLN:HE21	1:A:233:LEU:HD13	1.44	0.80
1:B:5:THR:HG22	3:B:370:HOH:O	1.85	0.77
1:B:38:PHE:HB2	1:B:63:HIS:HB2	1.69	0.75
1:B:186:GLN:HB2	1:B:187:PRO:HD3	1.70	0.74
1:B:186:GLN:H	1:B:186:GLN:CD	1.93	0.72
1:A:239:GLU:CD	1:A:239:GLU:H	1.91	0.71
1:B:244:GLN:HE22	1:B:247:LYS:HD3	1.56	0.71
1:A:21:VAL:HG13	1:A:219:GLU:HG3	1.71	0.70
1:B:86:LYS:HE2	3:B:337:HOH:O	1.90	0.70
1:B:24:ARG:HG2	1:B:24:ARG:NH1	2.04	0.70
1:B:7:VAL:HG21	1:B:220:PRO:HG3	1.75	0.69
1:A:219:GLU:HG2	3:A:302:HOH:O	1.91	0.69
1:A:217:ARG:HH11	1:A:217:ARG:HG3	1.58	0.68
1:A:162:ALA:O	1:A:165:VAL:HG22	1.95	0.66
1:B:79:GLU:HG2	1:B:117:LEU:CD1	2.25	0.66
1:B:177:GLY:HA2	1:B:210:PRO:HB3	1.78	0.66
1:B:92:GLU:CG	1:B:128:HIS:HB2	2.26	0.66
1:B:127:ILE:HD12	1:B:140:LEU:HD11	1.77	0.65
1:A:92:GLU:OE2	1:A:128:HIS:ND1	2.30	0.65
1:B:181:PHE:O	1:B:188:LYS:HE2	1.99	0.63
1:B:70:PHE:CD2	1:B:110:VAL:HG22	2.34	0.63
1:B:244:GLN:NE2	1:B:247:LYS:HD3	2.14	0.62
1:A:191:ALA:HB3	1:A:233:LEU:HD23	1.81	0.61
1:A:98:HIS:CB	1:A:130:ARG:HD3	2.31	0.61
1:A:98:HIS:HB2	1:A:130:ARG:HD3	1.84	0.60
1:B:57:TYR:CD1	1:B:86:LYS:HG3	2.37	0.60
1:A:92:GLU:CG	1:A:128:HIS:HB2	2.33	0.59
1:B:79:GLU:HG2	1:B:117:LEU:HD11	1.84	0.59
1:B:229:GLN:HG3	1:B:233:LEU:HD22	1.85	0.59
1:A:253:PHE:O	1:A:254:ASN:CB	2.51	0.57
1:B:7:VAL:HG23	1:B:205:ALA:HB3	1.86	0.57
1:B:244:GLN:HE21	1:B:248:ASN:HD21	1.52	0.57
1:A:40:LYS:O	1:A:44:GLU:HG3	2.04	0.57
1:A:229:GLN:NE2	1:A:233:LEU:HD13	2.18	0.57
1:B:217:ARG:HD2	1:B:218:ASN:O	2.05	0.56
1:A:177:GLY:HA2	1:A:210:PRO:HB3	1.86	0.56
1:B:6:HIS:O	1:B:203:THR:O	2.23	0.56
1:A:141:LEU:HD23	1:A:169:LEU:HD21	1.88	0.56
1:A:161:ILE:O	1:A:165:VAL:HG13	2.07	0.55
1:B:196:MSE:HG3	1:B:244:GLN:HG2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:ASP:HA	1:B:166:THR:HG22	1.90	0.53
1:A:158:SER:HB2	1:A:159:PRO:HD2	1.90	0.53
1:B:127:ILE:HD11	1:B:152:MSE:CE	2.38	0.53
1:B:92:GLU:HG2	1:B:128:HIS:HB2	1.91	0.53
1:A:79:GLU:HG3	1:A:121:LEU:HD11	1.90	0.52
1:A:186:GLN:O	1:A:190:VAL:HG23	2.11	0.51
1:B:68:ILE:O	1:B:68:ILE:HD13	2.11	0.51
1:B:79:GLU:HG2	1:B:117:LEU:HD13	1.92	0.51
1:B:253:PHE:O	1:B:254:ASN:CB	2.58	0.50
1:A:186:GLN:HB3	1:A:187:PRO:HD3	1.94	0.50
1:A:100:ASP:OD2	1:B:211:HIS:HE1	1.95	0.49
1:A:160:GLU:O	1:A:164:ILE:HG13	2.12	0.49
1:A:117:LEU:HD22	1:A:121:LEU:HD13	1.93	0.49
1:A:205:ALA:HA	1:A:218:ASN:HB3	1.94	0.49
1:A:38:PHE:HB2	1:A:63:HIS:HB2	1.95	0.48
1:B:11:ASP:OD2	1:B:12:GLU:N	2.46	0.48
1:A:217:ARG:HH11	1:A:217:ARG:CG	2.23	0.48
1:B:176:GLY:O	1:B:179:VAL:HG12	2.13	0.48
1:B:24:ARG:CG	1:B:24:ARG:NH1	2.73	0.48
1:B:67:ALA:O	1:B:70:PHE:CD1	2.67	0.48
1:B:231:ALA:HB2	1:B:241:VAL:HG21	1.95	0.48
1:B:75:LEU:HD23	1:B:75:LEU:C	2.34	0.47
1:A:152:MSE:HE3	3:A:375:HOH:O	2.14	0.47
1:B:246:THR:O	1:B:250:GLU:HG3	2.15	0.47
1:B:194:VAL:CG1	1:B:199:LEU:HD13	2.45	0.46
1:A:55:PHE:CE2	1:A:56:LEU:HD13	2.51	0.46
1:B:203:THR:HB	1:B:218:ASN:ND2	2.31	0.45
1:B:77:TRP:NE1	1:B:81:LEU:HD21	2.31	0.45
1:A:120:ARG:O	1:A:122:LYS:HD2	2.15	0.45
1:B:126:ILE:HD12	1:B:126:ILE:N	2.31	0.45
1:B:127:ILE:HG13	1:B:152:MSE:SE	2.67	0.45
1:B:229:GLN:HG3	1:B:233:LEU:CD2	2.46	0.45
1:A:217:ARG:HG3	1:A:217:ARG:O	2.15	0.45
1:B:203:THR:HB	1:B:218:ASN:HD21	1.82	0.45
1:B:38:PHE:CD2	1:B:63:HIS:HB2	2.52	0.45
1:B:39:ASN:HA	1:B:39:ASN:HD22	1.52	0.45
1:A:129:ASN:HB3	3:A:383:HOH:O	2.16	0.45
1:B:127:ILE:HD11	1:B:152:MSE:HE1	1.98	0.45
1:B:127:ILE:HD11	1:B:152:MSE:SE	2.67	0.44
1:B:120:ARG:O	1:B:122:LYS:HE2	2.16	0.44
1:B:205:ALA:HA	1:B:218:ASN:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:PRO:HA	1:A:181:PHE:CD2	2.53	0.44
1:A:84:HIS:CE1	1:A:86:LYS:HB2	2.53	0.44
1:A:39:ASN:HD22	1:A:39:ASN:HA	1.54	0.43
1:B:64:PRO:HB3	1:B:94:GLY:O	2.18	0.43
1:A:217:ARG:NH1	1:A:217:ARG:CG	2.81	0.43
1:A:48:LYS:HB3	1:A:48:LYS:HE2	1.84	0.42
1:B:70:PHE:CG	1:B:110:VAL:HG22	2.54	0.42
1:B:153:HIS:HA	1:B:174:SER:HB3	2.02	0.42
1:B:67:ALA:O	1:B:70:PHE:HD1	2.03	0.42
1:A:239:GLU:N	1:A:239:GLU:CD	2.68	0.42
1:B:144:HIS:HA	1:B:146:GLU:OE1	2.19	0.42
1:A:63:HIS:ND1	1:A:64:PRO:HD2	2.35	0.41
1:B:53:TYR:HB2	1:B:56:LEU:HD22	2.01	0.41
1:B:14:TYR:OH	1:B:205:ALA:HB1	2.21	0.41
1:B:2:LEU:HD11	1:B:201:VAL:HG21	2.02	0.41
1:B:194:VAL:HG11	1:B:199:LEU:HD13	2.01	0.41
1:A:110:VAL:HG12	1:A:114:GLN:HE21	1.86	0.41
1:A:205:ALA:CB	1:A:218:ASN:HB3	2.51	0.41
1:B:93:MSE:CG	1:B:127:ILE:HG22	2.51	0.41
1:B:70:PHE:CG	1:B:70:PHE:O	2.74	0.40
1:A:172:TYR:CZ	1:A:198:ARG:NH2	2.89	0.40
1:A:7:VAL:O	1:A:35:VAL:HA	2.21	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	251/265 (95%)	243 (97%)	8 (3%)	0	100	100
1	B	251/265 (95%)	241 (96%)	10 (4%)	0	100	100
All	All	502/530 (95%)	484 (96%)	18 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	216/227 (95%)	210 (97%)	6 (3%)	43	56
1	B	213/227 (94%)	199 (93%)	14 (7%)	16	19
All	All	429/454 (94%)	409 (95%)	20 (5%)	26	33

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	56	LEU
1	A	153	HIS
1	A	179	VAL
1	A	211	HIS
1	A	217	ARG
1	B	17	ASP
1	B	24	ARG
1	B	39	ASN
1	B	51	ASP
1	B	68	ILE
1	B	86	LYS
1	B	95	LEU
1	B	127	ILE
1	B	153	HIS
1	B	166	THR
1	B	175	LEU
1	B	199	LEU
1	B	222	ARG
1	B	233	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	167	ASN
1	A	183	ASN
1	A	211	HIS
1	A	229	GLN
1	A	244	GLN
1	A	248	ASN
1	B	39	ASN
1	B	134	GLN
1	B	167	ASN
1	B	183	ASN
1	B	211	HIS
1	B	244	GLN
1	B	248	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are 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 [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	248/265 (93%)	0.44	9 (3%) 42 41	12, 28, 39, 47	0
1	B	248/265 (93%)	0.57	13 (5%) 27 26	16, 30, 42, 49	0
All	All	496/530 (93%)	0.50	22 (4%) 34 32	12, 29, 42, 49	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	70	PHE	5.1
1	A	20	GLU	3.4
1	B	91	GLY	3.2
1	B	127	ILE	3.1
1	B	160	GLU	3.0
1	B	207	TYR	2.8
1	B	204	ASP	2.8
1	B	126	ILE	2.8
1	A	168	LYS	2.7
1	B	99	TRP	2.6
1	B	239	GLU	2.5
1	A	99	TRP	2.4
1	A	207	TYR	2.4
1	A	151	ILE	2.4
1	A	239	GLU	2.4
1	A	91	GLY	2.4
1	B	174	SER	2.2
1	B	59	ILE	2.2
1	B	238	TYR	2.1
1	B	5	THR	2.1
1	A	36	VAL	2.1
1	A	105	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 carbohydrates 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	NI	B	298	1/1	0.09	0.37	30,30,30,30	0
2	NI	A	299	1/1	0.43	0.28	22,22,22,22	0
2	NI	A	300	1/1	0.98	0.13	15,15,15,15	0
2	NI	B	297	1/1	0.99	0.13	21,21,21,21	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.