



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:16 AM UTC

PDB ID : 5DND / pdb_00005dnd
Title : Crystal structure of the Asn-bound guinea pig L-asparaginase 1 catalytic domain active site mutant T116A
Authors : Schalk, A.M.; Lavie, A.
Deposited on : 2015-09-09
Resolution : 2.29 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

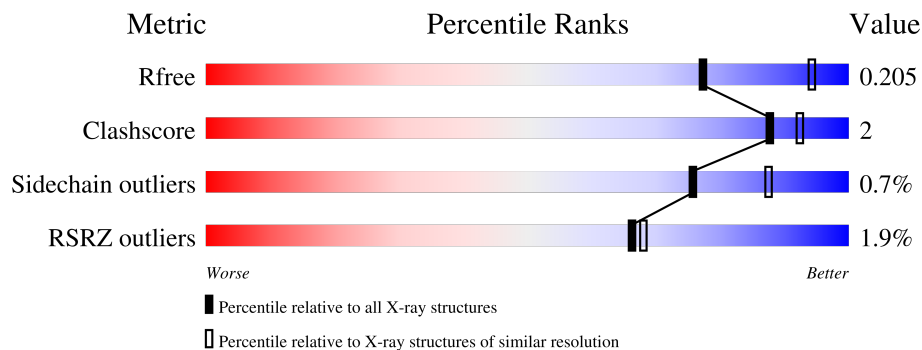
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	588	 57% 40%
1	B	588	 57% 40%
1	C	588	 58% 40%
1	D	588	 57% 39%

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 11313 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	353	2700	1729	466	489	16	0	0	0
1	B	355	2715	1737	469	493	16	0	0	0
1	C	354	2719	1743	469	491	16	0	1	0
1	D	357	2728	1744	471	497	16	0	0	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MET	-	initiating methionine	UNP H0W0T5
A	-21	GLY	-	expression tag	UNP H0W0T5
A	-20	SER	-	expression tag	UNP H0W0T5
A	-19	SER	-	expression tag	UNP H0W0T5
A	-18	HIS	-	expression tag	UNP H0W0T5
A	-17	HIS	-	expression tag	UNP H0W0T5
A	-16	HIS	-	expression tag	UNP H0W0T5
A	-15	HIS	-	expression tag	UNP H0W0T5
A	-14	HIS	-	expression tag	UNP H0W0T5
A	-13	HIS	-	expression tag	UNP H0W0T5
A	-12	SER	-	expression tag	UNP H0W0T5
A	-11	SER	-	expression tag	UNP H0W0T5
A	-10	GLY	-	expression tag	UNP H0W0T5
A	-9	GLY	-	expression tag	UNP H0W0T5
A	-8	ASN	-	expression tag	UNP H0W0T5
A	-7	GLU	-	expression tag	UNP H0W0T5
A	-6	ASN	-	expression tag	UNP H0W0T5
A	-5	LEU	-	expression tag	UNP H0W0T5
A	-4	TYR	-	expression tag	UNP H0W0T5
A	-3	PHE	-	expression tag	UNP H0W0T5
A	-2	GLN	-	expression tag	UNP H0W0T5

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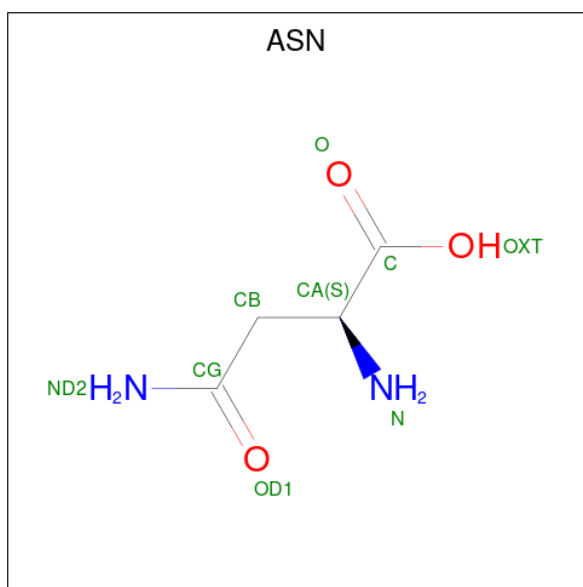
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP H0W0T5
A	0	HIS	-	expression tag	UNP H0W0T5
A	116	ALA	THR	engineered mutation	UNP H0W0T5
B	-22	MET	-	initiating methionine	UNP H0W0T5
B	-21	GLY	-	expression tag	UNP H0W0T5
B	-20	SER	-	expression tag	UNP H0W0T5
B	-19	SER	-	expression tag	UNP H0W0T5
B	-18	HIS	-	expression tag	UNP H0W0T5
B	-17	HIS	-	expression tag	UNP H0W0T5
B	-16	HIS	-	expression tag	UNP H0W0T5
B	-15	HIS	-	expression tag	UNP H0W0T5
B	-14	HIS	-	expression tag	UNP H0W0T5
B	-13	HIS	-	expression tag	UNP H0W0T5
B	-12	SER	-	expression tag	UNP H0W0T5
B	-11	SER	-	expression tag	UNP H0W0T5
B	-10	GLY	-	expression tag	UNP H0W0T5
B	-9	GLY	-	expression tag	UNP H0W0T5
B	-8	ASN	-	expression tag	UNP H0W0T5
B	-7	GLU	-	expression tag	UNP H0W0T5
B	-6	ASN	-	expression tag	UNP H0W0T5
B	-5	LEU	-	expression tag	UNP H0W0T5
B	-4	TYR	-	expression tag	UNP H0W0T5
B	-3	PHE	-	expression tag	UNP H0W0T5
B	-2	GLN	-	expression tag	UNP H0W0T5
B	-1	GLY	-	expression tag	UNP H0W0T5
B	0	HIS	-	expression tag	UNP H0W0T5
B	116	ALA	THR	engineered mutation	UNP H0W0T5
C	-22	MET	-	initiating methionine	UNP H0W0T5
C	-21	GLY	-	expression tag	UNP H0W0T5
C	-20	SER	-	expression tag	UNP H0W0T5
C	-19	SER	-	expression tag	UNP H0W0T5
C	-18	HIS	-	expression tag	UNP H0W0T5
C	-17	HIS	-	expression tag	UNP H0W0T5
C	-16	HIS	-	expression tag	UNP H0W0T5
C	-15	HIS	-	expression tag	UNP H0W0T5
C	-14	HIS	-	expression tag	UNP H0W0T5
C	-13	HIS	-	expression tag	UNP H0W0T5
C	-12	SER	-	expression tag	UNP H0W0T5
C	-11	SER	-	expression tag	UNP H0W0T5
C	-10	GLY	-	expression tag	UNP H0W0T5
C	-9	GLY	-	expression tag	UNP H0W0T5
C	-8	ASN	-	expression tag	UNP H0W0T5

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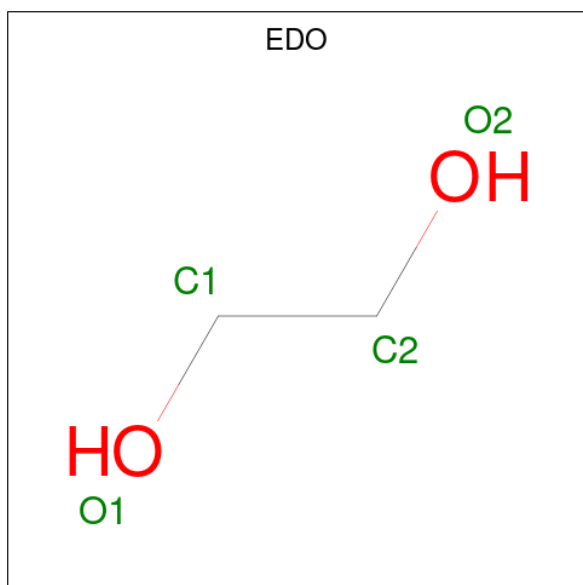
Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	GLU	-	expression tag	UNP H0W0T5
C	-6	ASN	-	expression tag	UNP H0W0T5
C	-5	LEU	-	expression tag	UNP H0W0T5
C	-4	TYR	-	expression tag	UNP H0W0T5
C	-3	PHE	-	expression tag	UNP H0W0T5
C	-2	GLN	-	expression tag	UNP H0W0T5
C	-1	GLY	-	expression tag	UNP H0W0T5
C	0	HIS	-	expression tag	UNP H0W0T5
C	116	ALA	THR	engineered mutation	UNP H0W0T5
D	-22	MET	-	initiating methionine	UNP H0W0T5
D	-21	GLY	-	expression tag	UNP H0W0T5
D	-20	SER	-	expression tag	UNP H0W0T5
D	-19	SER	-	expression tag	UNP H0W0T5
D	-18	HIS	-	expression tag	UNP H0W0T5
D	-17	HIS	-	expression tag	UNP H0W0T5
D	-16	HIS	-	expression tag	UNP H0W0T5
D	-15	HIS	-	expression tag	UNP H0W0T5
D	-14	HIS	-	expression tag	UNP H0W0T5
D	-13	HIS	-	expression tag	UNP H0W0T5
D	-12	SER	-	expression tag	UNP H0W0T5
D	-11	SER	-	expression tag	UNP H0W0T5
D	-10	GLY	-	expression tag	UNP H0W0T5
D	-9	GLY	-	expression tag	UNP H0W0T5
D	-8	ASN	-	expression tag	UNP H0W0T5
D	-7	GLU	-	expression tag	UNP H0W0T5
D	-6	ASN	-	expression tag	UNP H0W0T5
D	-5	LEU	-	expression tag	UNP H0W0T5
D	-4	TYR	-	expression tag	UNP H0W0T5
D	-3	PHE	-	expression tag	UNP H0W0T5
D	-2	GLN	-	expression tag	UNP H0W0T5
D	-1	GLY	-	expression tag	UNP H0W0T5
D	0	HIS	-	expression tag	UNP H0W0T5
D	116	ALA	THR	engineered mutation	UNP H0W0T5

- Molecule 2 is ASPARAGINE (CCD ID: ASN) (formula: C₄H₈N₂O₃).



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

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	113	Total	O	0	0
			113	113		
4	B	110	Total	O	0	0
			110	110		
4	C	97	Total	O	0	0
			97	97		
4	D	79	Total	O	0	0
			79	79		

4 Data and refinement statistics i

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	123.86Å 154.78Å 157.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.29 30.00 – 2.29	Depositor EDS
% Data completeness (in resolution range)	97.7 (30.00-2.29) 97.7 (30.00-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.208 , 0.242 (Not available) , 0.205	Depositor DCC
R_{free} test set	3316 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtrriage
Anisotropy	0.091	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.015 for -h,-l,-k	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11313	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.28% 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: 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	0.76	0/2756	0.82	2/3746 (0.1%)
1	B	0.75	0/2772	0.80	1/3770 (0.0%)
1	C	0.75	0/2781	0.80	0/3783
1	D	0.75	0/2785	0.81	0/3788
All	All	0.75	0/11094	0.81	3/15087 (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

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	69	GLY	CA-C-N	-6.24	113.86	120.66
1	A	69	GLY	C-N-CA	-6.24	113.86	120.66
1	B	186	VAL	CB-CA-C	-5.14	104.39	111.49

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	65	PRO	Peptide

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	2700	0	2772	13	1
1	B	2715	0	2786	13	1
1	C	2719	0	2789	13	0
1	D	2728	0	2795	14	0
2	A	9	0	5	0	0
2	B	9	0	5	1	0
2	C	9	0	5	0	0
2	D	9	0	5	1	0
3	B	4	0	6	0	0
3	C	4	0	6	0	0
3	D	8	0	12	0	0
4	A	113	0	0	1	0
4	B	110	0	0	1	0
4	C	97	0	0	0	0
4	D	79	0	0	1	0
All	All	11313	0	11186	43	1

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 2.

All (43) 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:C:281:GLN:OE1	1:C:284:ARG:NH2	2.00	0.94
1:C:150[B]:TRP:NE1	1:D:208:VAL:HG11	2.05	0.71
1:A:150:TRP:NE1	1:B:208:VAL:HG11	2.12	0.64
1:A:150:TRP:NE1	1:B:208:VAL:CG1	2.60	0.64
1:C:150[B]:TRP:NE1	1:D:208:VAL:CG1	2.63	0.61
1:C:47:ASP:OD2	1:C:71:ARG:NH2	2.38	0.57
1:B:47:ASP:OD2	1:B:71:ARG:NH2	2.38	0.57
1:A:47:ASP:OD2	1:A:71:ARG:NH2	2.38	0.56
1:D:47:ASP:OD2	1:D:71:ARG:NH2	2.38	0.56
1:A:208:VAL:HG21	1:B:150:TRP:CZ2	2.41	0.55
1:B:292:ILE:HD12	1:B:336:LEU:HD21	1.89	0.54
1:D:292:ILE:HD12	1:D:336:LEU:HD21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:TRP:HE1	1:B:208:VAL:HG12	1.72	0.54
1:C:119:MET:SD	1:C:174:LEU:HD13	2.48	0.54
1:C:150[B]:TRP:HE1	1:D:208:VAL:CG1	2.22	0.53
1:D:77:LEU:C	1:D:77:LEU:HD23	2.33	0.52
1:A:66:ALA:HA	4:A:889:HOH:O	2.10	0.51
1:A:292:ILE:HD12	1:A:336:LEU:HD21	1.92	0.51
1:C:292:ILE:HD12	1:C:336:LEU:HD21	1.93	0.50
1:D:40:ARG:NH1	1:D:58:ASP:O	2.45	0.49
1:C:150[B]:TRP:HE1	1:D:208:VAL:HG12	1.77	0.49
1:B:19:THR:OG1	2:B:601:ASN:CG	2.56	0.48
1:B:77:LEU:C	1:B:77:LEU:HD23	2.38	0.47
1:C:77:LEU:HD23	1:C:77:LEU:C	2.39	0.47
1:A:150:TRP:NE1	1:B:208:VAL:HG12	2.27	0.47
1:B:134:HIS:CD2	4:B:741:HOH:O	2.68	0.47
1:A:174:LEU:HD21	1:A:176:MET:HG3	1.97	0.47
1:C:119:MET:SD	1:C:174:LEU:CD1	3.03	0.47
1:A:77:LEU:C	1:A:77:LEU:HD23	2.40	0.47
1:D:19:THR:OG1	2:D:601:ASN:CG	2.58	0.46
1:B:174:LEU:HD21	1:B:176:MET:HG3	1.98	0.45
1:C:224:TRP:CD1	1:C:224:TRP:H	2.36	0.44
1:D:312:LEU:HD23	4:D:755:HOH:O	2.18	0.44
1:D:174:LEU:HD21	1:D:176:MET:HG3	1.98	0.43
1:B:224:TRP:CD1	1:B:224:TRP:H	2.37	0.42
1:D:85:SER:HB3	1:D:115:GLY:HA3	2.02	0.42
1:B:85:SER:HB3	1:B:115:GLY:HA3	2.02	0.42
1:C:208:VAL:HG21	1:D:150:TRP:CZ2	2.55	0.41
1:D:20:LEU:C	1:D:20:LEU:HD23	2.45	0.41
1:A:85:SER:HB3	1:A:115:GLY:HA3	2.03	0.40
1:A:125:MET:HB3	1:A:129:MET:HE3	2.02	0.40
1:C:125:MET:HB3	1:C:129:MET:HE3	2.02	0.40
1:A:159:GLY:HA3	1:A:175:PHE:CE2	2.57	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:GLU:OE1	1:B:342:SER:OG[8_555]	2.11	0.09

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	294/473 (62%)	293 (100%)	1 (0%)	86	93
1	B	296/473 (63%)	295 (100%)	1 (0%)	86	93
1	C	296/473 (63%)	294 (99%)	2 (1%)	76	87
1	D	297/473 (63%)	293 (99%)	4 (1%)	61	77
All	All	1183/1892 (62%)	1175 (99%)	8 (1%)	76	87

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	198	CYS
1	B	198	CYS
1	C	198	CYS
1	C	281	GLN
1	D	198	CYS
1	D	211	ASP
1	D	284	ARG
1	D	362	THR

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	23	GLN
1	A	54	GLN
1	A	106	GLN
1	A	179	GLN
1	B	23	GLN

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Mol	Chain	Res	Type
1	B	68	HIS
1	B	106	GLN
1	C	23	GLN
1	C	106	GLN
1	D	106	GLN
1	D	179	GLN
1	D	281	GLN
1	D	288	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	$\# Z > 2$
3	EDO	B	602	-	3,3,3	0.58	0	2,2,2	0.22	0
3	EDO	D	603	-	3,3,3	0.58	0	2,2,2	0.09	0
3	EDO	D	602	-	3,3,3	0.54	0	2,2,2	0.12	0
3	EDO	C	602	-	3,3,3	0.58	0	2,2,2	0.27	0
2	ASN	C	601	-	7,8,8	0.86	0	6,10,10	0.58	0
2	ASN	B	601	-	7,8,8	0.93	0	6,10,10	0.99	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ASN	A	700	-	7,8,8	0.98	1 (14%)	6,10,10	0.98	1 (16%)
2	ASN	D	601	-	7,8,8	0.77	0	6,10,10	1.20	1 (16%)

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
3	EDO	B	602	-	-	1/1/1/1	-
3	EDO	D	603	-	-	1/1/1/1	-
3	EDO	D	602	-	-	1/1/1/1	-
3	EDO	C	602	-	-	1/1/1/1	-
2	ASN	C	601	-	-	4/8/8/8	-
2	ASN	B	601	-	-	2/8/8/8	-
2	ASN	A	700	-	-	4/8/8/8	-
2	ASN	D	601	-	-	4/8/8/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	700	ASN	OXT-C	-2.50	1.22	1.30

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	ASN	OXT-C-O	-2.83	117.65	124.08
2	B	601	ASN	OXT-C-O	-2.32	118.81	124.08
2	A	700	ASN	OXT-C-O	-2.32	118.82	124.08

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	700	ASN	O-C-CA-N
2	B	601	ASN	O-C-CA-N
2	C	601	ASN	O-C-CA-N
2	D	601	ASN	O-C-CA-N
2	C	601	ASN	OXT-C-CA-N
2	D	601	ASN	OXT-C-CA-N

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Mol	Chain	Res	Type	Atoms
2	A	700	ASN	OXT-C-CA-N
2	B	601	ASN	OXT-C-CA-N
2	C	601	ASN	OXT-C-CA-CB
2	D	601	ASN	OXT-C-CA-CB
2	C	601	ASN	O-C-CA-CB
2	D	601	ASN	O-C-CA-CB
3	D	602	EDO	O1-C1-C2-O2
3	D	603	EDO	O1-C1-C2-O2
3	B	602	EDO	O1-C1-C2-O2
3	C	602	EDO	O1-C1-C2-O2
2	A	700	ASN	O-C-CA-CB
2	A	700	ASN	OXT-C-CA-CB

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	ASN	1	0
2	D	601	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

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, 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	353/588 (60%)	-0.18	8 (2%) 61 63	21, 32, 70, 110	0
1	B	355/588 (60%)	-0.17	5 (1%) 73 75	23, 33, 65, 113	0
1	C	354/588 (60%)	-0.19	7 (1%) 65 66	17, 33, 60, 108	1 (0%)
1	D	357/588 (60%)	-0.07	7 (1%) 65 66	22, 35, 70, 120	0
All	All	1419/2352 (60%)	-0.15	27 (1%) 66 68	17, 33, 68, 120	1 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	224	TRP	4.7
1	A	68	HIS	3.8
1	A	66	ALA	3.8
1	D	224	TRP	3.6
1	D	68	HIS	3.0
1	A	57	PRO	2.8
1	B	208	VAL	2.8
1	C	56	LEU	2.8
1	A	59	HIS	2.8
1	D	223	LYS	2.7
1	C	59	HIS	2.6
1	B	57	PRO	2.6
1	C	66	ALA	2.5
1	B	362	THR	2.5
1	B	224	TRP	2.5
1	D	59	HIS	2.5
1	C	57	PRO	2.4
1	D	302	GLY	2.3
1	A	56	LEU	2.3
1	A	60	ALA	2.3
1	D	67	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	68	HIS	2.3
1	C	302	GLY	2.3
1	C	77	LEU	2.1
1	B	222	VAL	2.1
1	A	67	SER	2.1
1	D	69	GLY	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 oligosaccharides 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, 95th 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(Å ²)	Q<0.9
3	EDO	C	602	4/4	0.79	0.18	51,55,57,61	0
3	EDO	D	602	4/4	0.87	0.11	42,46,46,47	0
3	EDO	B	602	4/4	0.92	0.10	33,37,38,38	0
3	EDO	D	603	4/4	0.94	0.10	34,37,37,38	0
2	ASN	B	601	9/9	0.95	0.07	30,34,36,38	0
2	ASN	C	601	9/9	0.95	0.08	30,32,34,35	0
2	ASN	A	700	9/9	0.95	0.07	26,27,29,33	0
2	ASN	D	601	9/9	0.96	0.06	26,28,30,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.