



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:52 PM GMT

PDB ID : 1YX2  
Title : Crystal Structure of the Probable Aminomethyltransferase from *Bacillus subtilis*  
Authors : Midwest Center for Structural Genomics (MCSG)  
Deposited on : 2005-02-19  
Resolution : 2.08 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

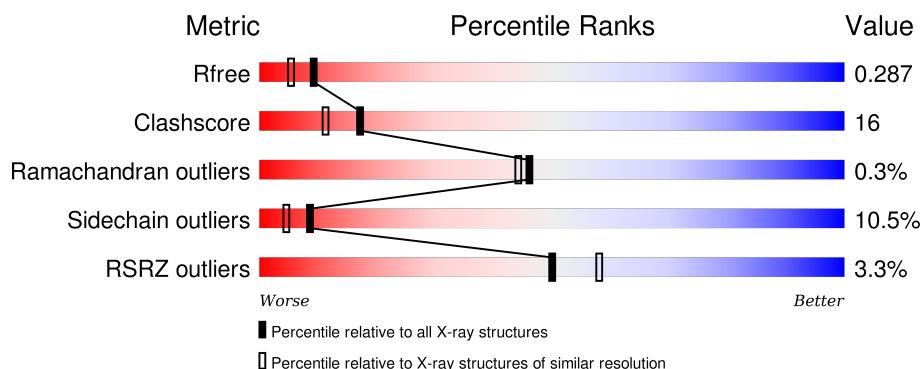
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.08 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	4546 (2.10-2.06)
Clashscore	102246	5101 (2.10-2.06)
Ramachandran outliers	100387	5048 (2.10-2.06)
Sidechain outliers	100360	5049 (2.10-2.06)
RSRZ outliers	91569	4556 (2.10-2.06)

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	365	 4% 65% 28% 6% .
1	B	365	 2% 74% 21% . .

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6482 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 Aminomethyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	Se	0	27	0
			2999	1895	517	578	3	6			
1	B	362	Total	C	N	O	S	Se	0	17	0
			2955	1870	508	567	3	7			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	CLONING ARTIFACT	UNP P54378
A	-1	ASN	-	CLONING ARTIFACT	UNP P54378
A	0	ALA	-	CLONING ARTIFACT	UNP P54378
A	1	MSE	MET	MODIFIED RESIDUE	UNP P54378
A	52	MSE	MET	MODIFIED RESIDUE	UNP P54378
A	70	MSE	MET	MODIFIED RESIDUE	UNP P54378
A	87	MSE	MET	MODIFIED RESIDUE	UNP P54378
A	124	MSE	MET	MODIFIED RESIDUE	UNP P54378
A	205	MSE	MET	MODIFIED RESIDUE	UNP P54378
A	237	ILE	VAL	CONFLICT	UNP P54378
A	290	MSE	MET	MODIFIED RESIDUE	UNP P54378
B	-2	SER	-	CLONING ARTIFACT	UNP P54378
B	-1	ASN	-	CLONING ARTIFACT	UNP P54378
B	0	ALA	-	CLONING ARTIFACT	UNP P54378
B	1	MSE	MET	MODIFIED RESIDUE	UNP P54378
B	52	MSE	MET	MODIFIED RESIDUE	UNP P54378
B	70	MSE	MET	MODIFIED RESIDUE	UNP P54378
B	87	MSE	MET	MODIFIED RESIDUE	UNP P54378
B	124	MSE	MET	MODIFIED RESIDUE	UNP P54378
B	205	MSE	MET	MODIFIED RESIDUE	UNP P54378
B	237	ILE	VAL	CONFLICT	UNP P54378
B	290	MSE	MET	MODIFIED RESIDUE	UNP P54378

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	2	2		

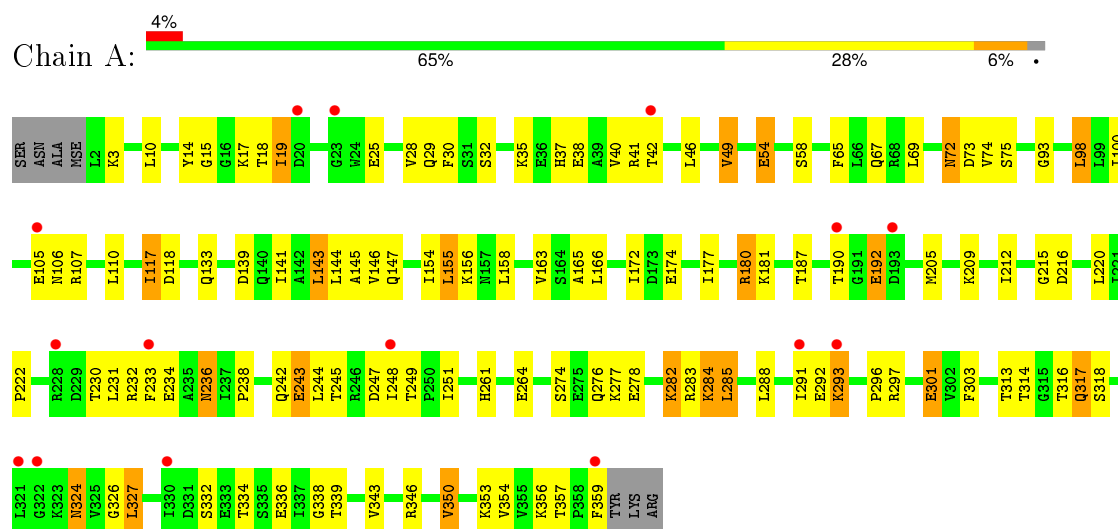
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	216	Total	O	0	0
			216	216		
3	B	308	Total	O	0	0
			308	308		

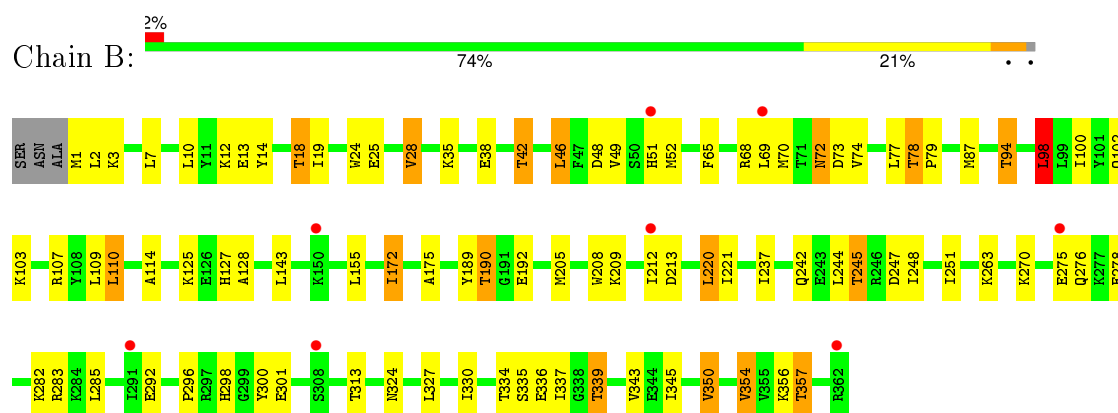
### 3 Residue-property plots

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: Aminomethyltransferase



#### • Molecule 1: Aminomethyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	47.63Å 88.09Å 88.76Å 90.00° 101.78° 90.00°	Depositor
Resolution (Å)	41.20 – 2.08 41.21 – 2.08	Depositor EDS
% Data completeness (in resolution range)	96.0 (41.20-2.08) 96.0 (41.21-2.08)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.2.0000	Depositor
R, $R_{free}$	0.212 , 0.288 0.211 , 0.287	Depositor DCC
$R_{free}$ test set	4121 reflections (11.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.8	Xtriage
Anisotropy	0.861	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 50.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 41476 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6482	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	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 44.44 % 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 1.5247e-04. 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, 0.375 respectively for untwinned datasets, and 0.333, 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: EDO

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	0.49	0/3041	0.68	2/4080 (0.0%)
1	B	0.53	0/2997	0.71	2/4019 (0.0%)
All	All	0.51	0/6038	0.69	4/8099 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	LEU	CA-CB-CG	8.33	134.45	115.30
1	A	98	LEU	CA-CB-CG	7.38	132.28	115.30
1	B	220	LEU	CA-CB-CG	6.75	130.82	115.30
1	A	220	LEU	CA-CB-CG	5.07	126.96	115.30

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	2999	0	3006	99	0
1	B	2955	0	2972	96	0
2	B	4	0	6	1	0
3	A	216	0	0	11	0
3	B	308	0	0	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6482	0	5984	195	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

All (195) 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:103[B]:LYS:HD2	1:B:107[B]:ARG:HB3	1.33	1.06
1:B:103[B]:LYS:HZ3	1:B:107[B]:ARG:HH21	1.04	1.02
1:A:249:THR:HG21	1:A:276:GLN:OE1	1.60	1.01
1:B:10[A]:LEU:HD22	1:B:14:TYR:HE1	1.22	0.99
1:A:244:LEU:HA	1:A:248[A]:ILE:HG21	1.48	0.94
1:B:103[B]:LYS:NZ	1:B:107[B]:ARG:HE	1.66	0.93
1:B:7:LEU:O	1:B:10[B]:LEU:HB3	1.69	0.92
1:A:238:PRO:HA	1:A:243[B]:GLU:HG2	1.51	0.92
1:A:187:THR:HG21	3:A:466:HOH:O	1.71	0.91
1:A:72:ASN:HD22	1:A:73:ASP:H	1.14	0.90
1:B:103[B]:LYS:HZ2	1:B:107[B]:ARG:HE	0.93	0.90
1:A:242:GLN:HG2	1:A:313:THR:O	1.72	0.89
1:A:336[A]:GLU:O	1:A:354[A]:VAL:HG11	1.73	0.88
1:B:245:THR:HG22	1:B:247:ASP:H	1.39	0.87
1:B:212[A]:ILE:HG23	3:B:1719:HOH:O	1.73	0.87
1:B:190:THR:HG22	1:B:192:GLU:H	1.41	0.85
1:B:103[B]:LYS:HD2	1:B:107[B]:ARG:CB	2.07	0.85
1:A:10:LEU:HD13	1:A:205:MSE:HE2	1.59	0.85
1:B:103[B]:LYS:HZ2	1:B:107[B]:ARG:NE	1.75	0.84
1:B:78:THR:HG22	1:B:79:PRO:HD2	1.62	0.79
1:B:10[B]:LEU:HD21	1:B:208:TRP:CE2	2.17	0.79
1:B:245:THR:HG21	3:B:1645:HOH:O	1.83	0.79
1:B:10[B]:LEU:HD11	1:B:208:TRP:CD1	2.18	0.78
1:B:72:ASN:HD22	1:B:73:ASP:H	1.30	0.78
1:B:292:GLU:HB2	1:B:350:VAL:HG23	1.65	0.78
1:B:209:LYS:HA	1:B:212[B]:ILE:HG12	1.65	0.77
1:A:274:SER:O	1:A:278[B]:GLU:HG3	1.86	0.75
1:B:103[B]:LYS:HZ3	1:B:107[B]:ARG:NH2	1.84	0.74
1:B:10[A]:LEU:HG	1:B:205:MSE:HE3	1.70	0.73
1:A:35:LYS:HB2	3:A:558:HOH:O	1.89	0.73
1:B:103[B]:LYS:CD	1:B:107[B]:ARG:HB3	2.15	0.73
1:A:72:ASN:HD22	1:A:73:ASP:N	1.84	0.73
1:B:51[A]:HIS:O	1:B:114:ALA:HB2	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243[A]:GLU:O	1:A:248[A]:ILE:HG12	1.89	0.72
1:B:245:THR:CG2	1:B:247:ASP:H	2.03	0.71
1:B:18:THR:HG21	1:B:25:GLU:OE1	1.91	0.71
1:B:209:LYS:O	1:B:212[B]:ILE:HG13	1.91	0.70
1:A:105:GLU:O	1:A:106[B]:ASN:HB2	1.92	0.70
1:B:10[A]:LEU:HD22	1:B:14:TYR:CE1	2.15	0.70
1:B:69[A]:LEU:HD22	1:B:87:MSE:SE	2.42	0.70
1:A:174:GLU:HG3	1:A:181:LYS:HD2	1.73	0.69
1:A:243[A]:GLU:OE1	1:A:313:THR:OG1	2.10	0.69
1:A:40:VAL:HG21	1:A:231:LEU:HD11	1.72	0.69
1:B:103[B]:LYS:NZ	1:B:107[B]:ARG:HH21	1.87	0.69
1:A:190:THR:HG23	1:A:231:LEU:HD13	1.75	0.68
1:B:7:LEU:O	1:B:10[B]:LEU:CB	2.42	0.68
1:B:94:THR:HG21	1:B:244:LEU:HD22	1.76	0.67
1:A:336[A]:GLU:O	1:A:354[A]:VAL:CG1	2.42	0.66
1:B:1:MSE:HE1	3:B:1621:HOH:O	1.95	0.66
1:A:147:GLN:NE2	3:A:514:HOH:O	2.29	0.66
1:A:245:THR:H	1:A:248[A]:ILE:CG2	2.09	0.65
1:A:65:PHE:O	1:A:69[B]:LEU:HD23	1.96	0.65
1:A:336[B]:GLU:O	1:A:354[B]:VAL:CG2	2.44	0.64
1:B:10[A]:LEU:HD23	1:B:13:GLU:OE1	1.98	0.64
1:B:10[B]:LEU:HD21	1:B:208:TRP:CD2	2.32	0.64
1:A:58:SER:HB3	1:A:107[B]:ARG:HG3	1.80	0.62
1:B:245:THR:HG22	1:B:247:ASP:N	2.13	0.62
1:A:155:LEU:HA	1:A:158:LEU:HD12	1.81	0.62
1:A:336[B]:GLU:O	1:A:354[B]:VAL:HG21	2.00	0.62
1:B:336:GLU:O	1:B:339:THR:HG23	2.00	0.62
1:B:103[B]:LYS:NZ	1:B:107[B]:ARG:NE	2.43	0.62
1:A:238:PRO:HA	1:A:243[B]:GLU:CG	2.30	0.61
1:A:288:LEU:HA	1:A:353[A]:LYS:O	2.02	0.60
1:B:209:LYS:O	1:B:212[B]:ILE:CG1	2.49	0.59
1:A:67:GLN:NE2	1:A:75:SER:OG	2.34	0.59
1:B:212[B]:ILE:HG13	1:B:213:ASP:N	2.14	0.59
1:B:68:ARG:HB2	1:B:69[B]:LEU:HD12	1.83	0.59
1:A:244:LEU:CA	1:A:248[A]:ILE:HG21	2.29	0.58
1:B:73:ASP:HA	1:B:263:LYS:HD3	1.86	0.58
1:B:72:ASN:HD22	1:B:73:ASP:N	2.00	0.57
1:B:69[B]:LEU:HD21	1:B:127:HIS:HB2	1.86	0.57
1:A:282:LYS:HG2	1:A:283:ARG:HG3	1.86	0.56
1:A:46[B]:LEU:HB3	1:A:222:PRO:HA	1.87	0.56
1:B:38:GLU:O	1:B:42:THR:HB	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:242:GLN:HG2	1:B:298:HIS:CD2	2.39	0.56
1:B:212[B]:ILE:CD1	3:B:1538:HOH:O	2.53	0.56
1:A:93:GLY:HA2	1:A:248[A]:ILE:O	2.06	0.56
1:B:79:PRO:HA	1:B:102:GLN:O	2.05	0.56
1:A:292:GLU:HB2	1:A:350:VAL:HG23	1.88	0.55
1:A:72:ASN:ND2	1:A:73:ASP:H	1.95	0.55
1:B:19:ILE:HD13	1:B:28:VAL:HG13	1.87	0.55
1:B:48:ASP:O	2:B:1501:EDO:H21	2.07	0.54
1:B:49:VAL:HG22	1:B:49:VAL:O	2.07	0.54
1:A:10:LEU:HG	1:A:14:TYR:HE1	1.72	0.54
1:B:70:MSE:HG3	1:B:100:ILE:HD11	1.88	0.54
1:A:288:LEU:HD23	1:A:354[B]:VAL:HG12	1.90	0.54
1:A:243[A]:GLU:O	1:A:248[A]:ILE:CG1	2.55	0.54
1:B:98:LEU:HD23	1:B:110:LEU:HB3	1.89	0.54
1:A:288:LEU:CD2	1:A:354[B]:VAL:HG12	2.38	0.53
1:A:156:LYS:HE2	3:A:575:HOH:O	2.07	0.53
1:A:177:ILE:O	1:A:180:ARG:HB2	2.08	0.53
1:A:243[A]:GLU:OE1	1:A:327:LEU:HB3	2.09	0.53
1:A:243[A]:GLU:CD	1:A:313:THR:HG1	2.12	0.53
1:A:243[A]:GLU:O	1:A:248[A]:ILE:CD1	2.57	0.52
1:A:245:THR:H	1:A:248[A]:ILE:HG22	1.75	0.52
1:A:261:HIS:CD2	1:A:277:LYS:HD3	2.45	0.52
1:B:296:PRO:HD2	1:B:324:ASN:HD21	1.73	0.52
1:A:32:SER:HB3	1:A:35:LYS:HG3	1.92	0.52
1:B:10[A]:LEU:HD12	1:B:205:MSE:HG2	1.92	0.51
1:A:54:GLU:HG3	1:A:141:ILE:HB	1.93	0.51
1:B:209:LYS:CA	1:B:212[B]:ILE:HG12	2.37	0.51
1:A:190:THR:HB	3:A:514:HOH:O	2.10	0.51
1:A:232:ARG:NH2	1:A:243[B]:GLU:OE1	2.44	0.51
1:A:233[A]:PHE:CE2	1:A:316:THR:HG22	2.46	0.50
1:B:24:TRP:CD1	1:B:51[B]:HIS:CD2	3.00	0.50
1:A:284[A]:LYS:HG3	1:A:285:LEU:N	2.26	0.50
1:A:245:THR:O	1:A:248[A]:ILE:HG22	2.12	0.50
1:A:209:LYS:O	1:A:212:ILE:HG13	2.12	0.50
1:A:17[A]:LYS:HD3	1:A:29:GLN:HG3	1.93	0.50
1:B:46:LEU:HD12	1:B:212[A]:ILE:HG13	1.93	0.49
1:B:337:ILE:HA	1:B:354:VAL:HG22	1.94	0.49
1:A:357:THR:HG23	3:A:529:HOH:O	2.12	0.49
1:A:243[A]:GLU:OE1	1:A:285:LEU:HD21	2.11	0.49
1:A:18:THR:CG2	1:A:25:GLU:HB2	2.42	0.49
1:A:233[A]:PHE:HZ	1:A:314:THR:O	1.96	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46[A]:LEU:HD12	1:A:145:ALA:O	2.13	0.49
1:A:301:GLU:HG2	1:A:303:PHE:CE1	2.48	0.48
1:A:317[B]:GLN:HG3	1:A:318:SER:N	2.27	0.48
1:B:189:TYR:CE1	1:B:237:ILE:CG2	2.96	0.48
1:B:189:TYR:CE1	1:B:237:ILE:HG21	2.48	0.48
1:A:49:VAL:HG22	1:A:49:VAL:O	2.13	0.48
1:A:165:ALA:HB3	3:A:489:HOH:O	2.13	0.47
1:B:357:THR:CG2	3:B:1786:HOH:O	2.62	0.47
1:A:166:LEU:HD21	1:A:172:ILE:HG13	1.96	0.47
1:B:24:TRP:CD1	1:B:51[B]:HIS:HD2	2.32	0.47
1:A:190:THR:HG22	1:A:192:GLU:HG2	1.97	0.47
1:A:49:VAL:HG22	1:A:143:LEU:HD13	1.95	0.47
1:A:296:PRO:HD2	1:A:324:ASN:OD1	2.15	0.47
1:B:94:THR:HG22	1:B:248:ILE:O	2.15	0.47
1:B:35[B]:LYS:HG2	1:B:221:ILE:CD1	2.44	0.47
1:A:216:ASP:HB3	3:A:421:HOH:O	2.15	0.46
1:A:46[A]:LEU:HD13	1:A:146:VAL:HG22	1.97	0.46
1:B:10[A]:LEU:CD2	1:B:13:GLU:OE1	2.64	0.46
1:A:14:TYR:HE2	1:A:212:ILE:HD13	1.78	0.46
1:B:172:ILE:HG12	1:B:175:ALA:HB2	1.98	0.46
1:A:297:ARG:NE	3:A:552:HOH:O	2.48	0.46
1:B:189:TYR:CD1	1:B:237:ILE:HG21	2.52	0.45
1:A:233[A]:PHE:HE1	1:A:314:THR:CG2	2.29	0.45
1:A:37:HIS:HE1	1:A:234:GLU:OE1	1.99	0.45
1:B:298:HIS:HD2	1:B:313:THR:O	1.99	0.45
1:B:212[B]:ILE:HD13	3:B:1538:HOH:O	2.16	0.45
1:B:10[A]:LEU:HD21	1:B:209:LYS:NZ	2.31	0.44
1:B:334:THR:HG22	1:B:334:THR:O	2.17	0.44
1:A:30:PHE:CG	1:A:222:PRO:HB2	2.53	0.44
1:A:41[A]:ARG:NH2	1:A:234:GLU:OE1	2.50	0.44
1:B:103[B]:LYS:CD	1:B:107[B]:ARG:NE	2.81	0.44
1:A:40:VAL:HG21	1:A:231:LEU:CD1	2.45	0.44
1:B:282:LYS:HG3	1:B:283:ARG:HG3	1.99	0.44
1:B:65:PHE:CE2	1:B:128:ALA:HA	2.53	0.44
1:B:275[B]:GLU:HG2	3:B:1625:HOH:O	2.17	0.44
1:A:233[B]:PHE:CD1	1:A:327:LEU:HD13	2.53	0.43
1:B:51[A]:HIS:CD2	1:B:51[A]:HIS:H	2.35	0.43
1:B:94:THR:CG2	1:B:248:ILE:O	2.66	0.43
1:A:19:ILE:HB	1:A:28:VAL:HG13	2.00	0.43
1:A:117:ILE:HG13	1:A:118:ASP:N	2.33	0.43
1:A:356[B]:LYS:HE3	1:A:359:PHE:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103[B]:LYS:HD3	1:B:107[B]:ARG:CZ	2.49	0.43
1:B:103[B]:LYS:NZ	1:B:107[B]:ARG:NH2	2.56	0.43
1:A:15:GLY:O	1:A:17[A]:LYS:HD2	2.19	0.43
1:A:100:ILE:HG12	1:A:110:LEU:HD22	2.00	0.43
1:A:336[B]:GLU:HG2	1:A:339:THR:OG1	2.19	0.43
1:A:236:ASN:HD22	1:A:236:ASN:HA	1.68	0.43
1:A:147:GLN:HE21	1:A:190:THR:HB	1.83	0.43
1:A:292:GLU:HB3	1:A:293[A]:LYS:HE2	2.00	0.43
1:A:233[A]:PHE:HE2	1:A:326:GLY:CA	2.32	0.43
1:B:263:LYS:O	1:B:270:LYS:NZ	2.43	0.42
1:A:293[B]:LYS:HG2	3:A:395:HOH:O	2.18	0.42
1:B:190:THR:HG22	1:B:192:GLU:N	2.22	0.42
1:B:78:THR:HG22	1:B:79:PRO:CD	2.42	0.42
1:B:296:PRO:CD	1:B:324:ASN:HD21	2.31	0.42
1:A:334:THR:HG22	1:A:339:THR:HG21	2.02	0.42
1:A:249:THR:HG22	1:A:251:ILE:N	2.35	0.42
1:A:324:ASN:HB2	3:A:490:HOH:O	2.19	0.42
1:A:19:ILE:HD13	1:A:28:VAL:CG2	2.50	0.42
1:A:338:GLY:O	1:A:353[A]:LYS:HD3	2.20	0.42
1:B:190:THR:CG2	1:B:192:GLU:HB2	2.49	0.42
1:B:107[A]:ARG:HB3	3:B:1598:HOH:O	2.20	0.41
1:A:243[A]:GLU:CD	1:A:313:THR:OG1	2.59	0.41
1:A:316:THR:HG23	1:A:317[B]:GLN:N	2.36	0.41
1:A:359:PHE:CD2	1:A:359:PHE:N	2.89	0.41
1:B:2:LEU:HD13	1:B:25:GLU:HB3	2.02	0.41
1:B:330:ILE:HD11	1:B:335:SER:HA	2.03	0.41
1:A:154:ILE:HG12	1:A:215:GLY:HA2	2.03	0.41
1:B:251:ILE:HB	1:B:276:GLN:HE21	1.84	0.41
1:B:68:ARG:NH1	3:B:1596:HOH:O	2.47	0.41
1:B:49:VAL:HG22	1:B:52:MSE:HE2	2.02	0.41
1:B:301:GLU:HG3	3:B:1521:HOH:O	2.20	0.41
1:B:336:GLU:O	1:B:339:THR:CG2	2.68	0.41
1:A:46[A]:LEU:HD11	1:A:144:LEU:HB3	2.03	0.41
1:B:24:TRP:CG	1:B:51[B]:HIS:CD2	3.09	0.40
1:B:3:LYS:NZ	3:B:1612:HOH:O	2.51	0.40
1:B:300:TYR:CD2	1:B:345:ILE:HG12	2.56	0.40
1:B:19:ILE:CD1	1:B:28:VAL:HG13	2.50	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	383/365 (105%)	364 (95%)	17 (4%)	2 (0%)	34	29
1	B	377/365 (103%)	359 (95%)	16 (4%)	2 (0%)	34	29
All	All	760/730 (104%)	723 (95%)	33 (4%)	4 (0%)	46	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	346[A]	ARG
1	A	346[B]	ARG
1	B	125[A]	LYS
1	B	125[B]	LYS

### 5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	321/293 (110%)	282 (88%)	39 (12%)	6	3
1	B	315/293 (108%)	285 (90%)	30 (10%)	11	6
All	All	636/586 (108%)	567 (89%)	69 (11%)	8	4

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	19	ILE

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Mol	Chain	Res	Type
1	A	38	GLU
1	A	42	THR
1	A	49	VAL
1	A	54	GLU
1	A	72	ASN
1	A	74	VAL
1	A	98	LEU
1	A	117	ILE
1	A	133	GLN
1	A	139[A]	ASP
1	A	139[B]	ASP
1	A	143	LEU
1	A	155	LEU
1	A	163	VAL
1	A	180	ARG
1	A	192	GLU
1	A	230	THR
1	A	236	ASN
1	A	243[A]	GLU
1	A	243[B]	GLU
1	A	247	ASP
1	A	264	GLU
1	A	282	LYS
1	A	284[A]	LYS
1	A	284[B]	LYS
1	A	285	LEU
1	A	291	ILE
1	A	293[A]	LYS
1	A	293[B]	LYS
1	A	301	GLU
1	A	317[A]	GLN
1	A	317[B]	GLN
1	A	324	ASN
1	A	327	LEU
1	A	332	SER
1	A	343	VAL
1	A	350	VAL
1	B	12[A]	LYS
1	B	12[B]	LYS
1	B	18	THR
1	B	28	VAL
1	B	42	THR

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Mol	Chain	Res	Type
1	B	46	LEU
1	B	72	ASN
1	B	74	VAL
1	B	77	LEU
1	B	78	THR
1	B	94	THR
1	B	98	LEU
1	B	109	LEU
1	B	110	LEU
1	B	143	LEU
1	B	155	LEU
1	B	172	ILE
1	B	190	THR
1	B	220	LEU
1	B	245	THR
1	B	278[A]	GLU
1	B	278[B]	GLU
1	B	285	LEU
1	B	327	LEU
1	B	339	THR
1	B	343	VAL
1	B	350	VAL
1	B	354	VAL
1	B	356	LYS
1	B	357	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	HIS
1	A	67	GLN
1	A	72	ASN
1	A	102	GLN
1	A	116	ASN
1	A	133	GLN
1	A	136	ASN
1	A	147	GLN
1	A	261	HIS
1	B	72	ASN
1	B	83	GLN
1	B	102	GLN
1	B	106	ASN

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Mol	Chain	Res	Type
1	B	116	ASN
1	B	136	ASN
1	B	140	GLN
1	B	147	GLN
1	B	276	GLN
1	B	298	HIS
1	B	317	GLN
1	B	324	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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	EDO	B	1501	-	3,3,3	0.63	0	2,2,2	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	B	1501	-	-	0/1/1/1	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1501	EDO	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	352/365 (96%)	0.27	15 (4%)	39 47	18, 34, 46, 50	3 (0%)
1	B	355/365 (97%)	-0.00	8 (2%)	64 69	15, 25, 42, 50	6 (1%)
All	All	707/730 (96%)	0.13	23 (3%)	50 58	15, 30, 44, 50	9 (1%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	321	LEU	3.5
1	A	248[A]	ILE	3.2
1	A	20[A]	ASP	3.1
1	A	23	GLY	3.0
1	B	362	ARG	3.0
1	A	359	PHE	3.0
1	B	291	ILE	2.9
1	B	308	SER	2.7
1	B	212[A]	ILE	2.6
1	A	291	ILE	2.5
1	A	322	GLY	2.5
1	A	193	ASP	2.3
1	B	69[A]	LEU	2.2
1	A	228[A]	ARG	2.2
1	A	293[A]	LYS	2.2
1	B	275[A]	GLU	2.1
1	B	150	LYS	2.1
1	A	105	GLU	2.1
1	B	51[A]	HIS	2.1
1	A	233[A]	PHE	2.1
1	A	190	THR	2.0
1	A	42	THR	2.0
1	A	330	ILE	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	EDO	B	1501	4/4	0.92	0.14	0.16	20,22,23,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.