



# Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 02:16 AM GMT

PDB ID : 3C20  
Title : Crystal Structure of Threonine-sensitive Aspartokinase from *Methanococcus jannaschii* with L-aspartate  
Authors : Liu, X.; Pavlovsky, A.G.; Viola, R.E.  
Deposited on : 2008-01-24  
Resolution : 2.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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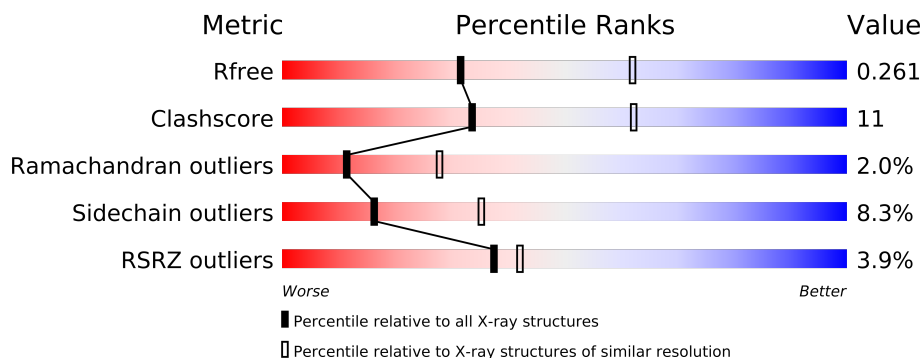
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.70 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))
$R_{free}$	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	473	
1	B	473	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	ASP	A	474	-	X
3	FMT	A	475	-	X
3	FMT	B	475	-	X

## 2 Entry composition i

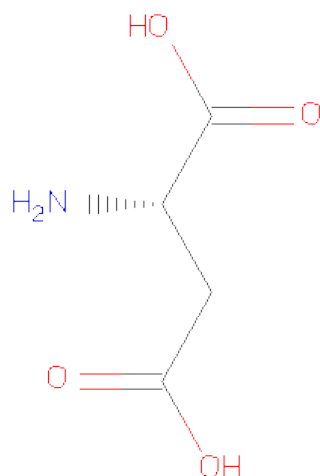
There are 4 unique types of molecules in this entry. The entry contains 7112 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Probable aspartokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	465	Total	C	N	O	S	0	0	0
			3538	2241	593	693	11			
1	B	466	Total	C	N	O	S	0	0	0
			3537	2242	595	690	10			

- Molecule 2 is ASPARTIC ACID (three-letter code: ASP) (formula: C<sub>4</sub>H<sub>7</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			9	4	1	4		
2	A	1	Total	C	N	O	0	0
			9	4	1	4		

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			3	1	2		
3	B	1	Total	C	O	0	0
			3	1	2		

- Molecule 4 is water.

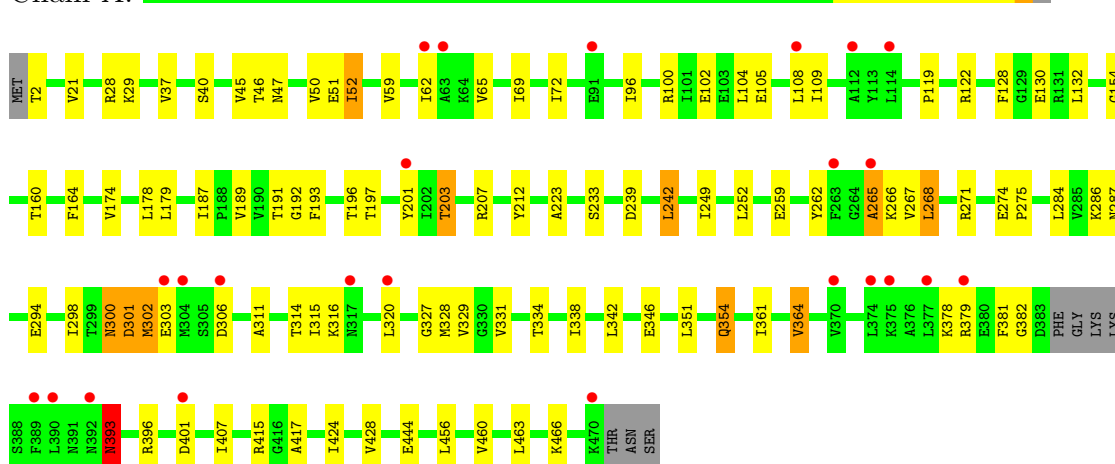
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	O	0	0
			4	4		
4	B	9	Total	O	0	0
			9	9		

### 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.

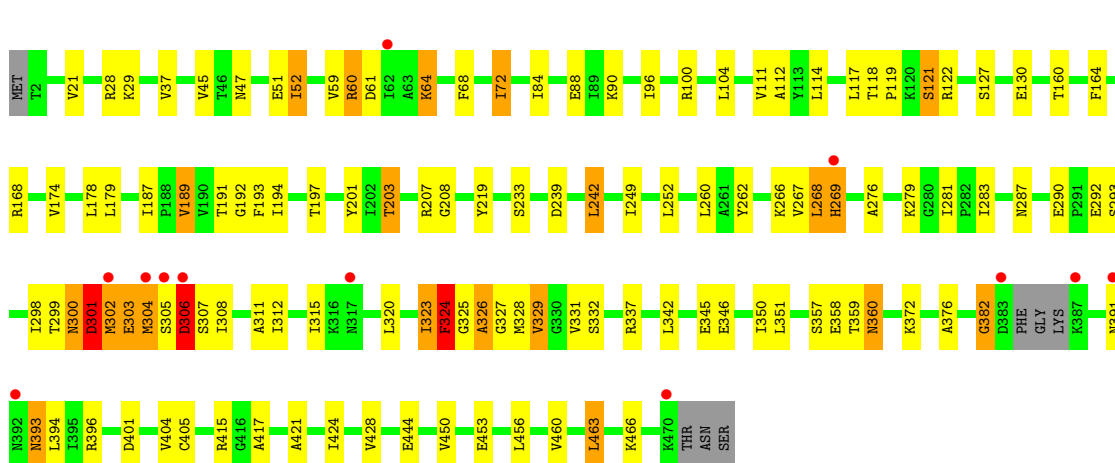
- Molecule 1: Probable aspartokinase

Chain A:



- Molecule 1: Probable aspartokinase

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.97Å 199.07Å 96.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 37.36 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.70) 99.8 (37.36-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.11 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.238 , 0.273 0.226 , 0.261	Depositor DCC
$R_{free}$ test set	1466 reflections (5.36%)	DCC
Wilson B-factor (Å <sup>2</sup> )	57.8	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 24.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 28855 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7112	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

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

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	0.39	0/3577	0.58	0/4819
1	B	0.43	0/3576	0.59	1/4818 (0.0%)
All	All	0.41	0/7153	0.58	1/9637 (0.0%)

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	3
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	306	ASP	N-CA-C	-5.80	95.33	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	265	ALA	Peptide
1	B	306	ASP	Peptide
1	B	323	ILE	Peptide
1	B	324	PHE	Peptide

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3538	0	3652	63	0
1	B	3537	0	3651	101	0
2	A	9	0	3	3	0
2	B	9	0	3	2	0
3	A	3	0	1	0	0
3	B	3	0	1	1	0
4	A	4	0	0	1	0
4	B	9	0	0	1	0
All	All	7112	0	7311	159	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

All (159) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:324:PHE:CZ	1:B:328:MET:CB	1.95	1.49
1:B:324:PHE:HD2	1:B:359:THR:C	1.51	1.14
1:B:324:PHE:CE1	1:B:328:MET:CB	2.34	1.09
1:B:345:GLU:HG3	1:B:376:ALA:HB2	1.33	1.07
1:A:351:LEU:HB2	1:A:364:VAL:CG1	1.88	1.03
1:B:324:PHE:HE2	1:B:358:GLU:O	1.45	0.98
1:B:324:PHE:HB3	1:B:325:GLY:HA3	1.45	0.96
1:B:324:PHE:HB3	1:B:359:THR:O	1.65	0.95
1:A:259:GLU:HA	1:B:357:SER:HB3	1.48	0.94
1:B:324:PHE:CD2	1:B:359:THR:C	2.42	0.93
1:B:324:PHE:CB	1:B:325:GLY:HA3	1.99	0.92
1:B:324:PHE:CG	1:B:325:GLY:CA	2.54	0.90
1:B:324:PHE:CG	1:B:325:GLY:HA2	2.07	0.89
1:A:351:LEU:HB2	1:A:364:VAL:HG12	1.58	0.84
1:B:324:PHE:CE2	1:B:328:MET:CB	2.60	0.84
1:B:324:PHE:CE2	1:B:358:GLU:O	2.29	0.84
1:B:324:PHE:HD2	1:B:360:ASN:N	1.75	0.83
1:B:324:PHE:CB	1:B:325:GLY:CA	2.56	0.83
1:A:327:GLY:HA2	1:B:168:ARG:HH21	1.43	0.83

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:323:ILE:O	1:B:324:PHE:HB2	1.75	0.82
1:B:324:PHE:CG	1:B:325:GLY:HA3	2.16	0.80
1:B:324:PHE:CD1	1:B:325:GLY:HA2	2.17	0.79
1:A:334:THR:O	1:A:338:ILE:HG12	1.82	0.79
1:B:421:ALA:H	3:B:475:FMT:H	1.50	0.77
1:B:324:PHE:HB2	1:B:360:ASN:HA	1.66	0.74
1:B:302:MET:O	1:B:303:GLU:CB	2.34	0.73
1:B:324:PHE:CD2	1:B:360:ASN:N	2.56	0.73
1:A:207:ARG:NH1	2:A:474:ASP:O	2.22	0.71
1:B:305:SER:O	1:B:306:ASP:C	2.30	0.70
1:B:207:ARG:HH11	2:B:474:ASP:N	1.90	0.70
1:B:324:PHE:CB	1:B:359:THR:O	2.37	0.70
1:A:267:VAL:O	1:A:268:LEU:HB2	1.92	0.69
1:B:324:PHE:HZ	1:B:328:MET:CB	1.98	0.69
1:A:301:ASP:O	1:A:301:ASP:CG	2.30	0.69
1:A:50:VAL:HG13	1:A:122:ARG:HH22	1.57	0.69
1:A:300:ASN:O	1:A:302:MET:N	2.24	0.68
1:B:197:THR:HG22	1:B:201:TYR:H	1.58	0.67
1:A:197:THR:HG22	1:A:201:TYR:H	1.59	0.67
1:B:267:VAL:O	1:B:268:LEU:HB2	1.94	0.67
1:A:46:THR:HG1	2:A:474:ASP:N	1.93	0.67
1:A:239:ASP:HB3	1:A:242:LEU:HD22	1.77	0.67
1:A:105:GLU:O	1:A:109:ILE:HG12	1.97	0.65
1:A:327:GLY:HA2	1:B:168:ARG:NH2	2.13	0.64
1:B:405:CYS:SG	1:B:453:GLU:HG3	2.38	0.64
1:B:269:HIS:CD2	1:B:269:HIS:H	2.14	0.64
1:A:301:ASP:C	1:A:302:MET:O	2.36	0.64
1:B:305:SER:C	1:B:306:ASP:O	2.30	0.62
1:A:351:LEU:HB2	1:A:364:VAL:HG13	1.78	0.61
1:A:40:SER:HB3	2:A:474:ASP:HB2	1.81	0.61
1:B:300:ASN:O	1:B:302:MET:HE3	2.00	0.61
1:B:302:MET:HA	1:B:302:MET:CE	2.32	0.59
1:A:29:LYS:HG3	1:A:187:ILE:HD11	1.84	0.59
1:B:29:LYS:HG3	1:B:187:ILE:HD11	1.85	0.59
1:A:259:GLU:HA	1:B:357:SER:CB	2.28	0.58
1:B:117:LEU:HD12	1:B:121:SER:HB3	1.86	0.58
1:B:326:ALA:O	1:B:329:VAL:CG1	2.52	0.57
1:B:208:GLY:H	2:B:474:ASP:N	2.02	0.57
1:B:262:TYR:CD2	1:B:315:ILE:HG12	2.41	0.56
1:A:456:LEU:O	1:A:460:VAL:HG23	2.06	0.55
1:B:59:VAL:HG12	1:B:59:VAL:O	2.07	0.55
1:B:239:ASP:HB3	1:B:242:LEU:HD22	1.88	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:323:ILE:O	1:B:324:PHE:CB	2.47	0.54
1:B:405:CYS:SG	1:B:456:LEU:HD22	2.48	0.54
1:A:300:ASN:C	1:A:302:MET:H	2.11	0.54
1:B:130:GLU:HG2	1:B:192:GLY:O	2.08	0.53
1:B:160:THR:OG1	1:B:203:THR:HG21	2.08	0.53
1:A:160:THR:OG1	1:A:203:THR:HG21	2.09	0.53
1:B:345:GLU:HG3	1:B:376:ALA:CB	2.23	0.53
1:B:301:ASP:O	1:B:302:MET:CB	2.55	0.52
1:A:122:ARG:HD2	4:A:476:HOH:O	2.09	0.52
1:B:292:GLU:OE1	1:B:292:GLU:HA	2.09	0.52
1:A:65:VAL:HG13	1:A:108:LEU:HD23	1.90	0.52
1:B:415:ARG:O	1:B:444:GLU:OE1	2.28	0.52
1:B:122:ARG:HD2	4:B:477:HOH:O	2.10	0.52
1:B:260:LEU:HD21	1:B:311:ALA:HB3	1.92	0.52
1:B:252:LEU:O	1:B:298:ILE:HA	2.10	0.52
1:B:324:PHE:CD2	1:B:359:THR:O	2.63	0.51
1:B:302:MET:HE2	1:B:302:MET:HA	1.93	0.51
1:A:252:LEU:O	1:A:298:ILE:HA	2.10	0.51
1:A:212:TYR:CE1	1:A:271:ARG:HG2	2.46	0.51
1:A:197:THR:HG22	1:A:201:TYR:N	2.25	0.51
1:A:47:ASN:OD1	1:A:207:ARG:NH2	2.43	0.51
1:B:302:MET:HE3	1:B:302:MET:CA	2.41	0.51
1:A:351:LEU:CB	1:A:364:VAL:HG12	2.37	0.51
1:B:456:LEU:O	1:B:460:VAL:HG23	2.11	0.51
1:A:262:TYR:CD2	1:A:315:ILE:HG12	2.47	0.50
1:A:274:GLU:HB3	1:A:275:PRO:HD3	1.93	0.50
1:A:301:ASP:OD1	1:A:301:ASP:O	2.29	0.49
1:B:197:THR:HG22	1:B:201:TYR:N	2.24	0.49
1:A:265:ALA:HA	1:A:266:LYS:HG2	1.94	0.49
1:B:130:GLU:HB3	1:B:191:THR:HB	1.94	0.49
1:A:424:ILE:O	1:A:428:VAL:HG23	2.13	0.49
1:A:301:ASP:O	1:A:302:MET:C	2.50	0.49
1:B:192:GLY:O	1:B:193:PHE:HB3	2.12	0.49
1:B:305:SER:OG	1:B:305:SER:O	2.30	0.49
1:A:267:VAL:O	1:A:268:LEU:CB	2.61	0.49
1:A:301:ASP:O	1:A:302:MET:O	2.29	0.49
1:B:47:ASN:OD1	1:B:207:ARG:NH2	2.45	0.48
1:B:174:VAL:CG1	1:B:178:LEU:HD12	2.43	0.48
1:B:302:MET:CE	1:B:302:MET:CA	2.90	0.48
1:B:269:HIS:HD2	1:B:269:HIS:H	1.59	0.48
1:B:307:SER:OG	1:B:308:ILE:N	2.47	0.48
1:B:405:CYS:SG	1:B:453:GLU:HA	2.53	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:424:ILE:O	1:B:428:VAL:HG23	2.14	0.48
1:A:174:VAL:CG1	1:A:178:LEU:HD12	2.43	0.48
1:B:283:ILE:HB	1:B:298:ILE:HB	1.95	0.47
1:A:174:VAL:HG13	1:A:178:LEU:HD12	1.96	0.47
1:A:415:ARG:O	1:A:444:GLU:OE1	2.32	0.47
1:B:233:SER:HA	1:B:287:ASN:HB2	1.97	0.47
1:A:62:ILE:HG23	1:A:109:ILE:HD12	1.96	0.47
1:B:84:ILE:O	1:B:90:LYS:HD2	2.14	0.47
1:B:60:ARG:HG2	1:B:112:ALA:O	2.15	0.46
1:B:249:ILE:HG21	1:B:252:LEU:HD13	1.96	0.46
1:A:128:PHE:O	1:A:132:LEU:HG	2.15	0.46
1:B:61:ASP:HB3	1:B:64:LYS:HG2	1.97	0.46
1:A:192:GLY:O	1:A:193:PHE:HB3	2.15	0.45
1:A:96:ILE:O	1:A:100:ARG:HG2	2.17	0.45
1:B:320:LEU:HB3	1:B:401:ASP:HB3	1.98	0.45
1:B:189:VAL:CG2	1:B:189:VAL:O	2.64	0.45
1:B:96:ILE:O	1:B:100:ARG:HG2	2.17	0.45
1:B:325:GLY:O	1:B:326:ALA:C	2.55	0.45
1:A:328:MET:HG2	1:A:334:THR:HG21	1.98	0.45
1:A:130:GLU:HB3	1:A:191:THR:HB	1.99	0.45
1:B:325:GLY:HA3	1:B:359:THR:O	2.17	0.45
1:A:354:GLN:HG3	1:A:361:ILE:HG12	2.00	0.44
1:B:320:LEU:HD22	1:B:450:VAL:HG11	1.99	0.44
1:B:219:TYR:CE1	1:B:279:LYS:HG3	2.52	0.44
1:B:68:PHE:HE2	1:B:104:LEU:HD11	1.81	0.44
1:B:127:SER:HB2	1:B:194:ILE:HG21	1.98	0.44
1:A:302:MET:C	1:A:303:GLU:HG3	2.38	0.44
1:A:320:LEU:HB3	1:A:401:ASP:HB3	2.00	0.44
1:A:119:PRO:HB2	1:A:164:PHE:HB2	2.00	0.44
1:B:325:GLY:O	1:B:327:GLY:N	2.51	0.44
1:B:382:GLY:N	1:B:393:ASN:HD21	2.16	0.43
1:A:381:PHE:HB3	1:A:393:ASN:HD21	1.83	0.43
1:B:324:PHE:CB	1:B:360:ASN:HA	2.42	0.43
1:B:276:ALA:HB2	1:B:283:ILE:HD11	2.00	0.43
1:B:189:VAL:HG23	1:B:189:VAL:O	2.19	0.43
1:B:303:GLU:O	1:B:304:MET:O	2.37	0.43
1:B:174:VAL:HG13	1:B:178:LEU:HD12	2.01	0.42
1:B:312:ILE:HD13	1:B:463:LEU:HB3	2.00	0.42
1:A:249:ILE:HD11	1:A:311:ALA:HB2	2.02	0.42
1:A:284:LEU:HG	1:A:286:LYS:HG3	2.00	0.42
1:A:354:GLN:NE2	1:B:350:ILE:O	2.45	0.42
1:B:290:GLU:OE2	1:B:293:SER:HB2	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:52:ILE:HG13	1:B:68:PHE:CG	2.54	0.42
1:A:300:ASN:C	1:A:302:MET:N	2.67	0.42
1:B:119:PRO:HB2	1:B:164:PHE:HB2	2.01	0.42
1:A:45:VAL:HG13	1:A:72:ILE:HD11	2.02	0.41
1:A:314:THR:HG22	1:A:407:ILE:HG12	2.02	0.41
1:A:154:GLY:HA3	1:A:196:THR:HB	2.01	0.41
1:A:2:THR:O	1:A:223:ALA:HB1	2.21	0.41
1:B:326:ALA:O	1:B:329:VAL:HG12	2.21	0.41
1:B:45:VAL:HG13	1:B:72:ILE:HD11	2.02	0.41
1:B:405:CYS:SG	1:B:456:LEU:HB2	2.61	0.41
1:A:233:SER:HA	1:A:287:ASN:HB2	2.03	0.41
1:B:328:MET:O	1:B:332:SER:OG	2.39	0.40
1:A:130:GLU:HG2	1:A:192:GLY:O	2.20	0.40
1:A:52:ILE:CG2	1:A:108:LEU:HD21	2.51	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	461/473 (98%)	431 (94%)	21 (5%)	9 (2%)	11	28
1	B	462/473 (98%)	429 (93%)	24 (5%)	9 (2%)	12	29
All	All	923/946 (98%)	860 (93%)	45 (5%)	18 (2%)	11	28

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	302	MET
1	A	417	ALA
1	B	304	MET
1	B	266	LYS
1	B	301	ASP
1	B	303	GLU

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Mol	Chain	Res	Type
1	B	417	ALA
1	A	268	LEU
1	A	382	GLY
1	B	268	LEU
1	B	326	ALA
1	B	382	GLY
1	A	301	ASP
1	A	393	ASN
1	A	59	VAL
1	A	306	ASP
1	B	331	VAL
1	A	331	VAL

### 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	387/397 (98%)	361 (93%)	26 (7%)	23	49
1	B	385/397 (97%)	347 (90%)	38 (10%)	11	26
All	All	772/794 (97%)	708 (92%)	64 (8%)	16	35

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	VAL
1	A	28	ARG
1	A	37	VAL
1	A	51	GLU
1	A	52	ILE
1	A	69	ILE
1	A	102	GLU
1	A	104	LEU
1	A	179	LEU
1	A	189	VAL
1	A	203	THR
1	A	242	LEU
1	A	294	GLU

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Mol	Chain	Res	Type
1	A	300	ASN
1	A	316	LYS
1	A	329	VAL
1	A	342	LEU
1	A	346	GLU
1	A	354	GLN
1	A	364	VAL
1	A	378	LYS
1	A	379	ARG
1	A	393	ASN
1	A	396	ARG
1	A	463	LEU
1	A	466	LYS
1	B	21	VAL
1	B	28	ARG
1	B	37	VAL
1	B	51	GLU
1	B	52	ILE
1	B	60	ARG
1	B	64	LYS
1	B	72	ILE
1	B	88	GLU
1	B	111	VAL
1	B	114	LEU
1	B	118	THR
1	B	121	SER
1	B	179	LEU
1	B	189	VAL
1	B	203	THR
1	B	242	LEU
1	B	269	HIS
1	B	281	ILE
1	B	299	THR
1	B	300	ASN
1	B	301	ASP
1	B	302	MET
1	B	324	PHE
1	B	329	VAL
1	B	337	ARG
1	B	342	LEU
1	B	346	GLU
1	B	351	LEU

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Mol	Chain	Res	Type
1	B	360	ASN
1	B	372	LYS
1	B	391	ASN
1	B	393	ASN
1	B	394	LEU
1	B	396	ARG
1	B	404	VAL
1	B	463	LEU
1	B	466	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	163	ASN
1	A	348	ASN
1	A	434	ASN
1	B	163	ASN
1	B	269	HIS
1	B	300	ASN
1	B	322	ASN
1	B	391	ASN
1	B	393	ASN
1	B	434	ASN
1	B	440	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

4 ligands are 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	ASP	A	474	-	8,8,8	0.95	0	10,10,10	1.29	2 (20%)
3	FMT	A	475	-	2,2,2	0.60	0	1,1,1	0.17	0
2	ASP	B	474	-	8,8,8	0.98	1 (12%)	10,10,10	1.01	0
3	FMT	B	475	-	2,2,2	0.60	0	1,1,1	0.12	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	ASP	A	474	-	-	0/8/8/8	0/0/0/0
3	FMT	A	475	-	-	0/0/0/0	0/0/0/0
2	ASP	B	474	-	-	0/8/8/8	0/0/0/0
3	FMT	B	475	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	474	ASP	OXT-C	-2.04	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	474	ASP	OXT-C-O	-2.42	118.60	124.07
2	A	474	ASP	OXT-C-CA	2.33	122.12	116.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.



## 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 ⓘ

### 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	465/473 (98%)	0.13	24 (5%) 26 29	23, 32, 46, 55	0
1	B	466/473 (98%)	0.09	12 (2%) 53 59	23, 32, 46, 55	0
All	All	931/946 (98%)	0.11	36 (3%) 37 42	23, 32, 46, 55	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	392	ASN	5.3
1	A	304	MET	4.2
1	B	305	SER	3.8
1	A	470	LYS	3.7
1	B	470	LYS	3.7
1	B	306	ASP	3.6
1	A	317	ASN	3.4
1	A	108	LEU	3.3
1	A	392	ASN	3.1
1	A	390	LEU	3.0
1	B	302	MET	2.9
1	A	306	ASP	2.9
1	A	63	ALA	2.9
1	A	303	GLU	2.8
1	B	304	MET	2.7
1	B	269	HIS	2.7
1	A	370	VAL	2.7
1	A	374	LEU	2.6
1	A	114	LEU	2.6
1	A	62	ILE	2.5
1	B	387	LYS	2.4
1	A	377	LEU	2.4
1	A	389	PHE	2.4
1	B	383	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	375	LYS	2.3
1	A	401	ASP	2.2
1	B	62	ILE	2.1
1	A	379	ARG	2.1
1	A	112	ALA	2.1
1	A	201	TYR	2.1
1	A	263	PHE	2.1
1	A	91	GLU	2.1
1	B	317	ASN	2.1
1	A	320	LEU	2.1
1	B	391	ASN	2.0
1	A	265	ALA	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	FMT	A	475	3/3	0.34	6.41	65,65,65,65	0
2	ASP	A	474	9/9	0.25	4.16	62,63,63,64	0
3	FMT	B	475	3/3	0.28	3.82	57,57,57,58	0
2	ASP	B	474	9/9	0.25	1.97	55,55,56,56	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.