



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:02 PM UTC

PDB ID : 2XB6 / pdb_00002xb6
Title : Revisited crystal structure of Neurexin1beta-Neurologin4 complex
Authors : Leone, P.; Comoletti, D.; Ferracci, G.; Conrod, S.; Garcia, S.U.; Taylor, P.; Bourne, Y.; Marchot, P.
Deposited on : 2010-04-07
Resolution : 2.60 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

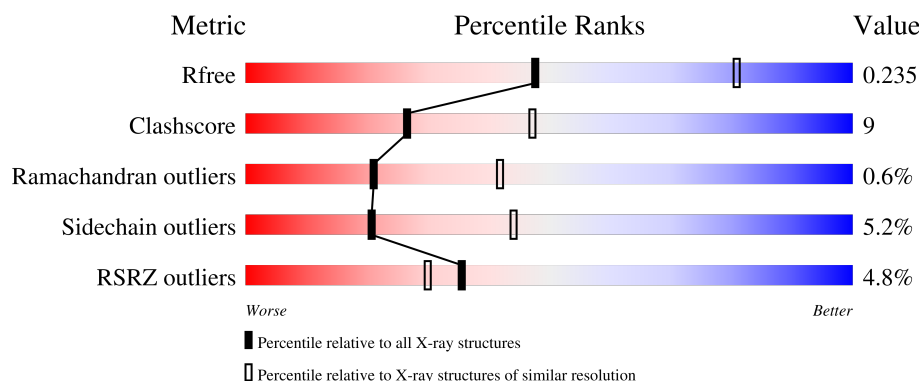
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	
1	B	588	
2	C	179	
2	D	179	

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
4	EDO	A	1601	-	-	X	-
4	EDO	A	1605	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 11720 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 NEUROLIGIN-4, X-LINKED.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	529	Total	C	N	O	S	0	0	0
			4182	2681	692	788	21			
1	B	541	Total	C	N	O	S	0	0	0
			4276	2738	707	810	21			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	ASP	-	expression tag	UNP Q8N0W4
A	-11	TYR	-	expression tag	UNP Q8N0W4
A	-10	LYS	-	expression tag	UNP Q8N0W4
A	-9	ASP	-	expression tag	UNP Q8N0W4
A	-8	ASP	-	expression tag	UNP Q8N0W4
A	-7	ASP	-	expression tag	UNP Q8N0W4
A	-6	ASP	-	expression tag	UNP Q8N0W4
A	-5	LYS	-	expression tag	UNP Q8N0W4
A	-4	LEU	-	expression tag	UNP Q8N0W4
A	-3	ALA	-	expression tag	UNP Q8N0W4
A	-2	ALA	-	expression tag	UNP Q8N0W4
A	-1	ALA	-	expression tag	UNP Q8N0W4
B	-12	ASP	-	expression tag	UNP Q8N0W4
B	-11	TYR	-	expression tag	UNP Q8N0W4
B	-10	LYS	-	expression tag	UNP Q8N0W4
B	-9	ASP	-	expression tag	UNP Q8N0W4
B	-8	ASP	-	expression tag	UNP Q8N0W4
B	-7	ASP	-	expression tag	UNP Q8N0W4
B	-6	ASP	-	expression tag	UNP Q8N0W4
B	-5	LYS	-	expression tag	UNP Q8N0W4
B	-4	LEU	-	expression tag	UNP Q8N0W4
B	-3	ALA	-	expression tag	UNP Q8N0W4
B	-2	ALA	-	expression tag	UNP Q8N0W4
B	-1	ALA	-	expression tag	UNP Q8N0W4
A	561	ARG	LYS	cloning artifact	UNP Q8N0W4

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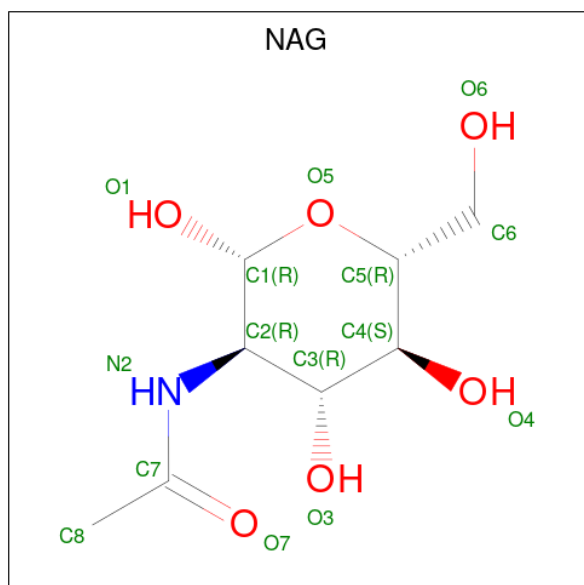
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Chain	Residue	Modelled	Actual	Comment	Reference
B	561	ARG	LYS	cloning artifact	UNP Q8N0W4

- Molecule 2 is a protein called NEUREXIN-1-BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	177	Total	C	N	O	S	0	0	0
			1359	857	243	258	1			
2	D	177	Total	C	N	O	S	0	0	0
			1359	857	243	258	1			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O		0	0
			14	8	1	5			
3	A	1	Total	C	N	O		0	0
			14	8	1	5			
3	B	1	Total	C	N	O		0	0
			14	8	1	5			
3	B	1	Total	C	N	O		0	0
			14	8	1	5			

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

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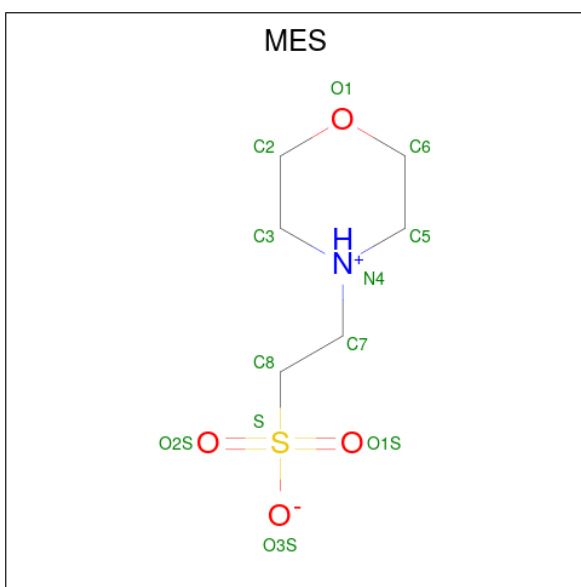
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0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

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Cl 2 2	0	0
5	B	3	Total Cl 3 3	0	0

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	1	Total	Ca	0	0
			1	1		
7	D	1	Total	Ca	0	0
			1	1		

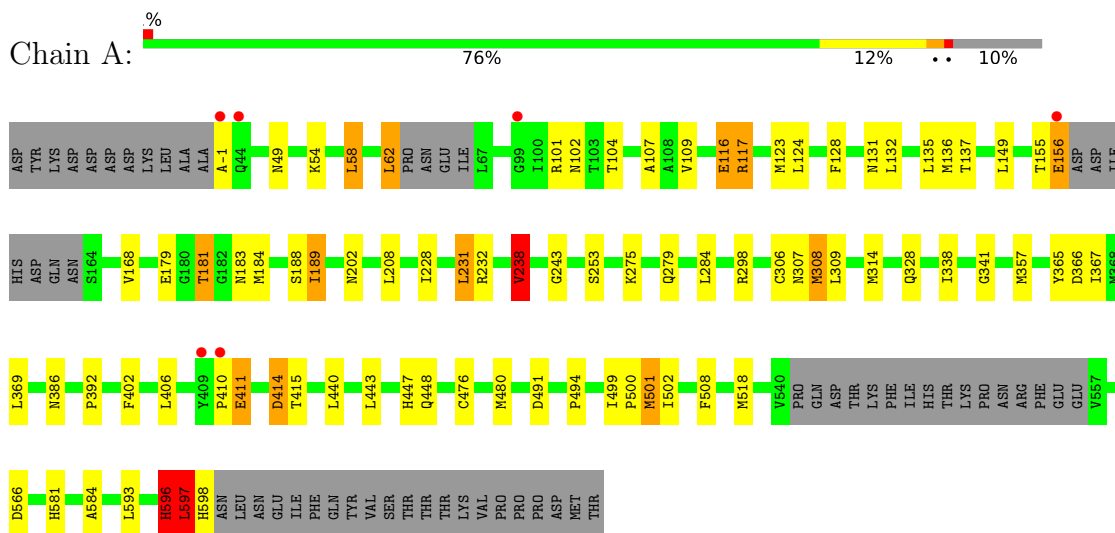
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	129	Total	O	0	0
			129	129		
8	B	162	Total	O	0	0
			162	162		
8	C	38	Total	O	0	0
			38	38		
8	D	20	Total	O	0	0
			20	20		

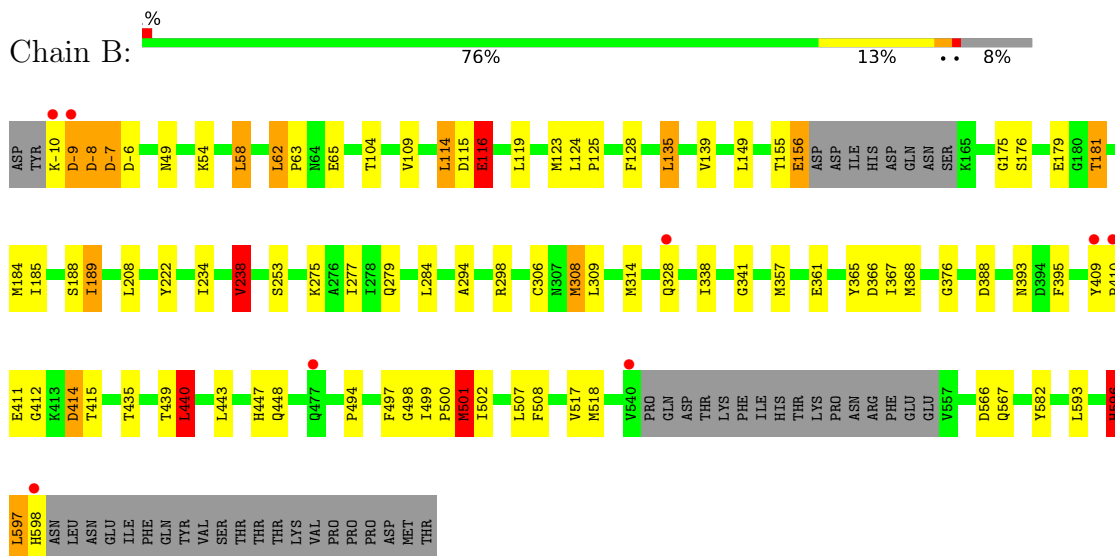
3 Residue-property plots

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.

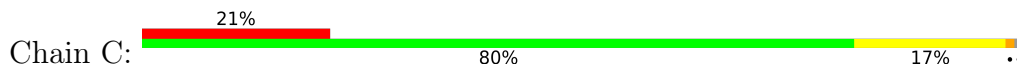
• Molecule 1: NEUROLIGIN-4, X-LINKED

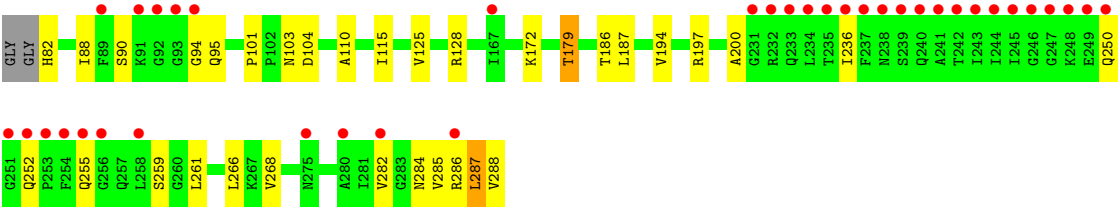


• Molecule 1: NEUROLIGIN-4, X-LINKED

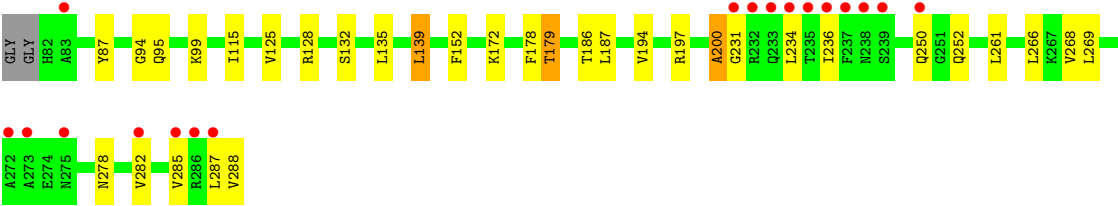
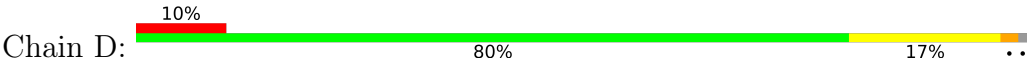


• Molecule 2: NEUREXIN-1-BETA





● Molecule 2: NEUREXIN-1-BETA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	136.31Å 198.78Å 85.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 30.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-2.60) 99.9 (30.00-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.204 , 0.236 0.202 , 0.235	Depositor DCC
R_{free} test set	3656 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.541	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11720	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, NAG, MES, CA, CL

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	0.86	4/4298 (0.1%)	0.91	2/5860 (0.0%)
1	B	0.88	3/4394 (0.1%)	0.91	3/5992 (0.1%)
2	C	1.17	2/1385 (0.1%)	1.02	2/1877 (0.1%)
2	D	1.40	2/1385 (0.1%)	0.98	4/1877 (0.2%)
All	All	0.99	11/11462 (0.1%)	0.93	11/15606 (0.1%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	200	ALA	C-N	40.78	1.86	1.33
2	C	200	ALA	C-N	25.08	1.66	1.33
2	C	197	ARG	CZ-NH1	-15.04	1.11	1.32
2	D	197	ARG	CZ-NH1	-14.54	1.12	1.32
1	A	-1	ALA	C-N	10.76	1.49	1.33
1	B	238	VAL	CB-CG1	-5.82	1.33	1.52
1	B	238	VAL	CB-CG2	-5.82	1.33	1.52
1	A	231	LEU	CG-CD1	-5.65	1.33	1.52
1	A	440	LEU	CG-CD2	-5.46	1.34	1.52
1	B	440	LEU	CG-CD1	-5.35	1.34	1.52
1	A	238	VAL	CB-CG1	-5.09	1.35	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	197	ARG	NE-CZ-NH2	15.93	133.54	119.20
2	C	197	ARG	NE-CZ-NH2	15.72	133.34	119.20
1	B	501	MET	CB-CG-SD	10.48	144.15	112.70
1	A	501	MET	CB-CG-SD	9.97	142.61	112.70
2	C	197	ARG	NE-CZ-NH1	-9.97	111.53	121.50
2	D	197	ARG	NE-CZ-NH1	-9.82	111.68	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	596	HIS	N-CA-C	-8.52	98.76	110.35
1	B	596	HIS	N-CA-C	-6.47	100.71	110.28
1	B	238	VAL	CB-CA-C	-5.32	103.91	112.16
2	D	200	ALA	CA-C-N	-5.25	113.26	121.87
2	D	200	ALA	C-N-CA	-5.25	113.26	121.87

There are no chirality outliers.

There are no planarity outliers.

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	4182	0	4027	75	0
1	B	4276	0	4116	85	0
2	C	1359	0	1347	22	0
2	D	1359	0	1346	25	0
3	A	28	0	26	3	0
3	B	28	0	26	1	0
4	A	40	0	60	12	0
4	B	56	0	84	9	0
4	C	24	0	36	1	0
5	A	2	0	0	0	0
5	B	3	0	0	0	0
6	C	12	0	12	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	129	0	0	3	0
8	B	162	0	0	1	0
8	C	38	0	0	1	0
8	D	20	0	0	2	0
All	All	11720	0	11080	209	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 9.

All (209) 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)
2:D:200:ALA:C	2:D:231:GLY:N	1.86	1.33
1:B:115:ASP:O	1:B:116:GLU:HB3	1.56	1.05
1:A:596:HIS:O	1:A:597:LEU:HB2	1.64	0.94
1:B:411:GLU:OE2	1:B:414:ASP:OD1	1.86	0.94
1:A:308:MET:HE2	1:A:308:MET:H	1.34	0.93
1:B:308:MET:H	1:B:308:MET:HE2	1.32	0.92
1:A:128:PHE:CE1	1:A:135:LEU:HD11	2.04	0.92
1:B:189:ILE:HD11	1:B:502:ILE:HG12	1.54	0.89
1:A:308:MET:H	1:A:308:MET:CE	1.91	0.84
1:A:128:PHE:CD1	1:A:135:LEU:HD11	2.12	0.83
1:B:189:ILE:HD11	1:B:502:ILE:CG1	2.08	0.83
2:C:186:THR:HG23	2:C:194:VAL:CG1	2.08	0.82
1:B:308:MET:H	1:B:308:MET:CE	1.91	0.82
2:D:186:THR:HG23	2:D:194:VAL:CG1	2.14	0.78
1:A:132:LEU:HD13	1:A:136:MET:HE3	1.68	0.76
1:B:306:CYS:C	1:B:308:MET:HE3	2.09	0.76
2:C:186:THR:CG2	2:C:194:VAL:CG1	2.64	0.76
1:B:596:HIS:O	1:B:597:LEU:HB2	1.86	0.75
1:A:306:CYS:C	1:A:308:MET:HE3	2.11	0.74
1:B:395:PHE:CD1	1:B:440:LEU:HD13	2.23	0.74
1:B:189:ILE:CD1	1:B:502:ILE:HG12	2.18	0.73
2:D:186:THR:CG2	2:D:194:VAL:HG13	2.21	0.70
1:A:480:MET:HE1	4:A:1605:EDO:O1	1.92	0.69
1:B:58:LEU:HD21	1:B:104:THR:HB	1.74	0.69
1:B:181:THR:HG22	1:B:184:MET:HE3	1.75	0.69
2:D:186:THR:CG2	2:D:194:VAL:CG1	2.71	0.68
2:C:287:LEU:HD13	2:C:287:LEU:O	1.94	0.68
1:B:181:THR:CG2	1:B:184:MET:HE3	2.24	0.68
1:A:202:ASN:CG	4:A:1601:EDO:H12	2.19	0.67
1:A:189:ILE:HD11	1:A:502:ILE:CG1	2.25	0.67
1:A:128:PHE:CD1	1:A:135:LEU:CD1	2.78	0.67
1:B:49:ASN:HD22	1:B:54:LYS:HG2	1.60	0.67
2:D:135:LEU:O	8:D:2005:HOH:O	2.13	0.66
1:B:365:TYR:HB2	1:B:367:ILE:HD11	1.78	0.66
1:A:414:ASP:OD1	1:A:414:ASP:N	2.26	0.65
1:A:107:ALA:HB3	4:A:1601:EDO:H22	1.79	0.64
1:A:365:TYR:O	1:A:367:ILE:HD13	1.96	0.64
2:C:186:THR:CG2	2:C:194:VAL:HG13	2.26	0.64
1:B:275:LYS:HG2	1:B:366:ASP:HB2	1.80	0.64
1:A:365:TYR:HB2	1:A:367:ILE:HD11	1.80	0.63
1:B:593:LEU:O	1:B:596:HIS:O	2.14	0.63
2:D:288:VAL:HG12	2:D:288:VAL:O	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:MET:HE2	1:B:176:SER:HA	1.79	0.63
2:D:115:ILE:HD12	2:D:261:LEU:HD13	1.79	0.63
1:B:498:GLY:O	1:B:501:MET:HB2	1.99	0.63
2:C:94:GLY:HA3	2:C:285:VAL:HG23	1.81	0.62
1:B:155:THR:O	1:B:156:GLU:HG2	1.99	0.61
1:B:596:HIS:O	1:B:597:LEU:CB	2.48	0.61
1:A:593:LEU:O	1:A:596:HIS:O	2.18	0.61
1:B:395:PHE:CD1	1:B:440:LEU:CD1	2.83	0.60
1:B:411:GLU:HG3	1:B:412:GLY:H	1.66	0.60
1:B:234:ILE:O	1:B:238:VAL:HG22	2.02	0.59
1:A:189:ILE:HD11	1:A:502:ILE:HG12	1.82	0.59
2:C:115:ILE:HD12	2:C:261:LEU:HD13	1.83	0.59
1:B:298:ARG:NH2	1:B:314:MET:HE2	2.18	0.59
1:B:567:GLN:HB3	4:B:1600:EDO:H12	1.85	0.59
1:B:116:GLU:HA	1:B:119:LEU:HD12	1.84	0.58
1:B:414:ASP:OD1	1:B:414:ASP:N	2.35	0.58
2:C:179:THR:HB	2:C:186:THR:HB	1.84	0.58
1:A:596:HIS:O	1:A:597:LEU:CB	2.43	0.58
1:B:181:THR:HG22	1:B:184:MET:CE	2.34	0.58
1:B:234:ILE:HG23	1:B:238:VAL:HG13	1.86	0.58
2:D:287:LEU:O	2:D:288:VAL:C	2.45	0.58
1:A:49:ASN:HD22	1:A:54:LYS:HG2	1.69	0.58
1:B:306:CYS:CA	1:B:308:MET:HE3	2.33	0.58
1:A:298:ARG:NH2	1:A:314:MET:HE2	2.18	0.57
1:A:338:ILE:HD12	1:A:341:GLY:HA3	1.86	0.57
1:B:365:TYR:O	1:B:367:ILE:HD13	2.04	0.57
2:D:200:ALA:C	2:D:231:GLY:CA	2.77	0.57
1:A:308:MET:HE2	1:A:308:MET:N	2.12	0.57
1:B:411:GLU:OE1	1:B:411:GLU:HA	2.05	0.57
1:A:275:LYS:HG2	1:A:366:ASP:HB2	1.87	0.57
2:D:179:THR:HB	2:D:186:THR:HB	1.86	0.56
1:B:308:MET:HE2	1:B:308:MET:N	2.11	0.56
1:A:58:LEU:HD21	1:A:104:THR:HB	1.88	0.56
1:A:306:CYS:CA	1:A:308:MET:HE3	2.35	0.56
3:A:700:NAG:C6	8:A:2124:HOH:O	2.50	0.56
2:C:287:LEU:O	2:C:288:VAL:C	2.49	0.56
2:D:139:LEU:HD11	2:D:178:PHE:CE2	2.41	0.55
1:B:365:TYR:HB2	1:B:367:ILE:CD1	2.37	0.55
1:A:386:ASN:ND2	4:A:1602:EDO:O2	2.39	0.55
2:D:287:LEU:O	2:D:287:LEU:HG	2.06	0.54
1:B:409:TYR:O	1:B:410:PRO:C	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:LEU:O	4:B:1611:EDO:O2	2.20	0.54
1:B:501:MET:HE2	1:B:517:VAL:HG13	1.88	0.54
1:B:284:LEU:HD21	1:B:357:MET:CE	2.38	0.54
1:B:361:GLU:CG	2:D:234:LEU:HD22	2.38	0.53
1:A:411:GLU:OE1	1:A:411:GLU:HA	2.09	0.53
2:C:261:LEU:HD23	2:C:268:VAL:HB	1.91	0.53
2:D:261:LEU:HD23	2:D:268:VAL:HB	1.89	0.53
1:A:443:LEU:C	1:A:443:LEU:HD23	2.34	0.52
1:A:101:ARG:NH2	8:A:2006:HOH:O	2.43	0.52
3:A:700:NAG:O6	8:A:2124:HOH:O	1.94	0.52
1:A:135:LEU:C	1:A:135:LEU:HD23	2.35	0.52
1:A:480:MET:HE2	4:A:1605:EDO:H21	1.92	0.52
2:C:88:ILE:HG23	2:C:286:ARG:HB3	1.90	0.52
2:D:95:GLN:HB3	2:D:282:VAL:HG12	1.91	0.52
1:A:202:ASN:CG	4:A:1601:EDO:C1	2.83	0.52
1:B:63:PRO:HG2	1:B:502:ILE:HD12	1.92	0.52
1:B:338:ILE:HD12	1:B:341:GLY:HA3	1.92	0.52
1:A:406:LEU:HD13	1:A:447:HIS:CE1	2.45	0.51
1:B:155:THR:O	1:B:156:GLU:CG	2.58	0.51
1:B:306:CYS:HA	1:B:308:MET:CE	2.41	0.51
2:C:95:GLN:HB3	2:C:282:VAL:HG12	1.92	0.51
1:A:189:ILE:CD1	1:A:502:ILE:HG12	2.41	0.51
1:A:306:CYS:HA	1:A:308:MET:CE	2.41	0.51
1:B:395:PHE:CE1	1:B:440:LEU:HD13	2.46	0.51
2:C:88:ILE:CG2	2:C:286:ARG:HB3	2.40	0.51
1:A:155:THR:O	1:A:156:GLU:HG2	2.09	0.51
1:B:181:THR:CG2	1:B:184:MET:CE	2.89	0.50
1:B:582:TYR:N	4:B:1600:EDO:H21	2.26	0.50
1:B:-8:ASP:O	1:B:-7:ASP:HB2	2.11	0.50
1:B:494:PRO:HG3	1:B:508:PHE:CD2	2.46	0.50
2:C:186:THR:HG22	2:C:187:LEU:N	2.27	0.50
1:A:155:THR:O	1:A:156:GLU:CG	2.60	0.49
1:A:253:SER:HA	1:A:279:GLN:O	2.11	0.49
1:A:168:VAL:HG21	1:A:238:VAL:HG21	1.94	0.49
1:A:447:HIS:ND1	1:A:448:GLN:NE2	2.57	0.49
1:B:124:LEU:HD23	1:B:175:GLY:HA3	1.94	0.49
1:A:107:ALA:C	4:A:1601:EDO:H22	2.38	0.48
1:A:181:THR:CG2	1:A:184:MET:HE3	2.43	0.48
1:A:284:LEU:HD11	1:A:357:MET:HE1	1.95	0.48
1:A:128:PHE:CE1	1:A:135:LEU:CD1	2.87	0.48
1:B:115:ASP:O	1:B:116:GLU:CB	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:CYS:HA	1:B:308:MET:HE3	1.94	0.48
1:B:443:LEU:HD23	1:B:443:LEU:C	2.38	0.48
1:B:-9:ASP:O	1:B:-7:ASP:N	2.47	0.48
1:B:128:PHE:CE1	1:B:135:LEU:HD22	2.48	0.48
1:A:366:ASP:C	1:A:367:ILE:HD12	2.38	0.48
1:A:494:PRO:HG3	1:A:508:PHE:CD2	2.49	0.48
1:B:65:GLU:HA	4:B:1611:EDO:H12	1.96	0.48
1:A:306:CYS:HA	1:A:308:MET:HE3	1.96	0.47
1:A:499:ILE:N	1:A:500:PRO:CD	2.77	0.47
2:C:90:SER:HB2	2:C:284:ASN:ND2	2.29	0.47
3:B:700:NAG:H62	4:B:1609:EDO:H11	1.96	0.47
2:C:186:THR:CG2	2:C:194:VAL:HG11	2.45	0.47
1:B:181:THR:HG23	1:B:184:MET:HE3	1.97	0.47
1:B:388:ASP:OD2	8:B:2106:HOH:O	2.20	0.47
1:A:132:LEU:HA	1:A:135:LEU:HB3	1.96	0.47
1:A:411:GLU:OE2	1:A:414:ASP:OD1	2.32	0.47
2:D:125:VAL:HG23	2:D:252:GLN:HE21	1.79	0.47
1:A:392:PRO:HD3	4:A:1603:EDO:H22	1.96	0.46
1:B:499:ILE:N	1:B:500:PRO:CD	2.78	0.46
2:D:139:LEU:HD12	2:D:152:PHE:HB3	1.97	0.46
1:A:365:TYR:HB2	1:A:367:ILE:CD1	2.44	0.46
2:C:101:PRO:HB2	2:C:103:ASN:OD1	2.15	0.46
1:B:63:PRO:HD2	1:B:502:ILE:HD12	1.98	0.46
2:C:255:GLN:OE1	8:C:2037:HOH:O	2.21	0.46
1:A:181:THR:HG22	1:A:184:MET:HE3	1.98	0.46
1:A:58:LEU:N	1:A:58:LEU:HD23	2.31	0.46
1:B:499:ILE:HD13	1:B:508:PHE:CD1	2.51	0.46
2:D:94:GLY:HA3	2:D:285:VAL:CG2	2.46	0.45
1:B:234:ILE:HG23	1:B:238:VAL:CG1	2.46	0.45
1:B:294:ALA:CB	4:B:1599:EDO:H11	2.46	0.45
1:A:476:CYS:SG	4:A:1605:EDO:H11	2.56	0.45
2:D:128:ARG:HD3	2:D:250:GLN:NE2	2.31	0.45
1:B:395:PHE:HD1	1:B:440:LEU:HD13	1.80	0.45
2:D:125:VAL:HG23	2:D:252:GLN:NE2	2.32	0.45
1:A:116:GLU:O	1:A:117:ARG:CB	2.65	0.45
1:A:181:THR:HG22	1:A:184:MET:CE	2.46	0.45
1:B:114:LEU:HD22	1:B:139:VAL:HG21	1.98	0.45
1:B:149:LEU:C	1:B:149:LEU:HD12	2.42	0.45
1:A:181:THR:CG2	1:A:184:MET:CE	2.95	0.45
1:B:597:LEU:O	1:B:598:HIS:HB2	2.17	0.44
2:C:186:THR:HG23	2:C:194:VAL:HG11	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:253:SER:HA	1:B:279:GLN:O	2.17	0.44
1:B:222:TYR:OH	4:B:1605:EDO:H22	2.18	0.44
1:B:366:ASP:C	1:B:367:ILE:HD12	2.43	0.44
1:B:294:ALA:HB3	4:B:1599:EDO:H11	1.98	0.44
1:A:597:LEU:O	1:A:598:HIS:HB2	2.18	0.44
1:B:58:LEU:HD21	1:B:104:THR:CB	2.44	0.44
2:C:128:ARG:HD3	2:C:250:GLN:NE2	2.33	0.44
1:A:102:ASN:CG	3:A:700:NAG:HN2	2.22	0.43
1:A:62:LEU:HD11	1:A:188:SER:HB3	1.99	0.43
1:A:58:LEU:HD23	1:A:104:THR:HG22	1.99	0.43
1:A:499:ILE:HD13	1:A:508:PHE:CD1	2.53	0.43
1:A:58:LEU:HD21	1:A:104:THR:CB	2.48	0.43
2:D:87:TYR:CD1	2:D:269:LEU:HD22	2.54	0.43
2:D:186:THR:HG22	2:D:187:LEU:N	2.34	0.43
1:A:183:ASN:HD21	4:A:1601:EDO:H21	1.84	0.42
2:D:186:THR:HG22	8:D:2012:HOH:O	2.17	0.42
1:A:402:PHE:CE1	1:A:406:LEU:HD12	2.54	0.42
1:B:-9:ASP:OD1	1:B:-8:ASP:N	2.52	0.42
2:C:82:HIS:ND1	2:C:259:SER:OG	2.45	0.42
1:A:238:VAL:HG22	1:A:243:GLY:HA3	2.02	0.42
1:A:284:LEU:HD21	1:A:357:MET:CE	2.50	0.42
1:A:581:HIS:HB3	1:A:584:ALA:HB2	2.00	0.42
1:B:58:LEU:HD23	1:B:104:THR:HG22	2.01	0.42
1:B:277:ILE:HA	1:B:368:MET:O	2.19	0.42
1:B:499:ILE:CD1	1:B:508:PHE:CD1	3.03	0.42
1:B:135:LEU:HG	1:B:507:LEU:HD21	2.01	0.42
1:B:447:HIS:ND1	1:B:448:GLN:NE2	2.64	0.42
1:B:125:PRO:HG2	1:B:128:PHE:HB2	2.00	0.42
1:A:149:LEU:C	1:A:149:LEU:HD12	2.45	0.41
2:C:110:ALA:HB1	4:C:1293:EDO:H22	2.01	0.41
1:A:369:LEU:HD23	1:A:369:LEU:N	2.34	0.41
2:D:99:LYS:O	2:D:278:ASN:HB3	2.20	0.41
2:C:125:VAL:HG23	2:C:252:GLN:HE21	1.85	0.41
2:D:94:GLY:HA3	2:D:285:VAL:HG22	2.02	0.41
1:B:62:LEU:HD11	1:B:188:SER:HB3	2.02	0.41
1:B:435:THR:O	1:B:439:THR:HG23	2.20	0.41
1:A:369:LEU:HD23	1:A:369:LEU:H	1.86	0.41
1:A:491:ASP:OD2	4:A:1605:EDO:H12	2.21	0.41
1:B:185:ILE:HG21	1:B:497:PHE:CZ	2.57	0.40
1:B:189:ILE:HD11	1:B:502:ILE:HG13	1.94	0.40
1:A:232:ARG:NH1	4:A:1599:EDO:O2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:-6:ASP:OD1	1:B:-6:ASP:C	2.64	0.40
1:B:376:GLY:HA2	4:B:1607:EDO:H11	2.04	0.40
1:A:410:PRO:HA	1:A:411:GLU:HA	1.83	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	521/588 (89%)	493 (95%)	26 (5%)	2 (0%)	30	51
1	B	535/588 (91%)	511 (96%)	19 (4%)	5 (1%)	14	30
2	C	175/179 (98%)	170 (97%)	5 (3%)	0	100	100
2	D	175/179 (98%)	168 (96%)	6 (3%)	1 (1%)	21	42
All	All	1406/1534 (92%)	1342 (95%)	56 (4%)	8 (1%)	21	42

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	-8	ASP
1	B	-9	ASP
1	B	-7	ASP
1	B	116	GLU
1	B	597	LEU
1	A	117	ARG
1	A	597	LEU
2	D	132	SER

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	453/510 (89%)	425 (94%)	28 (6%)	16	36
1	B	463/510 (91%)	439 (95%)	24 (5%)	21	44
2	C	143/143 (100%)	137 (96%)	6 (4%)	26	52
2	D	143/143 (100%)	138 (96%)	5 (4%)	32	59
All	All	1202/1306 (92%)	1139 (95%)	63 (5%)	21	44

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	LEU
1	A	62	LEU
1	A	109	VAL
1	A	116	GLU
1	A	123	MET
1	A	124	LEU
1	A	131	ASN
1	A	137	THR
1	A	156	GLU
1	A	179	GLU
1	A	181	THR
1	A	189	ILE
1	A	208	LEU
1	A	228	ILE
1	A	231	LEU
1	A	238	VAL
1	A	307	ASN
1	A	308	MET
1	A	309	LEU
1	A	328	GLN
1	A	411	GLU
1	A	414	ASP
1	A	415	THR
1	A	501	MET

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Mol	Chain	Res	Type
1	A	518	MET
1	A	566	ASP
1	A	596	HIS
1	A	597	LEU
1	B	-10	LYS
1	B	58	LEU
1	B	62	LEU
1	B	109	VAL
1	B	114	LEU
1	B	116	GLU
1	B	135	LEU
1	B	156	GLU
1	B	179	GLU
1	B	181	THR
1	B	189	ILE
1	B	208	LEU
1	B	238	VAL
1	B	308	MET
1	B	309	LEU
1	B	328	GLN
1	B	393	ASN
1	B	414	ASP
1	B	415	THR
1	B	440	LEU
1	B	501	MET
1	B	518	MET
1	B	566	ASP
1	B	596	HIS
2	C	104	ASP
2	C	172	LYS
2	C	179	THR
2	C	236	ILE
2	C	266	LEU
2	C	287	LEU
2	D	139	LEU
2	D	172	LYS
2	D	179	THR
2	D	236	ILE
2	D	266	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	51	ASN
1	A	89	GLN
1	A	140	GLN
1	A	150	ASN
1	A	183	ASN
1	A	322	ASN
1	A	329	GLN
1	A	386	ASN
1	A	405	ASN
1	A	448	GLN
1	A	460	HIS
1	A	462	GLN
1	A	515	ASN
1	A	529	ASN
1	B	49	ASN
1	B	51	ASN
1	B	89	GLN
1	B	229	GLN
1	B	292	GLN
1	B	322	ASN
1	B	329	GLN
1	B	373	GLN
1	B	405	ASN
1	B	448	GLN
1	B	460	HIS
1	B	515	ASN
1	B	529	ASN
1	B	571	HIS
1	B	596	HIS
2	C	252	GLN
2	C	255	GLN
2	C	257	GLN
2	C	270	ASN
2	C	284	ASN
2	D	252	GLN
2	D	257	GLN
2	D	270	ASN
2	D	284	ASN

5.3.3 RNA ⓘ

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](#)

Of 42 ligands modelled in this entry, 7 are monoatomic - leaving 35 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	$\# Z > 2$
4	EDO	B	1601	-	3,3,3	0.48	0	2,2,2	0.15	0
3	NAG	B	701	1	14,14,15	0.54	0	17,19,21	1.25	2 (11%)
4	EDO	A	1601	-	3,3,3	0.73	0	2,2,2	0.55	0
3	NAG	A	701	1	14,14,15	0.55	0	17,19,21	0.99	1 (5%)
4	EDO	B	1604	-	3,3,3	0.64	0	2,2,2	0.10	0
4	EDO	A	1605	-	3,3,3	0.56	0	2,2,2	0.16	0
4	EDO	C	1291	-	3,3,3	0.67	0	2,2,2	0.17	0
4	EDO	B	1603	-	3,3,3	0.48	0	2,2,2	0.33	0
4	EDO	C	1295	-	3,3,3	0.35	0	2,2,2	0.42	0
4	EDO	A	1599	-	3,3,3	0.56	0	2,2,2	0.12	0
4	EDO	A	1602	-	3,3,3	0.40	0	2,2,2	0.35	0
4	EDO	B	1605	-	3,3,3	0.61	0	2,2,2	0.23	0
4	EDO	A	1604	-	3,3,3	0.61	0	2,2,2	0.41	0
4	EDO	B	1600	-	3,3,3	0.44	0	2,2,2	0.57	0
4	EDO	A	1600	-	3,3,3	0.44	0	2,2,2	0.37	0
4	EDO	C	1293	-	3,3,3	0.54	0	2,2,2	0.07	0
4	EDO	C	1292	-	3,3,3	0.58	0	2,2,2	0.17	0
4	EDO	B	1606	-	3,3,3	0.59	0	2,2,2	0.16	0
4	EDO	B	1610	-	3,3,3	0.49	0	2,2,2	0.27	0
4	EDO	B	1611	-	3,3,3	0.40	0	2,2,2	0.33	0
4	EDO	B	1602	-	3,3,3	0.81	0	2,2,2	0.52	0
4	EDO	A	1607	-	3,3,3	0.57	0	2,2,2	0.11	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	1603	-	3,3,3	0.46	0	2,2,2	0.53	0
4	EDO	B	1609	-	3,3,3	0.49	0	2,2,2	0.40	0
4	EDO	A	1606	-	3,3,3	0.65	0	2,2,2	0.18	0
4	EDO	B	1608	-	3,3,3	0.52	0	2,2,2	0.31	0
6	MES	C	1289	-	12,12,12	2.24	1 (8%)	15,16,16	2.65	3 (20%)
3	NAG	B	700	1	14,14,15	0.54	0	17,19,21	1.14	1 (5%)
4	EDO	A	1608	-	3,3,3	0.48	0	2,2,2	0.23	0
4	EDO	C	1290	-	3,3,3	0.62	0	2,2,2	0.41	0
4	EDO	C	1294	-	3,3,3	0.40	0	2,2,2	0.21	0
4	EDO	B	1599	-	3,3,3	0.48	0	2,2,2	0.20	0
3	NAG	A	700	1	14,14,15	0.51	0	17,19,21	1.45	2 (11%)
4	EDO	B	1612	-	3,3,3	0.59	0	2,2,2	0.09	0
4	EDO	B	1607	-	3,3,3	0.90	0	2,2,2	0.96	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	EDO	B	1601	-	-	0/1/1/1	-
3	NAG	B	701	1	-	0/6/23/26	0/1/1/1
4	EDO	A	1601	-	-	1/1/1/1	-
3	NAG	A	701	1	-	2/6/23/26	0/1/1/1
4	EDO	B	1604	-	-	0/1/1/1	-
4	EDO	A	1605	-	-	0/1/1/1	-
4	EDO	C	1291	-	-	1/1/1/1	-
4	EDO	B	1603	-	-	0/1/1/1	-
4	EDO	C	1295	-	-	0/1/1/1	-
4	EDO	A	1599	-	-	1/1/1/1	-
4	EDO	A	1602	-	-	1/1/1/1	-
4	EDO	B	1605	-	-	1/1/1/1	-
4	EDO	A	1604	-	-	1/1/1/1	-
4	EDO	B	1600	-	-	1/1/1/1	-
4	EDO	A	1600	-	-	1/1/1/1	-
4	EDO	C	1293	-	-	1/1/1/1	-
4	EDO	C	1292	-	-	0/1/1/1	-
4	EDO	B	1606	-	-	1/1/1/1	-
4	EDO	B	1610	-	-	1/1/1/1	-
4	EDO	B	1611	-	-	1/1/1/1	-
4	EDO	B	1602	-	-	1/1/1/1	-
4	EDO	A	1607	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	1603	-	-	1/1/1/1	-
4	EDO	B	1609	-	-	0/1/1/1	-
4	EDO	A	1606	-	-	1/1/1/1	-
4	EDO	B	1608	-	-	1/1/1/1	-
6	MES	C	1289	-	-	3/6/14/14	0/1/1/1
3	NAG	B	700	1	-	0/6/23/26	0/1/1/1
4	EDO	A	1608	-	-	1/1/1/1	-
4	EDO	C	1290	-	-	1/1/1/1	-
4	EDO	C	1294	-	-	1/1/1/1	-
4	EDO	B	1599	-	-	0/1/1/1	-
3	NAG	A	700	1	-	3/6/23/26	0/1/1/1
4	EDO	B	1612	-	-	1/1/1/1	-
4	EDO	B	1607	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1289	MES	C8-S	-7.54	1.67	1.77

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1289	MES	O2S-S-C8	6.07	115.90	106.73
6	C	1289	MES	C5-N4-C3	5.80	121.34	108.84
6	C	1289	MES	C7-N4-C3	4.41	122.99	111.24
3	A	700	NAG	C1-C2-N2	-3.55	104.84	110.43
3	A	700	NAG	C2-N2-C7	3.13	127.10	122.90
3	B	701	NAG	C1-O5-C5	2.79	115.92	112.19
3	B	700	NAG	C1-C2-N2	-2.44	106.59	110.43
3	B	701	NAG	C1-C2-N2	-2.29	106.82	110.43
3	A	701	NAG	C1-O5-C5	-2.06	109.43	112.19

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	1289	MES	C8-C7-N4-C3
3	A	701	NAG	O5-C5-C6-O6
3	A	700	NAG	O5-C5-C6-O6
3	A	701	NAG	C4-C5-C6-O6
4	A	1600	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	A	1602	EDO	O1-C1-C2-O2
4	A	1603	EDO	O1-C1-C2-O2
4	A	1604	EDO	O1-C1-C2-O2
4	A	1606	EDO	O1-C1-C2-O2
4	A	1608	EDO	O1-C1-C2-O2
4	B	1606	EDO	O1-C1-C2-O2
4	C	1294	EDO	O1-C1-C2-O2
4	A	1601	EDO	O1-C1-C2-O2
4	B	1600	EDO	O1-C1-C2-O2
4	B	1602	EDO	O1-C1-C2-O2
4	B	1608	EDO	O1-C1-C2-O2
4	C	1293	EDO	O1-C1-C2-O2
3	A	700	NAG	C3-C2-N2-C7
4	C	1290	EDO	O1-C1-C2-O2
4	C	1291	EDO	O1-C1-C2-O2
6	C	1289	MES	C7-C8-S-O1S
3	A	700	NAG	C4-C5-C6-O6
4	B	1611	EDO	O1-C1-C2-O2
6	C	1289	MES	C7-C8-S-O3S
4	B	1605	EDO	O1-C1-C2-O2
4	A	1599	EDO	O1-C1-C2-O2
4	B	1610	EDO	O1-C1-C2-O2
4	B	1612	EDO	O1-C1-C2-O2

There are no ring outliers.

14 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1601	EDO	5	0
4	A	1605	EDO	4	0
4	A	1599	EDO	1	0
4	A	1602	EDO	1	0
4	B	1605	EDO	1	0
4	B	1600	EDO	2	0
4	C	1293	EDO	1	0
4	B	1611	EDO	2	0
4	A	1603	EDO	1	0
4	B	1609	EDO	1	0
3	B	700	NAG	1	0
4	B	1599	EDO	2	0
3	A	700	NAG	3	0
4	B	1607	EDO	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	D	1
2	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	200:ALA	C	231:GLY	N	1.86
1	C	200:ALA	C	231:GLY	N	1.66

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	529/588 (89%)	-0.20	6 (1%) 78 74	6, 21, 36, 54	0
1	B	541/588 (92%)	-0.29	8 (1%) 72 68	6, 21, 34, 62	0
2	C	177/179 (98%)	0.95	37 (20%) 2 2	18, 26, 42, 52	0
2	D	177/179 (98%)	0.51	18 (10%) 12 9	18, 26, 46, 54	0
All	All	1424/1534 (92%)	0.00	69 (4%) 35 30	6, 23, 40, 62	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	232	ARG	9.7
2	C	231	GLY	9.3
2	C	233	GLN	8.4
2	C	234	LEU	8.0
2	C	235	THR	7.2
2	D	231	GLY	6.9
2	C	237	PHE	6.6
2	C	246	GLY	6.2
2	C	238	ASN	5.6
2	D	232	ARG	5.4
2	C	241	ALA	5.2
2	C	244	ILE	5.2
2	C	239	SER	5.2
2	C	243	ILE	4.9
2	C	247	GLY	4.8
2	C	240	GLN	4.7
2	C	236	ILE	4.7
2	D	233	GLN	4.7
2	C	91	LYS	4.6
2	C	250	GLN	4.6
2	C	251	GLY	4.5

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Mol	Chain	Res	Type	RSRZ
2	C	242	THR	4.4
2	C	252	GLN	4.3
2	C	245	ILE	4.1
2	D	238	ASN	4.0
1	A	409	TYR	3.9
1	A	44	GLN	3.8
2	C	93	GLY	3.7
2	C	92	GLY	3.7
2	C	249	GLU	3.7
2	D	235	THR	3.6
2	D	234	LEU	3.6
2	C	253	PRO	3.3
2	C	254	PHE	3.2
2	C	248	LYS	3.1
1	B	410	PRO	3.1
1	B	477	GLN	3.0
1	A	410	PRO	2.9
2	D	83	ALA	2.9
2	D	273	ALA	2.8
1	B	540	VAL	2.8
2	D	237	PHE	2.8
2	C	255	GLN	2.7
2	D	286	ARG	2.6
2	D	285	VAL	2.6
1	B	328	GLN	2.6
1	B	598	HIS	2.5
2	C	94	GLY	2.5
2	C	280	ALA	2.5
2	D	272	ALA	2.5
2	C	167	ILE	2.5
2	C	275	ASN	2.4
2	C	258	LEU	2.4
1	B	-10	LYS	2.4
2	C	256	GLY	2.4
2	C	286	ARG	2.4
1	B	-9	ASP	2.3
2	D	282	VAL	2.3
1	B	409	TYR	2.3
2	C	89	PHE	2.3
2	D	239	SER	2.3
2	D	236	ILE	2.2
1	A	99	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	-1	ALA	2.1
2	D	287	LEU	2.1
2	C	282	VAL	2.1
1	A	156	GLU	2.0
2	D	250	GLN	2.0
2	D	275	ASN	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 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($\text{\AA}^2$)	Q<0.9
3	NAG	B	701	14/15	0.31	0.20	66,71,71,72	0
3	NAG	A	701	14/15	0.46	0.19	65,70,71,72	0
4	EDO	B	1604	4/4	0.63	0.21	66,67,68,69	0
3	NAG	A	700	14/15	0.67	0.15	62,66,68,69	0
4	EDO	A	1601	4/4	0.69	0.23	59,61,61,61	0
4	EDO	C	1293	4/4	0.71	0.33	86,87,87,87	0
5	CL	B	1615	1/1	0.71	0.22	82,82,82,82	0
4	EDO	C	1294	4/4	0.73	0.34	87,87,87,87	0
4	EDO	B	1602	4/4	0.74	0.26	56,58,58,59	0
4	EDO	A	1606	4/4	0.75	0.20	66,68,68,68	0
4	EDO	A	1600	4/4	0.75	0.21	58,59,59,59	0
4	EDO	B	1606	4/4	0.76	0.26	74,77,77,77	0
4	EDO	B	1607	4/4	0.76	0.29	50,51,52,53	0
4	EDO	B	1609	4/4	0.76	0.20	74,75,75,75	0
4	EDO	B	1612	4/4	0.77	0.28	70,71,72,72	0
3	NAG	B	700	14/15	0.77	0.12	59,64,65,66	0
4	EDO	B	1603	4/4	0.78	0.20	73,74,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	A	1599	4/4	0.80	0.19	77,78,78,79	0
4	EDO	B	1610	4/4	0.80	0.22	73,74,74,75	0
4	EDO	C	1290	4/4	0.82	0.22	53,55,57,58	0
4	EDO	A	1603	4/4	0.82	0.18	58,60,60,60	0
4	EDO	A	1604	4/4	0.83	0.20	57,60,60,60	0
4	EDO	B	1599	4/4	0.83	0.15	58,58,60,60	0
4	EDO	A	1602	4/4	0.84	0.20	62,65,65,65	0
4	EDO	A	1608	4/4	0.84	0.21	69,70,71,71	0
4	EDO	C	1291	4/4	0.84	0.19	59,61,62,62	0
4	EDO	B	1611	4/4	0.85	0.16	74,76,77,77	0
4	EDO	B	1605	4/4	0.87	0.16	54,55,56,56	0
4	EDO	A	1607	4/4	0.87	0.19	73,74,74,74	0
4	EDO	C	1292	4/4	0.88	0.15	67,68,68,69	0
4	EDO	B	1608	4/4	0.89	0.16	63,63,64,64	0
4	EDO	C	1295	4/4	0.90	0.17	65,65,66,67	0
4	EDO	A	1605	4/4	0.90	0.16	52,52,53,53	0
4	EDO	B	1600	4/4	0.92	0.22	48,51,51,54	0
4	EDO	B	1601	4/4	0.92	0.14	48,48,49,50	0
5	CL	A	1610	1/1	0.93	0.20	68,68,68,68	0
7	CA	C	1296	1/1	0.93	0.06	29,29,29,29	0
5	CL	B	1614	1/1	0.95	0.13	60,60,60,60	0
6	MES	C	1289	12/12	0.96	0.07	39,41,51,51	0
7	CA	D	1289	1/1	0.96	0.07	32,32,32,32	0
5	CL	A	1609	1/1	0.97	0.11	46,46,46,46	0
5	CL	B	1613	1/1	0.98	0.09	49,49,49,49	0

6.5 Other polymers

There are no such residues in this entry.