



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 04:34 PM JST

PDB ID : 8H4B
Title : Blasnase-T13A/M57P with L-asn
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Deposited on : 2022-10-10
Resolution : 2.00 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

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>.

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)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

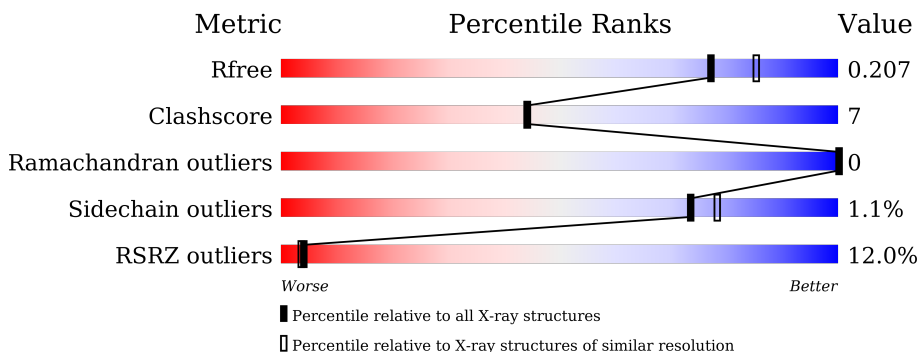
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 ≥ 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	328	 15% 88% 10% .
1	B	328	 9% 83% 14% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	FMT	B	404	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5457 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 L-asparaginase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	321	Total	C	N	O	S	0	0	0
			2497	1587	427	476	7			
1	B	320	Total	C	N	O	S	0	5	0
			2516	1602	429	478	7			

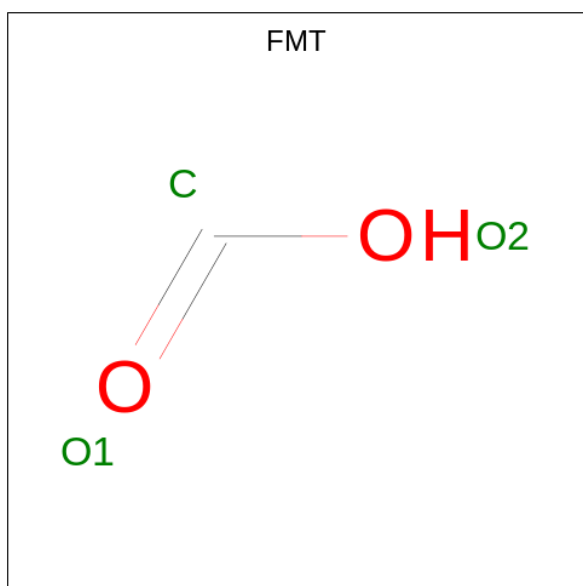
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	ALA	THR	engineered mutation	UNP A0A6I7U6Y2
A	57	PRO	MET	engineered mutation	UNP A0A6I7U6Y2
A	323	LEU	-	expression tag	UNP A0A6I7U6Y2
A	324	GLU	-	expression tag	UNP A0A6I7U6Y2
A	325	HIS	-	expression tag	UNP A0A6I7U6Y2
A	326	HIS	-	expression tag	UNP A0A6I7U6Y2
A	327	HIS	-	expression tag	UNP A0A6I7U6Y2
A	328	HIS	-	expression tag	UNP A0A6I7U6Y2
B	13	ALA	THR	engineered mutation	UNP A0A6I7U6Y2
B	57	PRO	MET	engineered mutation	UNP A0A6I7U6Y2
B	323	LEU	-	expression tag	UNP A0A6I7U6Y2
B	324	GLU	-	expression tag	UNP A0A6I7U6Y2
B	325	HIS	-	expression tag	UNP A0A6I7U6Y2
B	326	HIS	-	expression tag	UNP A0A6I7U6Y2
B	327	HIS	-	expression tag	UNP A0A6I7U6Y2
B	328	HIS	-	expression tag	UNP A0A6I7U6Y2

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

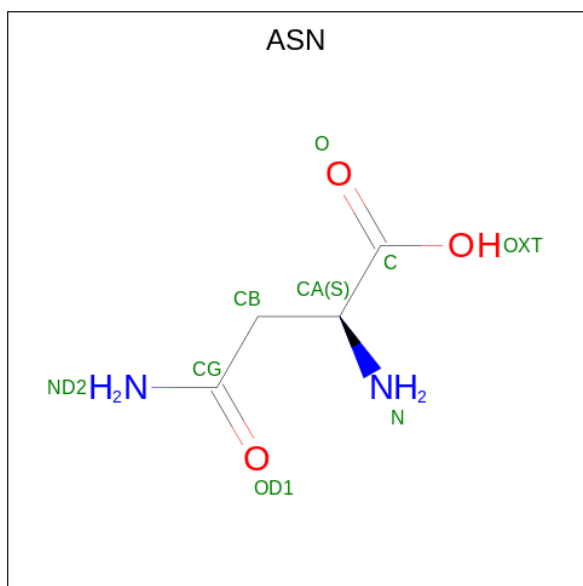
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Mg	4	0
			4	4		
2	B	2	Total	Mg	2	0
			2	2		

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



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

- Molecule 4 is ASPARAGINE (three-letter code: ASN) (formula: $\text{C}_4\text{H}_8\text{N}_2\text{O}_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			9	4	2	3		

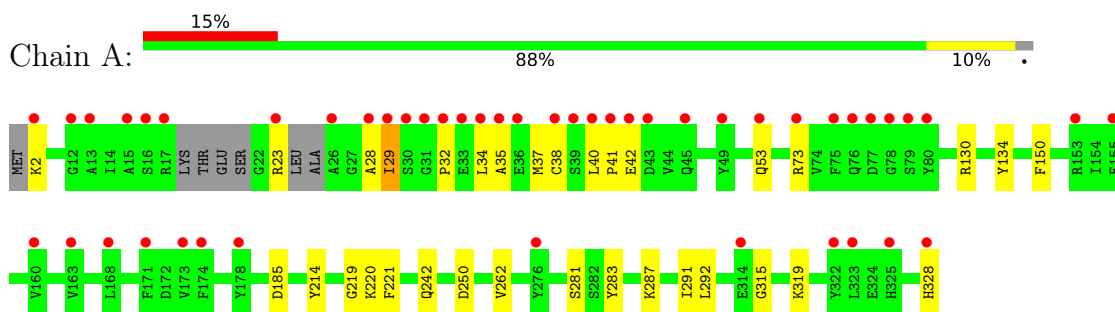
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	196	Total	O	0	0
			196	196		
5	B	224	Total	O	0	0
			224	224		

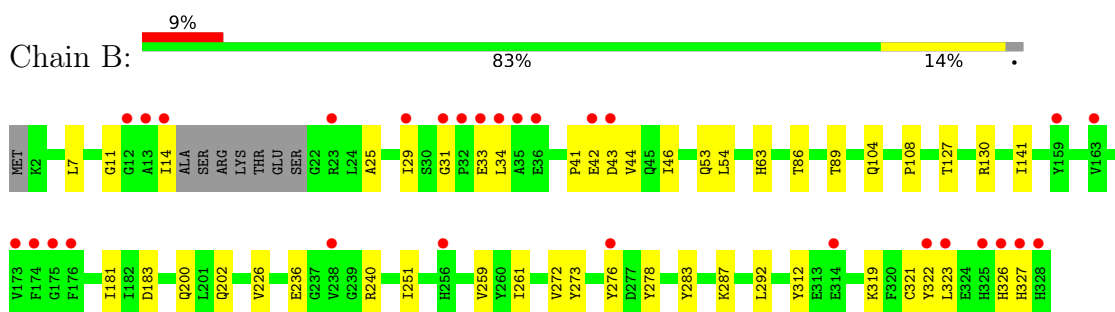
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: L-asparaginase



- Molecule 1: L-asparaginase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	91.54Å 91.54Å 232.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.64 – 2.00 49.64 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.64-2.00) 100.0 (49.64-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.00Å)	Xtrriage
Refinement program	PHENIX v1.16	Depositor
R, R_{free}	0.186 , 0.207 0.186 , 0.207	Depositor DCC
R_{free} test set	3312 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtrriage
Anisotropy	0.303	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5457	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: MG, 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	0.40	0/2547	0.58	0/3449
1	B	0.54	2/2570 (0.1%)	0.61	0/3481
All	All	0.47	2/5117 (0.0%)	0.59	0/6930

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	236	GLU	CD-OE2	-5.41	1.19	1.25
1	B	236	GLU	CD-OE1	-5.36	1.19	1.25

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	2497	0	2468	27	0
1	B	2516	0	2491	39	0
2	A	4	0	0	0	0
2	B	2	0	0	0	0
3	A	3	0	1	0	0
3	B	6	0	2	5	0
4	A	9	0	5	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	196	0	0	1	0
5	B	224	0	0	1	0
All	All	5457	0	4967	66	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 7.

All (66) 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:23:ARG:HH21	1:A:29:ILE:HG23	1.30	0.95
1:A:23:ARG:NH2	1:A:29:ILE:HG23	1.86	0.89
1:A:29:ILE:HG21	1:A:37:MET:HE1	1.60	0.84
1:B:89:THR:OG1	3:B:404:FMT:H	1.80	0.81
1:B:273:TYR:HD2	1:B:327:HIS:CG	2.01	0.79
1:B:273:TYR:CD2	1:B:327:HIS:CG	2.75	0.74
1:A:23:ARG:HB2	1:A:29:ILE:CD1	2.20	0.72
1:A:73:ARG:NH2	5:A:501:HOH:O	2.23	0.70
1:A:2:LYS:NZ	1:A:42:GLU:O	2.20	0.69
1:A:23:ARG:HB3	1:A:28:ALA:HB3	1.74	0.69
1:B:273:TYR:HD2	1:B:327:HIS:CD2	2.10	0.69
1:B:89:THR:H	3:B:404:FMT:H	1.61	0.65
1:B:89:THR:HG1	3:B:404:FMT:H	1.63	0.64
1:A:23:ARG:HB2	1:A:29:ILE:HD13	1.81	0.61
1:A:23:ARG:HB2	1:A:29:ILE:HD11	1.83	0.61
1:A:38:CYS:HB2	1:A:40:LEU:HD11	1.83	0.60
4:A:406:ASN:N	1:B:278:TYR:HH	1.99	0.60
1:A:35:ALA:HA	1:A:40:LEU:HD13	1.85	0.59
1:B:200:GLN:HE21	1:B:202:GLN:HE22	1.51	0.58
1:B:34:LEU:C	1:B:34:LEU:HD13	2.24	0.58
1:B:29:ILE:HG22	1:B:33:GLU:HB2	1.84	0.57
1:B:273:TYR:CE2	1:B:327:HIS:HB3	2.38	0.57
1:B:34:LEU:HD13	1:B:34:LEU:O	2.05	0.56
1:B:41:PRO:O	1:B:44:VAL:HG12	2.07	0.54
1:A:292:LEU:H	1:A:328:HIS:CE1	2.26	0.53
1:B:273:TYR:CD2	1:B:327:HIS:HB3	2.43	0.53
1:B:273:TYR:CD2	1:B:327:HIS:CB	2.92	0.52
1:B:226:VAL:HG22	1:B:259:VAL:HG21	1.90	0.52
1:B:89:THR:H	3:B:404:FMT:C	2.22	0.51
1:A:134:TYR:CE2	1:A:185:ASP:HB3	2.47	0.50
1:A:130:ARG:HD2	1:A:185:ASP:OD1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ARG:NH2	1:A:29:ILE:CG2	2.69	0.48
1:B:181:ILE:HD13	1:B:183:ASP:HB2	1.96	0.48
1:A:35:ALA:HA	1:A:40:LEU:CD1	2.42	0.47
1:B:240:ARG:O	1:B:272:VAL:HG13	2.14	0.47
1:B:29:ILE:CG2	1:B:33:GLU:HB2	2.44	0.47
1:B:14[B]:ILE:C	1:B:25:ALA:HB2	2.36	0.47
1:B:7:LEU:HD11	1:B:86:THR:HG23	1.97	0.46
1:A:315:GLY:O	1:A:319:LYS:HD2	2.16	0.46
1:B:321:CYS:HA	1:B:326:HIS:CE1	2.50	0.46
1:B:89:THR:CB	3:B:404:FMT:H	2.47	0.45
1:B:34:LEU:C	1:B:34:LEU:CD1	2.85	0.45
1:B:251:ILE:HG23	1:B:261:ILE:HD12	1.98	0.45
1:A:283:TYR:CZ	1:A:287:LYS:HD3	2.51	0.45
1:A:29:ILE:HB	1:A:34:LEU:CD1	2.47	0.45
1:A:220:LYS:HG3	1:A:221:PHE:CD1	2.52	0.45
1:B:31:GLY:HA3	1:B:46:ILE:O	2.17	0.44
1:B:108:PRO:HB3	1:B:141:ILE:HG23	1.99	0.44
1:A:29:ILE:HB	1:A:34:LEU:HD12	2.00	0.43
1:B:322:TYR:CE1	1:B:323:LEU:HD13	2.53	0.43
1:B:292:LEU:O	1:B:326:HIS:HD2	2.02	0.43
1:B:11[A]:GLY:O	1:B:53:GLN:HA	2.19	0.43
1:A:41:PRO:HD3	1:A:134:TYR:OH	2.19	0.43
1:B:283:TYR:CZ	1:B:287:LYS:HD3	2.54	0.43
1:B:29:ILE:CG2	1:B:33:GLU:CB	2.97	0.42
1:A:53:GLN:HA	1:A:53:GLN:OE1	2.19	0.42
1:B:41:PRO:HB2	1:B:43:ASP:OD1	2.19	0.42
1:A:23:ARG:NE	1:A:29:ILE:HD13	2.34	0.42
1:A:242:GLN:HG3	1:A:281:SER:HA	2.01	0.42
1:B:312:TYR:CD2	1:B:319:LYS:HD3	2.55	0.42
1:B:104:GLN:NE2	5:B:507:HOH:O	2.53	0.41
1:B:127:THR:HG22	1:B:130:ARG:NH1	2.34	0.41
1:A:219:GLY:HA3	1:A:250:ASP:OD2	2.20	0.41
1:B:54:LEU:HD11	1:B:63:HIS:CE1	2.55	0.41
1:B:200:GLN:HE21	1:B:202:GLN:NE2	2.18	0.40
1:A:262:VAL:HG22	1:A:291:ILE:HB	2.04	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	315/328 (96%)	301 (96%)	14 (4%)	0	100	100
1	B	320/328 (98%)	312 (98%)	8 (2%)	0	100	100
All	All	635/656 (97%)	613 (96%)	22 (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	265/271 (98%)	261 (98%)	4 (2%)	65	69
1	B	266/271 (98%)	264 (99%)	2 (1%)	81	86
All	All	531/542 (98%)	525 (99%)	6 (1%)	73	78

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ILE
1	A	32	PRO
1	A	150	PHE
1	A	214	TYR
1	B	42	GLU
1	B	276	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	328	HIS
1	B	202	GLN
1	B	326	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 for Mogul analysis.

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
3	FMT	B	404	-	2,2,2	0.01	0	1,1,1	0.13	0
3	FMT	A	405	-	2,2,2	0.72	0	1,1,1	0.25	0
4	ASN	A	406	-	6,8,8	0.90	0	8,10,10	1.22	2 (25%)
3	FMT	B	403	-	2,2,2	0.72	0	1,1,1	0.24	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
4	ASN	A	406	-	-	6/8/8/8	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	406	ASN	OXT-C-O	-2.55	118.30	124.09
4	A	406	ASN	OXT-C-CA	2.22	120.94	113.38

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	406	ASN	O-C-CA-N
4	A	406	ASN	C-CA-CB-CG
4	A	406	ASN	OXT-C-CA-N
4	A	406	ASN	O-C-CA-CB
4	A	406	ASN	OXT-C-CA-CB
4	A	406	ASN	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	404	FMT	5	0
4	A	406	ASN	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 [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, 95th 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 ²)	Q<0.9
1	A	321/328 (97%)	0.65	48 (14%) 2 2	22, 33, 75, 99	0
1	B	320/328 (97%)	0.24	29 (9%) 9 8	19, 30, 58, 80	0
All	All	641/656 (97%)	0.44	77 (12%) 4 3	19, 32, 62, 99	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	30	SER	8.3
1	A	34	LEU	7.9
1	A	32	PRO	6.7
1	A	42	GLU	6.4
1	A	36	GLU	6.4
1	A	35	ALA	6.4
1	A	29	ILE	5.8
1	A	43	ASP	5.4
1	A	38	CYS	5.2
1	B	14[A]	ILE	5.0
1	A	15	ALA	4.8
1	A	28	ALA	4.7
1	B	42	GLU	4.4
1	A	33	GLU	4.2
1	A	26	ALA	4.1
1	A	40	LEU	4.1
1	A	23	ARG	4.1
1	A	39	SER	3.9
1	A	41	PRO	3.9
1	B	325	HIS	3.9
1	B	13[A]	ALA	3.8
1	A	322	TYR	3.8
1	B	323	LEU	3.8
1	B	36	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	323	LEU	3.7
1	A	328	HIS	3.5
1	B	327	HIS	3.5
1	A	76	GLN	3.4
1	A	16	SER	3.3
1	B	322	TYR	3.3
1	B	326	HIS	3.3
1	B	174	PHE	3.3
1	A	173	VAL	3.2
1	B	314	GLU	3.2
1	A	17	ARG	3.2
1	A	155	PHE	3.2
1	A	2	LYS	3.2
1	B	33	GLU	3.1
1	B	276	TYR	3.1
1	B	34	LEU	3.1
1	A	31	GLY	3.0
1	A	163	VAL	2.9
1	A	325	HIS	2.9
1	B	32	PRO	2.9
1	B	328	HIS	2.9
1	A	160	VAL	2.9
1	B	256	HIS	2.8
1	A	276	TYR	2.8
1	B	175	GLY	2.7
1	A	174	PHE	2.7
1	B	12[A]	GLY	2.7
1	A	49	TYR	2.7
1	B	29	ILE	2.6
1	B	31	GLY	2.5
1	A	75	PHE	2.5
1	B	43	ASP	2.5
1	A	178	TYR	2.5
1	A	12	GLY	2.5
1	A	45	GLN	2.5
1	B	173	VAL	2.4
1	A	171	PHE	2.4
1	B	238	VAL	2.3
1	B	23	ARG	2.3
1	A	153	ARG	2.2
1	A	53	GLN	2.1
1	B	35	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	176	PHE	2.1
1	B	159	TYR	2.1
1	A	77	ASP	2.1
1	A	13	ALA	2.1
1	A	80	TYR	2.1
1	A	78	GLY	2.1
1	A	79	SER	2.1
1	A	168	LEU	2.0
1	A	314	GLU	2.0
1	A	73	ARG	2.0
1	B	163	VAL	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 monosaccharides in this entry.

6.4 Ligands [i](#)

LIGAND-RSR INFOmissingINFO

6.5 Other polymers [i](#)

There are no such residues in this entry.